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- (73) Patenthaver: **The Trustees of the University of Pennsylvania, 3160 Chestnut Street, Suite 200, Philadelphia, PA 19104, USA**
- (72) Opfinder: **Gao, Guangping, 4 Edward Dunn Way, Westborough, Massachusetts 01581, USA**
Vandenbergh, Luk, 2131 St Albans Street, Philadelphia, PA 19146, USA
Alvira, Mauricio R., 3937 Pine Street, Apt 3-F, Philadelphia, PA 19105, USA
Wilson, James M., 7 Fallbrook Lane, Glenn Mills, PA 19342, USA
- (74) Fuldmægtig i Danmark: **Patentgruppen A/S, Arosgården, Åboulevarden 31, 8000 Århus C, Danmark**
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Fortsættes ...

DESCRIPTION

BACKGROUND OF THE INVENTION

[0001] Adeno-associated virus (AAV), a member of the Parvovirus family, is a small nonenveloped, icosahedral virus with single-stranded linear DNA genomes of 4.7 kilobases (kb) to 6 kb. AAV is assigned to the genus, *Dependovirus*, because the virus was discovered as a contaminant in purified adenovirus stocks. AAV's life cycle includes a latent phase at which AAV genomes, after infection, are site specifically integrated into host chromosomes and an infectious phase in which, following either adenovirus or herpes simplex virus infection, the integrated genomes are subsequently rescued, replicated, and packaged into infectious viruses. The properties of non-pathogenicity, broad host range of infectivity, including non-dividing cells, and potential site-specific chromosomal integration make AAV an attractive tool for gene transfer.

[0002] Recent studies suggest that AAV vectors may be the preferred vehicle for gene delivery. To date, there have been several different well-characterized AAVs isolated from human or non-human primates (NHP).

[0003] It has been found that AAVs of different serotypes exhibit different transfection efficiencies, and also exhibit tropism for different cells or tissues. However, the relationship between these different serotypes has not previously been explored.

[0004] The applicant's earlier application, published as EP 1,310,571, discloses methods of detecting AAVs in a sample and methods of identifying the serotype of AAV sequences in a sample. It also discloses a number of AAV sequences but not those of the present invention.

[0005] What is desirable are AAV-based constructs for delivery of heterologous molecules.

SUMMARY OF THE INVENTION

[0006] The present invention involves "superfamilies" or "clades" of AAV of phylogenetically related sequences. These AAV clades provide a source of AAV sequences useful for targeting and/or delivering molecules to desired target cells or tissues.

[0007] In one aspect, the invention provides a recombinant adeno-associated virus (AAV) comprising an AAV capsid of serotype hu.37 having the sequence of amino acids 138 to 738 of SEQ ID NO: 88 and wherein the AAV further comprises a minigene having AAV inverted terminal repeats and a heterologous gene operably linked to regulatory sequences which direct its expression in a host cell.

[0008] The invention also provides an isolated capsid protein comprising a hu.37 adeno-associated (AAVhu.37) capsid protein selected from the group consisting of: vp1 capsid protein, amino acids (aa) 1 to 738, SEQ ID NO: 88; and vp2 capsid protein, amino acids (aa) 138 to 738, SEQ ID NO: 88.

[0009] In another aspect, the invention provides a method of generating a recombinant adeno-associated virus (AAV) comprising an AAV capsid comprising the steps of culturing a host cell containing: (a) a molecule encoding an AAV capsid protein; (b) a functional rep gene; (c) a minigene comprising AAV inverted terminal repeats (ITRs) and a transgene; and (d) sufficient helper functions to permit packaging of the minigene into the AAV capsid protein, wherein said host cell comprises a nucleic acid molecule selected from the group consisting of: vp1, nt 1 to 2217 of SEQ ID NO: 10; and vp2, nt 411 to 2217 of SEQ ID NO: 10.

[0010] The present invention also provides compositions containing these sequences, and uses therefor. Advantageously, these compositions are particularly well suited for use in compositions requiring re-administration of AAV vectors for therapeutic or prophylactic purposes.

[0011] These and other aspects of the invention will be readily apparent from the following detailed description of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0012]

Fig. 1 is a tree showing the phylogenetic relationship constructed using the Neighbor-Joining heuristic with Poisson correction distance measurement. The relationship was determined based on the isolated AAV vp1 capsid protein, with the isolated AAV grouped in clades. Groups of individual capsid clones are classified in clades based on their common ancestry. Clade nomenclature goes from A through F; subtypes are represented by the clade letter followed by a number.

Figs. 2A-2AE are an alignment of the amino acid sequences of AAV vp1 capsid proteins, with the numbering of the individual sequences reported, and previously published AAV1 [SEQ ID NO: 219]; AAV2 [SEQ ID NO: 221]; AAV3-3 [SEQ ID NO: 217]; AAV4-4 [SEQ ID NO: 218]; AAV5 [SEQ ID NO: 216]; AAV6 [SEQ ID NO: 220]; AAV7 [SEQ ID NO: 222]; AAV8 [SEQ ID NO: 223], and; rh. 25/42-15; 29.3/bb.1; cy.2; 29.5/bb.2; rh.32, rh.33, rh.34, rh.10; rh.24; rh.14, rh.16, rh.17, rh.12, rh.18, rh.21 (formerly termed 41.10); rh.25 (formerly termed 41.15); rh.2; rh.31; cy.3; cy.5; rh.13; cy.4; cy.6; rh.22; rh.19; rh.35; rh.37; rh.36; rh.23; rh.8; and ch.5 [US Published Patent Application No. 2003/0138772 A1 (Jul 24, 2003)]. The sequences include hu.14/AAV9 [SEQ ID NO: 123]; hu.17 [SEQ ID NO: 83], hu. 6 [SEQ ID NO: 84], hu.42 [SEQ ID NO: 85], rh.38 [SEQ ID NO: 86], hu.40 [SEQ ID NO: 87], hu.37 [SEQ ID NO: 88], rh.40 [SEQ ID NO: 92], rh.52 [SEQ ID NO: 96]; rh.53 [SEQ ID NO: 97]; rh.49 [SEQ ID NO: 103]; rh.51 [SEQ ID NO: 104]; rh.57 [SEQ ID NO: 105]; rh.58 [SEQ ID NO: 106], rh.61 [SEQ ID NO: 107]; rh.50 [SEQ ID NO: 108]; rh.43 [SEQ ID NO: 163]; rh.62 [SEQ ID NO: 114]; rh.48 [SEQ ID NO: 115]; 4-9/rh.54 (SEQ ID No: 116); and 4-19/rh.55 (SEQ ID Nos: 117); hu.31 [SEQ ID NO:121]; hu.32 [SEQ ID NO:122]; hu.34 [SEQ ID NO: 125]; hu.45 [SEQ ID NO: 127]; hu.47 [SEQ ID NO: 128]; hu.13 [SEQ ID NO:129]; hu.28 [SEQ ID NO: 130]; hu.29 [SEQ ID NO:132]; hu.19 [SEQ ID NO: 133]; hu.20 [SEQ ID NO: 134]; hu.21 [SEQ ID NO:135]; hu.23.2 [SEQ ID NO:137]; hu.22 [SEQ ID NO: 138]; hu.27 [SEQ ID NO: 140]; hu.4 [SEQ ID NO: 141]; hu.2 [SEQ ID NO: 143]; hu.1 [SEQ ID NO: 144]; hu.3 [SEQ ID NO: 145]; hu.25 [SEQ ID NO: 146]; hu.15 [SEQ ID NO: 147]; hu.16 [SEQ ID NO: 148]; hu.18 [SEQ ID NO: 149]; hu.7 [SEQ ID NO: 150]; hu.11 [SEQ ID NO: 153]; hu.9 [SEQ ID NO: 155]; hu.10 [SEQ ID NO: 156]; hu.48 [SEQ ID NO: 157]; hu.44 [SEQ ID NO: 158]; hu.46 [SEQ ID NO: 159]; hu.43 [SEQ ID NO: 160]; hu.35 [SEQ ID NO: 164]; hu.24 [SEQ ID NO: 136]; rh.64 [SEQ ID NO: 99]; hu.41 [SEQ ID NO: 91]; hu.39 [SEQ ID NO: 102]; hu.67 [SEQ ID NO: 198]; hu.66 [SEQ ID NO: 197]; hu.51 [SEQ ID NO: 190]; hu.52 [SEQ ID NO: 191]; hu.49 [SEQ ID NO: 189]; hu.56 [SEQ ID NO: 192]; hu.57 [SEQ ID NO: 193]; hu.58 [SEQ ID NO: 194]; hu.63 [SEQ ID NO: 195]; hu.64 [SEQ ID NO: 196]; hu.60 [SEQ ID NO: 184]; hu.61 [SEQ ID NO: 185]; hu.53 [SEQ ID NO: 186]; hu.55 [SEQ ID NO: 187]; hu.54 [SEQ ID NO: 188]; hu.6 [SEQ ID NO: 84]; and rh.56 [SEQ ID NO: 152]. These capsid sequences are also reproduced in the accompanying Sequence Listing.

Figs. 3A- 3CN are an alignment of the nucleic acid sequences of AAV vp1 capsid proteins, with the numbering of the individual sequences reported, and previously published AAV5 (SEQ ID NO: 199); AAV3-3 (SEQ ID NO: 200); AAV4-4 (SEQ ID NO: 201); AAV1 (SEQ ID NO: 202); AAV6 (SEQ ID NO: 203); AAV2(SEQ ID NO: 211); AAV7 (SEQ ID NO: 213) and AAV8 (SEQ ID NO: 214); rh. 25/42-15; 29.3/bb.1; cy.2; 29.5/bb.2; rh.32, rh.33, rh.34, rh.10; rh.24; rh.14, rh.16, rh.17, rh.12, rh.18, rh.21 (formerly termed 41.10); rh.25 (formerly termed 41.15; GenBank accession AY530557); rh.2; rh.31; cy.3; cy.5; rh.13; cy.4; cy.6; rh.22; rh.19; rh.35; rh.37; rh.36; rh.23; rh.8; and ch.5 [US Published Patent Application No. 2003/0138772 A1 (Jul 24, 2003)]. The nucleic acid sequences include, hu.14/AAV9 (SEQ ID No: 3); LG-4/rh.38 (SEQ ID No: 7); LG-10/rh.40 (SEQ ID No: 14); N721-8/rh.43 (SEQ ID No: 43); 1-8/rh.49 (SEQ ID NO: 25); 2-4/rh.50 (SEQ ID No: 23); 2-5/rh.51 (SEQ ID No: 22); 3-9/rh.52 (SEQ ID No: 18); 3-11/rh.53 (SEQ ID NO: 17); 5-3/rh.57 (SEQ ID No: 26); 5-22/rh.58 (SEQ ID No: 27); 2-3/rh.61 (SEQ ID NO: 21); 4-8/rh.64 (SEQ ID No: 15); 3.1/hu.6 (SEQ ID NO: 5); 33.12/hu.17 (SEQ ID NO:4); 106.1/hu.37 (SEQ ID No: 10); LG-9/hu.39 (SEQ ID No: 24); 114.3/hu.40 (SEQ ID No: 11); 127.2/hu.41 (SEQ ID NO:6); 127.5/hu.42 (SEQ ID No: 8); and hu.66 (SEQ ID NO: 173); 2-15/ rh.62 (SEQ ID NO: 33); 1-7/rh.48 (SEQ ID NO: 32); 4-9/rh.54 (SEQ ID No: 40); 4-19/rh.55 (SEQ ID NO: 37); 52/hu.19 (SEQ ID NO: 62), 52.1/hu.20 (SEQ ID NO: 63), 54.5/hu.23 (SEQ ID No: 60), 54.2/hu.22 (SEQ ID No: 67), 54.7/hu.24 (SEQ ID No: 66), 54.1/hu.21 (SEQ ID No: 65), 54.4R/hu.27 (SEQ ID No: 64); 46.2/hu.28 (SEQ ID No: 68); 46.6/hu.29 (SEQ ID No: 69); 128.1/hu.43 (SEQ ID No: 80); 128.3/hu.44 (SEQ ID No: 81) and 130.4/hu.48 (SEQ ID NO: 78); 3.1/hu.9 (SEQ ID No: 58); 16.8/hu.10 (SEQ ID No: 56); 16.12/hu.11 (SEQ ID No: 57); 145.1/hu.53 (SEQ ID No: 176); 145.6/hu.55 (SEQ ID No: 178); 145.5/hu.54 (SEQ ID No: 177); 7.3/hu.7 (SEQ ID No: 55); 52/hu.19 (SEQ ID No: 62); 33.4/hu.15 (SEQ ID No: 50); 33.8/hu.16 (SEQ ID No: 51); 58.2/hu.25 (SEQ ID No: 49); 161.10/hu.60 (SEQ ID No: 170); H-5/hu.3 (SEQ ID No: 44); H-1/hu.1 (SEQ ID No: 46); 161.6/hu.61 (SEQ ID No: 174); hu.31 (SEQ ID No: 1); hu.32 (SEQ ID No: 2); hu.46 (SEQ ID NO: 82); hu.34 (SEQ ID NO: 72); hu.47 (SEQ ID NO: 77); hu.63 (SEQ ID NO: 204); hu.56 (SEQ ID NO: 205); hu.45 (SEQ ID NO: 76); hu.57 (SEQ ID NO: 206); hu.35 (SEQ ID NO: 73); hu.58 (SEQ ID NO: 207); hu.51 (SEQ ID NO: 208); hu.49 (SEQ ID NO: 209); hu.52 (SEQ ID NO: 210); hu.13 (SEQ ID NO: 71); hu.64 (SEQ ID NO: 212); rh.56 (SEQ ID NO: 54); hu.2 (SEQ ID NO: 48); hu.18 (SEQ ID NO: 52); hu.4 (SEQ ID NO: 47); and hu.67 (SEQ ID NO: 215). These sequences are also reproduced in the accompanying Sequence Listing.

Figs. 4A - 4D provide an evaluation of gene transfer efficiency of primate AAV-based vectors *in vitro* and *in vivo*. AAV vectors were pseudotyped as described [Gao et al, Proc Natl Acad Sci USA, 99:11854-11859 (Sept. 3, 2002)] with capsids of AAVs 1, 2, 5, 7, 8 and 6 and ch.5, rh.34, cy.5, rh.20, rh.8 and AAV9. For *in vitro* study, Fig. 4A, 84-32 cells (293 cells expressing E4 of adenovirus serotypes) seeded in a 96 well plate were infected with pseudotyped AAVCMVEGFP vectors at an MOI of 1×10^4 GC per cell. Relative EGFP transduction efficiency was estimated as percentage of green cells using a UV microscope at 48 hours post-infection and shown on the Y axis. For *in vivo* study, the vectors expressing the secreted reporter gene A1AT were administered to the liver (Fig. 4B), lung (Fig. 4C) and muscle (Fig. 4D) of NCR nude mice (4-6 weeks old) at a dose of 1×10^{11}

GC per animal by intraportal (Fig. 4B), intratracheal (Fig. 4C) and intramuscular injections (Fig. 4D), respectively. Serum A1AT levels (ng/mL) were compared at day 28 post gene transfer and presented on the Y axis. The X axis indicates the AAVs analyzed and the clades to which they belong.

DETAILED DESCRIPTION OF THE INVENTION

[0013] In any arsenal of vectors useful in therapy or prophylaxis, a variety of distinct vectors capable of carrying a macromolecule to a target cell is desirable, in order to permit selection of a vector source for a desired application. To date, one of the concerns regarding the use of AAV as vectors was the lack of a variety of different virus sources. The clades of AAV discussed herein are useful for selecting phylogenetically related, or where desired for a selected regimen, phylogenetically distinct, AAV and for predicting function.

[0014] The term "substantial homology" or "substantial similarity," when referring to a nucleic acid, or fragment thereof, indicates that, when optimally aligned with appropriate nucleotide insertions or deletions with another nucleic acid (or its complementary strand), there is nucleotide sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or an open reading frame thereof, or another suitable fragment which is at least 15 nucleotides in length. Examples of suitable fragments are described herein.

[0015] The terms "sequence identity" "percent sequence identity" or "percent identical" in the context of nucleic acid sequences refers to the residues in the two sequences which are the same when aligned for maximum correspondence. The length of sequence identity comparison may be over the full-length of the genome, the full-length of a gene coding sequence, or a fragment of at least about 500 to 5000 nucleotides, is desired. However, identity among smaller fragments, *e.g.* of at least about nine nucleotides, usually at least about 20 to 24 nucleotides, at least about 28 to 32 nucleotides, at least about 36 or more nucleotides, may also be desired. Similarly, "percent sequence identity" may be readily determined for amino acid sequences, over the full-length of a protein, or a fragment thereof. Suitably, a fragment is at least about 8 amino acids in length, and may be up to about 700 amino acids. Examples of suitable fragments are described herein.

[0016] The term "substantial homology" or "substantial similarity," when referring to amino acids or fragments thereof, indicates that, when optimally aligned with appropriate amino acid insertions or deletions with another amino acid (or its complementary strand), there is amino acid sequence identity in at least about 95 to 99% of the aligned sequences. Preferably, the homology is over full-length sequence, or a protein thereof, *e.g.*, a cap protein, a rep protein, or a fragment thereof which is at least 8 amino acids, or more desirably, at least 15 amino acids in length. Examples of suitable fragments are described herein.

[0017] By the term "highly conserved" is meant at least 80% identity, preferably at least 90% identity, and more preferably, over 97% identity. Identity is readily determined by one of skill in the art by resort to algorithms and computer programs known by those of skill in the art.

[0018] Generally, when referring to "identity", "homology", or "similarity" between two different adeno-associated viruses, "identity", "homology" or "similarity" is determined in reference to "aligned" sequences. "Aligned" sequences or "alignments" refer to multiple nucleic acid sequences or protein (amino acids) sequences, often containing corrections for missing or additional bases or amino acids as compared to a reference sequence. In the examples, AAV alignments are performed using the published AAV2 or AAV1 sequences as a reference point. However, one of skill in the art can readily select another AAV sequence as a reference.

[0019] Alignments are performed using any of a variety of publicly or commercially available Multiple Sequence Alignment Programs. Examples of such programs include, "Clustal W", "CAP Sequence Assembly", "MAP", and "MEME", which are accessible through Web Servers on the internet. Other sources for such programs are known to those of skill in the art. Alternatively, Vector NTI utilities are also used. There are also a number of algorithms known in the art that can be used to measure nucleotide sequence identity, including those contained in the programs described above. As another example, polynucleotide sequences can be compared using Fasta™, a program in GCG Version 6.1. Fasta™ provides alignments and percent sequence identity of the regions of the best overlap between the query and search sequences. For instance, percent sequence identity between nucleic acid sequences can be determined using Fasta™ with its default parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1. Multiple sequence alignment programs are also available for amino acid sequences, *e.g.*, the "Clustal X", "MAP", "PIMA", "MSA", "BLOCKMAKER", "MEME", and "Match-Box" programs. Generally, any of these programs are used at default settings, although one of skill in the art can alter these settings

as needed. Alternatively, one of skill in the art can utilize another algorithm or computer program which provides at least the level of identity or alignment as that provided by the referenced algorithms and programs. See, e.g., J. D. Thomson et al, Nucl. Acids. Res., "A comprehensive comparison of multiple sequence alignments", 27(13):2682-2690 (1999).

[0020] The term "serotype" is a distinction with respect to an AAV having a capsid which is serologically distinct from other AAV serotypes. Serologic distinctiveness is determined on the basis of the lack of cross-reactivity between antibodies to the AAV as compared to other AAV.

[0021] Cross-reactivity is typically measured in a neutralizing antibody assay. For this assay polyclonal serum is generated against a specific AAV in a rabbit or other suitable animal model using the adeno-associated viruses. In this assay, the serum generated against a specific AAV is then tested in its ability to neutralize either the same (homologous) or a heterologous AAV. The dilution that achieves 50% neutralization is considered the neutralizing antibody titer. If for two AAVs the quotient of the heterologous titer divided by the homologous titer is lower than 16 in a reciprocal manner, those two vectors are considered as the same serotype. Conversely, if the ratio of the heterologous titer over the homologous titer is 16 or more in a reciprocal manner the two AAVs are considered distinct serotypes.

[0022] As used throughout this specification and the claims, the terms "comprising" and "including" are inclusive of other components, elements, integers, steps and the like. Conversely, the term "consisting" and its variants are exclusive of other components, elements, integers, steps and the like.

I. Clades

[0023] A clade is a group of AAV which are phylogenetically related to one another as determined using a Neighbor-Joining algorithm by a bootstrap value of at least 75% (of at least 1000 replicates) and a Poisson correction distance measurement of no more than 0.05, based on alignment of the AAV vp1 amino acid sequence.

[0024] The Neighbor-Joining algorithm has been described extensively in the literature. See, e.g., M. Nei and S. Kumar, Molecular Evolution and Phylogenetic (Oxford University Press, New York (2000). Computer programs are available that can be used to implement this algorithm. For example, the MEGA v2.1 program implements the modified Nei-Gojobori method. Using these techniques and computer programs, and the sequence of an AAV vp1 capsid protein, one of skill in the art can readily determine whether a selected AAV is contained in one of the clades identified herein, in another clade, or is outside these clades.

[0025] While the clades defined herein are based primarily upon naturally occurring AAV vp1 capsids, the clades are not limited to naturally occurring AAV. The clades can encompass non-naturally occurring AAV, including, without limitation, recombinant, modified or altered, chimeric, hybrid, synthetic, artificial, etc., AAV which are phylogenetically related as determined using a Neighbor-Joining algorithm at least 75% (of at least 1000 replicates) and a Poisson correction distance measurement of no more than 0.05, based on alignment of the AAV vp1 amino acid sequence.

[0026] The clades described herein include Clade A (represented by AAV1 and AAV6), Clade B (represented by AAV2) and Clade C (represented by the AAV2-AAV3 hybrid), Clade D (represented by AAV7), Clade E (represented by AAV8), and Clade F (represented by human AAV9). These clades are represented by a member of the clade that is a previously described AAV serotype. Previously described AAV1 and AAV6 are members of a single clade (Clade A) in which 4 isolates were recovered from 3 humans. Previously described AAV3 and AAV5 serotypes are clearly distinct from one another, but were not detected in the screen described herein, and have not been included in any of these clades.

[0027] Clade B (AAV2) and Clade C (the AAV2-AAV3 hybrid) are the most abundant of those found in humans (22 isolates from 12 individuals for AAV2 and 17 isolates from 8 individuals for Clade C).

[0028] There are a large number of sequences grouped in either Clade D (AAV7) or Clade E (AAV8). Interestingly, both of these clades are prevalent in different species. Clade D is unique to rhesus and cynomolgus macaques with 15 members being isolated from 10 different animals. Clade E is interesting because it is found in both human and nonhuman primates: 9 isolates were recovered from 7 humans and 21 isolates were obtained in 9 different nonhuman primates including rhesus macaques, a baboon and a pigtail monkey.

