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FIG. 1

(57) Abstract: The present invention relates to recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered to include amino acid sequences and/or amino acid substitutions that confer and/or enhance desired properties, particularly increased transduction in CNS or muscle cells relative to a rAAV having a reference capsid.

WO 2022/076750 A3

RECOMBINANT ADENO-ASSOCIATED VIRUSES FOR CNS OR MUSCLE DELIVERY

1. FIELD OF THE INVENTION

[0001] The present invention relates to recombinant adeno-associated viruses (rAAVs) having capsid proteins with one or more amino acid substitutions and/or peptide insertions that confer and/or enhance desired properties, including tissue tropisms. In particular, the invention provides engineered capsid proteins comprising one or more amino acid substitutions or peptide insertions that enhance the tropism of an AAV serotype for one or more tissue types as well as capsids that are not engineered but are found to confer muscle or CNS tropisms on rAAVs. Particularly, the one or more amino acid substitutions and/or insertions in the AAV capsid improve transduction, genome integration and/or transgene expression in heart and/or muscle tissue or the central nervous system while reducing tropism for the liver and/or the dorsal root ganglion and/or peripheral nerve cells. rAAVs having the capsid proteins disclosed herein are useful for delivering a transgene encoding a therapeutic protein for treatment of CNS or muscle disease.

2. BACKGROUND

[0002] The use of adeno-associated viruses (AAV) as gene delivery vectors is a promising avenue for the treatment of many unmet patient needs. Dozens of naturally occurring AAV capsids have been reported, and mining the natural diversity of AAV sequences in primate tissues has identified over a hundred variants, distributed in clades. AAVs belong to the parvovirus family and are single-stranded DNA viruses with relatively small genomes and simple genetic components. Without a helper virus, AAV establishes a latent infection. An AAV genome generally has a Rep gene and a Cap gene, flanked by inverted terminal repeats (ITRs), which serve as replication and packaging signals for vector production. The capsid proteins form capsids that carry genome DNA and can determine tissue tropism to deliver DNA into target cells.

[0003] Due to low pathogenicity and the promise of long-term, targeted gene expression, recombinant AAVs (rAAVs) have been used as gene transfer vectors, in which therapeutic sequences are packaged into various capsids. Such vectors have been used in preclinical gene therapy studies and over twenty gene therapy products are currently in clinical development.

Recombinant AAVs, such as recombinant AAV9 particles, have demonstrated desirable neurotropic properties and clinical trials using recombinant AAV9 for treatment of CNS disease are underway. Delivery to muscle and/or heart tissue is also desirable. Reduction of transduction of liver and/or dorsal root ganglion cells may also be desirable to reduce toxicity. However, attempts to enhance the neurotropic or muscle/heart tropic properties of rAAVs in human subjects have met with limited success.

[0004] There remains a need for rAAV vectors with enhanced neurotropic or with tropism for muscle and/or heart properties for use, *e.g.*, in treating disorders associated with the central nervous system or where expression in the heart and/or muscle are desirable, with minimal transduction in liver and/or dorsal root ganglion cells and/or peripheral nerve cells to minimize adverse effects. There also is a need for rAAV vectors with enhanced tissue-specific targeting and/or enhanced tissue-specific transduction to deliver therapies.

3. SUMMARY OF THE INVENTION

[0005] Provided are recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered to have one or more amino acid substitutions and/or peptide insertion that enhance tissue targeting, transduction and/or integration of the rAAV genome in CNS and/or muscle tissue relative to a reference capsid, for example, the parent capsid or an AAV8 or AAV9 capsid, while having reduced biodistribution in certain tissues, such as liver and dorsal root ganglion cells, relative to the distribution in CNS and/or muscle and/or relative to the parent capsid or a reference capsid, such as AAV8 or AAV9 capsid, to reduce toxicity. Biodistribution studies in mice and non-human primates permit assessment of relative transduction and transgene transcription and expression in tissue types of capsids, including engineered capsids (see, Examples 13-18, *infra*). Accordingly, provided herein are rAAVs with enhanced or increased biodistribution, including transduction, genome integration, transgene transcription and expression, in CNS tissues (including frontal cortex, hippocampus, cerebellum, midbrain) relative to a reference capsid (for example the unengineered, parental capsid that has been modified or AAV8 or AAV9), with reduced distribution, including transduction, genome integration, transgene transcription and expression in the liver and/or dorsal root ganglion cells (cervical, thoracic, and/or lumbar) compared to the biodistribution in CNS tissue and/or relative to an AAV with a reference capsid, such as the parental capsid or AAV8 or AAV9. Such rAAVs may be useful to deliver therapeutic proteins for the treatment of CNS disease. In addition, provided herein are rAAVs with enhanced or increased biodistribution, including transduction, genome integration, transgene transcription and expression, in skeletal muscle and/or cardiac muscle tissues relative to a reference capsid (for example the unengineered, parental capsid or AAV8 or AAV9), with reduced distribution, including transduction, genome integration, transgene transcription and expression in the liver and/or dorsal root ganglion cells (cervical, thoracic, and/or lumbar) compared to the biodistribution in muscle tissue and/or relative to an AAV with a reference capsid, such as the parental capsid or AAV8 or AAV9. Such rAAVs may be useful to deliver therapeutic proteins for the treatment of muscle disease.

[0006] In particular, provided are AAV9 capsid proteins or AAV8 capsid proteins (SEQ ID NO:67 or 66, respectively, and as numbered in **FIG. 7**) or having one or more amino acid substitutions (including, 2, 3 or 4 amino acid substitutions) that preferentially (in particular, at a greater level than rAAVs with the wild type AAV8 or AAV9 capsid) transduce (target) cells of the CNS, and, in certain embodiments, do not target or transduce, or have reduced transduction compared to rAAVs with wild type AAV8 or AAV9 capsids, the liver and/or the dorsal root ganglion and/or peripheral nerve cells. In other embodiments, provided are AAV9 capsid proteins or AAV8 capsid proteins (SEQ ID NO:67 or 66, respectively, and as numbered in **FIG. 7**) having one or more amino acid substitutions (including, 2, 3 or 4 amino acid substitutions) that preferentially (in particular, at a greater level than rAAVs with the wild type AAV9 capsid) transduce (target) cells of the heart and/or skeletal muscle, and, in certain embodiments, do not target or transduce, or have reduced transduction compared to rAAVs with wild type AAV8 or AAV9 capsids, the liver and/or the dorsal root ganglion and/or peripheral nerve cells. Such amino acid modifications include S263F/S269T/A273T of AAV9, and corresponding substitutions in other AAV type capsids (for example according to the alignment in **FIG. 7**), or W530R, Q474A, N272A, or G266A of AAV9, and corresponding substitutions in other AAV type capsids or A269S of AAV8 and corresponding substitutions in other AAV capsids (for example, according to the alignment in FIG. 7). Also provided are capsids, particularly AAV9 capsids having a peptide TLAAPFK (SEQ ID NO:1) inserted between Q588 and A589 (herein PHP.hDYN) or alternatively between S268 and S269 or between S454 and G455) or inserted in another AAV capsid at a corresponding position (see, e.g., **FIG. 7**). Or, alternatively, the capsid is an AAV9 PHP.eB capsid (which has the modifications A587D and Q588G and insertion of the peptide TLAVPFK (SEQ ID NO:20) between G588 and A589) and the peptide TILSRSTQTG (SEQ ID NO:15) between position 138 and 139, or the corresponding. Additional capsids have a Kidney1 peptide LPVAS inserted into the capsid, for example between S454 and G455 of AAV9, or alternatively between S268 and S269 or between Q588 and A589, or the corresponding position of a different capsid. In some embodiments, the capsids can comprise R697W substitution of AAV rh64R1. The capsids having these amino acid substitutions and insertions may further have substitutions of the NNN (asparagines) at 496 to 498 with AAA (alanines) of the AAV9 capsid or at positions 498 to 500 of the AAV8 capsid, or corresponding substitutions in other AAV type capsids. Engineered capsids include AAV8.BB.LD (A269S,498-NNN/AAA-500 substitutions in the amino acid sequence of AAV8, SEQ ID NO 66), AAV9.BB.LD (S263G/S269T/A273T, 496-NNN/AAA-498 substitutions in the amino acid sequence of AAV9, SEQ ID NO 67), AAV9.496-NNN/AAA-498 (SEQ ID NO: 31), AAV9.496-NNN/AAA-498.W503R (SEQ ID NO: 32), AAV9.W503R (SEQ ID NO: 33), or AAV9.Q474A (SEQ ID NO: 34). In other examples, the capsid can be AAV9.N272A.496-NNN-498 (SEQ ID NO:91) or AAV9.G266A.496-NNN-498 (SEQ ID NO: 92). In other embodiments, the capsid is not an engineered capsid, but is an AAVrh.10 capsid (SEQ ID NO: 69), an AAVrh.46 capsid (SEQ ID NO:93), an AAVrh.64.R1 capsid (SEQ ID NO: 90) or an AAVrh.73 capsid (SEQ ID NO: 88). In certain embodiments, transduction is measured by detection of transgene, such as GFP fluorescence.

[0007] The capsid protein to be engineered may be an AAV9 capsid protein but may also be any AAV capsid protein, such as AAV serotype 1 (SEQ ID NO:59); AAV serotype 2 (SEQ ID NO:60); AAV serotype 3 (SEQ ID NO:61), AAV serotype 3B, AAV serotype 4 (SEQ ID NO:62); AAV serotype 5 (SEQ ID NO:63); AAV serotype 6 (SEQ ID NO:64); 451-461 of AAV7 capsid (SEQ ID NO:65); 451-461 of AAV8 capsid (SEQ ID NO:66); AAV serotype 9 (SEQ ID NO:67); AAV serotype 9e (SEQ ID NO:68); AAV serotype rh10 (SEQ ID NO:69); AAV serotype rh20 (SEQ ID NO:70); and AAV serotype hu.37 (SEQ ID NO:71), AAV serotype rh39 (SEQ ID NO:73), and AAV serotype rh74 (SEQ ID NO:72 or SEQ ID NO:80), AAV serotype rh.34, AAV serotype hu.60, AAV serotype rh.21, AAV serotype rh.15, AAV serotype rh.24, AAV serotype hu.5, AAV serotype hu.10 (SEQ ID NO: 69), AAV serotype rh64R1 (SEQ ID NO:90), AAV serotype rh46 (SEQ ID NO:93), and AAV serotype rh73 (SEQ ID NO: 88) (see **FIG. 7** for alignment of certain sequences) and Table 17 for sequences. In some embodiments, the capsids of these vectors are not engineered. For example, unmodified AAV serotype rh64R1 (SEQ ID NO:90) AAV serotype rh.10 ((SEQ ID NO: 69) AAV serotype rh46 (SEQ ID NO:93), and AAV serotype rh73 (SEQ ID NO: 88) can be used in the disclosed methods and compositions.

[0008] In certain embodiments, provided are rAAVs incorporating the engineered capsids described herein, including rAAVs with genomes comprising a transgene of therapeutic interest, including a transgene encoding a therapeutic protein for treatment of a muscle, heart or CNS disease. Packaging cells for producing the rAAVs described herein are provided. Method of treatment by delivery of, and pharmaceutical compositions comprising, the engineered rAAVs described herein are also provided. Also provided are methods of manufacturing the rAAVs with the engineered capsids described herein.

[0009] The invention is illustrated by way of examples *infra* describing the construction of rAAV9 capsids engineered with amino acid substitutions and assaying of tissue distribution when administered to non-human primates.

3.1. Embodiments

[0010] 1. A recombinant AAV capsid protein comprising one or more amino acid substitutions relative to the wild type or unengineered capsid protein, in which the rAAV capsid protein is an AAV9 capsid protein (SEQ ID NO:67) with S263G/S269R/A273T substitutions, a G266A substitution, an N272A substitution, a W503R substitution, a Q474A substitution, 496-NNN/AAA-498 substitutions, has an insertion of the peptide TLAAPFK between Q588 and A589, S268 and S269, or S454 and G455, or is an AAV8 capsid (SEQ ID NO:6) with an A269S substitution or 498-NNN/AAA-500 substitutions, or corresponding substitutions or peptide insertions in a capsid protein of another AAV type capsid.

[0011] 2. The recombinant AAV capsid protein of embodiment 1 further comprising 498-NNN/AAA-500 amino acid substitutions for an AAV8 capsid protein (SEQ ID NO: 66) or 496-NNN/AAA-498 amino acid substitutions for an AAV9 capsid protein (SEQ ID NO:67), or corresponding substitutions in a capsid protein of another AAV type capsid.

[0012] 3. The recombinant AAV capsid protein of embodiments 1 or 2 which is an AAV8.BBB.LD capsid (SEQ ID NO: 27), an AAV9.BBB.LD capsid (SEQ ID NO: 29), an AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 31), AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 32), AAV9.W503R capsid (SEQ ID NO: 33), AAV9.Q474A capsid (SEQ ID NO: 34), AAV9.N272A.496-NNN/AAA-498 capsid (SEQ ID NO: 91) or AAV9.N266A.496-NNN/AAA-498 capsid (SEQ ID NO: 92).

[0013] 4. The recombinant AAV capsid protein of embodiments 1 to 3 in which the amino acid substitutions or insertions are in an AAV9 capsid, including an AABPHP.eB capsid, protein, or an AAV8 capsid.

[0014] 5. The recombinant AAV capsid protein of embodiment 1 or 2 wherein the AAV type capsid is AAV rh.34, AAV4, AAV5, AAV hu.26, AAV rh.31, AAV hu.13, AAV hu.26, AAV hu.56, AAV hu.53, AAV7, AAV rh.10, AAV rh.64.R1, AAV rh.46 or AAV rh.73.

[0015] 6. The recombinant AAV capsid protein of any of embodiments 1 to 5, which when incorporated into a rAAV vector, the rAAV vector has increased targeting, transduction or genome integration into CNS cells, relative to a rAAV vector incorporating the corresponding wild type capsid protein without the amino acid substitutions or peptide insertions.

[0016] 7. The recombinant capsid protein of embodiment 6, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into liver cells, relative to a rAAV vector incorporating the corresponding wild type capsid protein without the amino acid substitutions or peptide insertions.

[0017] 8. The recombinant capsid protein of embodiment 6 or 7, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into dorsal root ganglion cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

[0018] 9. The recombinant capsid protein of any of the embodiments 6 to 8, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into peripheral nerve cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

[0019] 10. The recombinant AAV capsid protein of any of embodiments 1 to 5, which when incorporated into a rAAV vector, the rAAV vector has increased targeting, transduction or genome integration into skeletal and/or cardiac muscle cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

[0020] 11. The recombinant capsid protein of embodiment 10, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into liver cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

[0021] 12. The recombinant capsid protein of embodiment 10 or 11, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into CNS cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertion.

[0022] 13. The recombinant capsid protein of any of embodiments 10 to 12, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into dorsal root ganglion cells, relative to an rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions

[0023] 14. A nucleic acid comprising a nucleotide sequence encoding the rAAV capsid protein of any of embodiments 1 to 13, or encoding an amino acid sequence sharing at least 80% identity therewith and retaining the biological activity of the capsid.

[0024] 15. The nucleic acid of embodiment 14 encoding the rAAV capsid protein of any of embodiments 1 to 13.

[0025] 16. A packaging cell capable of expressing the nucleic acid of embodiment 14 or 15 to produce AAV vectors comprising the capsid protein encoded by said nucleotide sequence.

[0026] 17 A rAAV vector comprising the capsid protein of any of embodiments 1 to 13.

[0027] 18. The rAAV vector of embodiment 17 further comprising a transgene encoding a therapeutic protein operably linked to a regulatory sequence for expression in the muscle and/or CNS cells.

[0028] 19. A pharmaceutical composition comprising the rAAV vector of embodiment 17 or 18 and a pharmaceutically acceptable carrier.

[0029] 20. A method of delivering a transgene to a cell, said method comprising contacting said cell with the rAAV vector of embodiment 17 or 18, wherein said transgene is delivered to said cell.

[0030] 21. The method of embodiment 20 in which the cell is a CNS cell, cardiac muscle cell or skeletal muscle cell.

[0031] 22. A method of delivering a transgene to a target tissue of a subject in need thereof, said method comprising administering to said subject the rAAV vector of embodiment 17 or 18, wherein the transgene is delivered to said target tissue.

[0032] 23. The method of embodiment 22 wherein the transgene is a muscle disease or heart disease therapeutic and said target tissue is cardiac muscle or skeletal muscle.

[0033] 24. The method of embodiment 23, wherein the rAAV is administered systemically, including intravenously or intramuscularly.

[0034] 25. The method of embodiment 22 wherein the transgene is a CNS disease therapeutic and said target tissue is CNS.

[0035] 26. The method of embodiment 25 wherein the rAAV is administered intrathecally or intracerebroventricularly.

[0036] 27. A pharmaceutical composition for use in delivering a transgene to a cell, said pharmaceutical composition comprising the rAAV vector of embodiment 17 or 18, wherein said transgene is delivered to said cell.

[0037] 28. A pharmaceutical composition for use in delivering a transgene encoding a therapeutic protein to a target tissue of a subject in need thereof, said pharmaceutical composition comprising the rAAV vector of embodiment 17 or 18, wherein the transgene is delivered to said target tissue.

[0038] 29. The pharmaceutical composition of embodiment 27 or 28 wherein said therapeutic protein is a muscle disease therapeutic or a heart disease therapeutic and said target tissue is cardiac muscle or skeletal muscle.

[0039] 30. The pharmaceutical composition of embodiment 27 to 29 wherein the rAAV exhibits at least 1.1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold greater transduction in cardiac muscle or skeletal muscle cells compared to a reference AAV capsid.

[0040] 31. The pharmaceutical composition of embodiment 27 to 30 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in liver compared to the reference AAV capsid.

[0041] 32. The pharmaceutical composition of embodiment 27 to 31 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in dorsal root ganglion cells compared to the reference AAV capsid.

[0042] 33. The pharmaceutical composition of embodiment 27, 28 or 32 wherein said therapeutic protein is a CNS disease therapeutic and said target tissue is CNS.

[0043] 34. The pharmaceutical composition of embodiment 27, 28, 32 or 33 wherein the rAAV exhibits at least 1.1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold greater transduction in CNS cells compared to a reference AAV capsid.

[0044] 35. The pharmaceutical composition of embodiment 27, 28, 33 to 34 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in liver compared to the reference AAV capsid.

[0045] 36. The pharmaceutical composition of embodiment 27, 28, 32 to 35 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in dorsal root ganglion cells compared to the reference AAV capsid.

[0046] 37. The pharmaceutical composition of embodiments 27 to 36, wherein the AAV reference capsid is AAV8 or AAV9.

[0047] 38. A method of treating a CNS disorder in a subject in need thereof, said method comprising administering a therapeutically effective amount of pharmaceutical composition of any of embodiments 27, 28, 32 to 37.

[0048] 39. A method of treating a muscle disorder in a subject in need thereof, said method comprising administering a therapeutically effective amount of the pharmaceutical composition of any of embodiments 27-31 and 37.

4. BRIEF DESCRIPTION OF THE FIGURES

[0049] **FIG. 1** depicts sequence comparison of the capsid amino acid sequences including the VR-IV loop of the adeno-associated virus type 9 (AAV9 VR-IV) from residues L447 to R476, (with residues 451-459 bracketed) to corresponding to regions of other AAVs. Figure discloses SEQ ID NOS:49-54, 50, and 55-58, respectively, in order of appearance. The top sequence is the consensus sequence, SEQ ID NO:48.

[0050] **FIG. 2** depicts a protein model of an AAV capsid structure, showing capsid variable regions VR-IV, VR-V and VR-VIII. The box highlights the loop region of VR-IV which provides surface-exposed amino acids as represented in the model.

[0051] **FIG. 3** depicts high packaging efficiency (titer) in terms of genome copies per mL (GC/mL) of wild type AAV9 and eight (8) candidate modified rAAV9 vectors (1090, 1091, 1092, 1093, 1094, 1095, 1096, and 1097), where the candidate vectors each contain a FLAG insert immediately after different sites within AAV9s VR-IV, from residues I451 to Q458, respectively. All vectors were packaged with luciferase transgene in 10 mL culture; error bars represent standard error of the mean.

[0052] **FIG. 4** demonstrates surface exposure of l VR-IV loop FLAG inserts in each of eight (8) candidate modified rAAV9 vectors (1090, 1091, 1092, 1093, 1094, 1095, 1096, and 1097), confirmed by immunoprecipitation of packaged vectors by binding to anti-FLAG resin.

[0053] **FIGs. 5A-5B** depict transduction efficiency in Lec2 cells, transduced with capsid vectors carrying the luciferase gene (as a transgene), which were packaged into either wild type AAV9 (9-luc), or into each of eight (8) candidate modified (FLAG peptide inserted) rAAV9 vectors (1090, 1091, 1092, 1093, 1094, 1095, 1096, and 1097); transduction activity is expressed as percent luciferase activity, taking the activity of 9-luc as 100% **(FIG. 5A)**, or as Relative Light Units (RLU) per microgram of protein **(FIG. 5B)**.

[0054] **FIGs. 6A-6E. FIG. 6A** depicts a bar graph illustrating that insertions immediately after S454 of AAV9 of varying peptide length and composition may affect production efficiencies of AAV particles in a packaging cell. Ten peptides of varying composition and length were inserted after S454 within AAV9 VR-IV. qPCR was performed on harvested supernatant of transfected suspension HEK293 cells five days post-transfection. The results depicted in the bar graph demonstrate that the nature of the insertions affects the ability of AAV particles to be produced and secreted by HEK293 cells, and indicated by overall yields (titer). (Error bars represent standard error of the mean length of peptide, which is noted on the Y-axis in parenthesis.) **FIGs. 6B-6E** depict fluorescence images of transduced cell cultures of the following cell lines: (**6B**) Lec2 cell line (**6C**) HT-22 cell line, (**6D**) hCMEC/D3 cell line, and (**6E**) C2C12 cell line. AAV9 wild type and S454 insertion homing peptide capsids containing GFP transgene were used to transduce the noted cell lines. P1 vector was not included in images due to extremely low transduction efficiency, and P8 vector was not included due to low titer. AAV9.S454.FLAG showed low transduction levels in every cell type tested.

[0055] **FIG. 7** depicts alignment of AAVs 1-9e, 3B, rh10, rh20, rh39, rh73, rh74 version 1 and version 2, hu12, hu21, hu26, hu37, hu51 and hu53 capsid sequences with insertion sites for heterologous peptides after the initiation codon of VP2, and within or near variable region 1 (VR-I), variable region 4 (VR-IV), and variable region 8 (VR-VIII), all highlighted in grey; a particular insertion site within variable region eight (VR-VIII) of each capsid protein is shown by the symbol "#" (after amino acid residue 588 according to the amino acid numbering of AAV9).

[0056] **FIG. 8** depicts copies of GFP (green fluorescent protein) transgene in mice brain cells, following administration of the AAV vectors: AAV9; AAV.PHP.eB, also referred to herein as AAV9e (AAV9 with the peptide TLAVPFK (SEQ ID NO:20) inserted between positions 588 and 589 and modifications A587D/A588G); AAV.hDyn (AAV9 with TLAAPFK (SEQ ID NO:1) between 588 and 589); AAV.PHP.S (AAV9 with the peptide QAVRTSL (SEQ ID NO:16) inserted between positions 588 and 589); and AAV.PHP.SH (AAV9 with the peptide QAVRTSH (SEQ ID NO:17) inserted between positions 588 and 589).

[0057] **FIGs. 9A-9C** depict the amino acid sequences for a recombinant AAV9 vector including a peptide insertion of TLAAPFK (SEQ ID NO:1) between Q588 and A589 (**FIG. 9A**), between S268 and S269 of VR-III (**FIG. 9B**), and between S454 and G455 of VR-IV (**FIG. 9C**), each with the TLAAPFK (SEQ ID NO:1) insert shown in bold.

[0058] **FIGs. 10A-10B** depict an *in vitro* transwell assay for AAV vectors crossing a blood brain barrier (BBB) cell layer (**FIG. 10A**), and results showing that AAV.hDyn (indicated by inverted triangles) crosses the BBB cell layer of the assay faster than AAV9 (squares), as well as faster and to a greater extent than AAV2 (circles) (**FIG. 10B**).

[0059] **FIG. 11** depicts results of Next Generation Sequencing (NGS) analysis of brain gDNA from mice to which pools of engineered and native capsids have been intravenously administered, revealing relative abundances in tissues of the mice of the different capsids in the pool. Three different pools were injected into mice. Dotted lines indicate which vectors were pooled together. Parental AAV9 was included in each pool as control (Pool 1: BC01, Pool 2: BC31, Pool 3: BC01). Bar codes for each capsid of the pool are listed in **Tables 6a-6c**.

[0060] **FIGs. 12A-12H** depict an *in vivo* transduction profile of AAV.hDyn in female C57Bl/6 mice, showing copy number/microgram gDNA in naïve mice, or mice injected with either AAV9 or AAV.hDyn in brain (**FIG. 12A**), liver (**FIG. 12B**), heart (**FIG. 12C**), lung (**FIG. 12D**), kidney (**FIG. 12E**), skeletal muscle (**FIG. 12F**), sciatic nerve (**FIG. 12G**), and ovary (**FIG. 12H**), where AAV.hDyn shows increased brain bio-distribution compared to AAV9.

[0061] **FIGs. 13A-13C** depict distribution of GFP from AAV.hDyn throughout the brain, where images of immunohistochemical staining of brain sections from the striatum (**FIG. 13A**), hippocampus (**FIG. 13B**), and cortex (**FIG. 13C**) revealed a comprehensive transduction of the brain by the modified vector.

[0062] **FIG. 14** depicts *in vivo* kidney to liver transduction efficiency ratio of genetically engineered AAV9 vectors containing insertions of homing peptides immediately after amino acid 454. Details on peptides used in this study are outlined in **Table 6**.

[0063] **FIG. 15** depicts the relative abundance (RA) of the viral genomes (normalized to input) in the frontal cortex of the cynomolgus monkey model.

[0064] . **FIGS. 16 and 17** depict the Relative Abundance of the viral genomes (normalized to input) in the hippocampus and the cerebellum of the cynomolgus monkey model, respectively. The RA of AAV.rh34 is shown by the shaded column on the left side of the graphs and the RA of AAV9 reference is showed by the shaded column in the middle of the graphs. FIGS. 16 and 17 show that AAV.rh34 is a top performing capsid in the intravenous administration pool.

[0065] **FIG. 18** depicts a Venn diagram of the: top 45 performers in FC (highest RA to AAV9), and bottom 45 performers in the cervical, thoracic, and lumbar DRGs (lowest RA to

AAV9) and the AAVrh34 capsid is shown as the only capsid that was present in each group of 45 amongst the pool of capsids.

[0066] **FIG. 19** depicts the RA of the viral genomes (normalized to input and AAV9 control) in the frontal cortex of the cynomolgus monkey model.

[0067] **FIG. 20** depicts the RA of the viral genomes (normalized to input) in the hippocampus of the cynomolgus monkey model.

[0068] **FIG. 21** depicts the RA of the viral genomes (normalized to input) in the midbrain of the cynomolgus monkey model.

[0069] **FIG. 22** depicts the RA of the viral genomes (normalized to input) in the cerebellum of the cynomolgus monkey model.

[0070] **FIG. 23** depicts the RA of the viral genomes (normalized to input) in the cervical DRGs of the cynomolgus monkey model.

[0071] **FIG. 24** depicts the RA of the viral genomes (normalized to input) in the lumbar DRGs of the cynomolgus monkey model.

[0072] **FIG. 25** depicts a Venn diagram of the top performing 15 capsids transducing the frontal cortex, hippocampus, midbrain and cerebellum following ICV administration. As indicated in the diagram, AAV6, AAV8.BBB, AAV.rh.46, and AAV1 were the only AAVs represented in each of the top performing groups.

[0073] **FIG. 26** depicts a Venn diagram of the top performing 45 capsids transducing the hippocampus and the 45 capsids with the lowest transduction values for DRG, to identify hippocampus-targeting DRG friendly capsids. As indicated in the diagram, AAV.hu.60, AAV.rh.21, AAV.PHP.hB, AAV.rh.15, AAV.rh.24, AAV9.W503R, hu.5, AAV9.Q474A, and AAV.hu.10 were the only AAVs represented in each of the groups.

[0074] **FIG. 27** depicts a Venn diagram of the top performing 40 capsids transducing the heart, biceps, and gastrocnemius and the 40 capsids with the lowest transduction values for the liver, to identify muscle-targeting capsids that have reduced targeting to the liver. As indicated in the diagram, AAV.PHPeB.VP2Herp was the only AAVs represented in each of the groups.

[0075] **FIG. 28** depicts a Venn diagram of the top performing 15 capsids transducing the heart, biceps, and gastrocnemius muscle.

[0076] **FIGS. 29A and B** depict the RA of the viral genomes (normalized to input) in the gastrocnemius and the liver of the cynomolgus monkey model, respectively.

[0077] **FIG. 30A and 30B** depict the number of genome copies of DNA (A) or RNA (B) of select "liver-detargeting" (LD) vectors as detected in the liver of NHPs following IV administration of the capsid library.

[0078] **FIG. 31** depicts the biodistribution of select "liver-detargeting" (LD) vectors compared to their parental AAV9 capsid in various tissues, in NHPs following IV administration of the capsid library.

[0079] **FIG. 32** depicts the biodistribution of select LD vectors compared to their parental AAV8 capsid in various tissues, in NHPs following IV administration of the capsid library.

[0080] **FIGs 33A and 33B**. **FIG 33A** depicts the change in relative abundance for point mutations affecting AAV9 transduction (or liver transduction) as compared to AAV9. The four mutants depicted in this study demonstrate retention in the blood when compared to wild-type AAV9. **FIG 33B** shows the change in relative abundance for the AAV8 and AAV9 mutants combining the NNN/AAA mutation with the transport motif BBB (A269S, in AAV8; S263G/S269T/A273T, in AAV9), as compared to parental capsid (AAV8 or AAV9, respectively).

[0081] **FIG. 34A and FIG. 34B**. **FIG. 34A** shows the increase in blood retention 3-24 hr relative to AAV9. **FIG. 34B** shows the increase in blood retention 3-24 hr relative to parental AAV.

[0082] **FIG. 35** depicts the biodistribution of select AAV vectors in muscle tissues, including cardiac muscle, as well as cerebrum, liver and pancreas in wild-type B6 mice following IV administration of the capsid library.

[0083] **FIGs. 36A-36H** depicts biodistribution of various capsids in wild-type B6 mice compared to that of mdx mouse tissue.

5. DETAILED DESCRIPTION

[0084] Provided are recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered relative to a reference capsid protein, such that the rAAV has enhance desired properties, such as increased tissue targeting, including transduction, genome integration and transgene expression, particularly, preferentially, relative to the reference capsid protein (e.g., the unengineered or wild type capsid), to CNS or to heart and/or skeletal muscle tissue. In embodiments, the engineered capsid has reduced tropism (i.e., tissue targeting, transduction and integration of the rAAV genome) relative to the reference capsid for liver, dorsal root ganglion and/or peripheral nervous tissue to reduce toxicity of the AAV gene therapy. The modifications include amino acid substitutions (including 1, 2, 3, 4, 5, 6, 7 or 8 amino acid substitutions) and/or peptide insertions (4 to 20, or 7 contiguous amino acids, and in embodiments no more than 12 contiguous amino acids from a heterologous protein) as described herein. The AAV capsid protein to be engineered is, in certain embodiments, an AAV9 capsid protein or an AAV8 capsid protein. In other embodiments, the AAV capsid to be engineered is an AAV rh.34, AAV4, AAV5, AAV hu.26, AAV rh.31, AAV hu.13, AAV hu.56, AAV hu.53, AAV7, AAV rh64R1, AAV rh46 or AAV rh73 capsid protein. (See FIG. 7 and Table 17 for sequences)

[0085] Accordingly provided are engineered capsids having one or more amino acid substitutions that promote transduction and/or tissue tropism, particularly for enhanced, relative to an unengineered capsid, targeting for heart and/or skeletal muscle and, in embodiments, reduced, relative to an unengineered capsid, targeting for liver, dorsal root ganglion, and/or peripheral nervous tissue. In embodiments, the amino acid substitutions are S263F/S269T/A273T of AAV9, and corresponding substitutions in other AAV type capsids (for example according to the alignment in **FIG. 7**), or W530R, Q474A, N272A, or G266A of AAV9, and corresponding substitutions in other AAV type capsids or A269S of AAV8 and corresponding substitutions in other AAV capsids (for example, according to the alignment in FIG. 7). Also provided are capsids, particularly AAV9 capsids having a peptide TLAAPFK (SEQ ID NO:1) inserted between Q588 and A589 (herein PHP.hDYN) or alternatively between S268 and S269 or between S454 and G455) or inserted in another AAV capsid at a corresponding position (see, e.g., **FIG. 7**). Or, alternatively, the capsid is an AAV9 PHP.eB capsid (which has the modifications A587D and Q588G and insertion of the peptide TLAVPFK (SEQ ID NO:20) between G588 and A589) and the peptide TILSRSTQTG (SEQ ID NO:15) between position 138 and 139, or the corresponding. Additional capsids have a Kidney1 peptide LPVAS inserted into the capsid, for example between S454 and G455 of AAV9, or alternatively between S268 and S269 or between Q588 and A589, or the corresponding position of a different capsid. In some embodiments, the capsids can comprise R697W substitution of AAV rh64R1. The capsids having these amino acid substitutions and insertions may further have substitutions of the NNN (asparagines) at 496 to 498 with AAA (alanines) of the AAV9 capsid or at positions 498 to 500 of the AAV8 capsid, or corresponding substitutions in other AAV type capsids. Engineered capsids include AAV8.BB.LD (A269S,498-NNN/AAA-500 substitutions in the amino acid sequence of AAV8, SEQ ID NO 66), AAV9.BB.LD (S263G/S269T/A273T, 496-NNN/AAA-498 substitutions in the amino acid sequence of AAV9, SEQ ID NO 67), AAV9.496-NNN/AAA-498 (SEQ ID NO: 31), AAV9.496-NNN/AAA-498.W503R (SEQ ID NO: 32), AAV9.W503R (SEQ ID NO: 33), or AAV9.Q474A (SEQ ID NO: 34). In other examples, the capsid can be AAV9.N272A.496-NNN-498 (SEQ ID NO:91) or AAV9.G266A.496-NNN-498 (SEQ ID NO: 92). In other embodiments, the capsid is not an engineered capsid, but is an AAVrh.10 capsid (SEQ ID NO: 69), an AAVrh.46 capsid (SEQ ID NO:93), an AAVrh.64.R1 capsid (SEQ ID NO: 90) or an AAVrh.73 capsid (SEQ ID NO: 88). In certain embodiments, transduction is measured by detection of transgene, such as GFP fluorescence. The capsids having these amino acid substitutions and insertions may further have substitutions of the NNN (asparagines) at 496 to 498 with AAA (alanines) of the AAV9 capsid, or corresponding substitutions in other AAV type capsids. This engineered capsid may exhibit preferential targeting for heart and/or skeletal muscle, and reduced targeting (compared to an AAV bearing the unengineered capsid) for liver and/or dorsal root ganglion cells and/or peripheral nervous system tissue, and may particularly useful for delivery of a transgene encoding a therapeutic protein for treatment of a muscle disease.

[0086] In another embodiment, provided is a recombinant capsid protein, including an engineered AAV9 capsid protein, and an rAAV comprising the capsid protein, in which the peptide TLAVPFK (SEQ ID NO:20) is inserted between G588 and A589 of AAV9, and, in particular, the capsid protein also has amino acid substitutions A587D/Q588G (PHP.eB) and further has the peptide TILSRSTQTG (SEQ ID NO:15) inserted after position 138 of AAV9 (collectively, AAVPHPeB.VP2Herp; see Table 17), or in the corresponding positions of another AAV. Additional capsids have a Kidney1 peptide LPVAS (SEQ ID NO:6) (or alternatively CLPVASC (SEQ ID NO:5)) inserted into the capsid, for example between S454 and G455 of AAV9 (see Table 17), or alternatively between S268 and S269 or between Q588 and A589, or the corresponding position of a different capsid. Such an engineered capsid may exhibit preferential targeting for heart and skeletal muscle, and reduced targeting (as compared to an AAV having the unengineered capsid) for liver and/or dorsal root ganglion cells and may particularly useful for delivery of a transgene encoding a therapeutic protein for treatment of a muscle disease (such as, but not limited to a muscular dystrophy).

[0087] In embodiments the engineered rAAV exhibits at least 1.1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold greater transduction in cardiac muscle and/or skeletal muscle cells compared to a reference AAV capsid, including an AAV9 capsid or an AAV8 capsid, or the parental capsid. In particular embodiments, the muscle is gastrocnemius muscle, bicep, tricep and/or heart muscle. In further embodiments, the engineered rAAV exhibits of 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in liver compared to the reference AAV capsid compared to a reference AAV capsid, including an AAV9 capsid or an AAV8 capsid, or the parental capsid. In further embodiments, the rAAV exhibits of 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in dorsal root ganglion cells (including in cervical, thoracic or lumbar DRG cells) compared to the reference AAV capsid. The enhanced and/or reduce transduction may be with any mode of administration, by intravenous administration, intramuscular administration, or any type of systemic administration, intrathecal administration or ICV administration.

[0088] Also provided are engineered capsids having one or more amino acid substitutions that promote transduction and/or tissue tropism, particularly for enhanced, relative to an unengineered capsid, targeting for CNS and, in embodiments, reduced, relative to an unengineered capsid, targeting for liver, dorsal root ganglion, and/or peripheral nervous tissue. In embodiments, the amino acid substitutions areA269S of AAV8 (or at a corresponding position in a different AAV serotype capsid), S263G/S269T/A273T of AAV9 (or at a corresponding position in a different AAV serotype capsid), N272A or N266A of AAV9 (or at a corresponding position in a different AAV serotype capsid), Q474A of AAV9 (or at a corresponding position in a different AAV serotype capsid), or W503R of AAV9 (or at a corresponding position in a different AAV serotype capsid), or R697W of rh64R1 (or at a corresponding position in a different AAV serotype capsid). The capsids having these amino acid substitutions and insertions may further have or alternatively have substitutions of the NNN (asparagines) at 496 to 498 with AAA (alanines) of the AAV9 capsid (SEQ ID NO: 67) or have substitutions of the NNN (asparagines) at 498 to 4500 with AAA (alanines) of the AAV8 capsid (SEQ ID NO: 66), or corresponding substitutions in other AAV type capsids. This engineered capsid may exhibit preferential targeting for CNS, and reduced targeting (compared to an AAV bearing the unengineered capsid) for liver and/or dorsal root ganglion cells and/or peripheral nervous system tissue, and may particularly useful for delivery of a transgene encoding a therapeutic protein for treatment of a CNS disease.

[0089] Also provided are recombinant capsid proteins, and rAAVs comprising them, that have inserted peptides that target and/or promote rAAV cellular uptake, transduction and/or genome integration in CNS tissue and, in embodiments, reduced, relative to an unengineered capsid, targeting for liver, dorsal root ganglion, and/or peripheral nervous tissue, for example, the peptide TILSRSTQTG (SEQ ID NO:15); TLAVPFK (SEQ ID NO:20); or TLAAPFK

(SEQ ID NO:1). In particular embodiments the peptide TLAAPFK (SEQ ID NO:1) is inserted between Q588 and A589 of AAV9 (AAV9.hDyn; see Table 17), or the corresponding position of another AAV (see FIG. 7). Alternatively, the capsid is rh.34, rh.10, rh.46, rh.73, or rh64.R1 (Fig. 7 or Table 17 for sequence), or an engineered form of rh.34, rh.10, rh.46, rh.73, or rh64.R1. These engineered capsids may exhibit preferential targeting for CNS, and reduced targeting (compared to an AAV bearing the unengineered capsid) for liver and/or dorsal root ganglion cells and/or peripheral nervous system tissue, and may particularly useful for delivery of a transgene encoding a therapeutic protein for treatment of a CNS disease.

[0090] In embodiments the engineered rAAV exhibits at least 1.1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold greater transduction in CNS tissue compared to a reference AAV capsid, such as the parental capsid or AAV8 or AAV9. The CNS tissue may be one or more of the frontal cortex, hippocampus, cerebellum, midbrain and/or hindbrain. In further embodiments, the engineered rAAV exhibits of 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in liver compared to the reference AAV capsid such as the parental capsid or AAV8 or AAV9. In further embodiments, the rAAV exhibits of 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in dorsal root ganglion cells (including in cervical, thoracic or lumbar DRG cells) compared to the reference AAV capsid such as the parental capsid or AAV8 or AAV9. The enhanced and/or reduce transduction may be with any mode of administration, by intravenous administration, intramuscular administration, or any type of systemic administration, intrathecal administration or ICV administration.

[0091] Recombinant vectors comprising the capsid proteins also are provided, along with pharmaceutical compositions thereof, nucleic acids encoding the capsid proteins, and methods of making and using the capsid proteins and rAAV vectors having the engineered capsids for targeted delivery, improved transduction and/or treatment of disorders associated with the target tissue.

[0092] As used throughout, AAV "serotype" refers to an AAV having an immunologically distinct capsid, a naturally-occurring capsid, or an engineered capsid.

5.1. Definitions

[0093] The term "AAV" or "adeno-associated virus" refers to a Dependoparvovirus within the Parvoviridae genus of viruses. The AAV can be an AAV derived from a naturally occurring "wild-type" virus, an AAV derived from a rAAV genome packaged into a capsid comprising capsid proteins encoded by a naturally occurring cap gene and/or from a rAAV genome packaged into a capsid comprising capsid proteins encoded by a non-naturally occurring capsid cap gene. An example of the latter includes a rAAV having a capsid protein comprising a peptide insertion into the amino acid sequence of the naturally-occurring capsid.

[0094] The term "rAAV" refers to a "recombinant AAV." In some embodiments, a recombinant AAV has an AAV genome in which part or all of the rep and cap genes have been replaced with heterologous sequences.

[0095] The term "rep-cap helper plasmid" refers to a plasmid that provides the viral rep and cap gene function and aids the production of AAVs from rAAV genomes lacking functional rep and/or the cap gene sequences.

[0096] The term "cap gene" refers to the nucleic acid sequences that encode capsid proteins that form or help form the capsid coat of the virus. For AAV, the capsid protein may be VP1, VP2, or VP3.

[0097] The term "rep gene" refers to the nucleic acid sequences that encode the non-structural protein needed for replication and production of virus.

[0098] As used herein, the terms "nucleic acids" and "nucleotide sequences" include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), combinations of DNA and RNA molecules or hybrid DNA/RNA molecules, and analogs of DNA or RNA molecules. Such analogs can be generated using, for example, nucleotide analogs, which include, but are not limited to, inosine or tritylated bases. Such analogs can also comprise DNA or RNA molecules comprising modified backbones that lend beneficial attributes to the molecules such as, for example, nuclease resistance or an increased ability to cross cellular membranes. The nucleic acids or nucleotide sequences can be single-stranded, double-stranded, may contain both single-stranded and double-stranded portions, and may contain triple-stranded portions, but preferably is double-stranded DNA.

[0099] As used herein, the terms "subject", "host", and "patient" are used interchangeably. As used herein, a subject is a mammal such as a non-primate (*e.g.*, cows, pigs, horses, cats, dogs, rats etc.) or a primate (*e.g.*, monkey and human), or, in certain embodiments, a human.

[00100] As used herein, the terms "therapeutic agent" refers to any agent which can be used in treating, managing, or ameliorating symptoms associated with a disease or disorder, where the disease or disorder is associated with a function to be provided by a transgene. As used herein, a "therapeutically effective amount" refers to the amount of agent, (*e.g.*, an amount of product expressed by the transgene) that provides at least one therapeutic benefit in the treatment or management of the target disease or disorder, when administered to a subject suffering therefrom. Further, a therapeutically effective amount with respect to an agent of the invention means that amount of agent alone, or when in combination with other therapies, that provides at least one therapeutic benefit in the treatment or management of the disease or disorder.

[00101] As used herein, the term "prophylactic agent" refers to any agent which can be used in the prevention, delay, or slowing down of the progression of a disease or disorder, where the disease or disorder is associated with a function to be provided by a transgene. As used herein, a "prophylactically effective amount" refers to the amount of the prophylactic agent (*e.g.*, an amount of product expressed by the transgene) that provides at least one prophylactic benefit in the prevention or delay of the target disease or disorder, when administered to a subject predisposed thereto. A prophylactically effective amount also may refer to the amount of agent sufficient to prevent or delay the occurrence of the target disease or disorder; or slow the progression of the target disease or disorder; the amount sufficient to delay or minimize the onset of the target disease or disorder; or the amount sufficient to prevent or delay the recurrence or spread thereof. A prophylactically effective amount also may refer to the amount of agent sufficient to prevent or delay the exacerbation of symptoms of a target disease or disorder. Further, a prophylactically effective amount with respect to a prophylactic agent of the invention means that amount of prophylactic agent alone, or when in combination with other agents, that provides at least one prophylactic benefit in the prevention or delay of the disease or disorder.

[00102] A prophylactic agent of the invention can be administered to a subject "pre-disposed" to a target disease or disorder. A subject that is "pre-disposed" to a disease or disorder is one that shows symptoms associated with the development of the disease or disorder, or that has a genetic makeup, environmental exposure, or other risk factor for such a disease or disorder, but where the symptoms are not yet at the level to be diagnosed as the disease or disorder. For example, a patient with a family history of a disease associated with a missing gene (to be provided by a transgene) may qualify as one predisposed thereto. Further, a patient with a dormant tumor that persists after removal of a primary tumor may qualify as one predisposed to recurrence of a tumor.

[00103] The "central nervous system" ("CNS") as used herein refers to neural tissue reaches by a circulating agent after crossing a blood-brain barrier, and includes, for example, the brain, optic nerves, cranial nerves, and spinal cord. The CNS also includes the cerebrospinal fluid, which fills the central canal of the spinal cord as well as the ventricles of the brain.

5.2. Recombinant AAV Capsids and Vectors

[00104] Provided are recombinant adeno-associated viruses (rAAVs) having capsid proteins engineered relative to a reference capsid protein, such that the rAAV has enhance desired properties, such as increased tissue targeting, including transduction, genome integration and transgene expression, particularly, preferentially, relative to the reference capsid protein (e.g., the unengineered or wild type capsid), to CNS or to heart and/or skeletal muscle tissue. In embodiments, the engineered capsid has reduced tropism (i.e., tissue targeting, transduction and integration of the rAAV genome) relative to the reference capsid for liver, dorsal root ganglion and/or peripheral nervous tissue to reduce toxicity of the AAV gene therapy. The modifications include amino acid substitutions (including 1, 2, 3, 4, 5, 6, 7 or 8 amino acid substitutions) and/or peptide insertions (4 to 20, or 7 contiguous amino acids, and in embodiments no more than 12 contiguous amino acids from a heterologous protein) as described herein.

5.2.1 Engineered Capsids with Amino Acid Substitutions

[00105] In some embodiments, AAV capsids were modified by introducing selected single to multiple amino acid substitutions which increase effective gene delivery to the CNS or to cardiac or skeletal muscle, detarget the liver and/or dorsal root ganglion to reduce toxicity, and/or reduce immune responses of neutralizing antibodies.

[00106] In particular embodiments the capsids have one or more amino acid substitutions including a W503R substitution, a Q474 substitutional a N272A or N266A substitution in AAV9 or the corresponding substitution in another AAV serotype or an A269S substitution in AAV8 or the corresponding substitution in another AAV serotype. rAAV having a capsid with the Q474A substitution may be particularly useful for delivery to skeletal and/or cardiac muscle or CNS tissue and rAAV having a capsid with the W503R substitution may be particularly useful for delivery to CNS tissue, particularly with reduced, compared to reference capsid containing rAAVs, transduction in the liver and/or DRGs. Other substitutions include S263G/S269R/A273T substitutions in AAV9 or A587D/Q588G in AAV9 or corresponding substitutions in other AAV serotypes. In some embodiments, the rAAV capsid can have a R697W substitution. The capsids having these amino acid substitutions and insertions may further have substitutions of the NNN (asparagines) at 496 to 498 with AAA (alanines) of the AAV9 capsid, or of the NNN (asparagines) at 498 to 500 with AAA (alanines) of the AAV8 capsid corresponding substitutions in other AAV type capsids. Other AAV serotypes that may be used for the amino acid substitutions and that may be the reference capsid include AAV8, AAV rh.34, AAV4, AAV5, AAV hu.26, AAV rh.31, AAV hu.13, AAV hu.26, AAV hu.56, AAV hu.53, AAV7, rh64R1, rh46 or rh73. In particular embodiments for CNS delivery, the capsid is rh34, either unmodified or serving as the parental capsid to be modified as detailed herein.

[00107] Effective gene delivery to the CNS by intravenously administered rAAV vectors requires crossing the blood brain barrier. Key clusters of residues on the AAVrh.10 capsid that enabled transport across the brain vasculature and widespread neuronal transduction in mice have recently been reported. Specifically, AAVrh.10-derived amino acids N262, G263, T264, S265, G267, S268, T269, and T273 were identified as key residues that promote crossing the BBB (Albright et al, 2018, Mapping the Structural Determinants Required for AAVrh.10 Transport across the Blood-Brain Barrier). Amino acid substitutions in capsids, such as AAV8 and AAV9 capsids that promote rAAV crossing of the blood brain barrier, transduction, detargeting of the liver and/or reduction in immune responses have been identified.

[00108] In some embodiments, provided are capsids having one or more amino acid substitutions that promote transduction and/or tissue tropism of the rAAV having the modified capsid. In particular embodiments, provided are capsids having a single mutation at amino acid 269 of the AAV8 capsid replacing alanine with serine (A269S) (see, **Tables 5a-5c**, herein referred to as AAV8.BBB) and amino acid substitutions at corresponding positions in other AAV types. In some embodiments, provided are capsids having multiple substitutions at amino acids 263, 269, and 273 of the AAV9 capsid resulting in the following substitutions: S263G, S269T, and A273T (herein referred to as AAV9.BBB) or substitutions corresponding to these positions in other AAV types.

[00109] Exposure to the AAV capsid can generate an immune response of neutralizing antibodies. One approach to overcome this response is to map the AAV-specific neutralizing epitopes and rationally design an AAV capsid able to evade neutralization. A monoclonal antibody, specific for intact AAV9 capsids, with high neutralizing titer has recently been described (Giles et al, 2018, Mapping an Adeno-associated Virus 9-Specific Neutralizing Epitope To Develop Next-Generation Gene Delivery Vectors). The epitope was mapped to the 3-fold axis of symmetry on the capsid, specifically to residues 496-NNN-498 and 588-QAQAQT-592 of AAV9 (SEQ ID NO:8). Capsid mutagenesis demonstrated that single amino acid substitution within this epitope markedly reduced binding and neutralization. In addition, in vivo studies showed that mutations in the epitope conferred a “liver-detargeting” phenotype to the mutant vectors, suggesting that the same residues are also responsible for AAV9 tropism. Liver detargeting has also been associated with substitution of amino acid 503 replacing tryptophan with arginine. Presence of the W503R mutation in the AAV9 capsid was associated with low glycan binding avidity (Shen *et al*, 2012, Glycan Binding Avidity Determines the Systemic Fate of Adeno-Associated Virus Type 9).

[00110] In some embodiments, provided are capsids in which the AAV8.BBB and AAV9.BBB capsids were further modified by substituting asparagines at amino acid positions 498, 499, and 500 of AAV8 (herein referred to as AAV8.BBB.LD) or 496, 497, and 498 of AAV9 (herein referred to as AAV9.BBB.LD) with alanines. In some embodiments, the AAVrh10 capsid was modified by substituting three asparagines at amino acid positions 498, 499, and 500 to alanines (AAVrh10.LD) (**Tables 5a-5c**).

[00111] In some embodiments, provided are capsids having three asparagines at amino acid positions 496, 497, and 498 of the AAV9 capsid replaced with alanines and also tryptophan at amino acid 503 of the AAV9 capsid with arginine or capsids with substitutions corresponding to these positions in other AAV types. In some embodiments, provided are capsids having glutamine at amino acid position 474 of the AAV9 capsid substituted with alanine or capsids with substitutions corresponding to this position in other AAV types.

[00112] In some embodiments, the capsid is an AAV8.BB.LD capsid (A269S,498-NNN/AAA-500 substitutions in the amino acid sequence of AAV8, SEQ ID NO 66), an AAV9.BBB.LD capsid (S263G/S269T/A273T, 496-NNN/AAA-498 substitutions in the amino acid sequence of AAV9, SEQ ID NO 67), an AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 31), an AAV9.496-NNN/AAA-498.W503R capsid (SEQ ID NO: 32), an AAV9.W503R capsid (SEQ ID NO: 33), or an AAV9.Q474A capsid (SEQ ID NO: 34). In other examples, the capsid can be an AAV9.N272A.496-NNN-498 capsid (SEQ ID NO:91) or an AAV9.G266A.496-NNN-498 capsid (SEQ ID NO: 92).

[00113] In some embodiments, the rAAVs described herein increase tissue-specific (such as, but not limited to, CNS or skeletal and/or cardiac muscle) cell transduction in a subject (a human, non-human-primate, or mouse subject) or in cell culture, compared to the rAAV not comprising the amino acid substitution. In some embodiments, the increase in tissue specific cell transduction is at least 2, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 fold more than that without the modification. For example, in some embodiments, there is a 50-80 fold increase in tissue specific cell transduction compared to transduction with the same AAV type without the modification. The increase in transduction may be assessed using methods described in the Examples herein and known in the art.

[00114] In some embodiments, the rAAVs described herein increase the incorporation of rAAV genomes into a cell or tissue type in a subject (a human, non-human primate or mouse subject) or in cell culture to the rAAV not comprising the peptide insertion. In some embodiments, the increase in genome integration is at least 2, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 fold more than an AAV having a capsid without the modification (i.e., the parental capsid). For example, in some embodiments, there is a 50-80 fold increase in genome integration compared to genome integration with the same AAV type without the modification.

5.2.2 rAAV Vectors with Peptide Insertions

[00115] Provided are rAAVs having capsid proteins with one or more (generally one or two) peptide insertions wherein the peptide insertion increase effective gene delivery to the CNS or to cardiac or skeletal muscle and to detarget the liver and/or dorsal root ganglion to reduce toxicity relative to the parental capsid protein. In particular embodiments, the peptides include TLAVPFK, TLAAPFK, or TILSRSTQTG (or an at least 4, 5, 6, 7 amino acid portion thereof). The peptides may be inserted into the AAV9 capsid, for example after the positions 138; 262-273; 452-461; 585-593 of AAV9 cap, particularly after position 138, 454 or 588 of AAV9 or a corresponding position in another AAV as detailed herein. In particular embodiments, the capsid has the peptide TLAVPFK (SEQ ID NO:20) is inserted between G588 and A589 of AAV9, and, in particular, the capsid protein also has amino acid substitutions A587D/Q588G (PHP.eB) and further has the peptide TILSRSTQTG (SEQ ID NO:15) inserted after position 138 of AAV9 (collectively, AAVPHPeB.VP2Herp; see Table 17), or in the corresponding positions of another AAV. Additional capsids have a Kidney1 peptide LPVAS inserted into the capsid, for example between 454 and 455 of AAV9 (see Table 17), or alternatively or alternatively between S268 and S269 or between Q588 and A589 of AAV9 or the corresponding position of another AAV serotype. Such an engineered capsid may exhibit preferential targeting for heart and skeletal muscle, and reduced targeting (as compared to an AAV having the unengineered capsid) for liver and/or dorsal root ganglion cells and may particularly useful for delivery of a transgene encoding a therapeutic protein for treatment of a muscle disease (such as, but not limited to a muscular dystrophy).

[00116] In some embodiments, the peptide insertion comprises at least 4, 5, 6, 7, 8, 9, or all 10 consecutive amino acids of sequence TILSRSTQTG (SEQ ID NO:15), preferably which contains the TQT or STQT (SEQ ID NO:9) motif. In some embodiments, the peptide insertion consists of at least 4, 5, 6, 7, 8, 9, or all 10 consecutive amino acids of sequence TILSRSTQTG (SEQ ID NO:15), preferably which contains the TQT or STQT (SEQ ID NO:9) motif.

[00117] In certain embodiments, the peptide insertion may be a sequence of consecutive amino acids from a domain that targets kidney tissue, or a conformation analog designed to mimic the three-dimensional structure of said domain. In some embodiments, the kidney-homing domain comprises the sequence CLPVASC (SEQ ID NO:5) (*see*, *e.g.*, US 5,622,699). In some embodiments, the peptide insertion from said kidney-homing domain comprises at least 4, 5, 6, or all 7 amino acids from sequence CLPVASC (SEQ ID NO:5). In some embodiments, the peptide insertion comprises or consists of the sequence CLPVASC (SEQ ID NO:5).

[00118] It has been found that both of the cysteine residues in certain homing peptides can be deleted without significantly affecting the organ homing activity of the peptide. For example, a peptide having the sequence LPVAS (SEQ ID NO:6) also can be a kidney-homing peptide. Methods for determining the necessity of a cysteine residue or of amino acid residues N-terminal or C-terminal to a cysteine residue for organ homing activity of a peptide are routine and well known in the art. Thus, in some embodiments, the peptide insertion comprises at least 4 or all 5 amino acids from sequence LPVAS (SEQ ID NO:6). In some embodiments, the peptide insertion comprises or consists of the sequence LPVAS (SEQ ID NO:6).

[00119] In particular embodiments, provided are rAAVs having a capsid that has the peptide TLAAPFK (SEQ ID NO:1) is inserted between Q588 and A589 of AAV9 (AAV9.hDyn; see Table 17), or the corresponding position of another AAV (see, e.g., FIG. 7). Such an engineered capsid may exhibit preferential targeting for CNS tissue, and reduced targeting (as compared to an AAV having the unengineered capsid) for liver and/or dorsal root ganglion cells and may particularly useful for delivery of a transgene encoding a therapeutic protein for treatment of a CNS disease.

[00120] Provided are capsids with peptide insertions at positions amenable to peptide insertions within and near the AAV9 capsid VR-IV loop (see **FIG. 2**) and corresponding regions on the VR-IV loop of capsids of other AAV types. Though previous studies analyzed potential positions in various AAVs, none identified the AAV9 VR-IV as amenable for this purpose (consider, *e.g.*, Wu *et al*, 2000, "Mutational Analysis of the Adeno-Associated Virus Type 2 (AAV2) Capsid Gene and Construction of AAV2 Vectors with Altered Tropism," *J of Virology* 74(18):8635-8647; Lochrie *et al*, 2006, "Adeno-associated virus (AAV) capsid genes isolated from rat and mouse liver genomic DNA define two new AAV species distantly related to AAV-5," *Virology* 353:68-82; Shi and Bartlett, 2003, "RGD Inclusion in VP3 Provides Adeno-Associated Virus Type 2 (AAV2)-Based Vectors with a Heparan Sulfate-Independent Cell Entry Mechanism," *Molecular Therapy* 7(4):515525-; Nicklin *et al.*, 2001, "Efficient and Selective AAV2-Mediated Gene Transfer Directed to Human Vascular Endothelial Cells" *Molecular Therapy* 4(2):174-181; Grifman *et al.*, 2001, "Incorporation of Tumor-Targeting Peptides into Recombinant Adeno-associated Virus Capsids," *Molecular Therapy* 3(6):964-975; Girod *et al.* 1999, "Genetic capsid modifications allow efficient re-targeting of adeno-associated virus type 2," *Nature Medicine* 3(9):1052-1056; Douar *et al.*, 2003, "Deleterious effect of peptide insertions in a permissive site of the AAV2 capsid, *"Virology* 309:203-208; and Ponnazhagan, *et al.* 2001, *J. of Virology* 75(19):9493-9501).

[00121] Accordingly, provided are rAAV vectors carrying peptide insertions at these points, in particular, within surface-exposed variable regions in the capsid coat, particularly within or near the variable region IV of the capsid protein. In some embodiments, the rAAV capsid protein comprises a peptide insertion immediately after (*i.e.*, connected by a peptide bond C-terminal to) an amino acid residue corresponding to one of amino acids 451 to 461 of AAV9 capsid protein (amino acid sequence SEQ ID NO:67 and see **FIG.** 7 for alignment of capsid protein amino acid sequence of other AAV serotypes with amino acid sequence of the AAV9 capsid and Table 17 for other capsid sequences), where said peptide insertion is surface exposed when the capsid protein is packaged as an AAV particle. The peptide insertion should not delete any residues of the AAV capsid protein. Generally, the peptide insertion occurs in a variable (poorly conserved) region of the capsid protein, compared with other serotypes, and in a surface exposed loop.

[00122] A peptide insertion described as inserted "at" a given site refers to insertion immediately after, that is having a peptide bond to the carboxy group of, the residue normally found at that site in the wild type virus. For example, insertion at Q588 in AAV9 means that the peptide insertion appears between Q588 and the consecutive amino acid (A589) in the AAV9 wildtype capsid protein sequence (SEQ ID NO:67). In embodiments, there is no deletion of amino acid residues at or near (within 5, 10, 15 residues or within the structural loop that is the site of the insertion) the point of insertion.