[0029] In two other animals the hybrid nature of certain sequences was proven, although all sequences in this case seem to have originated through individual and different recombinations of two co-infecting viruses (in both animals a Clade D with a

Clade E virus). None of these recombinants were identified in other animals or subjects.

[0030] Since Clade C (the AAV2-AAV3 hybrid) clade was identified in 6 different human subjects, the recombination event resulted in a fit progeny. In the case of the AAV7-AAV8 hybrids on the other hand, only few conclusions can be drawn as to the implication of recombination in AAV evolution. These recombination events show that AAV is capable of recombining, thereby creating in-frame genes and in some cases packagable and/or infectious capsid structures. Clade C (the AAV2-AAV3 hybrid clade) on the other hand is a group of viruses that has acquired a selective advantage through recombination that made them sustain certain environmental pressures.

A. Clade A (represented by AAV1 and AAV6):

[0031] Clade A is characterized by containing the previously published AAV1 and AAV6. See, e.g., International Publication No. WO 00/28061, 18 May 2000; Rutledge et al, J Virol, 72(1):309-319 (Jan 1998). In addition, this clade contains AAV including, without limitation, 128.1/hu. 43 [SEQ ID NOs: 80 and 160]; 128.3/hu. 44 [SEQ ID NOs: 81 and 158]; 130.4/hu.48 [SEQ ID NO: 78 and 157]; hu.46 [SEQ ID NOs: 82 and 159]; modified hu. 43 capsid [SEQ ID NO:236]; and modified hu. 46 capsid [SEQ ID NO:224].

[0032] One or more of the members of this clade has a capsid with an amino acid identity of at least 85% identity, at least 90% identity, at least 95% identity, or at least 97% identity over the full-length of the vp1, the vp2, or the vp3 of the AAV1 and/or AAV6 capsid.

[0033] Clade A also contains AAV which do not comprise a capsid of any of AAV1 or AAV6. These AAV may include, without limitation, an AAV having a capsid derived from one or more of 128.1/hu. 43 [SEQ ID NOs: 80 and 160]; modified hu.43 [SEQ ID NO:236] 128.3/hu. 44 [SEQ ID NOs: 81 and 158]; hu.46 [SEQ ID NOs: 82 and 159]; modified hu. 46 [SEQ ID NO:224]; and 130.4/hu.48 [SEQ ID NO: 78 and 157].

B. Clade B (AAV2 Clade):

[0034] Clade B is characterized by containing, at a minimum, the previously described AAV2 and AAV including, 52/hu.19 [SEQ ID NOs: 62 and 133], 52.1/hu.20 [SEQ ID NOs: 63 and 134], 54.5/hu.23 [SEQ ID NOs: 60 and 137], 54.2/hu.22 [SEQ ID NOs: 67 and 138], 54.7/hu.24 [SEQ ID NOs: 66 and 136], 54.1/hu.21 [SEQ ID NOs: 65 and 135], 54.4R/hu.27 [SEQ ID NOs: 64 and 140]; 46.2/hu.28 [SEQ ID NOs: 68 and 130]; 46.6/hu.29 [SEQ ID NOs: 69 and 132]; modified hu. 29 [SEQ ID NO: 225]; 172.1/hu.63 [SEQ ID NO: 171 and 195; GenBank Accession No. AY530624]; 172.2/hu. 64 [SEQ ID NO: 172 and 196; GenBank Accession No. AY530625]; 24.5/hu.13 [SEQ ID NO: 71 and 129; GenBank Accession No. AY530578]; 145.6/hu.56 [SEQ ID NO: 168 and 192]; hu.57 [SEQ ID NOs: 169 and 193]; 136.1/hu.49 [SEQ ID NO: 165 and 189]; 156.1/hu.58 [SEQ ID NO: 179 and 194]; 72.2/hu.34 [SEQ ID NO: 72 and 125; GenBank Accession No. AY530598]; 72.3/hu.35 [SEQ ID NO: 73 and 164; GenBank Accession No. AY530599]; 130.1/hu.47 [SEQ ID NO: 77 and 128]; 129.1/hu.45 (SEQ ID NO: 76 and 127; GenBank Accession No. AY530608); 140.1/hu.51 [SEQ ID NO: 161 and 190; GenBank Accession No. AY530613]; and 140.2/hu.52 [SEQ ID NO: 167 and 191; GenBank Accession No. AY530614].

[0035] One or more of the members of this clade has a capsid with an amino acid identity of at least 85% identity, at least 90% identity, at least 95% identity, or at least 97% identity over the full-length of the vp1, the vp2, or the vp3 of the AAV2 capsid.

[0036] Clade B also contains AAV which do not have an AAV2 capsid. These AAV may include, without limitation, an AAV having a capsid derived from one or more of the following: 52/hu.19 [SEQ ID NOs: 62 and 133], 52.1/hu.20 [SEQ ID NOs: 63 and 134], 54.5/hu.23 [SEQ ID NOs: 60 and 137], 54.2/hu.22 [SEQ ID NOs: 67 and 138], 54.7/hu.24 [SEQ ID NOs: 66 and 136], 54.1/hu.21 [SEQ ID NOs: 65 and 135], 54.4R/hu.27 [SEQ ID NOs: 64 and 140]; 46.2/hu.28 [SEQ ID NOs: 68 and 130]; 46.6/hu.29 [SEQ ID NOs: 69 and 132]; modified hu. 29 [SEQ ID NO: 225]; 172.1/hu.63 [SEQ ID NO: 171 and 195]; 172.2/hu. 64 [SEQ ID NO: 172 and 196]; 24.5/hu.13 [SEQ ID NO: 71 and 129]; 145.6/hu.56 [SEQ ID NO: 168 and 192; GenBank Accession No. AY530618]; hu.57 [SEQ ID NOs: 169 and 193; GenBank Accession No. AY530619]; 136.1/hu.49 [SEQ ID NO: 165 and 189; GenBank Accession No. AY530612]; 156.1/hu.58 [SEQ ID NO: 179 and 194; GenBank Accession No. AY530620]; 72.2/hu.34 [SEQ ID NO: 72 and 125]; 72.3/hu.35 [SEQ ID NO: 73 and 164]; 129.1/hu.45 [SEQ ID NO: 76 and 127]; 130.1/hu.47 [SEQ ID NO:77 and 128; GenBank Accession No. AY530610]; 140.1/hu.51 [SEQ ID NO: 161 and 190; GenBank Accession No. AY530613]; and 140.2/hu.52 [SEQ ID NO: 167 and 191; GenBank Accession No. AY530614].

C. Clade C (AAV2-AAV3 Hybrid Clade)

[0037] Clade C is characterized by containing AAV that are hybrids of the previously published AAV2 and AAV3 such as H-6/hu.4; H-2/hu.2 [US Patent Application 2003/0138772 (Jun 24, 2003)]. In addition, this clade contains AAV including, without limitation, 3.1/hu.9 [SEQ ID Nos: 58 and 155]; 16.8/hu.10 [SEQ ID Nos: 56 and 156]; 16.12/hu.11 [SEQ ID Nos: 57 and 153]; 145.1/hu.53 [SEQ ID Nos: 176 and 186]; 145.6/hu.55 [SEQ ID Nos: 178 and 187]; 145.5/hu.54 [SEQ ID Nos: 177 and 188]; 7.3/hu.7 [SEQ ID Nos: 55 and 150; now deposited as GenBank Accession No. AY530628]; modified hu. 7 [SEQ ID NO: 226]; 33.4/hu.15 [SEQ ID Nos: 50 and 147]; 33.8/hu.16 [SEQ ID Nos: 51 and 148]; hu.18 [SEQ ID NOs: 52 and 149]; 58.2/hu.25 [SEQ ID Nos: 49 and 146]; 161.10/hu.60 [SEQ ID Nos: 170 and 184]; H-5/hu.3 [SEQ ID Nos: 44 and 145]; H-1/hu.1 [SEQ ID Nos: 46 and 144]; and 161.6/hu.61 [SEQ ID Nos: 174 and 185].

[0038] One or more of the members of this clade has a capsid with an amino acid identity of at least 85% identity, at least 90% identity, at least 95% identity, or at least 97% identity over the full-length of the vp1, the vp2, or the vp3 of the hu.4 and/or hu.2 capsid.

[0039] Clade C (the AAV2-AAV3 hybrid clade) also contains AAV which do not comprise a capsid of hu.2 or hu.4. These AAV may include, without limitation, an AAV having a capsid derived from one or more of 3.1/hu.9 [SEQ ID Nos: 58 and 155]; 16.8/hu.10 [SEQ ID Nos: 56 and 156]; 16.12/hu.11 [SEQ ID Nos: 57 and 153]; 145.1/hu.53 [SEQ ID Nos: 176 and 186]; 145.6/hu.55 [SEQ ID Nos: 178 and 187]; 145.5/hu.54 [SEQ ID Nos: 177 and 188]; 7.3/hu.7 [SEQ ID Nos: 55 and 150]; modified hu.7 [SEQ ID NO:226]; 33.4/hu.15 [SEQ ID Nos: 50 and 147]; 33.8/hu.16 [SEQ ID Nos: 51 and 148]; 58.2/hu.25 [SEQ ID Nos: 49 and 146]; 161.10/hu.60 [SEQ ID Nos: 170 and 184]; H-5/hu.3 [SEQ ID Nos: 44 and 145]; H-1/hu.1 [SEQ ID Nos: 46 and 144]; and 161.6/hu.61 [SEQ ID Nos: 174 and 185].

D. Clade D (AAV7 clade)

[0040] Clade D is characterized by containing the previously described AAV7 [G. Gao et al, Proc. Natl Acad. Sci USA, 99:11854-9 (Sep. 3, 2002)]. The nucleic acid sequences encoding the AAV7 capsid are reproduced in SEQ ID NO: 184; the amino acid sequences of the AAV7 capsid are reproduced in SEQ ID NO: 185. In addition, the clade contains a number of previously described AAV sequences, including: cy.2; cy.3; cy.4; cy.5; cy.6; rh.13; rh.37; rh. 36; and rh.35 [US Published Patent Application No. US 2003/0138772 A1 (July 24 2003)]. Additionally, the AAV7 clade contains AAV sequences, including, without limitation, 2-15/ rh.62 [SEQ ID Nos: 33 and 114]; 1-7/rh.48 [SEQ ID Nos: 32 and 115]; 4-9/rh.54 [SEQ ID Nos: 40 and 116]; and 4-19/rh.55 [SEQ ID Nos: 37 and 117]; modified cy. 5 [SEQ ID NO: 227]; modified rh.13 [SEQ ID NO: 228]; and modified rh. 37 [SEQ ID NO: 229].

[0041] One or more of the members of this clade has a capsid with an amino acid identity of at least 85% identity, at least 90% identity, at least 95% identity, or at least 97% identity over the full-length of the vp1, the vp2, or the vp3 of the AAV7 capsid, SEQ ID NO: 184 and 185.

[0042] Clade D also contains AAV which do not comprise a capsid of any of cy.2; cy.3; cy.4; cy.5; cy.6; rh.13; rh.37; rh. 36; and rh.35. These AAV may include, without limitation, an AAV having a capsid derived from one or more of the following 2-15/ rh.62 [SEQ ID Nos: 33 and 114]; 1-7/rh.48 [SEQ ID Nos: 32 and 115]; 4-9/rh.54 [SEQ ID Nos: 40 and 116]; and 4-19/rh.55 [SEQ ID Nos: 37 and 117].

E. Clade E (AAV8 clade)

[0043] Clade E is characterized by containing the previously described AAV8 [G. Gao et al, Proc. Natl Acad. Sci USA, 99:11854-9 (Sep. 3, 2002)], 43.1/rh.2; 44.2/rh.10; rh. 25; 29.3/bb.1; and 29.5/bb.2 [US Published Patent Application No. US 2003/0138772 A1 (Jul 24 2003)].

[0044] This clade comprises AAV sequences, including, without limitation, including, e.g., 30.10/pi.1 [SEQ ID NOs: 28 and 93], 30.12/pi.2 [SEQ ID NOs: 30 and 95], 30.19/pi.3 [SEQ ID NOs: 29 and 94], LG-4/rh.38 [SEQ ID Nos: 7 and 86]; LG-10/rh.40 [SEQ ID Nos: 14 and 92]; N721-8/rh.43 [SEQ ID Nos: 43 and 163]; 1-8/rh.49 [SEQ ID NOs: 25 and 103]; 2-4/rh.50 [SEQ ID Nos: 23 and 108]; 2-5/rh.51 [SEQ ID Nos: 22 and 104]; 3-9/rh.52 [SEQ ID Nos: 18 and 96]; 3-11/rh.53 [SEQ ID NOs: 17 and 97]; 5-3/rh.57

[SEQ ID Nos: 26 and 105]; 5-22/rh.58 [SEQ ID Nos: 27 and 58]; 2-3/rh.61 [SEQ ID NOs: 21 and 107]; 4-8/rh.64 [SEQ ID Nos: 15 and 99]; 3.1/hu.6 [SEQ ID NO: 5 and 84]; 33.12/hu.17 [SEQ ID NO:4 and 83]; 106.1/hu.37 [SEQ ID Nos: 10 and 88]; LG-9/hu.39 [SEQ ID Nos: 24 and 102]; 114.3/hu. 40 [SEQ ID Nos: 11 and 87]; 127.2/hu.41 [SEQ ID NO:6 and 91]; 127.5/hu.42 [SEQ ID Nos: 8 and 85]; hu. 66 [SEQ ID NOs: 173 and 197]; and hu.67 [SEQ ID NOs: 174 and 198]. This clade further includes modified rh. 2 [SEQ ID NO: 231]; modified rh. 58 [SEQ ID NO: 232]; modified rh. 64 [SEQ ID NO: 233].

[0045] One or more of the members of this clade has a capsid with an amino acid identity of at least 85% identity, at least 90% identity, at least 95% identity, or at least 97% identity over the full-length of the vp 1, the vp2, or the vp3 of the AAV8 capsid. The nucleic acid sequences encoding the AAV8 capsid are reproduced in SEQ ID NO: 186 and the amino acid sequences of the capsid are reproduced in SEQ ID NO:187.

[0046] Clade E also contains AAV which do not comprise a capsid of any of AAV8, rh.8; 44.2/rh.10; rh. 25; 29.3/bb.1; and 29.5/bb.2 [US Published Patent Application No. US 2003/0138772 A1 (Jul 24 2003)]. These AAV may include, without limitation, an AAV having a capsid derived from one or more of the following: 30.10/pi.1 [SEQ ID NOs:28 and 93], 30.12/pi.2 [SEQ ID NOs:30 and 95], 30.19/pi.3 [SEQ ID NOs:29 and 94], LG-4/rh.38 [SEQ ID Nos: 7 and 86]; LG-10/rh.40 [SEQ ID Nos: 14 and 92]; N721-8/rh.43 [SEQ ID Nos: 43 and 163];1-8/rh.49 [SEQ ID NOs: 25 and 103]; 2-4/rh.50 [SEQ ID Nos: 23 and 108]; 2-5/rh.51 [SEQ ID NOs: 22 and 104]; 3-9/rh.52 [SEQ ID Nos: 18 and 96]; 3-11/rh.53 [SEQ ID NOs: 17 and 97]; 5-3/rh.57 [SEQ ID Nos: 26 and 105]; 5-22/rh.58 [SEQ ID Nos: 27 and 58]; modified rh. 58 [SEQ ID NO: 232]; 2-3/rh.61 [SEQ ID NOs: 21 and 107]; 4-8/rh.64 [SEQ ID NOs: 15 and 99]; modified rh. 64[SEQ ID NO: 233]; 3.1/hu.6 [SEQ ID NO: 5 and 84]; 33.12/hu.17 [SEQ ID NO:4 and 83]; 106.1/hu.37 [SEQ ID Nos: 10 and 88]; LG-9/hu.39 [SEQ ID Nos: 24 and 102]; 114.3/hu. 40 [SEQ ID Nos: 11 and 87]; 127.2/hu.41 [SEQ ID NO:6 and 91]; 127.5/hu.42 [SEQ ID Nos: 8 and 85]; hu. 66 [SEQ ID NOs: 173 and 197]; and hu.67 [SEQ ID NOs: 174 and 198].

F. Clade F (AAV 9 Clade)

[0047] This clade is identified by the name of an AAV serotype identified herein as hu.14/AAV9 [SEQ ID Nos: 3 and 123]. In addition, this clade contains other sequences including, hu.31 [SEQ ID NOs:1 and 121]; and hu.32 [SEQ ID Nos: 2 and 122].

[0048] One or more of the members of this clade has a capsid with an amino acid identity of at least 85% identity, at least 90% identity, at least 95% identity, or at least 97% identity over the full-length of the vp1, the vp2, or the vp3 of the AAV9 capsid, SEQ ID NO: 3 and 123.

[0049] Clade F includes, without limitation, an AAV having a capsid derived from one or more of hu.14/AAV9 [SEQ ID Nos: 3 and 123], hu.31 [SEQ ID NOs:1 and 121] and hu.32 [SEQ ID Nos: 1 and 122].

[0050] The AAV clades are useful for a variety of purposes, including providing ready collections of related AAV for generating viral vectors, and for generating targeting molecules. These clades may also be used as tools for a variety of purposes that will be readily apparent to one of skill in the art.

II. NOVEL AAV SEQUENCES

[0051] The invention provides the recombinant AAVs, isolated capsid proteins, methods of generation, transfected host cells and compositions, as defined in the claims, which are characterized by capsids of AAV serotype hu.37.

[0052] The nucleic acid sequences and amino acid sequences of a number of AAV are also of interest. Many of these sequences include those described above as members of a clade, as summarized below.

[0053] 128.1/hu. 43 [SEQ ID Nos: 80 and 160 GenBank Accession No. AY530606]; modified hu. 43 [SEQ ID NO:236]; 128.3/hu. 44 [SEQ ID Nos: 81 and 158; GenBank Accession No. AY530607] and 130.4/hu.48 [SEQ ID NO: 78 and 157; GenBank Accession No. AY530611]; from the Clade A;

[0054] 52/hu.19 [SEQ ID NOs: 62 and 133; GenBank Accession No. AY530584], 52.1/hu.20 [SEQ ID NOs: 63 and 134; GenBank Accession No. AY530586], 54.5/hu.23 [SEQ ID Nos: 60 and 137; GenBank Accession No. AY530589], 54.2/hu.22 [SEQ ID Nos: 67 and 138; GenBank Accession No. AY530588], 54.7/hu.24 [SEQ ID Nos: 66 and 136; GenBank Accession No. AY530590], 54.1/hu.21 [SEQ ID Nos: 65 and 135; GenBank Accession No. AY530587], 54.4R/hu.27 [SEQ ID Nos: 64 and 140; GenBank

Accession No. AY530592]; 46.2/hu.28 [SEQ ID Nos: 68 and 130; GenBank Accession No. AY530593]; 46.6/hu.29 [SEQ ID Nos: 69 and 132; GenBank Accession No. AY530594]; modified hu. 29 [SEQ ID NO: 225]; 172.1/hu.63 [SEQ ID NO: 171 and 195]; and 140.2/hu.52 (SEQ ID NO: 167 and 191; from Clade B;

[0055] 3.1/hu.9 [SEQ ID Nos: 58 and 155; GenBank Accession No. AY530626]; 16.8/hu.10 [SEQ ID Nos: 56 and 156; GenBank Accession No. AY530576]; 16.12/hu.11 [SEQ ID Nos: 57 and 153; GenBank Accession No. AY530577]; 145.1/hu.53 [SEQ ID Nos: 176 and 186; GenBank Accession No. AY530615]; 145.6/hu.55 [SEQ ID Nos: 178 and 187; GenBank Accession No. AY530617]; 145.5/hu.54 [SEQ ID Nos: 177 and 188; GenBank Accession No. AY530616]; 7.3/hu.7 [SEQ ID Nos: 55 and 150; GenBank Accession No. AY530628]; modified hu. 7 [SEQ ID NO: 226]; hu.18 [SEQ ID Nos: 52 and 149; GenBank Accession No. AY530583]; 33.4/hu.15 [SEQ ID Nos: 50 and 147; GenBank Accession No. AY530580]; 33.8/hu.16 [SEQ ID Nos: 51 and 148; GenBank Accession No. AY530581]; 58.2/hu.25 [SEQ ID Nos: 49 and 146; GenBank Accession No. AY530591]; 161.10/hu.60 [SEQ ID Nos: 170 and 184; GenBank Accession No. AY530622]; H-5/hu.3 [SEQ ID Nos: 44 and 145; GenBank Accession No. AY530595]; H-1/hu.1 [SEQ ID Nos: 46 and 144; GenBank Accession No. AY530575]; and 161.6/hu.61 [SEQ ID Nos: 174 and 185; GenBank Accession No. AY530623] from Clade C;

[0056] 2-15/ rh.62 [SEQ ID Nos: 33 and 114; GenBank Accession No. AY530573]; 1-7/rh.48 [SEQ ID Nos: 32 and 115; GenBank Accession No. AY530561]; 4-9/rh.54 [SEQ ID Nos: 40 and 116; GenBank Accession No. AY530567]; and 4-19/rh.55 [SEQ ID Nos: 37 and 117; GenBank Accession No. AY530568]; modified cy. 5 [SEQ ID NO: 227]; modified rh.13 [SEQ ID NO: 228]; and modified rh. 37 [SEQ ID NO: 229] from the Clade D;

[0057] 30.10/pi.1 [SEQ ID NOs:28 and 93; GenBank Accession No. AY53055], 30.12/pi.2 [SEQ ID NOs:30 and 95; GenBank Accession No. AY 530554], 30.19/pi.3 [SEQ ID NOs:29 and 94; GenBank Accession No. AY530555], LG-4/rh.38 [SEQ ID Nos: 7 and 86; GenBank Accession No. AY 530558]; LG-10/rh.40 [SEQ ID Nos: 14 and 92; GenBank Accession No. AY530559]; N721-8/rh.43 [SEQ ID Nos: 43 and 163; GenBank Accession No. AY530560];1-8/rh.49 [SEQ ID NOs: 25 and 103; GenBank Accession No. AY530561]; 2-4/rh.50 [SEQ ID Nos: 23 and 108; GenBank Accession No. AY530563]; 2-5/rh.51 [SEQ ID Nos: 22 and 104; GenBank Accession No. 530564]; 3-9/rh.52 [SEQ ID Nos: 18 and 96; GenBank Accession No. AY530565]; 3-11/rh.53 [SEQ ID Nos: 17 and 97; GenBank Accession No. AY530566]; 5-3/rh.57 [SEQ ID Nos: 26 and 105; GenBank Accession No. AY530569]; 5-22/rh.58 [SEQ ID Nos: 27 and 58; GenBank Accession No. 530570]; modified rh. 58 [SEQ ID NO: 232]; 2-3/rh.61 [SEQ ID Nos: 21 and 107; GenBank Accession No. AY530572]; 4-8/rh.64 [SEQ ID Nos: 15 and 99; GenBank Accession No. AY530574]; modified rh. 64[SEQ ID NO: 233]; 3.1/hu.6 [SEQ ID NO: 5 and 84; GenBank Accession No. AY530621]; 33.12/hu.17 [SEQ ID NO:4 and 83; GenBank Accession No. AY530582]; 106.1/hu.37 [SEQ ID Nos: 10 and 88; GenBank Accession No. AY530600]; LG-9/hu.39 [SEQ ID Nos: 24 and 102; GenBank Accession No. AY530601]; 114.3/hu. 40 [SEQ ID Nos: 11 and 87; GenBank Accession No. AY530603]; 127.2/hu.41 [SEQ ID NO:6 and 91; GenBank Accession No. AY530604]; 127.5/hu.42 [SEQ ID Nos: 8 and 85; GenBank Accession No. AY530605]; and hu. 66 [SEQ ID NOs: 173 and 197; GenBank Accession No. AY530626]; and hu.67 [SEQ ID NOs: 174 and 198; GenBank Accession No. AY530627]; and modified rh.2 [SEQ ID NO:231]; from Clade E;

[0058] hu.14/AAV9 [SEQ ID Nos: 3 and 123; GenBank Accession No. AY530579], hu.31 [SEQ ID NOs:1 and 121; AY530596] and hu.32 [SEQ ID Nos: 1 and 122; GenBank Accession No. AY530597] from Clade F.