[00123] In particular embodiments, the capsid protein is an AAV9 capsid protein and the insertion occurs immediately after at least one of the amino acid residues 451 to 461. In particular embodiments, the peptide insertion occurs immediately after amino acid I451, N452, G453, S454, G455, Q456, N457, Q458, Q459, T460, or L461 of the AAV9 capsid (amino acid sequence SEQ ID NO:67). In certain embodiments, the peptide is inserted between residues S454 and G455 of AAV9 capsid protein or between the residues corresponding to S454 and G455 of an AAV capsid protein other than an AAV9 capsid protein (amino acid sequence SEQ ID NO:67).

[00124] In other embodiments, provided are engineered capsid proteins comprising targeting peptides heterologous to the capsid protein that are inserted into the AAV capsid protein such that, when incorporated into the AAV vector the heterologous peptide is surface exposed.

[00125] In other embodiments, the capsid protein is from at least one AAV type selected from AAV serotype 1 (AAV1), serotype 2 (AAV2), serotype 3 (AAV3), serotype 4 (AAV4), serotype 5 (AAV5), serotype 6 (AAV6), serotype 7 (AAV7), serotype 8 (AAV8), serotype rh8 (AAVrh8), serotype 9e (AAV9e), serotype rh10 (AAVrh10), serotype rh20 (AAVrh20), serotype rh39 (AAVrh39), serotype hu.37 (AAVhu.37), serotype rh74 (AAVrh74, versions 1 and 2), serotype rh34 (AAVrh34), serotype hu26 (AAVhu26), serotype rh31 (AAVrh31), serotype hu56 (AAVhu56), serotype hu53 (AAVhu53), serotype rh64R1 (AAVrh64R1), serotype rh46 (AAVrh46), and serotype rh73 (AAVrh73) (see **FIG.** 7 or **Table 17**), and the insertion occurs immediately after an amino acid residue corresponding to at least one of the amino acid residues 451 to 461. The alignments of these different AAV serotypes, as shown in **FIG.** 7, indicates "corresponding" amino acid residues in the different capsid amino acid sequences such that a "corresponding" amino acid residue is lined up at the same position in the alignment as the residue in the reference sequence. In some particular embodiments, the peptide insertion occurs immediately after one of the amino acid residues within: 450-459 of AAV1 capsid (SEQ ID NO:59); 449-458 of AAV2 capsid (SEQ ID NO:60); 449-459 of AAV3 capsid (SEQ ID NO:61); 443-453 of AAV4 capsid (SEQ ID NO:62); 442-445 of AAV5 capsid (SEQ ID NO:63); 450-459 of AAV6 capsid (SEQ ID NO:64); 451-461 of AAV7 capsid (SEQ ID NO:65); 451-461 of AAV8 capsid (SEQ ID NO:66); 451-461 of AAV9 capsid (SEQ ID NO:67); 452-461 of AAV9e capsid (SEQ ID NO:68); 452-461 of AAVrh10 capsid (SEQ ID NO:69); 452-461 of AAVrh20 capsid (SEQ ID NO:70); 452-461 of AAVhu.37 (SEQ ID NO:71); 452-461 of AAVrh74 (SEQ ID NO:72 or SEQ ID NO:80); or 452-461 of AAVrh39 (SEQ ID NO:73), in the sequences depicted in **FIG.** 7. In certain embodiments, the rAAV capsid protein comprises a peptide insertion immediately after (*i.e.*, C-terminal to) amino acid 588 of AAV9 capsid protein (having the amino acid sequence of SEQ ID NO:67 and see **FIG.** 7), where said peptide insertion is surface exposed when the capsid protein is packaged as an

AAV particle. In other embodiments, the rAAV capsid protein has a peptide insertion that is not immediately after amino acid 588 of AAV9 or corresponding to amino acid 588 of AAV9.

[00126] In specific embodiments, the peptide is inserted after 138; 262-272; 450-459; or 585-593 of AAV1 capsid (SEQ ID NO:59); 138; 262-272; 449-458; or 584-592 of AAV2 capsid (SEQ ID NO:60); 138; 262-272; 449-459; or 585-593 of AAV3 capsid (SEQ ID NO:61); 137; 256-262; 443-453; or 583-591 of AAV4 capsid (SEQ ID NO:62); 137; 252-262; 442-445; or 574-582 of AAV5 capsid (SEQ ID NO:63); 138; 262-272; 450-459; 585-593 of AAV6 capsid (SEQ ID NO:64); 138; 263-273; 451-461; 586-594 of AAV7 capsid (SEQ ID NO:65); 138; 263-274; 452-461; 587-595 of AAV8 capsid (SEQ ID NO:66); 138; 262-273; 452-461; 585-593 of AAV9 capsid (SEQ ID NO:67); 138; 262-273; 452-461; 585-593 of AAV9e capsid (SEQ ID NO:68); 138; 263-274; 452-461; 587-595 of AAVrh10 capsid (SEQ ID NO:69); 138; 263-274; 452-461; 587-595 of AAVrh20 capsid (SEQ ID NO:70); 138; 263-274; 452-461; 587-595 of AAVrh74 capsid (SEQ ID NO:72 or SEQ ID NO:80) , 138; 263-274; 452-461; 587-595 of AAVhu37 capsid (SEQ ID NO:71); or 138; 263-274; 452-461; 587-595 of AAVrh39 capsid (SEQ ID NO:73) (as numbered in **FIG. 7**).

[00127] Generally, the peptide insertion is sequence of contiguous amino acids from a heterologous protein or domain thereof. The peptide to be inserted typically is long enough to retain a particular biological function, characteristic, or feature of the protein or domain from which it is derived. The peptide to be inserted typically is short enough to allow the capsid protein to form a coat, similarly or substantially similarly to the native capsid protein without the insertion. In preferred embodiments, the peptide insertion is from about 4 to about 30 amino acid residues in length, about 4 to about 20, about 4 to about 15, about 5 to about 10, or about 7 amino acids in length. The peptide sequences for insertion are at least 4 amino acids in length and may be 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids in length. In some embodiments, the peptide sequences are 16, 17, 18, 19, or 20 amino acids in length. In embodiments, the peptide is no more than 7 amino acids, 10 amino acids or 12 amino acids in length.

[00128] A "peptide insertion from a heterologous protein" in an AAV capsid protein refers to an amino acid sequence that has been introduced into the capsid protein and that is not native to any AAV serotype capsid. Non-limiting examples include a peptide of a human protein in an AAV capsid protein.

[00129] In some embodiments, the rAAVs described herein increase tissue-specific (such as, but not limited to, CNS or skeletal and/or cardiac muscle) cell transduction in a subject (a human, non-human-primate, or mouse subject) or in cell culture, compared to the rAAV not comprising the amino acid substitution. In some embodiments, the increase in tissue specific cell transduction is at least 2, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 fold more than that without the peptide insertion. For example, in some embodiments, there is a 50-80 fold increase in tissue specific cell transduction compared to transduction with the same AAV type without the modification. The increase in transduction may be assessed using methods described in the Examples herein and known in the art.

[00130] In some embodiments, the rAAVs described herein increase the incorporation of rAAV genomes into a cell or tissue type, particularly CNS or heart and/or skeletal muscle in a subject (a human, non-human primate or mouse subject) or in cell culture to the rAAV not comprising the peptide insertion. In some embodiments, the increase in genome integration is at least 2, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 fold more than an AAV having a capsid without the peptide insertion. For example, in some embodiments, there is a 50-80 fold increase in genome integration compared to genome integration with the same AAV type without a peptide insert.

[00131] In another aspect, provided are libraries of capsids, including heterologous peptide insertion libraries or libraries of capsids having one or more amino acid substitutions. A heterologous peptide insertion library refers to a collection of rAAV vectors that carry the same peptide insertion at different insertion sites in the virus capsid, *e.g.*, at different positions within a given variable region of the capsid or different variant peptides or even one or more amino acid substitutions. Provided are methods of screening the rAAVs having capsids from the library for enhance of improved properties such as tissue tropism, including enhanced transduction in CNS or cardiac and/or skeletal muscle tissue and, including, reduced transduction in liver and/or DRG cells. Generally, the capsid proteins used comprise AAV genomes that contain modified rep and cap sequences to prevent the replication of the virus under conditions in which it could normally replicate (co-infection of a mammalian cell along with a helper virus such as adenovirus). The members of the peptide insertion libraries may then be assayed for functional display of the peptide on the rAAV surface, tissue targeting and/or gene transduction.

5.2.3 Additional AAV Capsid Insertion Sites

[00132] The follow summarizes insertion sites for the peptides described herein immediately after amino acid residues of AAV capsids as set forth below (see also, **FIG. 7**):

AAV1: 138; 262-272; 450-459; 595-593; and in a particular embodiment, between 453-454 (SEQ ID NO:59).

AAV2: 138; 262-272; 449-458; 584-592; and in particular embodiment, between 452-453 (SEQ ID NO:60).

AAV3: 138; 262-272; 449-459; 585-593; and in particular embodiment, between 452-453 (SEQ ID NO:61).

AAV4: 137; 256-262; 443-453; 583-591; and in particular embodiment, between 446-447 (SEQ ID NO:62).

AAV5: 137; 252-262; 442-445; 574-582; and in particular embodiment, between 445-446 (SEQ ID NO:63).

AAV6: 138; 262-272; 450-459; 585-593; and in particular embodiment, between 452-453 (SEQ ID NO:64).

AAV7: 138; 263-273; 451-461; 586-594; and in particular embodiment, between 453-454 (SEQ ID NO:65).

AAV8: 138; 263-274; 451-461; 587-595; and in particular embodiment, between 453-454 (SEQ ID NO:66).

AAV9: 138; 262-273; 452-461; 585-593; and in particular embodiment, between 454-455 (SEQ ID NO:67).

AAV9e: 138; 262-273; 452-461; 585-593; and in particular embodiment, between 454-455 (SEQ ID NO:68).

AAVrh10: 138; 263-274; 452-461; 587-595; and in particular embodiment, between 454-455 (SEQ ID NO:69).

AAVrh20: 138; 263-274; 452-461; 587-595; and in particular embodiment, between 454-455 (SEQ ID NO:70).

AAVrh39: 138; 263-274; 452-461; 587-595; and in particular embodiment, between 454-455 (SEQ ID NO:73).

AAVrh74: 138; 263-274; 452-461; 587-595; and in particular embodiment, between 454-455 (SEQ ID NO:72 or SEQ ID NO:80).

AAVhu.37: 138; 263-274; 452-461; 587-595; and in particular embodiment, between 454-455 (SEQ ID NO:71)

[00133] In particular embodiments, the peptide insertion occurs between amino acid residues 588-589 of the AAV9 capsid, or between corresponding residues of another AAV type capsid as determined by an amino acid sequence alignment (for example, as in **FIG. 7**). In particular embodiments, the peptide insertion occurs immediately after amino acid residue I451 to L461, S268 and Q588 of the AAV9 capsid sequence, or immediately after corresponding residues of another AAV capsid sequence (**FIG. 7**).

[00134] In some embodiments, one or more peptide insertions can be used in a single system. In some embodiments, the capsid is chosen and/or further modified to reduce recognition of the AAV particles by the subject's immune system, such as avoiding pre-existing antibodies in the subject. In some embodiments. In some embodiments, the capsid is chosen and/or further modified to enhance desired tropism/targeting.

5.2.4 AAV Vectors

[00135] Also provided are AAV vectors comprising the engineered capsids. In some embodiments, the AAV vectors are non-replicating and do not include the nucleotide sequences encoding the rep or cap proteins (these are supplied by the packaging cells in the manufacture of the rAAV vectors). In some embodiments, AAV-based vectors comprise components from one or more serotypes of AAV. In some embodiments, AAV based vectors provided herein comprise capsid components from one or more of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, AAV16, AAV.rh8, AAV.rh10, AAV.rh20, AAV.rh39, AAV.Rh74, AAV.RHM4-1, AAV.hu37, AAV.Anc80, AAV.Anc80L65, AAV.7m8, AAV.PHP.B, AAV.PHP.eB, AAV2.5, AAV2tYF, AAV3B, AAV.LK03, AAV.HSC1, AAV.HSC2, AAV.HSC3, AAV.HSC4, AAV.HSC5, AAV.HSC6, AAV.HSC7, AAV.HSC8, AAV.HSC9, AAV.HSC10, AAV.HSC11, AAV.HSC12, AAV.HSC13, AAV.HSC14, AAV.HSC15, AAV.HSC16, AAVrh34, AAVhu26, AAVrh31, AAVhu56, AAVhu53, AAVrh64R1, AAVrh46, and AAVrh73, or other rAAV particles, or combinations of two or more thereof. In some embodiments, AAV based vectors provided herein comprise components from one or more of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, AAV16, AAV.rh8, AAV.rh10, AAV.rh20, AAV.rh39, AAV.Rh74, AAV.RHM4-1, AAV.hu37, AAV.Anc80, AAV.Anc80L65, AAV.7m8, AAV.PHP.B, AAV.PHP.eB, AAV2.5, AAV2tYF, AAV3B, AAV.LK03, AAV.HSC1, AAV.HSC2, AAV.HSC3, AAV.HSC4, AAV.HSC5, AAV.HSC6, AAV.HSC7, AAV.HSC8, AAV.HSC9, AAV.HSC10,

AAV.HSC11, AAV.HSC12, AAV.HSC13, AAV.HSC14, AAV.HSC15, or AAV.HSC16, AAVrh34, AAVhu26, AAVrh31, AAVhu56, AAVhu53, AAVrh64R1, AAVrh46, and AAVrh73, or other rAAV particles, or combinations of two or more thereof serotypes. In some embodiments, rAAV particles comprise a capsid protein at least 80% or more identical, *e.g.*, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, etc., i.e. up to 100% identical, to *e.g.*, VP1, VP2 and/or VP3 sequence of an AAV capsid serotype selected from AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, AAV13, AAV14, AAV15, AAV16, AAV.rh8, AAV.rh10, AAV.rh20, AAV.rh39, AAV.Rh74, AAV.RHM4-1, AAV.hu37, AAV.Anc80, rAAV.Anc80L65, AAV.7m8, AAV.PHP.B, AAV.PHP.eB, AAV2.5, AAV2tYF, AAV3B, AAV.LK03, AAV.HSC1, AAV.HSC2, AAV.HSC3, AAV.HSC4, AAV.HSC5, AAV.HSC6, AAV.HSC7, AAV.HSC8, AAV.HSC9, AAV.HSC10, AAV.HSC11, AAV.HSC12, AAV.HSC13, AAV.HSC14, AAV.HSC15, or AAV.HSC16, AAVrh34, AAVhu26, AAVrh31, AAVhu56, AAVhu53, AAVrh64R1, AAVrh46, and AAVrh73, or a derivative, modification, or pseudotype thereof. These engineered AAV vectors may comprise a genome comprising a transgene encoding a therapeutic protein.

[00136] In particular embodiments, the recombinant AAV for use in compositions and methods herein is Anc80 or Anc80L65 (see, *e.g.*, Zinn *et al.*, 2015, *Cell Rep.* 12(6): 1056-1068, which is incorporated by reference in its entirety). In particular embodiments, the recombinant AAV for use in compositions and methods herein is AAV.7m8 (including variants thereof) (see, *e.g.*, US 9,193,956; US 9,458,517; US 9,587,282; US 2016/0376323, and WO 2018/075798, each of which is incorporated herein by reference in its entirety). In particular embodiments, the AAV for use in compositions and methods herein is any AAV disclosed in US 9,585,971, such as AAV-PHP.B. In particular embodiments, the AAV for use in compositions and methods herein is an AAV2/Rec2 or AAV2/Rec3 vector, which has hybrid capsid sequences derived from AAV8 and serotypes cy5, rh20 or rh39 (see, *e.g.*, Issa *et al.*, 2013, PLoS One 8(4): e60361, which is incorporated by reference herein for these vectors). In particular embodiments, the AAV for use in compositions and methods herein is an AAV disclosed in any of the following, each of which is incorporated herein by reference in its entirety: US 7,282,199; US 7,906,111; US 8,524,446; US 8,999,678; US 8,628,966; US 8,927,514; US 8,734,809; US9,284,357; US 9,409,953; US 9,169,299; US 9,193,956; US 9,458,517; US 9,587,282; US 2015/0374803; US 2015/0126588; US 2017/0067908; US 2013/0224836; US 2016/0215024; US 2017/0051257; PCT/US2015/034799; and

PCT/EP2015/053335. In some embodiments, rAAV particles have a capsid protein at least 80% or more identical, *e.g.*, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, etc., i.e. up to 100% identical, to the VP1, VP2 and/or VP3 sequence of an AAV capsid disclosed in any of the following patents and patent applications, each of which is incorporated herein by reference in its entirety: United States Patent Nos. 7,282,199; 7,906,111; 8,524,446; 8,999,678; 8,628,966; 8,927,514; 8,734,809; US 9,284,357; 9,409,953; 9,169,299; 9,193,956; 9,458,517; and 9,587,282; US patent application publication nos. 2015/0374803; 2015/0126588; 2017/0067908; 2013/0224836; 2016/0215024; 2017/0051257; and International Patent Application Nos. PCT/US2015/034799; PCT/EP2015/053335.

[00137] In some embodiments, rAAV particles comprise any AAV capsid disclosed in United States Patent No. 9,840,719 and WO 2015/013313, such as AAV.Rh74 and RHM4-1, each of which is incorporated herein by reference in its entirety. In some embodiments, rAAV particles comprise any AAV capsid disclosed in WO 2014/172669, such as AAV rh.74, which is incorporated herein by reference in its entirety. In some embodiments, rAAV particles comprise the capsid of AAV2/5, as described in Georgiadis *et al.,* 2016, Gene Therapy 23: 857-862 and Georgiadis *et al.,* 2018, Gene Therapy 25: 450, each of which is incorporated by reference in its entirety. In some embodiments, rAAV particles comprise any AAV capsid disclosed in WO 2017/070491, such as AAV2tYF, which is incorporated herein by reference in its entirety. In some embodiments, rAAV particles comprise the capsids of AAVLK03 or AAV3B, as described in Puzzo *et al.,* 2017, Sci. Transl. Med. 29(9): 418, which is incorporated by reference in its entirety. In some embodiments, rAAV particles comprise any AAV capsid disclosed in US Pat Nos. 8,628,966; US 8,927,514; US 9,923,120 and WO 2016/049230, such as HSC1, HSC2, HSC3, HSC4, HSC5, HSC6, HSC7, HSC8, HSC9, HSC10, HSC11, HSC12, HSC13, HSC14, HSC15, or HSC16, each of which is incorporated by reference in its entirety.

[00138] In some embodiments, rAAV particles have a capsid protein disclosed in Intl. Appl. Publ. No. WO 2003/052051 (see, *e.g.*, SEQ ID NO: 2 of '051 publication), WO 2005/033321 (see, *e.g.*, SEQ ID NOs: 123 and 88 of '321 publication), WO 03/042397 (see, *e.g.*, SEQ ID NOs: 2, 81, 85, and 97 of '397 publication), WO 2006/068888 (see, *e.g.*, SEQ ID NOs: 1 and 3-6 of '888 publication), WO 2006/110689, (see, *e.g.*, SEQ ID NOs: 5-38 of '689 publication) WO2009/104964 (see, *e.g.*, SEQ ID NOs: 1-5, 7, 9, 20, 22, 24 and 31 of '964 publication), WO 2010/127097 (see, *e.g.*, SEQ ID NOs: 5-38 of '097 publication), and WO 2015/191508 (see, *e.g.*, SEQ ID NOs: 80-294 of '508 publication), and U.S. Appl. Publ. No. 20150023924 (see, *e.g.*, SEQ ID NOs: 1, 5-10 of ′924 publication), the contents of each of which is herein incorporated by reference in its entirety. In some embodiments, rAAV particles have a capsid protein at least 80% or more identical, *e.g.*, 85%, 85%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, etc., i.e. up to 100% identical, to the VP1, VP2 and/or VP3 sequence of an AAV capsid disclosed in Intl. Appl. Publ. No. WO 2003/052051 (see, *e.g.*, SEQ ID NO: 2 of ′051 publication), WO 2005/033321 (see, *e.g.*, SEQ ID NOs: 123 and 88 of ′321 publication), WO 03/042397 (see, *e.g.*, SEQ ID NOs: 2, 81, 85, and 97 of ′397 publication), WO 2006/068888 (see, *e.g.*, SEQ ID NOs: 1 and 3-6 of ′888 publication), WO 2006/110689 (see, *e.g.*, SEQ ID NOs: 5-38 of ′689 publication) WO2009/104964 (see, *e.g.*, SEQ ID NOs: 1-5, 7, 9, 20, 22, 24 and 31 of 964 publication), W0 2010/127097 (see, *e.g.*, SEQ ID NOs: 5-38 of ′097 publication), and WO 2015/191508 (see, *e.g.*, SEQ ID NOs: 80-294 of ′508 publication), and U.S. Appl. Publ. No. 20150023924 (see, *e.g.*, SEQ ID NOs: 1, 5-10 of ′924 publication).

[00139] In additional embodiments, rAAV particles comprise a pseudotyped AAV capsid. In some embodiments, the pseudotyped AAV capsids are rAAV2/8 or rAAV2/9 pseudotyped AAV capsids. Methods for producing and using pseudotyped rAAV particles are known in the art (see, *e.g.*, Duan *et al.*, J. Virol., 75:7662-7671 (2001); Halbert *et al.*, J. Virol., 74:1524-1532 (2000); Zolotukhin *et al.*, Methods 28:158-167 (2002); and Auricchio *et al.*, Hum. Molec. Genet. 10:3075-3081, (2001).

[00140] In certain embodiments, a single-stranded AAV (ssAAV) may be used. In certain embodiments, a self-complementary vector, *e.g.*, scAAV, may be used (*see, e.g.*, Wu, 2007, *Human Gene Therapy*, 18(2):171-82; McCarty *et al*, 2001, *Gene Therapy*, 8(16):1248-1254; US 6,596,535; US 7,125,717; and US 7,456,683, each of which is incorporated herein by reference in its entirety).

5.3. Methods of Making rAAV Particles

[00141] Another aspect of the present invention involves making rAAV particles having the capsids disclosed herein. In some embodiments, an rAAV particle is made by providing a nucleotide comprising the nucleic acid sequence encoding any of the capsid proteins described herein; and using a packaging cell system to prepare corresponding rAAV particles with capsid coats made up of the capsid protein. In some embodiments, the nucleic acid sequence encodes a sequence having at least 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.9%, identity to the sequence of a capsid protein molecule described herein, and retains (or substantially retains) biological function of the capsid protein. In some embodiments, the nucleic acid encodes a sequence having at least 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 99.9%, identity to the sequence of the one of the capsid proteins described herein, for example, those with sequences in Table 17 or otherwise described herein (see also **FIG. 7**), while retaining (or substantially retaining) biological function of the capsid protein.

[00142] The capsid protein, coat, and rAAV particles may be produced by techniques known in the art. In some embodiments, the viral genome comprises at least one inverted terminal repeat to allow packaging into a vector. In some embodiments, the viral genome further comprises a cap gene and/or a rep gene for expression and splicing of the cap gene. In other embodiments, the cap and rep genes are provided by a packaging cell and not present in the viral genome.

[00143] In some embodiments, the nucleic acid encoding the engineered capsid protein is cloned into an AAV Rep-Cap helper plasmid in place of the existing capsid gene. When introduced together into host cells, this plasmid helps package an rAAV genome into the engineered capsid protein as the capsid coat. Packaging cells can be any cell type possessing the genes necessary to promote AAV genome replication, capsid assembly, and packaging. Nonlimiting examples include 293 cells or derivatives thereof, HELA cells, or insect cells.

[00144] Standard techniques can be used for recombinant DNA, oligonucleotide synthesis, and tissue culture and transformation (*e.g.*, electroporation, lipofection). Enzymatic reactions and purification techniques can be performed according to manufacturer's specifications or as commonly accomplished in the art or as described herein. The foregoing techniques and procedures can be generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification. See, e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual (2d ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. (1989)), which is incorporated herein by reference for any purpose. Unless specific definitions are provided, the nomenclatures utilized in connection with, and the laboratory procedures and techniques of, analytical chemistry, synthetic organic chemistry, and medicinal and pharmaceutical chemistry described herein are those well-known and commonly used in the art. Standard techniques can be used for chemical syntheses, chemical analyses, pharmaceutical preparation, formulation, and delivery, and treatment of patients. Nucleic acid sequences of AAV-based viral vectors, and methods of making recombinant AAV and AAV capsids, are taught, *e.g.*, in US 7,282,199; US 7,790,449; US 8,318,480; US 8,962,332; and PCT/EP2014/076466, each of which is incorporated herein by reference in its entirety.

[00145] In some embodiments, the rAAVs provide transgene delivery vectors that can be used in therapeutic and prophylactic applications, as discussed in more detail below. In some embodiments, the rAAV vector also includes regulatory control elements known to one skilled in the art to influence the expression of the RNA and/or protein products encoded by nucleic acids (transgenes) within target cells of the subject. Regulatory control elements and may be tissue-specific, that is, active (or substantially more active or significantly more active) only in the target cell/tissue. In specific embodiments, the AAV vector comprises a regulatory sequence, such as a promoter, operably linked to the transgene that allows for expression in target tissues. The promoter may be a constitutive promoter, for example, the CB7 promoter. Additional promoters include: cytomegalovirus (CMV) promoter, Rous sarcoma virus (RSV) promoter, MMT promoter, EF-1 alpha promoter, UB6 promoter, chicken beta-actin promoter, CAG promoter, RPE65 promoter, opsin promoter, the TBG (Thyroxine-binding Globulin) promoter, the APOA2 promoter, SERPINA1 (hAAT) promoter, or MIR122 promoter. In some embodiments, particularly where it may be desirable to turn off transgene expression, an inducible promoter is used, *e.g.*, hypoxia-inducible or rapamycin-inducible promoter.

[00146] Provided in particular embodiments are AAV vectors comprising a viral genome comprising an expression cassette for expression of the transgene, under the control of regulatory elements, and flanked by ITRs and an engineered viral capsid as described herein or is at least 95%, 96%, 97%, 98%, 99% or 99.9% identical to the amino acid sequence of the a capsid protein described herein (see **Table 17,** *e.g.*), while retaining the biological function of the engineered capsid. In certain embodiments, the encoded engineered capsid has the sequence of an AAV8.BBB.LD capsid (SEQ ID NO: 27), an AAV9.BBB.LD capsid (SEQ ID NO: 29), an AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 31), AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 32), AAV9.W503R capsid (SEQ ID NO: 33), AAV9.Q474A capsid (SEQ ID NO: 34), AAV9.N272A.496-NNN/AAA-498 capsid (SEQ ID NO: 91) or AAV9.N266A.496-NNN/AAA-498 capsid (SEQ ID NO: 92). Also provided are engineered AAV vectors other than AAV9 vectors, such as engineered AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV9e, AAVrh10, AAVrh20, AAVhu.37, AAVrh39, AAVrh74, AAVrh34, AAVhu26, AAVrh31, AAVhu56, AAVhu53, AAVrh.46, AAVrh.64.R1, AAV.rh.73 vectors, including with the amino acid substitutions and/or peptide insert as described herein and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 amino acid substitutions relative to the wild type or unengineered sequence for that AAV type and that retains its biological function.

[00147] The recombinant adenovirus can be a first-generation vector, with an E1 deletion, with or without an E3 deletion, and with the expression cassette inserted into either deleted region. The recombinant adenovirus can be a second-generation vector, which contains full or partial deletions of the E2 and E4 regions. A helper-dependent adenovirus retains only the adenovirus inverted terminal repeats and the packaging signal (phi). The transgene generally is inserted between the packaging signal and the 3'ITR, with or without stuffer sequences to keep the genome close to wild-type size of approximately 36 kb. An exemplary protocol for production of adenoviral vectors may be found in Alba *et al.*, 2005, "Gutless adenovirus: last generation adenovirus for gene therapy," *Gene Therapy* 12:S18-S27, which is incorporated by reference herein in its entirety

[00148] The rAAV vector for delivering the transgene to target tissues, cells, or organs, has a tropism for that particular target tissue, cell, or organ. Tissue-specific promoters may also be used. The construct further can include expression control elements that enhance expression of the transgene driven by the vector (*e.g.*, introns such as the chicken β-actin intron, minute virus of mice (MVM) intron, human factor IX intron (*e.g.*, FIX truncated intron 1), β-globin splice donor/immunoglobulin heavy chain spice acceptor intron, adenovirus splice donor /immunoglobulin splice acceptor intron, SV40 late splice donor /splice acceptor (19S/16S) intron, and hybrid adenovirus splice donor/IgG splice acceptor intron and polyA signals such as the rabbit β-globin polyA signal, human growth hormone (hGH) polyA signal, SV40 late polyA signal, synthetic polyA (SPA) signal, and bovine growth hormone (bGH) polyA signal. *See*, *e.g.*, Powell and Rivera-Soto, 2015, *Discov. Med.*, 19(102):49-57.

[00149] In certain embodiments, nucleic acids sequences disclosed herein may be codon-optimized, for example, via any codon-optimization technique known to one of skill in the art (*see, e.g.*, review by Quax et al., 2015, Mol Cell 59:149-161).

[00150] In a specific embodiment, the constructs described herein comprise the following components: (1) AAV2 inverted terminal repeats that flank the expression cassette; (2) control elements, which include a) a promoter and, optionally, enhancer elements to promote expression of the transgene in CNS and/or muscle cells, b) optionally an intron sequence, such as a chicken β-actin intron, and c) a polyadenylation sequence, such as an SV40 polyA or rabbit β-globin poly A signal; and (3) transgene providing (*e.g.*, coding for) a nucleic acid or protein product of interest.

[00151] The viral vectors provided herein may be manufactured using host cells, *e.g.*, mammalian host cells, including host cells from humans, monkeys, mice, rats, rabbits, or hamsters. Nonlimiting examples include: A549, WEHI, 10T1/2, BHK, MDCK, COS1, COS7, BSC 1, BSC 40, BMT 10, VERO, W138, HeLa, 293, Saos, C2C12, L, HT1080, HepG2, primary fibroblast, hepatocyte, and myoblast cells. Typically, the host cells are stably transformed with the sequences encoding the transgene and associated elements (*i.e.*, the vector genome), and genetic components for producing viruses in the host cells, such as the replication and capsid genes (*e.g.*, the rep and cap genes of AAV). For a method of producing recombinant AAV vectors with AAV8 capsids, see Section IV of the Detailed Description of U.S. Patent No. 7,282,199 B2, which is incorporated herein by reference in its entirety. Genome copy titers of said vectors may be determined, for example, by TAQMAN® analysis. Virions may be recovered, for example, by $CsCl_2$ sedimentation. Alternatively, baculovirus expression systems in insect cells may be used to produce AAV vectors. For a review, see Aponte-Ubillus *et al.*, 2018, *Appl. Microbiol. Biotechnol.* 102:1045-1054, which is incorporated by reference herein in its entirety for manufacturing techniques.

[00152] In vitro assays, *e.g.*, cell culture assays, can be used to measure transgene expression from a vector described herein, thus indicating, *e.g.*, potency of the vector. For example, the PER.C6® Cell Line (Lonza), a cell line derived from human embryonic retinal cells, or retinal pigment epithelial cells, *e.g.*, the retinal pigment epithelial cell line hTERT RPE-1 (available from ATCC®), can be used to assess transgene expression. Alternatively, cell lines derived from liver or other cell types may be used, for example, but not limited, to HuH-7, HEK293, fibrosarcoma HT-1080, HKB-11, and CAP cells. Once expressed, characteristics of the expressed product (*i.e.*, transgene product) can be determined, including determination of the glycosylation and tyrosine sulfation patterns, using assays known in the art.

5.4. Therapeutic and Prophylactic Uses

[00153] Another aspect relates to therapies which involve administering a transgene via a rAAV vector according to the invention to a subject in need thereof, for delaying, preventing, treating, and/or managing a disease or disorder, and/or ameliorating one or more symptoms associated therewith. A subject in need thereof includes a subject suffering from the disease or disorder, or a subject pre-disposed thereto, *e.g.*, a subject at risk of developing or having a recurrence of the disease or disorder. Generally, a rAAV carrying a particular transgene will find use with respect to a given disease or disorder in a subject where the subject’s native gene, corresponding to the transgene, is defective in providing the correct gene product, or correct amounts of the gene product. The transgene then can provide a copy of a gene that is defective in the subject.

[00154] Generally, the transgene comprises cDNA that restores protein function to a subject having a genetic mutation(s) in the corresponding native gene. In some embodiments, the cDNA comprises associated RNA for performing genomic engineering, such as genome editing via homologous recombination. In some embodiments, the transgene encodes a therapeutic RNA, such as a shRNA, artificial miRNA, or element that influences splicing.

[00155] **Tables 1A-1B** below provides a list of transgenes that may be used in any of the rAAV vectors described herein, in particular, in the novel insertion sites described herein, to treat or prevent the disease with which the transgene is associated, also listed in **Tables 1A-1B.** As described herein, the AAV vector may be engineered as described herein to target the appropriate tissue for delivery of the transgene to effect the therapeutic or prophylactic use. The appropriate AAV serotype may be chosen to engineer to optimize the tissue tropism and transduction of the vector.

Table 1A

Disease	**Transgene**	**Possible AAV serotype for delivery of transgene**
MPS I	alpha-L-iduronidase (IDUA)	AAV9
MPS II (Hunter Syndrome)	iduronate-2-sulfatase (IDS)	AAV9
ceroid lipofuscinosis (Batten disease)	(CLN1, CLN2, CLN10, CLN13), a soluble lysosomal protein (CLN5), a protein in the secretory pathway (CLN11), two cytoplasmic proteins that also peripherally associate with membranes (CLN4, CLN14), and many transmembrane proteins with different subcellular locations (CLN3, CLN6, CLN7, CLN8, CLN12)	AAV9
MPS IIIa (Sanfilippo type A Syndrome)	heparan sulfate sulfatase (also called N-sulfoglucosamine sulfohydrolase (SGSH))	AAV9, Rh10
MPS IIIB (Sanfilippo type B Syndrome)	N-acetyl-alpha-D-glucosaminidase (NAGLU)	AAV9

Disease	Transgene	Possible AAV serotype for delivery of transgene
MPS VI (Maroteaux-Lamy Syndrome)	arylsulfatase B	AAV8
Morquio syndrome (MPS IV)	Beta galactosidase or galactosamine-6-sulfatase	AAV9
Gaucher disease (type 1, II and III)	Glucocerebrosidase, GBA1	AAV9
Parkinson's Disease	Glucocerebrosidase; GBA1	AAV9
Parkinson's Disease	dopamine decarboxylase	AAV2
Pompe	acid maltase; GAA	AAV9
Metachromatic leukodystrophy	Aryl sulfatase A	Rh10
MPS VII (Sly syndrome)	beta-glucuronidase	
MPS VIII	glucosamine-6-sulfate sulfatase	
MPS IX	hyaluronidase	
Niemann-Pick disease	sphingomyelinase	
Niemann-Pick disease without sphingomyelinase deficiency	a npc1 gene encoding a cholesterol metabolizing enzyme	
Tay-Sachs disease	Alpha subunit of beta-hexosaminidase	
Sandhoff disease	both alpha and beta subunit of beta-hexosaminidase	
Fabry Disease	alpha-galactosidase	
Fucosidosis	Fucosidase (FUCA1 gene)	
Alpha-mannosidosis	alpha-mannosidase	
Beta-mannosidosis	Beta-mannosidase	

Disease	**Transgene**	**Possible AAV serotype for delivery of transgene**
Wolman disease	cholesterol ester hydrolase	
Parkinson’s disease	Neurturin	
Parkinson’s disease	glial derived growth factor (GDGF)	
Parkinson’s disease	tyrosine hydroxylase	
Parkinson’s disease	glutamic acid decarboxylase.	
No disease listed	fibroblast growth factor-2 (FGF-2)	
No disease listed	brain derived growth factor (BDGF)	
No disease listed (Galactosialidosis (Goldberg syndrome))	neuraminidase deficiency with betagalactosidase deficiency	
Spinal Muscular Atrophy (SMA)	SMN	AAV9
Friedreich's ataxia	Frataxin	AAV9 PHP.B
Amyotrophic lateral sclerosis (ALS)	SOD1	Rh10
Glycogen Storage Disease 1a	Glucose-6-phosphatase	AAV8
XLMTM	MTM1	AAV8 or AAV9
Crigler Najjar	UGT1A1	AAV8
CPVT	CASQ2	AAV9
Rett syndrome	MECP2	AAV9
Achromatopsia	CNGB3, CNGA3, GNAT2, PDE6C	AAV8
Choroidermia	CDM	AAV8
Danon Disease	LAMP2	AAV9

Table 1B

Disease	**Transgene**	**Possible AAV serotype for delivery of transgene**
Cystic Fibrosis	CFTR	AAV2
Duchenne Muscular Dystrophy	Mini-Dystrophin or Micro-dystrophin Gene	AAV2, AAV8 or AAV9
Limb Girdle Muscular Dystrophy Type 2C|Gamma-sarcoglycanopathy	human-alpha-sarcoglycan	AAV1
Advanced Heart Failure	SERCA2a	AAV6
Rheumatoid Arthritis	TNFR:Fc Fusion Gene	AAV2
Leber Congenital Amaurosis	GAA	AAV1
Limb Girdle Muscular Dystrophy Type 2C|Gamma-sarcoglycanopathy	gamma-sarcoglycan	AAV1
Retinitis Pigmentosa	hMERTK	AAV2
Age-Related Macular Degeneration	sFLT01	AAV2
Becker Muscular Dystrophy and Sporadic Inclusion Body Myositis	huFollistatin344	AAV1
Parkinson's Disease	GDNF	AAV2
Metachromatic Leukodystrophy (MLD)	cuARSA	AAVrh.10
Hepatitis C	anti-HCV shRNA	AAV8
Limb Girdle Muscular Dystrophy Type 2D	hSGCA	AAVrh74*
Human Immunodeficiency Virus Infections; HIV Infections (HIV-1)	PG9DP	AAV1
Acute Intermittant Porphyria	PBGD	AAV5
Leber's Hereditary Optical Neuropathy	P1ND4v2	AAV2
Alpha-1 Antitrypsin Deficiency	alpha1AT	AAVrh10
Pompe Disease	hGAA	AAV9
X-linked Retinoschisis	RS1	AAV8
Choroideremia	hCHM	AAV2
Giant Axonal Neuropathy	JeT-GAN	AAV9
Duchenne Muscular Dystrophy	rmicro-Dystrophin	AAVrh74*
X-linked Retinoschisis	hRS1	AAV2
Squamous Cell Head and Neck Cancer; Radiation Induced Xerostomia	hAQP1	AAV2
Hemophilia B	Factor IX	AAVrh10/ Rh74
Homozygous FH	hLDLR	AAV8
Dysferlinopathies	rAAVrh74.MHCK7.DYSF.DV	AAVrh74
Hemophilia B	AAV6 ZFP nuclease	AAV6
MPS I	AAV6 ZFP nuclease	AAV6
Rheumatoid Arthritis	NF-kB.IFN-β	AAV5

Disease	**Transgene**	**Possible AAV serotype for delivery of transgene**
Batten / CLN6	CLN6	AAV9
Sanfilippo Disease Type A	hSGSH	AAV9
Osteoarthritis	5IL-1Ra	AAV2.5
Achromatopsia	CNGA3	AAV2tYF
Achromatopsia	CNGB3	AAV8
Ornithine Transcarbamylase (OTC) Deficiency	OTC	scAAV8
Hemophilia A	Factor VIII	LK03/AAV3B
Mucopolysaccharidosis II	ZFP nuclease	AAV6
Hemophilia A	ZFP nuclease	AAV6
Wet AMD	anti-VEGF	AAV8
X-Linked Retinitis Pigmentosa	PGR	AAV2
Mucopolysaccharidosis Type VI	hARSB	AAV8
Leber Hereditary Optic Neuropathy	ND4	AAV2
X-Linked Myotubular Myopathy	MTM1	AAV8
Crigler-Najjar Syndrome	UGT1A1	AAV8
Achromatopsia	CNGB3	AAV8
Retinitis Pigmentosa	hPDE6B	AAV5
X-Linked Retinitis Pigmentosa	RPGR	AAV2tYF
Mucopolysaccharidosis Type 3 B	hNAGLU	AAV9
Duchenne Muscular Dystrophy	GALGT2	AAVrh74
Arthritis, Rheumatoid; Arthritis, Psoriatic; Ankylosing Spondylitis	TNFR:Fc Fusion Gene	AAV2
Idiopathic Parkinson's Disease	Neurturin	AAV2
Alzheimer's Disease	NGF	AAV2
Human Immunodeficiency Virus Infections; HIV Infections (HIV-1)	tgAAC09	AAV2
Familial Lipoprotein Lipase Deficiency	LPL	AAV1
Idiopathic Parkinson's Disease	Neurturin	AAV2
Alpha-1 Antitrypsin Deficiency	hAAT	AAV1
Leber Congenital Amaurosis (LCA) 2	hRPE65v2	AAV2
Batten Disease; Late Infantile Neuronal Lipofuscinosis	CLN2	AAVrh.10
Parkinson's Disease	GAD	AAV2
Sanfilippo Disease Type A/ Mucopolysaccharidosis Type IIIA	N-sulfoglucosamine sulfohydrolase (SGSH) gene	AAVrh.10
Congestive Heart Failure	SERC2a	AAV1
Becker Muscular Dystrophy and Sporadic Inclusion Body Myositis	rAAV1.CMV.huFollistatin344	AAV1
Parkinson's Disease	hAADC-2	AAV2

Disease	Transgene	Possible AAV serotype for delivery of transgene
Choroideremia	REP1	AAV2
CEA Specific AAV-DC-CTL Treatment in Stage IV Gastric Cancer	CEA	AAV2
Gastric Cancer	MUC1-peptide-DC-CTL	
Leber's Hereditary Optical Neuropathy	scAAV2-P1ND4v2	scAAV2
Aromatic Amino Acid Decarboxylase Deficiency	hAADC	AAV2
Hemophilia B	Factor IX	AAVrh10
Parkinson's Disease	AADC	AAV2
Leber Hereditary Optic Neuropathy	Genetic: GS010|Drug: Placebo	AAV2
SMA - Spinal Muscular Atrophy|Gene Therapy	SMN	AAV9
Hemophilia A	B-Domain Deleted Factor VIII	AAV8
MPS I	IDUA	AAV9
MPS II	IDS	AAV9
CLN3-Related Neuronal Ceroid-Lipofuscinosis (Batten)	CLN3	AAV9
Limb-Girdle Muscular Dystrophy, Type 2E	hSGCB	rh74
Alzheimer Disease	APOE2	rh10
Retinitis Pigmentosa	hMERKTK	AAV2
Retinitis Pigmentosa	RLBP1	AAV8
Wet AMD	Anti-VEGF antibody	AAV2.7m8

[00156] For example, a rAAV vector comprising a transgene encoding glial derived growth factor (GDGF) finds use treating/preventing/managing Parkinson’s disease. Generally, the rAAV vector is administered systemically. For example, the rAAV vector may be provided by intravenous, intrathecal, intra-nasal, and/or intra-peritoneal administration.

[00157] In certain embodiments, the transgene encodes a microdystrophin (for example, as disclosed in WO WO2021/108755, WO2002/029056, WO2016/115543, WO2015/197232, WO2016/177911, US7892824B2, US9624282B2, and WO2017221145, which are hereby incorporated by reference in their entirety) and is useful for treatment of dystrophinopathies, such as muscular dystrophy. Example 18 herein shows the relative abundance of capsids AAV7, AAV8, AAV9, AAVrh.10, AAVrh.46, AAVrh.64.R1, and AAVrh.73 after intravenous administration to wild-type mice compared to *mdx* mice (animal model for muscular dystrophy). rAAV particles having these capsids, or an engineered forms thereof, may be useful for delivery of transgenes encoding microdystrophins or other dystrophinopathy therapeutic proteins to muscle cells, including skeletal and/or cardiac muscle, while having reduced delivery to liver cells, for treatment of muscular dystrophies, such as, Duchenne Muscular Dystrophy.

[00158] In particular aspects, the rAAVs of the present invention find use in delivery to target tissues, or target cell types, including cell matrix associated with the target cell types, associated with the disorder or disease to be treated/prevented. A disease or disorder associated with a particular tissue or cell type is one that largely affects the particular tissue or cell type, in comparison to other tissue of cell types of the body, or one where the effects or symptoms of the disorder appear in the particular tissue or cell type. Methods of delivering a transgene to a target tissue of a subject in need thereof involve administering to the subject tan rAAV where the peptide insertion is a homing peptide. In the case of Parkinson’s, for example, a rAAV vector comprising a peptide insertion that directs the rAAV to neural tissue can be used, in particular, where the peptide insertion facilitates the rAAV in crossing the blood brain barrier to the CNS.

[00159] For a disease or disorder associated with neural tissue, an rAAV vector can be used that comprises a peptide insertion from a neural tissue-homing domain, such as any described herein. Diseases/disorders associated with neural tissue include Alzheimer's disease, amyotrophic lateral sclerosis (ALS), amyotrophic lateral sclerosis (ALS), Battens disease, Batten’s Juvenile NCL form, Canavan disease, chronic pain, Friedreich’s ataxia, glioblastoma multiforme, Huntington's disease, Late Infantile neuronal ceroid lipofuscinosis (LINCL), lysosomal storage disorders, Leber’s congenital amaurosis, multiple sclerosis, Parkinson's disease, Pompe disease, Rett syndrome, spinal cord injury, spinal muscular atrophy (SMA), stroke, and traumatic brain injury. The vector further can contain a transgene for therapeutic/prophylactic benefit to a subject suffering from, or at risk of developing, the disease or disorder (see Tables 1A-1B).

[00160] The rAAV vectors of the invention also can facilitate delivery, in particular, targeted delivery, of oligonucleotides, drugs, imaging agents, inorganic nanoparticles, liposomes, antibodies to target cells or tissues. The rAAV vectors also can facilitate delivery, in particular, targeted delivery, of non-coding DNA, RNA, or oligonucleotides to target tissues.

[00161] The agents may be provided as pharmaceutically acceptable compositions as known in the art and/or as described herein. Also, the rAAV molecule of the invention may be administered alone or in combination with other prophylactic and/or therapeutic agents.

[00162] The dosage amounts and frequencies of administration provided herein are encompassed by the terms therapeutically effective and prophylactically effective. The dosage and frequency will typically vary according to factors specific for each patient depending on the specific therapeutic or prophylactic agents administered, the severity and type of disease, the route of administration, as well as age, body weight, response, and the past medical history of the patient, and should be decided according to the judgment of the practitioner and each patient's circumstances. Suitable regimens can be selected by one skilled in the art by considering such factors and by following, for example, dosages reported in the literature and recommended in the Physician 's Desk Reference (56th ed., 2002). Prophylactic and/or therapeutic agents can be administered repeatedly. Several aspects of the procedure may vary such as the temporal regimen of administering the prophylactic or therapeutic agents, and whether such agents are administered separately or as an admixture.

[00163] The amount of an agent of the invention that will be effective can be determined by standard clinical techniques. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems. For any agent used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC_{50} (*i.e.*, the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[00164] Prophylactic and/or therapeutic agents, as well as combinations thereof, can be tested in suitable animal model systems prior to use in humans. Such animal model systems include, but are not limited to, rats, mice, chicken, cows, monkeys, pigs, dogs, rabbits, *etc*. Any animal system well-known in the art may be used. Such model systems are widely used and well known to the skilled artisan. In some embodiments, animal model systems for a CNS condition are used that are based on rats, mice, or other small mammal other than a primate.

[00165] Once the prophylactic and/or therapeutic agents of the invention have been tested in an animal model, they can be tested in clinical trials to establish their efficacy. Establishing clinical trials will be done in accordance with common methodologies known to one skilled in the art, and the optimal dosages and routes of administration as well as toxicity profiles of agents of the invention can be established. For example, a clinical trial can be designed to test a rAAV molecule of the invention for efficacy and toxicity in human patients.

[00166] Toxicity and efficacy of the prophylactic and/or therapeutic agents of the instant invention can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, *e.g.*, for determining the LD_{50} (the dose lethal to 50% of the population) and the ED_{50} (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD_{50}/ED_{50}. Prophylactic and/or therapeutic agents that exhibit large therapeutic indices are preferred. While prophylactic and/or therapeutic agents that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such agents to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[00167] A rAAV molecule of the invention generally will be administered for a time and in an amount effective for obtain a desired therapeutic and/or prophylactic benefit. The data obtained from the cell culture assays and animal studies can be used in formulating a range and/or schedule for dosage of the prophylactic and/or therapeutic agents for use in humans. The dosage of such agents lies within a range of circulating concentrations that include the ED_{50} with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized.

[00168] A therapeutically effective dosage of an rAAV vector for patients is generally from about 0.1 ml to about 100 ml of solution containing concentrations of from about $1x10^9$ to about $1x10^{16}$ genomes rAAV vector, or about $1x10^{10}$ to about $1x10^{15}$, about $1x10^{12}$ to about $1x10^{16}$, or about $1x10^{14}$ to about $1x10^{16}$ AAV genomes. Levels of expression of the transgene can be monitored to determine/adjust dosage amounts, frequency, scheduling, and the like.

[00169] Treatment of a subject with a therapeutically or prophylactically effective amount of the agents of the invention can include a single treatment or can include a series of treatments. For example, pharmaceutical compositions comprising an agent of the invention may be administered once, or may be administered in a series of 2, 3 or 4 or more times, for example, weekly, monthly or every two months, 3 months, 6 months or one year until the series of doses has been administered.

[00170] The rAAV molecules of the invention may be administered alone or in combination with other prophylactic and/or therapeutic agents. Each prophylactic or therapeutic agent may be administered at the same time or sequentially in any order at different points in time; however, if not administered at the same time, they should be administered sufficiently close in time so as to provide the desired therapeutic or prophylactic effect. Each therapeutic agent can be administered separately, in any appropriate form and by any suitable route.

[00171] In various embodiments, the different prophylactic and/or therapeutic agents are administered less than 1 hour apart, at about 1 hour apart, at about 1 hour to about 2 hours apart, at about 2 hours to about 3 hours apart, at about 3 hours to about 4 hours apart, at about 4 hours to about 5 hours apart, at about 5 hours to about 6 hours apart, at about 6 hours to about 7 hours apart, at about 7 hours to about 8 hours apart, at about 8 hours to about 9 hours apart, at about 9 hours to about 10 hours apart, at about 10 hours to about 11 hours apart, at about 11 hours to about 12 hours apart, no more than 24 hours apart, or no more than 48 hours apart. In certain embodiments, two or more agents are administered within the same patient visit.

[00172] Methods of administering agents of the invention include, but are not limited to, parenteral administration (*e.g.*, intradermal, intramuscular, intraperitoneal, intravenous, and subcutaneous, including infusion or bolus injection), epidural, and by absorption through epithelial or mucocutaneous or mucosal linings (*e.g.*, intranasal, oral mucosa, rectal, and intestinal mucosa, *etc.*). In particular embodiments, such as where the transgene is intended to be expressed in the CNS, the vector is administered via lumbar puncture or via cisterna magna.

[00173] In certain embodiments, the agents of the invention are administered intravenously and may be administered together with other biologically active agents.

[00174] In another specific embodiment, agents of the invention may be delivered in a sustained release formulation, *e.g.*, where the formulations provide extended release and thus extended half-life of the administered agent. Controlled release systems suitable for use include, without limitation, diffusion-controlled, solvent-controlled, and chemically-controlled systems. Diffusion controlled systems include, for example reservoir devices, in which the molecules of the invention are enclosed within a device such that release of the molecules is controlled by permeation through a diffusion barrier. Common reservoir devices include, for example, membranes, capsules, microcapsules, liposomes, and hollow fibers. Monolithic (matrix) device are a second type of diffusion controlled system, wherein the dual antigen-binding molecules are dispersed or dissolved in an rate-controlling matrix (*e.g.*, a polymer matrix). Agents of the invention can be homogeneously dispersed throughout a rate-controlling matrix and the rate of release is controlled by diffusion through the matrix. Polymers suitable for use in the monolithic matrix device include naturally occurring polymers, synthetic polymers and synthetically modified natural polymers, as well as polymer derivatives.

[00175] Any technique known to one of skill in the art can be used to produce sustained release formulations comprising one or more agents described herein. See, *e.g.* U.S. Pat. No. 4,526,938; PCT publication WO 91/05548; PCT publication WO 96/20698; Ning et al., "Intratumoral Radioimmunotheraphy of a Human Colon Cancer Xenograft Using a Sustained-Release Gel," *Radiotherapy & Oncology*, 39:179 189, 1996; Song et al., "Antibody Mediated Lung Targeting of Long-Circulating Emulsions," PDA *Journal of Pharmaceutical Science & Technology*, 50:372 397, 1995; Cleek et al., "Biodegradable Polymeric Carriers for a bFGF Antibody for Cardiovascular Application," *Pro. Intl. Symp. Control. Rel. Bioact. Mater.*, 24:853 854, 1997; and Lam et al., "Microencapsulation of Recombinant Humanized Monoclonal Antibody for Local Delivery," *Proc. Int'l. Symp. Control Rel. Bioact. Mater.*, 24:759 760, 1997, each of which is incorporated herein by reference in its entirety. In one embodiment, a pump may be used in a controlled release system (see Langer, *supra*; Sefton, *CRC Crit. Ref. Biomed. Eng.*, 14:20, 1987; Buchwald et al., *Surgery*, 88:507, 1980; and Saudek et al., *N. Engl. J. Med.*, 321:574, 1989). In another embodiment, polymeric materials can be used to achieve controlled release of agents comprising dual antigen-binding molecule, or antigen-binding fragments thereof (see *e.g.*, Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Fla. (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, N.Y. (1984); Ranger and Peppas, J., *Macromol. Sci. Rev. Macromol. Chem.*, 23:61, 1983; see also Levy et al., *Science*, 228:190, 1985; During et al., *Ann. Neurol.*, 25:351, 1989; Howard et al., J. *Neurosurg.*, 7 1:105, 1989); U.S. Pat. No. 5,679,377; U.S. Pat. No. 5,916,597; U.S. Pat. No. 5,912,015; U.S. Pat. No. 5,989,463; U.S. Pat. No. 5,128,326; PCT Publication No. WO 99/15154; and PCT Publication No. WO 99/20253). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target (*e.g.*, an affected joint), thus requiring only a fraction of the systemic dose (see, *e.g.*, Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115 138 (1984)). Other controlled release systems are discussed in the review by Langer, *Science*, 249:1527 1533, 1990.

[00176] In addition, rAAVs can be used for *in vivo* delivery of transgenes for scientific studies such as optogenetics, gene knock-down with miRNAs, recombinase delivery for conditional gene deletion, gene editing with CRISPRs, and the like.

5.5. Pharmaceutical Compositions and Kits

[00177] The invention further provides a pharmaceutical composition comprising a pharmaceutically acceptable carrier and an agent of the invention, said agent comprising a rAAV molecule of the invention. In some embodiments, the pharmaceutical composition comprises rAAV combined with a pharmaceutically acceptable carrier for administration to a subject. In one embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant (*e.g.*, Freund's complete and incomplete adjuvant), excipient, or vehicle with which the agent is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable, or synthetic origin, including, *e.g.*, peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a common carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. Additional examples of pharmaceutically acceptable carriers, excipients, and stabilizers include, but are not limited to, buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight polypeptides; proteins, such as serum albumin and gelatin; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™ as known in the art. The pharmaceutical composition of the present invention can also include a lubricant, a wetting agent, a sweetener, a flavoring agent, an emulsifier, a suspending agent, and a preservative, in addition to the above ingredients. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like.

[00178] In certain embodiments of the invention, pharmaceutical compositions are provided for use in accordance with the methods of the invention, said pharmaceutical compositions comprising a therapeutically and/or prophylactically effective amount of an agent of the invention along with a pharmaceutically acceptable carrier.

[00179] In certain embodiments, the agent of the invention is substantially purified (*i.e.*, substantially free from substances that limit its effect or produce undesired side-effects). In a specific embodiment, the host or subject is an animal, *e.g.*, a mammal such as non-primate (*e.g.*, cows, pigs, horses, cats, dogs, rats etc.) and a primate (*e.g.*, monkey such as, a cynomolgus monkey and a human). In a certain embodiment, the host is a human.

[00180] The invention provides further kits that can be used in the above methods. In one embodiment, a kit comprises one or more agents of the invention, *e.g.*, in one or more containers. In another embodiment, a kit further comprises one or more other prophylactic or therapeutic agents useful for the treatment of a condition, in one or more containers.

[00181] The invention also provides agents of the invention packaged in a hermetically sealed container such as an ampoule or sachette indicating the quantity of the agent or active agent. In one embodiment, the agent is supplied as a dry sterilized lyophilized powder or water free concentrate in a hermetically sealed container and can be reconstituted, *e.g.*, with water or saline, to the appropriate concentration for administration to a subject. Typically, the agent is supplied as a dry sterile lyophilized powder in a hermetically sealed container at a unit dosage of at least 5 mg, more often at least 10 mg, at least 15 mg, at least 25 mg, at least 35 mg, at least 45 mg, at least 50 mg, or at least 75 mg. The lyophilized agent should be stored at between 2 and 8°C in its original container and the agent should be administered within 12 hours, usually within 6 hours, within 5 hours, within 3 hours, or within 1 hour after being reconstituted. In an alternative embodiment, an agent of the invention is supplied in liquid form in a hermetically sealed container indicating the quantity and concentration of agent or active agent. Typically, the liquid form of the agent is supplied in a hermetically sealed container at least 1 mg/ml, at least 2.5 mg/ml, at least 5 mg/ml, at least 8 mg/ml, at least 10 mg/ml, at least 15 mg/kg, or at least 25 mg/ml.

[00182] The compositions of the invention include bulk drug compositions useful in the manufacture of pharmaceutical compositions (*e.g.*, impure or non-sterile compositions) as well as pharmaceutical compositions (i.e., compositions that are suitable for administration to a subject or patient). Bulk drug compositions can be used in the preparation of unit dosage forms, *e.g.*, comprising a prophylactically or therapeutically effective amount of an agent disclosed herein or a combination of those agents and a pharmaceutically acceptable carrier.

[00183] The invention further provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the agents of the invention. Additionally, one or more other prophylactic or therapeutic agents useful for the treatment of the target disease or disorder can also be included in the pharmaceutical pack or kit. The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use, or sale for human administration.

[00184] Generally, the ingredients of compositions of the invention are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water-free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of agent or active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

6. EXAMPLES

[00185] The following examples report an analysis of surface-exposed loops on the AAV9 capsid to identify candidates for capsid engineering via insertional mutagenesis. The invention is illustrated by way of examples, describing the construction of rAAV9 capsids engineered to contain 7-mer peptides designed on the basis of the human axonemal dynein heavy chain tail. Briefly, three criteria were used for selecting surface loops that might be amenable to short peptide insertions: 1) minimal side chain interactions with adjacent loops; 2) variable sequence and structure between serotypes (lack of conserved sequences); and 3) the potential for interrupting commonly targeted neutralizing antibody epitopes. A panel of peptide insertion mutants was constructed and the individual mutants were screened for viable capsid assembly, peptide surface exposure, and potency. The top candidates were then used as templates for insertion of homing peptides to test if these peptide insertion points could be used to re-target rAAV vectors to tissues of interest. Further examples, demonstrate the increased transduction and tissue tropism for certain of the modified AAV capsids described herein.

6.1. Example 1 – Analysis of AAV9 capsid

[00186] **FIGs. 1 and 2** depict analysis of variable region four of the adeno-associated virus type 9 (AAV9 VR-IV) by amino acid sequence comparison to other AAVs VR-IV **(FIG. 1)** and protein model **(FIG. 2)**. As seen, AAV9 VR-IV is exposed on the surface at the tip or outer surface of the 3-fold spike. Further analysis indicated that there are few side chain interactions between VR-IV and VR-V and that the sequence and structure of VR-IV is variable amongst AAV serotypes, and further that there is potential for interrupting a commonly-targeted neutralizing antibody epitope and thus, reducing immunogenicity of the modified capsid.

6.2. Example 2 – Construction of AAV9 mutants

[00187] Eight AAV9 mutants were constructed, to each include a heterologous peptide but at different insertion points in the VR-IV loop. The heterologous peptide was a FLAG tag that was inserted immediately following the following residues in vectors identified as pRGNX1090-1097, as shown in **Table 2.**

Table 2

Vector designation	AAV9 VR-IV Insertion site for FLAG tag
pRGNX1090	I451
pRGNX1091	N452
pRGNX1092	G453
pRGNX1093	S454
pRGNX1094	G455
pRGNX1095	Q456
pRGNX1096	N457
pRGNX1097	Q458

6.3. Example 3 – Analysis of Packaging Efficiency

[00188] **FIG. 3** depicts high packaging efficiency in terms of genome copies per mL (GC/mL) of wild type AAV9 and eight (8) candidate rAAV9 vectors (1090, 1091, 1092, 1093, 1094, 1095, 1096, and 1097), where the candidate vectors each contain a FLAG insert at different sites within AAV9's VR-IV. All vectors were packaged with luciferase transgene in 10 mL culture to facilitate determining which insertion points did not interrupt capsid packaging; error bars represent standard error of the mean.