[0059] In addition, AAV sequences, including, rh.59 [SEQ ID NO: 49 and 110]; rh.60 [SEQ ID NO: 31 and 120; GenBank Accession No. AY530571], modified ch.5 [SEQ ID NO: 234]; and modified rh. 8 [SEQ ID NO: 235], are outside the definition of the clades described above.

[0060] Also of relevance are fragments of the AAV sequences. Each of these fragments may be readily utilized in a variety of vector systems and host cells. Among desirable AAV fragments are the cap proteins, including the vp1, vp2, vp3 and hypervariable regions. Where desired, the methodology described in published US Patent Publication No. US 2003/0138772 A1 (July 24 2003)] can be used to obtain the rep sequences for the AAV clones identified above. Such rep sequences include, e.g., rep 78, rep 68, rep 52, and rep 40, and the sequences encoding these proteins. Similarly, other fragments of these clones may be obtained using the techniques described in the referenced patent publication, including the AAV inverted terminal repeat (ITRs), AAV P 19 sequences, AAV P40 sequences, the rep binding site, and the terminal resolute site (TRS). Still other suitable fragments will be readily apparent to those of skill in the art.

[0061] The capsid of the invention can be readily utilized in a variety of vector systems and host cells. Such fragments may be used alone, in combination with other AAV sequences or fragments, or in combination with elements from other AAV or non-AAV viral sequences. In one particularly desirable embodiment, a vector contains the AAV cap and/or rep sequences of the invention.

[0062] The AAV sequences and fragments thereof are useful in production of rAAV, and are also useful as antisense delivery vectors, gene therapy vectors, or vaccine vectors. The invention further provides nucleic acid molecules, gene delivery vectors,

and host cells which contain the AAV sequences of the invention.

[0063] Suitable fragments can be determined using the information provided herein.

[0064] As described herein, the vectors of the invention containing the AAV capsid proteins of the invention are particularly well suited for use in applications in which the neutralizing antibodies diminish the effectiveness of other AAV serotype based vectors, as well as other viral vectors. The rAAV vectors of the invention are particularly advantageous in rAAV readministration and repeat gene therapy.

[0065] These and other embodiments and advantages of the invention are described in more detail below.

A. AAV Serotype 9/hu14 Sequences

[0066] Of interest are the nucleic acid sequences and amino acids of an AAV, which is termed interchangeably herein as clone hu.14 (formerly termed 28.4) and huAAV9. As defined herein, serotype AAV9 refers to AAV having a capsid which generates antibodies which cross-react serologically with the capsid having the sequence of hu. 14 [SEQ ID NO: 123] and which antibodies do not cross-react serologically with antibodies generated to the capsids of any of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7 or AAV8.

1. Nucleic Acid Sequences

[0067] The AAV9 nucleic acid sequences include the DNA sequences of SEQ ID NO: 3, which consists of 2211 nucleotides.

[0068] The nucleic acid sequences further encompass the strand which is complementary to SEQ ID NO: 3, as well as the RNA and cDNA sequences corresponding to SEQ ID NO: 3, and its complementary strand. Also included in the nucleic acid sequences are natural variants and engineered modifications of SEQ ID NO: 3 and its complementary strand. Such modifications include, for example, labels that are known in the art, methylation, and substitution of one or more of the naturally occurring nucleotides with a degenerate nucleotide.

[0069] Further included are nucleic acid sequences which are greater than about 90%, more preferably at least about 95%, and most preferably at least about 98 to 99%, identical or homologous to SEQ ID NO: 3.

[0070] Also included are fragments of SEQ ID NO: 3, its complementary strand, and cDNA and RNA complementary thereto. Suitable fragments are at least 15 nucleotides in length, and encompass functional fragments, *i.e.*, fragments which are of biological interest. Such fragments include the sequences encoding the three variable proteins (vp) of the AAV9/HU.14 capsid which are alternative splice variants: vp1 [nt 1 to 2211 of SEQ ID NO:3]; vp2 [about nt 411 to 2211 of SEQ ID NO:3]; and vp 3 [about nt 609 to 2211 of SEQ ID NO:3]. Other suitable fragments of SEQ ID NO: 3, include the fragment which contains the start codon for the AAV9/HU.14 capsid protein, and the fragments encoding the hypervariable regions of the vp1 capsid protein, which are described herein.

[0071] In addition to including the nucleic acid sequences provided in the figures and Sequence Listing, the present disclosure includes nucleic acid molecules and sequences which are designed to express the amino acid sequences, proteins and peptides of the AAV serotypes described herein. Thus, the disclosure includes nucleic acid sequences which encode the following AAV amino acid sequences and artificial AAV serotypes generated using these sequences and/or unique fragments thereof.

[0072] As used herein, artificial AAV serotypes include, without limitation, AAVs with a non-naturally occurring capsid protein. Such an artificial capsid may be generated by any suitable technique, using AAV sequences described herein (e.g., a fragment of a vp1 capsid protein) in combination with heterologous sequences which may be obtained from another AAV serotype (known or novel), non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source. An artificial AAV serotype may be, without limitation, a chimeric AAV capsid, a recombinant AAV capsid, or a "humanized" AAV capsid.

2. HU.14/AAV9 Amino Acid Sequences, Proteins and Peptides

[0073] Of interest are proteins and fragments thereof which are encoded by the hu.14/AAV9 nucleic acids, and hu.14/AAV9 proteins and fragments which are generated by other methods. As used herein, these proteins include the assembled capsid. The disclosure further encompasses AAV serotypes generated using sequences of the AAV serotypes described herein, which are generated using synthetic, recombinant or other techniques known to those of skill in the art. The disclosure is not limited to AAV amino acid sequences, peptides and proteins expressed from the AAV nucleic acid sequences disclosed herein, but encompasses amino acid sequences, peptides and proteins generated by other methods known in the art, including, *e.g.*, by chemical synthesis, by other synthetic techniques, or by other methods. The sequences of any of the AAV capsids provided herein can be readily generated using a variety of techniques.

[0074] Suitable production techniques are well known to those of skill in the art. See, *e.g.*, Sambrook et al, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (Cold Spring Harbor, NY). Alternatively, peptides can also be synthesized by the well-known solid phase peptide synthesis methods (Merrifield, *J. Am. Chem. Soc.*, 85:2149 (1962); Stewart and Young, *Solid Phase Peptide Synthesis* (Freeman, San Francisco, 1969) pp. 27-62). These and other suitable production methods are within the knowledge of those of skill in the art.

[0075] Particularly desirable proteins include the AAV capsid proteins, which are encoded by the nucleotide sequences identified above. The AAV capsid is composed of three proteins, vp1, vp2 and vp3, which are alternative splice variants. The full-length sequence provided in Fig. 2 is that of vp1. The AAV9/HU.14 capsid proteins include vp1 [amino acids (aa) 1 to 736 of SEQ ID NO: 123], vp2 [about aa 138 to 736 of SEQ ID NO: 123], vp3 [about aa 203 to 736 of SEQ ID NO: 123], and functional fragments thereof. Other desirable fragments of the capsid protein include the constant and variable regions, located between hypervariable regions (HVR). Other desirable fragments of the capsid protein include the HVR themselves.

[0076] An algorithm developed to determine areas of sequence divergence in AAV2 has yielded 12 hypervariable regions (HVR) of which 5 overlap or are part of the four previously described variable regions. [Chiorini et al, *J. Virol.*, 73:1309-19 (1999); Rutledge et al, *J. Virol.*, 72:309-319] Using this algorithm and/or the alignment techniques described herein, the HVR of the AAV serotypes are determined. For example, the HVR are located as follows: HVR1, aa 146-152; HVR2, aa 182-186; HVR3, aa 262-264; HVR4, aa 381-383; HVR5, aa 450-474; HVR6, aa 490-495; HVR7, aa 500-504; HVR8, aa 514-522; HVR9, aa 534-555; HVR10, aa 581-594; HVR11, aa 658-667; and HVR12, aa 705-719 [the numbering system is based on an alignment which uses the AAV2 vp1 as a point of reference]. Using the alignment provided herein performed using the Clustal X program at default settings, or using other commercially or publicly available alignment programs at default settings such as are described herein, one of skill in the art can readily determine corresponding fragments of the AAV.

[0077] Still other desirable fragments of the AAV9/HU.14 capsid protein include amino acids 1 to 184 of SEQ ID NO: 123, amino acids 199 to 259; amino acids 274 to 446; amino acids 603 to 659; amino acids 670 to 706; amino acids 724 to 736 of SEQ ID NO: 123; aa 185 - 198; aa 260-273; aa447-477; aa495-602; aa660-669; and aa707-723. Additionally, examples of other suitable fragments of AAV capsids include, with respect to the numbering of AAV9 [SEQ ID NO: 123], aa 24 - 42, aa 25 - 28; aa 81 - 85; aa133-165; aa 134 - 165; aa 137-143; aa 154-156; aa 194-208; aa 261-274; aa 262-274; aa 171-173; aa 413-417; aa 449-478; aa 494-525; aa 534-571; aa 581-601; aa 660-671; aa 709-723. Using the alignment provided herein performed using the Clustal X program at default settings, or using other commercially or publicly available alignment programs at default settings, one of skill in the art can readily determine corresponding fragments of the novel AAV capsids of the invention.

[0078] Still other desirable AAV9/HU.14 proteins include the rep proteins include rep68/78 and rep40/52.

[0079] Suitably, fragments are at least 8 amino acids in length. However, fragments of other desired lengths may be readily utilized. Such fragments may be produced recombinantly or by other suitable means, *e.g.*, chemical synthesis.

[0080] Also of interest are other AAV9/HU.14 sequences which are identified using the sequence information provided herein. For example, given the AAV9/HU.14 sequences provided herein, infectious AAV9/HU.14 may be isolated using genome walking technology (Siebert *et al.*, 1995, *Nucleic Acid Research*, **23**:1087-1088, Frieznier-Degen *et al.*, 1986, *J. Biol. Chem.* **261**:6972-6985, BD Biosciences Clontech, Palo Alto, CA). Genome walking is particularly well suited for identifying and isolating the sequences adjacent to the sequences identified according to the method described herein. This technique is also useful for isolating inverted terminal repeat (ITRs) of the AAV9/HU.14 serotype, based upon the AAV capsid and rep sequences provided herein.

[0081] The sequences, proteins, and fragments of the invention may be produced by any suitable means, including recombinant production, chemical synthesis, or other synthetic means. Such production methods are within the knowledge of those of skill in the art and are not a limitation of the present invention.

III. Production of rAAV with Novel AAV Capsids

[0082] The invention encompasses novel AAV capsid sequences which are free of DNA and/or cellular material with which these viruses are associated in nature.

[0083] In another aspect, the present invention provides molecules that utilize the novel AAV sequences of the invention, for production of molecules useful in delivery of a heterologous gene or other nucleic acid sequences to a target cell.

[0084] In another aspect, the present invention provides molecules that utilize the AAV sequences of the invention, for production of viral vectors useful in delivery of a heterologous gene or other nucleic acid sequences to a target cell.

[0085] The molecules of the invention which contain AAV sequences include any genetic element (vector) which may be delivered to a host cell, *e.g.*, naked DNA, a plasmid, phage, transposon, cosmid, episome, a protein in a non-viral delivery vehicle (*e.g.*, a lipid-based carrier), virus, etc., which transfers the sequences carried thereon. The selected vector may be delivered by any suitable method, including transfection, electroporation, liposome delivery, membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, *e.g.*, Sambrook et al, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, NY.

[0086] In one embodiment, the vectors of the invention contain, *inter alia*, sequences encoding an AAV capsid of the invention. Optionally, vectors of the invention may contain both AAV cap and rep proteins. In vectors in which both AAV *rep* and *cap* are provided, the AAV *rep* and AAV *cap* sequences can originate from an AAV of the same clade. Alternatively, the present invention provides vectors in which the *rep* sequences are from an AAV source which differs from that which is providing the *cap* sequences. In one embodiment, the *rep* and *cap* sequences are expressed from separate sources (*e.g.*, separate vectors, or a host cell and a vector). In another embodiment, these *rep* sequences are fused in frame to *cap* sequences of a different AAV source to form a chimeric AAV vector. Optionally, the vectors of the invention are vectors packaged in an AAV capsid of the invention. These vectors and other vectors described herein can further contain a minigene comprising a selected transgene which is flanked by AAV 5' ITR and AAV 3' ITR.

[0087] Thus, for example, the vectors described herein contain nucleic acid sequences encoding an intact AAV capsid which may be from a single AAV sequence (*e.g.*, AAV9/HU.14). Such a capsid may comprise amino acids 1 to 736 of SEQ ID NO: 123. Alternatively, these vectors contain sequences encoding artificial capsids which contain one or more fragments of the AAV9/HU.14 capsid fused to heterologous AAV or non-AAV capsid proteins (or fragments thereof). These artificial capsid proteins are selected from non-contiguous portions of the AAV9/HU.14 capsid or from capsids of other AAVs. For example, a rAAV may have a capsid protein comprising one or more of the AAV9/HU.14 capsid regions selected from the vp2 and/or vp3, or from vp 1, or fragments thereof selected from amino acids 1 to 184, amino acids 199 to 259; amino acids 274 to 446; amino acids 603 to 659; amino acids 670 to 706; amino acids 724 to 738 of the AAV9/HU.14 capsid, SEQ ID NO: 123. In another example, it may be desirable to alter the start codon of the vp3 protein to GTG. Alternatively, the rAAV may contain one or more of the AAV serotype 9 capsid protein hypervariable regions which are identified herein, or other fragment including, without limitation, aa 185 - 198; aa 260-273; aa447-477; aa495-602; aa660-669; and aa707-723 of the AAV9/HU.14 capsid. See, SEQ ID NO: 123. These modifications may be to increase expression, yield, and/or to improve purification in the selected expression systems, or for another desired purpose (*e.g.*, to change tropism or alter neutralizing antibody epitopes).

[0088] The vectors described herein, *e.g.*, a plasmid, are useful for a variety of purposes, but are particularly well suited for use in production of a rAAV containing a capsid comprising AAV sequences or a fragment thereof. These vectors, including rAAV, their elements, construction, and uses are described in detail herein.

[0089] In one aspect, the invention provides a method of generating a recombinant adeno-associated virus (AAV) as claimed in claim 6.

[0090] The components required to be cultured in the host cell to package an AAV minigene in an AAV capsid may be provided to the host cell *in trans*. Alternatively, any one or more of the required components (*e.g.*, minigene, *rep* sequences, *cap* sequences, and/or helper functions) may be provided by a stable host cell which has been engineered to contain one or more of the required components using methods known to those of skill in the art. Most suitably, such a stable host cell will contain the required component(s) under the control of an inducible promoter. However, the required component(s) may be under the control of a constitutive promoter. Examples of suitable inducible and constitutive promoters are provided herein, in the discussion of

regulatory elements suitable for use with the transgene. In still another alternative, a selected stable host cell may contain selected component(s) under the control of a constitutive promoter and other selected component(s) under the control of one or more inducible promoters. For example, a stable host cell may be generated which is derived from 293 cells (which contain E1 helper functions under the control of a constitutive promoter), but which contains the rep and/or cap proteins under the control of inducible promoters. Still other stable host cells may be generated by one of skill in the art.

[0091] The minigene, *rep* sequences, *cap* sequences, and helper functions required for producing the rAAV of the invention may be delivered to the packaging host cell in the form of any genetic element which transfer the sequences carried thereon. The selected genetic element may be delivered by any suitable method, including those described herein. The methods used to construct any embodiment of this invention are known to those with skill in nucleic acid manipulation and include genetic engineering, recombinant engineering, and synthetic techniques. See, e.g., Sambrook et al, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, NY. Similarly, methods of generating rAAV virions are well known and the selection of a suitable method is not a limitation on the present invention. See, e.g., K. Fisher et al, *J. Virol.*, 70:520-532 (1993) and US Patent No. 5,478,745.

[0092] Unless otherwise specified, the AAV ITRs, and other selected AAV components described herein, may be readily selected from among any AAV, including, without limitation, AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV9. These ITRs or other AAV components may be readily isolated using techniques available to those of skill in the art from an AAV sequence. Such AAV may be isolated or obtained from academic, commercial, or public sources (e.g., the American Type Culture Collection, Manassas, VA). Alternatively, the AAV sequences may be obtained through synthetic or other suitable means by reference to published sequences such as are available in the literature or in databases such as, e.g., GenBank®, PubMed®, or the like.

A. The Minigene

[0093] The minigene is composed of, at a minimum, a transgene and its regulatory sequences, and 5' and 3' AAV inverted terminal repeats (ITRs). In one desirable embodiment, the ITRs of AAV serotype 2 are used. However, ITRs from other suitable sources may be selected. It is this minigene that is packaged into a capsid protein and delivered to a selected host cell.

1. The transgene

[0094] The transgene is a nucleic acid sequence, heterologous to the vector sequences flanking the transgene, which encodes a polypeptide, protein, or other product, of interest. The nucleic acid coding sequence is operatively linked to regulatory components in a manner which permits transgene transcription, translation, and/or expression in a host cell.

[0095] The composition of the transgene sequence will depend upon the use to which the resulting vector will be put. For example, one type of transgene sequence includes a reporter sequence, which upon expression produces a detectable signal. Such reporter sequences include, without limitation, DNA sequences encoding β -lactamase, β -galactosidase (LacZ), alkaline phosphatase, thymidine kinase, green fluorescent protein (GFP), enhanced GFP (EGFP), chloramphenicol acetyltransferase (CAT), luciferase, membrane bound proteins including, for example, CD2, CD4, CD8, the influenza hemagglutinin protein, and others well known in the art, to which high affinity antibodies directed thereto exist or can be produced by conventional means, and fusion proteins comprising a membrane bound protein appropriately fused to an antigen tag domain from, among others, hemagglutinin or Myc.

[0096] These coding sequences, when associated with regulatory elements which drive their expression, provide signals detectable by conventional means, including enzymatic, radiographic, colorimetric, fluorescence or other spectrographic assays, fluorescent activating cell sorting assays and immunological assays, including enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and immunohistochemistry. For example, where the marker sequence is the LacZ gene, the presence of the vector carrying the signal is detected by assays for beta-galactosidase activity. Where the transgene is green fluorescent protein or luciferase, the vector carrying the signal may be measured visually by color or light production in a luminometer.

[0097] However, desirably, the transgene is a non-marker sequence encoding a product which is useful in biology and medicine, such as proteins, peptides, RNA, enzymes, dominant negative mutants, or catalytic RNAs. Desirable RNA molecules include tRNA, dsRNA, ribosomal RNA, catalytic RNAs, siRNA, small hairpin RNA, trans-splicing RNA, and antisense RNAs. One example of a useful RNA sequence is a sequence which inhibits or extinguishes expression of a targeted nucleic acid sequence in the treated animal. Typically, suitable target sequences include oncologic targets and viral diseases. See, for examples of such targets the

oncologic targets and viruses identified below in the section relating to immunogens.

[0098] The transgene may be used to correct or ameliorate gene deficiencies, which may include deficiencies in which normal genes are expressed at less than normal levels or deficiencies in which the functional gene product is not expressed. Alternatively, the transgene may provide a product to a cell which is not natively expressed in the cell type or in the host. A preferred type of transgene sequence encodes a therapeutic protein or polypeptide which is expressed in a host cell. The invention further includes using multiple transgenes. In certain situations, a different transgene may be used to encode each subunit of a protein, or to encode different peptides or proteins. This is desirable when the size of the DNA encoding the protein subunit is large, *e.g.*, for an immunoglobulin, the platelet-derived growth factor, or a dystrophin protein. In order for the cell to produce the multi-subunit protein, a cell is infected with the recombinant virus containing each of the different subunits. Alternatively, different subunits of a protein may be encoded by the same transgene. In this case, a single transgene includes the DNA encoding each of the subunits, with the DNA for each subunit separated by an internal ribozyme entry site (IRES). This is desirable when the size of the DNA encoding each of the subunits is small, *e.g.*, the total size of the DNA encoding the subunits and the IRES is less than five kilobases. As an alternative to an IRES, the DNA may be separated by sequences encoding a 2A peptide, which self-cleaves in a post-translational event. See, *e.g.*, M.L. Donnelly, et al, J. Gen. Virol., 78(Pt 1):13-21 (Jan 1997); Furler, S., et al, Gene Ther., 8(11):864-873 (June 2001); Klump H., et al., Gene Ther., 8(10):811-817 (May 2001). This 2A peptide is significantly smaller than an IRES, making it well suited for use when space is a limiting factor. More often, when the transgene is large, consists of multi-subunits, or two transgenes are co-delivered, rAAV carrying the desired transgene(s) or subunits are co-administered to allow them to concatamerize *in vivo* to form a single vector genome. In such an embodiment, a first AAV may carry an expression cassette which expresses a single transgene and a second AAV may carry an expression cassette which expresses a different transgene for co-expression in the host cell. However, the selected transgene may encode any biologically active product or other product, *e.g.*, a product desirable for study.

[0099] Suitable transgenes may be readily selected by one of skill in the art. The selection of the transgene is not considered to be a limitation of this invention.

2. Regulatory Elements

[0100] In addition to the major elements identified above for the minigene, the vector also includes conventional control elements which are operably linked to the transgene in a manner which permits its transcription, translation and/or expression in a cell transfected with the plasmid vector or infected with the virus produced by the invention. As used herein, "operably linked" sequences include both expression control sequences that are contiguous with the gene of interest and expression control sequences that act *in trans* or at a distance to control the gene of interest.

[0101] Expression control sequences include appropriate transcription initiation, termination, promoter and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation (polyA) signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (*i.e.*, Kozak consensus sequence); sequences that enhance protein stability; and when desired, sequences that enhance secretion of the encoded product. A great number of expression control sequences, including promoters which are native, constitutive, inducible and/or tissue-specific, are known in the art and may be utilized.

[0102] Examples of constitutive promoters include, without limitation, the retroviral Rous sarcoma virus (RSV) LTR promoter (optionally with the RSV enhancer), the cytomegalovirus (CMV) promoter (optionally with the CMV enhancer) [see, *e.g.*, Boshart et al, Cell, 41:521-530 (1985)], the SV40 promoter, the dihydrofolate reductase promoter, the β -actin promoter, the phosphoglycerol kinase (PGK) promoter, and the EF1 promoter [Invitrogen]. Inducible promoters allow regulation of gene expression and can be regulated by exogenously supplied compounds, environmental factors such as temperature, or the presence of a specific physiological state, *e.g.*, acute phase, a particular differentiation state of the cell, or in replicating cells only. Inducible promoters and inducible systems are available from a variety of commercial sources, including, without limitation, Invitrogen, Clontech and Ariad. Many other systems have been described and can be readily selected by one of skill in the art. Examples of inducible promoters regulated by exogenously supplied compounds, include, the zinc-inducible sheep metallothioneine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system [International Patent Publication No. WO 98/10088]; the ecdysone insect promoter [No et al, Proc. Natl. Acad. Sci. USA, 93:3346-3351 (1996)], the tetracycline-repressible system [Gossen et al, Proc. Natl. Acad. Sci. USA, 89:5547-5551 (1992)], the tetracycline-inducible system [Gossen et al, Science, 268:1766-1769 (1995), see also Harvey et al, Curr. Opin. Chem. Biol., 2:512-518 (1998)], the RU486-inducible system [Wang et al, Nat. Biotech., 15:239-243 (1997) and Wang et al, Gene Ther., 4:432-441 (1997)] and the rapamycin-inducible system [Magari et al, J. Clin. Invest., 100:2865-2872 (1997)]. Other types of

inducible promoters which may be useful in this context are those which are regulated by a specific physiological state, *e.g.*, temperature, acute phase, a particular differentiation state of the cell, or in replicating cells only.

[0103] In another embodiment, the native promoter for the transgene will be used. The native promoter may be preferred when it is desired that expression of the transgene should mimic the native expression. The native promoter may be used when expression of the transgene must be regulated temporally or developmentally, or in a tissue-specific manner, or in response to specific transcriptional stimuli. In a further embodiment, other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

[0104] Another embodiment of the transgene includes a gene operably linked to a tissue-specific promoter. For instance, if expression in skeletal muscle is desired, a promoter active in muscle should be used. These include the promoters from genes encoding skeletal β -actin, myosin light chain 2A, dystrophin, muscle creatine kinase, as well as synthetic muscle promoters with activities higher than naturally-occurring promoters (see Li et al., *Nat. Biotech.*, 17:241-245 (1999)). Examples of promoters that are tissue-specific are known for liver (albumin, Miyatake et al., *J. Virol.*, 71:5124-32 (1997); hepatitis B virus core promoter, Sandig et al., *Gene Ther.*, 3:1002-9 (1996); alpha-fetoprotein (AFP), Arbutnot et al., *Hum. Gene Ther.*, 7:1503-14 (1996)), bone osteocalcin (Stein et al., *Mol. Biol. Rep.*, 24:185-96 (1997)); bone sialoprotein (Chen et al., *J. Bone Miner. Res.*, 11:654-64 (1996)), lymphocytes (CD2, Hansal et al., *J. Immunol.*, 161:1063-8 (1998); immunoglobulin heavy chain; T cell receptor chain), neuronal such as neuron-specific enolase (NSE) promoter (Andersen et al., *Cell. Mol. Neurobiol.*, 13:503-15 (1993)), neurofilament light-chain gene (Piccioli et al., *Proc. Natl. Acad. Sci. USA*, 88:5611-5 (1991)), and the neuron-specific vgf gene (Piccioli et al., *Neuron*, 15:373-84 (1995)), among others.

[0105] Optionally, plasmids carrying therapeutically useful transgenes may also include selectable markers or reporter genes may include sequences encoding geneticin, hygromycin or purimycin resistance, among others. Such selectable reporters or marker genes (preferably located outside the viral genome to be rescued by the method of the invention) can be used to signal the presence of the plasmids in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication. Selection of these and other promoters and vector elements are conventional and many such sequences are available [see, *e.g.*, Sambrook et al, and references cited therein].

[0106] The combination of the transgene, promoter/enhancer, and 5' and 3' AAV ITRs is referred to as a "minigene" for ease of reference herein. Provided with the teachings of this invention, the design of such a minigene can be made by resort to conventional techniques.

3. Delivery of the Minigene to a Packaging Host Cell

[0107] The minigene can be carried on any suitable vector, *e.g.*, a plasmid, which is delivered to a host cell. The plasmids useful in this invention may be engineered such that they are suitable for replication and, optionally, integration in prokaryotic cells, mammalian cells, or both. These plasmids (or other vectors carrying the 5' AAV ITR-heterologous molecule-3' AAV ITR) contain sequences permitting replication of the minigene in eukaryotes and/or prokaryotes and selection markers for these systems. Selectable markers or reporter genes may include sequences encoding geneticin, hygromycin or purimycin resistance, among others. The plasmids may also contain certain selectable reporters or marker genes that can be used to signal the presence of the vector in bacterial cells, such as ampicillin resistance. Other components of the plasmid may include an origin of replication and an amplicon, such as the amplicon system employing the Epstein Barr virus nuclear antigen. This amplicon system, or other similar amplicon components permit high copy episomal replication in the cells. Preferably, the molecule carrying the minigene is transfected into the cell, where it may exist transiently. Alternatively, the minigene (carrying the 5' AAV ITR-heterologous molecule-3' ITR) may be stably integrated into the genome of the host cell, either chromosomally or as an episome. In certain embodiments, the minigene may be present in multiple copies, optionally in head-to-head, head-to-tail, or tail-to-tail concatamers. Suitable transfection techniques are known and may readily be utilized to deliver the minigene to the host cell.

[0108] Generally, when delivering the vector comprising the minigene by transfection, the vector is delivered in an amount from about 5 μ g to about 100 μ g DNA, about 10 μ g to about 50 μ g DNA to about 1×10^4 cells to about 1×10^{13} cells, or about 1×10^5 cells. However, the relative amounts of vector DNA to host cells may be adjusted, taking into consideration such factors as the selected vector, the delivery method and the host cells selected.

B. Rep and Cap Sequences

[0109] In addition to the minigene, the host cell contains the sequences which drive expression of a novel AAV capsid protein of the invention (or a capsid protein comprising a fragment thereof) in the host cell and rep sequences of the same source as the source of the AAV ITRs found in the minigene, or a cross-complementing source. The AAV *cap* and *rep* sequences may be independently obtained from an AAV source as described above and may be introduced into the host cell in any manner known to one in the art as described above. Additionally, when pseudotyping an AAV vector in (e.g., an AAV9/HU.14 capsid), the sequences encoding each of the essential rep proteins may be supplied by different AAV sources (e.g., AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8). For example, the *rep78/68* sequences may be from AAV2, whereas the *rep52/40* sequences may be from AAV8.

[0110] In one embodiment, the host cell stably contains the capsid protein under the control of a suitable promoter, such as those described above. Most desirably, in this embodiment, the capsid protein is expressed under the control of an inducible promoter. In another embodiment, the capsid protein is supplied to the host cell in *trans*. When delivered to the host cell in *trans*, the capsid protein may be delivered via a plasmid which contains the sequences necessary to direct expression of the selected capsid protein in the host cell. Most desirably, when delivered to the host cell in *trans*, the plasmid carrying the capsid protein also carries other sequences required for packaging the rAAV, e.g., the *rep* sequences.

[0111] In another embodiment, the host cell stably contains the *rep* sequences under the control of a suitable promoter, such as those described above. Most desirably, in this embodiment, the essential rep proteins are expressed under the control of an inducible promoter. In another embodiment, the rep proteins are supplied to the host cell in *trans*. When delivered to the host cell in *trans*, the rep proteins may be delivered via a plasmid which contains the sequences necessary to direct expression of the selected rep proteins in the host cell. Most desirably, when delivered to the host cell in *trans*, the plasmid carrying the capsid protein also carries other sequences required for packaging the rAAV, e.g., the *rep* and *cap* sequences.

[0112] Thus, in one embodiment, the *rep* and *cap* sequences may be transfected into the host cell on a single nucleic acid molecule and exist stably in the cell as an episome. In another embodiment, the *rep* and *cap* sequences are stably integrated into the chromosome of the cell. Another embodiment has the *rep* and *cap* sequences transiently expressed in the host cell. For example, a useful nucleic acid molecule for such transfection comprises, from 5' to 3', a promoter, an optional spacer interposed between the promoter and the start site of the *rep* gene sequence, an AAV *rep* gene sequence, and an AAV *cap* gene sequence.

[0113] Optionally, the *rep* and/or *cap* sequences may be supplied on a vector that contains other DNA sequences that are to be introduced into the host cells. For instance, the vector may contain the rAAV construct comprising the minigene. The vector may comprise one or more of the genes encoding the helper functions, e.g., the adenoviral proteins E1, E2a, and E4 ORF6, and the gene for VAI RNA.

[0114] Preferably, the promoter used in this construct may be any of the constitutive, inducible or native promoters known to one of skill in the art or as discussed above. In one embodiment, an AAV P5 promoter sequence is employed. The selection of the AAV to provide any of these sequences does not limit the invention.

[0115] In another preferred embodiment, the promoter for *rep* is an inducible promoter, such as are discussed above in connection with the transgene regulatory elements. One preferred promoter for *rep* expression is the T7 promoter. The vector comprising the *rep* gene regulated by the T7 promoter and the *cap* gene, is transfected or transformed into a cell which either constitutively or inducibly expresses the T7 polymerase. See International Patent Publication No. WO 98/10088, published March 12, 1998.

[0116] The spacer is an optional element in the design of the vector. The spacer is a DNA sequence interposed between the promoter and the *rep* gene ATG start site. The spacer may have any desired design; that is, it may be a random sequence of nucleotides, or alternatively, it may encode a gene product, such as a marker gene. The spacer may contain genes which typically incorporate start/stop and polyA sites. The spacer may be a non-coding DNA sequence from a prokaryote or eukaryote, a repetitive non-coding sequence, a coding sequence without transcriptional controls or a coding sequence with transcriptional controls. Two exemplary sources of spacer sequences are the phage ladder sequences or yeast ladder sequences, which are available commercially, e.g., from Gibco or Invitrogen, among others. The spacer may be of any size sufficient to reduce expression of the *rep78* and *rep68* gene products, leaving the *rep52*, *rep40* and *cap* gene products expressed at normal levels. The length of the spacer may therefore range from about 10 bp to about 10.0 kbp, preferably in the range of about 100 bp to about 8.0 kbp. To reduce the possibility of recombination, the spacer is preferably less than 2 kbp in length; however, the invention is not so limited.

[0117] Although the molecule(s) providing *rep* and *cap* may exist in the host cell transiently (i.e., through transfection), it is preferred that one or both of the *rep* and *cap* proteins and the promoter(s) controlling their expression be stably expressed in the

host cell, e.g., as an episome or by integration into the chromosome of the host cell. The methods employed for constructing embodiments of this invention are conventional genetic engineering or recombinant engineering techniques such as those described in the references above. While this specification provides illustrative examples of specific constructs, using the information provided herein, one of skill in the art may select and design other suitable constructs, using a choice of spacers, P5 promoters, and other elements, including at least one translational start and stop signal, and the optional addition of polyadenylation sites.

[0118] In another embodiment of this invention, the rep or cap protein may be provided stably by a host cell.

C. The Helper Functions

[0119] The packaging host cell also requires helper functions in order to package the rAAV of the invention. Optionally, these functions may be supplied by a herpesvirus. Most desirably, the necessary helper functions are each provided from a human or non-human primate adenovirus source, such as those described above and/or are available from a variety of sources, including the American Type Culture Collection (ATCC), Manassas, VA (US). In one currently preferred embodiment, the host cell is provided with and/or contains an E1a gene product, an E1b gene product, an E2a gene product, and/or an E4 ORF6 gene product. The host cell may contain other adenoviral genes such as VAI RNA, but these genes are not required. In a preferred embodiment, no other adenovirus genes or gene functions are present in the host cell.

[0120] By "adenoviral DNA which expresses the E1a gene product", it is meant any adenovirus sequence encoding E1a or any functional E1a portion. Adenoviral DNA which expresses the E2a gene product and adenoviral DNA which expresses the E4 ORF6 gene products are defined similarly. Also included are any alleles or other modifications of the adenoviral gene or functional portion thereof. Such modifications may be deliberately introduced by resort to conventional genetic engineering or mutagenic techniques to enhance the adenoviral function in some manner, as well as naturally occurring allelic variants thereof. Such modifications and methods for manipulating DNA to achieve these adenovirus gene functions are known to those of skill in the art.

[0121] The adenovirus E1a, E1b, E2a, and/or E4ORF6 gene products, as well as any other desired helper functions, can be provided using any means that allows their expression in a cell. Each of the sequences encoding these products may be on a separate vector, or one or more genes may be on the same vector. The vector may be any vector known in the art or disclosed above, including plasmids, cosmids and viruses. Introduction into the host cell of the vector may be achieved by any means known in the art or as disclosed above, including transfection, infection, electroporation, liposome delivery, membrane fusion techniques, high velocity DNA-coated pellets, viral infection and protoplast fusion, among others. One or more of the adenoviral genes may be stably integrated into the genome of the host cell, stably expressed as episomes, or expressed transiently. The gene products may all be expressed transiently, on an episome or stably integrated, or some of the gene products may be expressed stably while others are expressed transiently. Furthermore, the promoters for each of the adenoviral genes may be selected independently from a constitutive promoter, an inducible promoter or a native adenoviral promoter. The promoters may be regulated by a specific physiological state of the organism or cell (*i.e.*, by the differentiation state or in replicating or quiescent cells) or by exogenously added factors, for example.

D. Host Cells And Packaging Cell Lines

[0122] The host cell itself may be selected from any biological organism, including prokaryotic (e.g., bacterial) cells, and eukaryotic cells, including, insect cells, yeast cells and mammalian cells. Particularly desirable host cells are selected from among any mammalian species, including, without limitation, cells such as A549, WEHI, 3T3, 10T1/2, BHK, MDCK, COS 1, COS 7, BSC 1, BSC 40, BMT 10, VERO, WI38, HeLa, 293 cells (which express functional adenoviral E1), Saos, C2C12, L cells, HT1080, HepG2 and primary fibroblast, hepatocyte and myoblast cells derived from mammals including human, monkey, mouse, rat, rabbit, and hamster. The selection of the mammalian species providing the cells is not a limitation of this invention; nor is the type of mammalian cell, *i.e.*, fibroblast, hepatocyte, tumor cell, etc. The requirements for the cell used is that it not carry any adenovirus gene other than E1, E2a and/or E4 ORF6; it not contain any other virus gene which could result in homologous recombination of a contaminating virus during the production of rAAV; and it is capable of infection or transfection of DNA and expression of the transfected DNA. In a preferred embodiment, the host cell is one that has *rep* and *cap* stably transfected in the cell.

[0123] One host cell useful in the present invention is a host cell stably transformed with the sequences encoding rep and cap, and which is transfected with the adenovirus E1, E2a, and E4ORF6 DNA and a construct carrying the minigene as described

above. Stable *rep* and/or *cap* expressing cell lines, such as B-50 (International Patent Application Publication No. WO 99/15685), or those described in US Patent No. 5,658,785, may also be similarly employed. Another desirable host cell contains the minimum adenoviral DNA which is sufficient to express E4 ORF6. Yet other cell lines can be constructed using the novel AAV9 *cap* sequences of the invention.

[0124] The preparation of a host cell according to this invention involves techniques such as assembly of selected DNA sequences. This assembly may be accomplished utilizing conventional techniques. Such techniques include cDNA and genomic cloning, which are well known and are described in Sambrook et al., cited above, use of overlapping oligonucleotide sequences of the adenovirus and AAV genomes, combined with polymerase chain reaction, synthetic methods, and any other suitable methods which provide the desired nucleotide sequence.

[0125] Introduction of the molecules (as plasmids or viruses) into the host cell may also be accomplished using techniques known to the skilled artisan and as discussed throughout the specification. In preferred embodiment, standard transfection techniques are used, *e.g.*, CaPO₄ transfection or electroporation, and/or infection by hybrid adenovirus/AAV vectors into cell lines such as the human embryonic kidney cell line HEK 293 (a human kidney cell line containing functional adenovirus E1 genes which provides *trans*-acting E1 proteins).

[0126] The AAV9/HU.14 based vectors which are generated by one of skill in the art are beneficial for gene delivery to selected host cells and gene therapy patients since no neutralization antibodies to AAV9/HU.14 have been found in the human population. One of skill in the art may readily prepare other rAAV viral vectors containing the AAV9/HU.14 capsid proteins provided herein using a variety of techniques known to those of skill in the art. One may similarly prepare still other rAAV viral vectors containing AAV9/HU.14 sequence and AAV capsids from another source.

[0127] One of skill in the art will readily understand that the novel AAV sequences of the invention can be readily adapted for use in these and other viral vector systems for *in vitro*, *ex vivo* or *in vivo* gene delivery. Similarly, one of skill in the art can readily select other fragments of the AAV genome of the invention for use in a variety of rAAV and non-rAAV vector systems. Such vector systems may include, *e.g.*, lentiviruses, retroviruses, poxviruses, vaccinia viruses, and adenoviral systems, among others. Selection of these vector systems is not a limitation of the present invention.

[0128] Thus, the invention further provides vectors generated using the nucleic acid and amino acid sequences of the novel AAV of the invention. Such vectors are useful for a variety of purposes, including for delivery of therapeutic molecules and for use in vaccine regimens. Particularly desirable for delivery of therapeutic molecules are recombinant AAV containing capsids of the novel AAV of the invention. These, or other vector constructs containing novel AAV sequences of the invention may be used in vaccine regimens, *e.g.*, for co-delivery of a cytokine, or for delivery of the immunogen itself.

IV. Recombinant Viruses And Uses Therefor

[0129] Using the techniques described herein, one of skill in the art can generate a rAAV having a capsid of an AAV of the invention or having a capsid containing one or more fragments of an AAV of the invention. In one embodiment, a full-length capsid may be generated which contains one or more fragments of the novel AAV capsid of the invention fused in frame with sequences from another selected AAV, or from heterologous (*i.e.*, non-contiguous) portions of the same AAV. For example, a rAAV may contain one or more of the hypervariable region sequences of AAV9/HU.14. Alternatively, the unique AAV sequences of the invention may be used in constructs containing other viral or non-viral sequences. Optionally, a recombinant virus may carry AAV *rep* sequences encoding one or more of the AAV *rep* proteins.

A. Delivery of Viruses

[0130] Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

[0131] In one desirable embodiment, the invention enables AAV-mediated delivery of a transgene to a host.

[0132] Optionally, a sample from the host may be first assayed for the presence of antibodies to a selected AAV source (*e.g.*, a serotype). A variety of assay formats for detecting neutralizing antibodies are well known to those of skill in the art. The selection of such an assay is not a limitation of the present invention. See, *e.g.*, Fisher et al, *Nature Med.*, 3(3):306-312 (March 1997) and W. C. Manning et al, *Human Gene Therapy*, 9:477-485 (March 1, 1998). The results of this assay may be used to determine

which AAV vector containing capsid proteins of a particular source are preferred for delivery, e.g., by the absence of neutralizing antibodies specific for that capsid source.

[0133] In one aspect of this method, the delivery of vector with AAV capsid proteins of the invention may precede or follow delivery of a gene via a vector with a different AAV capsid protein. Thus, gene delivery via rAAV vectors may be used for repeat gene delivery to a selected host cell. Desirably, subsequently administered rAAV vectors carry the same transgene as the first rAAV vector, but the subsequently administered vectors contain capsid proteins of sources (and preferably, different serotypes) which differ from the first vector. For example, if a first vector has AAV9/HU.14 capsid proteins, subsequently administered vectors may have capsid proteins selected from among the other AAV, optionally, from another serotype or from another clade.

[0134] Optionally, multiple rAAV vectors can be used to deliver large transgenes or multiple transgenes by co-administration of rAAV vectors concatamerize *in vivo* to form a single vector genome. In such an embodiment, a first AAV may carry an expression cassette which expresses a single transgene (or a subunit thereof) and a second AAV may carry an expression cassette which expresses a second transgene (or a different subunit) for co-expression in the host cell. A first AAV may carry an expression cassette which is a first piece of a polycistronic construct (e.g., a promoter and transgene, or subunit) and a second AAV may carry an expression cassette which is a second piece of a polycistronic construct (e.g., transgene or subunit and a polyA sequence). These two pieces of a polycistronic construct *concatamerize in vivo* to form a single vector genome that co-expresses the transgenes delivered by the first and second AAV. In such embodiments, the rAAV vector carrying the first expression cassette and the rAAV vector carrying the second expression cassette can be delivered in a single pharmaceutical composition. In other embodiments, the two or more rAAV vectors are delivered as separate pharmaceutical compositions which can be administered substantially simultaneously, or shortly before or after one another.

[0135] The above-described recombinant vectors may be delivered to host cells according to published methods. The rAAV, preferably suspended in a physiologically compatible carrier, may be administered to a human or non-human mammalian patient. Suitable carriers may be readily selected by one of skill in the art in view of the indication for which the transfer virus is directed. For example, one suitable carrier includes saline, which may be formulated with a variety of buffering solutions (e.g., phosphate buffered saline). Other exemplary carriers include sterile saline, lactose, sucrose, calcium phosphate, gelatin, dextran, agar, pectin, peanut oil, sesame oil, and water. The selection of the carrier is not a limitation of the present invention.

[0136] Optionally, the compositions of the invention may contain, in addition to the rAAV and carrier(s), other conventional pharmaceutical ingredients, such as preservatives, or chemical stabilizers. Suitable exemplary preservatives include chlorobutanol, potassium sorbate, sorbic acid, sulfur dioxide, propyl gallate, the parabens, ethyl vanillin, glycerin, phenol, and parachlorophenol. Suitable chemical stabilizers include gelatin and albumin.