[00189] As seen, all candidates package with high efficiency.

6.4. Example 4 – Analysis of Surface FLAG exposure

[00190] **FIG. 4** depicts surface exposure of FLAG inserts in each of eight (8) candidate rAAV9 vectors (1090, 1091, 1092, 1093, 1094, 1095, 1096, and 1097), confirmed by immunoprecipitation of transduced vectors by binding to anti-FLAG resin. Binding to anti-FLAG indicates insertion points that allow formation of capsids that display the peptide insertion on the surface.

[00191] Transduced cells were lysed and centrifuged. 500 µL of cell culture supernatant was loaded on 20 µL agarose-FLAG beads and eluted with SDS-PAGE loading buffer also loaded directly on the gel. For a negative control, 293-ssc supernatant was used that contained no FLAG inserts.

[00192] As seen, 1090 had the lowest titer of the candidate vectors, indicating the least protein pulled down. Very low titers also were seen with the positive control. It is likely that not a sufficient amount of positive control had been loaded for visualization on SDS-PAGE.

6.5. Example 5 – Analysis of Transduction Efficiency

[00193] **FIGs. 5A-5B** depict transduction efficiency in Lec2 cells, transduced with capsid vectors carrying the luciferase gene as a transgene, that was packaged into either wild type AAV9 (9-luc), or into each of eight (8) candidate rAAV9 vectors (1090, 1091, 1092, 1093, 1094, 1095, 1096, and 1097); activity is expressed as percent luciferase activity, taking the activity of 9-luc as 100% (**FIG. 5A**), or as Relative Light Units (RLU) per microgram of protein (**FIG. 5B**).

[00194] CHO-derived Lec2 cells were grown in αMEM and 10% FBS. The Lec2 cells were transduced at a MOI of about $2x10^8$ GC vector (a MOI of about 10,000) and were treated with ViraDuctin reagent (similar results were observed on transducing Lec2 cells at a MOI of about

10,000 GC/cell but treated with 40 µg/mL zinc chloride ($ZnCl_2$); results not shown). Lec2 cells are proline auxotrophs from CHO.

[00195] As seen, transduction efficiency *in vitro* is lower than that obtained using wild type AAV9 (9-luc). Nonetheless, previous studies have shown that introduction of a homing peptide can decrease *in vitro* gene transfer in non-target cells (such as 293, Lec2, or HeLa), while significantly increasing *in vitro* gene transfer in target cells (*see*, *e.g.*, Nicklin *et al.* 2001; and Grifman *et al.* 2001).

6.6. Example 6 – Analysis of Packaging Efficiency as a Factor of Insertion Peptide Composition and Length

[00196] **FIG. 6A** depicts a bar graph illustrating that insertions immediately after S454 of AAV9 capsid (SEQ ID NO:67) of varying peptide length and composition may affect production efficiencies of AAV particles in a packaging cell line. Ten peptides of varying composition and length were inserted after S454 (between residues 454 and 455) within AAV9 VR-IV. qPCR was performed on harvested supernatant of transfected suspension HEK293 cells five days post-transfection. The results depicted in the bar graph demonstrate that the nature and length of the insertions may affect the ability of AAV particles to be produced at high titer and packaged in 293 cells. (Error bars represent standard error of the mean length of peptide, which is noted on the Y-axis in parenthesis.)

[00197] AAV9 vectors having a capsid protein containing a homing peptide of the following peptide sequences (**Table 3**) at the S454 insertion site were studied. Suspension-adapted HEK293 cells were seeded at $1x10^6$ cells/mL one day before transduction in 10mL of media. Triple plasmid DNA transfections were done with PEIpro® (Polypus transfection) at a DNA:PEI ratio of 1:1.75. Cells were spun down and supernatant harvested five days post-transfection and stored at -80°C.

Table 3.

Peptide#	Tissue or Target Designation	Peptide Sequence	SEQ ID NO:
P1	Bone1 (D8)	DDDDDDDD	2
P2	Brain1	LSSRLDA	3
P3	Brain2	CLSSRLDAC	4
P4	Kidney1	LPVAS	6
P5	Kidney2	CLPVASC	5
P6	Muscle1	ASSLNIA	7
P7	TfR1	HAIYPRH	10
P8	TfR2	THRPPMWSPVWP	11

Peptide#	Tissue or Target Designation	Peptide Sequence	SEQ ID NO:
P9	TfR3	RTIGPSV	12
P10	TfR4	CRTIGPSVC	13

[00198] qPCR was performed on harvested supernatant of transfected suspension HEK293 cells five days post-transfection. Samples were subjected to DNase I treatment to remove residual plasmid or cellular DNA and then heat treated to inactivate DNase I and denature capsids. Samples were titered via qPCR using TaqMan Universal PCR Master Mix, No AmpEraseUNG (ThermoFisherScientific) and primer/probe against the polyA sequence packaged in the transgene construct. Standard curves were established using RGX-501 vector BDS.

[00199] Peptide insertions directly after S454 ranging from 5 to 10 amino acids in length produced AAV particles having adequate titer, whereas an upper size limit is possible, with significant packaging deficiencies observed for the peptide insertion having a length of 12 amino acids.

6.7. Example 7 - Homing peptides alter the transduction properties of AAV9 in vitro when inserted after S454.

[00200] **FIGs. 6B-E** depict fluorescence images of cell cultures of (**FIG. 6B**) Lec2 cell line (sialic acid-deficient epithelial cell line) (**FIG. 6C**) HT-22 cell line (neuronal cell line), (**FIG. 6D**) hCMEC/D3 cell line (brain endothelial cell line), and (**FIG. 6E**) C2C12 cell line (muscle cell line). AAV9 wild type and S454 insertion homing peptide capsids of **Table 3** containing GFP transgene were used to transduce the noted cell lines.

[00201] Cell lines were plated at 5-20x10^3 cells/well (depending on the cell line) in 96-well 24 hours before transduction. Cells were transduced with AAV9-GFP vectors (with or without insertions) at 1x10^{10} particles/well and analyzed via Cytation5 (BioTek) 48-96 hours after transduction, depending on the difference in expression rate in each cell line. Lec2 cells were cultured as in Example 5, blood-brain barrier hCMEC/D3 (EMD Millipore) cells were cultured according to manufacturer's protocol, HT-22 and HUH7 cells were cultured in DMEM and 10% FBS, and C2C12 myoblasts were plated in DMEM and 10% FBS and differentiated for three days pre-transfection in DMEM supplemented with 2% horse serum and 0.1% insulin. AAV9.S454.FLAG showed low transduction levels in every cell type tested.

[00202] Images show that homing peptides can alter the transduction properties of AAV9 *in vitro* when inserted after S454 in the AAV9 capsid protein, as compared to unmodified AAV9 capsid. P7 (TfR1 peptide, HAIYPRH (SEQ ID NO:10)) for all cell lines show the highest rate of transduction followed by P9 (TfR3 peptide, RTIGPSV (SEQ ID NO:12)). P4 (Kidney1 peptide, LPVAS (SEQ ID NO:6)) showed a slightly higher rate of transduction than that of AAV9 wildtype for all cell types. Higher transduction rates were observed for P6 (Muscle1 peptide, ASSLNIA (SEQ ID NO:7)) in the brain endothelial hCMEC/D3 cell line and the C2C12 muscle cell line cultures as compared to the Lec2 and HT-22 cell line cultures. P1 vector was not included in images due to extremely low transduction efficiency, and P8 vector was not included due to low titer.

6.8. Example 8 – Analysis of AAV capsids for peptide insertion points

[00203] **FIG. 7** depicts alignment of AAVs 1-9e, rh10, rh20, rh39, rh74, hu12, hu21, hu26, hu37, hu51 and hu53 capsid sequences within insertion sites for capsid sequences within insertion sites for human peptides within or near the initiation codon of VP2, variable region 1 (VR-I), variable region 4 (VR-IV), and variable region 8 (VR-VIII) highlighted in grey; a particular insertion site within variable region eight (VR-VIII) of each capsid protein is shown by the symbol "#" (after amino acid residue 588 according to the amino acid numbering of AAV9).

6.9. Example 9 – Comparison of AAV Genome Copies/μg genomic DNA of Various Vectors

[00204] **FIG. 8** depicts copies of GFP (green fluorescent protein) transgene expressed in mouse brain cells, following administration of the AAV vectors: AAV9; AAV.PHP.eB; AAV.hDyn (AAV9 with TLAAPFK (SEQ ID NO:1) between 588-589 with no other amino acid modifications to the capsid sequence); AAV.PHP.S; and AAV.PHP.SH (see **Table 17**).

[00205] AAV.PHP.B is a capsid having a TLAVPFK (SEQ ID NO:20) insertion in AAV9 capsid, with no other amino acid modifications to the capsid sequence. AAV.PHP.eB is a capsid having a TLAVPFK (SEQ ID NO:20) insertion in AAV9 capsid, with two amino acid modifications of the capsid sequence upstream of the PHP.B insertion (see also **Table 17**). **Table 4A** summarizes the capsids utilized in the study.

Table. 4A

Name	**Parent capsid**	**Mutation**	**Location of insertion 2**	**Peptide 2**	**SEQ ID NO:**
AAV9	AAV9	-	-	-	
PHP.B	AAV9	-	588_589	TLAVPFK	20
PHP.eB	AAV9	586A_587Q delinsDG	588_589	TLAVPFK	20
AAV.hDyn	AAV9	-	588_589	TLAAPFK	1
AAV.PHP.S	AAV9	-	588_589	QAVRTSL	16
AAV.PHP.SH	AAV9	-	588_589	QAVRTSH	17

Materials and Methods

[00206] Constructs of AAV9, AAV.PHPeB, AAV.hDyn, AAV.PHP.S and AAV.PHP.SH encoding GFP transgene were prepared and formulated in 1xPBS + 0.001% Pluronic. Female C57BL/6 mice were randomized into treatment groups base on Day 1 bodyweight. Five groups of female C57BL/6 mice were each intravenously administered AAV9.GFP, AAV.PHPeB.GFP, AAV.hDyn.GFP, AAV.PHP.S.GFP or AAV.PHP.SH.GFP in accordance with **Table 4B**, below. The dosing volume was 10 mL/kg (0.200 mL/20 g mouse). The mice were 8-12 weeks of age at the start date. At day 15 post administration, the animals were euthanized, and peripheral tissues were collected, including brain tissue, liver, forelimb biceps, heart, kidney, lung, ovaries, and the sciatic nerve.

Table 4B

Gr.	**N**	**Agent**	**Formulation dose**	**Route**	**Schedule**
1	9	AAV9	2.5E12 GC/kg	iv	day 1
2	5	PHPeB	2.5E12 GC/kg	iv	day 1
3	5	hDyn	2.5E12 GC/kg	iv	day 1
4	5	PHP.S	2.5E12 GC/kg	iv	day 1
5	5	PHP.SH	2.5E12 GC/kg	iv	day 1

[00207] Quantitiative PCR (qPCR) was used to determine the number of vector genomes per µg of brain genomic DNA. Brain samples from injected mice were processed and genomic DNA was isolated using Blood and Tissue Genomic DNA kit from Qiagen. The qPCR assay was run on a QuantStudio 5 instrument (Life Technologies Inc) using primer-probe combination specific for eGFP following a standard curve method.

[00208] The AAV vector genome copies per µg of brain genomic DNA was at least a log higher in mice that were administered AAV.hDyn compared to all other AAV serotypes: AAV9, AAV.PHPeB, PHP.S, and PHP.SH (see **FIG. 8**). As seen in this study, GC/µg genomic DNA is highest for AAV.hDyn, which is AAV9 capsid containing the "TLAAPFK" (SEQ ID NO:1) peptide insert (a peptide from human axonemal dynein) between residues 588-589 of the AAV9 capsid. The study demonstrated transduction in mouse brain at greater than 1E04 GC/µg transgene on average in 5 mice systemically administered AAV.hDyn carrying eGFP. Other modified AAV9 capsids, however, including the vector AAV.PHPeB, which contains the "TLAVPFK" (SEQ ID NO:20) sequence (a peptide from mouse dynein) demonstrated transduction in mouse brain at less than 1E03 GC/µg transgene upon systemic treatment.

6.10. Example 10 – Construction of rAAV Capsid containing TLAAPFK (SEQ ID NO: 2)

[00209] **FIG. 9A** depicts the amino acid sequence for a recombinant AAV9 vector capsid including a peptide insertion of amino acid sequence TLAAPFK (SEQ ID NO:1) between Q588 and A589 of VR-IIIV . Inserted peptide in bold.

[00210] **FIG. 9B** depicts the amino acid sequence for a recombinant AAV9 vector capsid including a peptide insertion of amino acid sequence TLAAPFK (SEQ ID NO:1) between S268 and S269 of VR-III. Inserted peptide in bold.

[00211] **FIG. 9C** depicts the amino acid sequence for a recombinant AAV9 vector capsid including a peptide insertion of amino acid sequence TLAAPFK (SEQ ID NO:1) between S454 and G455 of VR-IV. Inserted peptide in bold.

6.11. Example 11: Assessment of Modified Capsids *in vitro* and *in vivo*

[00212] AAV capsid sequences were modified either by peptide insertions or guided mutagenesis and pooled to give a bar-coded library packaged with a GFP expression cassette. The modified vectors were then evaluated in an *in vitro* assay, as well as for *in vivo* bio-distribution in mice using next generation sequencing (NGS) and quantitative PCR. AAV.hDyn was identified as a high brain transduction vector from this pool and was further evaluated in individual delivery studies in mice to characterize its transduction profile. Additionally, immunohistochemistry analysis of brain sections was performed to understand the cellular tropism of this vector.

6.11.1 Example 11A – *In vitro* testing of transduction an crossing blood brain barrier

[00213] The ability of the modified capsids to cross the blood brain barrier was tested in an *in vitro* transwell assay using hCMEC/D3 BBB cells (SCC066, Millipore-Sigma) (see **FIGs. 10A-10B**). More specifically, the assay was essentially adapted from Sade, H. *et al.* (2014 PLoS ONE 9(4): e96340) A human Blood-Brain Barrier transcytosis assay reveals Antibody Transcytosis influenced by pH-dependent Receptor Binding, April 2014, Vol. 9, Issue 4; and Zhang, X., Blood-brain barrier shuttle peptides enhance AAV transduction in the brain after systemic administration, 2018 *Biomaterials* 176: 71–83. Briefly, 5x10^4 hCMEC/D3 cells/cm^2 were seeded in collagen-coated transwell inserts in a 12-well plate. Each insert contained 500 µL media and the lower chamber contained 1 mL media. Media was replaced every second day. The supernatant was removed at 10 days post-seeding (the zero (0) time point). At this 0 time point, the cells were transduced by adding 1x10^9 GC of vector to the upper insert chamber media. 10µL lower chamber supernatant samples were removed for testing at intervals 0.5, 3, 6, and 23 hours post-transduction. Each condition (vector) was tested in duplicate, and measured for titer via qPCR against PolyA in triplicate.

[00214] **FIGS. 10A-10B** depict an *in vitro* transwell assay for AAV.hDyn (AAV9 with TLAAPFK (SEQ ID NO:1) between amino acid residues 588-589) crossing a blood brain barrier (BBB) cell layer **(FIG. 10A)**, and results showing that AAV.hDyn (indicated by inverted triangles in the figure) crosses the BBB cell layer of the assay faster than AAV9 (squares), as well as faster and to a greater extent than AAV2 (circles) **(FIG. 10B)**. The developed *in vitro* assay predicted enhanced BBB cross-trafficking and similar assays can be used to predict targeting to other organs as well.

6.11.2 Example 11B – Transduction and Biodistribution of modified capsids

6.11.2.1 Materials and Methods

[00215] Capsid modifications were performed on widely used AAV capsids including AAV8, AAV9, and AAVrh.10 by inserting various peptide sequences after the position S454 of the VR-IV (**Tables 5a-5c**) or after position Q588 of the VR-VIII surface exposed loop of the AAV capsid, as well as insertions after the initiation codon of VP2, which begins at amino acid 137 (AAV4, AAV4-4, and AAV5) or at amino acid 138 (AAV1, AAV2, AAV3, AAV3-3, AAV6, AAV7, AAV8, AAV9, AAV9e, rh.10, rh.20, rh.39, rh.74, and hu.37) **(FIG. 7)** (see also **Table 17** for certain capsid sequences). Selected single to multiple amino acid mutations were also used for modifying the capsids. See also, Yost *et al.*, Structure-guided engineering of surface exposed loops on AAV Capsids. 2019. ASGCT Annual Meeting; and Wu *et al.*, 2000 *J. Virology* (*supra*). It was confirmed that packaging efficiency was not negatively impacted following any of these capsid modifications in small scale.

[00216] rAAVs with certain modified capsids were tested for transduction *in vitro* in Lec2 cells as described above in Example 5. Modified AAVs tested for transduction in Lec2 cells as follows: eB 588 Ad, eB 588 Hep, eB 588 p79, eB 588 Rab, AAV9 588 Ad, AAV9 588 Hep, AAV9 588 p79, AAV9 588 Rab, eB VP2 Ad, eB VP2 Hep, eB VP2 p79, eB VP2 Rab, AAV9 VP2 Ad, AAV9 VP2 Hep, AAV9 VP2 p79, AAV9 VP2 Rab as compared to AAV9. See **Table 5B** below for identity of AAV capsids.

[00217] To test biodistribution, modified AAVs were packaged with an eGFP transgene cassette containing specific barcodes corresponding to each individual capsid. Novel barcoded vectors were pooled and injected into mice in order to increase the efficiency of screening.

[00218] To analyse the bio-distribution of genetically altered AAV vectors, various vectors encoding GFP were prepared and formulated in 1xPBS + 0.0001% Pluronic acid. All vectors were made with cis plasmids containing a ten (10) bp barcode to enable next-generation sequencing (NGS) library (pool) preparation. Three (3) vector pools (Study 1, Study 2 and Study 3 vectors) were injected intravenously into a cohort of 5 female C57Bl/6 mice in accordance with **Tables 5A-C**. The dosing volume was 10 mL/kg (0.2mL/20g mouse) for each.

[00219] The mice were randomized into treatment groups based on Day 1 bodyweight and their age at start date was 8-12 weeks. At day 15 post administration, the animals were euthanized and peripheral tissues were collected, including brain, kidney, liver, sciatic nerve, lung, heart, and muscle tissue. In the studies where selected capsids from the pool were injected individually, the same protocol was followed

[00220] Genomic DNA (gDNA) was isolated from tissue samples using DNeasy Blood and Tissue kit (69506) from Qiagen. Each vector's barcode region was amplified with primers containing overlaps for NGS and unique dual indexing (UDI) and multiplex sequencing strategies, as recommended by the manufacturer (Illumina). Illumina MiSeq using reagent nano and micro kits v2 (MS-103-1001/1002) were used to determine the relative abundance of each barcoded AAV vector per sample collected from the mice. Accordingly, each vector sample in **Tables 5A-C** below was barcoded as noted above to allow for each read to be identified and sorted before the final data analysis. The data was normalized based on the composition of AAVs in the originally injected pool and quantified using the total genome copy number obtained from qPCR analysis with a primer-probe combination specific to the barcoded sample.

Table 5A

Study 1	**Name**	**Capsid**	**Insertion Point**	**Peptide**	**Notes**
BC01	AAV9	AAV9	-	-	Blue bar**, FIG. 21**
BC02	PHP.eB	PHP.eB	588_589	TLAVPFK (SEQ ID NO:20)	
BC03	AAV8.BBB	Modified AAV8	-	-	A269S
BC04	AAV9.BBB	Modified AAV9	-	-	S263G/S269T/A273T
BC05	AAV8.BBB.LD	Modified AAV8	-	-	A269S, 498-NNN/AAA-500
BC06	AAV9.BBB.LD	Modified AAV9	-	-	S263G/S269T/A273T, 496-NNN/AAA-498
BC07	rh.10	rh.10	-	-	
BC08	rh.10.LD	Modified rh.10	-	-	498-NNN/AAA-500
BC09	AAV.hDyn	modifiedAAV9	588_589	TLAAPFK (SEQ ID NO:1)	Orange bar, **FIG. 21**
BC10	PHP.S	PHP.S	588_589	QAVRTSL (SEQ ID NO:16)	-
BC11	PHP.SH	PHP.SH	588_589	QAVRTSH (SEQ ID NO:17)	-
BC13	rh39	rh.39	-	-	-

Table 5B

Study 2	Name	Capsid	Insertion Point	Peptide	Notes
BC20	eB 588 Ad	PHP.eB	588_589	SITLVKSTQTV (SEQ ID NO:14)	Replaces TLAVPFK peptide (SEQ ID NO:20)
BC21	eB 588 Hep	PHP.eB	588_589	TILSRSTQTG (SEQ ID NO:15)	Replaces TLAVPFK peptide (SEQ ID NO:20)
BC22	eB 588 p79	PHP.eB	588_589	VVMVGEKPITITQ HSVETEG (SEQ ID NO:18)	Replaces TLAVPFK peptide (SEQ ID NO:20)
BC23	eB 588 Rab	PHP.eB	588_589	RSSEEDKSTQTT (SEQ ID NO:19)	Replaces TLAVPFK peptide (SEQ ID NO:20)
BC24	9 588 Ad	AAV9	588_589	SITLVKSTQTV (SEQ ID NO:14)	
BC25	9 588 Hep	AAV9	588_589	TILSRSTQTG (SEQ ID NO:15)	
BC26	9 588 p79	AAV9	588_589	VVMVGEKPITITQ HSVETEG (SEQ ID NO:18)	
BC27	9 588 Rab	AAV9	588_589	RSSEEDKSTQTT (SEQ ID NO:19)	
BC28	eB VP2 Ad	PHP.eB	138_139	SITLVKSTQTV (SEQ ID NO:14)	Also has TLAVPFK (SEQ ID NO:20) insert after residue 588
BC29	eB VP2 Hep	PHP.eB	138_139	TILSRSTQTG (SEQ ID NO:15)	Also has TLAVPFK (SEQ ID NO:20) insert after residue 588

Study 2	Name	Capsid	Insertion Point	Peptide	Notes
BC30	eB VP2 p79	PHP.eB	138_139	VVMVGEKPITITQ HSVETEG (SEQ ID NO:18)	Also has TLAVPFK (SEQ ID NO:20) insert after residue 588
BC31	AAV9	AAV9	-	-	
BC32	eB VP2 Rab	PHP.eB	138_139	RSSEEDKSTQTT (SEQ ID NO:19)	Also has TLAVPFK (SEQ ID NO:20) insert after residue 588
BC33	9 VP2 Ad	AAV9	138_139	SITLVKSTQTV (SEQ ID NO:14)	
BC34	9 VP2 Hep	AAV9	138_139	TILSRSTQTG (SEQ ID NO:15)	
BC35	9 VP2 p79	AAV9	138_139	VVMVGEKPITITQ HSVETEG (SEQ ID NO:18)	
BC36	9 VP2 Rab	AAV9	138_139	RSSEEDKSTQTT (SEQ ID NO:19)	

Table 5C

Study 3	Name	Capsid	Insertion Point	Peptide	Notes
BC01	AAV9	AAV9	-	-	
BC03	AAV8-BBB	AAV8	-	-	A269S
BC07	rh10	rh.10	-	-	
BC09	AAV.hDyn	AAV.hDyn	588_589	TLAAPFK (SEQ ID NO:1)	
BC12	PHP.B	PHP.B	588_589	TLAVPFK (SEQ ID NO:20)	

Study 3	**Name**	**Capsid**	**Insertion Point**	**Peptide**	**Notes**
BC20	AAV9 S454-D8	AAV9	454_455	DDDDDDDD (SEQ ID NO:2)	
BC22	AAV9 S454-Brain1	AAV9	454_455	LSSRLDA (SEQ ID NO:3)	
BC23	AAV9 S454-Brian1C	AAV9	454_455	CLSSRLDAC (SEQ ID NO:4)	
BC24	AAV9 S454-Kidney1	AAV9	454_455	LPVAS (SEQ ID NO:6)	
BC25	AAV9 S454-Kidney1C	AAV9	454_455	CLPVASC (SEQ ID NO:5)	
BC26	AAV9 S454-Muscle1	AAV9	454_455	ASSLNIA (SEQ ID NO:7)	
BC27	AAV9 S454-TfR1	AAV9	454_455	HAIYPRH (SEQ ID NO:10)	
BC29	AAV9 S454-TfR3	AAV9	454_455	RTIGPSV (SEQ ID NO:12)	
BC30	AAV9 S454-TfR4	AAV9	454_455	CRTIGPSVC (SEQ ID NO:13)	
BC31	AAV9 S454-FLAG	AAV9	454_455	DYKDDDDK (SEQ ID NO:21)	
BC37	pRGX1005-PHP.eB (no BC)	PHP.eB	588_589	TLAVPFK (SEQ ID NO:20)	

[00221] In the studies where selected capsids from the pool were injected individually, qPCR was used to determine the number of vector genomes per µg of tissue genomic DNA. qPCR was done on a QuantStudio 5 (Life Technologies, Inc.) using primer-probe combination specific for eGFP following a standard curve method (**FIG. 12**).

[00222] From the study where individual vectors were injected into mice for characterization, formalin fixed mouse brains were sectioned at 40μm thickness on a vibrating blade microtome (VT1000S, Leica) and the floating sections were probed with antibodies against GFP to look at the cellular distribution of the delivered vectors.

[00223] More specifically, fixed brains from the mice injected with AAV.hDyn were sectioned using a Vibratome (Leica, VT-1000) and the GFP expression was evaluated using an anti-GFP antibody (AB3080, Millipore Sigma), Vectastain ABC kit (PK-6100, Vector Labs) and DAB Peroxidase kit (SK-4100, Vector Labs). Broad distribution of GFP expressing cells were present throughout the brain in mice injected with AAV.hDyn, including distribution in the cortex, striatum, and hippocampus of the brain. **FIGS. 13A-13C** show the images from these regions and the scale bar is 400um (discussed below).

6.11.2.2 Results

[00224] Results are shown in **FIG. 11**, **FIGs. 12A-12H**, and **FIGs. 13A-13C**.

[00225] Data for the Lec2 cell transduction assay not shown. The AAV9 588 Hep (AAV9 with the peptide TILSRSTQTG (SEQ ID NO:15) 5 inserted after position 588) exhibited significantly greater transduction (4-fold) than wild type AAV9, and AAV9 VP2 Ad (AAV9 with the peptide SITLVKSTQTV (SEQ ID NO:14) inserted after position 138), AAV9 VP2 Hep (AAV9 with the peptide TILSRSTQTG (SEQ ID NO:15) inserted after position 138), and AAV9 VP2 Rab (AAV9 with the peptide RSSEEDKSTQTT (SEQ ID NO:19) inserted after position 138) exhibited slightly greater transduction of the Lec2 cells relative to AAV9. The other AAVs assayed exhibited lower levels of transduction than AAV9.

[00226] **FIG. 11** depicts results of Next Generation Sequencing (NGS) analysis of brain gDNA, revealing relative abundances (percent composition) of the capsid pool delivered to mouse brains following intravenous injection. The data was normalized based on the composition of AAVs in the originally injected pool and quantified using the total genome copy number obtained from qPCR analysis with a primer-probe combination specific to the eGFP sequence. Data shown are from three different experiments. Dotted lines indicate which vectors were pooled together. Parental AAV9 was used as standard and included in each pool. The “BC” identifiers are as indicated in Tables 5A, 5B and 5C above.

[00227] **FIGs. 12A-12H** depict an *in vivo* transduction profile of AAV.hDyn in female C57Bl/6 mice, showing copy number/microgram gDNA in naïve mice, or mice injected with either AAV9 or AAV.hDyn in brain (**FIG. 12A**), liver (**FIG. 12B**), heart (**FIG. 12C**), lung (**FIG. 12D**), kidney (**FIG. 12E**), skeletal muscle (**FIG. 12F**), sciatic nerve (**FIG. 12G**), and ovary (**FIG. 12H**), where AAV.hDyn shows increased brain bio-distribution compared to AAV9. The AAV vector genome copies per µg of brain genomic DNA was at least a log higher in mice that were administered AAV.hDyn compared to the parental AAV9 vector.

[00228] **FIGs. 13A-13C** show images from the regions analysed in the Immunohistochemical Analysis described above; scale bar is 400 µm. **FIGs. 13A-13C** depict distribution of GFP from AAV.hDyn throughout the brain, where images of immunohistochemical staining of brain sections from the striatum (**FIG. 13A**), hippocampus (**FIG. 13B**), and cortex (**FIG. 13C**) revealed a global transduction of the brain by the modified vector.

6.11.2.3 Conclusions

[00229] AAV capsid modifications performed either by insertions in surface exposed loops of VR-IV and VR-VIII or by specific amino acid mutations did not affect their packaging efficiency and were able to produce similar titers in the production system described herein.

[00230] Intravenous administration of AAV.hDyn to mice resulted in higher relative abundance of the viral genome and greater brain cell transduction than other modified AAV vectors and AAV9 tested.

Table 6. Homing peptides used in biodistribution study

Name	**Capsid**	**Location of Peptide Insertion**	**Peptide Name**	**Peptide Sequence**	**SEQ ID NO:**
AAV9	AAV9	454_455	-	-	
AAV9 S454-P2	AAV9	454_455	Brain1	LSSRLDA	3
AAV9 S454-P3	AAV9	454_455	Brain2 (Brain1C)	CLSSRLDAC	4
AAV9 S454-P4	AAV9	454_455	Kidney1	LPVAS	6
AAV9 S454-P5	AAV9	454_455	Kidney2 (Kidney 1C)	CLPVASC	5
AAV9 S454-P6	AAV9	454_455	Muscle1	ASSLNIA	7

Name	**Capsid**	**Location of Peptide Insertion**	**Peptide Name**	**Peptide Sequence**	**SEQ ID NO:**
AAV9 S454-P7	AAV9	454_455	Tfr1	HAIYPRH	10
AAV9 S454-P9	AAV9	454_455	Tfr3	RTIGPSV	12
AAV9 S454-P10	AAV9	454_455	Tfr4	CRTIGPSVC	13

[00231] AAV capsid modifications performed by insertions of different homing peptides in surface exposed loop VR-IV did not affect their packaging efficiency and were able to produce similar titers in the production system described herein.

[00232] Intravenous administration of AAV9 S454 Kidney1 and AAV9 S454 Kidney1C to mice resulted in higher relative abundance of the viral genome and greater kidney cell transduction than other modified AAV9 vectors and the parental AAV9 vector tested. Intravenous administration of the AAV9 S454 Kidney1 or AAV9 S454 Muscle1 vector to mice resulted also in lower liver cell transduction.

6.12. Example 12– Construction of rAAV Capsid containing TLAVPFK (SEQ ID NO:20)

[00233] **FIG. 25** depicts the amino acid sequence for a recombinant AAV9 vector capsid including a peptide insertion of amino acid sequence TLAVPFK (SEQ ID NO:20) between S454 and G455 of VR-IV.

6.13. Example 13 – Biodistribution of an rAAV Vector Pool in Cynomolgus Monkeys

[00234] The administration, *in vivo* and post-mortem observations, and biodistribution of a pool of recombinant AAVs having engineered capsids and a GFP transgene will be evaluated following a single intravenous, intracerebroventricular or intravitreal injection in cynomolgus monkeys (**Table 7**). The pool contains multiple capsids each of which contains a unique barcode identification allowing identification using next generation sequencing (NGS) analysis following administration to cynomolgus monkeys. The cynomolgus monkey is chosen as the test system because of its established usefulness and acceptance as a model for AAV biodistribution studies in a large animal species and for further translation to human. All animals on this study are naïve with respect to prior treatment. The pool may comprise at least the following recombinant AAVs having the engineered capsids listed in **Table 7**.

Table 7. Recombinant AAVs for Cynomolgus monkey study

Name	Capsid	Capsid modification	Location of insertion	Peptide	Peptide SEQ ID NO:
AAV8	AAV8	-	-	-	
AAV8.BBB	Modified AAV8	A269S	-	-	
AAV8.BBB.LD	Modified AAV8	A269S, 498-NNN/AAA-500	-	-	
AAV9	AAV9	-	-	-	
AAV9 S454-Brain1	AAV9	-	454_455	LSSRLDA	3
AAV9 S454-Brain1C	AAV9	-	454_455	CLSSRLDAC	4
AAV9 S454-D8	AAV9	-	454_455	DDDDDDDD	2
AAV9 S454-Kidney1	AAV9	-	454_455	LPVAS	6
AAV9 S454-Kidney1C	AAV9	-	454_455	CLPVASC	5
AAV9 S454-Muscle1	AAV9	-	454_455	ASSLNIA	7
AAV9 S454-Tfr1	AAV9	-	454_455	HAIYPRH	10
AAV9 S454-Tfr3	AAV9	-	454_455	RTIGPSV	1219
AAV9 S454-TfR3C	AAV9	-	454_455	CRTIGPSVC	13
AAV9.496NNN/AAA498	Modified AAV9	498-NNN/AAA-500	-	-	
AAV9.496NNN/AAA498.W503R	Modified AAV9	498-NNN/AAA-500, W503R	-	-	
AAV9.N272A.496NNN/AAA498	Modified AAV9	N272A, 496-NNN/AAA-498			
AAV9.G266A.496NNN/AAA498	Modified AAV9	G266A, 496-NNN/AAA-498			
AAV9.588Ad	AAV9	-	588_589	SITLVKSTQTV	14
AAV9.588Herp	AAV9	-	588_589	TILSRSTQTG	15
AAV9.BBB	Modified AAV9	S263G/S269T/A273T	-	-	

Name	**Capsid**	**Capsid modification**	**Location of insertion**	**Peptide**	**Peptide SEQ ID NO:**
AAV9.BBB.LD	Modified AAV9	S263G/S269T/A273T, 496-NNN/AAA-498	-	-	
AAV9.Q474A	Modified AAV9	Q474A	-	-	
AAV9.W503R	Modified AAV9	W503R	-	-	
AAVPHPeB.VP2Ad	PHP.eB	-	138_139	SITLVKSTQTV	14
AAVPHPeB.VP2Herp	PHP.eB	-	138_139	TILSRSTQTG	15
PHP.B	AAV9	-	588_589	TLAVPFK	20
PHP.eB	Modified PHP.B	A587D, Q588G	588_589	TLAVPFK	20
PHP.hB					
PHP.S	AAV9	-	588_589	QAVRTSL	16
PHP.SH	AAV9	-	588_589	QAVRTSH	17

6.13.1. Study Design

[00235] Nine female cynomolgus animals will be used. Animals judged suitable for experimentation based on clinical sign data and prescreening antibody titers will be placed in study groups by body weight using computer-generated random numbers. Three different routes of administration will be used and relevant tissues collected to evaluate the biodistribution (measured by NGS and PCR) associated with the different routes. Three animals will be implanted with a catheter in the left lateral ventricle for intracerebroventricular (ICV) dose administration (Group 1), three animals will receive a single intravenous infusion (Group 2) and three animals will receive a single intravitreal injection (Group 3). Two animals will serve as replacement animals and will be implanted if required. Animals in Group 1 will have an MRI scan to determine coordinates for proper ICV catheter placement.

[00236] The IV infusion will be administered at a rate of 3 mL/min followed by 0.2 mL of vehicle to flush the dose from the IV catheter. The three intravenous animals will receive a single dose of the pooled recombinant AAVs at a volume of 4 mL/kg. The total dose (vg) and dose volume (mL/kg) will be recorded in the raw data. Based on literature review and previous studies in non-human primates, the IV dose of 1×10^{13} GC/kg body weight was determined to be required to have the desired distribution in the CNS from a systemic delivery as well as the peripheral tissues including skeletal muscle.

[00237] The ICV implanted animals will receive a single bolus dose at a volume of 1 mL of AAV-NAV-GFPbc (by slow infusion, approximately 0.1 mL/min) followed by 0.1 mL of vehicle to flush the dose from the catheter system. The ICV dose is based on distribution data from a previous non-human primate study to support current clinical programs.

[00238] The intravitreal (IVT) injection will be administered bilateral as a bolus injection at a dose volume of 50 μL.

6.13.2. Observations and Examinations

[00239] Clinical signs will be recorded at least once daily beginning approximately two weeks prior to initiation of dosing and continuing throughout the study period. The animals will be observed for signs of clinical effects, illness, and/or death. Additional observations may be recorded based upon the condition of the animal at the discretion of the Study Director and/or technicians.

[00240] Ophthalmological examinations will be performed on Group 3 animals prior to dose administration, and on Days 2, 8, 15 and 22. All animals will be sedated with ketamine hydrochloride IM for the ophthalmologic examinations performed following Day 1. For the examinations on Day 1, the animals will be sedated with injectable anesthesia (refer to Section 15.3.3). The eyes will be dilated with 1% tropicamide prior to the examination. The examination will include slit-lamp biomicroscopy and indirect ophthalmoscopy. Additionally, applanation tonometry will be performed on Group 3 animals prior to dosing, immediately following dose administration (~10 to 15 minutes) and on Days 2 and 22.

[00241] Blood samples (~3 mL) will be collected from a peripheral vein for neutralizing antibodies analysis approximately 2 to 3 weeks prior to dose administration.

6.13.3. Bioanalytical Sample Collection

[00242] Whole blood samples (~0.5 mL) will be collected from a peripheral vein for bioanalytical analysis (AAV capsid clearance) prior to dose administration, 3 (±10 minutes), 6 (±10 minutes) and 24 (±0.5 hour) hours following dose administration from animals in Group 2 (IV) only. The samples will be collected using a syringe and needle, transferred to two K_2 EDTA tubes and the times recorded.

[00243] Blood samples (~5 mL) will be collected from fasted animals from a peripheral vein for PBMC analysis prior to dose administration (Day 1), on Days 8 and 15 and prior to necropsy (Day 22). The samples will be obtained using lithium heparin tubes and the times recorded.

[00244] Blood samples will be collected from a peripheral vein for bioanalytical analysis prior to dose administration (Day 1, 2 mL) and necropsy (Day 22, 5 mL). The samples will be collected in clot tubes and the times recorded. The tubes will be maintained at room temperature until fully clotted, then centrifuged at approximately 2400 rpm at room temperature for 15 minutes. The serum will be harvested, placed in labeled vials (necropsy sample split into 1 mL aliquots), frozen in liquid nitrogen, and stored at -60°C or below.

[00245] CSF (~1.5 mL) will be collected prior to dose administration from a cisterna magna spinal tap from animals in Group 1 only. CSF (~2 mL) will be collected immediately prior to necropsy from a cisterna magna spinal tap from all animals (Groups 1 to 3). An attempt to collect CSF will be made but due to unsuccessful spinal taps, samples may not be collected at all intervals from an animal(s). Upon collection, the samples will be stored on ice until processing.

6.13.4. Necroscopy

[00246] A gross necropsy will be performed on any animal found dead or sacrificed moribund, and at the scheduled necropsy, following at least 21 days of treatment (Day 22). All animals, except those found dead, will be sedated with 8 mg/kg of ketamine HCl IM, maintained on an isoflurane/oxygen mixture and provided with an intravenous bolus of heparin sodium, 200 IU/kg. The animals will be perfused via the left cardiac ventricle with 0.001% sodium nitrite in saline. Animals found dead will be necropsied but will not be perfused.

[00247] The following tissues will be saved from all animals (including those found dead): Bone marrow, brain, cecum, colon, dorsal nerve roots and ganglion, duodenum, esophagus, eyes with optic nerves, gross lesions, heart, ileum, jejunum, kidneys, knee joint, liver, lungs with bronchi, lymph nodes, ovaries, pancreas, sciatic nerve, skeletal muscle, spinal cord, spleen, thyroids, trachea, and vagus nerve.

6.13.5. Bioanalytical Analysis

[00248] The whole blood collected from animals in Group 2 (IV) will be evaluated by qPCR and Next-Generation Sequencing (NGS).

[00249] PBMC samples collected from all animals will be evaluated by flow cytometry and enzyme-linked immune absorbent spot (ELISpot), if required.

[00250] The presence of circulating neutralizing antibodies as well as free vector in the serum and/or CSF will be evaluated by ELISA and cell based assays, as needed.

[00251] The vector copy number and number of transcripts in tissues will be examined by quantitative PCR and NGS methods.

6.14. Example 14 -Study of CNS Biodistribution with Intravenous Administration

[00252] A procedure like that described in Example 13 was used to study the biodistribution of a pool of rAAV capsids administered intravenously to cynomolgus monkey model. Several capsids exhibited good spread in CNS with high relative abundance (RA, compared to AAV9 reference capsid) in most brain regions, notably AAV4, AAV5, rh 34, hu 26, rh31, and hu13. Favorable capsids exhibiting CNS-tropism have DNA RA values resulting in greater than 1.1-fold increase in DNA values in at least one CNS region, except dorsal root ganglion (DRG).

[00253] **FIG. 15** depicts the relative abundance (RA) of the viral genomes (normalized to input) in the frontal cortex of the cynomolgus monkey model, and **Table 8** lists the RA values for those capsids with the highest RA shown in FIG. 15.

Table 8:

Sample No.	Serotype	Relative Abundance	p-value
BC085	AAV4	32643.06	<0.0001
BC086	AAV5	836.64	0.0043
BC076	AAV.rh34	735.19	0.0296
BC049	AAV.hu26	606.37	ns
BC059	AAV.hu56	518.54	ns
BC057	AAV.hu53	444.2	ns
BC088	AAV7	427.28	ns
BC003	AAV8.BBB	359.84	ns
BC044	AAV.hu13	341.58	ns
BC075	AAV.rh31	339.86	ns

[00254] . **FIGS. 16 and 17** depict the RA of the viral genomes (normalized to input) in the hippocampus and the cerebellum of the cynomolgus monkey model, respectively. The RA of AAV.rh34 is shown by the shaded column on the left side of the graphs and the RA of AAV9 reference is showed by the shaded column in the middle or the graphs. FIGS. 16 and 17 show that AAV.rh34 is a top performing capsid in the intravenous administration pool

[00255] AAV.rh34, displayed a favorable profile with respect to CNS toxicity as well. The rh34 capsid displayed decreased transduction in dorsal root ganglion (DRG) while exhibiting a high frontal cortex tropism (transduction efficiency). AAVrh34 exhibits an increased RA to AAV9 in CNS regions as follows: 1.8-fold in Hippocampus, 7.4-fold in frontal cortex, 1.9-fold in amygdala, 6.0-fold in medulla, 3.1-fold in midbrain, 1.2-fold in hypothalamus, 8.8-fold in thalamus, 13-fold in globus pallidus, 5.7-fold in SNc, 3.5-fold in dorsal raphe, 2.0-fold in claustrum, 13-fold in putamen, 9-fold in occipital cortex, and 9.6-fold in cerebellum. Additionally, AAVrh34 exhibits a decreased RA in: DRGs: 90-99.5% ,Liver: ~99%, Biceps: ~30%, Sciatic nerve: 83%, and Optic nerve: 17%.

[00256] **FIG. 18** depicts a Venn diagram of the: top 45 performers in FC (highest RA to AAV9), and bottom 45 performers in the cervical, thoracic, and lumbar DRGs (lowest RA to AAV9) and the AAVrh34 capsid is shown as the only capsid that was present in each group of 45 amongst the pool of capsids. AAV capsids with a combination of these recited characteristics are considered "DRG-friendly" capsids, such that their low rate of transduction in DRG should have minimal neurotoxicity and/or reduced or negligible axonopathy symptoms in a subject administered the AAV capsid.

6.15. Example 15: Study of CNS Biodistribution with Intracerebroventricular (ICV) Administration

[00257] A procedure like that described in Example 13 with ICV administration was used to study the biodistribution of a pool of rAAV capsids to cynomolgus monkey model. Several capsids exhibited good spread in CNS with high relative abundance (RA, compared to AAV9 reference capsid) in most brain regions, notably AAV4, AAV5, rh 34, hu 26, rh31,and hu13. Favorable capsids exhibiting CNS-tropism have DNA relative abundance values resulting in greater than 1.1-fold increase in DNA values in at least one CNS region, except dorsal root ganglion (DRG).

[00258] **FIG. 19** depicts the RA of the viral genomes (normalized to input) in the frontal cortex of the cynomolgus monkey model, and **Table 9** lists the RA values for those capsids with the highest RA shown in FIG. 19.

Table 9.

Sample No.	Serotype	RA	p-value
BC083	AAV1	1499.86	<0.0001
BC003	AAV8.BBB	762.42	0.0151
BC077	AAV.rh4	659.09	ns
BC054	AAV.hu38	638.06	ns
BC086	AAV5	612.54	ns
BC079	AAV.rh46	588.72	ns
BC089	AAV8.BBB	574.48	ns
BC087	AAV6	520.67	ns
BC081	AAV.rh72	512.76	ns

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[00259] **FIG. 20** depicts the relative abundance of the viral genomes (normalized to input) in the hippocampus of the cynomolgus monkey model, and **Table 10** lists the RA values for those capsids with the highest RA shown in FIG. 20.

[00260] **Table 10**.

Sorted BC	Normalized Sorted Relative Abundance	Serotype	p-value
BC105	125921.21	AAV2	ns
BC062	81149.18	AAV2 7m8	ns
BC087	50962.40	AAV6	ns
BC083	25800.48	AAV1	ns
BC032	8113.37	AAVrh2	ns
BC126	4169.21	AAVrh73	ns
BC102	3673.77	AAV8Y733F	ns
BC085	3397.77	AAV4	ns
BC003	3279.18	AAV8.BBB	0.007
BC073	2609.49	AAVrh24	ns

[00261] **FIG. 21** depicts the relative abundance (RA) of the viral genomes (normalized to input) in the midbrain of the cynomolgus monkey model, and **Table 11** lists the RA values for those capsids with the highest RA shown in FIG. 21.

[00262] **Table 11.**

Sorted BC	Normalized Sorted Relative Abundance	Serotype	p-value
BC062	2077.07	AAV 7m8	<0.0001
BC085	1057.83	AAV4	0.0002
BC087	859.50	AAV6	0.0104
BC015	833.34	AAV27m8	0.0164
BC086	827.35	AAV5	0.0181
BC096	417.06	AAV8 Y444F	0.9781
BC098	407.57	AAV8 Y447F	ns
BC079	383.98	AAVrh46	ns
BC083	301.08	AAV1	ns
BC102	295.67	AAV8 Y733F	ns

[00263] **FIG. 22** depicts the RA of the viral genomes (normalized to input) in the cerebellum of the cynomolgus monkey model, and **Table 12** lists the RA values for those capsids with the highest RA shown in FIG. 22.

[00264] Table 12.

Sorted BC	Normalized Sorted RA	Serotype	p-value
BC083	1170.50	AAV1	<0.0001
BC003	671.84	AAV8.BBB	<0.0001
BC077	531.50	AAV rh4	0.0004
BC079	515.31	AAVrh46	0.0008
BC054	510.51	AAVhu38	0.001
BC100	479.36	AAV8Y707F	0.0038
BC127	470.57	AAVrh2.R1.V651F	0.0054
BC081	467.79	AAVrh72	0.006
BC053	447.81	AAVhu37	0.0128
BC091	445.93	AAV9Y6F	0.0137

[00265] **FIG. 23** depicts the RA of the viral genomes (normalized to input) in the cervical DRGs of the cynomolgus monkey model, and **Table 13** lists the RA values for those capsids with the highest RA shown in FIG. 23.

[00266] Table 13.

Sorted BC	Normalized sorted RA	Serotype	p-value
BC062	12040.24	AAV2 7m8	<0.0001
BC015	9522.20	AAV2	<0.0001
BC126	7170.76	AAVrh73	ns (0.2422)
BC086	4760.90	AAV5	<0.0001
BC084	2640.55	AAV3B	ns
BC083	1808.40	AAV1	ns
BC003	1192.23	AAV8.BBB	ns
BC085	922.02	AAV4	ns
BC087	875.60	AAV6	ns
BC077	826.27	AAVrh4	ns

[00267] **FIG. 24** depicts the RA of the viral genomes (normalized to input) in the lumbar DRGs of the cynomolgus monkey model, and **Table 14** lists the RA values for those capsids with the highest RA shown in FIG. 24.

[00268] Table 14.

Sorted BC	Normalized sorted RA	Serotype	p-value
BC015	5649.13	AAV2	ns (0.9996)
BC126	4840.36	AAVrh73	<0.0001
BC083	4002.82	AAV1	0.0021

BC086	3794.13	AAV5	0.0051
BC003	2847.53	AAV8.BBB	ns
BC131	2427.59	AAVrh64.R1	ns
BC062	2367.34	AAV2 7m8	ns
BC100	2000.82	AAV8 Y707F	ns
BC077	1988.30	AAV rh4	ns
BC053	1947.15	AAVhu37	ns

[00269] **FIG. 25** depicts a Venn diagram of the top performing 15 capsids transducing the frontal cortex, hippocampus, midbrain and cerebellum following ICV administration. As indicated in the diagram, AAV6, AAV8.BBB, AAV.rh.46, and AAV1 were the only AAVs represented in each of the top performing groups.

[00270] **FIG. 26** depicts a Venn diagram of the top performing 45 capsids transducing the hippocampus and the 45 capsids with the lowest transduction values for DRG, to identify hippocampus-targeting DRG friendly capsids. As indicated in the diagram, AAV.hu.60, AAV.rh.21, AAV.PHP.hB, AAV.rh.15, AAV.rh.24, AAV9.W503R, hu.5, AAV9.Q474A, and AAV.hu.10 were the only AAVs represented in each of the groups.

6.16. Example 16 -Study of Muscle and Liver Biodistribution with Intravenous (IV) Administration

[00271] A procedure like that described in Example 13 with IV administration was used to study the muscle and liver biodistribution of a pool of rAAV capsids to cynomolgus monkey model.

[00272] **FIG. 27** depicts a Venn diagram of the top performing 40 capsids transducing the heart, biceps, and gastrocnemius and the 40 capsids with the lowest transduction values for the liver, to identify muscle-targeting liver-friendly capsids. As indicated in the diagram, AAV.PHPeB.VP2Herp was the only AAVs represented in each of the groups.

[00273] **FIG. 28** depicts a Venn diagram of the top performing 15 capsids transducing the heart, biceps, and gastrocnemius and **Table 15** provides a list of the top performing capsids in three different cells of the diagram.

Table 15.

Diagram Cell	**Total**	**Serotype**
biceps, gastrocnemius, heart	4	Hu.10, AAV3B, AAV2.7m8, AAV9.Q474A
biceps, gastrocnemius,	1	AAV5
heart	3	Rh.15, PHP.hB, modified AAV8

[00274] FIGS. 29A and B depict the RA of the viral genomes (normalized to input) in the gastrocnemius and the liver of the cynomolgus monkey model, respectively.

[00275] Table 16 provides the rank of each capsid by RA values for the cynomolgus monkey model and the MDX mouse model. Capsids were ranked relative to one another in each animal to decrease variability across animals. Gastrocnemius, TA, heart, bicep, and triceps contributed 70% to the ranking for the MDX Mouse Model and the gastrocnemius, heart, and biceps contributed 70% to the ranking for the cynomolgus monkey model. Liver RA contributed 30% to rankings for each animal. The overall ranking was determined by weighting the ranking for each animal 50%.

Table 16.

Serotype	NH/C. Monkey Rank	MDX Rank	Overall Rank
AAV9.W503R	3	1	1
AAV9.Q474A	4	10	3
AAV9.BBB	15	2	4
AAV9 S454-Kidney 1	2	21	7
AAV.hu32	7	17	9
AAV.rh13	24	5	12
AAV.rh15	8	25	13
AAV9 S454-Kidney 1C	5	31	17
AAV9	36	6	18

6.17. Example 17: Study of Liver Detargeting Biodistribution following Intravenous Administration of Capsid Library

[00276] Pooled barcoded vectors were administered to NHPs by IV injection. The pooled mixture consists of 118 different AAV capsids, including natural isolates and engineered AAVs, as described herein, expressing the GFP reporter gene from the universal CAG promoter. The intravenous study followed the protocol described in Examples 13 and 14, infra. Several capsids exhibited tropism that "detargeted" the liver, as such, mutated capsids exhibited lower abundance in liver tissue than the parental capsid (AAV9), e.g. AAV8.BBB.LD (A269S, 498-NNN/AAA-500), AAV9.BBB.LD (S263G/S269T/A273T, 496-NNN/AAA-498), AAV9.496-NNN-498, AAV9.496-NNN-498.W503R, AAV9.W503R, and AAV9.Q474A. AAV8 capsids having the NNN/AAA mutation exhibit overall approximately an 11-fold reduction in transduction in liver, and 42-fold reduction in expression of transcript in liver. AAV9 capsids having the NNN/AAA and W503R mutation exhibits approximately a 400-fold reduction in transduction in liver, and results in zero expression of transcript in liver. In some instances, brain distribution of these modified vectors was also diminished. AAV8.BBB.LD additionally exhibits a high level of transduction in gastrocnemius muscle.

[00277] **FIG. 31** depicts the biodistribution of select "liver-detargeting" (LD) vectors compared to their parental AAV9 capsid in various tissues, in NHPs following IV administration of the capsid library. **FIG. 32** depicts the biodistribution of select LD vectors compared to their parental AAV8 capsid in various tissues, in NHPs following IV administration of the capsid library.

[00278] Studies also show the change in relative abundance (adjusted for input, normalized to 1) between the abundance for each barcode (and therefore capsid) at 3hr post and 24hr post IV capsid library administration (RA at 3hr/RA at 24hr). Individual animals are indicated by different shape data points (3 animals total) (**FIGs 33A** and **33B**).

[00279] A fold change >1 indicates that the capsid makes up a lower percentage of the total capsid "pool" present in the blood at 24hr compared to 3hr after dosing (i.e. faster blood clearance). A fold change <1 indicates that the capsid makes up a greater percentage of the total capsid "pool" present in the blood at 24hr compared to 3hr after dosing (i.e. slower clearance). Historically, slower clearance correlates with lower liver transduction/liver detargeting.

[00280] As represented by increase in blood retention, a depiction of the change in abundance for a given capsid in a given animal was plotted. Allowing for the calculation of the fold increase in blood retention over the baseline retention of AAV9, for example, the representations **(FIGs 34A and 34B)** compare that change in abundance value of the select capsid to the change in abundance of the parental capsid (setting the parental capsid to 1). Thus, various mutations to the AAV9 capsid increase retention in the circulation by 3 to 5 fold (see. e.g. FIG. 34A).

6.18 Example 18 -Study of Muscle, Liver and Brain Biodistribution with Intravenous (IV) Administration of Capsid Pool to *mdx* mice

[00281] Pooled barcoded vectors were administered to *mdx* mice by IV (tail vein) injection. The pooled mixture consists of 118 different AAV capsids, including natural isolates and engineered AAVs, as described herein, expressing the GFP reporter gene from the universal CAG promoter. The IV study followed a protocol analogous to that described in Examples 12 and 16, *infra.*

[00282] At 3 week sacrifice, tissues were harvested and samples were collected in tubes with RNAlater (per manufacturer's instructions) and flash frozen at -80ºC until DNA and RNA analysis (biodistribution of each vector in the pool) were performed by NGS (see **FIGs. 36A-36H**).

6.19 Capsid Amino Acid Sequences

[00283] **Table 17** provides the amino acid sequences of certain engineered capsid proteins described and/or used in studies described herein. Heterologous peptides and amino acid substitutions are indicated in gray shading.

Table 17. Capsid Amino Acid Sequences

Capsid Name	Insert or Substitution	Amino Acid Sequence
PHP.S *(California Institute of Technology-Chan et al 2017)*	QAVRTSL (SEQ ID NO:16) (588_589)	1 MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 61 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 121 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 181 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 241 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 301 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 361 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 421 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSRT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 481 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 541 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQQA VRTSLAQAQT 601 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 661 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 721 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:22)
PHP.SH	QAVRTSH (SEQ ID NO:17)	1 MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 61 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 121 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 181 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI

Capsid Name	Insert or Substitution	Amino Acid Sequence
	(588_589)	241 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 301 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 361 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 421 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSRT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 481 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 541 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQQA VRTSHAQAQT 601 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 661 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 721 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:23)
PHP.B *(California Institute of Technology GenBank entry: ALU85156.1-Deverman et al 2016)*	TLAVPFK (SEQ ID NO:20) (588_589)	1 MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 61 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 121 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 181 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 241 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 301 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 361 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 421 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSRT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 481 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 541 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQTL AVPFKAQAQT 601 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 661 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 721 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:24)
PHP.eB *(California Institute of Technology-Chan et al 2017)*	TLAVPFK (SEQ ID NO: 27) (588_589)	1 MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 61 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 121 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 181 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 241 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 301 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 361 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 421 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSRT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 481 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 541 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQS**DG**TL AVPFKAQAQT 601 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 661 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 721 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:25)
AAV8.BBB	A269S	MAADGYLPDW LEDNLSEGIR EWWALKPGAP KPKANQQKQD DGRGLVLPGY KYLGPFNGLD 60 KGEPVNAADA AALEHDKAYD QQLQAGDNPY LRYNHADAEF QERLQEDTSF GGNLGRAVFQ 120 AKKRVLEPLG LVEEGAKTAP GKKRPVEPSP QRSPDSSTGI GKKGQQPARK RLNFGQTGDS 180 ESVPDPQPLG EPPAAPSGVG PNTMAAGGGA PMADNNEGAD GVGSSSGNWH CDSTWLGDRV 240 ITTSTRTWAL PTYNNHLYKQ ISNGTSGGST NDNTYFGYST PWGYFDFNRF HCHFSPRDWQ 300 RLINNNWGFR PKRLSFKLFN IQVKEVTQNE GTKTIANNLT STIQVFTDSE YQLPYVLGSA 360 HQGCLPPFPA DVFMIPQYGY LTLNNGSQAV GRSSFYCLEY FPSQMLRTGN NFQFTYTFED 420 VPFHSSYAHS QSLDRLMNPL IDQYLYYLSR TQTTGGTANT QTLGFSQGGP NTMANQAKNW 480 LPGPCYRQQR VSTTTGQNNN SNFAWTAGTK YHLNGRNSLA NPGIAMATHK DDEERFFPSN 540 GILIFGKQNA ARDNADYSDV MLTSEEEIKT TNPVATEEYG IVADNLQQQN TAPQIGTVNS 600 QGALPGMVWQ NRDVYLQGPI WAKIPHTDGN FHPSPLMGGF GLKHPPPQIL IKNTPVPADP 660 PTTFNQSKLN SFITQYSTGQ VSVEIEWELQ KENSKRWNPE IQYTSNYYKS TSVDFAVNTE 720 GVYSEPRPIG TRYLTRNL (SEQ ID NO:26)
AAV8.BBB.LD	A269S, 498_NNN/AAA_500	MAADGYLPDW LEDNLSEGIR EWWALKPGAP KPKANQQKQD DGRGLVLPGY KYLGPFNGLD 60 KGEPVNAADA AALEHDKAYD QQLQAGDNPY LRYNHADAEF QERLQEDTSF GGNLGRAVFQ 120 AKKRVLEPLG LVEEGAKTAP GKKRPVEPSP QRSPDSSTGI GKKGQQPARK RLNFGQTGDS 180 ESVPDPQPLG EPPAAPSGVG PNTMAAGGGA PMADNNEGAD GVGSSSGNWH CDSTWLGDRV 240 ITTSTRTWAL PTYNNHLYKQ ISNGTSGGST NDNTYFGYST PWGYFDFNRF HCHFSPRDWQ 300 RLINNNWGFR PKRLSFKLFN IQVKEVTQNE GTKTIANNLT STIQVFTDSE YQLPYVLGSA 360 HQGCLPPFPA DVFMIPQYGY LTLNNGSQAV GRSSFYCLEY FPSQMLRTGN NFQFTYTFED 420 VPFHSSYAHS QSLDRLMNPL IDQYLYYLSR TQTTGGTANT QTLGFSQGGP NTMANQAKNW 480 LPGPCYRQQR VSTTTGQAAA SNFAWTAGTK YHLNGRNSLA NPGIAMATHK DDEERFFPSN 540 GILIFGKQNA ARDNADYSDV MLTSEEEIKT TNPVATEEYG IVADNLQQQN TAPQIGTVNS 600 QGALPGMVWQ NRDVYLQGPI WAKIPHTDGN FHPSPLMGGF GLKHPPPQIL IKNTPVPADP 660

Capsid Name	Insert or Substitution	Amino Acid Sequence
		PTTFNQSKLN SFITQYSTGQ VSVEIEWELQ KENSKRWNPE IQYTSNYYKS TSVDFAVNTE 720 GVYSEPRPIG TRYLTRNL (SEQ ID NO:27)
AAV9. BBB	S263G/S269T/A273T	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNGTSGGSTN DNTYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:28)
AAV9. BBB. LD	S263G/S269T/A273T, 496_NNN/AAA_498	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNGTSGGSTN DNTYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQAAASE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:29)
AAVrh.10.LD	498_NNN/AAA_500	MAADGYLPDW LEDNLSEGIR EWWDLKPGAP KPKANQQKQD DGRGLVLPGY 50 KYLGPFNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LRYNHADAEF 100 QERLQEDTSF GGNLGRAVFQ AKKRVLEPLG LVEEGAKTAP GKKRPVEPSP 150 QRSPDSSTGI GKKGQQPAKK RLNFGQTGDS ESVPDPQPIG EPPAGPSGLG 200 SGTMAAGGGA PMADNNEGAD GVGSSSGNWH CDSTWLGDRV ITTSTRTWAL 250 PTYNNHLYKQ ISNGTSGGST NDNTYFGYST PWGYFDFNRF HCHFSPRDWQ 300 RLINNNWGFR PKRLNFKLFN IQVKEVTQNE GTKTIANNLT STIQVFTDSE 350 YQLPYVLGSA HQGCLPPFPA DVFMIPQYGY LTLNNGSQAV GRSSFYCLEY 400 FPSQMLRTGN NFEFSYQFED VPFHSSYAHS QSLDRLMNPL IDQYLYYLSR 450 TQSTGGTAGT QQLLFSQAGP NNMSAQAKNW LPGPCYRQQR VSTTLSQAAA 500 SNFAWTGATK YHLNGRDSLV NPGVAMATHK DDEERFFPSS GVLMFGKQGA 550 GKDNVDYSSV MLTSEEEIKT TNPVATEQYG VVADNLQQQN AAPIVGAVNS 600 QGALPGMVWQ NRDVYLQGPI WAKIPHTDGN FHPSPLMGGF GLKHPPPQIL 650 IKNTPVPADP PTTFSQAKLA SFITQYSTGQ VSVEIEWELQ KENSKRWNPE 700 IQYTSNYYKS TNVDFAVNTD GTYSEPRPIG TRYLTRNL (SEQ ID NO:30)
AAV9. 496NNN/AAA498	498_NNN/AAA_500	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQAAASE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:31)
AAV9. 496NNN/AAA498. W503R	496NNN/AAA498, W503R	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480

Capsid Name	Insert or Substitution	Amino Acid Sequence
		GPSYRQQRVS TTVTQAAASE FARPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:32)
AAV9 W503 R	W503R	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQNNNSE FARPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:33)
AAV9 Q474A	Q474A	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVAGRNYIP 480 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:34)
AAV9 S454-D8	Bone1, DDDDDDDD (SEQ ID NO: 9) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSDDDDDD DDGQNQQTLKF SVAGPSNMAV481 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 541 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 601 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 661 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 721 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:35)
AAV9 S454-Brain1	Brain1, LSSRLDA (SEQ ID NO: 10) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSLSSRLD AGQNQQTLKF SVAGPSNMAV 480 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:36)
AAV9 S454-Brain2	Brain2/ Brain1C, CLSSRLDAC (SEQ ID	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420

Capsid Name	Insert or Substitution	Amino Acid Sequence
	NO: 11) (454_455)	PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSCLSSRL DACGQNQQTL KFSVAGPSNM AV 482 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 542 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 602 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 662 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 722 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:37)
AAV9 S454-Kidney 1	Kidney1, LPVAS (SEQ ID NO: 13) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSLPVASG QNQQTLKFSV AGPSNMAV 478 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 538 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 598 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 658 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 718 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:38)
AAV9 S454-Kidney 2	Kidney2/ Kidney1C, CLPVASC (SEQ ID NO: 12) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSCLPVAS CGQNQQTLKF SVAGPSNMAV 480 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:39)
AAV9 S454-Muscle 1	Muscle1, ASSLNIA (SEQ ID NO: 14) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSASSLNI AGQNQQTLKF SVAGPSNMAV 480 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:40)
AAV9 S454-Tfr1	Tfr1, HAIYPR (SEQ ID NO: 59) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSHAIYPR HGQNQQTLKF SVAGPSNMAV 480 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:41)
AAV9 S454-Tfr3	Tfr3, RTIGPSV (SEQ ID	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300

Capsid Name	Insert or Substitution	Amino Acid Sequence
	NO: 19) (454_455)	LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSRTIGPS VGQNQQTLKF SVAGPSNMAV 480 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:42)
AAV9 S454-Tfr4 (AAV9 S454-TfR3C)	Tfr4, CRTIGPSVC (SEQ ID NO: 20) (454_455)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSCRTIGP SVCGQNQQTL KFSVAGPSNMAV 482 QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 542 FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 602 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 662 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 722 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:43)
AAV9. 588Ad (9 588 Ad)	SITLVKSTQTV (SEQ ID NO: 21), DLC-AS1 (588_589)	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQNNNSI TLVKSTQTVS EFAWPGASSW ALNGRNSLMN PGPAMASHKE 540 GEDRFFPLSG SLIFGKQGTG RDNVDADKVM ITNEEEIKTT NPVATESYGQ VATNHQSAQA 600 QAQTGWVQNQ GILPGMVWQD RDVYLQGPIW AKIPHTDGNF HPSPLMGGFG MKHPPPQILI 660 KNTPVPADPP TAFNKDKLNS FITQYSTGQV SVEIEWELQK ENSKRWNPEI QYTSNYYKSN 720 NVEFAVNTEG VYSEPRPIGT RYLTRNL (SEQ ID NO:44)
AAV9. 588 Herp (9 588 Hep)	TILSRSTQTG (SEQ ID NO: 22), DLC-AS2, 588_589	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQNNNTI LSRSTQTGSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG 540 EDRFFPLSGS LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ 600 AQTGWVQNQG ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK 660 NTPVPADPPT AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN 720 VEFAVNTEG VYSEPRPIGT RYLTRNL (SEQ ID NO:45)
AAV**P** **HPeB**. VP2Ad	SITLVKSTQTV (SEQ ID NO: 21), DLC-AS1 (138_139)	1 MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 61 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 121 AKKRLLEPLG LVEEAAKTTI LSRSTQTGAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 191 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 251 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 311 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 371 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 431 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSRT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 491 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 551 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQS**DG**TL AVPFKAQAQT 611 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 671 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 731 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:46)

Capsid Name	Insert or Substitution	Amino Acid Sequence
AAV**PHPeB**. VP2Herp	TILSRSTQTG (SEQ ID NO: 22), DLC-AS2, (138_139)	1 MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 61 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 121 AKKRLLEPLG LVEEAAKTSI TLVKSTQTVA PGKKRPVEQS PQEPDSSAGI GKSGAQPAKK RLNFGQTGDT E 192 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 252 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 312 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 372 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 432 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSRT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 492 GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 552 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQS**DG**TL AVPFKAQAQT 612 GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 672 VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 732 AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO:47)
rh34	-	MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYEYLGPFNGLDKGEPVNAAD AAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLGLVEEGAKT APGKKRPLESPQEPDSSSGIGKKGKQPAKKRLNFEEDTGAGDGPPEGSDTSAMSSDIEMRAAPGGNAVD AGQGSDGVGNASGDWHCDSTWSEGKVTTTSTRTWVLPTYNNHLYLRLGTTSNSNTYNGFSTPWGYFDFN RFHCHFSPRDWQRLINNNWGLRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVM DAGQEGSLPPFPNDVFMVPQYGYCGIVTGENQNQTDRNAFYCLEYFPSQMLRTGNNFETAYNFEKVPFH SMYAHSQSLDGLMNPLLDQYLWHLQSTTSGETLNQGNAATTFGKIRSGDFAFYRKNWLPGPCVKQQRFS KTASQNYKIPASGGNALLKYDTHYTLNNRWSNIAPGPPMATAGPSDGDFSNAQLIFPGPSVTGNTTTSA NNLLFTSEEEIAATNPRDTDMFGQIADNNQNATTAPITGNVTAMGVLPGMVWQNRDIYYQGPIWAKIPH ADGHFHPSPLIGGFGLKHPPPQIFIKNTPVPAYPATTFTAARVDSFITQYSTGQVAVQIEWEIEKERSK RWNPEVQFTSNCGNQSSMLWAPDTTGKYTEPRVIGSRYLTNHL (SEQ ID NO:82)
hu.31	-	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPGNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGSQPAKKK LNFGQTGDTE SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH EGCLPPFPAD VFMIPQYGYL TLNDGGQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVSTEGV YSEPRPIGTR YLTRNL (SEQ ID NO:83)
rh.31	-	KAYDQQLKAG DNPYLRYNHA DAEFQERLQE DTSFGGNLGR AVFQAKKRVL EPLGLVETPA KTAPGKKRPV DSPDSTSGIG KKGQQPAKKR LNFGQTGDSE SVPDPQPIGE PPAGPSGLGS GTMAAGGGAP MADNNEGADG VGNASGNWHC DSTWLGDRVI TTSTRTWALP TYNNHLYKQI SSQSAGSTND NVYFGYSTPW GYFDFNRFHC HFSPRDWQRL INNNWGFRPK KLNFKLFNIQ VKEVTTNDGV TTIANNLTST VQVFSDSEYQ LPYVLGSAHQ GCLPPFPADV FMIPQYGYLT LNNGSQSVGR SSFYCLEYFP SQMLRTGNNF TFSYTFEDVP FHSSYAHSQS LDRLMNPLID QYLYYLARTQ SNAGGTAGNR ELQFYQGGPT TMAEQAKNWL PGPCFRQQRV SKTLDQNNNS NFAWTGATKY HLNXRNSLVN PGVAMATHKD DEERFFPSSG VLIFGKTGAA NKTTLENVLM TNEEEIRPTN PVATEEYGIV SSNLQAASTA AQTQVVNNQG ALPGMVWQNR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGL KHPPPQILIK NTPVPANPPE VFTPAKFASF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNFDKQTG VDFAVDSQGV YSEP (SEQ ID NO:84)
hu.12	-	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHQDDSRGLVLPGYKYLGPFNGLD KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPVEPDSSSGTGKAGHQPARKRLNFGQTGDAD SVPDPQPLGQPPAAPTSLGSTTMATGSGAPMADNNEGADGVGNSSGNWHCDSQWLGDRVI TTSTRTWALPTYNNHLYKQISSQSGASNDNHYFGYSTPWGYFDFNRFHCHFSPRDWQRLI NNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGSAHQG CLPPFPADVFMVPQYGYLTLNNGSQAVGRPSFYCLEYFPSQMLRTGNNFTFSYTFEDVPF HSSYAHSQSLDRLMNPLIDQYLYYLNRTQSNSGTLQQSRLLFSQAGPTSMSLQAKNWLPG PCYRQQRLSKQANDNNNSNFPWTAATKYHLNGRDSLVNPGPAMASHKDDEEKFFPMHGTL

Capsid Name	Insert or Substitution	Amino Acid Sequence
		IFGKQGTNANDADLEHVMITDEEEIRTTNPVATEQYGNVSNNLQNSNTGPTTENVNHQGA LPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPQIMIKNTPVPANPPTN FSSAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVY SEPRPIGTRYLTRNL (SEQ ID NO:85)
hu.13	-	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPFNGLD KGEPVNEADA AALEHDKAYD RQLDSGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRVLEPLG LVEEPVKTAP GKKRPVEHSP AEPDSSSGTG KAGQQPARKR LNFGQTGDAD SVPDPQPLGQ PPAAPSGLGT NTMASGSGAP MADNNEGADG VGNSSGNWHC DSTWMGDRVI TTSTRTWALP TYNNHLYKQI SSQSGASNDN HYFGYSTPWG YFDFNRFHCH FSPRDWQRLI NNNWGFRPKR LNFKLFNIQV KEVTQNDGTT TIANNLTSTV QVFTDSEYQL PYVLGSAHQG CLPPFPADVF MVPQYGYLTL NNGSQAVGRS SFYCLEYFPS QMLRTGNNFT FSYTFEDVPF HSSYAHSQSL DRLMNPLIDQ YLYYLSRTNT PSGTTTQSRL QFSQAGASDI RDQSRNWLPG PCYRQQRVSK TSADNNNSEY SWTGATKYHL NGRDSLVNPG PAMASHKDDE EKFFPQSGVL IFGKQGSEKT NVDIEKVMIT DEEEIRTTNP VATEQYGSVS TNLQGGNTQA ATADVNTQGV LPGMVWQDRD VYLQGPIWAK IPHTDGHFHP SPLMGGFGLK HPPPQILIKN TPVPANPSTT FSAAKFASFI TQYSTGQVSV EIEWELQKEN SKRWNPEIQY TSNYNKSVNV DFTVDTNGVY SEPRPIGTRY LTRNL (SEQ ID NO:85)
hu.21	-	MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLDKGEPVNEAD AAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLGLVEEPVKT APGKKRPVEHSPAEPDSSSGTGKAGQQPARKRLNFGQTGDADSVPDPRPLGQPPAAPSGLGTNTMASGS GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTSTRTWALPTYNNHLYKQISSQSGASNDNHYFGYS TPWGYFDFNRFHCHFSPRDWQRLINNNWGFRPKRLSFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTD SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFTFSYT FEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTNTPSGTTTMSRLQFSQAGASDIRDQSRNWLPGPCY RQQRVSKTAADNNNSDYSWTGATKYHLNGRDSLVNPGPAMASHKDDEEKYFPQSGVLIFGKQDSGKTNV DIEKVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYLQGPIWAKI PHTDGHFHPSPLMGGFGLKHPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKEN SKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL (SEQ ID NO:74)
hu.26	-	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPFNGLD KGEPVNEADA AALEHDKAYD RQLDSGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRILEPLG LVEEPVKTAP GKKRPVEHSP AEPDSSSGTG KAGQQPARKR LNFGQTGDAD SVPDPQPLGQ PPAAPSGLGT NTMASGSGAP MADNNEGADG VGNSSGNWHC DSTWMGDRVI TTSTRTWALP TYNNHLYKQI SSQSGASNDN HYFGYSTPWG YFDFNRFHCH FSPRDWQRLI NNNWGFRPKR LSFKLFNIQV KEVTQNDGTT TIANNLTSTV QVFTDSEYQL PYVLGSAHQG CLPPFPADVF MVPQYGYLTL NNGSQAVGRS SFYCLEYFPS QMLRTGNNFT FSYTFEDVPF HSSYAHSQSL DRLMNPLIDQ YLYYLSRTNT PSGTTTMSRL QFSQAGASDI RDQSRNWLPG PCYRQQRVSK TAADNNNSDY SWTGATKYHL NGRDSLVNPG PAMASHKDDE EKYFPQSGVL IFGKQDSGKT NVDIEKVMIT DEEEIRTTNP VATEQYGSVS TNLQSGNTQA ATSDVNTQGV LPGMVWQDRD VYLQGPIWAK IPHTDGHFHP SPLMGGFGLK HPPPQILIKN TPVPANPSTT FSAAKFASFI TQYSTGQVSV EIEWELQKEN SKRWNPEIQY TSNYNKSVNV DFTVDTNGVY SEPRPIGTRY LTRNL (SEQ ID NO:76)
hu.53	-	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPFNGLD KGEPVNEADA AALEHDKAYD RQLDSGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRVLEPLG LVEEPVKTAP GKKRPVEHSP AEPDSSSGTG KAGQQPARKR LNFGQTGDAD SVPDPQPLRQ PPAAPTSLGS TTMATGSGAP MADNNEGADG VGNSSGNWHC DSQWLGDRVI TTSTRTWALP TYNNHLYKQI SSQSGASNDN HYFGYSTPWG YFDFNRFHCH FSPRDWQRLI NNNWGFRPKR LNFKLFNIQV KEVTQNDGTT TIANNLTSTV QVFTDSEYQL PYVLGSAHQG CLPPFPADVF MVPQYGYLTL NNGSQAVGRS SFYCLEYFPS QMLRTGNNFQ FSYTFEDVPF HSSYAHSQSL DRLMNPLIDQ YLYYLNRTQT ASGTQQSRLL FSQAGPTSMS LQAKNWLPGP CYRQQRLSKQ ANDNNNSNFP WTGATKYYLN GRDSLVNPGP AMASHKDDEE KFFPMHGTLI FGKEGTNATN AELENVMITD EEEIRTTNPV ATEQYGYVSN NLQNSNTAAS TETVNHQGAL PGMVWQDRDV YLQGPIWAKI PHTDGHFHPS PLMGGFGLKH PPPQIMIKNT PVPANPPTNF SSAKFASFIT QYSTGQVSVE IEWELQKENS KRWNPEIQYT SNYNKSVNVD FTVDTNGVYS EPRPIGTRYL TRNL (SEQ ID NO:77)
hu.56	-	MAADGYLPDW LEDTLSEGIR QWWKLKPGPP PPKPAERHKD DSRGLVLPGY KYLGPFNGLD KGEPVNEADA AALEHDKAYD RQLDSGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ AKKRVLEPLG LVEEPVKTAP GKKRPVEHSP VEPDSSSGTG KAGNQPARKR LNFGQTGDAD SVPDPQPLGQ PPASPSGLGT NTMATGSGAP MADNNEGADG VGNSSGNWHC DSTWMGDRVV TTSTRTWALP TYNNHLYKQI SSQSGASNDN HYFGYSTPWG YFDFNRFHCH FSPRDWQRLI

Capsid Name	Insert or Substitution	Amino Acid Sequence
		NNNWGFRPKR LNFKLFNIQV KEVTQNDGTT TIANNLTSTV QVFTDLEYQL PYVLGSAHQG CLPPFPADVF MVPQYGYLTL NNGSQAVGRS SFYCLEYFPS QMLRTGNNFT FSYTFEDVPF HSSYAHSQSL DRLMNPLIDQ YLYYLSRTNT PSGTTTQSRL QFSQAGASDI RDQSRNWLPG PCYRQQRVSK TAADNNNSEY SWTGATKYHL NGRDSLVNPG PAMASHKDDE EKFFPQSGVL IFGKQGSEKT NVDIEKVMIT DEEEIRTTNP VATEQYGSVS TNLQSGNTQA ATSDVNTQGV LPGMVWQDRD VYLQGPIWAK IPHTDGHFHP SPLMGGFGLK HPPPQILIKN TPVPANPSTT FSAAKFASFI TQYSTGQVSV EIEWELQKEN SKRWNPEIQY TSNYNKSVNV DFTVDTNGVY SEPRPIGTRY LTRNL (SEQ ID NO:86)
Rh.64R1	R697W	MAADGYLPDW LEDNLSEGIR EWWDLKPGAP KPKANQQKQD DGRGLVLPGY KYLGPFNGLD KGEPVNAADA AALEHDKAYD QQLKAGDNPY LRYNHADAEF QERLQEDTSF GGNLGRAVFQ AKKRVLEPLG LVEEGAKTAP GKKRPVEPSP QRSPDSSTGI GKKGQQPARK RLNFGQTGDS ESVPDPQPIG EPPAAPSSVG SGTMAAGGGA PMADNNEGAD GVGSSSGNWH CDSTWLGDRV ITTSTRTWAL PTYNNHLYKQ ISNGTSGGST NDNTYFGYST PWGYFDFNRF HCHFSPRDWQ RLINNNWGFR PKRLSFKLFN IQVKEVTQNE GTKTIANNLT STIQVFTDSE YQLPYVLGSA HQGCLPPFPA DVFMIPQYGY LTLNNGSQAV GRSSFYCLEY FPSQMLRTGN NFSFSYTFED VPFHSSYAHS QSLDRLMNPL IDQYLYYLSR TQSTGGTAGT QQLLFSQAGP SNMSAQARNW LPGPCYRQQR VSTTLSQNNN SNFAWTGATK YHLNGRDSLV NPGVAMATNK DDEDRFFPSS GILMFGKQGA GKDNVDYSNV MLTSEEEIKT TNPVATEQYG VVADNLQQQN TAPIVGAVNS QGALPGMVWQ NRDVYLQGPI WAKIPHTDGN FHPSPLMGGF GLKHPPPQIL IKNTPVPADP PTAFNQAKLN SFITQYSTGQ VSVEIVWELQ KENSKRWNPE (SEQ ID NO:90)
AAV9.N272A.496NNN/AAA498	N272A 498_NNN/AAA_500	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DAAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQAAASE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:91)
AAV9.G266A.496NNN/AAA498	G266A 498_NNN/AAA_500	MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60 KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120 AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180 SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240 TTSTRTWALP TYNNHLYKQI SNSTSAGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300 LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360 EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420 PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480 GPSYRQQRVS TTVTQAAASE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540 LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQAQ AQTGWVQNQG 600 ILPGMVWQDR DVYLQGPIWA KIPHTDGNFH PSPLMGGFGM KHPPPQILIK NTPVPADPPT 660 AFNKDKLNSF ITQYSTGQVS VEIEWELQKE NSKRWNPEIQ YTSNYYKSNN VEFAVNTEGV 720 YSEPRPIGTR YLTRNL (SEQ ID NO:92)
Rh.46		MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS ESVPDPQPIGEPPAAPSSVGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDRV ITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDWQ RLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGSA HQGCLPPFPADVFMIPQYGYLTLNNGSQAVGRSSFYCLEYFPSQMLRTGNNFSFSYTFED VPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQSTGGTAGTQQLLFSQAGPSNMSAQARNW LPGPCYRQQRVSTTLSQNNNSNFAWTGATKYHLNGRDSLVNPGVAMATNKDDEDRFFPSS GILMFGKQGAGKDNVDYSNVMLTSEEEIKATNPVATEQYGVVADNLQQQNTAPIVGAVNS QGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPQILIKNTPVPADP PTAFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSTNVDFAVNTE GVYSEPRPIGTRYLTRNL (SEQ ID NO:93)

7. Equivalents

[00284] Although the invention is described in detail with reference to specific embodiments thereof, it will be understood that variations which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims. Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

[00285] All publications, patents and patent applications mentioned in this specification are herein incorporated by reference into the specification to the same extent as if each individual publication, patent or patent application was specifically and individually indicated to be incorporated herein by reference in their entireties.

[00286] The discussion herein provides a better understanding of the nature of the problems confronting the art and should not be construed in any way as an admission as to prior art nor should the citation of any reference herein be construed as an admission that such reference constitutes “prior art” to the instant application.

[00287] All references including patent applications and publications cited herein are incorporated herein by reference in their entirety and for all purposes to the same extent as if each individual publication or patent or patent application was specifically and individually indicated to be incorporated by reference in its entirety for all purposes. Many modifications and variations of this invention can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. The specific embodiments described herein are offered by way of example only, and the invention is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

We claim:

1. A recombinant AAV capsid protein comprising one or more amino acid substitutions relative to the wild type or unengineered capsid protein, in which the rAAV capsid protein is an AAV9 capsid protein (SEQ ID NO:67) with S263G/S269R/A273T substitutions, a G266A substitution, an N272A substitution, a W503R substitution, a Q474A substitution, 496-NNN/AAA-498 substitutions, has an insertion of the peptide TLAAPFK (SEQ ID NO:1) between Q588 and A589, S268 and S269, or S454 and G455, or is an AAV8 capsid (SEQ ID NO:6) with an A269S substitution or 498-NNN/AAA-500 substitutions, or corresponding substitutions or peptide insertions in a capsid protein of another AAV type capsid.

2. The recombinant AAV capsid protein of claim 1 further comprising 498-NNN/AAA-500 amino acid substitutions for an AAV8 capsid protein (SEQ ID NO: 66) or 496-NNN/AAA-498 amino acid substitutions for an AAV9 capsid protein (SEQ ID NO:67), or corresponding substitutions in a capsid protein of another AAV type capsid.

3. The recombinant AAV capsid protein of claims 1 or 2 which is an AAV8.BBB.LD capsid (SEQ ID NO: 27), an AAV9.BBB.LD capsid (SEQ ID NO: 29), an AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 31), AAV9.496-NNN/AAA-498 capsid (SEQ ID NO: 32), AAV9.W503R capsid (SEQ ID NO: 33), AAV9.Q474A capsid (SEQ ID NO: 34), AAV9.N272A.496-NNN/AAA-498 capsid (SEQ ID NO: 91) or AAV9.N266A.496-NNN/AAA-498 capsid (SEQ ID NO: 92).

4. The recombinant AAV capsid protein of claims 1 to 3 in which the amino acid substitutions or insertions are in an AAV9 capsid, including an AABPHP.eB capsid, protein, or an AAV8 capsid.

5. The recombinant AAV capsid protein of claim 1 or 2 wherein the AAV type capsid is AAV rh.34, AAV4, AAV5, AAV hu.26, AAV rh.31, AAV hu.13, AAV hu.26, AAV hu.56, AAV hu.53, AAV7, AAV rh.10, AAV rh.64.R1, AAV rh.46 or AAV rh.73.

6. The recombinant AAV capsid protein of any of claims 1 to 5, which when incorporated into a rAAV vector, the rAAV vector has increased targeting, transduction or genome integration into CNS cells, relative to a rAAV vector incorporating the corresponding wild type capsid protein without the amino acid substitutions or peptide insertions.

7. The recombinant capsid protein of claim 6, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration

into liver cells, relative to a rAAV vector incorporating the corresponding wild type capsid protein without the amino acid substitutions or peptide insertions.

8. The recombinant capsid protein of claim 6 or 7, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into dorsal root ganglion cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

9. The recombinant capsid protein of any of the claims 6 to 8, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into peripheral nerve cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

10. The recombinant AAV capsid protein of any of claims 1 to 5, which when incorporated into a rAAV vector, the rAAV vector has increased targeting, transduction or genome integration into skeletal and/or cardiac muscle cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

11. The recombinant capsid protein of claim 10, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into liver cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertions.

12. The recombinant capsid protein of claim 10 or 11, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into CNS cells, relative to a rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions or peptide insertion.

13. The recombinant capsid protein of any of claims 10 to 12, which when incorporated into a rAAV vector, the rAAV vector has decreased targeting, transduction or genome integration into dorsal root ganglion cells, relative to an rAAV vector incorporating the corresponding capsid protein without the amino acid substitutions

14. A nucleic acid comprising a nucleotide sequence encoding the rAAV capsid protein of any of claims 1 to 13, or encoding an amino acid sequence sharing at least 80% identity therewith and retaining the biological activity of the capsid.

15. The nucleic acid of claim 14 encoding the rAAV capsid protein of any of claims 1 to 13.

16. A packaging cell capable of expressing the nucleic acid of claim 14 or 15 to produce AAV vectors comprising the capsid protein encoded by said nucleotide sequence.

17. A rAAV vector comprising the capsid protein of any of claims 1 to 13.

18. The rAAV vector of claim 17 further comprising a transgene encoding a therapeutic protein operably linked to a regulatory sequence for expression in the muscle and/or CNS cells.

19. A pharmaceutical composition comprising the rAAV vector of claim 17 or 18 and a pharmaceutically acceptable carrier.

20. A method of delivering a transgene to a cell, said method comprising contacting said cell with the rAAV vector of claim 17 or 18, wherein said transgene is delivered to said cell.

21. The method of claim 20 in which the cell is a CNS cell, cardiac muscle cell or skeletal muscle cell.

22. A method of delivering a transgene to a target tissue of a subject in need thereof, said method comprising administering to said subject the rAAV vector of claim 17 or 18, wherein the transgene is delivered to said target tissue.

23. The method of claim 22 wherein the transgene is a muscle disease or heart disease therapeutic and said target tissue is cardiac muscle or skeletal muscle.

24. The method of claim 23, wherein the rAAV is administered systemically, including intravenously or intramuscularly.

25. The method of claim 22 wherein the transgene is a CNS disease therapeutic and said target tissue is CNS.

26. The method of claim 25 wherein the rAAV is administered intrathecally or intracerebroventricularly.

27. A pharmaceutical composition for use in delivering a transgene to a cell, said pharmaceutical composition comprising the rAAV vector of claim 17 or 18, wherein said transgene is delivered to said cell.

28. A pharmaceutical composition for use in delivering a transgene encoding a therapeutic protein to a target tissue of a subject in need thereof, said pharmaceutical composition comprising the rAAV vector of claim 17 or 18, wherein the transgene is delivered to said target tissue.

29. The pharmaceutical composition of claim 27 or 28 wherein said therapeutic protein is a muscle disease therapeutic or a heart disease therapeutic and said target tissue is cardiac muscle or skeletal muscle.

30. The pharmaceutical composition of claim 27 to 29 wherein the rAAV exhibits at least 1.1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold greater transduction in cardiac muscle or skeletal muscle cells compared to a reference AAV capsid.

31. The pharmaceutical composition of claim 27 to 30 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in liver compared to the reference AAV capsid.

32. The pharmaceutical composition of claim 27 to 31 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in dorsal root ganglion cells compared to the reference AAV capsid.

33. The pharmaceutical composition of claim 27, 28 or 32 wherein said therapeutic protein is a CNS disease therapeutic and said target tissue is CNS.

34. The pharmaceutical composition of claim 27, 28, 32 or 33 wherein the rAAV exhibits at least 1.1-fold, 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, or 10-fold greater transduction in CNS cells compared to a reference AAV capsid.

35. The pharmaceutical composition of claim 27, 28, 33 to 34 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in liver compared to the reference AAV capsid.

36. The pharmaceutical composition of claim 27, 28, 32 to 35 wherein the rAAV exhibits at least 50%, 60%, 70%, 80%, 90%, 95% or 99% less transduction in dorsal root ganglion cells compared to the reference AAV capsid.

37. The pharmaceutical composition of claims 27 to 36, wherein the AAV reference capsid is AAV8 or AAV9.

38. A method of treating a CNS disorder in a subject in need thereof, said method comprising administering a therapeutically effective amount of pharmaceutical composition of any of claims 27, 28, 32 to 37.

39. A method of treating a muscle disorder in a subject in need thereof, said method comprising administering a therapeutically effective amount of the pharmaceutical composition of any of claims 27-31 and 37.

40. The rAAV vector of claim 18, wherein the transgene is selected from Table 1A or Table 1B.

41. The method of claim 20, or 22-26, wherein the transgene is selected from Table 1A or Table 1B.

42. The pharmaceutical composition for use in delivering a transgene of claim 27 or 28, wherein the transgene is selected from Table 1A or Table 1B.

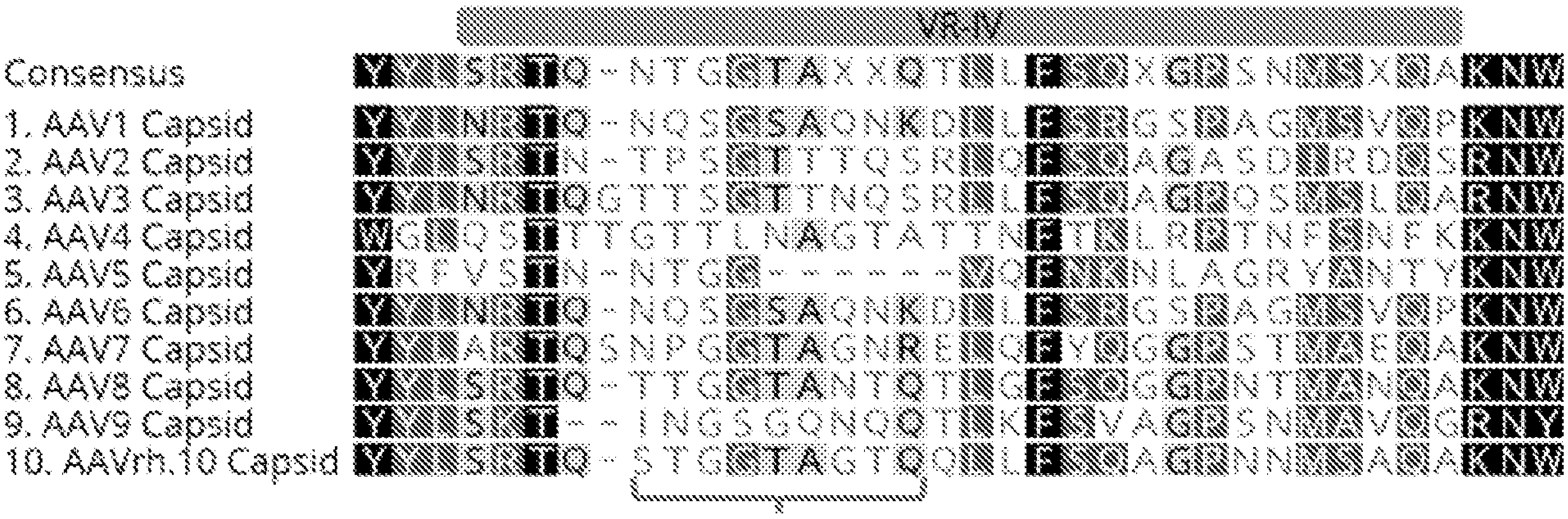
VR-IV
Consensus
1. AAV1 Capsid
2. AAV2 Capsid
3. AAV3 Capsid
4. AAV4 Capsid
5. AAV5 Capsid
6. AAV6 Capsid
7. AAV7 Capsid
8. AAV8 Capsid
9. AAV9 Capsid
10. AAVrh.10 Capsid

FIG. 1

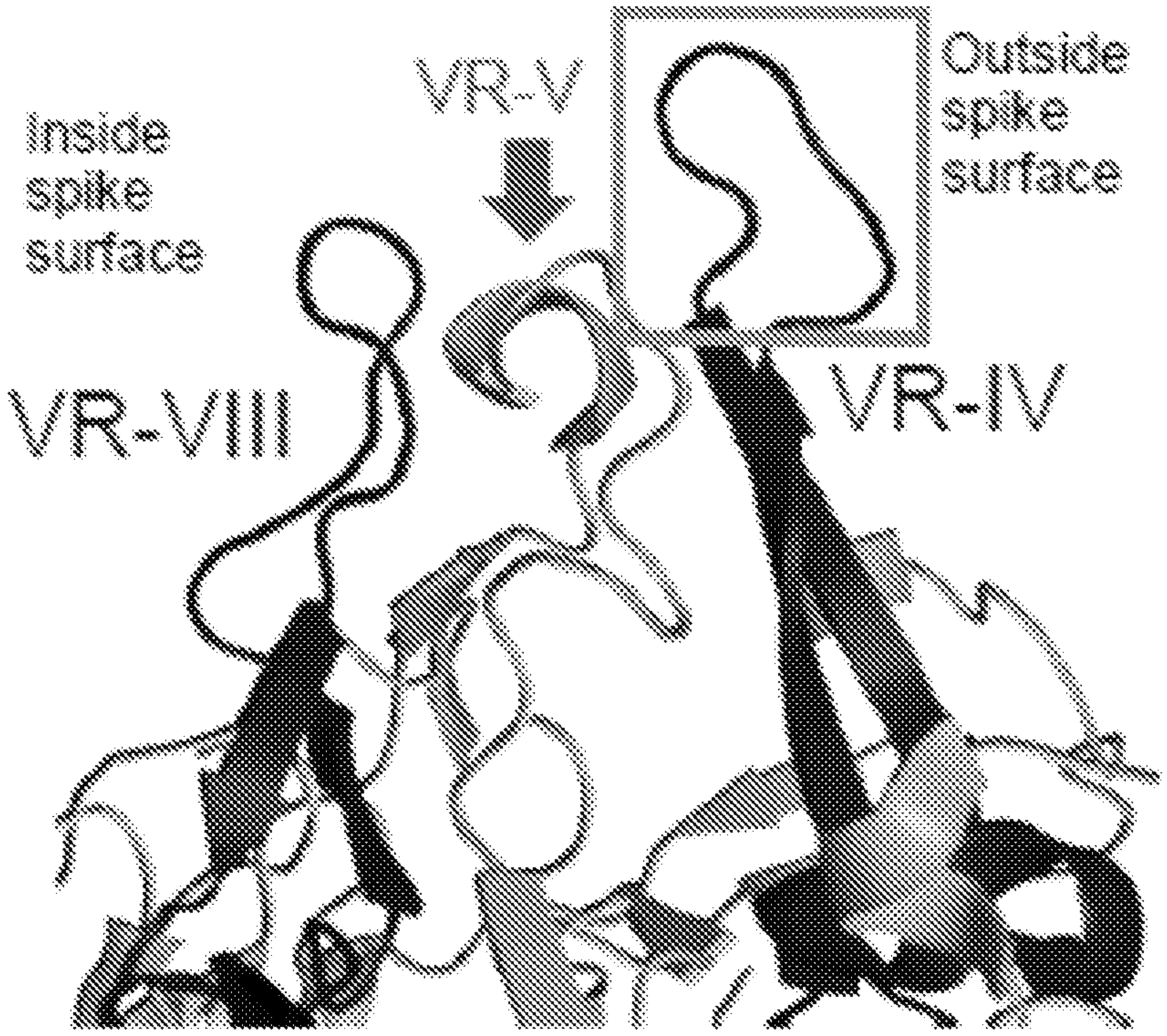
Inside
spike
surface
VR-V
Outside
spike
surface
VR-VIII
VR-IV

FIG. 2

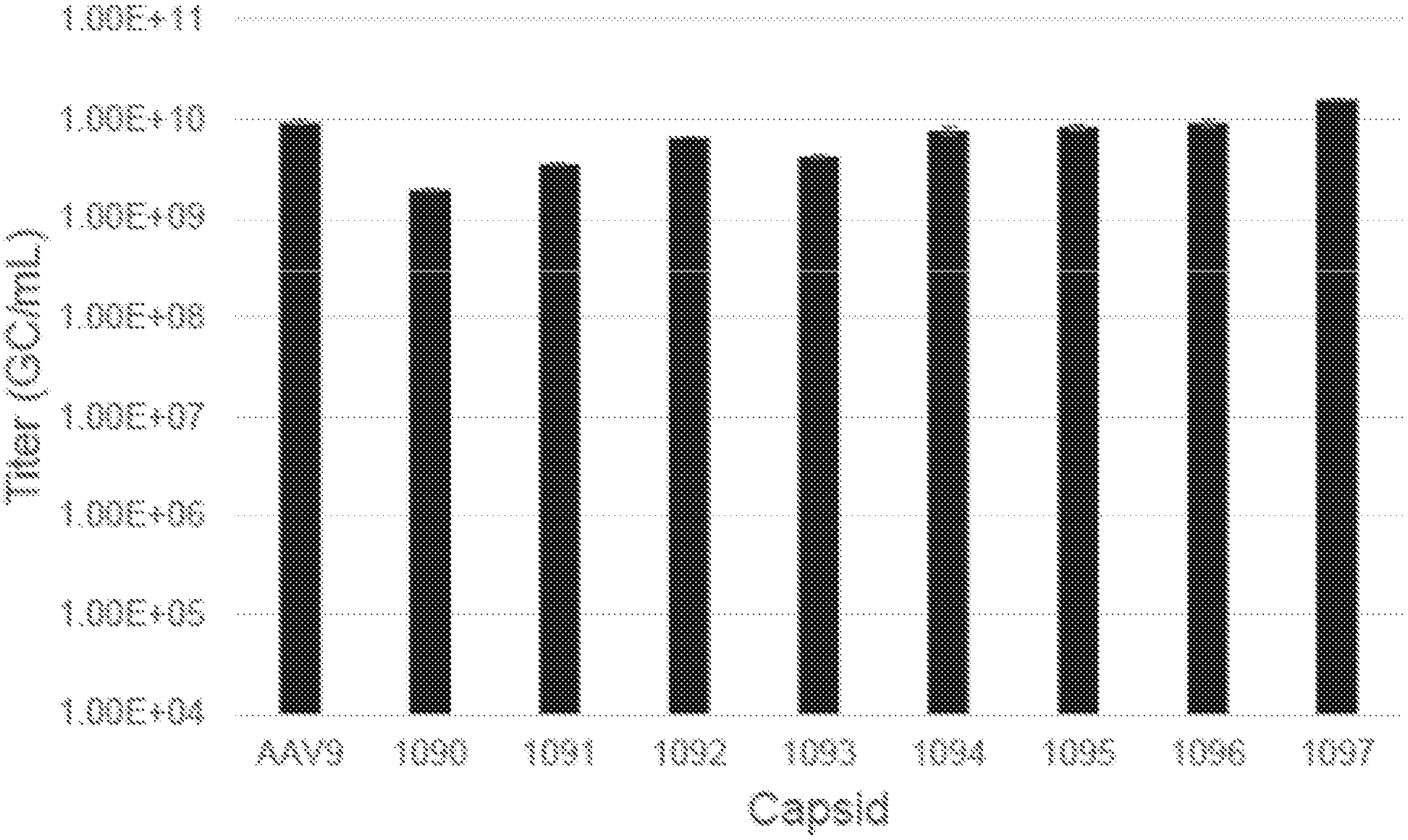
1.00E+11
1.00E+10
1.00E+09
1.00E+08
1.00E+07
1.00E+06
1.00E+05
1.00E+04
Titer (GC/mL)
AAV9
1090
1091
1092
1093
1094
1095
1096
1097
Capsid

FIG. 3

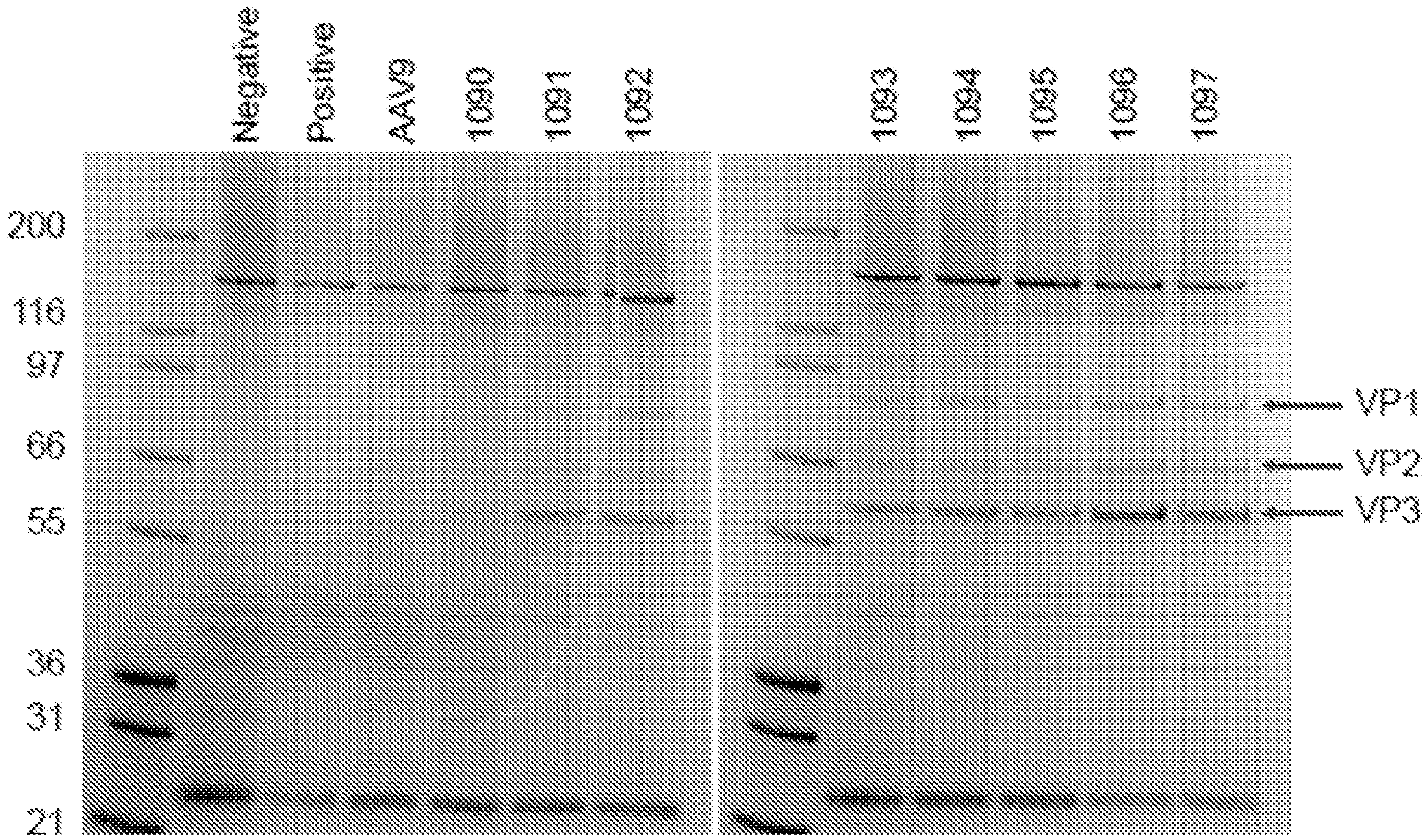
Negative
Positive
AAV9
1090
1091
1092
1093
1094
1095
1096
1097
200
116
97
66
55
36
31
21
VP1
VP2
VP3

FIG. 4

Capsid	% of 9-luc wt
9-luc	100
1090	8.9
1091	6.1
1092	3.2
1093	8.2
1094	4.9
1095	4.0
1096	2.8
1097	2.8

FIG. 5A

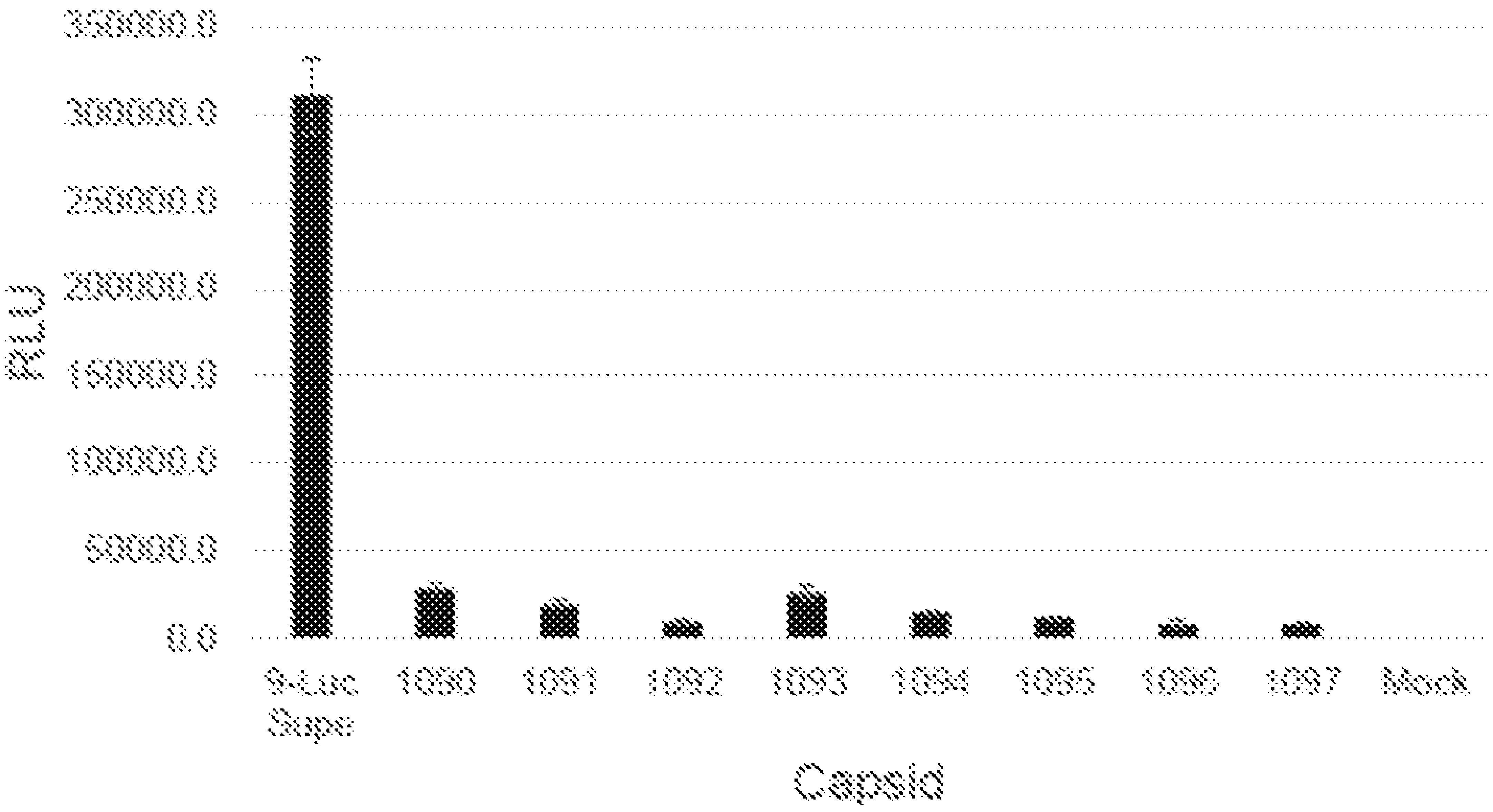

FIG. 5B

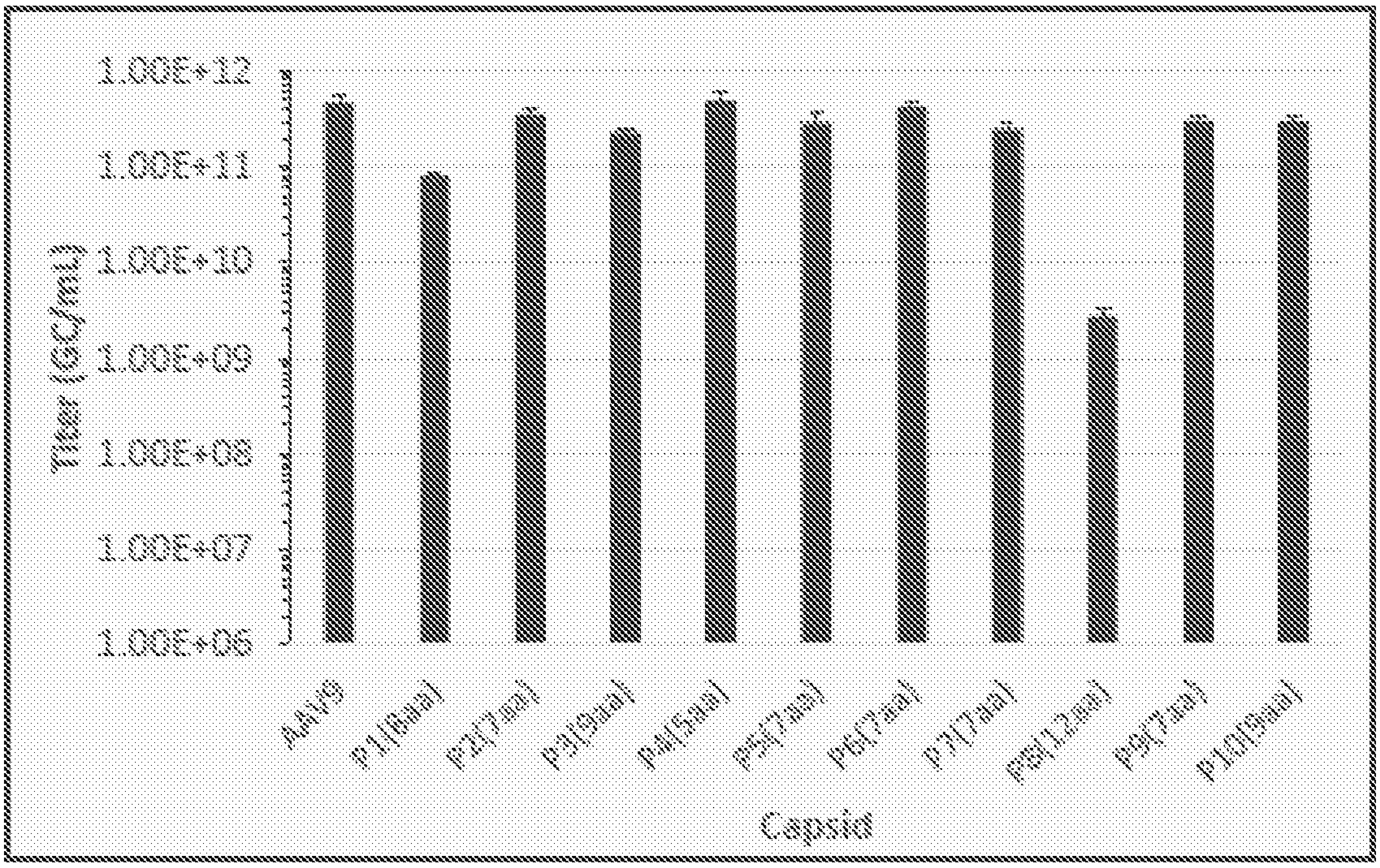

FIG. 6A

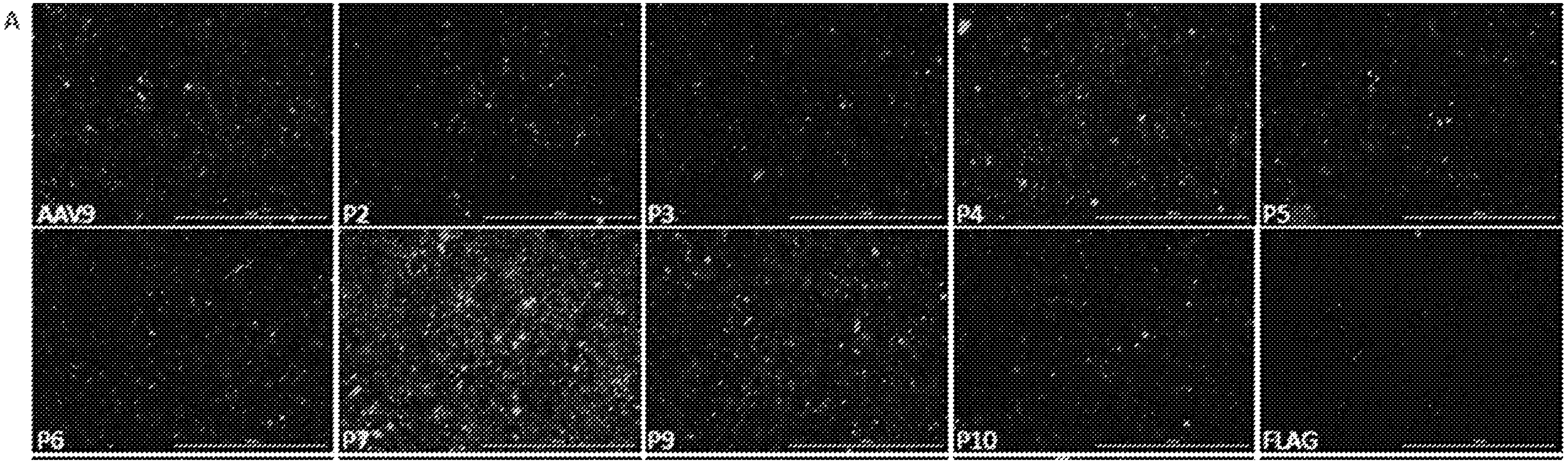

FIG. 6B - LEC2 cell line

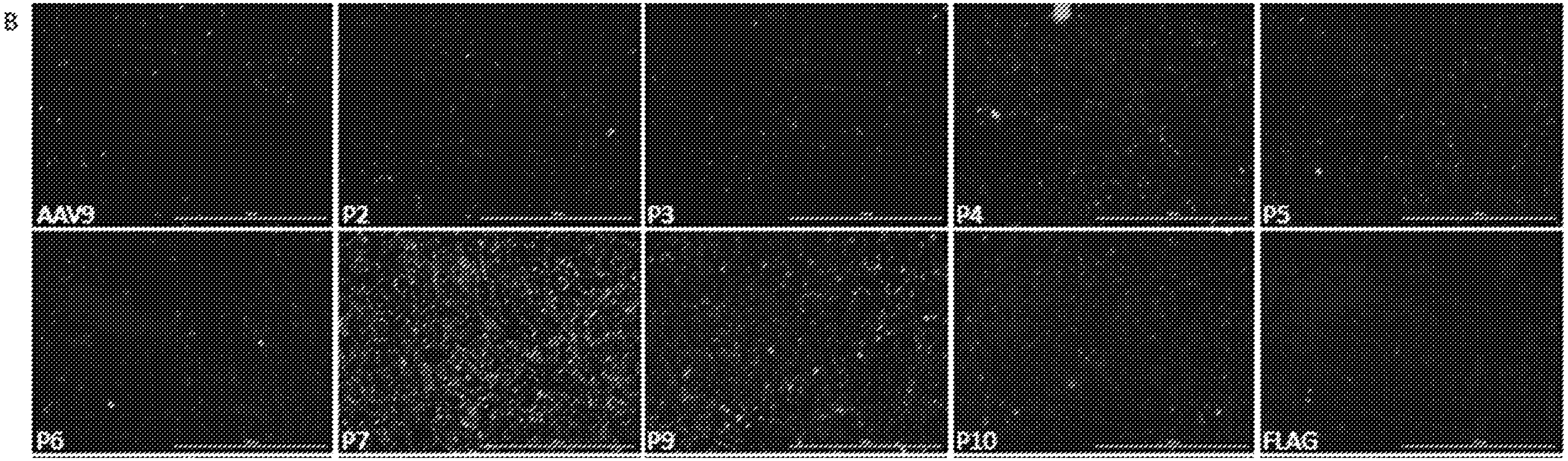

FIG. 6C - HT-22 cell line

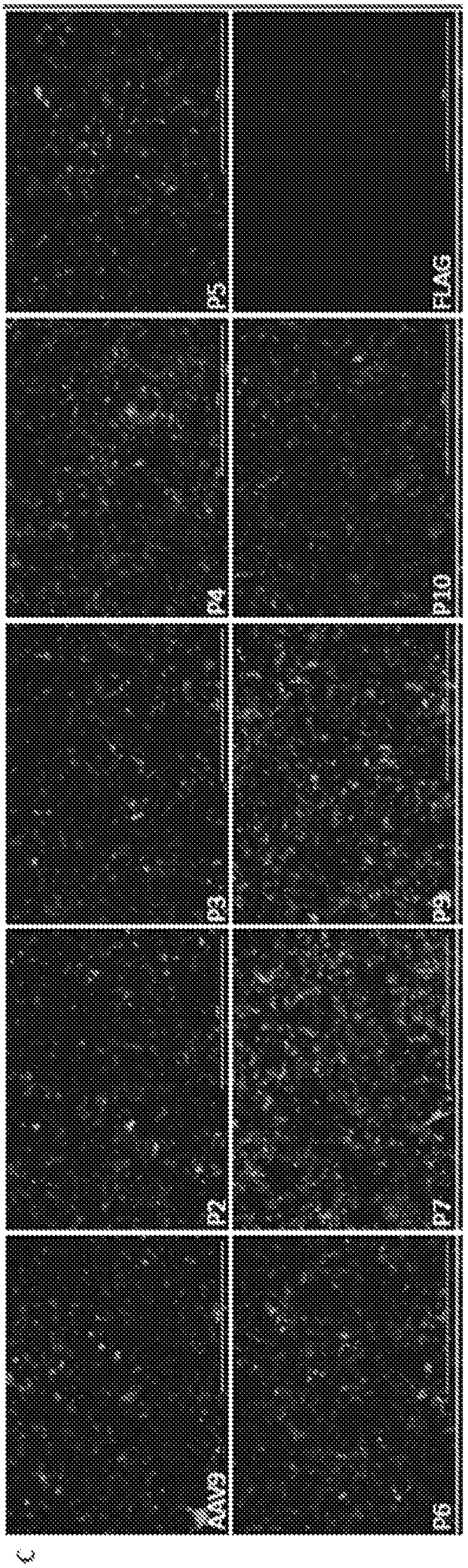

FIG. 6D - hCMEC/D3cell line

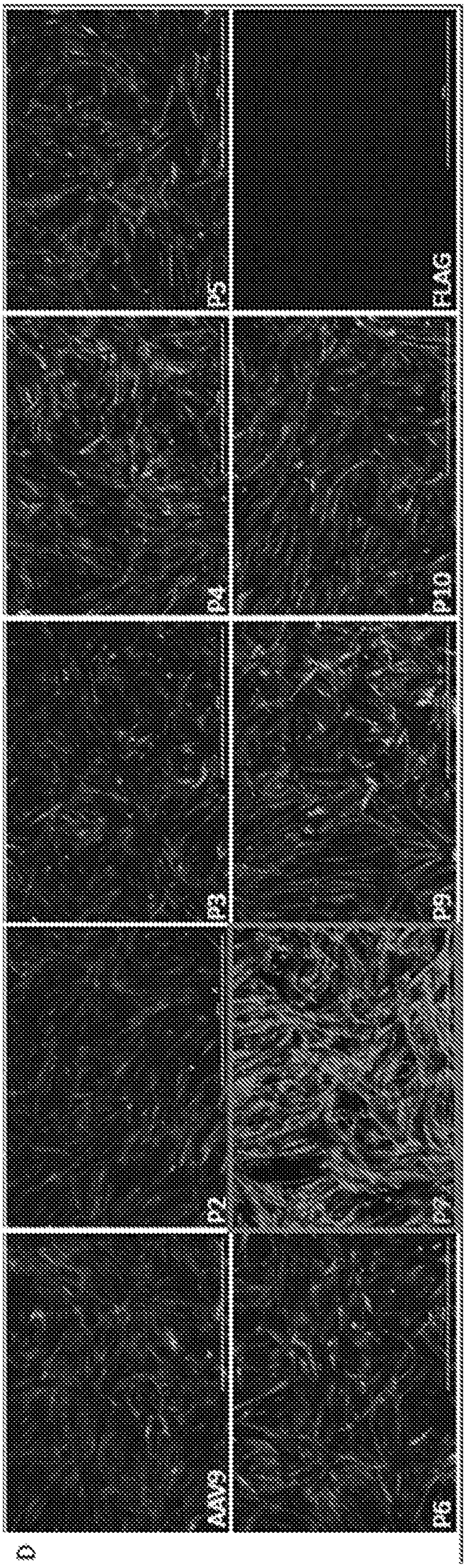

FIG. 6E - C2C12 cell line

FIG. 7 ALIGNMENT OF AAVS 1-9, 3B, 9e, RH10, RH20, RH39, RH73, RH74, HU37, HU12, HU21, HU26, HU37, HU51 and HU53 CAPSID WITH INSERTION SITES HIGHLIGHTED IN GREY