[0137] The vectors are administered in sufficient amounts to transfect the cells and to provide sufficient levels of gene transfer and expression to provide a therapeutic benefit without undue adverse effects, or with medically acceptable physiological effects, which can be determined by those skilled in the medical arts. Conventional and pharmaceutically acceptable routes of administration include, but are not limited to, direct delivery to a desired organ (e.g., the liver (optionally via the hepatic artery) or lung), oral, inhalation, intranasal, intratracheal, intraarterial, intraocular, intravenous, intramuscular, subcutaneous, intradermal, and other parental routes of administration. Routes of administration may be combined, if desired.

[0138] Dosages of the viral vector will depend primarily on factors such as the condition being treated, the age, weight and health of the patient, and may thus vary among patients. For example, a therapeutically effective human dosage of the viral vector is generally in the range of from about 0.1 mL to about 100 mL of solution containing concentrations of from about 1×10^9 to 1×10^{16} genomes virus vector. A preferred human dosage for delivery to large organs (e.g., liver, muscle, heart and lung) may be about 5×10^{10} to 5×10^{13} AAV genomes per 1 kg, at a volume of about 1 to 100 mL. A preferred dosage for delivery to eye is about 5×10^9 to 5×10^{12} genome copies, at a volume of about 0.1 mL to 1 mL. The dosage will be adjusted to balance the therapeutic benefit against any side effects and such dosages may vary depending upon the therapeutic application for which the recombinant vector is employed. The levels of expression of the transgene can be monitored to determine the frequency of dosage resulting in viral vectors, preferably AAV vectors containing the minigene. Optionally, dosage regimens similar to those described for therapeutic purposes may be utilized for immunization using the compositions of the invention.

[0139] Examples of therapeutic products and immunogenic products for delivery by the AAV-containing vectors of the invention are provided below. These vectors may be used for a variety of therapeutic or vaccinal regimens, as described herein. Additionally, these vectors may be delivered in combination with one or more other vectors or active ingredients in a desired therapeutic and/or vaccinal regimen.

B. Therapeutic Transgenes

[0140] Useful therapeutic products encoded by the transgene include hormones and growth and differentiation factors including, without limitation, insulin, glucagon, growth hormone (GH), parathyroid hormone (PTH), growth hormone releasing factor (GRF), follicle stimulating hormone (FSH), luteinizing hormone (LH), human chorionic gonadotropin (hCG), vascular endothelial growth factor (VEGF), angiopoietins, angiostatin, granulocyte colony stimulating factor (GCSF), erythropoietin (EPO), connective tissue growth factor (CTGF), basic fibroblast growth factor (bFGF), acidic fibroblast growth factor (aFGF), epidermal growth factor (EGF), platelet-derived growth factor (PDGF), insulin growth factors I and II (IGF-I and IGF-II), any one of the transforming growth factor α superfamily, including TGF α , activins, inhibins, or any of the bone morphogenic proteins (BMP) BMPs 1-15, any one of the heregulin/neuregulin/ARIA/neu differentiation factor (NDF) family of growth factors, nerve growth factor (NGF), brain-derived neurotrophic factor (BDNF), neurotrophins NT-3 and NT-4/5, ciliary neurotrophic factor (CNTF), glial cell line derived neurotrophic factor (GDNF), neurturin, agrin, any one of the family of semaphorins/collapsins, netrin-1 and netrin-2, hepatocyte growth factor (HGF), ephrins, noggin, sonic hedgehog and tyrosine hydroxylase.

[0141] Other useful transgene products include proteins that regulate the immune system including, without limitation, cytokines and lymphokines such as thrombopoietin (TPO), interleukins (IL) IL-1 through IL-25 (including, *e.g.*, IL-2, IL-4, IL-12 and IL-18), monocyte chemoattractant protein, leukemia inhibitory factor, granulocyte-macrophage colony stimulating factor, Fas ligand, tumor necrosis factors α and β , interferons α , β , and γ , stem cell factor, flk-2/flt3 ligand. Gene products produced by the immune system are also useful in the invention. These include, without limitations, immunoglobulins IgG, IgM, IgA, IgD and IgE, chimeric immunoglobulins, humanized antibodies, single chain antibodies, T cell receptors, chimeric T cell receptors, single chain T cell receptors, class I and class II MHC molecules, as well as engineered immunoglobulins and MHC molecules. Useful gene products also include complement regulatory proteins such as complement regulatory proteins, membrane cofactor protein (MCP), decay accelerating factor (DAF), CR1, CF2 and CD59.

[0142] Still other useful gene products include any one of the receptors for the hormones, growth factors, cytokines, lymphokines, regulatory proteins and immune system proteins. The invention encompasses the use of receptors for cholesterol regulation and/or lipid modulation, including the low density lipoprotein (LDL) receptor, high density lipoprotein (HDL) receptor, the very low density lipoprotein (VLDL) receptor, and scavenger receptors. The invention also encompasses the use of gene products such as members of the steroid hormone receptor superfamily including glucocorticoid receptors and estrogen receptors, Vitamin D receptors and other nuclear receptors. In addition, useful gene products include transcription factors such as *jun*, *fos*, *max*, *mad*, serum response factor (SRF), AP-1, AP2, *myb*, MyoD and myogenin, ETS-box containing proteins, TFE3, E2F, ATF1, ATF2, ATF3, ATF4, ZF5, NFAT, CREB, HNF-4, C/EBP, SP1, CCAAT-box binding proteins, interferon regulation factor (IRF-1), Wilms tumor protein, ETS-binding protein, STAT, GATA-box binding proteins, *e.g.*, GATA-3, and the forkhead family of winged helix proteins.

[0143] Other useful gene products include, carbamoyl synthetase I, ornithine transcarbamylase, arginosuccinate synthetase, arginosuccinate lyase, arginase, fumarylacetylacetate hydrolase, phenylalanine hydroxylase, alpha-1 antitrypsin, glucose-6-phosphatase, porphobilinogen deaminase, cystathione beta-synthase, branched chain ketoacid decarboxylase, albumin, isovaleryl-coA dehydrogenase, propionyl CoA carboxylase, methyl malonyl CoA mutase, glutaryl CoA dehydrogenase, insulin, beta-glucosidase, pyruvate carboxylase, hepatic phosphorylase, phosphorylase kinase, glycine decarboxylase, H-protein, T-protein, a cystic fibrosis transmembrane regulator (CFTR) sequence, and a dystrophin gene product [*e.g.*, a mini- or micro-dystrophin]. Still other useful gene products include enzymes such as may be useful in enzyme replacement therapy, which is useful in a variety of conditions resulting from deficient activity of enzyme. For example, enzymes that contain mannose-6-phosphate may be utilized in therapies for lysosomal storage diseases (*e.g.*, a suitable gene includes that encoding β -glucuronidase (GUSB)).

[0144] Still other useful gene products include those used for treatment of hemophilia, including hemophilia B (including Factor IX) and hemophilia A (including Factor VIII and its variants, such as the light chain and heavy chain of the heterodimer and the B-deleted domain; US Patent No. 6,200,560 and US Patent No. 6,221,349). The Factor VIII gene codes for 2351 amino acids and the protein has six domains, designated from the amino to the terminal carboxy terminus as A1-A2-B-A3-C1-C2 [Wood et al, Nature, 312:330 (1984); Vehar et al., Nature 312:337 (1984); and Toole et al, Nature, 342:337 (1984)]. Human Factor VIII is processed within the cell to yield a heterodimer primarily comprising a heavy chain containing the A1, A2 and B domains and a light chain containing the A3, C1 and C2 domains. Both the single chain polypeptide and the heterodimer circulate in the plasma as inactive precursors, until activated by thrombin cleavage between the A2 and B domains, which releases the B domain and results in a heavy chain consisting of the A1 and A2 domains. The B domain is deleted in the activated procoagulant form of the protein. Additionally, in the native protein, two polypeptide chains ("a" and "b"), flanking the B domain, are bound to a divalent

calcium cation.

[0145] In some embodiments, the minigene comprises first 57 base pairs of the Factor VIII heavy chain which encodes the 10 amino acid signal sequence, as well as the human growth hormone (hGH) polyadenylation sequence. In alternative embodiments, the minigene further comprises the A1 and A2 domains, as well as 5 amino acids from the N-terminus of the B domain, and/or 85 amino acids of the C-terminus of the B domain, as well as the A3, C1 and C2 domains. In yet other embodiments, the nucleic acids encoding Factor VIII heavy chain and light chain are provided in a single minigene separated by 42 nucleic acids coding for 14 amino acids of the B domain [US Patent No. 6,200,560].

[0146] As used herein, a therapeutically effective amount is an amount of AAV vector that produces sufficient amounts of Factor VIII to decrease the time it takes for a subject's blood to clot. Generally, severe hemophiliacs having less than 1% of normal levels of Factor VIII have a whole blood clotting time of greater than 60 minutes as compared to approximately 10 minutes for non-hemophiliacs.

[0147] The present invention is not limited to any specific Factor VIII sequence. Many natural and recombinant forms of Factor VIII have been isolated and generated. Examples of naturally occurring and recombinant forms of Factor VII can be found in the patent and scientific literature including, US Patent No. 5,563,045, US Patent No. 5,451,521, US Patent No. 5,422,260, US Patent No. 5,004,803, US Patent No. 4,757,006, US Patent No. 5,661,008, US Patent No. 5,789,203, US Patent No. 5,681,746, US Patent No. 5,595,886, US Patent No. 5,045,455, US Patent No. 5,668,108, US Patent No. 5,633,150, US Patent No. 5,693,499, US Patent No. 5,587,310, US Patent No. 5,171,844, US Patent No. 5,149,637, US Patent No. 5,112,950, US Patent No. 4,886,876; International Patent Publication Nos. WO 94/11503, WO 87/07144, WO 92/16557, WO 91/09122, WO 97/03195, WO 96/21035, and WO 91/07490; European Patent Application Nos. EP 0 672 138, EP 0 270 618, EP 0 182 448, EP 0 162 067, EP 0 786 474, EP 0 533 862, EP 0 506 757, EP 0 874 057, EP 0 795 021, EP 0 670 332, EP 0 500 734, EP 0 232 112, and EP 0 160 457; Sanberg et al., XXth Int. Congress of the World Fed. Of Hemophilia (1992), and Lind et al., Eur. J. Biochem., 232:19 (1995).

[0148] Nucleic acids sequences coding for the above-described Factor VIII can be obtained using recombinant methods or by deriving the sequence from a vector known to include the same. Furthermore, the desired sequence can be isolated directly from cells and tissues containing the same, using standard techniques, such as phenol extraction and PCR of cDNA or genomic DNA [See, e.g., Sambrook et al]. Nucleotide sequences can also be produced synthetically, rather than cloned. The complete sequence can be assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence [See, e.g., Edge, Nature 292:757 (1981); Nambari et al, Science, 223:1299 (1984); and Jay et al, J. Biol. Chem. 259:6311 (1984)].

[0149] Furthermore, the invention is not limited to human Factor VIII. Indeed, it is intended that the present invention encompass the use of Factor VIII from animals other than humans, including but not limited to companion animals (e.g., canine, felines, and equines), livestock (e.g., bovines, caprines and ovines), laboratory animals, marine mammals, large cats, etc.

[0150] The AAV vectors may contain a nucleic acid coding for fragments of Factor VIII which is itself not biologically active, yet when administered into the subject improves or restores the blood clotting time. For example, as discussed above, the Factor VIII protein comprises two polypeptide chains: a heavy chain and a light chain separated by a B-domain which is cleaved during processing. As demonstrated by the present invention, co-transducing recipient cells with the Factor VIII heavy and light chains leads to the expression of biologically active Factor VIII. Because most hemophiliacs contain a mutation or deletion in only one of the chains (e.g., heavy or light chain), it may be possible to administer only the chain defective in the patient to supply the other chain.

[0151] Other useful gene products include non-naturally occurring polypeptides, such as chimeric or hybrid polypeptides having a non-naturally occurring amino acid sequence containing insertions, deletions or amino acid substitutions. For example, single-chain engineered immunoglobulins could be useful in certain immunocompromised patients. Other types of non-naturally occurring gene sequences include antisense molecules and catalytic nucleic acids, such as ribozymes, which could be used to reduce overexpression of a target.

[0152] Reduction and/or modulation of expression of a gene is particularly desirable for treatment of hyperproliferative conditions characterized by hyperproliferating cells, as are cancers and psoriasis. Target polypeptides include those polypeptides which are produced exclusively or at higher levels in hyperproliferative cells as compared to normal cells. Target antigens include polypeptides encoded by oncogenes such as myb, myc, fyn, and the translocation gene bcr/abl, ras, src, P53, neu, trk and EGRF. In addition to oncogene products as target antigens, target polypeptides for anti-cancer treatments and protective regimens include variable regions of antibodies made by B cell lymphomas and variable regions of T cell receptors of T cell lymphomas which, in some embodiments, are also used as target antigens for autoimmune disease. Other tumor-associated

polypeptides can be used as target polypeptides such as polypeptides which are found at higher levels in tumor cells including the polypeptide recognized by monoclonal antibody 17-1A and folate binding polypeptides.

[0153] Other suitable therapeutic polypeptides and proteins include those which may be useful for treating individuals suffering from autoimmune diseases and disorders by conferring a broad based protective immune response against targets that are associated with autoimmunity including cell receptors and cells which produce "self"-directed antibodies. T cell mediated autoimmune diseases include Rheumatoid arthritis (RA), multiple sclerosis (MS), Sjögren's syndrome, sarcoidosis, insulin dependent diabetes mellitus (IDDM), autoimmune thyroiditis, reactive arthritis, ankylosing spondylitis, scleroderma, polymyositis, dermatomyositis, psoriasis, vasculitis, Wegener's granulomatosis, Crohn's disease and ulcerative colitis. Each of these diseases is characterized by T cell receptors (TCRs) that bind to endogenous antigens and initiate the inflammatory cascade associated with autoimmune diseases.

C. Immunogenic Transgenes

[0154] Suitably, the AAV vectors of the invention avoid the generation of immune responses to the AAV sequences contained within the vector. However, these vectors may nonetheless be formulated in a manner that permits the expression of a transgene carried by the vectors to induce an immune response to a selected antigen. For example, in order to promote an immune response, the transgene may be expressed from a constitutive promoter, the vector can be adjuvanted as described herein, and/or the vector can be put into degenerating tissue.

[0155] Examples of suitable immunogenic transgenes include those selected from a variety of viral families. Examples of desirable viral families against which an immune response would be desirable include, the picornavirus family, which includes the genera rhinoviruses, which are responsible for about 50% of cases of the common cold; the genera enteroviruses, which include polioviruses, coxsackieviruses, echoviruses, and human enteroviruses such as hepatitis A virus; and the genera aphthoviruses, which are responsible for foot and mouth diseases, primarily in non-human animals. Within the picornavirus family of viruses, target antigens include the VP1, VP2, VP3, VP4, and VPG. Other viral families include the astroviruses and the calicivirus family. The calicivirus family encompasses the Norwalk group of viruses, which are an important causative agent of epidemic gastroenteritis. Still another viral family desirable for use in targeting antigens for inducing immune responses in humans and non-human animals is the togavirus family, which includes the genera alphavirus, which include Sindbis viruses, Ross River virus, and Venezuelan, Eastern & Western Equine encephalitis, and rubivirus, including Rubella virus. The flaviviridae family includes dengue, yellow fever, Japanese encephalitis, St. Louis encephalitis and tick borne encephalitis viruses. Other target antigens may be generated from the Hepatitis C or the coronavirus family, which includes a number of non-human viruses such as infectious bronchitis virus (poultry), porcine transmissible gastroenteric virus (pig), porcine hemagglutinin encephalomyelitis virus (pig), feline infectious peritonitis virus (cat), feline enteric coronavirus (cat), canine coronavirus (dog), and human respiratory coronaviruses, which may cause the common cold and/or non-A, B or C hepatitis, and which include the putative cause of sudden acute respiratory syndrome (SARS). Within the coronavirus family, target antigens include the E1 (also called M or matrix protein), E2 (also called S or Spike protein), E3 (also called HE or hemagglutinin-esterase) glycoprotein (not present in all coronaviruses), or N (nucleocapsid). Still other antigens may be targeted against the arterivirus family and the rhabdovirus family. The rhabdovirus family includes the genera vesiculovirus (e.g., Vesicular Stomatitis Virus), and the general lyssavirus (e.g., rabies). Within the rhabdovirus family, suitable antigens may be derived from the G protein or the N protein. The family filoviridae, which includes hemorrhagic fever viruses such as Marburg and Ebola virus may be a suitable source of antigens. The paramyxovirus family includes parainfluenza Virus Type 1, parainfluenza Virus Type 3, bovine parainfluenza Virus Type 3, rubulavirus (mumps virus, parainfluenza Virus Type 2, parainfluenza virus Type 4, Newcastle disease virus (chickens), rinderpest, morbillivirus, which includes measles and canine distemper, and pneumovirus, which includes respiratory syncytial virus. The influenza virus is classified within the family orthomyxovirus and is a suitable source of antigen (e.g., the HA protein, the N1 protein). The bunyavirus family includes the genera bunyavirus (California encephalitis, La Crosse), phlebovirus (Rift Valley Fever), hantavirus (pneumonia is a hemorrhagic fever virus),airovirus (Nairobi sheep disease) and various unassigned bunyaviruses. The arenavirus family provides a source of antigens against LCM and Lassa fever virus. Another source of antigens is the bornavirus family. The reovirus family includes the genera reovirus, rotavirus (which causes acute gastroenteritis in children), orbiviruses, and cultivirus (Colorado Tick fever, Leishmaniasis (humans), equine encephalosis, blue tongue). The retrovirus family includes the sub-family oncovirinae which encompasses such human and veterinary diseases as feline leukemia virus, HTLV-I and HTLV-II, lentivirinae (which includes HIV, simian immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, and spumavirinae). The papovavirus family includes the sub-family polyomaviruses (BKU and JCU viruses) and the sub-family papillomavirus (associated with cancers or malignant progression of papilloma). The adenovirus family includes viruses (EX, AD7, ARD, O.B.) which cause respiratory disease and/or enteritis. The parvovirus family includes feline parvovirus (feline enteritis), feline panleucopeniavirus, canine parvovirus, and porcine parvovirus. The herpesvirus family includes the sub-family

alphaherpesvirinae, which encompasses the genera simplexvirus (HSV1, HSV2), varicellovirus (pseudorabies, varicella zoster) and the sub-family betaherpesvirinae, which includes the genera cytomegalovirus (HCMV, muromegalovirus) and the sub-family gammaherpesvirinae, which includes the genera lymphocryptovirus, EBV (Burkitt's lymphoma), human herpesviruses 6A, 6B and 7, Kaposi's sarcoma-associated herpesvirus and cercopithecine herpesvirus (B virus), infectious rhinotracheitis, Marek's disease virus, and rhadinovirus. The poxvirus family includes the sub-family chordopoxvirinae, which encompasses the genera orthopoxvirus (*Variola major* (Smallpox) and *Vaccinia* (Cowpox)), parapoxvirus, avipoxvirus, capripoxvirus, leporipoxvirus, suipoxvirus, and the sub-family entomopoxvirinae. The hepadnavirus family includes the Hepatitis B virus. One unclassified virus which may be suitable source of antigens is the Hepatitis delta virus, Hepatitis E virus, and prions. Another virus which is a source of antigens is Nipah Virus. Still other viral sources may include avian infectious bursal disease virus and porcine respiratory and reproductive syndrome virus. The alphavirus family includes equine arteritis virus and various Encephalitis viruses.

[0156] The present invention may also encompass the use of immunogens which are useful to immunize a human or non-human animal against other pathogens including bacteria, fungi, parasitic microorganisms or multicellular parasites which infect human and non-human vertebrates, or from a cancer cell or tumor cell. Examples of bacterial pathogens include pathogenic gram-positive cocci include pneumococci; staphylococci (and the toxins produced thereby, e.g., enterotoxin B); and streptococci. Pathogenic gram-negative cocci include meningococcus; gonococcus. Pathogenic enteric gram-negative bacilli include enterobacteriaceae; pseudomonas, acinetobacteria and eikenella; melioidosis; salmonella; shigella; haemophilus; moraxella; *H. ducreyi* (which causes chancroid); brucella species (brucellosis); *Francisella tularensis* (which causes tularemia); *Yersinia pestis* (plague) and other yersinia (pasteurella); streptobacillus moniliformis and spirillum; Gram-positive bacilli include listeria monocytogenes; erysipelotheix rhusiopathiae; *Corynebacterium diphtheria* (diphtheria); cholera; *B. anthracis* (anthrax); donovanosis (granuloma inguinale); and bartonellosis. Diseases caused by pathogenic anaerobic bacteria include tetanus; botulism (*Clostridium botulinum* and its toxin); *Clostridium perfringens* and its epsilon toxin; other clostridia; tuberculosis; leprosy; and other mycobacteria. Pathogenic spirochetal diseases include syphilis; treponematoses: yaws, pinta and endemic syphilis; and leptospirosis. Other infections caused by higher pathogen bacteria and pathogenic fungi include glanders (*Burkholderia mallei*); actinomycosis; nocardiosis; cryptococcosis, blastomycosis, histoplasmosis and coccidioidomycosis; candidiasis, aspergillosis, and mucormycosis; sporotrichosis; paracoccidioidomycosis, petriellidiosis, torulopsosis, mycetoma and chromomycosis; and dermatophytosis. Rickettsial infections include Typhus fever, Rocky Mountain spotted fever, Q fever (*Coxiella burnetii*), and Rickettsialpox. Examples of mycoplasma and chlamydial infections include: mycoplasma pneumoniae; lymphogranuloma venereum; psittacosis; and perinatal chlamydial infections. Pathogenic eukaryotes encompass pathogenic protozoans and helminths and infections produced thereby include: amebiasis; malaria; leishmaniasis; trypanosomiasis; toxoplasmosis; *Pneumocystis carinii*; *Trichans*; *Toxoplasma gondii*; babesiosis; giardiasis; trichinosis; filariasis; schistosomiasis; nematodes; trematodes or flukes; and cestode (tapeworm) infections.

[0157] Many of these organisms and/or the toxins produced thereby have been identified by the Centers for Disease Control [(CDC), Department of Health and Human Services, USA], as agents which have potential for use in biological attacks. For example, some of these biological agents, include, *Bacillus anthracis* (anthrax), *Clostridium botulinum* and its toxin (botulism), *Yersinia pestis* (plague), variola major (smallpox), *Francisella tularensis* (tularemia), and viral hemorrhagic fevers [filoviruses (e.g., Ebola, Marburg), and arenaviruses (e.g., Lassa, Machupo)], all of which are currently classified as Category A agents; *Coxiella burnetii* (Q fever); Brucella species (brucellosis), *Burkholderia mallei* (glanders), *Burkholderia pseudomallei* (melioidosis), *Ricin* *communis* and its toxin (ricin toxin), *Clostridium perfringens* and its toxin (epsilon toxin), *Staphylococcus* species and their toxins (enterotoxin B), *Chlamydia psittaci* (psittacosis), water safety threats (e.g., *Vibrio cholerae*, *Cryptosporidium parvum*), Typhus fever (*Rickettsia powazekii*), and viral encephalitis (alphaviruses, e.g., Venezuelan equine encephalitis; eastern equine encephalitis; western equine encephalitis); all of which are currently classified as Category B agents; and Nipah virus and hantaviruses, which are currently classified as Category C agents. In addition, other organisms, which are so classified or differently classified, may be identified and/or used for such a purpose in the future. It will be readily understood that the viral vectors and other constructs described herein are useful to deliver antigens from these organisms, viruses, their toxins or other by-products, which will prevent and/or treat infection or other adverse reactions with these biological agents.

[0158] Administration of the vectors of the invention to deliver immunogens against the variable region of the T cells elicit an immune response including CTLs to eliminate those T cells. In rheumatoid arthritis (RA), several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-3, V-14, V-17 and V-17. Thus, delivery of a nucleic acid sequence that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in RA. In multiple sclerosis (MS), several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-7 and V-10. Thus, delivery of a nucleic acid sequence that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in MS. In scleroderma, several specific variable regions of TCRs which are involved in the disease have been characterized. These TCRs include V-6, V-8, V-14 and V-16, V-3C, V-7, V-14, V-15, V-16, V-28 and V-12. Thus, delivery of a nucleic acid molecule that encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in scleroderma.

[0159] Thus, a rAAV-derived recombinant viral vector of the invention provides an efficient gene transfer vehicle which can deliver a selected transgene to a selected host cell *in vivo* or *ex vivo* even where the organism has neutralizing antibodies to one or more AAV sources. In one embodiment, the rAAV and the cells are mixed *ex vivo*; the infected cells are cultured using conventional methodologies; and the transduced cells are re-infused into the patient.

[0160] These compositions are particularly well suited to gene delivery for therapeutic purposes and for immunization, including inducing protective immunity. Further, the compositions of the invention may also be used for production of a desired gene product *in vitro*. For *in vitro* production, a desired product (e.g., a protein) may be obtained from a desired culture following transfection of host cells with a rAAV containing the molecule encoding the desired product and culturing the cell culture under conditions which permit expression. The expressed product may then be purified and isolated, as desired. Suitable techniques for transfection, cell culturing, purification, and isolation are known to those of skill in the art.

[0161] The following examples illustrate several aspects and embodiments of the invention.

EXAMPLE 1 - Computational analysis of primate AAV sequences

A. Collection of primate tissues

[0162] Sources of nonhuman primate tissues were described previously [N. Muzyczka, K. I. Berns, in Fields Virology D. M. Knipe, P. M. Howley, Eds. (Lippincott Williams & Wilkins, Philadelphia, 2001), vol. 2, pp. 2327-2359]. Human tissues were collected from either surgical procedures or postmortem examination or organ donors through two major national human tissue providers, Cooperative Human Tissue Network (CHTN) and National Disease Research Interchange (NDRI). Human tissues used for this study were comprised of 18 different tissue types that included colon, liver, lung, spleen, kidney, brain, small bowel, bone marrow, heart, lymph nodes, skeletal muscle, ovary, pancreas, stomach, esophagus, cervix, testis and prostate. The tissue samples came from a diverse group of individuals of different gender, races (Caucasian, African-American, Asian and Hispanic) and ages (23 - 83 years). Among 259 samples from 250 individuals analyzed, approximately 28% of tissues were associated with pathology.

B. Detection and isolation of AAV sequences

[0163] Total cellular DNAs were extracted from human and nonhuman primate tissues as described previously [R. W. Atchison, et al., Science 194, 754-756 (1965)]. Molecular prevalence and tissue distribution of AAVs in humans were determined by either signature or full-length cap PCR using the primers and conditions that were similar to those used for the nonhuman primate analysis. The same PCR cloning strategy used for the isolation and characterization of an expanded family of AAVs in nonhuman primates was deployed in the isolation of AAVs from selected human tissues. Briefly, a 3.1 kb fragment containing a part of rep and full length cap sequence was amplified from tissue DNAs by PCR and Topo-cloned (Invitrogen). The human AAV clones were initially analyzed by restriction mapping to help identify diversity of AAV sequences, which were subsequently subjected to full sequence analysis by SeqWright (SeqWright, Houston, TX) with an accuracy of 99.9%. A total of 67 capsid clones isolated from human tissues were characterized (hu.1 - hu.67). From nonhuman primate tissues, 86 cap clones were sequenced, among which 70 clones were from rhesus macaques, 6 clones from cynomolgus macaques, 3 clones from pigtailed macaques, 2 clones from a baboon and 5 clones from a chimpanzee.

C. Analysis of AAV sequences

[0164] From all contiguous sequences, AAV capsid viral protein (vp1) open reading frames (ORFs) were analyzed. The AAV capsid VP1 protein sequences were aligned with the ClustalX1.81™ program [H. D. Mayor, J. L. Melnick, Nature 210, 331-332 (1966)] and an in-frame DNA alignment was produced with the BioEdit™ [U. Bantel-Schaal, H. Zur Hausen, Virology 134, 52-63 (1984)] software package. Phylogenies were inferred with the MEGAT™ v2.1 and the TreePuzzle™ package. Neighbor-Joining, Maximum Parsimony, and Maximum Likelihood [M. Nei, S. Kumar, Molecular Evolution and Phylogenetics (Oxford University Press, New York, 2000); H. A. Schmidt, K. Strimmer, M. Vingron, A. von Haeseler, Bioinformatics 18, 502-4 (Mar, 2002); N. Saitou, M. Nei, Mol Biol Evol 4, 406-25 (Jul, 1987)] algorithms were used to confirm similar clustering of sequences in monophyletic groups.

[0165] Clades were then defined from a Neighbor-Joining phylogenetic tree of all protein sequences. The amino-acid distances were estimated by making use of Poisson-correction. Bootstrap analysis was performed with a 1000 replicates. Sequences were considered monophyletic when they had a connecting node within a 0.05 genetic distance. A group of sequences originating from 3 or more sources was considered a clade. The phylogeny of AAV was further evaluated for evidence of recombination through a sequential analysis. Homoplasy was screened for by implementation of the Split Decomposition algorithm [H. J. Bandelt, A. W. Dress, *Mol Phylogenet Evol* 1, 242-52 (Sep. 1992)]. Splits that were picked up in this manner were then further analyzed for recombination making use of the Bootscan algorithm in the Simplot software [M. Nei and S. Kumar, *Molecular Evolution and Phylogenetics* (Oxford University Press, New York, 2000)]. A sliding window of 400nt (10nt/step) was used to obtain 100 bootstrap replicate neighbor-joining trees. Subsequently, Split Decomposition and Neighbor-Joining phylogenies were inferred from the putative recombination fragments. Significant improvement of bootstrap values, reduction of splits and regrouping of the hybrid sequences with their parental sources were considered the criterion for recombination.

[0166] A number of different cap sequences amplified from 8 different human subjects showed phylogenetic relationships to AAV2 (5') and AAV3 (3') around a common breakpoint at position 1400 of the Cap DNA sequence, consistent with recombination and the formation of a hybrid virus. This is the general region of the cap gene where recombination was detected from isolates from a mesenteric lymph node of a rhesus macaque [Gao et al., *Proc Natl Acad Sci USA* 100, 6081-6086 (May 13, 2002)]. An overall codon based Z- test for selection was performed implementing the Neib-Gojobori method [R. M. Kotin, *Hum Gene Ther* 5, 793-801 (Jul, 1994)].

[0167] The phylogenetic analyses were repeated excluding the clones that were positively identified as hybrids. In this analysis, goose and avian AAVs were included as outgroups [(I. Bossis, J. A. Chiorini, *J Virol* 77, 6799-810 (Jun. 2003)]. Figure 1 is a neighbor-joining tree; similar relationships were obtained using maximum parsimony and maximum likelihood analyses.

[0168] This analysis demonstrated 11 phylogenetic groups, which are summarized in Table 1. The species origin of the 6 AAV clades and 5 individual AAV clones (or sets of clones) is represented by the number or sources from which the sequences were retrieved in the sampling. The total number of sequences gathered per species and per grouping is shown in between brackets. References for previously described sequences per clade are in the right column. Rhesus - rhesus macaques; cyno - cynomolgus macaques; chimp - chimpanzees; pigtail - pigtail macaques.

Table 1

Classification of the number of sources (sequences) per species and per clade or clone						
	Human	Rhesus	Cyno	Baboon	Chimp	Pigtail
<u>Clade/representative</u>						
A / AAV1 (AAV6)	3(4)					
B / AAV2	12(22)					
C / AAV2-AAV3	8(17)					
hybrid						
D / AAV7		5(10)	5(5)			
E / AAV8	7(9)	7(16)		1(2)		1(3)
F / AAV9	3(3)					
<u>Clones</u>						
AAV3						
AAV4		1(3)				
AAV5						
Ch.5					1(1)	
Rh.8		2(2)				

[0169] Since, as noted above, recombination is not implemented in the standard phylogenetic algorithms used, in order to build a proper phylogenetic tree, those sequences were excluded from the analysis, of which their recombinative ancestry was established. A neighbor-joining analysis of all non-recombined sequences is represented side by side with the clades that did evolve making use of recombination. A similar output was generated with the different algorithm used and with the nucleotide sequence as input.

[0170] Additional experiments were performed to evaluate the relationship of phylogenetic relatedness to function as measured by serologic activity and tropism, as described in the following examples.

EXAMPLE 2 - Serological analysis of novel human AAVs

[0171] The last clade obtained as described in the preceding example was derived from isolates of 3 humans and did not contain a previously described serotype. Polyclonal antisera were generated against a representative member of this clade and a comprehensive study of serologic cross reactivity between the previously described serotypes was performed. This showed that the new human clade is serologically distinct from the other known serotypes and therefore is called Clade F (represented by AAV9).

[0172] Rabbit polyclonal antibodies against AAV serotypes 1-9 were generated by intramuscularly inoculating the animals with 1×10^{13} genome copies each of AAV vectors together with an equal volume of incomplete Freud's adjuvant. The injections were repeated at day 34 to boost antibody titers. Serological cross reactivity between AAV 1-9 was determined by assessing the inhibitory effect of rabbit antisera on transduction of 293 cells by vectors carrying a reporter gene (AAVCMVEGFP, which carries enhanced green fluorescent protein) pseudotyped with capsids derived from different AAV sources. Transduction of 84-31 cells by AAVCMVEGFP vectors was assessed under a UV microscope. In assessing serologic relationships between two AAVs, the ability of both heterologous and homologous sera to neutralize vectors from each AAV were tested. If neutralization by the serum was at least 16-fold lower against heterologous vectors than homologous vectors in a reciprocal manner, the two AAVs are considered distinct serotypes. Neutralization titers were defined as described previously [(G. P. Gao et al., Proc Natl Acad Sci U S A 99, 11854-9 (Sep 3, 2002))].

Table 2

Serologic evaluation of novel AAV vectors									
Vector pseudotypes used in the neutralization assay									
from rabbit immunized with:	AAV2/1	AAV2/2	AAV2/3	AAV2/4	AAV2/5	AAV2/6	AAV2/7	AAV2/8	AAV2/9
AAV2/1	1/163,840	No NAB	No NAB	No NAB	1/40,960	1/40,960	1/40	No NAB	No NAB
AAV2/2	1/80	1/81,920	1/5,120	1/20	No NAB	1/80	1/40	1/40	No NAB
AAV2/3	1/1,280	1/2,560	1/40,960	1/20	1/40	1/2,560	1/1,280	1/1,280	No NAB
AAV2/4	1/20	No NAB	No NAB	1/1,280	1/40	No NAB	No NAB	No NAB	1/40
AAV2/5	1/20,480	No NAB	1/80	No NAB	1/163,840	1/5,120	1/40	No NAB	No NAB
AAV2/6	1/81,920	No NAB	1/640	1/40	1/40	1/327,680	1/40	No NAB	1/40
AAV2/7	1/1,280	1/640	1/1,280	1/20	No NAB	1/1,280	1/163,840	1/5,120	1/80
AAV2/8	1/20	1/1,280	1/1,280	No NAB	1/20	No NAB	1/640	1/327,680	1/2,560
AAV2/9	No NAB	No NAB	No NAB	No NAB	No NAB	No NAB	1/20	1/640	1/20,480

[0173] These data confirm the phylogenetic groupings of the different clones and clades except for unanticipated serological reactivity of the structurally distinct AAV5 and AAV1 serotypes (*i.e.*, ratio of heterologous/homologous titer were 1/4 and 1/8 in reciprocal titrations).

[0174] The result further indicated that AAVhu.14 had a distinct serological property and did not have significant cross reactivity with antisera generated from any known AAV serotypes. The serological distinctiveness of AAVhu.14 was further supported by its uniqueness in the capsid structure which shared less than 85% amino acid sequence identity with all other AAV serotypes compared in this study. Those findings provided the basis for us to name AAVhu.14 as a new serotype, AAV9.

EXAMPLE 3 - Evaluation of primate AAVs as gene transfer vectors

[0175] The biological tropisms of AAVs were studied by generating vector pseudotyped in which recombinant AAV2 genomes expressing either GFP or the secreted reporter gene α -1 antitrypsin (A1AT) were packaged with capsids derived from various clones and one representative member from each primate AAV clade for comparison. For instance, the data obtained from AAV1 was used to represent Clade A, followed by AAV2 for Clade B, Rh.34 for AAV4, AAV7 for Clade D, AAV8 for Clade E, and AAVHu.14 for Clade F. AAV5, AAVCh.5 and AAVRh.8 stand as single AAV genotypes for the comparison.

[0176] The vectors were evaluated for transduction efficiency *in vitro*, based on GFP transduction, and transduction efficiency *in vivo* in liver, muscle or lung (Fig. 4).

A. *In Vitro*

[0177] Vectors expressing enhanced green fluorescent protein (EGFP) were used to examine their *in vitro* transduction efficiency in 84-31 cells and to study their serological properties. For functional analysis, *in vitro* transduction of different AAVCMVEGFP vectors was measured in 84-31 cells that were seeded in a 96 well plate and infected with pseudotyped AAVCMVEGFP vectors at an MOI of 1×10^4 GC per cell. AAV vectors were pseudotyped with capsids of AAVs 1, 2, 5, 7, 8 and 6 other novel AAVs (Ch.5, Rh.34, Cy5, rh.20, Rh.8 and AAV9) using the technique described in G. Gao et al., Proc Natl Acad Sci U S A 99, 11854-9 (Sep 3, 2002). Relative EGFP transduction efficiency was scored as 0, 1, 2 and 3 corresponding to 0-10%, 10-30%, 30-70% and 70-100% of green cells estimated using a UV microscope at 48 hours post infection.

B. *In Vivo*

[0178] For *in vivo* studies, human α -antitrypsin (A1AT) was selected as a sensitive and quantitative reporter gene in the vectors and expressed under the control of CMV-enhanced chicken β -actin promoter. Employment of the CB promoter enables high levels of tissue non-specific and constitutive A1AT gene transfer to be achieved and also permits use of the same vector preparation for gene transfer studies in any tissue of interest. Four to six week old NCR nude mice were treated with novel AAV vectors (AAVCBhA1AT) at a dose of 1×10^{11} genome copies per animal through intraportal, intratracheal and intramuscular injections for liver, lung and muscle directed gene transfer, respectively. Serum samples were collected at different time points post gene transfer and A1AT concentrations were determined by an ELISA-based assay and scored as 0, 1, 2 and 3 relative to different serum A1AT levels at day 28 post gene transfer, depending on the route of vector administration (Liver: 0 = A1AT < 400 ng/ml, 1 = A1AT 400-1000 ng/ml, 2 = A1AT 1000-10,000 ng/ml, 3 = A1AT > 10,000 ng/ml; Lung: 0 = A1AT < 200 ng/ml, 1 = A1AT 200-1000 ng/ml, 2 = A1AT 1000-10,000 ng/ml, 3 = A1AT > 10,000 ng/ml; Muscle: 0 = A1AT < 100 ng/ml, 1 = A1AT 100-1000 ng/ml, 2 = A1AT 1000-10,000 ng/ml, 3 = A1AT > 10,000 ng/ml).

[0179] A human AAV, clone 28.4/hu.14 (now named AAV9), has the ability to transduce liver at a efficiency similar to AAV8, lung 2 logs better than AAV5 and muscle superior to AAV1, whereas the performance of two other human clones, 24.5 and 16.12 (hu.12 and hu.13) was marginal in all 3 target tissues. Clone N721.8 (AAVRh.43) is also a high performer in all three tissues.

[0180] To further analyze gene transfer efficiency of AAV9 and rh 43 in comparison with that of bench markers for liver (AAV8), lung (AAV5) and muscle (AAV1), a dose response experiment was carried out. Both new vectors demonstrated at least 10 fold more gene transfer than AAV1 in muscle, similar performance to AAV8 in liver and 2 logs more efficient than AAV5 in lung.

[0181] A group of AAVs demonstrated efficient gene transfer in all 3 tissues that was similar or superior to the performance of their bench marker in each tissue has emerged. To date, 3 novel AAVs have fallen into this category, two from rhesus (rh10 and 43) and one from human (hu.14 or AAV9). A direct comparison of relative gene transfer efficiency of those 3 AAVs to their bench markers in the murine liver, lung and muscle suggests that some primate AAVs with the best fitness might have evolved from rigorous biological selection and evolution as "super" viruses. These are particularly well suited for gene transfer applications.

C. Profiles of Biological Activity

[0182] Unique profiles of biological activity, in terms of efficiency of gene transfer, were demonstrated for the different AAVs with substantial concordance within members of a set of clones or clade. However, *in vitro* transduction did not predict the efficiency of

gene transfer *in vivo*. An algorithm for comparing the biological activity between two different AAV pseudotypes was developed based on relative scoring of the level of transgene expression and a cumulative analysis of differences.

[0183] Cumulative differences of the gene transfer scores *in vitro* and *in vivo* between pairs of AAVs were calculated and presented in the table (ND = not determined) according to the following formula. Cumulative functional difference in terms of scores between vectors A and B = *in vitro* (A - B) + lung (A - B) + liver (A - B) + muscle (A - B). The smaller the number, the more similar in function the AAVs. In the grey shaded area, the percentage difference in sequence is represented in bold italic. The percentage difference in cap structure was determined by dividing the number of amino-acid differences after a pairwise deletion of gaps by 750, the length of the VP1 protein sequence alignment.

	AAV1	AAV2	AAV3	Ch.5	AAV4	AAV5	AAV7	AAV8	Rh.8	AAV9
AAV1	0	5	ND	4	4	4	2	4	5	4
AAV2	16.3	0	ND	3	2	4	7	7	6	9
AAV3	13.2	12.3	0	ND	ND	ND	ND	ND	ND	ND
Ch.5	15.5	10.5	11.5	0	2	4	6	6	5	8
AAV4	33.7	36.7	34.8	34.9	0	2	7	6	5	8
AAV5	39.1	38.8	38.5	38.4	42.7	0	4	4	3	6
AAV7	14.1	16.7	14.9	15.6	33.2	38.5	0	2	3	2
AAV8	15.6	16.4	14	15.6	33.2	38.9	11.6	0	1	2
Rh.8	14.1	15.2	14.3	14.4	33.7	39.6	12.1	8.8	0	3
AAV9	17.2	17.3	15.6	14.8	34.5	39.7	17.5	14.3	12.5	0

[0184] These studies point out a number of issues relevant to the study of parvoviruses in humans. The prevalence of endogenous AAV sequences in a wide array of human tissues suggests that natural infections with this group of viruses are quite common. The wide tissue distribution of viral sequences and the frequent detection in liver, spleen and gut indicate that transmission occurs via the gastrointestinal track and that viremia may be a feature of the infection.

[0185] The tremendous diversity of sequence present in both human and nonhuman primates has functional correlates in terms of tropism and serology, suggesting it is driven by real biological pressures such as immune escape. Clearly, recombination contributes to this diversity as evidenced by the second most common human clade, which is a hybrid of two previously described AAVs.

[0186] Inspection of the topology of the phylogenetic analysis reveals insight into the relationship between the evolution of the virus and its host restriction. The entire genus of dependoviruses appears to be derived from avian AAV consistent with Lukashov and Goudsmit [(V. V. Lukashov, J. Goudsmit, J Virol 75, 2729-40 (Mar, 2001)]. The AAV4 and AAV5 isolates diverged early from the subsequent development of the other AAVs. The next important node divides the species into two major monophilic groups. The first group contains clones isolated solely from humans and includes Clade B, AAV3 clone, Clade C and Clade A; the only exception to the species restriction of this group is the single clone from chimpanzees, called ch.5. The other monophilic group, representing the remaining members of the genus, is derived from both human and nonhuman primates. This group includes Clade D and the rh.8 clone, which were isolated exclusively from macaques, and the Clade F, which is human specific. The remaining clade within this group (*i.e.*, Clade E) has members from both humans and a number of nonhuman primate species suggesting transmission of this clade across species barriers. It is interesting that the capsid structures of Clade E members isolated from some humans are essentially identical to some from nonhuman primates, indicating that very little host adaptation has occurred. Analysis of the biology of AAV8 derived vectors demonstrated a broad range of tissue tropism with high levels of gene transfer, which is consistent with a more promiscuous range of infectivity, and may explain its apparent zoonosis. An even greater range and efficiency of gene transfer was noted for the Clade F, highlighting the potential for cross species transmission, which to date has not been detected.

[0187] The presence of latent AAVs widely disseminated throughout human and nonhuman primates and their apparent predisposition to recombine and to cross species barriers raises important issues. This combination of events has the potential to lead to the emergence of new infectious agents with modified virulence. Assessing this potential is confounded by the fact that the clinical sequelae of AAV infections in primates has yet to be defined. In addition, the high prevalence of AAV sequences in liver may contribute to dissemination of the virus in the human population in the setting of allogeneic and xenogenic liver transplantation. Finally, the finding of endogenous AAVs in humans has implications in the use of AAV for human gene therapy.

The fact that wild type AAV is so prevalent in primates without ever being associated with a malignancy suggests it is not particularly oncogenic. In fact, expression of AAV rep genes has been shown to suppress transformation P. L. Hermonat, Virology 172, 253-61 (Sep, 1989)].

EXAMPLE 4 - AAV 2/9 Vector for the Treatment of Cystic Fibrosis Airway Disease

[0188] To date, CFTR gene transfer to the lung for the treatment of CF airway disease has been limited by poor vector performance combined with the significant barriers that the airway epithelium poses to effective gene transfer. The AAV2 genome packaged in the AAV9 capsid (AAV2/9) was compared to AAV2/5 in various airway model systems.