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                                  |         |         |         |         |         |
AAV1                    MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
AAV2                    MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD 60
AAV3                    MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLD 60
AAV3-3                  MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLD 60
AAV3B                   MAADGYLPDWLEDNLSEGIREWWALKPGVPQPKANQQHQDNRRGLVLPGYKYLGPGNGLD 60
AAV4                    -MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQQHQDNARGLVLPGYKYLGPGNGLD 59
AAV4-4                  -MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQQHQDNARGLVLPGYKYLGPGNGLD 59
AAV5                    MSFVDHPPDWLEE-VGEGLREFLGLEAGPPKPKPNQQHQDQARGLVLPGYNYLGPGNGLD 59
AAV6                    MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
AAV7                    MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLD 60
AAV8                    MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
AAV9                    MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPGNGLD 60
AAV9e                   MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPGNGLD 60
rh.10                   MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
rh.20                   MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
rh.39                   MAADGYLPDWLEDNLSEGIREWWALKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
rh.73                   MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
rh.74v1                 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLD 60
rh.74v2                 MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDNGRGLVLPGYKYLGPFNGLD 60
hu.12                   MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHQDDSRGLVLPGYKYLGPFNGLD 60
hu.21                   MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD 60
hu.26                   MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD 60
hu.37                   MAADGYLPDWLEDNLSEGIREWWDLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLD 60
hu.51                   MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD 60
hu.53                   MAADGYLPDWLEDTLSEGIRQWWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPFNGLD 60
                            .: *****: :.**:*::  *: * * **  ::::*: ********:**** ****
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                                 |         |         |         |         |         |
AAV1                    KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV2                    KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
AAV3                    KGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV3-3                  KGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV3B                   KGEPVNEADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV4                    KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQ 119
AAV4-4                  KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQQRLQGDTSFGGNLGRAVFQ 119
AAV5                    RGEPVNRADEVAREHDISYNEQLEAGDNPYLKYNHADAEFQEKLADDTSFGGNLGKAVFQ 119
AAV6                    KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV7                    KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV8                    KGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
AAV9                    KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
AAV9e                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
rh.10                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
rh.20                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
rh.39                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
rh.73                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
rh.74v1                 KGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
rh.74v2                 KGEPVNAADAAALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
hu.12                   KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
hu.21                   KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
hu.26                   KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
hu.37                   KGEPVNAADAAALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQ 120
hu.51                   KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120
hu.53                   KGEPVNEADAAALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQ 120

                                 |         |         |         |         |         |
AAV1                    AKKRVLEPLGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS 179
AAV2                    AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
AAV3                    AKKRILEPLGLVEEAAKTAPGKKGAVDQSPQ-EPDSSSGVGKSGKQPARKRLNFGQTGDS 179
AAV3-3                  AKKRILEPLGLVEEAAKTAPGKKGAVDQSPQ-EPDSSSGVGKSGKQPARKRLNFGQTGDS 179
AAV3B                   AKKRILEPLGLVEEAAKTAPGKKRPVDQSPQ-EPDSSSGVGKSGKQPARKRLNFGQTGDS 179
AAV4                    AKKRVLEPLGLVEQAGETAPGKKRPLIESPQ-QPDSSTGIGKKGKQPAKKKLVFEDETGA 178
AAV4-4                  AKKRVLEPLGLVEQAGETAPGKKRPLIESPQ-QPDSSTGIGKKGKQPAKKKLVFEDETGA 178
AAV5                    AKKRVLEPFGLVEEGAKTAPTGKRIDDHFPKRKKARTEEDSKP-----------STSSDA 168
AAV6                    AKKRVLEPFGLVEEGAKTAPGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDS 179
AAV7                    AKKRVLEPLGLVEEGAKTAPAKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS 180
AAV8                    AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS 180
AAV9                    AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSAGIGKSGAQPAKKRLNFGQTGDT 179
AAV9e                   AKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQ-EPDSSAGIGKSGAQPAKKRLNFGQTGDT 179
rh.10                   AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS 180
rh.20                   AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKTGQQPAKKRLNFGQTGDS 180
rh.39                   AKKRVLEPLGLVEEAAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS 180
rh.73                   AKKRVLEPLGLVEEGAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPARKRLNFGQTGDS 180
rh.74v1                 AKKRVLEPLGLVESPVKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS 180
rh.74v2                 AKKRVLEPLGLVESPVKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS 180
hu.12                   AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTGDA 179
hu.21                   AKKRILEPLGLVEEPVKTAPGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
hu.26                   AKKRILEPLGLVEEPVKTAPGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
hu.37                   AKKRVLEPLGLVEEAAKTAPGKKRPVEPSPQRSPDSSTGIGKKGQQPAKKRLNFGQTGDS 180
hu.51                   AKKRVLEPLGLVGEPVKTAPGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
hu.53                   AKKRVLEPLGLVEEPVKTAPGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDA 179
                        ****:***:****.  :***  *      *  .   :   .*                .:
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                       |         |         |         |         |         |
AAV1          ESVP-DPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR 238
AAV2          DSVP-DPQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDR 238
AAV3          ESVP-DPQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDR 238
AAV3-3        ESVP-DPQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDR 238
AAV3B         ESVP-DPQPLGEPPAAPTSLGSNTMASGGGAPMADNNEGADGVGNSSGNWHCDSQWLGDR 238
AAV4          GDGP----PEGSTSGAMS--DDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGH 232
AAV4-4        GDGP----PEGSTSGAMS--DDSEMRAAAGGAAVEGGQGADGVGNASGDWHCDSTWSEGH 232
AAV5          EAGPSGSQQLQIPAQPASSLGADTMSAGGGGPLGDNNQGADGVGNASGDWHCDSTWMGDR 228
AAV6          ESVP-DPQPLGEPPATPAAVGPTTMASGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR 238
AAV7          ESVP-DPQPLGEPPAAPSSVGSGTVAAGGGAPMADNNEGADGVGNASGNWHCDSTWLGDR 239
AAV8          ESVP-DPQPLGEPPAAPSGVGPNTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
AAV9          ESVP-DPQPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDR 238
AAV9e         ESVP-DPQPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWHCDSQWLGDR 238
rh.10         ESVP-DPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
rh.20         ESVP-DPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
rh.39         ESVP-DPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
rh.73         ESVP-DPQPLGEPPAAPSSVGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
rh.74v1       ESVP-DPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
rh.74v2       ESVP-DPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
hu.12         DSVP-DPQPLGQPPAAPTSLGSTTMATGSGAPMADNNEGADGVGNSSGNWHCDSQWLGDR 238
hu.21         DSVP-DPRPLGQPPAAPSGLGTNTMASGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDR 238
hu.26         DSVP-DPQPLGQPPAAPSGLGTNTMASGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDR 238
hu.37         ESVP-DPQPIGEPPAGPSGLGSGTMAAGGGAPMADNNEGADGVGSSSGNWHCDSTWLGDR 239
hu.51         DSVP-DPQPLGQPPAAPSGLGTNTMATGSGAPMADNNEGADGVGNSSGNWHCDSTWMGDR 238
hu.53         DSVP-DPQPLRQPPAAPTSLGSTTMATGSGAPMADNNEGADGVGNSSGNWHCDSQWLGDR 238
                 *             :  .   : :..*.   :..:******.:**:***** *  .:

              |         |         |         |         |         |
AAV1          VITTSTRTWALPTYNNHLYKQISSAST-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 297
AAV2          VITTSTRTWALPTYNNHLYKQISSQ-S-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
AAV3          VITTSTRTWALPTYNNHLYKQISSQ-S-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
AAV3-3        VITTSTRTWALPTYNNHLYKQISSQ-S-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
AAV3B         VITTSTRTWALPTYNNHLYKQISSQ-S-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
AAV4          VTTTSTRTWVLPTYNNHLYKRLGE-----SLQSNTYNGFSTPWGYFDFNRFHCHFSPRDW 287
AAV4-4        VTTTSTRTWVLPTYNNHLYKRLGE-----SLQSNTYNGFSTPWGYFDFNRFHCHFSPRDW 287
AAV5          VVTKSTRTWVLPSYNNHQYREIKSGSVD-GSNANAYFGYSTPWGYFDFNRFHSHWSPRDW 287
AAV6          VITTSTRTWALPTYNNHLYKQISSAST-GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 297
AAV7          VITTSTRTWALPTYNNHLYKQISSETA-GSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 298
AAV8          VITTSTRTWALPTYNNHLYKQISNGTSGGATNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
AAV9          VITTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDW 298
AAV9e         VITTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFSPRDW 298
rh.10         VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
rh.20         VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
rh.39         VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
rh.73         VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
rh.74v1       VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
rh.74v2       VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
hu.12         VITTSTRTWALPTYNNHLYKQISSQS--GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
hu.21         VITTSTRTWALPTYNNHLYKQISSQS--GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
hu.26         VITTSTRTWALPTYNNHLYKQISSQS--GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
hu.37         VITTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGYSTPWGYFDFNRFHCHFSPRDW 299
hu.51         VITTSTRTWALPTYNNHLYKQISSQS--GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
hu.53         VITTSTRTWALPTYNNHLYKQISSQS--GASNDNHYFGYSTPWGYFDFNRFHCHFSPRDW 296
              * *.*****.**:**** *:.:       . : * * *:*************.*:*****
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                          |         |         |         |         |         |
AAV1             QRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS 357
AAV2             QRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
AAV3             QRLINNNWGFRPKKLSFKLFNIQVRGVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
AAV3-3           QRLINNNWGFRPKKLSFKLFNIQVRGVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
AAV3B            QRLINNNWGFRPKKLSFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
AAV4             QRLINNNWGMRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDA 347
AAV4-4           QRLINNNWGMRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFADSSYELPYVMDA 347
AAV5             QRLINNYWGFRPRSLRVKIFNIQVKEVTVQDSTTTIANNLTSTVQVFTDDDYQLPYVVGN 347
AAV6             QRLINNNWGFRPKRLNFKLFNIQVKEVTTNDGVTTIANNLTSTVQVFSDSEYQLPYVLGS 357
AAV7             QRLINNNWGFRPKKLRFKLFNIQVKEVTTNDGVTTIANNLTSTIQVFSDSEYQLPYVLGS 358
AAV8             QRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
AAV9             QRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGS 358
AAV9e            QRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTSTVQVFTDSDYQLPYVLGS 358
rh.10            QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
rh.20            QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
rh.39            QRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
rh.73            QRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
rh.74v1          QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
rh.74v2          QRLINNNWGFRPKRLNFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
hu.12            QRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 359
hu.21            QRLINNNWGFRPKRLSFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
hu.26            QRLINNNWGFRPKRLSFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
hu.37            QRLINNNWGFRPKRLSFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTDSEYQLPYVLGS 359
hu.51            QRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
hu.53            QRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTTIANNLTSTVQVFTDSEYQLPYVLGS 356
                 ****** **:**: : .*:*****: ** .:. .*:*******:*:*:*..*:****:.

                          |         |         |         |         |         |
AAV1             AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY 414
AAV2             AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY 413
AAV3             AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY 413
AAV3-3           AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY 413
AAV3B            AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY 413
AAV4             GQEGSLPPFPNDVFMVPQYGYCGLVTGNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITY 407
AAV4-4           GQEGSLPPFPNDVFMVPQYGYCGLVTGNTSQQQTDRNAFYCLEYFPSQMLRTGNNFEITY 407
AAV5             GTEGCLPAFPPQVFTLPQYGYATLNRDNT-ENPTERSSFFCLEYFPSKMLRTGNNFEFTY 406
AAV6             AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY 414
AAV7             AHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFSY 415
AAV8             AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFTY 416
AAV9             AHEGCLPPFPADVFMIPQYGYLTLNDG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY 415
AAV9e            AHEGCLPPFPADVFMIPQYGYLTLNDG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY 415
rh.10            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
rh.20            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
rh.39            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
rh.73            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFSY 416
rh.74v1          AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
rh.74v2          AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
hu.12            AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRPSFYCLEYFPSQMLRTGNNFTFSY 413
hu.21            AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY 413
hu.26            AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY 413
hu.37            AHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFSY 416
hu.51            AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFSY 413
hu.53            AHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFSY 413
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                 |         |         |         |         |         |
AAV1             TFEEVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQN-QSGSAQNKDLLFSRGSPAGMSV 473
AAV2             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTN-TPSGTTTQSRLQFSQAGASDIRD 472
AAV3             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSL 473
AAV3-3           TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSL 473
AAV3B            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQGTTSGTTNQSRLLFSQAGPQSMSL 473
AAV4             SFEKVPFHSMYAHSQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATTNFTKLRPTNFSN 467
AAV4-4           SFEKVPFHSMYAHSQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATTNFTKLRPTNFSN 467
AAV5             NFEEVPFHSSFAPSQNLFKLANPLVDQYLYRFVSTNNTG-------GVQFNKNLAGRYAN 459
AAV6             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQN-QSGSAQNKDLLFSRGSPAGMSV 473
AAV7             SFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLARTQSNPGGTAGNRELQFYQGGPSTMAE 475
AAV8             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQT-TGGTANTQTLGFSQGGPNTMAN 475
AAV9             EFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTINGS--GQNQQTLKFSVAGPSNMAV 473
AAV9e            EFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTINGS--GQNQQTLKFSVAGPSNMAV 473
rh.10            QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTAGTQQLLFSQAGPNNMSA 475
rh.20            QFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTAGTQQLLFSQAGPNNMSA 475
rh.39            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTQGTQQLLFSQAGPANMSA 475
rh73             TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTAGTQQLLFSQAGPSNMSA 475
rh.74v1          NFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTAGTQQLLFSQAGPNNMSA 475
rh.74v2          NFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTAGTQQLLFSQAGPNNMSA 475
hu.12            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQS-NSGTLQQSRLLFSQAGPTSMSL 472
hu.21            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTN-TPSGTTTMSRLQFSQAGASDIRD 472
hu.26            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTN-TPSGTTTMSRLQFSQAGASDIRD 472
hu.37            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTQS-TGGTQGTQQLLFSQAGPANMSA 475
hu.51            TFEDVPFHSGYAHSQSLDRLMNPLIDQYLYYLSTTN-TPSGTTTQSRLQFSQAGASDIRD 472
hu.53            TFEDVPFHSSYAHSQSLDRLMNPLIDQYLYYLNRTQ-TASGTQ-QSRLLFSQAGPTSMSL 471
                  **.***** :* **.* :* ***:****: :  *              *

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AAV1             QPKNWLPGPCYRQQRVSKTKTDNNNSNF-----TWTGASKYNLNGRESIINPGTAMASHK 528
AAV2             QSRNWLPGPCYRQQRVSKTSADNNNSEY-----SWTGATKYHLNGRDSLVNPGPAMASHK 527
AAV3             QARNWLPGPCYRQQRLSKTANDNNNSNF-----PWTAASKYHLNGRDSLVNPGPAMASHK 528
AAV3-3           QARNWLPGPCYRQQRLSKTANDNNNSNF-----PWTAASKYHLNGRDSLVNPGPAMASHK 528
AAV3B            QARNWLPGPCYRQQRLSKTANDNNNSNF-----PWTAASKYHLNGRDSLVNPGPAMASHK 528
AAV4             FKKNWLPGPSIKQQGFSKTANQNYKIPATGSDSLIKYETHSTLDGRWSALTPGPPMATAG 527
AAV4-4           FKKNWLPGPSIKQQGFSKTANQNYKIPATGSDSLIKYETHSTLDGRWSALTPGPPMATAG 527
AAV5             TYKNWFPGPMGRTQGWNLGSGVNRASVS-----AFATTNRMELEGASYQVPPQPNGMTNN 514
AAV6             QPKNWLPGPCYRQQRVSKTKTDNNNSNF-----TWTGASKYNLNGRESIINPGTAMASHK 528
AAV7             QAKNWLPGPCFRQQRVSKTLDQNNNSNF-----AWTGATKYHLNGRNSLVNPGVAMATHK 530
AAV8             QAKNWLPGPCYRQQRVSTTTGQNNNSNF-----AWTAGTKYHLNGRNSLANPGIAMATHK 530
AAV9             QGRNYIPGPSYRQQRVSTTVTQNNNSEF-----AWPGASSWALNGRNSLMNPGPAMASHK 528
AAV9e            QGRNYIPGPSYRQQRVSTTVTQNNNSEF-----AWPGASSWALNGRNSLMNPGPAMASHK 528
rh.10            QAKNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATHK 530
rh.20            QAKNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATHK 530
rh.39            QAKNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATHK 530
rh.73            QARNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATNK 530
rh.74v1          QAKNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATHK 530
rh.74v2          QAKNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATHK 530
hu.12            QAKNWLPGPCYRQQRLSKQANDNNNSNF-----PWTAATKYHLNGRDSLVNPGPAMASHK 527
hu.21            QSRNWLPGPCYRQQRVSKTAADNNNSDY-----SWTGATKYHLNGRDSLVNPGPAMASHK 527
hu.26            QSRNWLPGPCYRQQRVSKTAADNNNSDY-----SWTGATKYHLNGRDSLVNPGPAMASHK 527
hu.37            QAKNWLPGPCYRQQRVSTTLSQNNNSNF-----AWTGATKYHLNGRDSLVNPGVAMATHK 530
hu.51            QSRNWLPGPCYRQQRVSKTSADNNNSEY-----SWTGATKYHLNGRDSLVNPGPAMASHK 527
hu.53            QAKNWLPGPCYRQQRLSKQANDNNNSNF-----PWTGATKYYLNGRDSLVNPGPAMASHK 526
                   :*::***  : *  .     *               .   *:*      *     :
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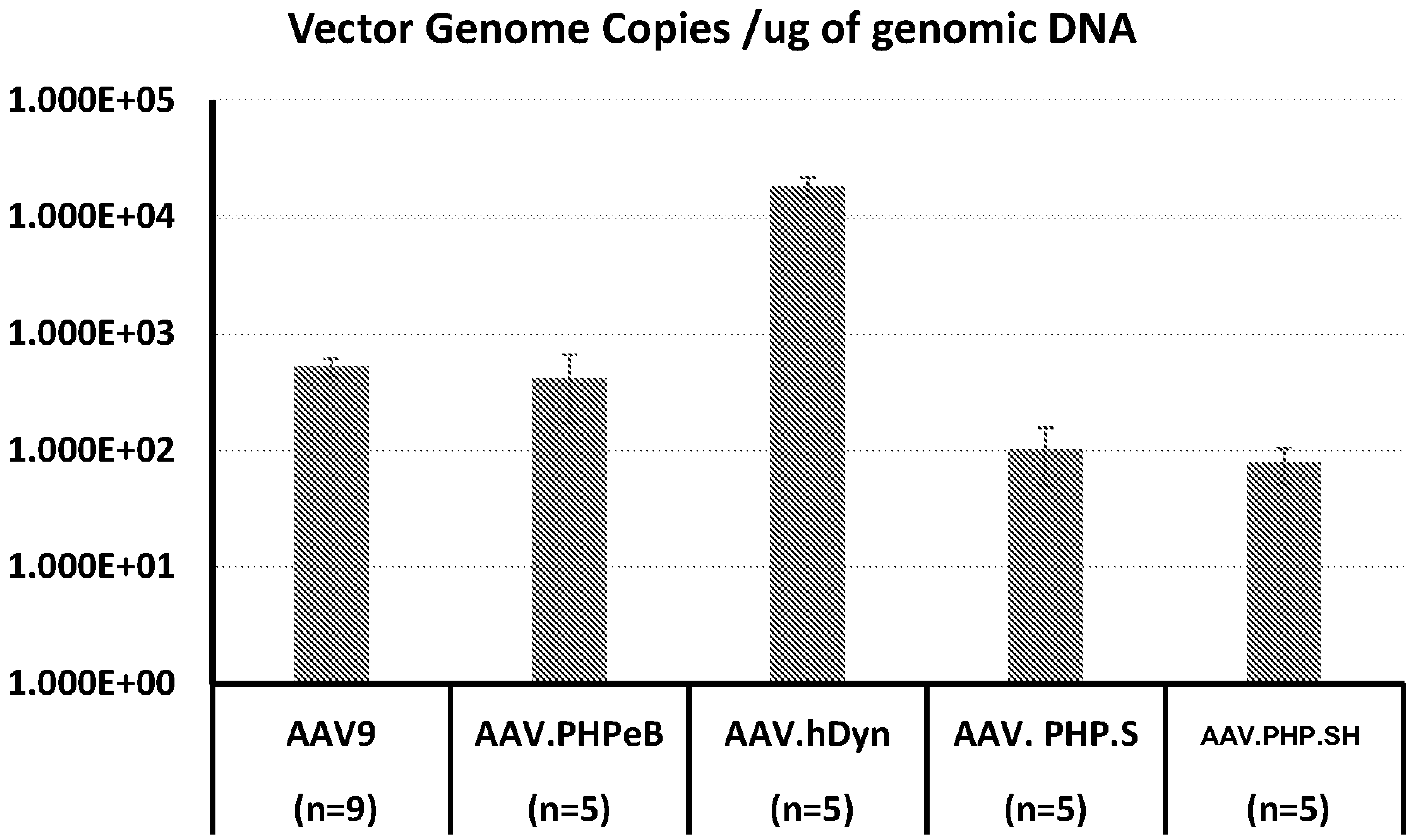
                          |         |         |         |         |         |
AAV1             DDEDKFFPMSGVMIFGKESAGA---SNTALDNVMITDEEEIKATNPVATERFGTVAVNFQ 585
AAV2             DDEEKFFPQSGVLIFGKQGSEK---TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQ 584
AAV3             DDEEKFFPMHGNLIFGKEGTTA---SNAELDNVMITDEEEIRTTNPVATEQYGTVANNLQ 585
AAV3-3           DDEEKFFPMHGNLIFGKEGTTA---SNAELDNVMITDEEEIRTTNPVATEQYGTVANNLQ 585
AAV3B            DDEEKFFPMHGNLIFGKEGTTA---SNAELDNVMITDEEEIRTTNPVATEQYGTVANNLQ 585
AAV4             PADSKFSN-SQLIFAGPKQNGN---TATVPGTLIFTSEEELAATNATDTDMWGNLPGGDQ 583
AAV4-4           PADSKFSN-SQLIFAGPKQNGN---TATVPGTLIFTSEEELAATNATDTDMWGNLPGGDQ 583
AAV5             LQGSNTYALENTMIFNSQPANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQ 574
AAV6             DDKDKFFPMSGVMIFGKESAGA---SNTALDNVMITDEEEIKATNPVATERFGTVAVNLQ 585
AAV7             DDEDRFFPSSGVLIFGKTGATN----KTTLENVLMTNEEEIRPTNPVATEEYGIVSSNLQ 586
AAV8             DDEERFFPSNGILIFGKQNAAR---DNADYSDVMLTSEEEIKTTNPVATEEYGIVADNLQ 587
AAV9             EGEDRFFPLSGSLIFGKQGTGR---DNVDADKVMITNEEEIKTTNPVATESYGQVATNHQ 585
AAV9e            EGEDRFFPLSGSLIFGKQGTGR---DNVDADKVMITNEEEIKTTNPVATESYGQVATNHQ 585
rh.10            DDEERFFPSSGVLMFGKQGAGK---DNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
rh.20            DDEERFFPSSGVLMFGKQGAGK---DNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
rh.39            DDEERFFPSSGVLMFGKQGAGR---DNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
rh.73            DDEDRFFPSSGILMFGKQGAGK---DNVDYSNVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
rh.74v1          DDEERFFPSSGVLMFGKQGAGK---DNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
rh.74v2          DDEERFFPSSGVLMFGKQGAGK---DNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
hu.12            DDEEKFFPMHGTLIFGKQGTNA---NDADLEHVMITDEEEIRTTNPVATEQYGNVSNNLQ 584
hu.21            DDEEKYFPQSGVLIFGKQDSGK---TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQ 584
hu.26            DDEEKYFPQSGVLIFGKQDSGK---TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQ 584
hu.37            DDEERFFPSSGVLMFGKQGAGR---DNVDYSSVMLTSEEEIKTTNPVATEQYGVVADNLQ 587
hu.51            DNEEKFFPQSGVLIFGKQGSEK---TNVDIEKVMITDEEEIRTTNPVATEQYGSVSTNLQ 584
hu.53            DDEEKFFPMHGTLIFGKEGTNA---TNAELENVMITDEEEIRTTNPVATEQYGYVSNNLQ 583
                    ..       :: .                :::*.*.*   .* .  :  * :  . *

                  |         |         |         |         |         |
AAV1             SSS#TDPATGDVHAMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKN-PPP 645
AAV2             RGN#RQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 644
AAV3             SSN#TAPTTGTVNHQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 645
AAV3-3           SSN#TAPTTGTVNHQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 645
AAV3B            SSN#TAPTTRTVNDQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 645
AAV4             SNS#NLPTVDRLTALGAVPGMVWQNRDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKH-PPP 643
AAV4-4           SNS#NLPTVDRLTALGAVPGMVWQNRDIYYQGPIWAKIPHTDGHFHPSPLIGGFGLKH-PPP 643
AAV5             SST#TAPATGTYNLQEIVPGSVWMERDVYLQGPIWAKIPETGAHFHPSPAMGGFGLKH-PPP 634
AAV6             SSS#TDPATGDVHVMGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 645
AAV7             AAN#TAAQTQVVNNQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 646
AAV8             QQN#TAPQIGTVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
AAV9             SAQ#AQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGMKH-PPP 645
AAV9e            SDG#AQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGMKH-PPP 645
AAVrh10          QQN#AAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
AAVrh20          QQN#AAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
rh.39            QTN#TGPIVGNVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
rh.73            RQN#TAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
rh.74v1          QQN#AAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
rh.74v2          QQN#AAPIVGAVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
hu.12            NSN#TGPTTENVNHQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 644
hu.21            SGN#TQAATSDVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 644
hu.26            SGN#TQAATSDVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 644
hu.37            QTN#TGPIVGNVNSQGALPGMVWQNRDVYLQGPIWAKIPHTDGNFHPSPLMGGFGLKH-PPP 647
hu.51            RGN#RQAATADVNTQGVLPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKHHPPP 645
hu.53            NSN#TAASTETVNHQGALPGMVWQDRDVYLQGPIWAKIPHTDGHFHPSPLMGGFGLKH-PPP 644
                                  :** ** :**:* *********.*..:***** :****:*:***
```

```
                                 |         |         |         |         |         |
AAV1                    QILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNY 705
AAV2                    QILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 704
AAV3                    QIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 705
AAV3-3                  QIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 705
AAV3B                   QIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 705
AAV4                    QIFIKNTPVPANPATTFSSTPVNSFITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNY 703
AAV4-4                  QIFIKNTPVPANPATTFSSTPVNSFITQYSTGQVSVQIDWEIQKERSKRWNPEVQFTSNY 703
AAV5                    MMLIKNTPVPGNI-TSFSDVPVSSFITQYSTGQVTVEMEWELKKENSKRWNPEIQYTNNY 693
AAV6                    QILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIEWELQKENSKRWNPEVQYTSNY 705
AAV7                    QILIKNTPVPANPPEVFTPAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNF 706
AAV8                    QILIKNTPVPADPPTTFNQSKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
AAV9                    QILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 705
AAV9e                   QILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 705
rh.10                   QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
rh.20                   QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
rh.39                   QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
rh.73                   QILIKNTPVPADPPTAFNQAKLNSFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
rh.74v1                 QILIKNTPVPADPPTTFTKAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
rh.74v2                 QILIKNTPVPADPPTTFNQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
hu.12                   QIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 704
rh.21                   QILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 704
hu.26                   QILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 704
hu.37                   QILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 707
hu.51                   QILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 705
hu.53                   QIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNY 704
                         ::*******.:    *.   . ***********:*:::**::**.*******:*:*.*:

                                  |         |         |
AAV1                    AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736 (SEQ ID NO: 59)
AAV2                    NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735 (SEQ ID NO: 60)
AAV3                    NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 61)
AAV3-3                  NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 78)
AAV3B                   NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 87)
AAV4                    GQQNSLLWAPDAAGKYTEPRAIGTRYLTHHL 734 (SEQ ID NO: 62)
AAV4-4                  GQQNSLLWAPDAAGKYTEPRAIGTRYLTHHL 734 (SEQ ID NO: 79)
AAV5                    NDPQFVDFAPDSTGEYRTTRPIGTRYLTRPL 724 (SEQ ID NO: 63)
AAV6                    AKSANVDFTVDNNGLYTEPRPIGTRYLTRPL 736 (SEQ ID NO: 64)
AAV7                    EKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL 737 (SEQ ID NO: 65)
AAV8                    YKSTSVDFAVNTEGVYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 66)
AAV9                    YKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 67)
AAV9e                   YKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 68)
rh.10                   YKSTNVDFAVNTDGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 69)
rh.20                   YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 70)
rh.39                   YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 73)
rh.73                   YKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL 739 (SEQ ID NO: 88)
rh.74v1                 YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 72)
rh.74v2                 YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 80)
hu.12                   NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735 (SEQ ID NO: 75)
hu.21                   NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735 (SEQ ID NO: 74)
hu.26                   NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 735 (SEQ ID NO: 76)
hu.37                   YKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL 738 (SEQ ID NO: 71)
hu.51                   NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 736 (SEQ ID NO: 89)
hu.53                   NKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL 737 (SEQ ID NO: 77)
                         .   : :: :  * *   * *******: *
```

FIG. 8


Vector Genome Copies /ug of genomic DNA
1.000E+05
1.000E+04
1.000E+03
1.000E+02
1.000E+01
1.000E+00
AAV9
(n=9)
AAV.PHPeB
(n=5)
AAV.hDyn
(n=5)
AAV. PHP.S
(n=5)
AAV.PHP.SH
(n=5)

FIGs. 9A-9C AAV9- TLAAPFK (SEQ ID NO: 1)

MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60
KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120
AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180
SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240
TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300
LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360
EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420
PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGSGQNQQT LKFSVAGPSN MAVQGRNYIP 480
GPSYRQQRVS TTVTQNNNSE FAWPGASSWA LNGRNSLMNP GPAMASHKEG EDRFFPLSGS 540
LIFGKQGTGR DNVDADKVMI TNEEEIKTTN PVATESYGQV ATNHQSAQ**TL** **AAPFK**AQAQT 600
GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660
VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720
AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 125)

FIG. 9A (TLAAPFK (SEQ ID NO: 1) INSERTION BETWEEN Q588 AND A589)

MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60
KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120
AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180
SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240
TTSTRTWALP TYNNHLYKQI SNSTSGGS**TL** **AAPFK**SNDNA YFGYSTPWGY FDFNRFHCHF 300
SPRDWQRLIN NNWGFRPKRL NFKLFNIQVK EVTDNNGVKT IANNLTSTVQ VFTDSDYQLP 360
YVLGSAHEGC LPPFPADVFM IPQYGYLTLN DGSQAVGRSS FYCLEYFPSQ MLRTGNNFQF 420
SYEFENVPFH SSYAHSQSLD RLMNPLIDQY LYYLSKTING SGQNQQTLKF SVAGPSNMAV 480
QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540
FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600
GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660
VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720
AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 126)

FIG. 9B (TLAAPFK (SEQ ID NO: 1) INSERTION BETWEEN S268 AND S269

MAADGYLPDW LEDNLSEGIR EWWALKPGAP QPKANQQHQD NARGLVLPGY KYLGPGNGLD 60
KGEPVNAADA AALEHDKAYD QQLKAGDNPY LKYNHADAEF QERLKEDTSF GGNLGRAVFQ 120
AKKRLLEPLG LVEEAAKTAP GKKRPVEQSP QEPDSSAGIG KSGAQPAKKR LNFGQTGDTE 180
SVPDPQPIGE PPAAPSGVGS LTMASGGGAP VADNNEGADG VGSSSGNWHC DSQWLGDRVI 240
TTSTRTWALP TYNNHLYKQI SNSTSGGSSN DNAYFGYSTP WGYFDFNRFH CHFSPRDWQR 300
LINNNWGFRP KRLNFKLFNI QVKEVTDNNG VKTIANNLTS TVQVFTDSDY QLPYVLGSAH 360
EGCLPPFPAD VFMIPQYGYL TLNDGSQAVG RSSFYCLEYF PSQMLRTGNN FQFSYEFENV 420
PFHSSYAHSQ SLDRLMNPLI DQYLYYLSKT INGS**TLAAPF** **K**GQNQQTLKF SVAGPSNMAV 480
QGRNYIPGPS YRQQRVSTTV TQNNNSEFAW PGASSWALNG RNSLMNPGPA MASHKEGEDR 540
FFPLSGSLIF GKQGTGRDNV DADKVMITNE EEIKTTNPVA TESYGQVATN HQSAQAQAQT 600
GWVQNQGILP GMVWQDRDVY LQGPIWAKIP HTDGNFHPSP LMGGFGMKHP PPQILIKNTP 660
VPADPPTAFN KDKLNSFITQ YSTGQVSVEI EWELQKENSK RWNPEIQYTS NYYKSNNVEF 720
AVNTEGVYSE PRPIGTRYLT RNL (SEQ ID NO: 127)

FIG. 9C (TLAAPFK (SEQ ID NO:1) INSERTION BETWEEN S454 AND G455)

FIGs. 10A-10B

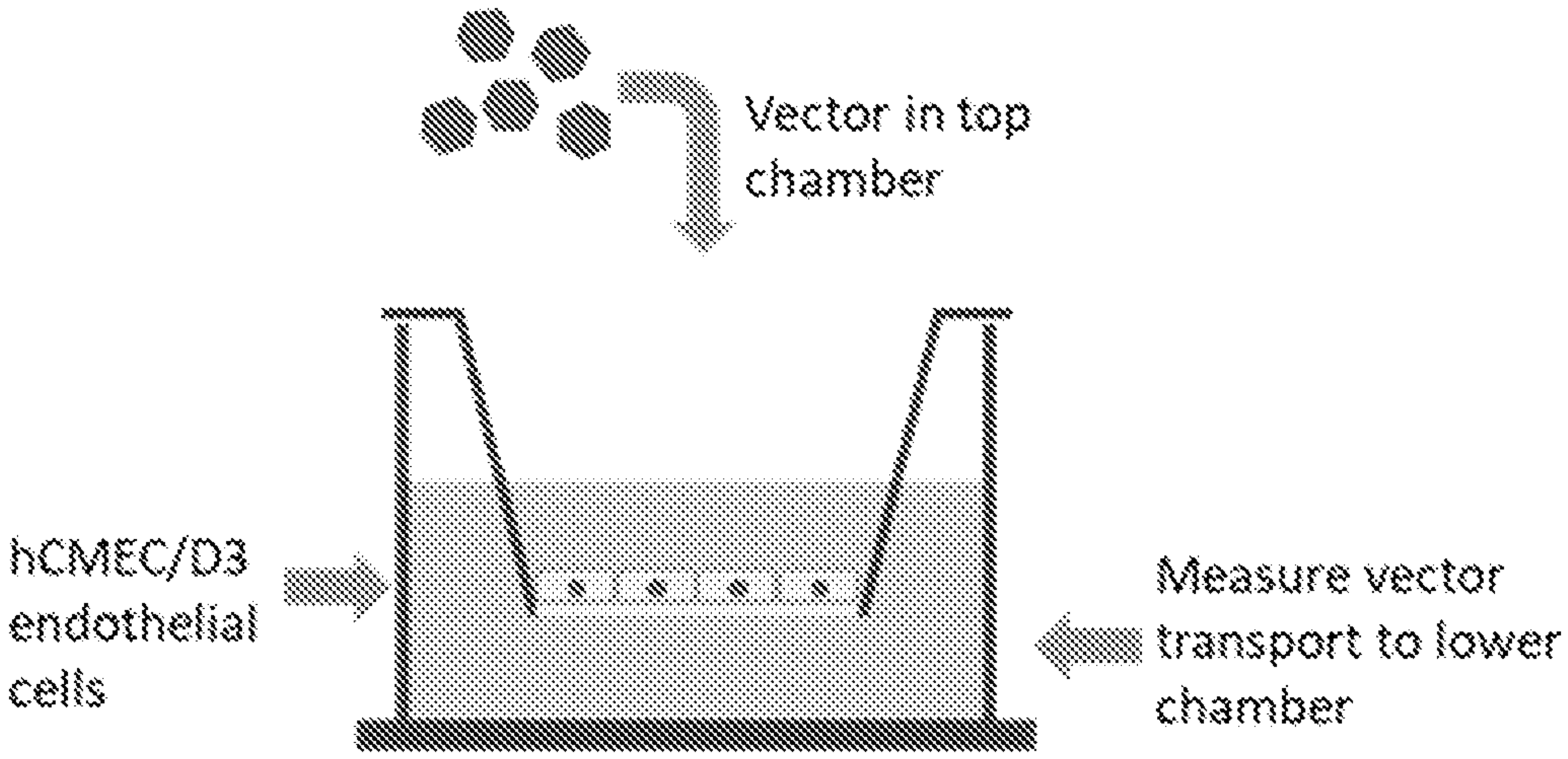


FIG. 10A

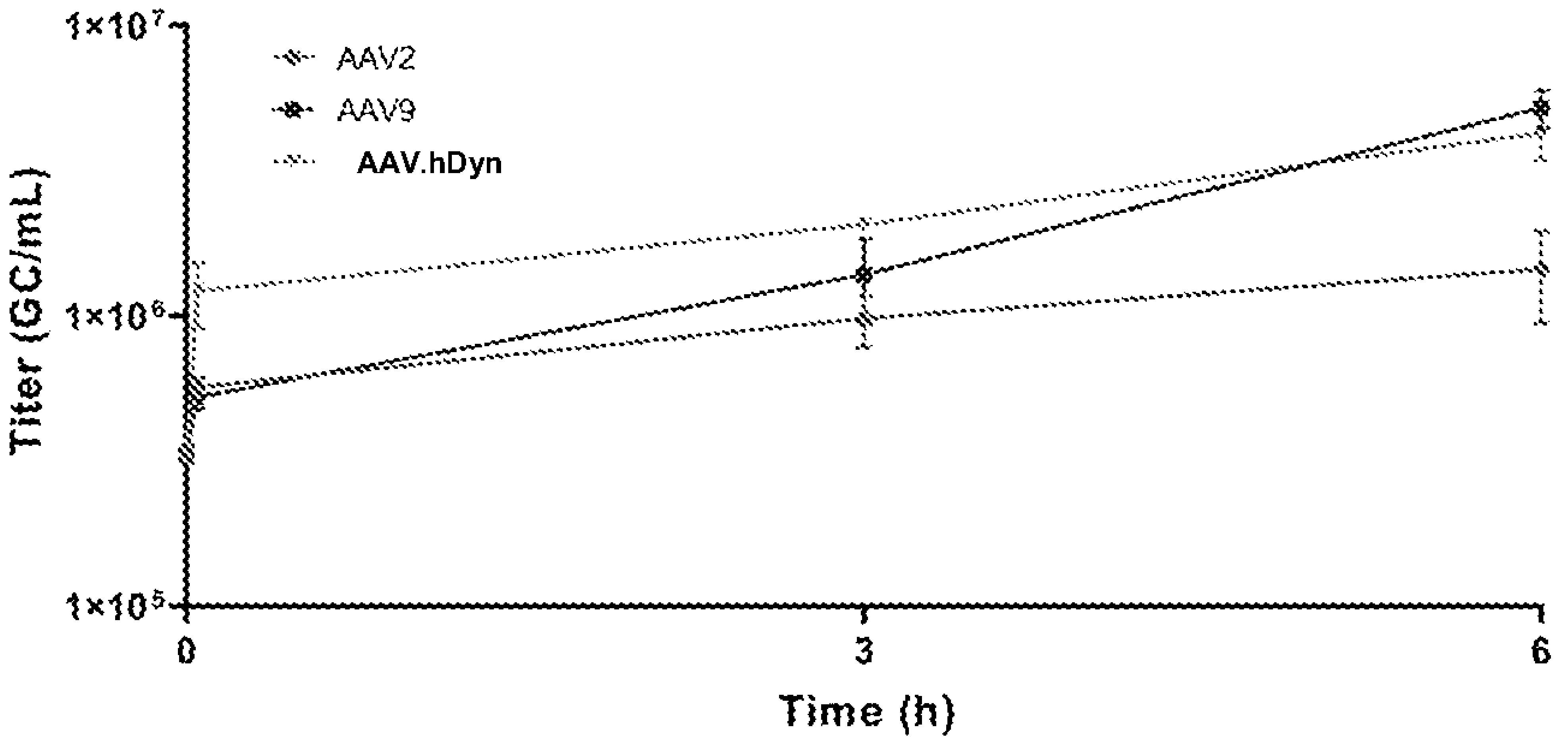


FIG. 10B

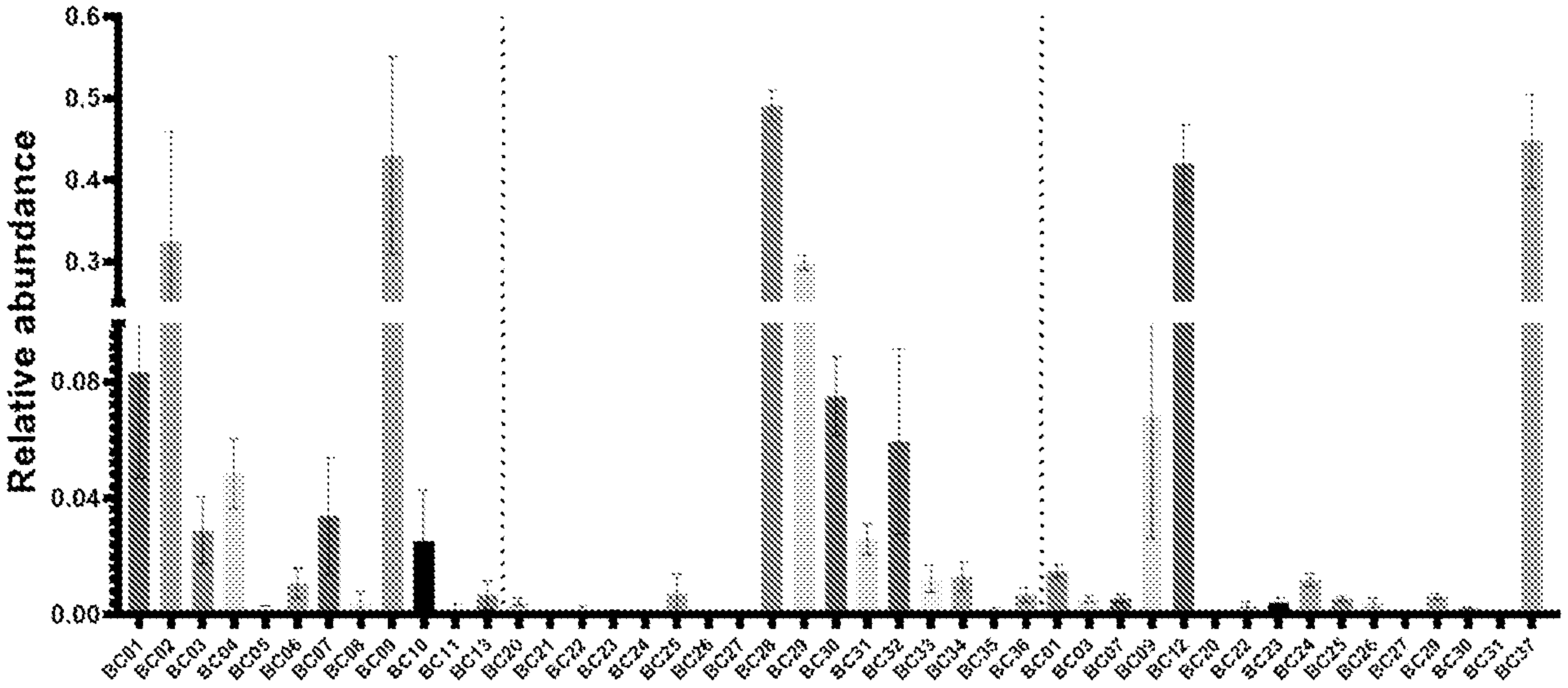

Relative abundance
0.6
0.5
0.4
0.3
0.08
0.04
0.00
BC01
BC02
BC03
BC04
BC05
BC06
BC07
BC08
BC09
BC10
BC11
BC13
BC20
BC21
BC22
BC23
BC24
BC25
BC26
BC27
BC28
BC29
BC30
BC31
BC32
BC33
BC34
BC35
BC36
BC01
BC03
BC07
BC09
BC12
BC20
BC22
BC23
BC24
BC25
BC26
BC27
BC29
BC30
BC31
BC37

FIG. 11

FIGs. 12A-12H

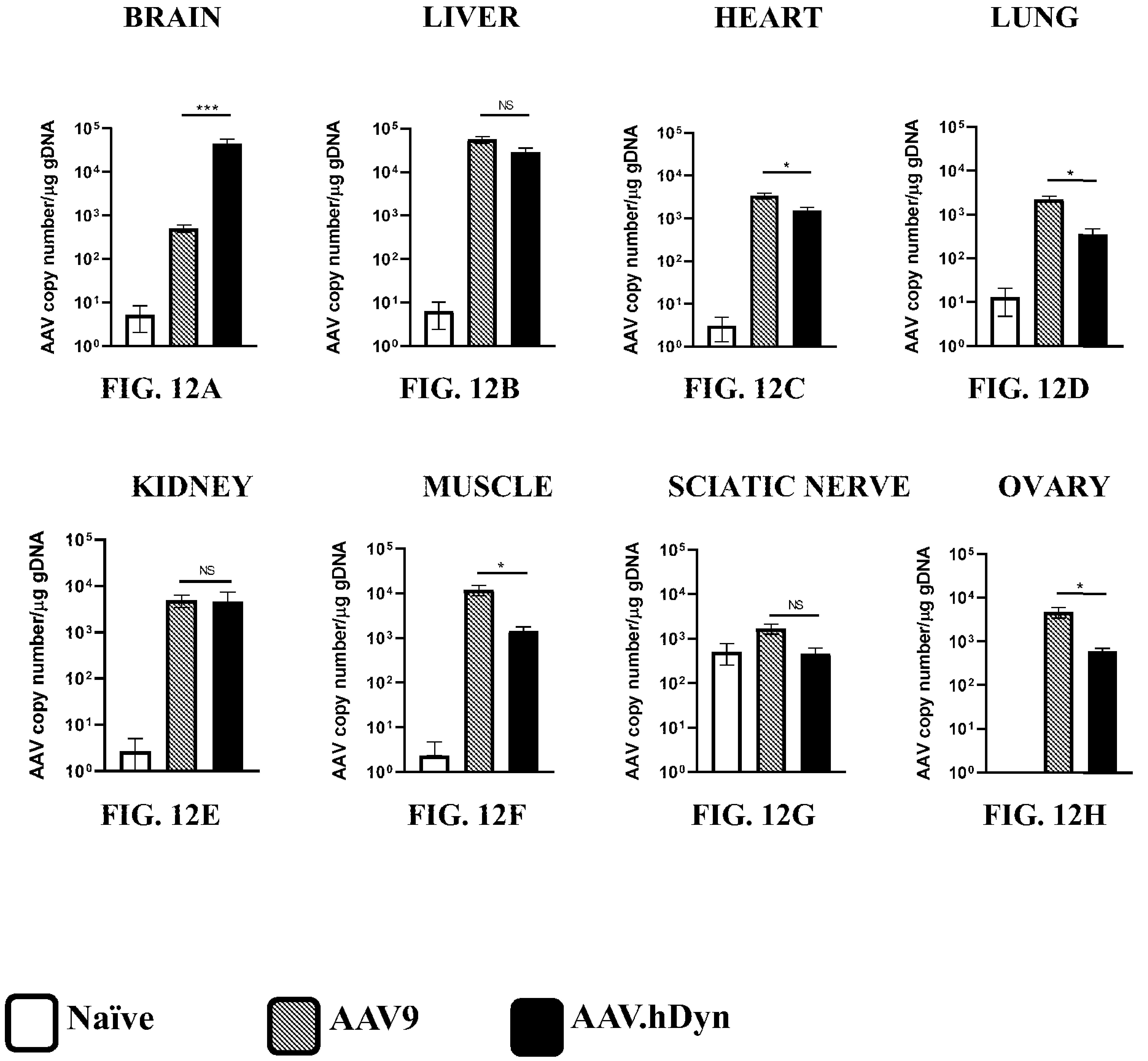


FIG. 12A FIG. 12B FIG. 12C FIG. 12D

FIG. 12E FIG. 12F FIG. 12G FIG. 12H

FIGs. 13A-13C

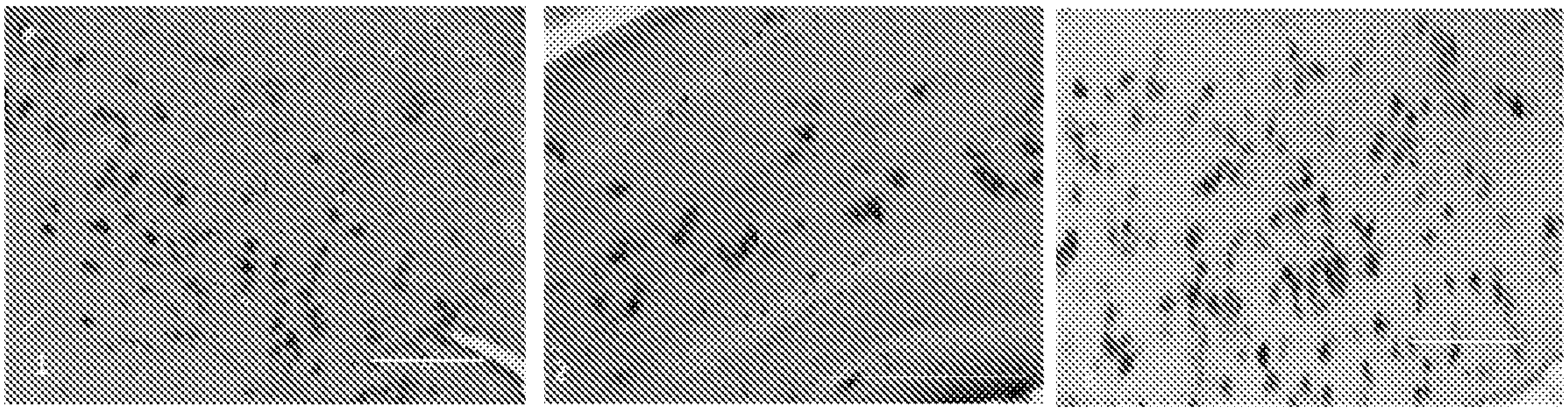


FIG. 13A FIG. 13B FIG.13C

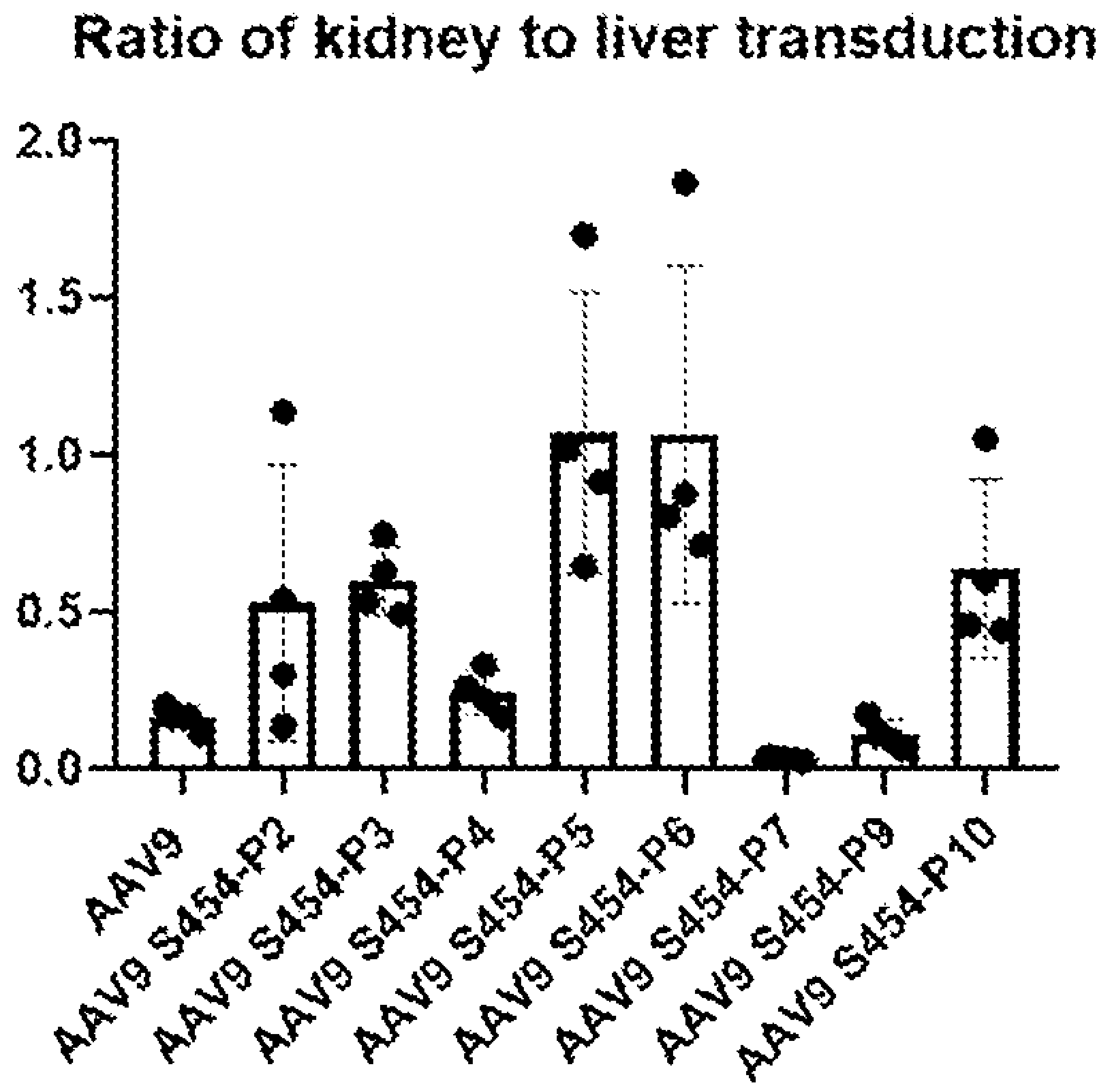

Ratio of kidney to liver transduction
2.0
1.5
1.0
0.5
0.0
AAV9
AAV9 S454-P2
AAV9 S454-P3
AAV9 S454-P4
AAV9 S454-P5
AAV9 S454-P6
AAV9 S454-P7
AAV9 S454-P9
AAV9 S454-P10

FIG. 14

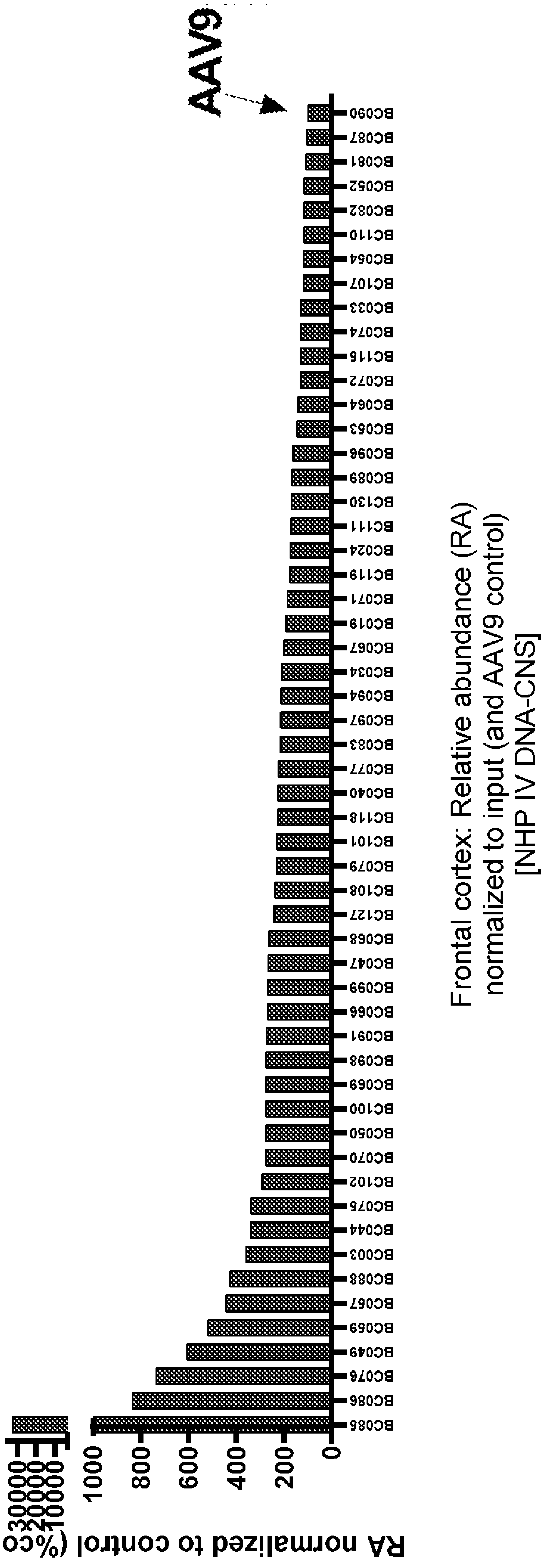

AAV9
RA normalized to control (%control)
30000
20000
10000
1000
800
600
400
200
0
BC085
BC086
BC076
BC049
BC059
BC057
BC088
BC003
BC044
BC075
BC102
BC070
BC050
BC100
BC069
BC098
BC091
BC066
BC099
BC047
BC068
BC127
BC108
BC079
BC101
BC118
BC040
BC077
BC083
BC097
BC094
BC034
BC067
BC019
BC071
BC119
BC024
BC111
BC130
BC089
BC096
BC053
BC064
BC072
BC115
BC074
BC033
BC107
BC054
BC110
BC082
BC052
BC081
BC087
BC090
Frontal cortex: Relative abundance (RA)
normalized to input (and AAV9 control)
[NHP IV DNA-CNS]

FIG. 15

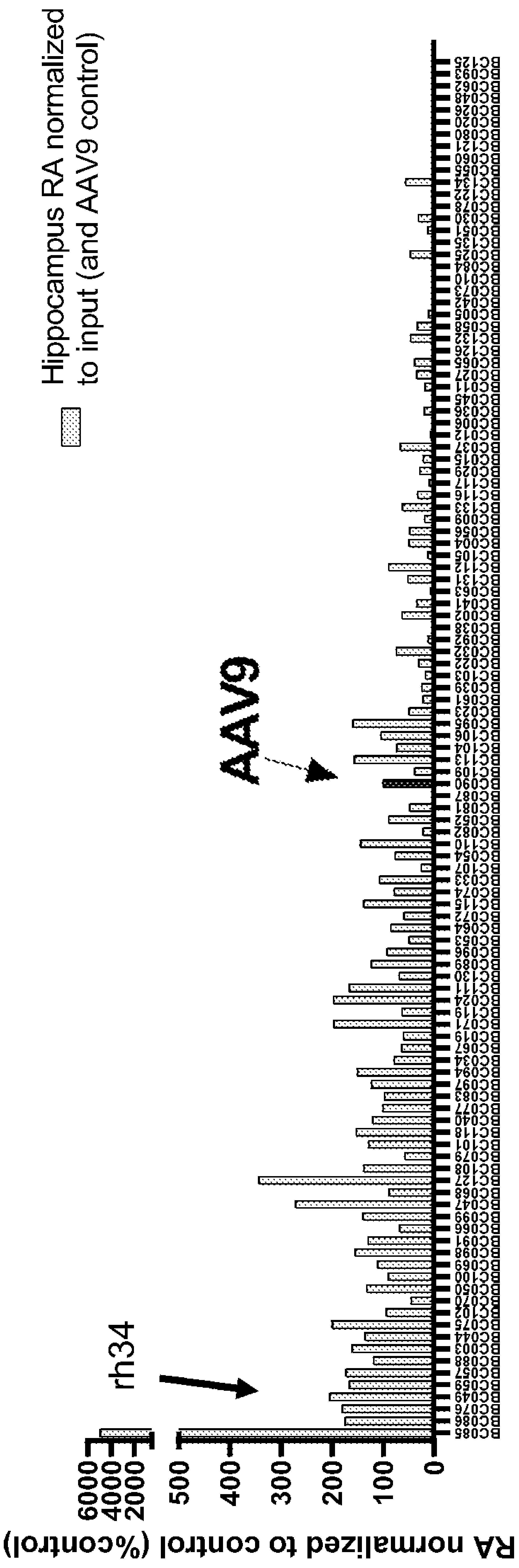

Hippocampus RA normalized to input (and AAV9 control)
RA normalized to control (%control)
0
100
200
300
400
500
2000
4000
6000
rh34
AAV9
BC085
BC086
BC076
BC049
BC059
BC057
BC088
BC003
BC044
BC075
BC102
BC070
BC050
BC100
BC069
BC098
BC091
BC066
BC099
BC047
BC068
BC127
BC108
BC079
BC101
BC118
BC040
BC077
BC083
BC097
BC094
BC034
BC067
BC019
BC071
BC119
BC024
BC111
BC130
BC089
BC096
BC053
BC064
BC072
BC115
BC074
BC033
BC107
BC054
BC110
BC082
BC052
BC081
BC087
BC090
BC109
BC113
BC104
BC106
BC095
BC023
BC061
BC039
BC103
BC022
BC032
BC092
BC038
BC002
BC041
BC063
BC131
BC112
BC105
BC004
BC056
BC009
BC133
BC116
BC117
BC029
BC015
BC037
BC012
BC006
BC036
BC045
BC011
BC027
BC065
BC126
BC132
BC058
BC005
BC042
BC073
BC010
BC084
BC025
BC135
BC051
BC030
BC078
BC122
BC134
BC055
BC060
BC121
BC080
BC020
BC026
BC048
BC062
BC093
BC125

FIG. 16

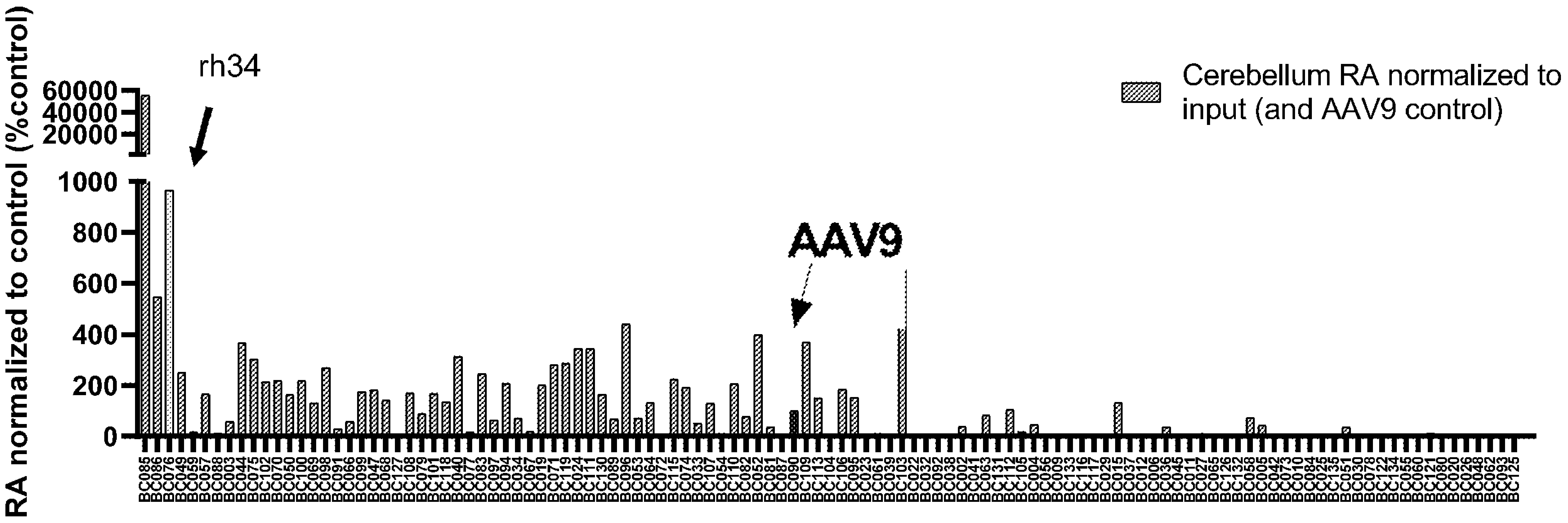

rh34
AAV9
Cerebellum RA normalized to input (and AAV9 control)
RA normalized to control (%control)
60000
40000
20000
1000
800
600
400
200
0
BC085
BC086
BC076
BC049
BC059
BC057
BC088
BC003
BC044
BC075
BC102
BC070
BC050
BC100
BC069
BC098
BC091
BC066
BC099
BC047
BC068
BC127
BC108
BC079
BC101
BC118
BC040
BC077
BC083
BC097
BC094
BC034
BC067
BC019
BC071
BC119
BC024
BC111
BC130
BC089
BC096
BC053
BC064
BC072
BC115
BC074
BC033
BC107
BC054
BC110
BC082
BC052
BC081
BC087
BC090
BC109
BC113
BC104
BC106
BC095
BC023
BC061
BC039
BC103
BC022
BC032
BC092
BC038
BC002
BC041
BC063
BC131
BC112
BC105
BC004
BC056
BC009
BC133
BC116
BC117
BC029
BC015
BC037
BC012
BC006
BC036
BC045
BC011
BC027
BC065
BC126
BC132
BC058
BC005
BC042
BC073
BC010
BC084
BC025
BC135
BC051
BC030
BC078
BC122
BC134
BC055
BC060
BC121
BC080
BC020
BC026
BC048
BC062
BC093
BC125

FIG. 17

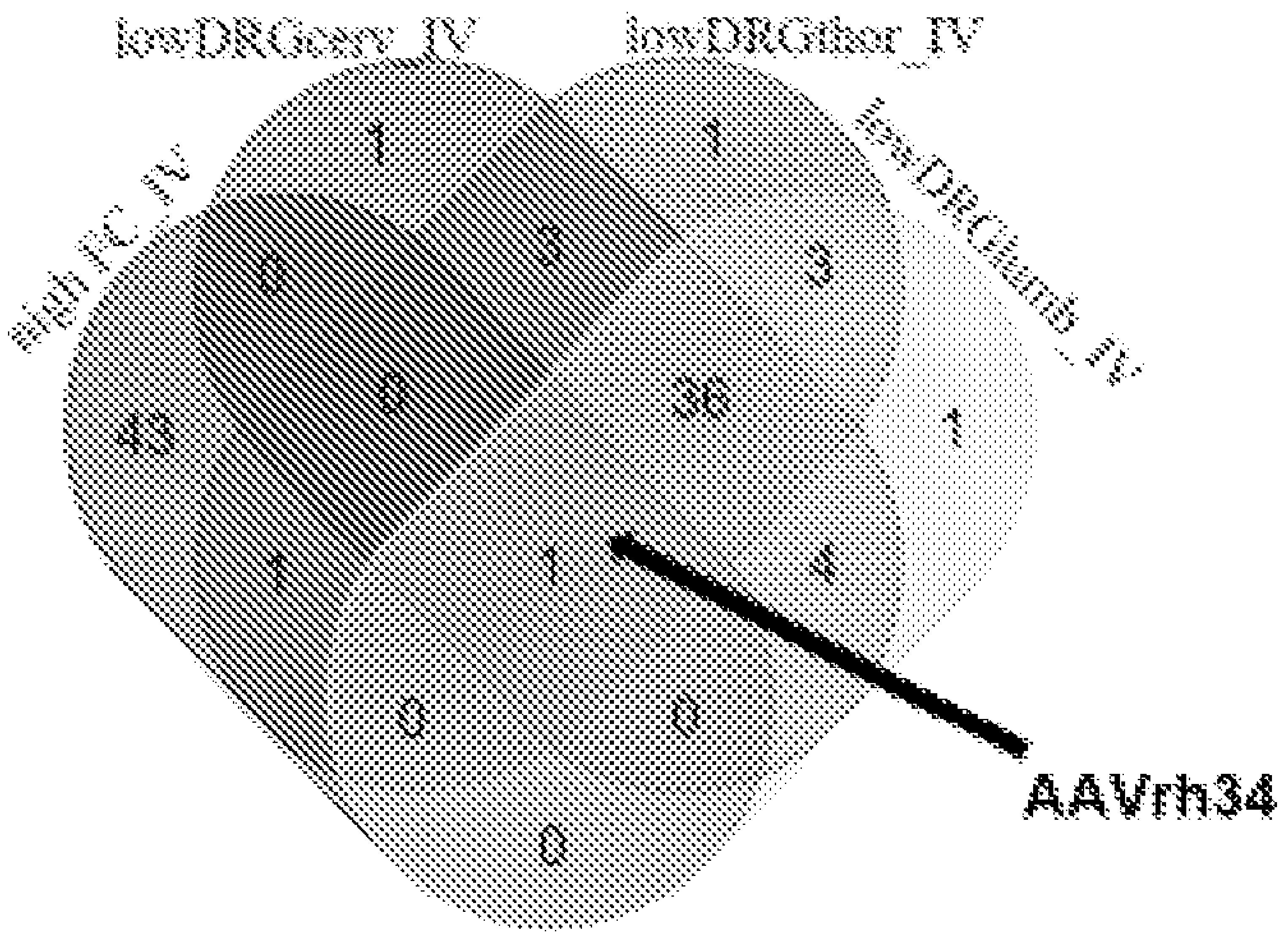

lowDRGcerv_IV
lowDRGthor_IV
lowDRGlumb_IV
high FC_IV
1
1
0
3
3
0
43
36
1
1
1
4
0
0
0
AAVrh34

FIG. 18

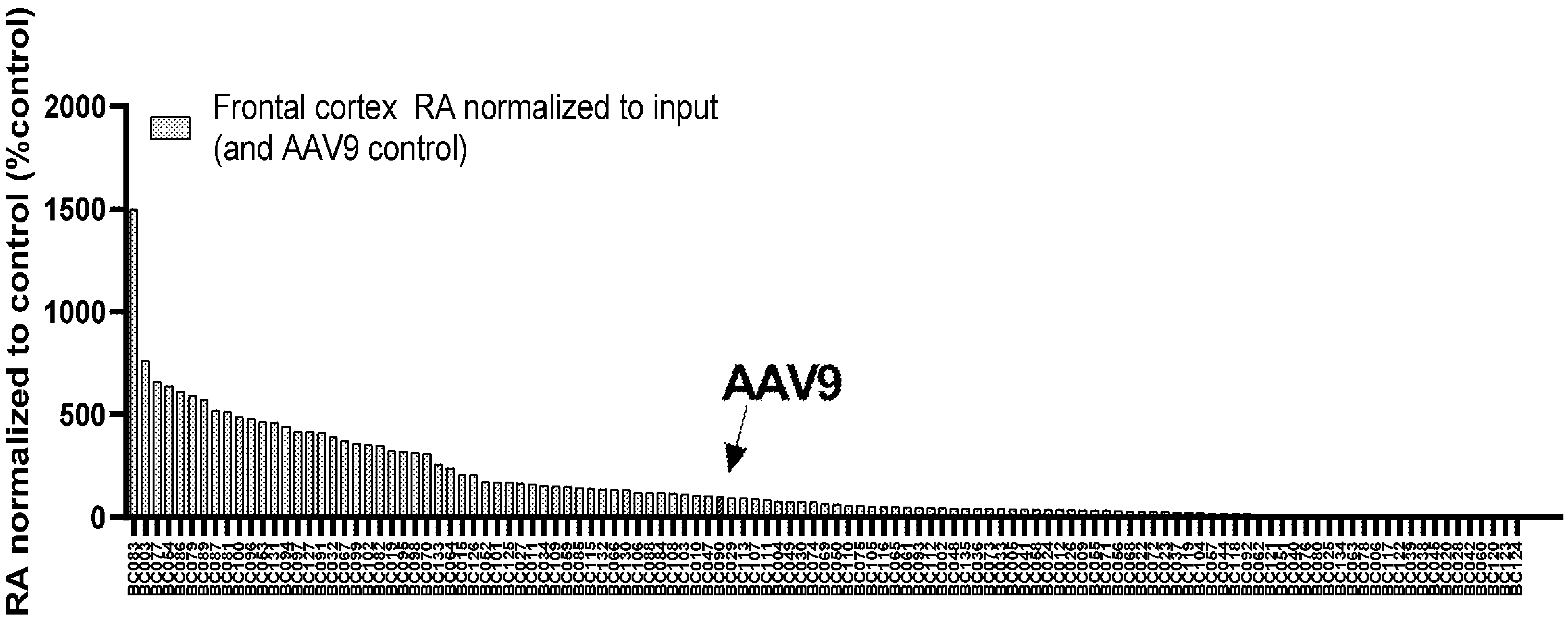

RA normalized to control (%control)
2000
1500
1000
500
0
Frontal cortex RA normalized to input
(and AAV9 control)
AAV9
BC083
BC003
BC077
BC054
BC086
BC079
BC089
BC087
BC081
BC100
BC096
BC053
BC131
BC094
BC097
BC127
BC091
BC032
BC067
BC099
BC102
BC092
BC095
BC098
BC070
BC133
BC054
BC016
BC126
BC052
BC101
BC125
BC027
BC071
BC034
BC109
BC059
BC086
BC115
BC135
BC066
BC130
BC106
BC088
BC084
BC108
BC103
BC010
BC047
BC090
BC023
BC107
BC111
BC004
BC049
BC030
BC074
BC069
BC050
BC110
BC076
BC106
BC116
BC065
BC061
BC093
BC112
BC002
BC048
BC135
BC036
BC073
BC033
BC005
BC041
BC068
BC024
BC012
BC026
BC009
BC055
BC071
BC066
BC068
BC022
BC072
BC037
BC119
BC104
BC057
BC014
BC118
BC092
BC062
BC121
BC051
BC040
BC080
BC025
BC134
BC063
BC078
BC006
BC117
BC122
BC039
BC038
BC046
BC028
BC042
BC060
BC120
BC124

FIG. 19

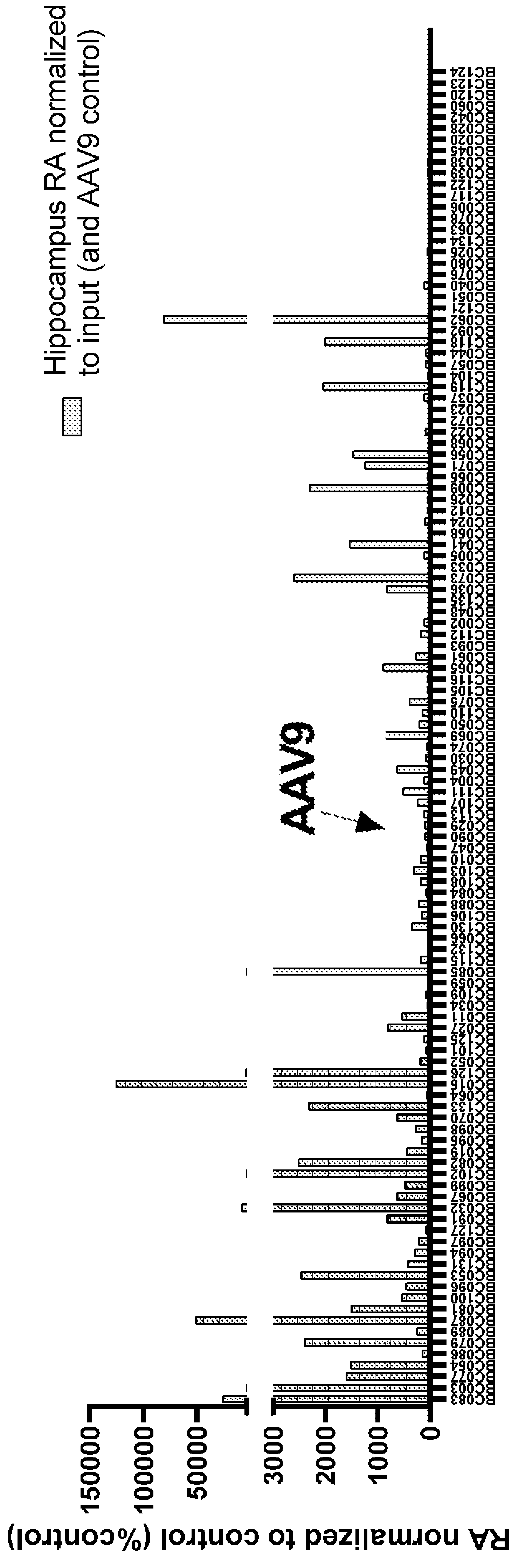

Hippocampus RA normalized to input (and AAV9 control)
AAV9
RA normalized to control (%control)
150000
100000
50000
3000
2000
1000
0

FIG. 20

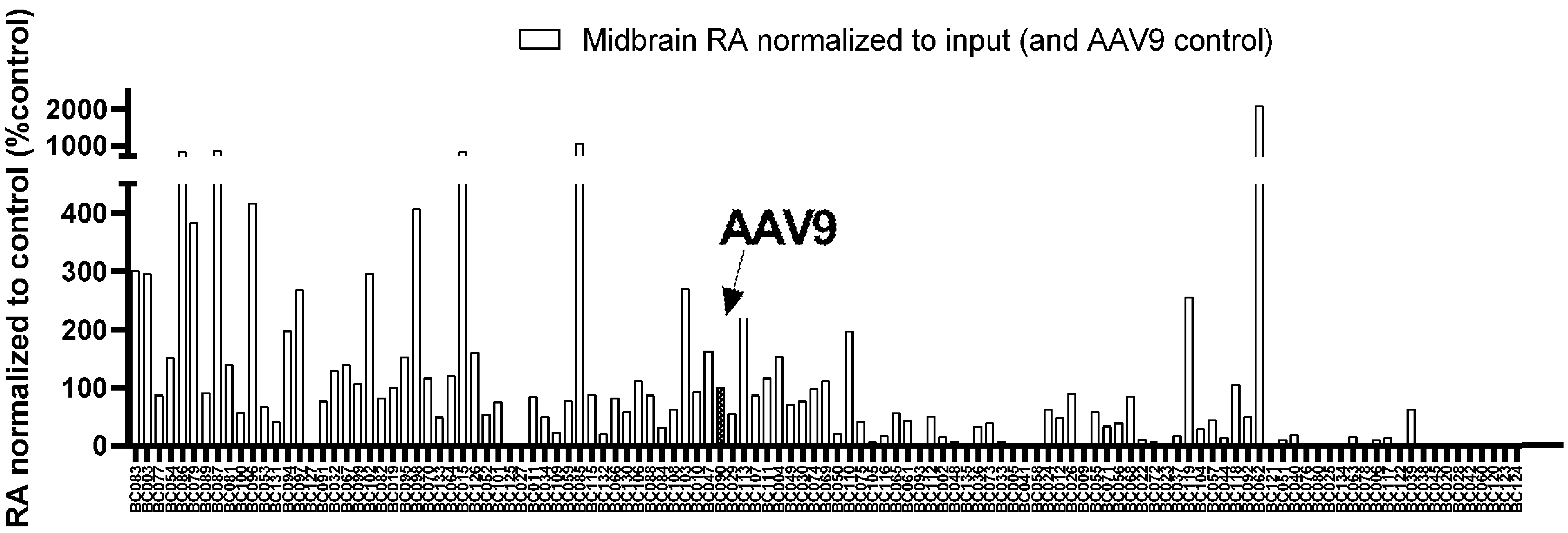
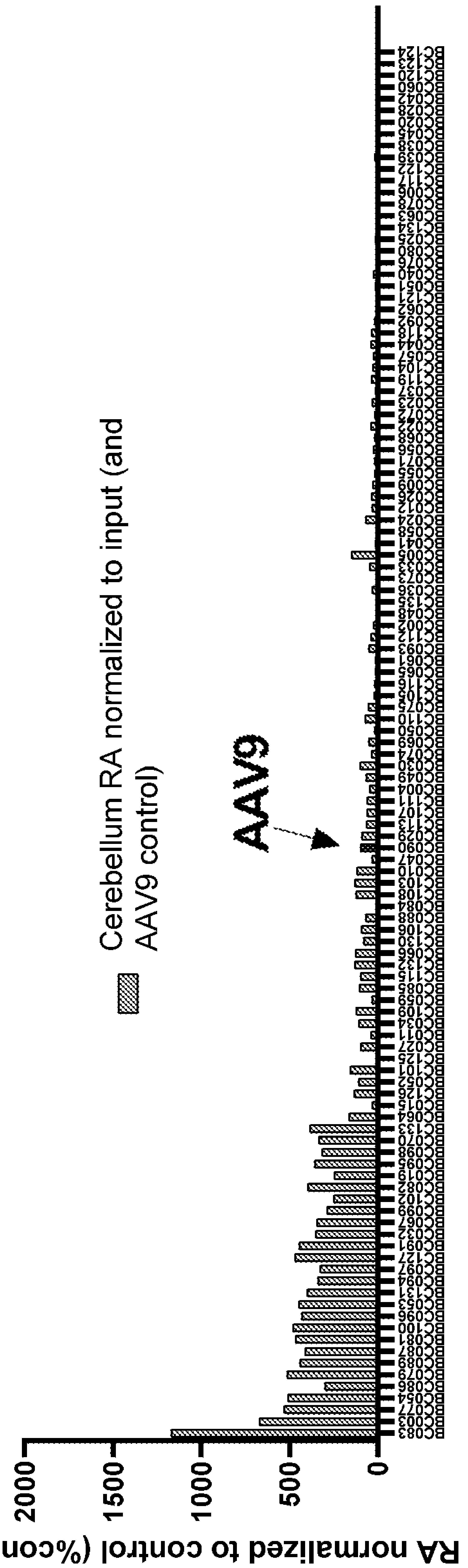

Midbrain RA normalized to input (and AAV9 control)
RA normalized to control (%control)
2000
1000
400
300
200
100
0
AAV9
BC083
BC003
BC077
BC054
BC086
BC079
BC089
BC087
BC081
BC100
BC096
BC053
BC131
BC094
BC097
BC127
BC091
BC032
BC067
BC099
BC102
BC082
BC019
BC095
BC098
BC070
BC133
BC064
BC015
BC126
BC052
BC101
BC125
BC027
BC011
BC034
BC109
BC059
BC085
BC115
BC132
BC066
BC130
BC106
BC088
BC084
BC108
BC103
BC010
BC047
BC090
BC029
BC113
BC107
BC111
BC004
BC049
BC030
BC074
BC069
BC050
BC110
BC075
BC105
BC116
BC065
BC061
BC093
BC112
BC002
BC048
BC135
BC036
BC073
BC033
BC005
BC041
BC058
BC024
BC012
BC026
BC009
BC055
BC071
BC056
BC068
BC022
BC072
BC023
BC037
BC119
BC104
BC057
BC044
BC118
BC092
BC062
BC121
BC051
BC040
BC076
BC080
BC025
BC134
BC063
BC078
BC006
BC117
BC122
BC039
BC038
BC045
BC020
BC028
BC042
BC060
BC120
BC123
BC124

FIG. 21


RA normalized to control (%control)
0
500
1000
1500
2000
BC083
BC003
BC077
BC054
BC086
BC079
BC089
BC087
BC081
BC100
BC096
BC053
BC131
BC094
BC097
BC127
BC091
BC032
BC067
BC099
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BC019
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BC030
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BC050
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BC093
BC112
BC002
BC048
BC135
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BC073
BC033
BC005
BC041
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BC012
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BC092
BC062
BC121
BC051
BC040
BC076
BC080
BC025
BC134
BC063
BC078
BC006
BC117
BC122
BC039
BC038
BC045
BC020
BC028
BC042
BC060
BC120
BC123
BC124
▨ Cerebellum RA normalized to input (and AAV9 control)
AAV9

FIG. 22

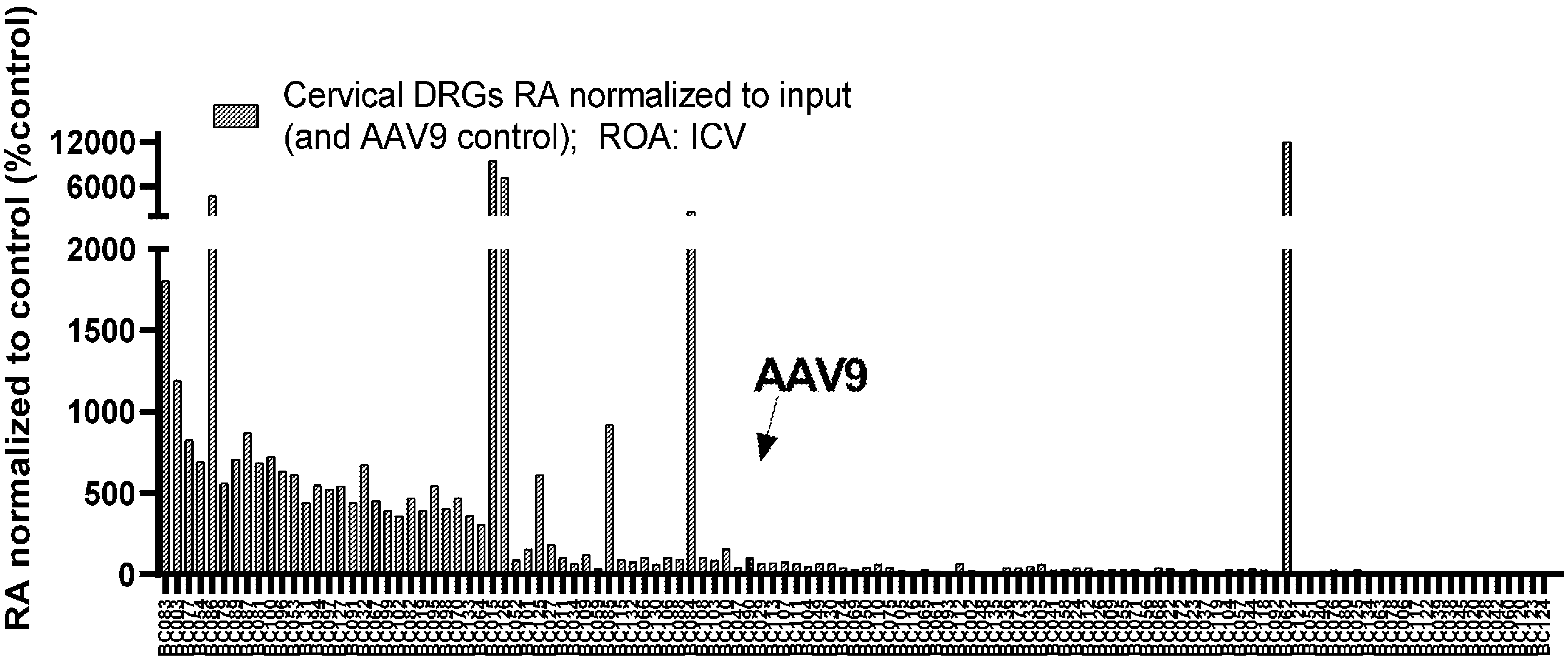

Cervical DRGs RA normalized to input
(and AAV9 control); ROA: ICV
RA normalized to control (%control)
12000
6000
2000
1500
1000
500
0
AAV9
BC083
BC124

FIG. 23

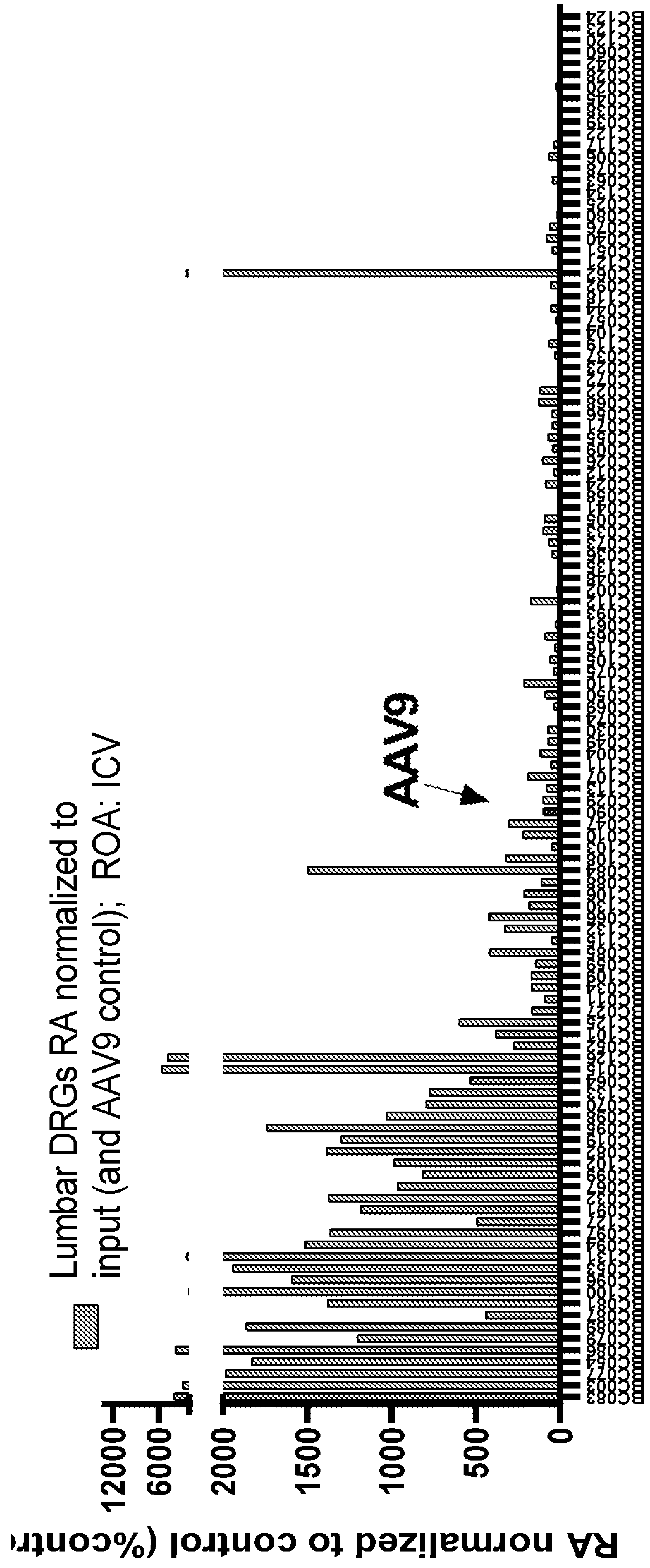

Lumbar DRGs RA normalized to input (and AAV9 control); ROA: ICV
AAV9
RA normalized to control (%contr
12000
6000
2000
1500
1000
500
0

FIG. 24

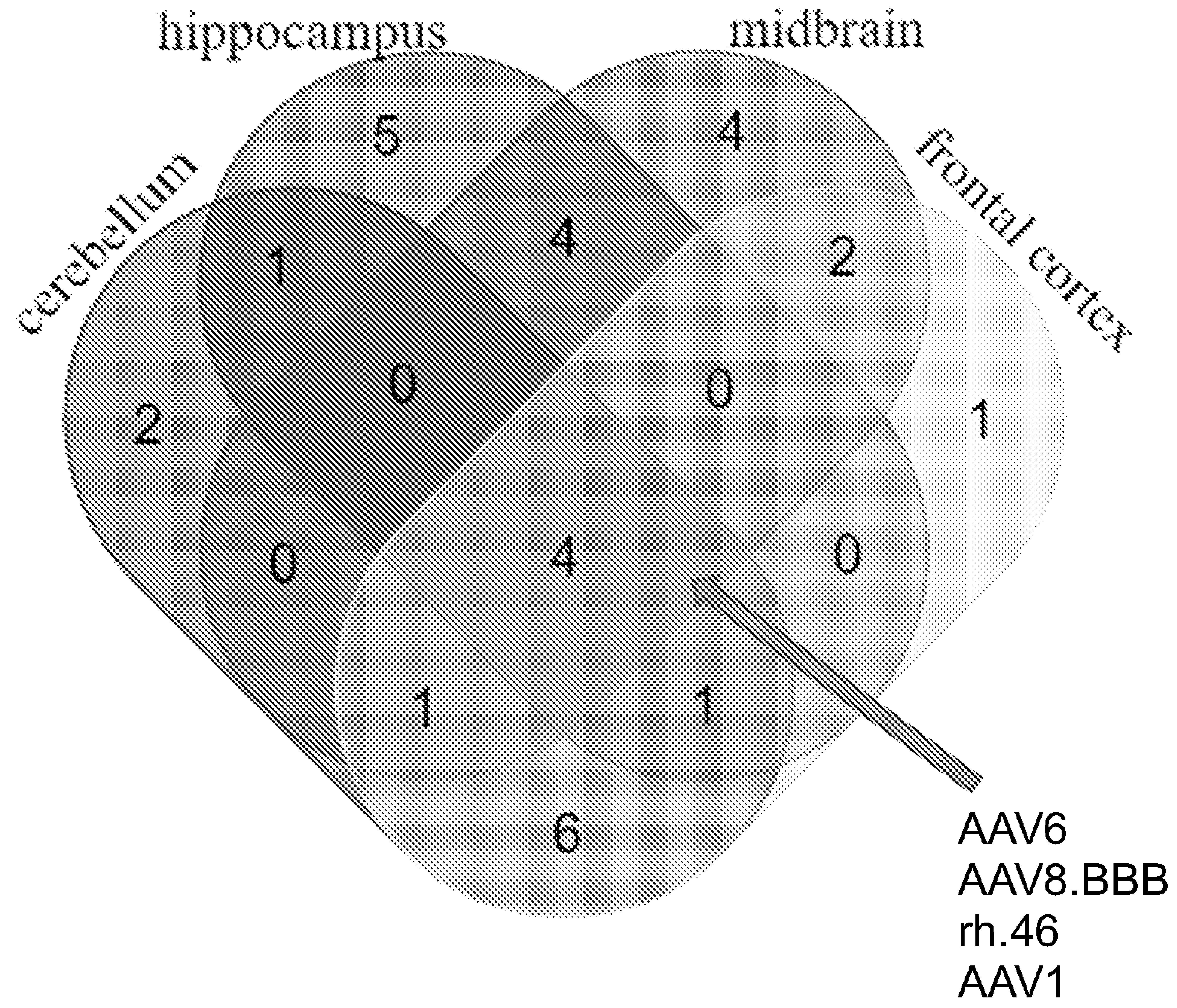

hippocampus
midbrain
cerebellum
frontal cortex
5
4
1
4
2
2
0
0
1
0
4
0
1
1
6
AAV6
AAV8.BBB
rh.46
AAV1

FIG. 25

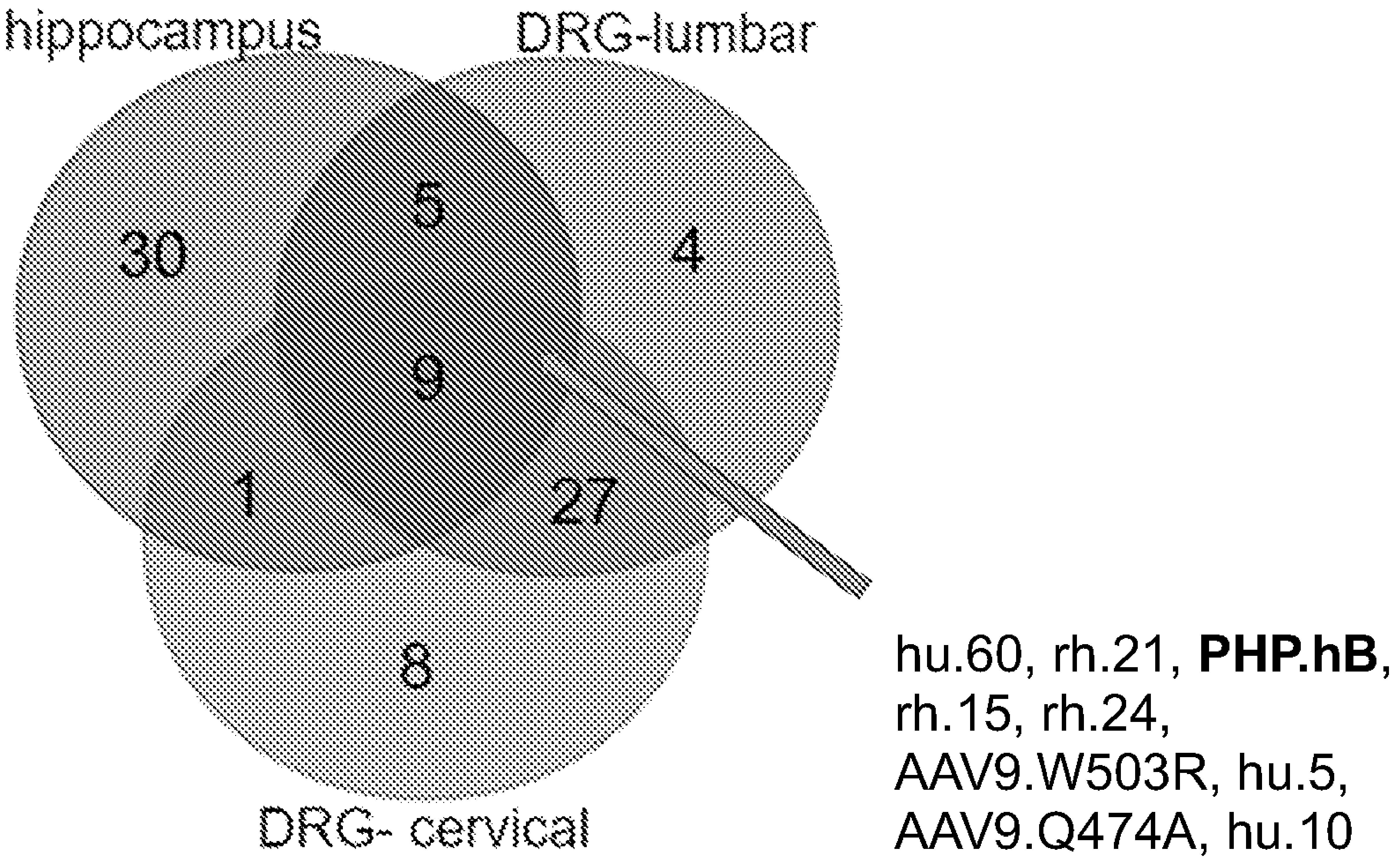
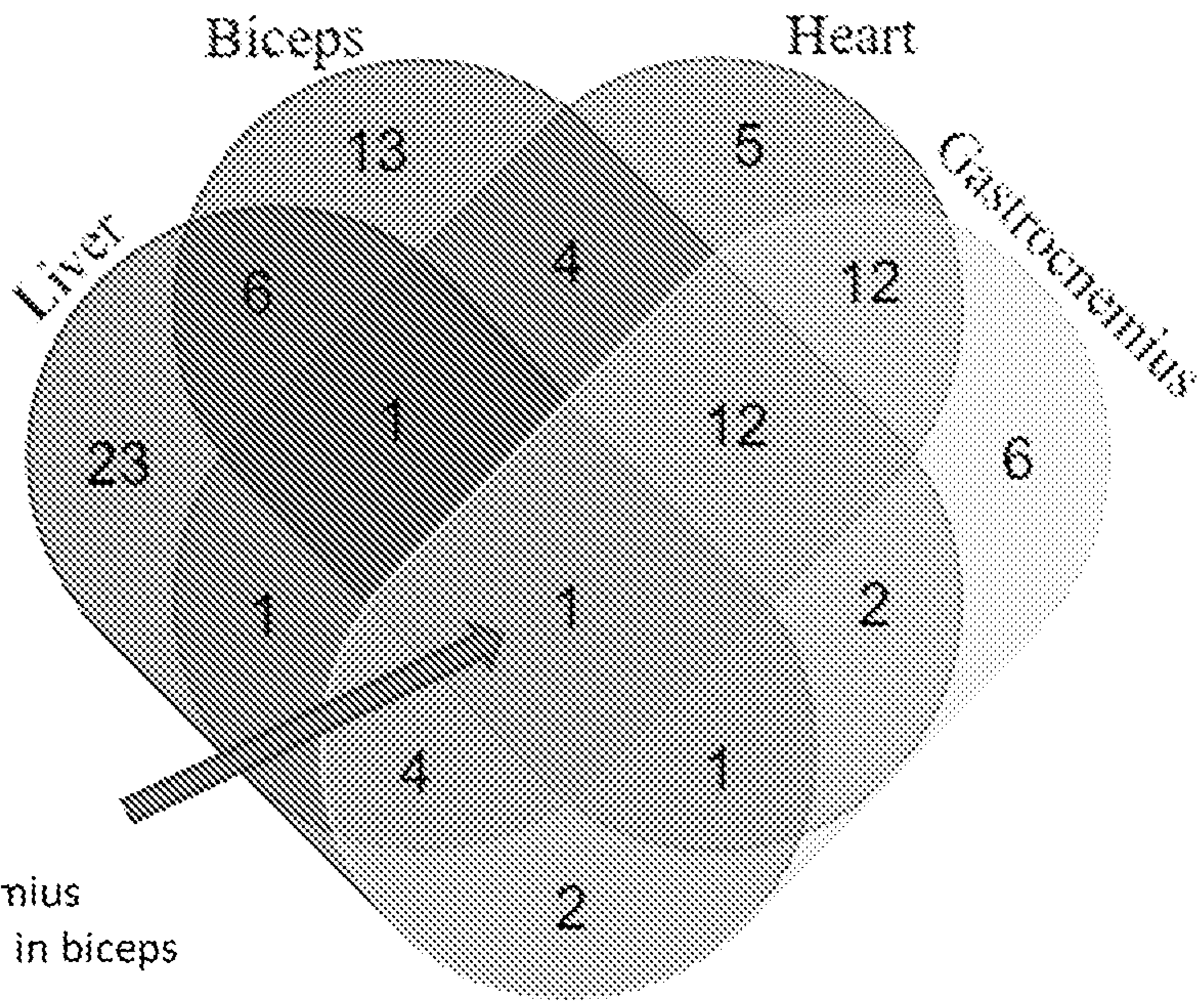

hippocampus
DRG-lumbar
30
5
4
9
1
27
8
DRG- cervical
hu.60, rh.21, **PHP.hB**,
rh.15, rh.24,
AAV9.W503R, hu.5,
AAV9.Q474A, hu.10

FIG. 26



AAVPHPeB.VP2Herp
100x lower in liver
2x higher in heart
4x higher in gastrocnemius
Comparable to control in biceps

FIG. 27

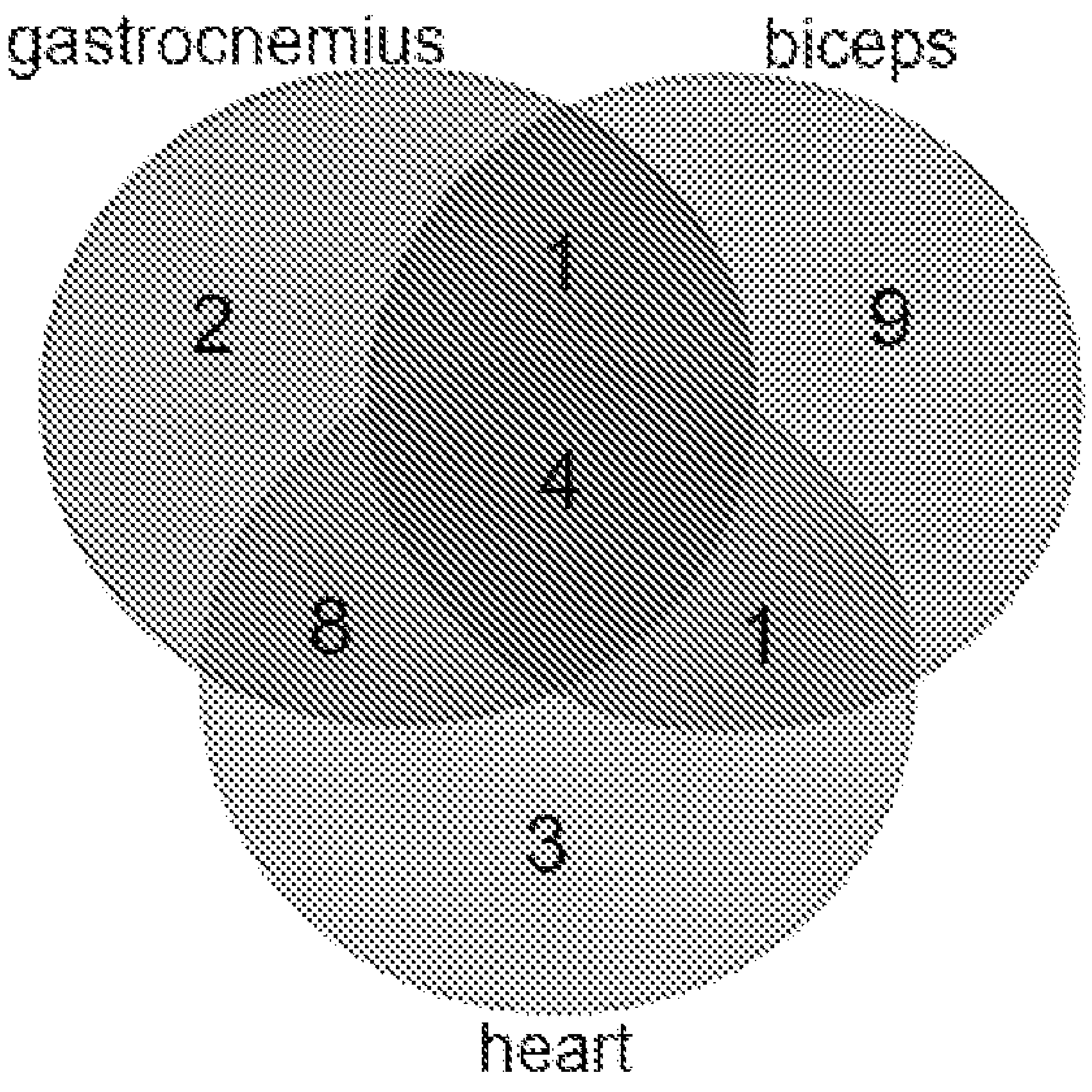


FIG. 28

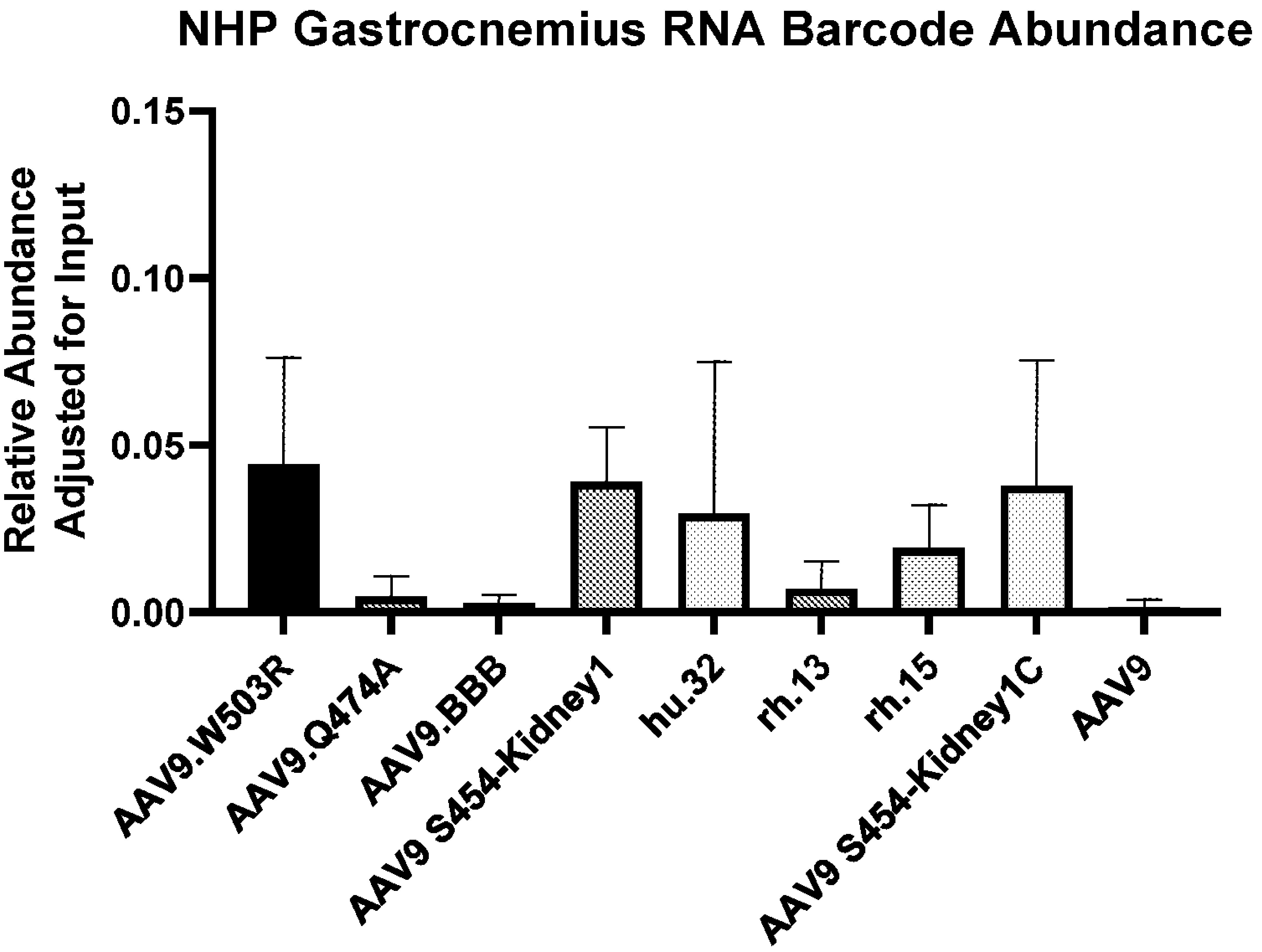

NHP Gastrocnemius RNA Barcode Abundance
Relative Abundance Adjusted for Input
0.15
0.10
0.05
0.00
AAV9.W503R
AAV9.Q474A
AAV9.BBB
AAV9 S454-Kidney1
hu.32
rh.13
rh.15
AAV9 S454-Kidney1C
AAV9

FIG. 29A

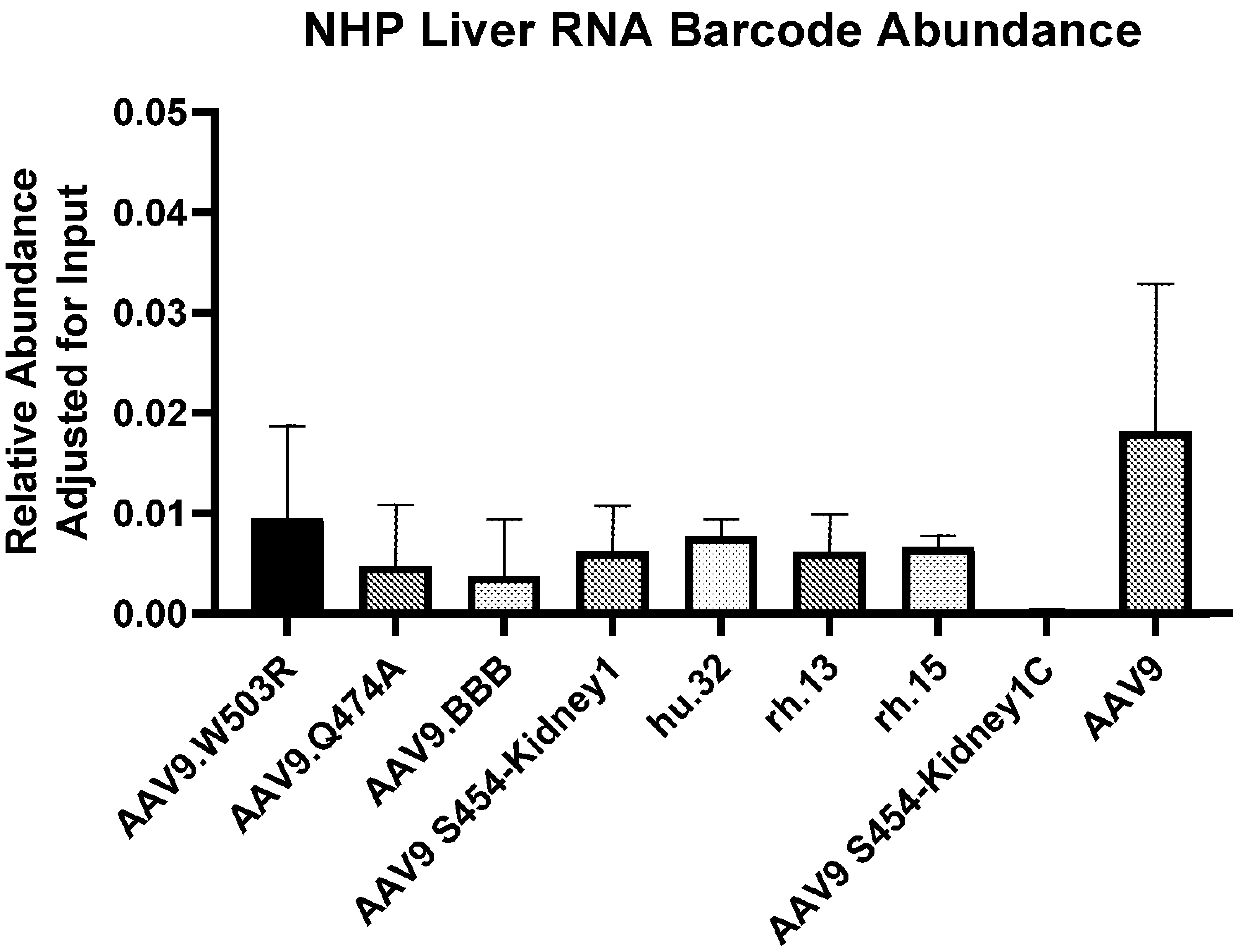

NHP Liver RNA Barcode Abundance
Relative Abundance Adjusted for Input
0.05
0.04
0.03
0.02
0.01
0.00
AAV9.W503R
AAV9.Q474A
AAV9.BBB
AAV9 S454-Kidney1
hu.32
rh.13
rh.15
AAV9 S454-Kidney1C
AAV9

FIG. 29B

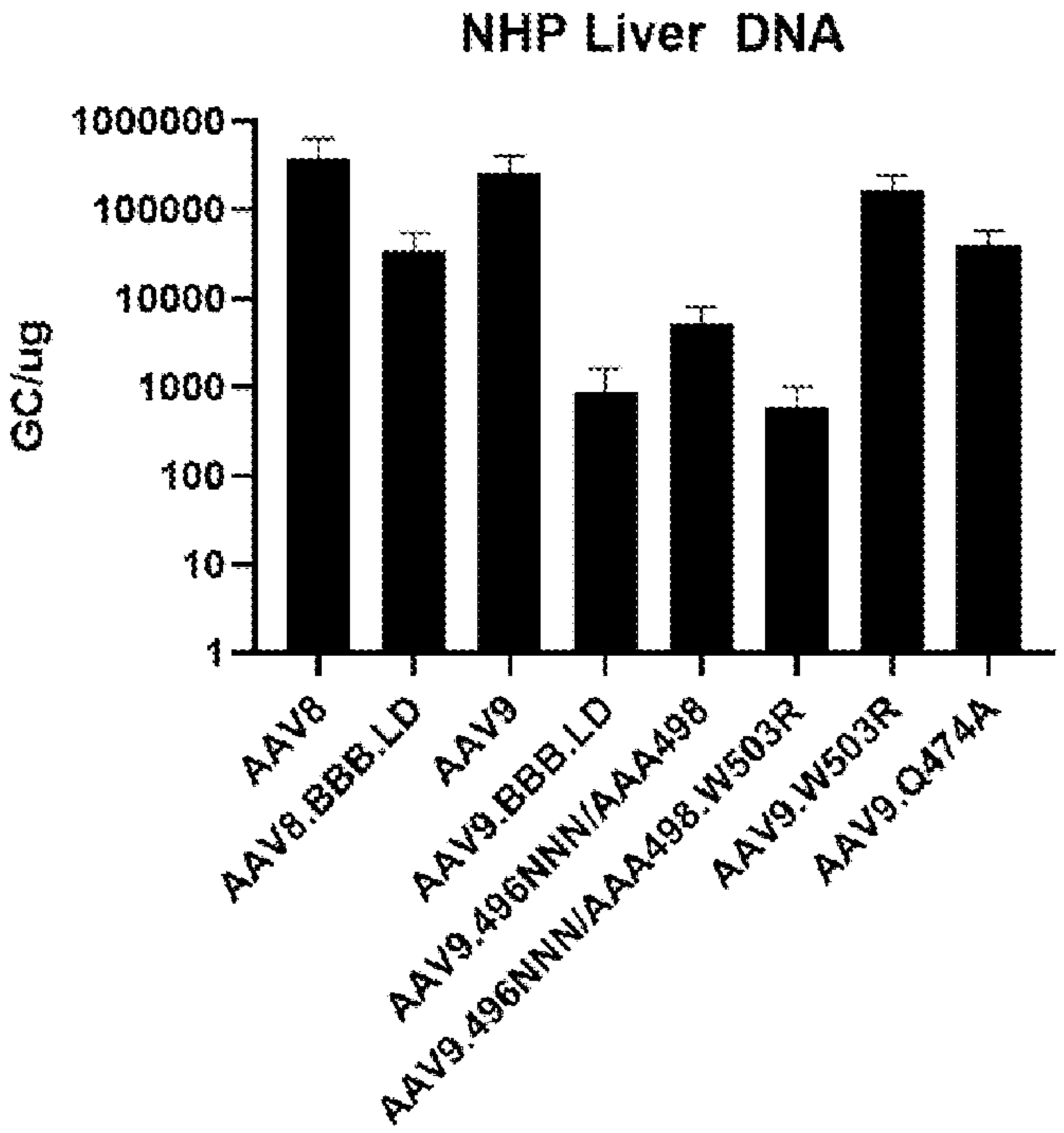


FIG. 30A

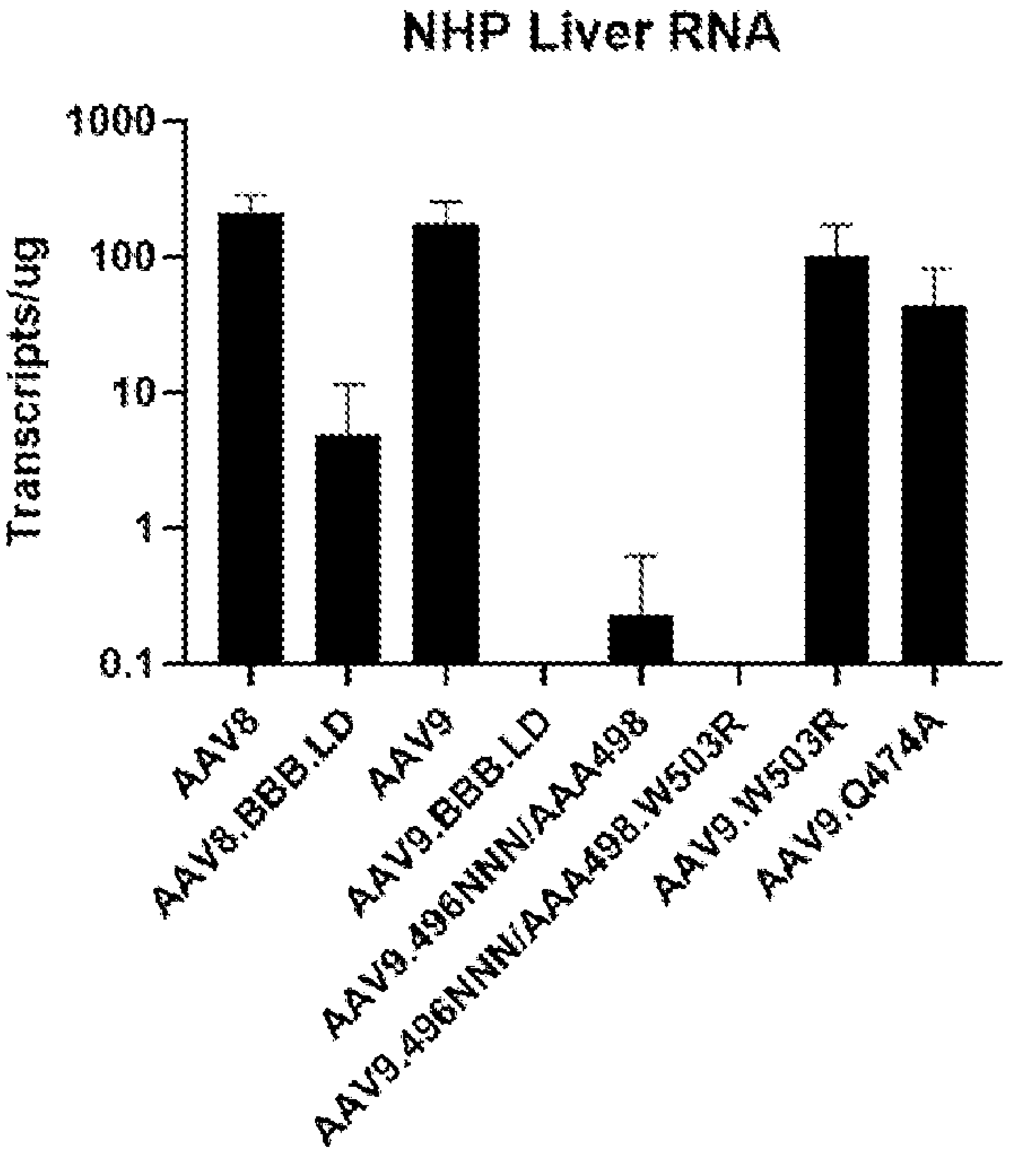


FIG. 30B

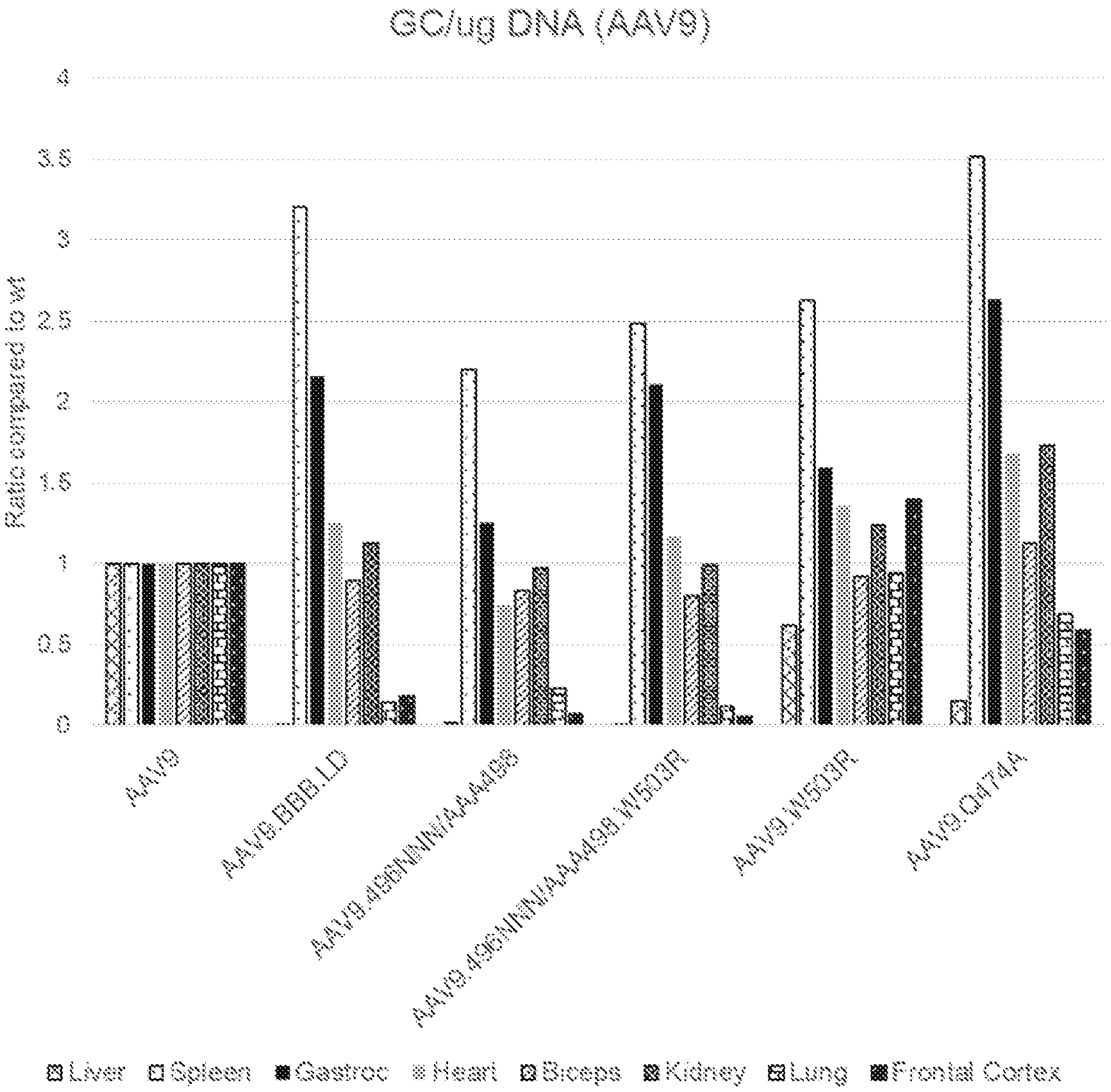

GC/ug DNA (AAV9)
Ratio compared to wt
4
3.5
3
2.5
2
1.5
1
0.5
0
AAV9
AAV9.BBB.LD
AAV9.496NNN/AAA498
AAV9.496NNN/AAA498.W503R
AAV9.W503R
AAV9.Q474A
Liver
Spleen
Gastroc
Heart
Biceps
Kidney
Lung
Frontal Cortex

FIG. 31

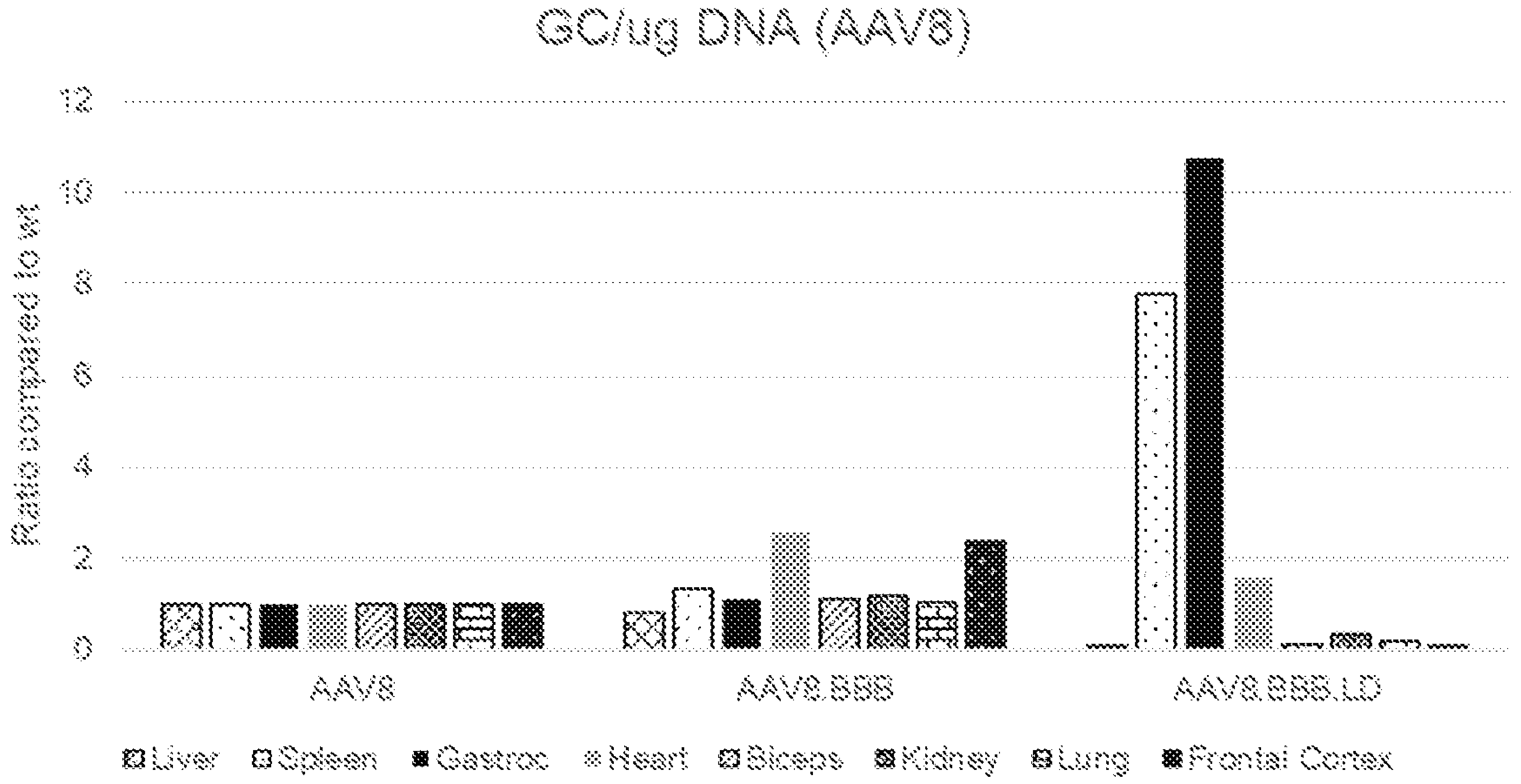

GC/ug DNA (AAV8)
Ratio compared to wt
12
10
8
6
4
2
0
AAV8
AAV8.BBB
AAV8.BBB.LD
Liver
Spleen
Gastroc
Heart
Biceps
Kidney
Lung
Frontal Cortex

FIG. 32

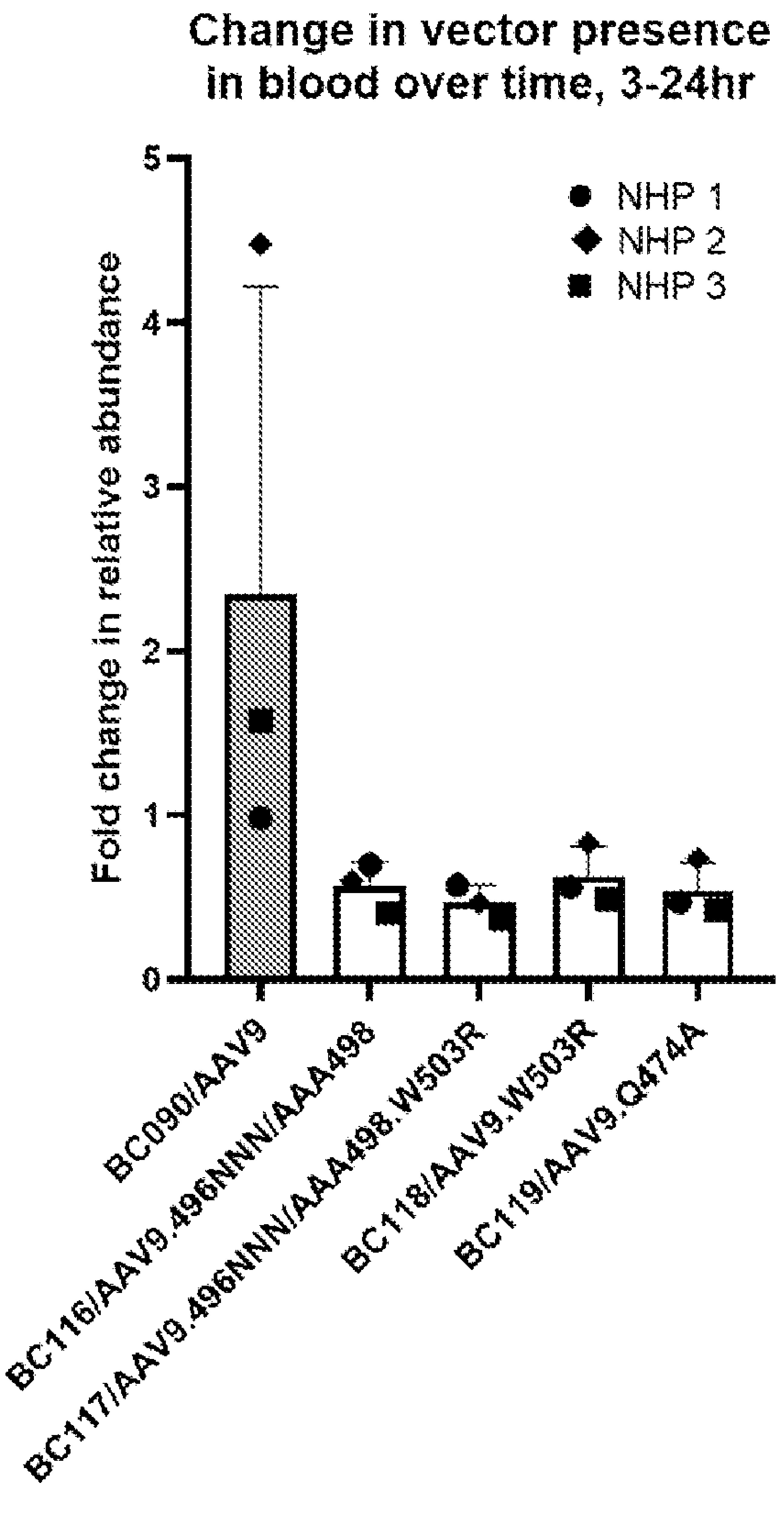

Change in vector presence
in blood over time, 3-24hr
Fold change in relative abundance
0
1
2
3
4
5
● NHP 1
◆ NHP 2
■ NHP 3
BC090/AAV9
BC116/AAV9.496NNN/AAA498
BC117/AAV9.496NNN/AAA498.W503R
BC118/AAV9.W503R
BC119/AAV9.Q474A

FIG. 33A

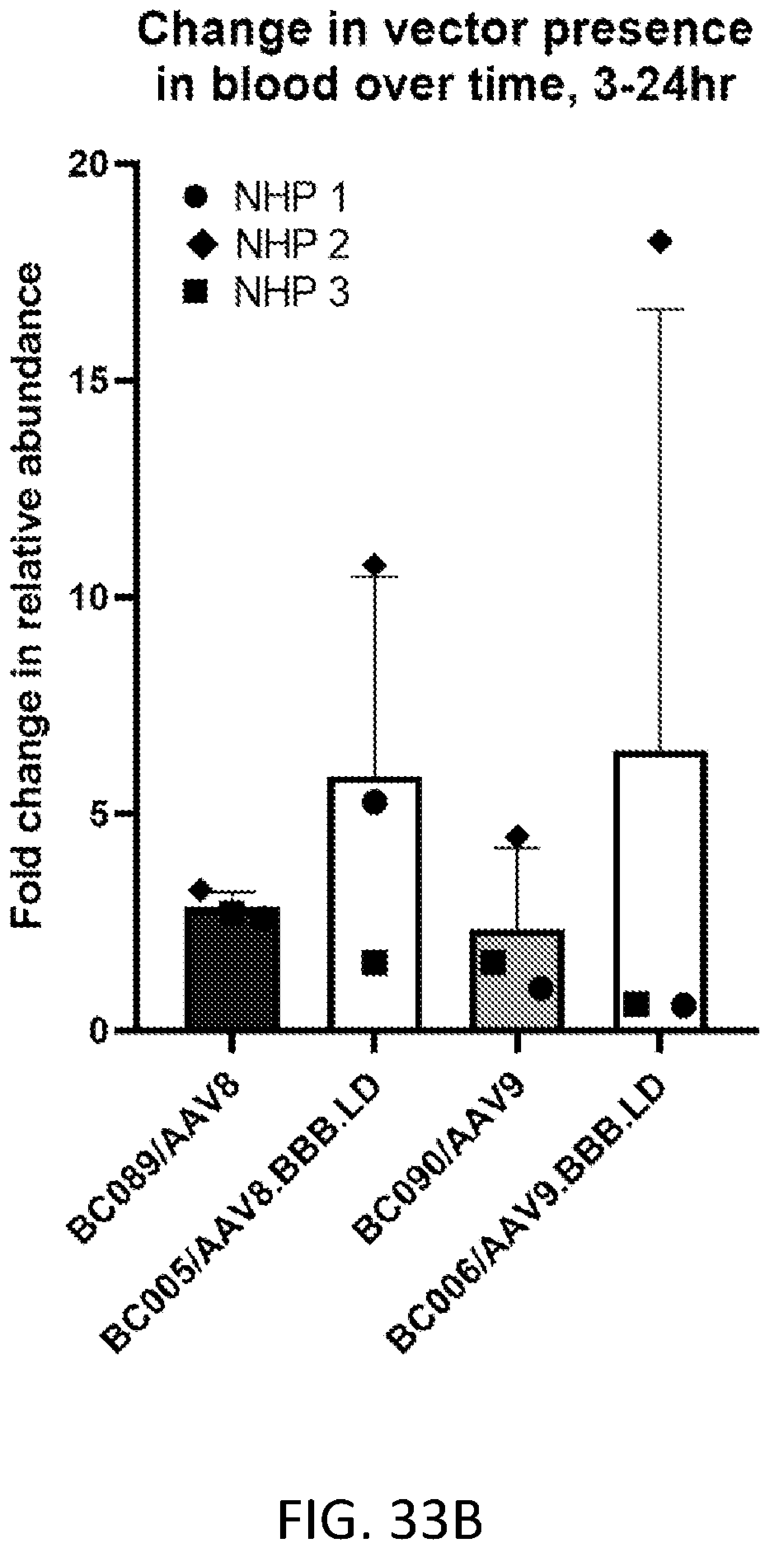

Change in vector presence in blood over time, 3-24hr
Fold change in relative abundance
0
5
10
15
20
● NHP 1
◆ NHP 2
■ NHP 3
BC089/AAV8
BC005/AAV8.BBB.LD
BC090/AAV9
BC006/AAV9.BBB.LD

FIG. 33B

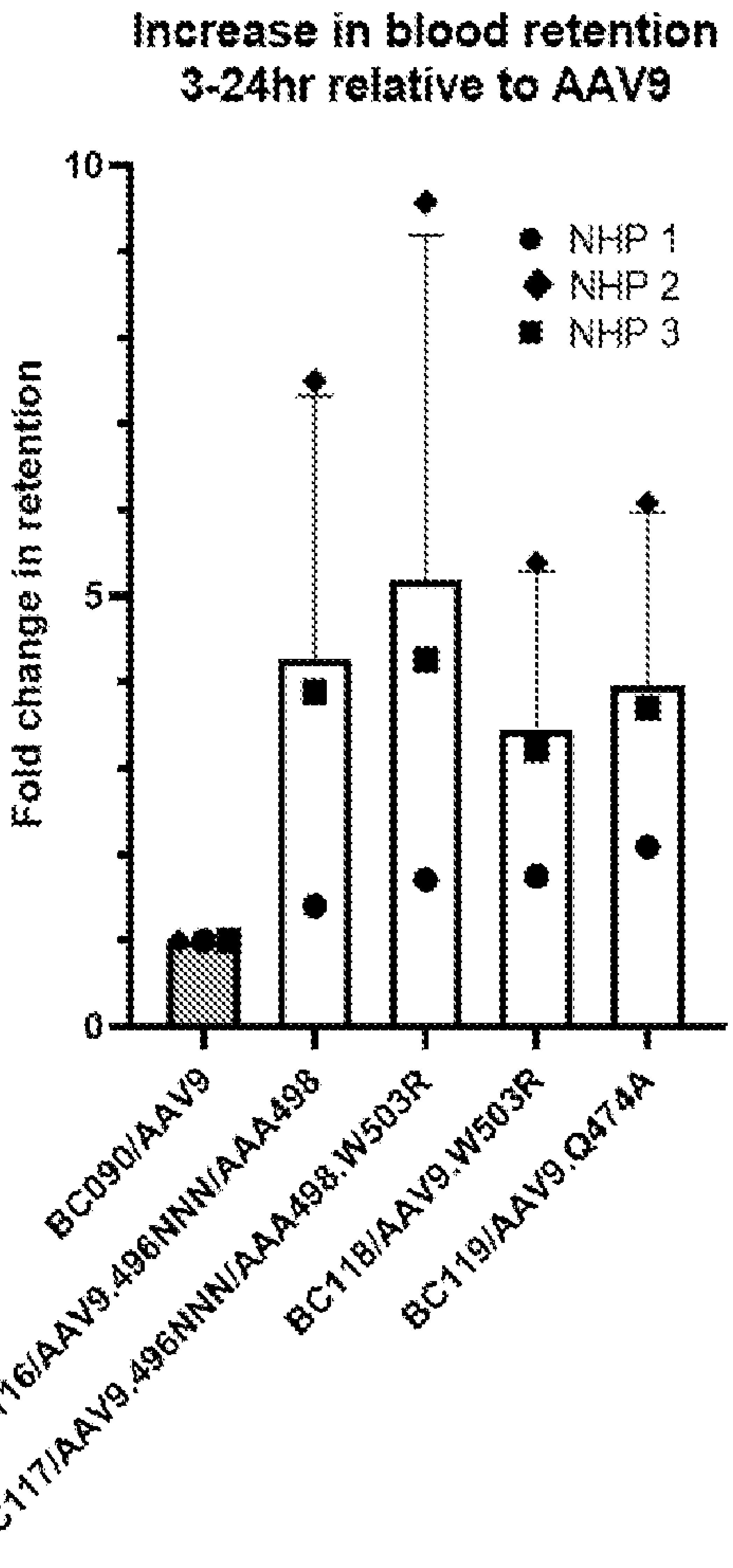


FIG. 34A

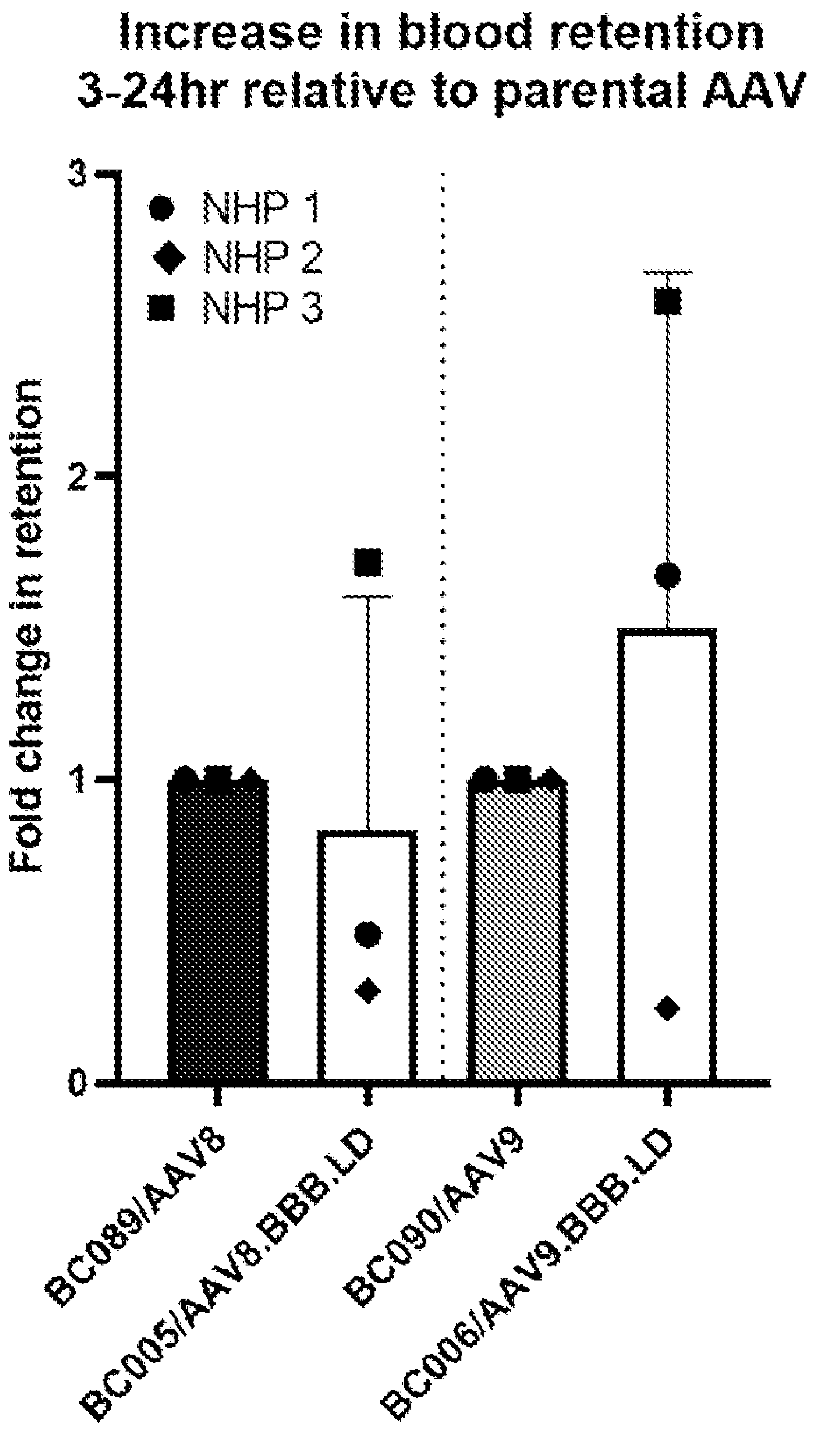


FIG. 34B

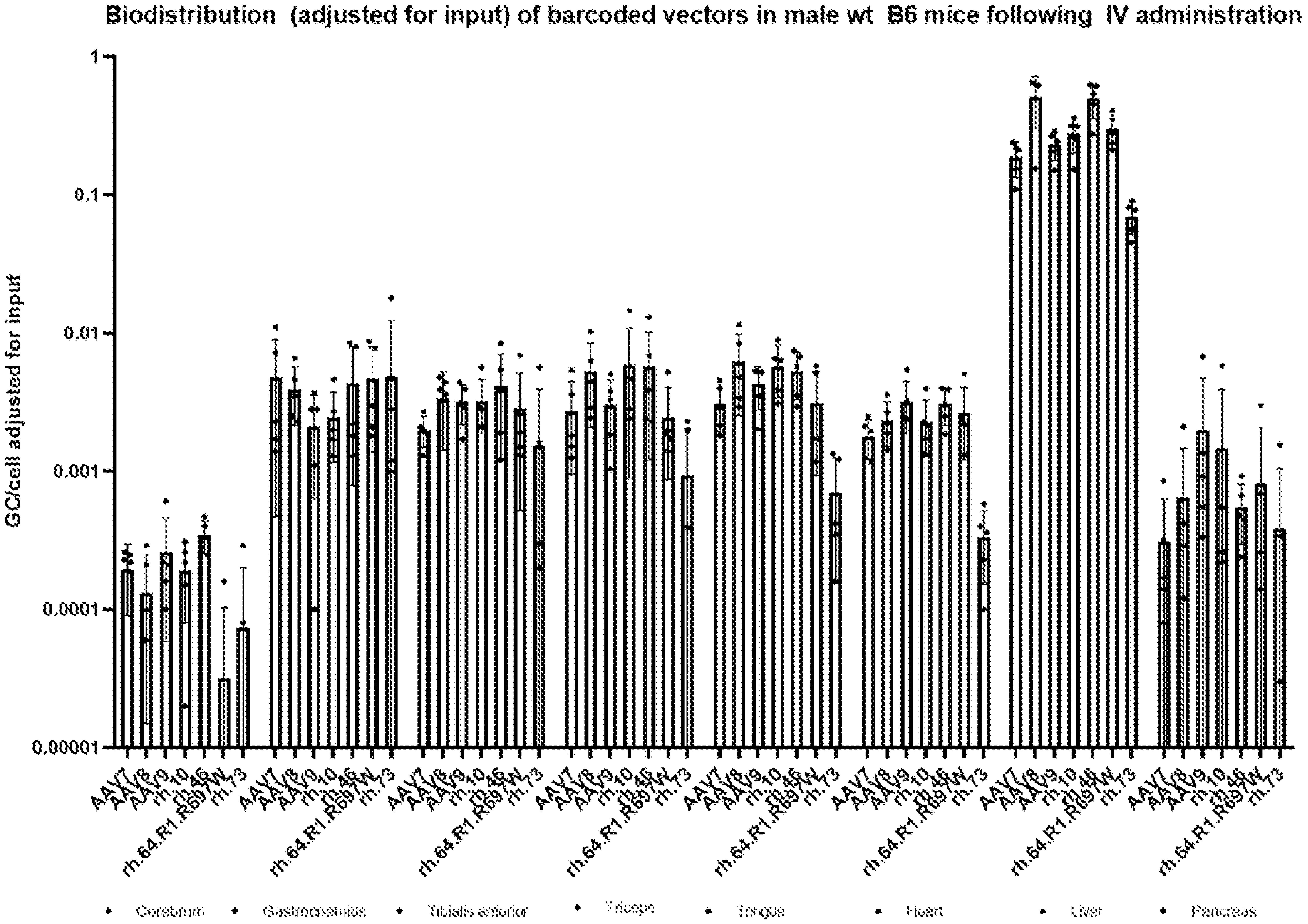

Biodistribution (adjusted for input) of barcoded vectors in male wt B6 mice following IV administration
GC/cell adjusted for input
1
0.1
0.01
0.001
0.0001
0.00001
AAV7
AAV8
AAV9
rh.10
rh.46
rh.64.R1.R697W
rh.73
Cerebrum
Gastrocnemius
Tibialis anterior
Triceps
Tongue
Heart
Liver
Pancreas

FIG. 35

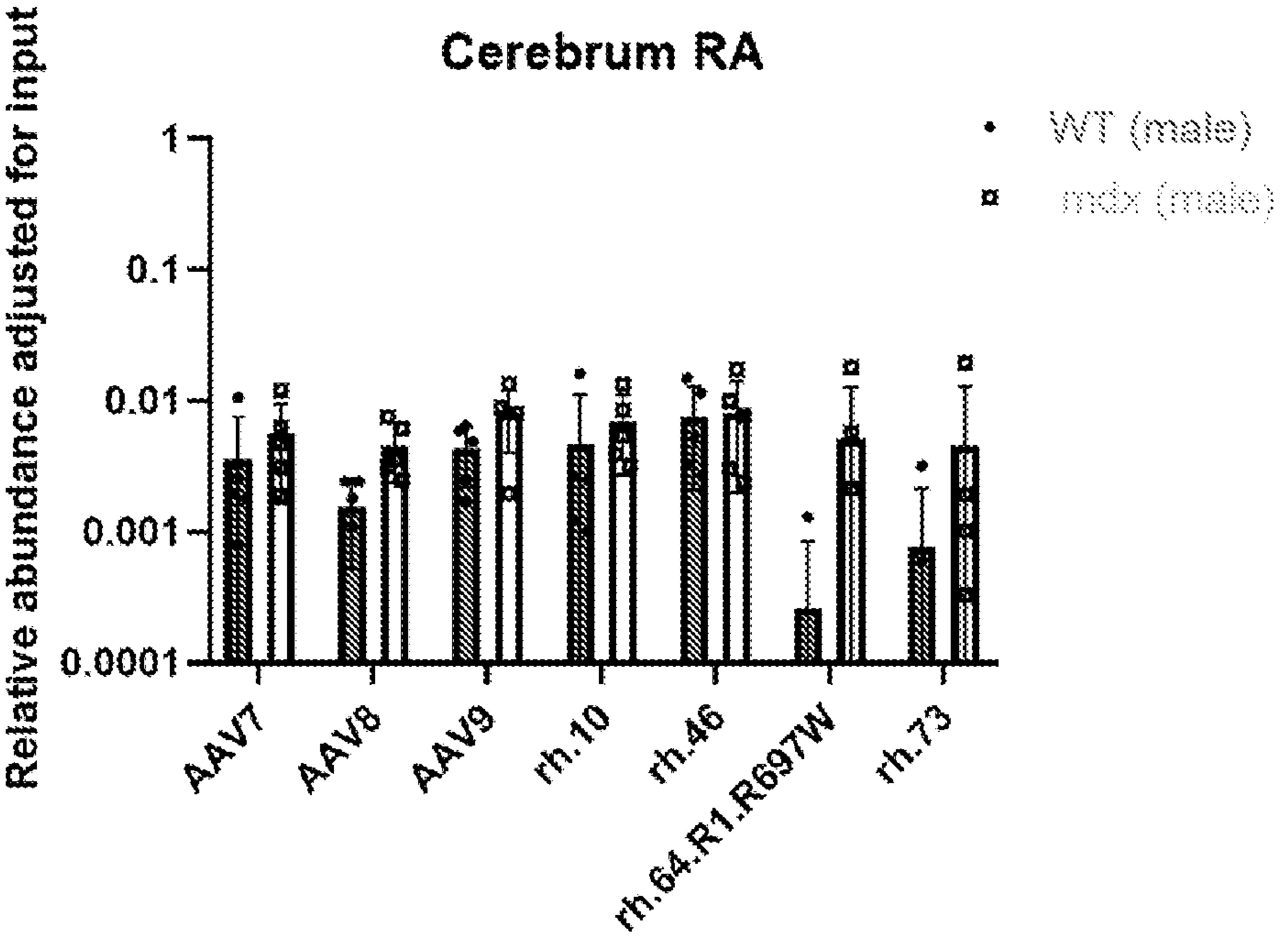


FIG. 36A

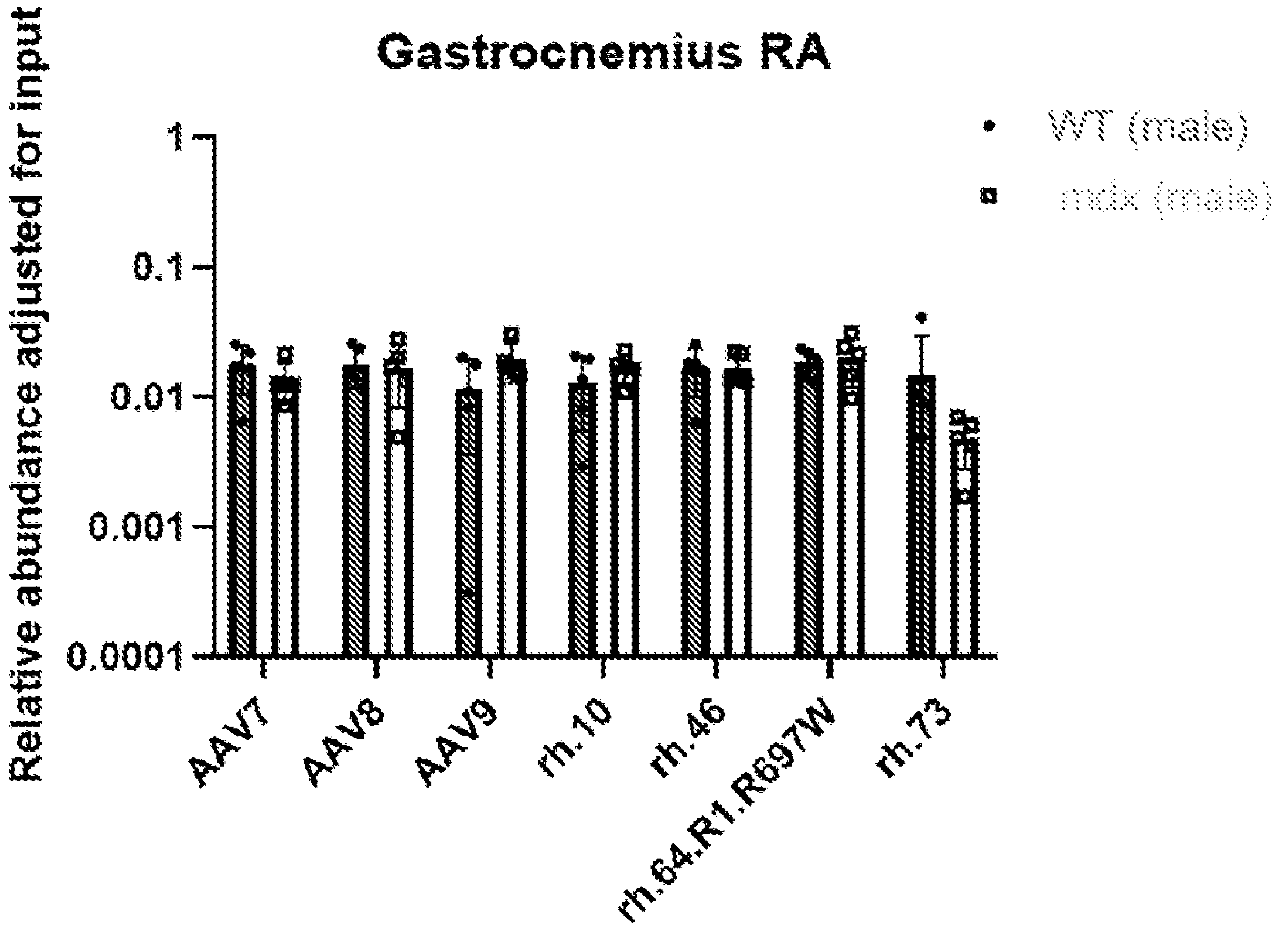


FIG. 36B

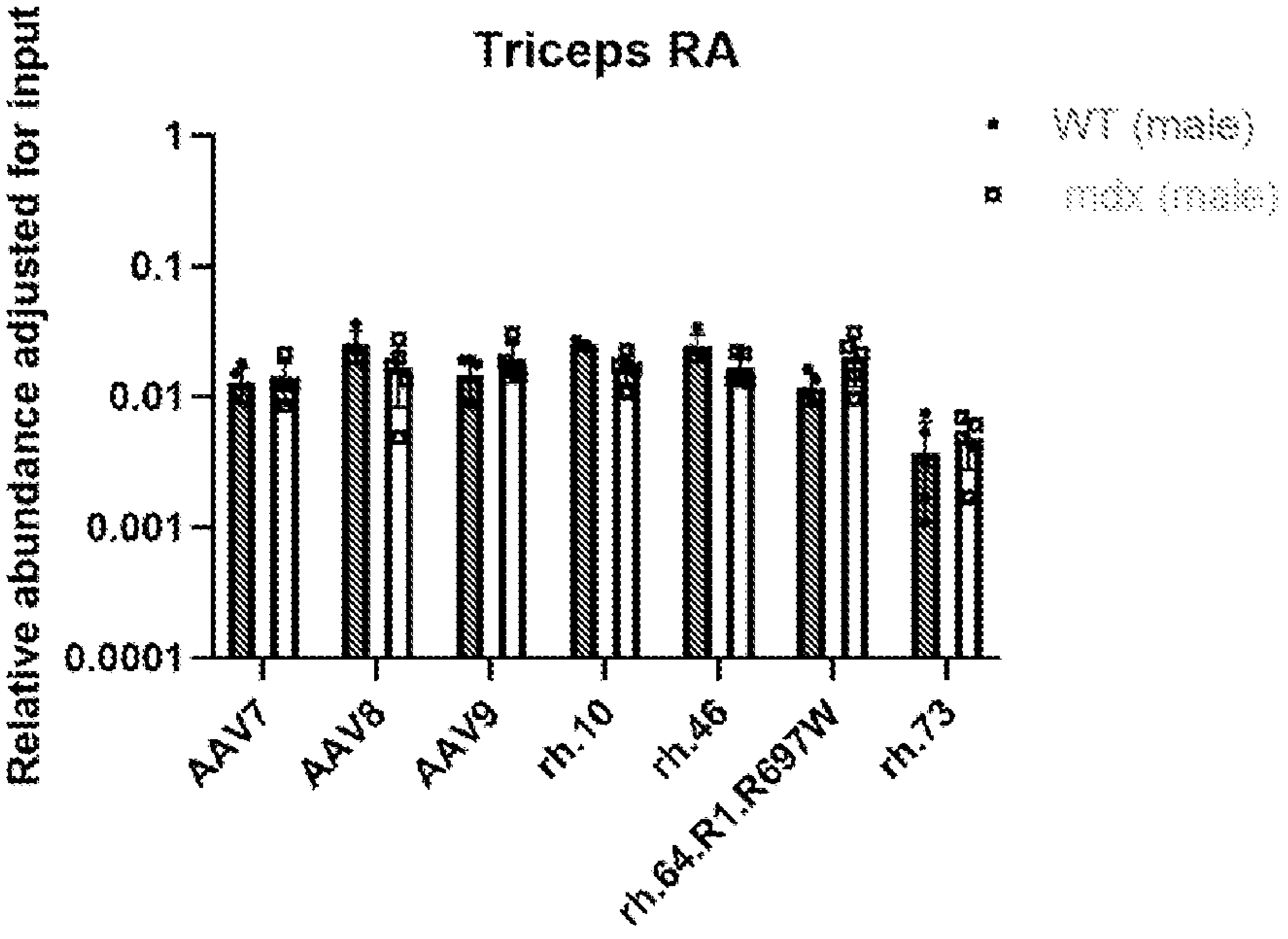


FIG. 36C

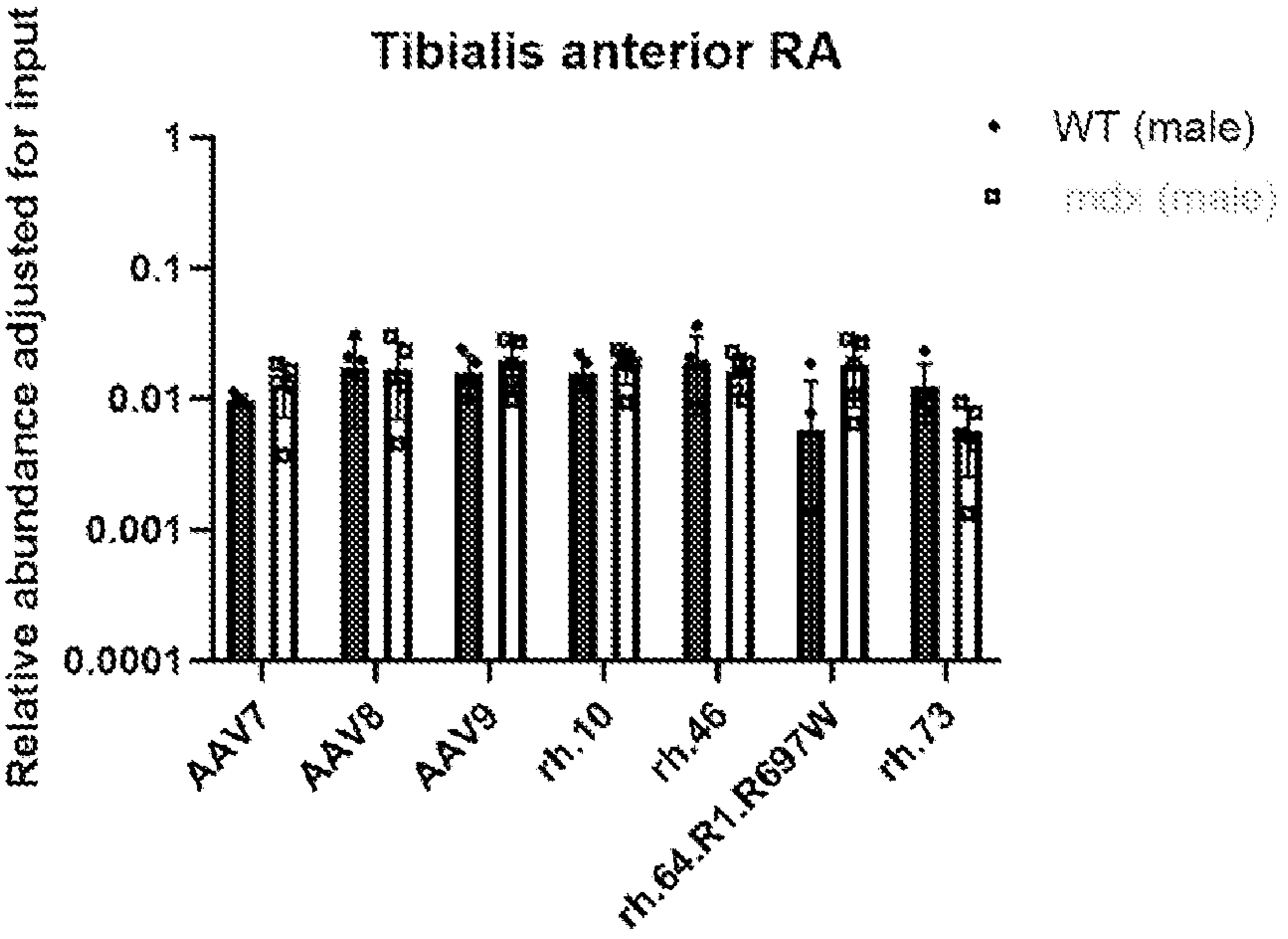


FIG. 36D

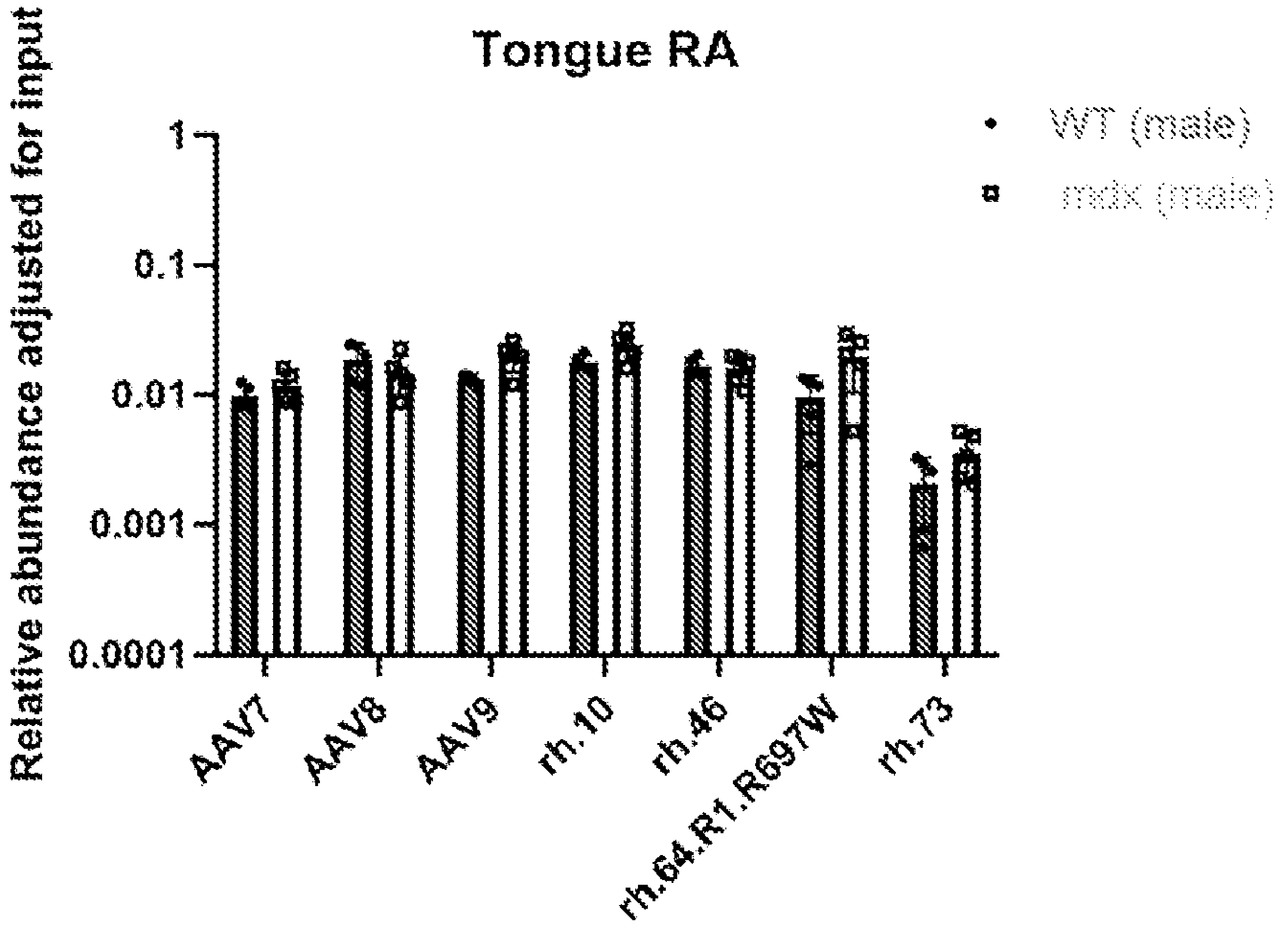


FIG. 36E

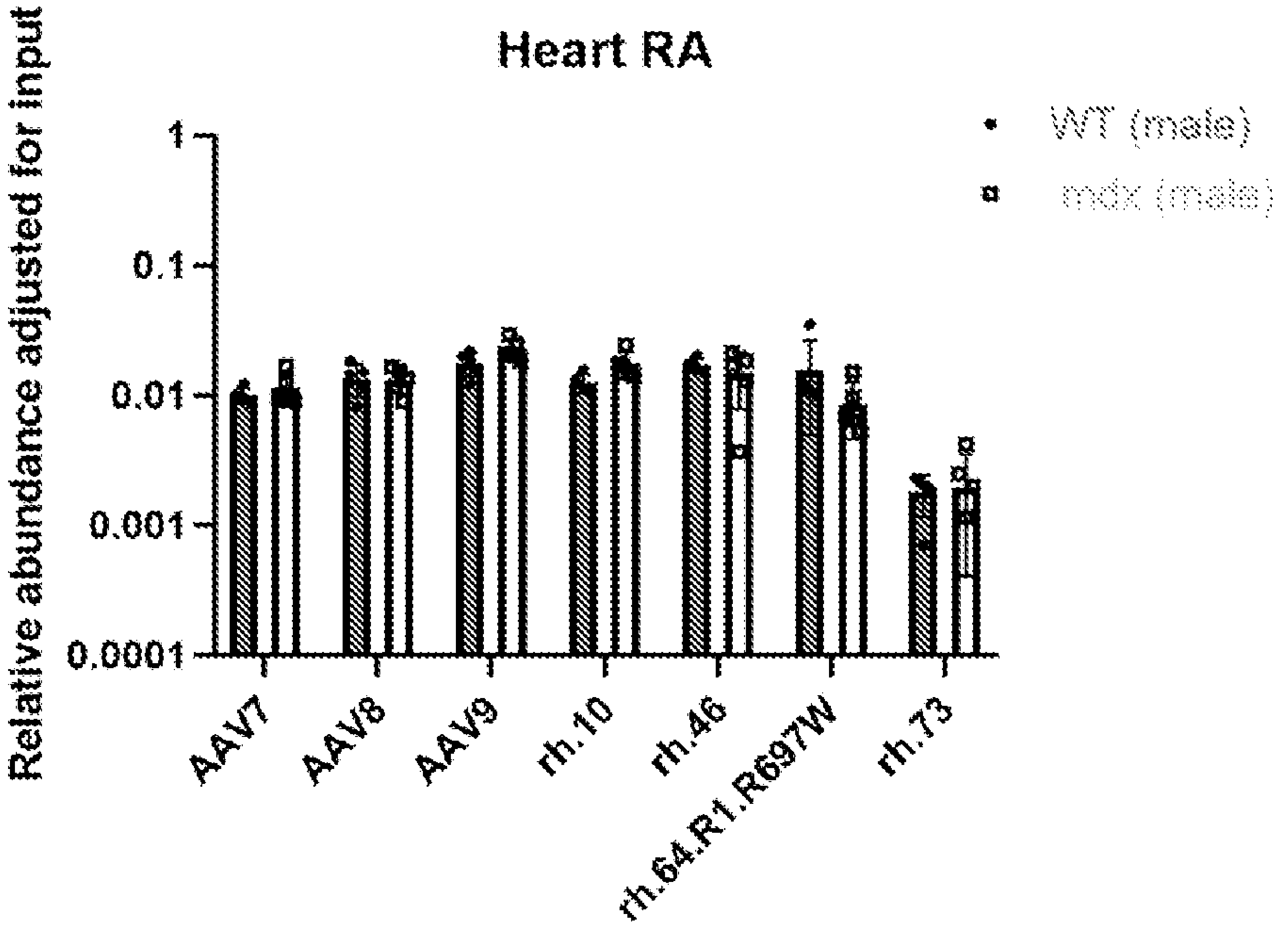


FIG. 36F

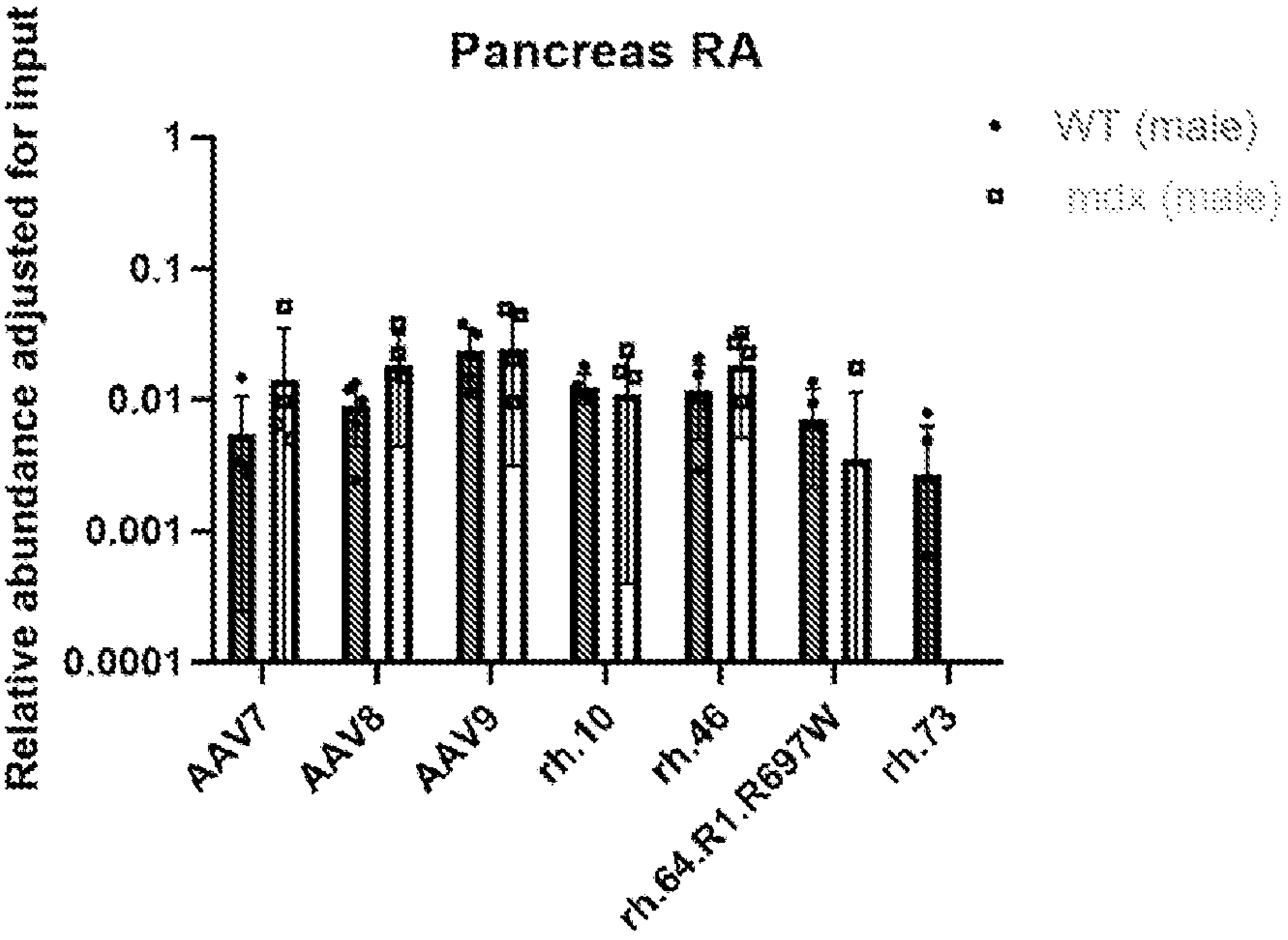


FIG. 36G

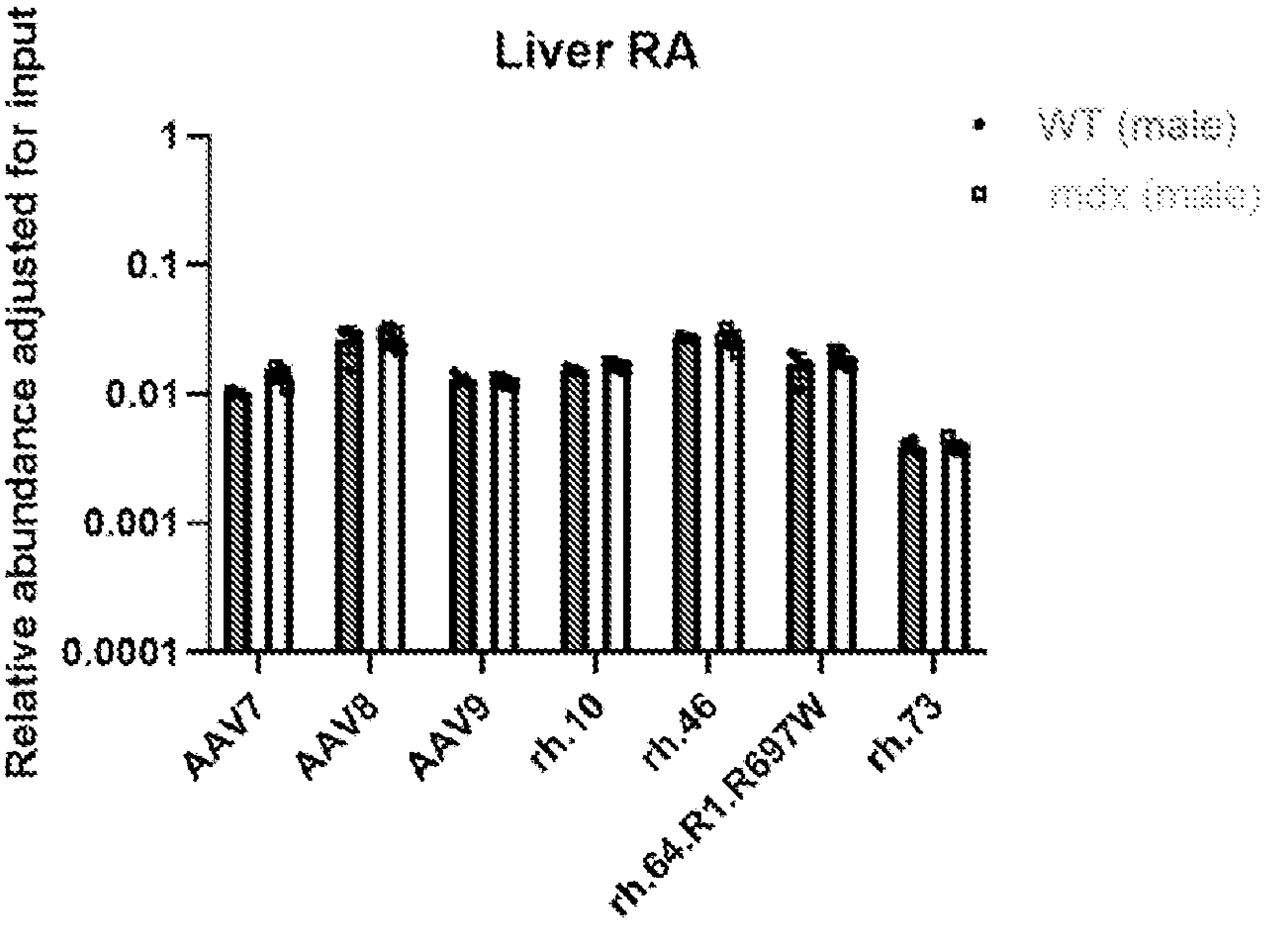


FIG. 36H

SEQUENCE LISTING

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<110>  REGENXBIO INC.

<120>  RECOMBINANT ADENO-ASSOCIATED VIRUSES FOR CNS OR MUSCLE DELIVERY

<130>  38013.0013P1

<150>  63/088,988
<151>  2020-10-07

<160>  93

<170>  PatentIn version 3.5

<210>  1
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  1

Thr Leu Ala Ala Pro Phe Lys
1               5


<210>  2
<211>  8
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  2

Asp Asp Asp Asp Asp Asp Asp Asp
1               5


<210>  3
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide
```

```
<400>  3

Leu Ser Ser Arg Leu Asp Ala
1               5


<210>  4
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capside peptide

<400>  4

Cys Leu Ser Ser Arg Leu Asp Ala Cys
1               5


<210>  5
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capside peptide

<400>  5

Cys Leu Pro Val Ala Ser Cys
1               5


<210>  6
<211>  5
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capside peptide

<400>  6

Leu Pro Val Ala Ser
1               5


<210>  7
```