[0189] A 50 μ l single dose of 1×10^{11} genome copies (gc) of AAV2/9 expressing either the nuclear targeted β -galactosidase (nLacZ) gene or the green fluorescence protein (GFP) gene under the transcriptional control of the chicken β -actin promoter was instilled intranasally into nude and also C57B1/6 mice. Twenty-one days later, the lung and nose were processed for gene expression. In control animals transduced with AAV2/9-GFP, no LacZ positive cells were seen. AAV2/9-nLacZ successfully transduced mainly airways, whereas AAV2/5-nLacZ transduced mainly alveoli and few airways. Across the nasal airway epithelium, both AAV2/5 and AAV2/9 transduced ciliated and non-ciliated epithelial cells.

[0190] Epithelial cell specific promoters are currently being evaluated to improve targeting to the airway cells *in vivo*. Based on the *in vivo* findings, the gene transfer efficiency of AAV2/9 to human airway epithelial cells was tested next. Airway epithelial cells were isolated from human trachea and bronchi and grown at air-liquid-interface (ALI) on collagen coated membrane supports. Once the cells polarized and differentiated, they were transduced with AAV2/9 or AAV2/5 expressing GFP from the apical as well as the basolateral side. Both AAV2/5 and AAV2/9 were successful at transducing epithelial cells from the basolateral surface. However, when applied onto the apical surface AAV2/9 resulted in a 10-fold increase in the number of transduced cells compared to AAV2/5. Currently, the gene transfer performance of AAV2/9 in the lungs and nasal airways of nonhuman primates is being evaluated.

[0191] This experiment demonstrates that AAV2/9 can efficiently transduce the airways of murine lung and well-differentiated human airway epithelial cells grown at ALI.

EXAMPLE 5 - Comparison of direct injection of AAV1 (2/1) and AAV9(2/9) in adult rat hearts

[0192] Two adult (3 month old) rats received a single injection of 5×10^{11} particles of AAV2/1 or AAV2/9 in the left ventricle

[0193] The results were spectacular, with significantly more expression observed in the adult rat heart with AAV2/9 vectors as compared to AAV2/1, as assessed by lacZ histochemistry. AAV2/9 also shows superior gene transfer in neonatal mouse heart.

EXAMPLE 6 - AAV2/9 Vector for Hemophilia B Gene Therapy

[0194] In this study, AAV 2/9 vectors are shown to be more efficient and less immunogenic vectors for both liver and muscle-directed gene therapy for hemophilia B than the traditional AAV sources.

[0195] For a liver-directed approach, evaluation of the AAV2/9 pseudotyped vector was performed in mouse and dog hemophilic models. In immunocompetent hemophilia B mice (in C57BL/6 background), long-term superphysiological levels of canine Factor IX (cFIX, 41-70 μ g/ml) and shortened activated partial thromboplastin time (aPTT) have been achieved following intraportal injection of 1×10^{11} genome copies (GC)/mouse of AAV2/7, 2/8, and 2/9 vectors in which the cFIX is expressed under a liver specific promoter (LSP) and woodchuck hepatitis B post-transcriptional responsive element (WPRE). A 10-fold lower dose (1×10^{10} GC/mouse) of AAV2/8 vector generated normal level of cFIX and aPTT time. In University of North Carolina (UNC) hemophilia B dogs, it was previously demonstrated that administration of an AAV2/8 vector into a dog previously treated with an AAV2 vector was successful; cFIX expression peaked at 10 μ g/ml day 6 after the 2nd intraportal injection (dose= 5×10^{12} GC/kg), then gradually decreased and stabilized around 700ng/ml (16% of the normal level) throughout the study (1 1/2 years). This level was about 3-fold higher than that from a hemophilia B dog that received a single injection of AAV2-cFIX at the similar dose. Recently, two naive hemophilia B dogs were injected with AAV2/8 vectors intraportally at the dose of 5.25×10^{12} GC/kg. cFIX levels

in one dog (male) reached 30% of normal level (1.5 µg/ml) ten weeks after injection and has sustained at 1.3-1.5 µg/ml, while the second dog (female) maintained cFIX expression at about 10% of normal level. Whole blood clotting time (WBCT) and aPTT were both shortened after the injection, suggesting the antigen was biologically active. Liver enzymes (aspartate amino transferase (SGOT), alanine amino transferase (SGPT) in both dogs remained in the normal range after surgery. These AAV were also evaluated for muscle-targeted gene therapy of hemophilia B. AAV-CMV-cFIX-WPRE [an AAV carrying cFIX under the control of a CMV promoter and containing the WPRE] packaged with six different AAV sources were compared in immunocompetent hemophilia B mice (in C57BL/6 background) after intramuscular injection at the dose of 1×10^{11} GC/mouse. cFIX gene expression and antibody formation were monitored. Highest expression was detected in the plasma of the mice injected with AAV2/8 vectors (1460±392 ng/ml at day 42), followed by AAV2/9 (773±171 ng/ml at day 42) and AAV2/7 (500±311 ng/ml at day 42). Levels were maintained for 5 months. Surprisingly, cFIX expression by AAV2/1 ranged from 0-253 ng/ml (average: 66±82 ng/ml). Anti-cFIX inhibitor (IgG) was detected in some of the AAV2/1-injected mice. cFIX expression levels in these mice correlated well with inhibitor levels. Further screening of inhibitor formation was performed on day 28 samples for all AAV. Hemophilia B mice showed highest inhibitor formation against AAV2/2, followed by AAV2/5, and AAV2/1. Only sporadic and low level inhibitors were detected in animals injected with AAV2/7, AAV2/8 and AAV2/9. Thus, the advantages of the new AAV serotype 2/9 vectors for muscle-directed gene therapy for hemophilia B as more efficient and safe vectors without eliciting any significant anti-FIX antibody formation are shown.

EXAMPLE 7 - Rh.43 Vectors

A. Comparison of AAVrh.43 based A1AT expression vector with AAV8 and AAV9 in mouse liver directed gene transfer

[0196] AAVrh.43, which belongs to Clade E by phylogenetic analysis vector was compared to AAV8 and AAV9 for hA1AT levels after intraportal infusion to the mouse liver. More particularly, pseudotyped AAVrh.43, AAV2/8 and AAV2/9 vectors were compared in mouse liver-directed gene transfer. Pseudotyped vectors at doses of 1×10^{11} GC, 3×10^{10} GC and 1×10^{10} GC per animal were administrated to 4 - 6 week old C57BL/6 mouse intramuscularly. Serum samples were collected from animals at day 28 post vector infusion for the human alpha 1 anti-trypsin (hA1AT) assay.

[0197] The data indicated that the AAVrh.43 vector had indeed a performance similar to that of AAV9 in the mouse model.

B. Nuclear target LacZ gene transfer to mouse liver and muscle mediated by pseudotyped AAV vectors.

[0198] AAV9 and AAVrh.43 based vectors were compared to AAV1 and AAV2-based vector. The vectors were injected at a dose of 1×10^{11} GC per mouse either intraportally to target liver or intramuscularly to the right anterior tibialis muscle of C57BL/6 mice intramuscularly. The animals were sacrificed at day 28 post gene transfer and tissues of interest harvested for X-gal histochemical staining.

[0199] The AAVrh.43 vector demonstrated gene transfer efficiency that was close to AAV9 but at least 5 fold higher than AAV1. The property of AAVrh.43 was further analyzed in both liver and muscle using nuclear targeted LacZ gene as a reporter to visualize extend of gene transfer histochemically.

C. Comparison of AAVrh.43 based A1AT expression vector with AAV5 in mouse lung directed gene transfer

[0200] A rh.43-based vector also demonstrated superb gene transfer potency in lung tissue. Different doses (1×10^{10} , 3×10^{10} and 1×10^{11} GC per animal) of pseudotyped vectors were administrated to 4 - 6 week old C57BL/6 mouse lungs intratracheally. Serum samples were collected from animals at different time points for hA1AT assay.

[0201] This vector was compared to AAV5 at different doses for levels of hA1AT detected systematically after intratracheal instillation to the mouse lung. The data indicated that this novel vector was at least 100 fold more efficient than AAV5 in the mouse model.

EXAMPLE 8 - Novel human AAV based vectors in mouse models for liver and lung-directed gene transfer

[0202] The human clones, AAVhu.37, AAVhu.41 and AAVhu.47 were pseudotyped and examined for gene transfer potency in mouse tissues. AAVCBA1AT vectors pseudotyped with capsids of hu.37, hu.41 and hu.47 were prepared using the methods described herein and administrated to 4 - 6 week old C57BL/6 mouse through intraportal and intratracheal injections. Serum samples were collected from animals at day 14 post vector injection for hA1AT assay, which was performed in accordance with published techniques. AAVhu.47 belongs to AAV2 family (clade B) AAV2 and was isolated from a human bone marrow sample. AAVhu.37 and AAVhu.41 came from a human testis tissue and a human bone marrow sample respectively. Phylogenetically, they fall into the AAV 8 clade (clade E).

[0203] Serum A1AT analysis of injected animals indicated that AAV hu.41 and AAV hu.47 performed poorly in the three tissues tested. However, gene transfer potency of AAVhu.37 derived vector was similar to that of AAV8 in liver and AAV9 in lung

[0204] While the invention has been described with reference to particularly preferred embodiments, it will be appreciated that modifications can be made within the scope of the appended claims.

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Patentkrav

1. Rekombinant adenoassocieret virus (AAV), der omfatter et AAV hu.37-capsid med sekvensen af aminosyrer fra 138 til 738 af SEQ ID NO: 88, og hvor AAV'et yderligere omfatter et minigen med AAV-inverterede terminale gentagelsessekvenser og et heterologt gen, som er operativt forbundet til regulatoriske sekvenser, der styrer dets udtryk i en værtscelle.
5
2. Rekombinant AAV ifølge krav 1, hvor AAV hu.37-capsidet har en aminosyresekvens, der omfatter aminosyrerne 1 til 738 af SEQ ID NO: 88.
10
3. Rekombinant AAV ifølge krav 2, hvor capsidet er kodet af nukleinsyresekvensen af SEQ ID NO: 10.
4. Rekombinant AAV ifølge et hvilket som helst af kravene 1 til 3, hvor de inverterede terminale gentagelsessekvenser er fra et AAV, der er heterologt med det AAV hu.37, som tilvejebringer capsidproteinet.
15
5. Isoleret capsidprotein, der omfatter et hu.37-adenoassocieret virus (AAV hu.37)-capsidprotein, som er valgt fra gruppen bestående af:
20
 - vp1-capsidprotein, aminosyrerne (aa) 1 til 738, SEQ ID NO: 88, og
 - vp2-capsidprotein, aa 138 til 738, SEQ ID NO: 88.
6. Fremgangsmåde til generering af et rekombinant adenoassocieret virus (AAV), der omfatter et AAV-capsid, hvilken fremgangsmåde omfatter trinnene til dyrkning af en værtscelle, som indeholder:
25
 - (a) et molekyle, der koder for et AAV-capsidprotein, (b) et funktionelt rep gen, (c) et minigen, som omfatter AAV-inverterede terminale gentagelsessekvenser (ITR'er) og et transgen, og (d) tilstrækkelige

hjelperfunktioner til at tillade pakning af minigenet i AAV-capsidproteinet, hvor værtscellen omfatter et nukleinsyremolekyle, der er valgt fra gruppen bestående af:

vp1, nt 1 til 2217 af SEQ ID NO: 10, og

5 vp2, nt 411 til 2217 af SEQ ID NO: 10.

7. Fremgangsmåde ifølge krav 6, hvor molekylet omfatter en AAV-sekvens, der koder for et AAV-capsidprotein og et funktionelt AAV rep protein.

10 **8.** Fremgangsmåde ifølge krav 6 eller 7, hvor molekylet er et plasmid.

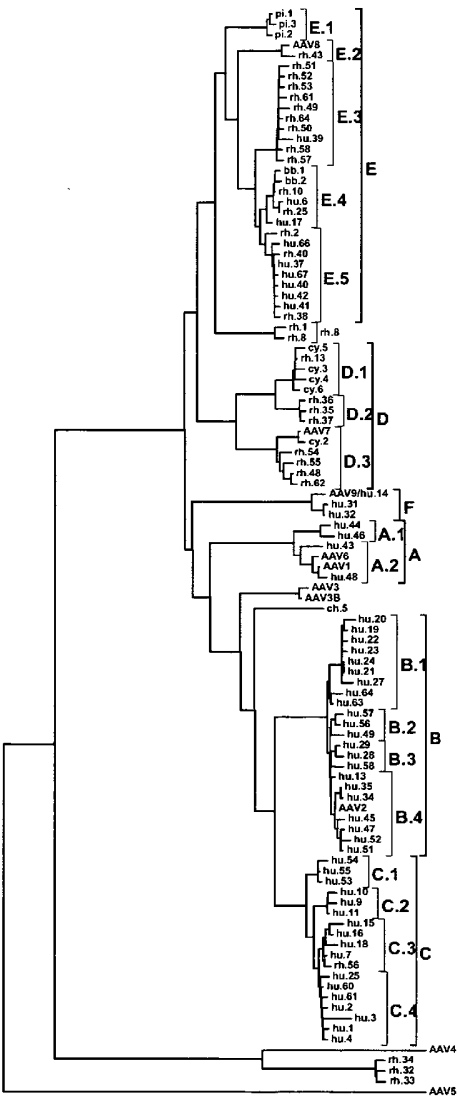
9. Værtscelle, der omfatter det adenoassocierede virus ifølge krav 1.

15 **10.** Præparat, der omfatter et rekombinant AAV ifølge et hvilket som helst af kravene 1 til 4 og en farmaceutisk bærer.

11. AAV ifølge et hvilket som helst af kravene 1 til 4 til levering af et molekyle til en celle.

DRAWINGS

FIG. 1



AAV5	1	MSFVDFPDWLEEE-VGEGLREFFLGEAGPPKPKPNQHQDQARGLIVLPGYNYLGPNGLDRGEPVNRAD	70
AAV3-3	1	MAADGYLPDWLEDNLSGIREWALWALKPGVPQKANKQHQDNRRGLVLPGYKYLGPGNGLDKGEPVNEAD	60
AAV4-4	1	-MTDGYLPDWLEDNLSGIREWALWALQPGAKPKPKANKQHQDNARGLIVLPGYKYLGPGNGLDKGEPVNEAD	50
AAV1-A	1	MAADGYLPDWLEDNLSGIREWDLKPGAKPKPKANKQKQDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	40
hu.46-A	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	30
hu.48-A	1	MAADGYLPDWLEDTLSGIREWDLKPGAKPKPKANKQKQDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	20
hu.44-A	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	10
hu.43-A	1	MAADGYLPDWLEDNLSGIREWDLKPGAKPKPKANKQKQDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
AAV6-A	1	MAADGYLPDWLEDNLSGIREWDLKPGAKPKANKQKQDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.34-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.47-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHRDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.29-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.63-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.56-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.45-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHRDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.57-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPP-KPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.35-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.58-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.28-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.51-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.19-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.49-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.52-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.13-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
AAV2-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.20-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.24-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	
hu.64-B	1	MAADGYLPDWLEDTLSGIRQWKKLPGPPPKPAERHKDDSGRLVLPGYKYLGPFNGLDKGEPVNEAD	

FIG. 2A

hu. 27-B	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 21-B	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 22-B	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 7-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 61-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 56-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 9-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 54-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 53-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 60-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 55-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 2-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 1-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 18-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 3-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 25-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 16-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 15-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 11-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 10-C	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 54-D	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 48-D	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 55-D	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 62-D	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
AAV7-D	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 52-E	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
rh. 51-E	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA
hu. 39-E	1	MAADGYLPWLEDTLSEGI RQWVKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFBNGLDKGEPVNEADA

FIG. 2B

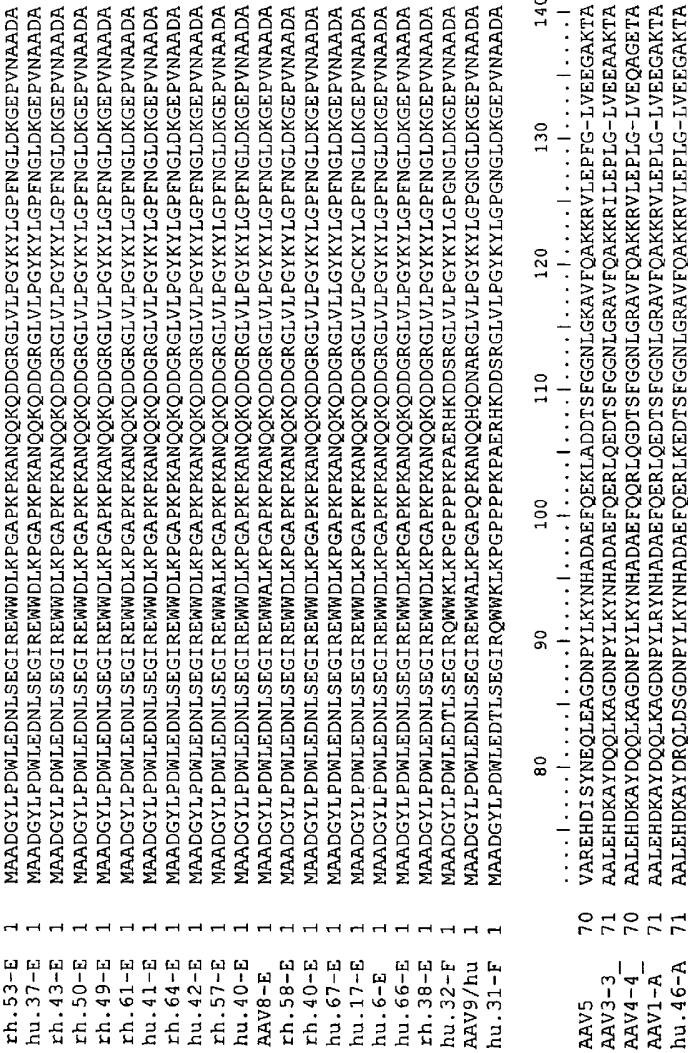


FIG. 2C

hu. 48-A	71	AALEHDKAYDQQLKAGDNPYLYRNHADAEFQERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEGAKTA
hu. 44-A	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEGAEATA
hu. 43-A	71	AALEHDKAYDQQLKAGDNPYLYRNHADAEFQERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAAKTA
AAV6-A	71	AALEHDKAYDQQLKAGDNPYLYRNHADAEFQERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEGAKTA
hu. 34-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 47-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 29-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 63-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 56-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 45-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 57-B	70	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 35-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 58-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 28-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 51-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 19-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 49-B	71	AALEYDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 52-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 13-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
AAV2-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 20-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 24-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 64-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 27-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 21-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 22-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 23-B	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 7-C	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
hu. 61-C	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA
rh. 56-C	71	AALEHDKAYDRQLDSGDNPYLYKNHADAEFQERLKEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEPVKTA

FIG. 2D

hu. 9-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 54-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 53-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 60-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 55-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 2-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 1-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 18-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 3-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 25-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 15-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 16-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 11-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 10-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
hu. 4-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEPPVKTA
rh. 54-D	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 48-D	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 55-D	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 62-D	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
AAW7-D	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 52-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 51-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
hu. 39-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 53-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
hu. 37-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 43-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 50-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 49-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
rh. 61-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA
hu. 41-E	71	AALEHDKAYDQQLKAGDNPYLYRYNHADADEFQERLKEDTSFGNLSGRAVFOAKKRVLEPLG-LVEEAAKTA

FIG. 2E

rh. 64-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 42-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
rh. 57-E	71	AALEHDKAYDQOLQAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 40-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
AAV8-E	71	AALEHDKAYDQOLQAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
rh. 58-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
rh. 40-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 67-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 17-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 6-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 66-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
rh. 38-E	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 32-F	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
AAV9/hu	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA
hu. 31-F	71	AALEHDKAYDQOLKAGDNPYLRYNHADAEFOERLQEDTSFGGNLGRAVFOAKKRVLEPLG-LVEEAKTA

AAV5	139	PTGKRIDDHFP-----
AAV3-3	140	PGKKGAVDQSPQ-EPDSSGVGKSGKQPARKRNFNGQTDSEVPD-PQPLGEPPTAAPTSLGSNTMASGG
AAV4-4	139	PGKKRPLIESPQ-QPDSSTGIGKKGKQPAKKLVFEDDTGAGDGP----PEGSTSGAMS--DDSEMRAAA
AAV1-A	140	PGKKRPEVEQSPQ-EPDSSGIGKTGQQPAKKRNFNGQTDSEVPD-PQPLGEPPTAAPTAAVGPPTTMASGG
hu. 46-A	140	PGKKRPEVEQSPQ-EPDSSGIGKTGQQPAKKRNFNGQTDSEVPD-PQPLGEPPTAAPTAAVGPPTTMASGG
hu. 48-A	140	PGKKRPEVEQSPQ-EPDSSGIGKTGQQPAKKRNFNGQTDSEVPD-PQPLGEPPTAAPTAAVGPPTTMASGG
hu. 44-A	140	PGKKRPEVEQSPQ-EPDSSGIGKTGQQPAKKRNFNGQTDSEVPD-PQPLGEPPTAAPTAAVGPPTTMASGG
hu. 43-A	140	PGKKRPEVEQSPQ-EPDSSGIGKTGQQPAKKRNFNGQTDSEVPD-PQPLGEPPTAAPTAAVGPPTTMASGG
AAV6-A	140	PGKKRPEVEQSPQ-EPDSSGIGKTGQQPAKKRNFNGQTDSEVPD-PQPLGEPPTAAPTAAVGPPTTMASGG
hu. 34-B	140	PGKKRPEVEHSPV-EPDSSSGTGKAGQQPARKRNFNGQTDADSVDP-PQPLGQPPAAPSGLGTNTMATGS
hu. 47-B	140	PGKKRPEVEHSPV-EPDSSSGTGKAGQQPARKRNFNGQTDADSVDP-PQPLGQPPAAPSGLGTNTMATGS
hu. 29-B	140	PGKKRPEVEHSPA-EPDSSSGTGKSGNQPAKKRNFNGQTDSDSVDP-PQPLGQPPAAPSGLGTNTMATGS

FIG. 2F

hu.63-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.56-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.45-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.57-B 139 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.35-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.58-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.28-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.51-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.19-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.49-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.52-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.13-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 AAV2-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.20-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.24-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.64-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.27-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.21-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.22-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.23-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.7-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.61-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 ch.56-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.9-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.54-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.53-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.60-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.55-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.2-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS
 hu.1-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQOPARKRLNFGQTGDADSVDP-PQPLGQPPAAPPSGLGTTNTMATGS

FIG. 2G

hu.18-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.3-C 141 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.25-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.15-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.16-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.11-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.10-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
hu.4-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDDADSVDP-PQPLGQPPAAPSGLGSTTMAAGS
rh.54-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.48-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.55-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.62-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
AAV7-D 140 PAKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.52-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.51-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
hu.39-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.53-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
hu.37-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.43-E 140 PGKKRPVEQSPQ-EPDSSSGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.50-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.49-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.61-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
hu.41-E 140 PGKKRPVEPPORSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.64-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
hu.42-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.57-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
hu.40-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
AAV8-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.58-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG
rh.40-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSVDP-PQPLGEPFAGPSGLGSGTMAAGG