<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capside peptide

<400> 7

Ala Ser Ser Leu Asn Ile Ala
1   5

<210> 8
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capside peptide

<400> 8

Gln Ala Gln Ala Gln Thr
1   5

<210> 9
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capside peptide

<400> 9

Ser Thr Gln Thr
1

<210> 10
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capside peptide

<400> 10

```
His Ala Ile Tyr Pro Arg His
1               5


<210>  11
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  11

Thr His Arg Pro Pro Met Trp Ser Pro Val Trp Pro
1               5                   10


<210>  12
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  12

Arg Thr Ile Gly Pro Ser Val
1               5


<210>  13
<211>  9
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  13

Cys Arg Thr Ile Gly Pro Ser Val Cys
1               5


<210>  14
<211>  11
<212>  PRT
```

```
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  14

Ser Ile Thr Leu Val Lys Ser Thr Gln Thr Val
1               5                   10


<210>  15
<211>  10
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  15

Thr Ile Leu Ser Arg Ser Thr Gln Thr Gly
1               5                   10


<210>  16
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  16

Gln Ala Val Arg Thr Ser Leu
1               5


<210>  17
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  17

Gln Ala Val Arg Thr Ser His
```

```
1               5


<210>  18
<211>  20
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  18

Val Val Met Val Gly Glu Lys Pro Ile Thr Ile Thr Gln His Ser Val
1               5                   10                  15


Glu Thr Glu Gly
            20


<210>  19
<211>  12
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  19

Arg Ser Ser Glu Glu Asp Lys Ser Thr Gln Thr Thr
1               5                   10


<210>  20
<211>  7
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid peptide

<400>  20

Thr Leu Ala Val Pro Phe Lys
1               5


<210>  21
```

<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid peptide

<400> 21

```
Asp Tyr Lys Asp Asp Asp Asp Lys
1               5
```

<210> 22
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 22

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

305   310   315   320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325   330   335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340   345   350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355   360   365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370   375   380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405   410   415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420   425   430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435   440   445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450   455   460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465   470   475   480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485   490   495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500   505   510

```
Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Gln Ala Val Arg
            580                 585                 590

Thr Ser Leu Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
```

```
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  23
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  23

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
```

```
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Gln Ala Val Arg
            580                 585                 590

Thr Ser His Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720
```

```
Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735


Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  24
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  24

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180   185   190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195   200   205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210   215   220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225   230   235   240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245   250   255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260   265   270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275   280   285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290   295   300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305   310   315   320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
```

```
                725                 730                 735


Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  25
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  25

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Arg Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735
```

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 26
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 26

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

```
Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
```

```
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540
```

```
Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

<210> 27
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 27

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile

```
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350
```

```
Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Ala Ala Ala Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
```

```
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
```

```
<210>  28
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  28

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160
```

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560
```

```
Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575


Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590


Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605


Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620


Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640


Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655


Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670


Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685


Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  29
<211>  736
<212>  PRT
<213>  Artificial Sequence
```

```
<220>
<223>  synthetic construct; capsid sequence

<400>  29

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
```

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Ala
                485                 490                 495

Ala Ala Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
```

```
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  30
<211>  738
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  30

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
```

```
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Ala Ala Ala Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu



<210>  31
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  31

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415
```

```
Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Ala
                485                 490                 495

Ala Ala Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

```
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  32
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  32

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
```

```
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Ala
                485                 490                 495

Ala Ala Ser Glu Phe Ala Arg Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640
```

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 33
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 33

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

```
Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
```

260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
450 455 460

```
Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Arg Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
```

660 665 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
675 680 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
690 695 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705 710 715 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 34
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 34

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Ala Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

```
Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700


Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720


Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  35
<211>  744
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  35

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Asp Asp Asp Asp Asp Asp Asp Asp Gly Gln
    450                 455                 460

Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala
465                 470                 475                 480

Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg
                485                 490                 495

Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro
            500                 505                 510
```

```
Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro
        515                 520                 525

Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro
    530                 535                 540

Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn
545                 550                 555                 560

Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr
                565                 570                 575

Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His
            580                 585                 590

Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly
        595                 600                 605

Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly
    610                 615                 620

Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser
625                 630                 635                 640

Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu
                645                 650                 655

Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys
            660                 665                 670

Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser
        675                 680                 685

Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn
    690                 695                 700

Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu
```

```
705                 710                 715                 720

Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly
                725                 730                 735

Thr Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  36
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  36

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320
```

```
Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Leu Ser Ser Arg Leu Asp Ala Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
```

```
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
545                 550                 555                 560

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
                565                 570                 575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
            580                 585                 590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720
```

```
Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735


Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  37
<211>  745
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  37

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

325 330 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
340 345 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
355 360 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
370 375 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385 390 395 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
405 410 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
420 425 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
435 440 445

Lys Thr Ile Asn Gly Ser Cys Leu Ser Ser Arg Leu Asp Ala Cys Gly
450 455 460

Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met
465 470 475 480

Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln
485 490 495

Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp
500 505 510

Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn
515 520 525

```
Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe
    530                 535                 540

Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp
545                 550                 555                 560

Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys
                565                 570                 575

Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn
            580                 585                 590

His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln
        595                 600                 605

Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
    610                 615                 620

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
625                 630                 635                 640

Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile
                645                 650                 655

Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn
            660                 665                 670

Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
        675                 680                 685

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
    690                 695                 700

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val
705                 710                 715                 720

Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile
```

```
                725                 730                 735


Gly Thr Arg Tyr Leu Thr Arg Asn Leu
            740                 745



<210>  38
<211>  741
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  38

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
```

130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145 150 155 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
165 170 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
180 185 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
195 200 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
210 215 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225 230 235 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
245 250 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
260 265 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
275 280 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
290 295 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305 310 315 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
325 330 335

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Leu Pro Val Ala Ser Gly Gln Asn Gln Gln
    450                 455                 460

Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly
465                 470                 475                 480

Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr
                485                 490                 495

Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser
            500                 505                 510

Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala
        515                 520                 525

Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly
```

```
    530                 535                 540

Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala
545                 550                 555                 560

Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro
                565                 570                 575

Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala
            580                 585                 590

Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro
        595                 600                 605

Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
    610                 615                 620

Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met
625                 630                 635                 640

Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn
                645                 650                 655

Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu
            660                 665                 670

Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile
        675                 680                 685

Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile
    690                 695                 700

Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val
705                 710                 715                 720

Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr
                725                 730                 735
```

```
Leu Thr Arg Asn Leu
            740


<210>  39
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  39

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140
```

```
Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
```

```
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Cys Leu Pro Val Ala Ser Cys Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540
```

```
Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
545                 550                 555                 560

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
                565                 570                 575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
            580                 585                 590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
```

740

<210> 40
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 40

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
100 105 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
115 120 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
130 135 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly

```
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Ala Ser Ser Leu Asn Ile Ala Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
```

```
545                 550                 555                 560

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
                565                 570                 575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
            580                 585                 590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740
```

<210> 41
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 41

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

```
Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
```

```
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser His Ala Ile Tyr Pro Arg His Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
545                 550                 555                 560
```

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
                565   570   575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
            580   585   590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595   600   605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610   615   620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625   630   635   640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645   650   655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660   665   670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675   680   685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690   695   700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705   710   715   720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725   730   735

Arg Tyr Leu Thr Arg Asn Leu
            740

<210> 42

<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 42

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Arg Thr Ile Gly Pro Ser Val Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
545                 550                 555                 560

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
```

565 570 575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
580 585 590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
595 600 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
610 615 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625 630 635 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
645 650 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
660 665 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
675 680 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
690 695 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 43
<211> 745
<212> PRT

<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 43

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145   150   155   160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165   170   175

```
Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
```

```
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Cys Arg Thr Ile Gly Pro Ser Val Cys Gly
    450                 455                 460

Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met
465                 470                 475                 480

Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln
                485                 490                 495

Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp
            500                 505                 510

Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn
        515                 520                 525

Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe
    530                 535                 540

Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp
545                 550                 555                 560

Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys
                565                 570                 575
```

Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn
580 585 590

His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln
595 600 605

Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln
610 615 620

Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro
625 630 635 640

Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile
645 650 655

Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn
660 665 670

Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val
675 680 685

Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp
690 695 700

Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val
705 710 715 720

Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile
725 730 735

Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 44
<211> 747
<212> PRT
<213> Artificial Sequence

```
<220>
<223>  synthetic construct; capsid sequence

<400>  44

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
```

```
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380
```

```
Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Ile Thr Leu Val Lys Ser Thr Gln Thr Val Ser Glu Phe
            500                 505                 510

Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu
        515                 520                 525

Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg
    530                 535                 540

Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly
545                 550                 555                 560

Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu
                565                 570                 575

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala
```

580 585 590

Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln
595 600 605

Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr
610 615 620

Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe
625 630 635 640

His Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro
645 650 655

Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala
660 665 670

Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly
675 680 685

Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys
690 695 700

Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn
705 710 715 720

Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg
725 730 735

Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
740 745

<210> 45
<211> 746
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

```
<400>  45

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

385   390   395   400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405   410   415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420   425   430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435   440   445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450   455   460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465   470   475   480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485   490   495

Asn Asn Thr Ile Leu Ser Arg Ser Thr Gln Thr Gly Ser Glu Phe Ala
            500   505   510

Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met
        515   520   525

Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe
    530   535   540

Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg
545   550   555   560

Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile
                565   570   575

Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr
            580   585   590

```
Asn His Gln Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn
        595                 600                 605


Gln Gly Ile Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu
    610                 615                 620


Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His
625                 630                 635                 640


Pro Ser Pro Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln
                645                 650                 655


Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe
            660                 665                 670


Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln
        675                 680                 685


Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg
    690                 695                 700


Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn
705                 710                 715                 720


Val Glu Phe Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro
                725                 730                 735


Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
            740                 745


<210>  46
<211>  753
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  46
```

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Thr Ile Leu Ser Arg Ser
    130                 135                 140

Thr Gln Thr Gly Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser Pro
145                 150                 155                 160

Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys Ser Gly Ala Gln Pro
                165                 170                 175

Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Thr Glu Ser Val
            180                 185                 190

Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Ala Pro Ser Gly Val
```

```
        195                 200                 205

Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala Pro Val Ala Asp Asn
    210                 215                 220

Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His Cys
225                 230                 235                 240

Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg Thr
                245                 250                 255

Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser Asn
            260                 265                 270

Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser
        275                 280                 285

Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser
    290                 295                 300

Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro
305                 310                 315                 320

Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr
                325                 330                 335

Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val
            340                 345                 350

Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser
        355                 360                 365

Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile
    370                 375                 380

Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly
385                 390                 395                 400
```

```
Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg
                405                 410                 415

Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe
            420                 425                 430

His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro
        435                 440                 445

Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Ile Asn Gly Ser
    450                 455                 460

Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn
465                 470                 475                 480

Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln
                485                 490                 495

Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala
            500                 505                 510

Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met
        515                 520                 525

Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe
    530                 535                 540

Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg
545                 550                 555                 560

Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile
                565                 570                 575

Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr
            580                 585                 590

Asn His Gln Ser Asp Gly Thr Leu Ala Val Pro Phe Lys Ala Gln Ala
```

```
        595                 600                 605

Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp
    610                 615                 620

Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
625                 630                 635                 640

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
                645                 650                 655

Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
            660                 665                 670

Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile
        675                 680                 685

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
    690                 695                 700

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
705                 710                 715                 720

Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly
                725                 730                 735

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
            740                 745                 750

Leu



<210>  47
<211>  754
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence
```

```
<400>  47

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ser Ile Thr Leu Val Lys
    130                 135                 140


Ser Thr Gln Thr Val Ala Pro Gly Lys Lys Arg Pro Val Glu Gln Ser
145                 150                 155                 160


Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly Lys Ser Gly Ala Gln
                165                 170                 175


Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr Gly Asp Thr Glu Ser
            180                 185                 190
```

```
Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro Ala Ala Pro Ser Gly
        195                 200                 205

Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly Ala Pro Val Ala Asp
    210                 215                 220

Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser Ser Gly Asn Trp His
225                 230                 235                 240

Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile Thr Thr Ser Thr Arg
                245                 250                 255

Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Gln Ile Ser
            260                 265                 270

Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn Ala Tyr Phe Gly Tyr
        275                 280                 285

Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe
    290                 295                 300

Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg
305                 310                 315                 320

Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val
                325                 330                 335

Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr
            340                 345                 350

Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly
        355                 360                 365

Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met
    370                 375                 380

Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val
```

385   390   395   400

Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu
                405   410   415

Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro
            420   425   430

Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn
        435   440   445

Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr Ile Asn Gly
    450   455   460

Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser
465   470   475   480

Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg
                485   490   495

Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe
            500   505   510

Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu
        515   520   525

Met Asn Pro Gly Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg
    530   535   540

Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly
545   550   555   560

Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu
                565   570   575

Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala
            580   585   590

```
Thr Asn His Gln Ser Asp Gly Thr Leu Ala Val Pro Phe Lys Ala Gln
        595                 600                 605


Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val
    610                 615                 620


Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
625                 630                 635                 640


Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
                645                 650                 655


Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
            660                 665                 670


Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe
        675                 680                 685


Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
    690                 695                 700


Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
705                 710                 715                 720


Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu
                725                 730                 735


Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
            740                 745                 750


Asn Leu



<210>  48
<211>  35
<212>  PRT
<213>  Artificial Sequence
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```
<220>
<223>  synthetic construct; capsid sequence


<220>
<221>  misc_feature
<222>  (14)..(15)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (23)..(23)
<223>  Xaa can be any naturally occurring amino acid

<220>
<221>  misc_feature
<222>  (30)..(30)
<223>  Xaa can be any naturally occurring amino acid

<400>  48

Tyr Tyr Leu Ser Arg Thr Gln Asn Thr Gly Gly Thr Ala Xaa Xaa Gln
1               5                   10                  15


Thr Leu Leu Phe Ser Gln Xaa Gly Pro Ser Asn Met Ser Xaa Gln Ala
            20                  25                  30


Lys Asn Trp
        35


<210>  49
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  49

Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys
1               5                   10                  15


Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro
            20                  25                  30
```

```
Lys Asn Trp
        35


<210>  50
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  50

Tyr Tyr Leu Asn Arg Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys
1               5                   10                  15


Asp Leu Leu Phe Ser Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro
            20                  25                  30


Lys Asn Trp
        35


<210>  51
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  51

Tyr Tyr Leu Ser Arg Thr Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser
1               5                   10                  15


Arg Leu Gln Phe Ser Gln Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser
            20                  25                  30


Arg Asn Trp
        35


<210>  52
```

```
<211>  36
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  52

Tyr Tyr Leu Asn Arg Thr Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln
1               5                   10                  15


Ser Arg Leu Leu Phe Ser Gln Ala Gly Pro Gln Ser Met Ser Leu Gln
            20                  25                  30


Ala Arg Asn Trp
        35


<210>  53
<211>  36
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  53

Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu Asn Ala Gly Thr
1               5                   10                  15


Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn Phe Ser Asn Phe
            20                  25                  30


Lys Lys Asn Trp
        35


<210>  54
<211>  29
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence
```

```
<400>  54

Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln Phe Asn Lys
1               5                   10                  15


Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
            20                  25


<210>  55
<211>  36
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  55

Tyr Tyr Leu Ala Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn
1               5                   10                  15


Arg Glu Leu Gln Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln
            20                  25                  30


Ala Lys Asn Trp
        35


<210>  56
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  56

Tyr Tyr Leu Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln
1               5                   10                  15


Thr Leu Gly Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala
            20                  25                  30
```

```
Lys Asn Trp
        35


<210>  57
<211>  34
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  57

Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr
1               5                   10                  15


Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg
            20                  25                  30


Asn Tyr




<210>  58
<211>  35
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  58

Tyr Tyr Leu Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln
1               5                   10                  15


Gln Leu Leu Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala
            20                  25                  30


Lys Asn Trp
        35


<210>  59
```

<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 59

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145   150   155   160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr

```
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365
```

```
Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Glu Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
```

```
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Phe Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Ala Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys Asn Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705                 710                 715                 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
                725                 730                 735
```

<210> 60
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

```
<400>  60

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                      25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                      40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                     105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                     120                 125


Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160


Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                     185                 190
```

```
Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
```

```
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Arg Gly Asn Arg Gln Ala Ala Thr
            580                 585                 590
```

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595   600   605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610   615   620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625   630   635   640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645   650   655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660   665   670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675   680   685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690   695   700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705   710   715   720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 61
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 61

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

```
Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

```
    210                 215                 220


Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240


Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255


Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270


Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285


Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300


Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320


Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335


Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350


Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365


Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380


Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400


Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510

Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

    610   615   620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625   630   635   640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645   650   655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660   665   670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675   680   685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690   695   700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 62
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 62

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly

```
        35                  40                  45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50                  55                  60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65                  70                  75                  80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115                 120                 125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240
```

```
Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
```

```
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640
```

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645   650   655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660   665   670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675   680   685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690   695   700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705   710   715   720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725   730

<210> 63
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 63

Met Ser Phe Val Asp His Pro Pro Asp Trp Leu Glu Glu Val Gly Glu
1   5   10   15

Gly Leu Arg Glu Phe Leu Gly Leu Glu Ala Gly Pro Pro Lys Pro Lys
            20   25   30

Pro Asn Gln Gln His Gln Asp Gln Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Asn Tyr Leu Gly Pro Gly Asn Gly Leu Asp Arg Gly Glu Pro Val
    50   55   60

```
Asn Arg Ala Asp Glu Val Ala Arg Glu His Asp Ile Ser Tyr Asn Glu
65                  70                  75                  80

Gln Leu Glu Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85                  90                  95

Ala Glu Phe Gln Glu Lys Leu Ala Asp Asp Thr Ser Phe Gly Gly Asn
            100                 105                 110

Leu Gly Lys Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Phe
        115                 120                 125

Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Thr Gly Lys Arg Ile
    130                 135                 140

Asp Asp His Phe Pro Lys Arg Lys Lys Ala Arg Thr Glu Glu Asp Ser
145                 150                 155                 160

Lys Pro Ser Thr Ser Ser Asp Ala Glu Ala Gly Pro Ser Gly Ser Gln
                165                 170                 175

Gln Leu Gln Ile Pro Ala Gln Pro Ala Ser Ser Leu Gly Ala Asp Thr
            180                 185                 190

Met Ser Ala Gly Gly Gly Gly Pro Leu Gly Asp Asn Asn Gln Gly Ala
        195                 200                 205

Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys Asp Ser Thr Trp
    210                 215                 220

Met Gly Asp Arg Val Val Thr Lys Ser Thr Arg Thr Trp Val Leu Pro
225                 230                 235                 240

Ser Tyr Asn Asn His Gln Tyr Arg Glu Ile Lys Ser Gly Ser Val Asp
                245                 250                 255

Gly Ser Asn Ala Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr
```

```
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Ser His Trp Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Tyr Trp Gly Phe Arg Pro Arg Ser Leu Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Val Gln Asp Ser Thr
305                 310                 315                 320

Thr Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp
                325                 330                 335

Asp Asp Tyr Gln Leu Pro Tyr Val Val Gly Asn Gly Thr Glu Gly Cys
            340                 345                 350

Leu Pro Ala Phe Pro Pro Gln Val Phe Thr Leu Pro Gln Tyr Gly Tyr
        355                 360                 365

Ala Thr Leu Asn Arg Asp Asn Thr Glu Asn Pro Thr Glu Arg Ser Ser
    370                 375                 380

Phe Phe Cys Leu Glu Tyr Phe Pro Ser Lys Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Phe Thr Tyr Asn Phe Glu Glu Val Pro Phe His Ser Ser
                405                 410                 415

Phe Ala Pro Ser Gln Asn Leu Phe Lys Leu Ala Asn Pro Leu Val Asp
            420                 425                 430

Gln Tyr Leu Tyr Arg Phe Val Ser Thr Asn Asn Thr Gly Gly Val Gln
        435                 440                 445

Phe Asn Lys Asn Leu Ala Gly Arg Tyr Ala Asn Thr Tyr Lys Asn Trp
    450                 455                 460
```

```
Phe Pro Gly Pro Met Gly Arg Thr Gln Gly Trp Asn Leu Gly Ser Gly
465                 470                 475                 480

Val Asn Arg Ala Ser Val Ser Ala Phe Ala Thr Thr Asn Arg Met Glu
                485                 490                 495

Leu Glu Gly Ala Ser Tyr Gln Val Pro Pro Gln Pro Asn Gly Met Thr
            500                 505                 510

Asn Asn Leu Gln Gly Ser Asn Thr Tyr Ala Leu Glu Asn Thr Met Ile
        515                 520                 525

Phe Asn Ser Gln Pro Ala Asn Pro Gly Thr Thr Ala Thr Tyr Leu Glu
    530                 535                 540

Gly Asn Met Leu Ile Thr Ser Glu Ser Glu Thr Gln Pro Val Asn Arg
545                 550                 555                 560

Val Ala Tyr Asn Val Gly Gly Gln Met Ala Thr Asn Asn Gln Ser Ser
                565                 570                 575

Thr Thr Ala Pro Ala Thr Gly Thr Tyr Asn Leu Gln Glu Ile Val Pro
            580                 585                 590

Gly Ser Val Trp Met Glu Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp
        595                 600                 605

Ala Lys Ile Pro Glu Thr Gly Ala His Phe His Pro Ser Pro Ala Met
    610                 615                 620

Gly Gly Phe Gly Leu Lys His Pro Pro Pro Met Met Leu Ile Lys Asn
625                 630                 635                 640

Thr Pro Val Pro Gly Asn Ile Thr Ser Phe Ser Asp Val Pro Val Ser
                645                 650                 655

Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Thr Val Glu Met Glu
```

660 665 670

Trp Glu Leu Lys Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln
675 680 685

Tyr Thr Asn Asn Tyr Asn Asp Pro Gln Phe Val Asp Phe Ala Pro Asp
690 695 700

Ser Thr Gly Glu Tyr Arg Thr Thr Arg Pro Ile Gly Thr Arg Tyr Leu
705 710 715 720

Thr Arg Pro Leu

<210> 64
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 64

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Phe Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly
145                 150                 155                 160

Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Thr Pro Ala Ala Val Gly Pro Thr Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Ala Ser Thr Gly Ala Ser Asn Asp Asn His
            260                 265                 270

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        275                 280                 285
```

```
His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    290                 295                 300

Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln
305                 310                 315                 320

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                325                 330                 335

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            340                 345                 350

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        355                 360                 365

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    370                 375                 380

Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
385                 390                 395                 400

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                405                 410                 415

Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            420                 425                 430

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg
        435                 440                 445

Thr Gln Asn Gln Ser Gly Ser Ala Gln Asn Lys Asp Leu Leu Phe Ser
    450                 455                 460

Arg Gly Ser Pro Ala Gly Met Ser Val Gln Pro Lys Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Lys Thr Asp Asn
```

```
                485                 490                 495

Asn Asn Ser Asn Phe Thr Trp Thr Gly Ala Ser Lys Tyr Asn Leu Asn
            500                 505                 510

Gly Arg Glu Ser Ile Ile Asn Pro Gly Thr Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Lys Asp Lys Phe Phe Pro Met Ser Gly Val Met Ile Phe Gly
    530                 535                 540

Lys Glu Ser Ala Gly Ala Ser Asn Thr Ala Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr Glu Arg
                565                 570                 575

Phe Gly Thr Val Ala Val Asn Leu Gln Ser Ser Ser Thr Asp Pro Ala
            580                 585                 590

Thr Gly Asp Val His Val Met Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Ala Glu Phe Ser Ala Thr Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685
```

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Val Gln Tyr Thr Ser Asn
690 695 700

Tyr Ala Lys Ser Ala Asn Val Asp Phe Thr Val Asp Asn Asn Gly Leu
705 710 715 720

Tyr Thr Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Pro Leu
725 730 735

<210> 65
<211> 737
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 65

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
20 25 30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
85 90 95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
100 105 110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Ala Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Val Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn
    210                 215                 220

Ala Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Ser Glu Thr Ala Gly Ser Thr Asn Asp Asn
            260                 265                 270

Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Lys Leu Arg Phe Lys Leu Phe Asn Ile
```

```
305                 310                 315                 320

Gln Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Ile Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn
    370                 375                 380

Gly Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr Ser
                405                 410                 415

Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala
        435                 440                 445

Arg Thr Gln Ser Asn Pro Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln
    450                 455                 460

Phe Tyr Gln Gly Gly Pro Ser Thr Met Ala Glu Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Val Leu Ile
    530                 535                 540

Phe Gly Lys Thr Gly Ala Thr Asn Lys Thr Thr Leu Glu Asn Val Leu
545                 550                 555                 560

Met Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu
                565                 570                 575

Glu Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Asn Thr Ala Ala
            580                 585                 590

Gln Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp
        595                 600                 605

Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro
    610                 615                 620

His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly
625                 630                 635                 640

Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro
                645                 650                 655

Ala Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile
            660                 665                 670

Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu
        675                 680                 685

Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser
    690                 695                 700

Asn Phe Glu Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly
```

```
705                 710                 715                 720

Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn
                725                 730                 735

Leu



<210>  66
<211>  738
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  66

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
```

```
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Gly Val Gly Pro Asn Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ala Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320
```

```
Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Thr Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Thr Thr Gly Gly Thr Ala Asn Thr Gln Thr Leu Gly
    450                 455                 460

Phe Ser Gln Gly Gly Pro Asn Thr Met Ala Asn Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Thr Gly
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Ala Gly Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asn Ser Leu Ala Asn Pro Gly Ile Ala Met Ala Thr
```

```
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Asn Gly Ile Leu Ile
    530                 535                 540

Phe Gly Lys Gln Asn Ala Ala Arg Asp Asn Ala Asp Tyr Ser Asp Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Glu Tyr Gly Ile Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Gln Ile Gly Thr Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ser Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Ser Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720
```

```
Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735


Asn Leu




<210>  67
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  67

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125
```

```
Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
```

```
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525
```

```
Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
```

```
                725                 730                 735


<210>  68
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  68

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
```

```
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350
```

```
Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
```

```
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Asp Gly Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735

<210>  69
<211>  738
<212>  PRT
```

```
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  69

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175
```

```
Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
```

```
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575
```

```
Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Asp
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu


<210>  70
<211>  738
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> synthetic construct; capsid sequence

<400> 70

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

Gly Lys Thr Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165   170   175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro

```
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380
```

```
Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Gln Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
```

580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 71
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

```
<400>  71

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160


Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175


Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190
```

```
Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
```

```
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590
```

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 72
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 72

```
Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
```

195 200 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
210 215 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225 230 235 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
245 250 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
260 265 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
275 280 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
290 295 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305 310 315 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
325 330 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
340 345 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
355 360 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
370 375 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385 390 395 400

```
Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
```

```
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Thr Lys Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu



<210>  73
<211>  738
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  73

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
```

```
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205
```

```
Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
```

```
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Gln Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ala Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Arg Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Thr Asn Thr Gly
            580                 585                 590

Pro Ile Val Gly Asn Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605
```

```
Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Thr Phe Ser Gln Ala Lys Leu Ala Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu



<210>  74
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  74

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15
```

```
Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Arg Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
```

```
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415
```

```
Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
```

```
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  75
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  75

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Gln Asp Asp Ser Arg Gly Leu Val Leu Pro
```

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly His Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Pro Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
```

```
        435                 440                 445

Gln Ser Asn Ser Gly Thr Leu Gln Gln Ser Arg Leu Leu Phe Ser Gln
    450                 455                 460

Ala Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn
                485                 490                 495

Asn Ser Asn Phe Pro Trp Thr Ala Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Thr Asn Ala Asn Asp Ala Asp Leu Glu His Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Asn Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Gly Pro Thr Thr
            580                 585                 590

Glu Asn Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  76
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  76

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Met Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Asp Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Tyr Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Asp Ser Gly Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
```

```
            660                 665                 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  77
<211>  734
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  77

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
```

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Arg Gln Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Thr Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285
```

```
Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Thr Ala Ser Gly Thr Gln Gln Ser Arg Leu Leu Phe Ser Gln Ala
    450                 455                 460

Gly Pro Thr Ser Met Ser Leu Gln Ala Lys Asn Trp Leu Pro Gly Pro
465                 470                 475                 480

Cys Tyr Arg Gln Gln Arg Leu Ser Lys Gln Ala Asn Asp Asn Asn Asn
```

```
                485                 490                 495

Ser Asn Phe Pro Trp Thr Gly Ala Thr Lys Tyr Tyr Leu Asn Gly Arg
            500                 505                 510

Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp Asp
        515                 520                 525

Glu Glu Lys Phe Phe Pro Met His Gly Thr Leu Ile Phe Gly Lys Glu
    530                 535                 540

Gly Thr Asn Ala Thr Asn Ala Glu Leu Glu Asn Val Met Ile Thr Asp
545                 550                 555                 560

Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr Gly
                565                 570                 575

Tyr Val Ser Asn Asn Leu Gln Asn Ser Asn Thr Ala Ala Ser Thr Glu
            580                 585                 590

Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln Asp Arg
        595                 600                 605

Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Pro Thr Asn Phe Ser Ser Ala Lys Phe Ala Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys Glu
        675                 680                 685
```

Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr Asn
    690   695   700

Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr Ser
705   710   715   720

Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730

<210> 78
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 78

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Val Pro Gln Pro
            20   25   30

Lys Ala Asn Gln Gln His Gln Asp Asn Arg Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Ile Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Gly
    130                 135                 140

Ala Val Asp Gln Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Val Gly
145                 150                 155                 160

Lys Ser Gly Lys Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Leu Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Thr Ser Leu Gly Ser Asn Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Lys Leu Ser Phe Lys Leu Phe Asn Ile Gln Val
```

```
305                 310                 315                 320

Arg Gly Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Asn Arg Thr
        435                 440                 445

Gln Gly Thr Thr Ser Gly Thr Thr Asn Gln Ser Arg Leu Leu Phe Ser
    450                 455                 460

Gln Ala Gly Pro Gln Ser Met Ser Leu Gln Ala Arg Asn Trp Leu Pro
465                 470                 475                 480

Gly Pro Cys Tyr Arg Gln Gln Arg Leu Ser Lys Thr Ala Asn Asp Asn
                485                 490                 495

Asn Asn Ser Asn Phe Pro Trp Thr Ala Ala Ser Lys Tyr His Leu Asn
            500                 505                 510
```

```
Gly Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Asp Asp Glu Glu Lys Phe Phe Pro Met His Gly Asn Leu Ile Phe Gly
    530                 535                 540

Lys Glu Gly Thr Thr Ala Ser Asn Ala Glu Leu Asp Asn Val Met Ile
545                 550                 555                 560

Thr Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln
                565                 570                 575

Tyr Gly Thr Val Ala Asn Asn Leu Gln Ser Ser Asn Thr Ala Pro Thr
            580                 585                 590

Thr Gly Thr Val Asn His Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Met Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asn Pro Pro Thr Thr Phe Ser Pro Ala Lys Phe Ala Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val
```

705   710   715   720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725   730   735

<210> 79
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 79

Met Thr Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser Glu
1   5   10   15

Gly Val Arg Glu Trp Trp Ala Leu Gln Pro Gly Ala Pro Lys Pro Lys
            20   25   30

Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro Gly
        35   40   45

Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro Val
    50   55   60

Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp Gln
65   70   75   80

Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala Asp
                85   90   95

Ala Glu Phe Gln Gln Arg Leu Gln Gly Asp Thr Ser Phe Gly Gly Asn
            100   105   110

Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro Leu
        115   120   125

Gly Leu Val Glu Gln Ala Gly Glu Thr Ala Pro Gly Lys Lys Arg Pro

```
    130                 135                 140

Leu Ile Glu Ser Pro Gln Gln Pro Asp Ser Ser Thr Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Lys Leu Val Phe Glu Asp Glu Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Thr Ser Gly Ala Met Ser
            180                 185                 190

Asp Asp Ser Glu Met Arg Ala Ala Ala Gly Gly Ala Ala Val Glu Gly
        195                 200                 205

Gly Gln Gly Ala Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly His Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Lys Arg Leu Gly Glu
                245                 250                 255

Ser Leu Gln Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Met Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335
```

```
Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Leu Val Thr Gly Asn Thr Ser Gln Gln Gln Thr Asp Arg Asn
    370                 375                 380

Ala Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly
385                 390                 395                 400

Asn Asn Phe Glu Ile Thr Tyr Ser Phe Glu Lys Val Pro Phe His Ser
                405                 410                 415

Met Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile
            420                 425                 430

Asp Gln Tyr Leu Trp Gly Leu Gln Ser Thr Thr Thr Gly Thr Thr Leu
        435                 440                 445

Asn Ala Gly Thr Ala Thr Thr Asn Phe Thr Lys Leu Arg Pro Thr Asn
    450                 455                 460

Phe Ser Asn Phe Lys Lys Asn Trp Leu Pro Gly Pro Ser Ile Lys Gln
465                 470                 475                 480

Gln Gly Phe Ser Lys Thr Ala Asn Gln Asn Tyr Lys Ile Pro Ala Thr
                485                 490                 495

Gly Ser Asp Ser Leu Ile Lys Tyr Glu Thr His Ser Thr Leu Asp Gly
            500                 505                 510

Arg Trp Ser Ala Leu Thr Pro Gly Pro Pro Met Ala Thr Ala Gly Pro
        515                 520                 525

Ala Asp Ser Lys Phe Ser Asn Ser Gln Leu Ile Phe Ala Gly Pro Lys
```

```
    530                 535                 540

Gln Asn Gly Asn Thr Ala Thr Val Pro Gly Thr Leu Ile Phe Thr Ser
545                 550                 555                 560

Glu Glu Glu Leu Ala Ala Thr Asn Ala Thr Asp Thr Asp Met Trp Gly
                565                 570                 575

Asn Leu Pro Gly Gly Asp Gln Ser Asn Ser Asn Leu Pro Thr Val Asp
            580                 585                 590

Arg Leu Thr Ala Leu Gly Ala Val Pro Gly Met Val Trp Gln Asn Arg
        595                 600                 605

Asp Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr Asp
    610                 615                 620

Gly His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His
625                 630                 635                 640

Pro Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Asn Pro
                645                 650                 655

Ala Thr Thr Phe Ser Ser Thr Pro Val Asn Ser Phe Ile Thr Gln Tyr
            660                 665                 670

Ser Thr Gly Gln Val Ser Val Gln Ile Asp Trp Glu Ile Gln Lys Glu
        675                 680                 685

Arg Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Tyr Gly
    690                 695                 700

Gln Gln Asn Ser Leu Leu Trp Ala Pro Asp Ala Ala Gly Lys Tyr Thr
705                 710                 715                 720

Glu Pro Arg Ala Ile Gly Thr Arg Tyr Leu Thr His His Leu
                725                 730
```

<210> 80
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 80

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1   5   10   15

Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20   25   30

Lys Ala Asn Gln Gln Lys Gln Asp Asn Gly Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Gln Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Ser Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130   135   140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145   150   155   160

```
Gly Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
```

```
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Glu Phe Ser Tyr
                405                 410                 415

Asn Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Asn Asn Met Ser Ala Gln Ala Lys Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

His Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Ser Val
545                 550                 555                 560
```

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
565 570 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Ala Ala
580 585 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
595 600 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
610 615 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625 630 635 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
645 650 655

Pro Ala Asp Pro Pro Thr Thr Phe Asn Gln Ala Lys Leu Ala Ser Phe
660 665 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
675 680 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
690 695 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705 710 715 720

Gly Thr Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
725 730 735

Asn Leu

<210> 81

```
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  81

His Ala Ile Tyr Pro Arg
1               5


<210>  82
<211>  733
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  82

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Glu Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Leu Glu Ser Pro Gln Glu Pro Asp Ser Ser Ser Gly Ile Gly Lys
145                 150                 155                 160

Lys Gly Lys Gln Pro Ala Lys Lys Arg Leu Asn Phe Glu Glu Asp Thr
                165                 170                 175

Gly Ala Gly Asp Gly Pro Pro Glu Gly Ser Asp Thr Ser Ala Met Ser
            180                 185                 190

Ser Asp Ile Glu Met Arg Ala Ala Pro Gly Gly Asn Ala Val Asp Ala
        195                 200                 205

Gly Gln Gly Ser Asp Gly Val Gly Asn Ala Ser Gly Asp Trp His Cys
    210                 215                 220

Asp Ser Thr Trp Ser Glu Gly Lys Val Thr Thr Thr Ser Thr Arg Thr
225                 230                 235                 240

Trp Val Leu Pro Thr Tyr Asn Asn His Leu Tyr Leu Arg Leu Gly Thr
                245                 250                 255

Thr Ser Asn Ser Asn Thr Tyr Asn Gly Phe Ser Thr Pro Trp Gly Tyr
            260                 265                 270

Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln
        275                 280                 285

Arg Leu Ile Asn Asn Asn Trp Gly Leu Arg Pro Lys Ala Met Arg Val
    290                 295                 300

Lys Ile Phe Asn Ile Gln Val Lys Glu Val Thr Thr Ser Asn Gly Glu
```

```
305                 310                 315                 320

Thr Thr Val Ala Asn Asn Leu Thr Ser Thr Val Gln Ile Phe Ala Asp
                325                 330                 335

Ser Ser Tyr Glu Leu Pro Tyr Val Met Asp Ala Gly Gln Glu Gly Ser
            340                 345                 350

Leu Pro Pro Phe Pro Asn Asp Val Phe Met Val Pro Gln Tyr Gly Tyr
        355                 360                 365

Cys Gly Ile Val Thr Gly Glu Asn Gln Asn Gln Thr Asp Arg Asn Ala
    370                 375                 380

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
385                 390                 395                 400

Asn Phe Glu Thr Ala Tyr Asn Phe Glu Lys Val Pro Phe His Ser Met
                405                 410                 415

Tyr Ala His Ser Gln Ser Leu Asp Gly Leu Met Asn Pro Leu Leu Asp
            420                 425                 430

Gln Tyr Leu Trp His Leu Gln Ser Thr Thr Ser Gly Glu Thr Leu Asn
        435                 440                 445

Gln Gly Asn Ala Ala Thr Thr Phe Gly Lys Ile Arg Ser Gly Asp Phe
    450                 455                 460

Ala Phe Tyr Arg Lys Asn Trp Leu Pro Gly Pro Cys Val Lys Gln Gln
465                 470                 475                 480

Arg Phe Ser Lys Thr Ala Ser Gln Asn Tyr Lys Ile Pro Ala Ser Gly
                485                 490                 495

Gly Asn Ala Leu Leu Lys Tyr Asp Thr His Tyr Thr Leu Asn Asn Arg
            500                 505                 510
```

```
Trp Ser Asn Ile Ala Pro Gly Pro Pro Met Ala Thr Ala Gly Pro Ser
        515                 520                 525

Asp Gly Asp Phe Ser Asn Ala Gln Leu Ile Phe Pro Gly Pro Ser Val
    530                 535                 540

Thr Gly Asn Thr Thr Thr Ser Ala Asn Asn Leu Leu Phe Thr Ser Glu
545                 550                 555                 560

Glu Glu Ile Ala Ala Thr Asn Pro Arg Asp Thr Asp Met Phe Gly Gln
                565                 570                 575

Ile Ala Asp Asn Asn Gln Asn Ala Thr Thr Ala Pro Ile Thr Gly Asn
            580                 585                 590

Val Thr Ala Met Gly Val Leu Pro Gly Met Val Trp Gln Asn Arg Asp
        595                 600                 605

Ile Tyr Tyr Gln Gly Pro Ile Trp Ala Lys Ile Pro His Ala Asp Gly
    610                 615                 620

His Phe His Pro Ser Pro Leu Ile Gly Gly Phe Gly Leu Lys His Pro
625                 630                 635                 640

Pro Pro Gln Ile Phe Ile Lys Asn Thr Pro Val Pro Ala Tyr Pro Ala
                645                 650                 655

Thr Thr Phe Thr Ala Ala Arg Val Asp Ser Phe Ile Thr Gln Tyr Ser
            660                 665                 670

Thr Gly Gln Val Ala Val Gln Ile Glu Trp Glu Ile Glu Lys Glu Arg
        675                 680                 685

Ser Lys Arg Trp Asn Pro Glu Val Gln Phe Thr Ser Asn Cys Gly Asn
    690                 695                 700

Gln Ser Ser Met Leu Trp Ala Pro Asp Thr Thr Gly Lys Tyr Thr Glu
```

705   710   715   720

Pro Arg Val Ile Gly Ser Arg Tyr Leu Thr Asn His Leu
                725   730

<210> 83
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 83

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1   5   10   15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20   25   30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35   40   45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50   55   60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65   70   75   80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85   90   95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100   105   110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115   120   125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg

```
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ser Gln Pro Ala Lys Lys Lys Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335
```

```
Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Gly Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
```

```
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Ser Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

```
<210>  84
<211>  644
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence


<220>
<221>  misc_feature
<222>  (434)..(434)
<223>  Xaa can be any naturally occurring amino acid

<400>  84

Lys Ala Tyr Asp Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg
1               5                   10                  15


Tyr Asn His Ala Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr
            20                  25                  30


Ser Phe Gly Gly Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg
        35                  40                  45


Val Leu Glu Pro Leu Gly Leu Val Glu Thr Pro Ala Lys Thr Ala Pro
    50                  55                  60


Gly Lys Lys Arg Pro Val Asp Ser Pro Asp Ser Thr Ser Gly Ile Gly
65                  70                  75                  80


Lys Lys Gly Gln Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                85                  90                  95


Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            100                 105                 110


Ala Gly Pro Ser Gly Leu Gly Ser Gly Thr Met Ala Ala Gly Gly Gly
        115                 120                 125


Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ala
```

```
    130                 135                 140

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val Ile
145                 150                 155                 160

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                165                 170                 175

Tyr Lys Gln Ile Ser Ser Gln Ser Ala Gly Ser Thr Asn Asp Asn Val
            180                 185                 190

Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe
        195                 200                 205

His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn
    210                 215                 220

Trp Gly Phe Arg Pro Lys Lys Leu Asn Phe Lys Leu Phe Asn Ile Gln
225                 230                 235                 240

Val Lys Glu Val Thr Thr Asn Asp Gly Val Thr Thr Ile Ala Asn Asn
                245                 250                 255

Leu Thr Ser Thr Val Gln Val Phe Ser Asp Ser Glu Tyr Gln Leu Pro
            260                 265                 270

Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala
        275                 280                 285

Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly
    290                 295                 300

Ser Gln Ser Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro
305                 310                 315                 320

Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe
                325                 330                 335
```

```
Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp
            340                 345                 350

Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ala Arg
        355                 360                 365

Thr Gln Ser Asn Ala Gly Gly Thr Ala Gly Asn Arg Glu Leu Gln Phe
    370                 375                 380

Tyr Gln Gly Gly Pro Thr Thr Met Ala Glu Gln Ala Lys Asn Trp Leu
385                 390                 395                 400

Pro Gly Pro Cys Phe Arg Gln Gln Arg Val Ser Lys Thr Leu Asp Gln
                405                 410                 415

Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His Leu
            420                 425                 430

Asn Xaa Arg Asn Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr His
        435                 440                 445

Lys Asp Asp Glu Glu Arg Phe Phe Pro Ser Ser Gly Val Leu Ile Phe
    450                 455                 460

Gly Lys Thr Gly Ala Ala Asn Lys Thr Thr Leu Glu Asn Val Leu Met
465                 470                 475                 480

Thr Asn Glu Glu Glu Ile Arg Pro Thr Asn Pro Val Ala Thr Glu Glu
                485                 490                 495

Tyr Gly Ile Val Ser Ser Asn Leu Gln Ala Ala Ser Thr Ala Ala Gln
            500                 505                 510

Thr Gln Val Val Asn Asn Gln Gly Ala Leu Pro Gly Met Val Trp Gln
        515                 520                 525

Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
```

530 535 540

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu
545 550 555 560

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
565 570 575

Asn Pro Pro Glu Val Phe Thr Pro Ala Lys Phe Ala Ser Phe Ile Thr
580 585 590

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
595 600 605

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
610 615 620

Phe Asp Lys Gln Thr Gly Val Asp Phe Ala Val Asp Ser Gln Gly Val
625 630 635 640

Tyr Ser Glu Pro

<210> 85
<211> 735
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 85

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1 5 10 15

Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
20 25 30

Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro

```
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Ala Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Ser Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Ile
225                 230                 235                 240
```

```
Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Ser Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
```

```
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460

Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ser Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Gly Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ala Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640
```

```
His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655


Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
            660                 665                 670


Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
        675                 680                 685


Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
    690                 695                 700


Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705                 710                 715                 720


Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  86
<211>  735
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  86

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Thr Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Gln Trp Trp Lys Leu Lys Pro Gly Pro Pro Pro Pro
            20                  25                  30


Lys Pro Ala Glu Arg His Lys Asp Asp Ser Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60
```

```
Val Asn Glu Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Arg Gln Leu Asp Ser Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Pro Val Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu His Ser Pro Val Glu Pro Asp Ser Ser Ser Gly Thr Gly
145                 150                 155                 160

Lys Ala Gly Asn Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Ala Asp Ser Val Pro Asp Pro Gln Pro Leu Gly Gln Pro Pro
            180                 185                 190

Ala Ser Pro Ser Gly Leu Gly Thr Asn Thr Met Ala Thr Gly Ser Gly
        195                 200                 205

Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Asn Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Thr Trp Met Gly Asp Arg Val Val
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Ser Gln Ser Gly Ala Ser Asn Asp Asn His Tyr
```

```
            260                 265                 270

Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg Phe His
        275                 280                 285

Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn Asn Trp
    290                 295                 300

Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile Gln Val
305                 310                 315                 320

Lys Glu Val Thr Gln Asn Asp Gly Thr Thr Thr Ile Ala Asn Asn Leu
                325                 330                 335

Thr Ser Thr Val Gln Val Phe Thr Asp Leu Glu Tyr Gln Leu Pro Tyr
            340                 345                 350

Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe Pro Ala Asp
        355                 360                 365

Val Phe Met Val Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asn Gly Ser
    370                 375                 380

Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe Pro Ser
385                 390                 395                 400

Gln Met Leu Arg Thr Gly Asn Asn Phe Thr Phe Ser Tyr Thr Phe Glu
                405                 410                 415

Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu Asp Arg
            420                 425                 430

Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser Arg Thr
        435                 440                 445

Asn Thr Pro Ser Gly Thr Thr Thr Gln Ser Arg Leu Gln Phe Ser Gln
    450                 455                 460
```

```
Ala Gly Ala Ser Asp Ile Arg Asp Gln Ser Arg Asn Trp Leu Pro Gly
465                 470                 475                 480

Pro Cys Tyr Arg Gln Gln Arg Val Ser Lys Thr Ala Ala Asp Asn Asn
                485                 490                 495

Asn Ser Glu Tyr Ser Trp Thr Gly Ala Thr Lys Tyr His Leu Asn Gly
            500                 505                 510

Arg Asp Ser Leu Val Asn Pro Gly Pro Ala Met Ala Ser His Lys Asp
        515                 520                 525

Asp Glu Glu Lys Phe Phe Pro Gln Ser Gly Val Leu Ile Phe Gly Lys
    530                 535                 540

Gln Gly Ser Glu Lys Thr Asn Val Asp Ile Glu Lys Val Met Ile Thr
545                 550                 555                 560

Asp Glu Glu Glu Ile Arg Thr Thr Asn Pro Val Ala Thr Glu Gln Tyr
                565                 570                 575

Gly Ser Val Ser Thr Asn Leu Gln Ser Gly Asn Thr Gln Ala Ala Thr
            580                 585                 590

Ser Asp Val Asn Thr Gln Gly Val Leu Pro Gly Met Val Trp Gln Asp
        595                 600                 605

Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His Thr
    610                 615                 620

Asp Gly His Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Leu Lys
625                 630                 635                 640

His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala Asn
                645                 650                 655

Pro Ser Thr Thr Phe Ser Ala Ala Lys Phe Ala Ser Phe Ile Thr Gln
```

660 665 670

Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln Lys
675 680 685

Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn Tyr
690 695 700

Asn Lys Ser Val Asn Val Asp Phe Thr Val Asp Thr Asn Gly Val Tyr
705 710 715 720

Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
725 730 735

<210> 87
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 87

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala

```
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285
```

```
Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300


Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320


Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335


Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350


Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365


Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380


Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400


Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415


Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430


Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445


Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460


Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480


Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Asn
```

```
                485                 490                 495

Asn Asn Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Thr Leu Ala Ala
            580                 585                 590

Pro Phe Lys Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685
```

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
690 695 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705 710 715 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
725 730 735

Arg Tyr Leu Thr Arg Asn Leu
740

<210> 88
<211> 743
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

<400> 88

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1 5 10 15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
20 25 30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
35 40 45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
50 55 60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65 70 75 80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
85 90 95

```
Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Thr Leu Ala Ala
            260                 265                 270

Pro Phe Lys Ser Asn Asp Asn Ala Tyr Phe Gly Tyr Ser Thr Pro Trp
        275                 280                 285

Gly Tyr Phe Asp Phe Asn Arg Phe His Cys His Phe Ser Pro Arg Asp
```

```
    290                 295                 300

Trp Gln Arg Leu Ile Asn Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu
305                 310                 315                 320

Asn Phe Lys Leu Phe Asn Ile Gln Val Lys Glu Val Thr Asp Asn Asn
                325                 330                 335

Gly Val Lys Thr Ile Ala Asn Asn Leu Thr Ser Thr Val Gln Val Phe
            340                 345                 350

Thr Asp Ser Asp Tyr Gln Leu Pro Tyr Val Leu Gly Ser Ala His Glu
        355                 360                 365

Gly Cys Leu Pro Pro Phe Pro Ala Asp Val Phe Met Ile Pro Gln Tyr
    370                 375                 380

Gly Tyr Leu Thr Leu Asn Asp Gly Ser Gln Ala Val Gly Arg Ser Ser
385                 390                 395                 400

Phe Tyr Cys Leu Glu Tyr Phe Pro Ser Gln Met Leu Arg Thr Gly Asn
                405                 410                 415

Asn Phe Gln Phe Ser Tyr Glu Phe Glu Asn Val Pro Phe His Ser Ser
            420                 425                 430

Tyr Ala His Ser Gln Ser Leu Asp Arg Leu Met Asn Pro Leu Ile Asp
        435                 440                 445

Gln Tyr Leu Tyr Tyr Leu Ser Lys Thr Ile Asn Gly Ser Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495
```

```
Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
545                 550                 555                 560

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
                565                 570                 575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
            580                 585                 590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
```

```
    690                 695                 700

Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720

Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735

Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  89
<211>  743
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  89

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15

Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30

Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
```

```
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160

Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300
```

```
Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Thr Leu Ala Ala Pro Phe Lys Gly Gln Asn
    450                 455                 460

Gln Gln Thr Leu Lys Phe Ser Val Ala Gly Pro Ser Asn Met Ala Val
465                 470                 475                 480

Gln Gly Arg Asn Tyr Ile Pro Gly Pro Ser Tyr Arg Gln Gln Arg Val
                485                 490                 495

Ser Thr Thr Val Thr Gln Asn Asn Asn Ser Glu Phe Ala Trp Pro Gly
```

```
            500                 505                 510

Ala Ser Ser Trp Ala Leu Asn Gly Arg Asn Ser Leu Met Asn Pro Gly
        515                 520                 525

Pro Ala Met Ala Ser His Lys Glu Gly Glu Asp Arg Phe Phe Pro Leu
    530                 535                 540

Ser Gly Ser Leu Ile Phe Gly Lys Gln Gly Thr Gly Arg Asp Asn Val
545                 550                 555                 560

Asp Ala Asp Lys Val Met Ile Thr Asn Glu Glu Glu Ile Lys Thr Thr
                565                 570                 575

Asn Pro Val Ala Thr Glu Ser Tyr Gly Gln Val Ala Thr Asn His Gln
            580                 585                 590

Ser Ala Gln Ala Gln Ala Gln Thr Gly Trp Val Gln Asn Gln Gly Ile
        595                 600                 605

Leu Pro Gly Met Val Trp Gln Asp Arg Asp Val Tyr Leu Gln Gly Pro
    610                 615                 620

Ile Trp Ala Lys Ile Pro His Thr Asp Gly Asn Phe His Pro Ser Pro
625                 630                 635                 640

Leu Met Gly Gly Phe Gly Met Lys His Pro Pro Pro Gln Ile Leu Ile
                645                 650                 655

Lys Asn Thr Pro Val Pro Ala Asp Pro Pro Thr Ala Phe Asn Lys Asp
            660                 665                 670

Lys Leu Asn Ser Phe Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val
        675                 680                 685

Glu Ile Glu Trp Glu Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro
    690                 695                 700
```

```
Glu Ile Gln Tyr Thr Ser Asn Tyr Tyr Lys Ser Asn Asn Val Glu Phe
705                 710                 715                 720


Ala Val Asn Thr Glu Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr
                725                 730                 735


Arg Tyr Leu Thr Arg Asn Leu
            740


<210>  90
<211>  700
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  90

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30


Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110
```

```
Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
```

```
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415

Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510
```

```
Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Val Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu
    690                 695                 700

<210>  91
```

```
<211>  736
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  91

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
```

```
                165                 170                 175

Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190

Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Gly Gly Ser Ser Asn Asp Ala
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365
```

```
Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Ala
                485                 490                 495

Ala Ala Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
```

```
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590

Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735
```

<210> 92
<211> 736
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic construct; capsid sequence

```
<400>  92

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15


Glu Gly Ile Arg Glu Trp Trp Ala Leu Lys Pro Gly Ala Pro Gln Pro
            20                  25                  30


Lys Ala Asn Gln Gln His Gln Asp Asn Ala Arg Gly Leu Val Leu Pro
        35                  40                  45


Gly Tyr Lys Tyr Leu Gly Pro Gly Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60


Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80


Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Lys Tyr Asn His Ala
                85                  90                  95


Asp Ala Glu Phe Gln Glu Arg Leu Lys Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110


Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Leu Leu Glu Pro
        115                 120                 125


Leu Gly Leu Val Glu Glu Ala Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140


Pro Val Glu Gln Ser Pro Gln Glu Pro Asp Ser Ser Ala Gly Ile Gly
145                 150                 155                 160


Lys Ser Gly Ala Gln Pro Ala Lys Lys Arg Leu Asn Phe Gly Gln Thr
                165                 170                 175


Gly Asp Thr Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro Pro
            180                 185                 190
```

```
Ala Ala Pro Ser Gly Val Gly Ser Leu Thr Met Ala Ser Gly Gly Gly
        195                 200                 205

Ala Pro Val Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser Ser
    210                 215                 220

Ser Gly Asn Trp His Cys Asp Ser Gln Trp Leu Gly Asp Arg Val Ile
225                 230                 235                 240

Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His Leu
                245                 250                 255

Tyr Lys Gln Ile Ser Asn Ser Thr Ser Ala Gly Ser Ser Asn Asp Asn
            260                 265                 270

Ala Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn Arg
        275                 280                 285

Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn Asn
    290                 295                 300

Asn Trp Gly Phe Arg Pro Lys Arg Leu Asn Phe Lys Leu Phe Asn Ile
305                 310                 315                 320

Gln Val Lys Glu Val Thr Asp Asn Asn Gly Val Lys Thr Ile Ala Asn
                325                 330                 335

Asn Leu Thr Ser Thr Val Gln Val Phe Thr Asp Ser Asp Tyr Gln Leu
            340                 345                 350

Pro Tyr Val Leu Gly Ser Ala His Glu Gly Cys Leu Pro Pro Phe Pro
        355                 360                 365

Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn Asp
    370                 375                 380

Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr Phe
```

```
385                 390                 395                 400

Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Gln Phe Ser Tyr Glu
                405                 410                 415

Phe Glu Asn Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser Leu
            420                 425                 430

Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu Ser
        435                 440                 445

Lys Thr Ile Asn Gly Ser Gly Gln Asn Gln Gln Thr Leu Lys Phe Ser
    450                 455                 460

Val Ala Gly Pro Ser Asn Met Ala Val Gln Gly Arg Asn Tyr Ile Pro
465                 470                 475                 480

Gly Pro Ser Tyr Arg Gln Gln Arg Val Ser Thr Thr Val Thr Gln Ala
                485                 490                 495

Ala Ala Ser Glu Phe Ala Trp Pro Gly Ala Ser Ser Trp Ala Leu Asn
            500                 505                 510

Gly Arg Asn Ser Leu Met Asn Pro Gly Pro Ala Met Ala Ser His Lys
        515                 520                 525

Glu Gly Glu Asp Arg Phe Phe Pro Leu Ser Gly Ser Leu Ile Phe Gly
    530                 535                 540

Lys Gln Gly Thr Gly Arg Asp Asn Val Asp Ala Asp Lys Val Met Ile
545                 550                 555                 560

Thr Asn Glu Glu Glu Ile Lys Thr Thr Asn Pro Val Ala Thr Glu Ser
                565                 570                 575

Tyr Gly Gln Val Ala Thr Asn His Gln Ser Ala Gln Ala Gln Ala Gln
            580                 585                 590
```

```
Thr Gly Trp Val Gln Asn Gln Gly Ile Leu Pro Gly Met Val Trp Gln
        595                 600                 605

Asp Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile Pro His
    610                 615                 620

Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe Gly Met
625                 630                 635                 640

Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val Pro Ala
                645                 650                 655

Asp Pro Pro Thr Ala Phe Asn Lys Asp Lys Leu Asn Ser Phe Ile Thr
            660                 665                 670

Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu Leu Gln
        675                 680                 685

Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr Ser Asn
    690                 695                 700

Tyr Tyr Lys Ser Asn Asn Val Glu Phe Ala Val Asn Thr Glu Gly Val
705                 710                 715                 720

Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg Asn Leu
                725                 730                 735


<210>  93
<211>  738
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  synthetic construct; capsid sequence

<400>  93

Met Ala Ala Asp Gly Tyr Leu Pro Asp Trp Leu Glu Asp Asn Leu Ser
1               5                   10                  15
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Glu Gly Ile Arg Glu Trp Trp Asp Leu Lys Pro Gly Ala Pro Lys Pro
            20                  25                  30

Lys Ala Asn Gln Gln Lys Gln Asp Asp Gly Arg Gly Leu Val Leu Pro
        35                  40                  45

Gly Tyr Lys Tyr Leu Gly Pro Phe Asn Gly Leu Asp Lys Gly Glu Pro
    50                  55                  60

Val Asn Ala Ala Asp Ala Ala Ala Leu Glu His Asp Lys Ala Tyr Asp
65                  70                  75                  80

Gln Gln Leu Lys Ala Gly Asp Asn Pro Tyr Leu Arg Tyr Asn His Ala
                85                  90                  95

Asp Ala Glu Phe Gln Glu Arg Leu Gln Glu Asp Thr Ser Phe Gly Gly
            100                 105                 110

Asn Leu Gly Arg Ala Val Phe Gln Ala Lys Lys Arg Val Leu Glu Pro
        115                 120                 125

Leu Gly Leu Val Glu Glu Gly Ala Lys Thr Ala Pro Gly Lys Lys Arg
    130                 135                 140

Pro Val Glu Pro Ser Pro Gln Arg Ser Pro Asp Ser Ser Thr Gly Ile
145                 150                 155                 160

Gly Lys Lys Gly Gln Gln Pro Ala Arg Lys Arg Leu Asn Phe Gly Gln
                165                 170                 175

Thr Gly Asp Ser Glu Ser Val Pro Asp Pro Gln Pro Ile Gly Glu Pro
            180                 185                 190

Pro Ala Ala Pro Ser Ser Val Gly Ser Gly Thr Met Ala Ala Gly Gly
        195                 200                 205

Gly Ala Pro Met Ala Asp Asn Asn Glu Gly Ala Asp Gly Val Gly Ser
```

```
    210                 215                 220

Ser Ser Gly Asn Trp His Cys Asp Ser Thr Trp Leu Gly Asp Arg Val
225                 230                 235                 240

Ile Thr Thr Ser Thr Arg Thr Trp Ala Leu Pro Thr Tyr Asn Asn His
                245                 250                 255

Leu Tyr Lys Gln Ile Ser Asn Gly Thr Ser Gly Gly Ser Thr Asn Asp
            260                 265                 270

Asn Thr Tyr Phe Gly Tyr Ser Thr Pro Trp Gly Tyr Phe Asp Phe Asn
        275                 280                 285

Arg Phe His Cys His Phe Ser Pro Arg Asp Trp Gln Arg Leu Ile Asn
    290                 295                 300

Asn Asn Trp Gly Phe Arg Pro Lys Arg Leu Ser Phe Lys Leu Phe Asn
305                 310                 315                 320

Ile Gln Val Lys Glu Val Thr Gln Asn Glu Gly Thr Lys Thr Ile Ala
                325                 330                 335

Asn Asn Leu Thr Ser Thr Ile Gln Val Phe Thr Asp Ser Glu Tyr Gln
            340                 345                 350

Leu Pro Tyr Val Leu Gly Ser Ala His Gln Gly Cys Leu Pro Pro Phe
        355                 360                 365

Pro Ala Asp Val Phe Met Ile Pro Gln Tyr Gly Tyr Leu Thr Leu Asn
    370                 375                 380

Asn Gly Ser Gln Ala Val Gly Arg Ser Ser Phe Tyr Cys Leu Glu Tyr
385                 390                 395                 400

Phe Pro Ser Gln Met Leu Arg Thr Gly Asn Asn Phe Ser Phe Ser Tyr
                405                 410                 415
```

```
Thr Phe Glu Asp Val Pro Phe His Ser Ser Tyr Ala His Ser Gln Ser
            420                 425                 430

Leu Asp Arg Leu Met Asn Pro Leu Ile Asp Gln Tyr Leu Tyr Tyr Leu
        435                 440                 445

Ser Arg Thr Gln Ser Thr Gly Gly Thr Ala Gly Thr Gln Gln Leu Leu
    450                 455                 460

Phe Ser Gln Ala Gly Pro Ser Asn Met Ser Ala Gln Ala Arg Asn Trp
465                 470                 475                 480

Leu Pro Gly Pro Cys Tyr Arg Gln Gln Arg Val Ser Thr Thr Leu Ser
                485                 490                 495

Gln Asn Asn Asn Ser Asn Phe Ala Trp Thr Gly Ala Thr Lys Tyr His
            500                 505                 510

Leu Asn Gly Arg Asp Ser Leu Val Asn Pro Gly Val Ala Met Ala Thr
        515                 520                 525

Asn Lys Asp Asp Glu Asp Arg Phe Phe Pro Ser Ser Gly Ile Leu Met
    530                 535                 540

Phe Gly Lys Gln Gly Ala Gly Lys Asp Asn Val Asp Tyr Ser Asn Val
545                 550                 555                 560

Met Leu Thr Ser Glu Glu Glu Ile Lys Ala Thr Asn Pro Val Ala Thr
                565                 570                 575

Glu Gln Tyr Gly Val Val Ala Asp Asn Leu Gln Gln Gln Asn Thr Ala
            580                 585                 590

Pro Ile Val Gly Ala Val Asn Ser Gln Gly Ala Leu Pro Gly Met Val
        595                 600                 605

Trp Gln Asn Arg Asp Val Tyr Leu Gln Gly Pro Ile Trp Ala Lys Ile
```

```
    610                 615                 620

Pro His Thr Asp Gly Asn Phe His Pro Ser Pro Leu Met Gly Gly Phe
625                 630                 635                 640

Gly Leu Lys His Pro Pro Pro Gln Ile Leu Ile Lys Asn Thr Pro Val
                645                 650                 655

Pro Ala Asp Pro Pro Thr Ala Phe Asn Gln Ala Lys Leu Asn Ser Phe
            660                 665                 670

Ile Thr Gln Tyr Ser Thr Gly Gln Val Ser Val Glu Ile Glu Trp Glu
        675                 680                 685

Leu Gln Lys Glu Asn Ser Lys Arg Trp Asn Pro Glu Ile Gln Tyr Thr
    690                 695                 700

Ser Asn Tyr Tyr Lys Ser Thr Asn Val Asp Phe Ala Val Asn Thr Glu
705                 710                 715                 720

Gly Val Tyr Ser Glu Pro Arg Pro Ile Gly Thr Arg Tyr Leu Thr Arg
                725                 730                 735

Asn Leu
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