FIG. 2H

hu. 67-E	140	PGKKRPVPSQSPDSSSTGIGKKGOQPAKRLNFGQTGDSVDP-PQPIGEPPAGPSGLSGTMAAGG
hu. 17-E	140	PGKKRPVPSQSPDSSSTGIGKTGQQAQPAKRLNFGQTGDSVDP-PQPIGEPPAGPSGLSGTMAAGG
hu. 6-E	140	PGKKRPVPSQSPDSSSTGIGKTGQQAQPAKRLNFGQTGDSVDP-PQPIGEPPAGPSGLSGTMAAGG
hu. 66-E	140	PGKKRPVPSQSPDSSSTGIGKTGQQAQPAKRLNFGQTGDSVDP-PQPIGEPPAGPSGLSGTMAAGG
rh. 38-E	140	PGKKRPVPSQSPDSSSTGIGKKRQPAKRLNFGQTGDSVDP-PQPIGEPPAGPSGLSGTMAAGG
hu. 32-F	140	PGKKRPVEQSPQ-EPDSSAGIGKSGQPAKRLNFGQTGDSVDP-PQPIGEPPAAPSGLSLTMAAGG
AAV9/hu	140	PGKKRPVEQSPQ-EPDSSAGIGKSGQPAKRLNFGQTGDSVDP-PQPIGEPPAAPSGLSLTMAAGG
hu. 31-F	140	PGKKRPVEQSPQ-EPDSSAGIGKSGQPAKRLNFGQTGDSVDP-PQPIGEPPAAPSGLSLTMAAGG

AAV5	198	GCPLGDNQAGDVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--GSVDGSNANAYFGY	220	230	240	250	260	270	280
AAV3-3	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
AAV4-4	202	GGAAYEGGQAGDVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKRLG-----ESLQNTYNGF							
AAV1-A	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--ASTGASNDNHYFGY							
hu. 46-A	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--ASTGASNDNHYFGY							
hu. 48-A	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--TSTGASNDNHYFGY							
hu. 44-A	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--ASTGASNDNHYFGY							
hu. 43-A	209	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--ASTGASNDNHYFGY							
AAV6-A	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--ASTGASNDNHYFGY							
hu. 34-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 47-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 29-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 63-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 56-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 45-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 57-B	207	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 35-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 58-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							
hu. 28-B	208	GAPMADNNEGADVGNSGNDWHDSTWMDRVITKSTRTWLPSYNNHLYKQIS--SQSGASNDNHYFGY							

FIG. 21

hu.51-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.19-B 208 GAPMADNNEGADGVGNSSGNWYCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.49-B 208 GAPMADNNEGADGVGNSSGSWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.52-B 208 GAPMADNNEGADGVGNSSGNRCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.13-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
AAV2-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.20-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.24-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.64-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.27-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.21-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.22-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.23-B 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTCNHLYKQIS--SQSGASNDNHFFGY
hu.7-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.61-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
rh.56-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.9-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.54-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.53-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.60-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.55-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.2-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.1-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.18-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.3-C 209 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGACNDNHFFGY
hu.25-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.15-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.16-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.11-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY
hu.10-C 208 GAPMADNNEGADGVGNSSGNWCHCDSTWNGDRVITTTSTRTWTALPTYNHLYKQIS--SQSGASNDNHFFGY

FIG. 2J

hu.4-C 208 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQIS--SQSCASNDNHVFGY
 rh.54-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISS-QSAGSTNDNVFGY
 rh.48-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISS-QSAGSTNDNVFGY
 rh.55-D 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISS-QSAGSTNDNVFGY
 rh.62-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISS-QSAGSTNDNVFGY
 AAV7-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISS-ETAGSTNDNVFGY
 rh.52-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.51-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.39-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.53-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.37-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.43-E 208 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.50-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.49-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.61-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.41-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.64-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.42-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.57-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.40-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 AAV8-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.58-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.40-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.17-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.6-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.66-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 rh.38-E 209 GAPMADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNGTSGGSTNDNVFGY
 hu.32-F 208 GAPVADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNSTSGGSSNDNAVFGY
 AAV9/hu 208 GAPVADNNEGADGVGSSGNWHCDSTWLGDRVITTTSTRTWTALPTYNHLYKQISSNSTSGGSSNDNAVFGY

FIG. 2K

hu.31-F 208 GAPVADNNEGADYGSSSGNWHCDSQLGDRVITTTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGY

AAV5 267 STPWGYFDENREHSHSPRDWQRLNNWGFPRSLRVKIFNIQKVEVTQDSTTTIANNLTSTVQVFTD 350
 AAV3-3 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLSFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 AAV4-4 267 STPWGYFDENREHCHFSPRDWRLLNNWGMKAMVKIFNIQKVEVTQDSTTTIANNLTSTVQVFTD
 AAV1-A 277 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.46-A 277 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.48-A 277 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.44-A 277 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.43-A 278 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 AAV6-A 277 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.34-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.47-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.29-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.63-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.56-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.45-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.57-B 275 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.35-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.58-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.28-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.51-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.19-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.49-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.52-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.13-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 AAV2-B 276 STPWGYFDENREHCHFSPRDWRLLNNWGFPRKLNFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD
 hu.20-B 276 STPWGHFDENREHCHFSPRDWRLLNNWGFPRKLSFKLENIQKVEVTQDSTTTIANNLTSTVQVFTD

FIG. 2L

hu.24-B 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.64-B 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.27-B 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.21-B 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.22-B 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.23-B 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.7-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.61-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 rh.56-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.9-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.54-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.53-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.60-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.55-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.2-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.1-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.18-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.3-C 277 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.25-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.15-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.16-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.11-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.10-C 276 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 hu.4-C 276 STPWGYFDENREHCHESPRDWQRLVNNRGRPRKRLSFKLENIQKVEVTQNDGTTTIANLSTVQVFTD
 rh.54-D 278 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTNDGVTTIANNLSTVQVFS
 rh.48-D 278 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTNDGVTTIANNLSTVQVFS
 rh.55-D 278 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTNDGVTTIANNLSTVQVFS
 rh.62-D 278 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTNDGVTTIANNLSTVQVFS
 AAV7-D 278 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTNDGVTTIANNLSTVQVFS
 rh.52-E 279 STPWGYFDENREHCHESPRDWQRLINNNWGFPRKRLSFKLENIQKVEVTQNEGTIANSITSTIQTIVFTD

FIG. 2M

rh. 51-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 39-E	279	STPWGYLDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 53-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 37-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 43-E	278	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 50-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 49-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 61-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 41-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 64-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 42-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 57-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 40-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
AAV8-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 58-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 40-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 67-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 17-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 6-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 66-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
rh. 38-E	279	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 32-F	278	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
AAV9/hu	278	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
hu. 31-F	278	STPWGYFDENREHCHESPRDWORLI	NNNWGFRPKLSFKLENIQKVEVTQNEGKTI	ANNLTSTIQVFTD
AAV5	337	DDYQLPYVVGNGTEGCLPAFPQVFTL	PQYGYATLNRD-NTENPTERSSEFCLEYP	PSKVLRTGNNFET
AAV3-3	346	SEYQLPYVLGSAHQGCLPPFPADVFMV	PQYGYLTLLNNG---SQAVGRSSFCLEYP	PSKVLRTGNNFQS
AAV4-4	337	SSYELPYVMDAGQEGSLPPFPNDVFMV	PQYGYGLVTGNTSQQQTDORNAFCLEYP	PSQVLRGTGNNFET

FIG. 2N

AAV1-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.46-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.48-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.44-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.43-A 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 AAV6-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.34-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNE---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.47-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.29-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.63-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.56-B 346 LEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.45-B 346 SGYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.57-B 345 LEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.35-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.58-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.28-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.51-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.19-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.49-B 346 SEYQLPYVPGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.52-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.13-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 AAV2-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.20-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.24-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.64-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.27-B 346 SGYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.21-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.22-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.23-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES
 hu.7-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMIPOYGYTLNNG---SOAVGRSSFYCLEYFPQSOMLRTGNFTES

FIG. 20

hu.61-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.56-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.9-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.54-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.53-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.60-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.55-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.2-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.1-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.18-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.3-C 347 SEYQLPYVPGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSPFYCLEYFPQSMLRTGNNFQS
 hu.25-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSPFYCLEYFPQSMLRTGNNFQS
 hu.15-C 346 SGYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.16-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.11-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.10-C 346 SEYQLPYVLGSAHQGCLPPFPADVFTVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNLTF
 hu.4-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.54-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.48-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.55-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.62-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLND---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 AAW7-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.52-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTPNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.51-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.39-E 349 SEYQPPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.53-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 hu.37-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.43-E 348 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.50-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGYLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS
 rh.49-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMVPOYGNLTLNNG---SQVGRSSFYCLEYFPQSMLRTGNNFQS

FIG. 2P

rh. 61-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 41-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
rh. 64-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 42-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
rh. 57-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 40-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
AAV8-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
rh. 58-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
rh. 40-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 67-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 17-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 6-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 66-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
rh. 38-E 349 SEYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 32-F 348 SDYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNDG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
AAV9/hu 348 SDYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNDG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES
hu. 31-F 348 SDYQLPYVLGSAHQCLPPFPADVFMIPQYGYLTLNDG---SQAVGRSSFYCLEYFPQSQMLRTGNNFES

AAV5 406 YNFEVPEHSSFAPSQNLFLKLANPLVDQYLYRFSVTN-----NTGGVQFNKLAGRYANTYKNWFPGP
AAV3-3 413 YTFEDVPEHSSYAHSQSLDRMLNPLIDQYLYYLNRTQGTTSQTNGSRLLFSQAGPQMSLQARNWLPGP
AAV4-4 407 YSFEKVPESHSMYAHSQSLDRMLNPLIDQYLGWLGQSTTTGTTLNAGTATTNFTKLRPTNFSNFKKNWLPGP
AAV1-A 414 YTFEEVPEHSSYAHSQSLDRMLNPLIDQYLYYLNRTQ-NQSGSAQNKDILFSRGSFAGMSVQPKNWLPGP
hu. 46-A 414 YTFEEVPLHSSCAHSQSLDRMLNPLIDQYLYYLNRTQ-NQSGSAQNKDILFSRGSFAGMSVQPKNWLPGP
hu. 48-A 414 YTFEEVPEHSSYAHSQSLDRMLNPLIDQYLYYLNRTQ-NQSGSAQNKDILFSRGSFAGMSVQPKNWLPGP
hu. 44-A 414 YTFEEVPLHSSYAHSQSLDRMLNPLIDQYLYYLNRTQ-NQSGSAQNKDILFSRGSFAGMSVQPKNWLPGP
hu. 43-A 415 YTFEEVPLHSSYAHSQSLDRMLNPLIDQYLYYLNRTQ-NQSGSAQNKDILFSRGSFAGMSVQPKNWLPGP
AAV6-A 414 YTFEDVPEHSSYAHSQSLDRMLNPLIDQYLYYLNRTQ-NQSGSAQNKDILFSRGSFAGMSVQPKNWLPGP
hu. 34-B 413 YTFEDVPEHSSYAHSQSLGRMLNPLIDQYLYYLSRTN-TPSGTTTQSRLOFSQAGASDINDQSRNWLPGP

FIG. 2Q

hu. 47-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 29-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 63-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 56-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 45-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 57-B 412 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 35-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 58-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 28-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 51-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 19-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 49-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 52-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 13-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 AAV2-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 20-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 24-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 64-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 27-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 21-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 22-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 23-B 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 7-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 61-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 rh. 56-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 9-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 54-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 53-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 60-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP
 hu. 55-C 413 YTFEDVPFHSSYAHQSQSLDRMLMNP LI DOYLYYLSTTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP

FIG. 2R

hu.2-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.1-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.18-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.3-C 414 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.25-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.15-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.16-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.11-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.10-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 hu.4-C 413 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYINKTQ-TNSGTLQOSRLLFSQAGPTNMSLOAKNWLPGP
 rh.54-D 415 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYIARTOSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
 rh.48-D 415 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYIARTOSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
 rh.55-D 415 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYIARTOSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
 rh.62-D 415 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYIARTOSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
 AAV7-D 415 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYIARTOSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
 rh.52-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.51-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 hu.39-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.53-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 hu.37-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.43-E 415 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTQ-TGCTANTQTLGFSQGGPNTMANQAKNWLPGP
 rh.50-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.49-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.61-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 hu.41-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.64-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 hu.42-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 rh.57-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 hu.40-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTOS-TGCTAGTQQLLSSQAGPSNMSAQARNWLPGP
 AAV8-E 416 YTFEDVPFHSSYAHQSQSLDRMLNPLIDQYLYYLSRTQ-TGCTANTQTLGFSQGGPNTMANQAKNWLPGP

FIG. 28

rh. 58-E 416 YTFEDVPFHSSYAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTACTQQLLFSQAGPSNMSAQARNWLPGP
rh. 40-E 416 YTFEDVPFHSSYAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTQGTQQLLFSQAGPANMSAQAQKNWLPGP
hu. 67-E 416 YTFEDVPFHSSYAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTQGTQQLLFSQAGPANMSAQAQKNWLPGP
hu. 17-E 416 YTFEDVPFHSSYAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTAGTQQLLFSQAGPNMMSAQAQKNWLPGP
hu. 6-E 416 YQFEDVPFHSSYAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTAGTQQLLFSQAGPNMMSAQAQKNWLPGP
hu. 66-E 416 YTFEDVPFHSSCAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTQGTQQLLFSQAGPANMSAQAQKNWLPGP
rh. 38-E 416 YTFEDVPFHSSYAHQSLSLDRMLNPLIDQYLYLSRTOS--TGTQGTQQLLFSQAGPANMSAQAQKNWLPGP
hu. 32-F 415 YEFENVPFHSSYAHQSLSLDRMLNPLIDQYLYLSKTINGSG--QNQOTLKFSVAGPSNMAVQGRNYIPGP
AAV9/hu 415 YEFENVPFHSSYAHQSLSLDRMLNPLIDQYLYLSKTINGSG--QNQOTLKFSVAGPSNMAVQGRNYIPGP
hu. 31-F 415 YEFENVPFHSSYAHQSLSLDRMLNPLIDQYLYLSKTINGSG--QNQOTLKFSVAGPSNMAVQGRNYIPGP

AAV5 469 MGRTOGWNILGSGVN-----RASVSFAFATNRMELEGASYQVPPQPPNGMTNNLQGSNTYALENTMIENSOP
AAV3-3_ 483 CYROQRVSKTANDN-----NNSNFPWTAASKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPMHGNLIFGKEG
AAV4-4_ 477 SIKOQGFSTANQNYKIPATGSDSLIKYETHSTLDGRWSALTGGPPMATAGPADSKFS--NSQLIFAGPKQ
AAV1-A_ 483 CYROQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMGSGVMIFGKES
hu. 46-A 483 CYROQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMGSGVMIFGKES
hu. 48-A 483 CYROQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMGSGVMIFGKES
hu. 44-A 483 CYROQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMGSGVMIFGKES
hu. 43-A 484 CYROQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMGSGVMIFGKES
AAV6-A 483 CYROQRVSKTKTDN-----NNSNFTWTGASKYNLNGRESIINPGTAMASHKDDDEKFFPMGSGVMIFGKES
hu. 34-B 482 CYROQRVSKTSADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG
hu. 47-B 482 CYROQRVSKTSADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDNEKFFPOSGLVIFGKQG
hu. 29-B 482 CYROQRVSKTSADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG
hu. 63-B 482 CYROQRVSKTSADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG
hu. 56-B 482 CYROQRVSKTAADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG
hu. 45-B 482 CYROQRVSKTSADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG
hu. 57-B 481 CYROQRVSKTAADN-----NNGEYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG
hu. 35-B 482 CYROQRVSKTSADN-----NNSYSWTGATKYHLNGRDLSLVNPGPPAMASHKDDDEKFFPOSGLVIFGKQG

FIG. 2T

hu.58-B 482 CYRQORVSKTSADN-----NNSEYSWIGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.28-B 482 CYRQORVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.51-B 482 CYRQORVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.19-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.49-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.52-B 482 CYRQORVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.13-B 482 CYRQORVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 AAV2-B 482 CYRQORVSKTSADN-----NNSEYSHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.20-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.24-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.64-B 482 CYRQORVSKTSADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.27-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.21-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.22-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.23-B 482 CYRQORVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPQSGVLIFFGKQG
 hu.7-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.61-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 rh.56-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.9-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.54-C 481 CYRQORLSKQANDN-----NNSNFPWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKEG
 hu.53-C 481 CYRQORLSKQANDN-----NNSNFPWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKEG
 hu.60-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.55-C 481 CYRQORLSKQANDN-----NNSNFPWTGATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKEG
 hu.2-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.1-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.18-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.3-C 483 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.25-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.15-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG
 hu.16-C 482 CYRQORLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNGPAMASHKDDDEKFFPMHGTLLIFFGKQG

FIG. 2U

hu.11-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYRLNGRDSLVPGPAMASHKDDERKFFPMHGTLIFGKQG
 hu.10-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDERKFFPMHGTLIFGKQG
 hu.4-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDERKFFPMHGTLIFGKQG
 rh.54-D 485 CEROQVSKTLDQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLIFGKTG
 rh.48-D 485 CEROQVSKTLDQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLIFGKTG
 rh.55-D 485 CEROQVSKTLDQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLIFGKTG
 rh.62-D 485 CEROQVSKTLDQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLIFGKTG
 AAV7-D 485 CEROQVSKTLDQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLIFGKTG
 rh.52-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.51-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 hu.39-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.53-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 hu.37-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 rh.43-E 484 CEROQVSTTSGN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.50-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.49-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.61-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 hu.41-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.64-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 hu.42-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 rh.57-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 hu.40-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 AAV8-E 485 CEROQVSTTSGN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.58-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGILMFGKQG
 rh.40-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 hu.67-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 hu.17-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 hu.6-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 hu.66-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG
 rh.38-E 485 CEROQVSTTSLQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDERFFPSSGVLMEFGKQG

FIG. 2V

hu.32-F	483	SYRQQRVSTTVTQN-----NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG	570	580	590	600	610	620	630
AAV9/hu	483	SYRQQRVSTTVTQN-----NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG							
hu.31-F	483	SYRQQRVSTTVTQN-----NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG							
AAV5	534	ANPGTATYLEGNMLITSESETQPNRVAYNYGQGMATNNOSSTTAPATGTYNLOEIVPGSVMMERDQVYL							
AAV3-3	548	T--TASNALD-NVMI TDEEEI RTTNPVATEQYGTVANLQSSNLTPTGTVNHQALPGMVWQDRDQVYL							
AAV4-4	546	N--GNTATVPG-TLIFTSEELATNTDWMGNLPGGDSNSNLTPTVDRLTALGAVPGMVWQDRDIYY							
AAV1-A	548	A--GASNTALD-NVMI TDEEEI KATNPVATERFGTVAVNFQSSSTDPATGVDVHAMGALPGMVWQDRDQVYL							
hu.46-A	548	A--GASNTALD-NVMI TDEEEI KATNPVATERFGTVAVNFQSSSTDPATGVDVHAMGALPGMVWQDRDQVYL							
hu.48-A	548	A--GASNTALD-NVMI TDEEEI KATNPVATERFGTVAVNFQSSSTDPATGVDVHAMGALPGMVWQDRDQVYL							
hu.44-A	548	A--GASNTALD-NVMI TDEEEI KATNPVATERFGTVAVNFQSSSTDPATGVDVHAMGALPGMVWQDRDQVYL							
hu.43-A	549	A--GASNTALD-NVMI TDEEEI KATNPVATERFGTVAVNFQSSSTDPATGVDVHAMGALPGMVWQDRDQVYL							
AAV6-A	548	A--GASNTALD-NVMI TDEEEI KATNPVATERFGTVAVNFQSSSTDPATGVDVHAMGALPGMVWQDRDQVYL							
hu.34-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.47-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.29-B	547	P--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.63-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.56-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.45-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.57-B	546	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.35-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.58-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.28-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.51-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.19-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.49-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.52-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							
hu.13-B	547	S--EKTINVDIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRNQAATAADVNTQGVLPGMVWQDRDQVYL							

FIG. 2W

AAV2-B 547 S--EKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNROAATADVNTQGVLPGMVWQDRDYYL
hu.20-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.24-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.64-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.27-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.21-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.22-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.23-B 547 S--GKTNDIE-KVMTDEEEIRTPNPVATEQYGSVSTNLRGNTOAATSDVNTQGVLPGMVWQDRDYYL
hu.7-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.61-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
rh.56-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.9-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.54-C 546 T--NATNAELE-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTAASSTETVNHOGALPGMVWQDRDYYL
hu.53-C 546 T--NATNAELE-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTAASSTETVNHOGALPGMVWQDRDYYL
hu.60-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.55-C 546 T--NATNAELE-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.2-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.1-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.18-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.3-C 548 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.25-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.15-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.16-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.11-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.10-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
hu.4-C 547 T--NANDADLD-NVMTDEEEIRTPNPVATEQYGVVSNLNQNSNTGPTTGTNVNHOQALPGMVWQDRDYYL
rh.54-D 550 A--TN-KTTLE-NVMTNEEEIRTPNPVATEEYGVVSNLNQNSNTAAQTQVNNQOGALPGMVWQDRDYYL
rh.48-D 550 A--AN-KTTLE-NVMTNEEEIRTPNPVATEEYGVVSNLNQNSNTAAQTQVNNQOGALPGMVWQDRDYYL
rh.55-D 550 A--AN-KTTLE-NVMTNEEEIRTPNPVATEEYGVVSNLNQNSNTAAQTQVNNQOGALPGMVWQDRDYYL
rh.62-D 550 A--AN-KTTLE-NVMTNEEEIRTPNPVATEEYGVVSNLNQNSNTAAQTQVNNQOGALPGMVWQDRDYYL

FIG. 2X

[illegible]

FIG. 2Y

AAV3-3 615 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPTTFSAPKFAFASITQYSTGQVSVEIE
AAV4-4- 613 QGPIWAKIPHDTDGHFHPSPILGGFGLKHPPPPQILIKNTVPANPATTFSTSPVNSFITQYSTGQVSQID
AAV1-A- 615 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPAEFSAFKFASITQYSTGQVSVEIE
hu.46-A 615 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPAEFSAFKFASITQYSTGQVSVEIE
hu.48-A 615 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPAEFSAFKFASITQYSTGQVSVEIE
hu.44-A 615 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPAEFSAFKFASITQYSTGQVSVEIE
hu.43-A 616 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPAEFSAFKFASITQYSTGQVSVEIE
AAV6-A 615 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPPAEFSAFKFASITQYSTGQVSVEIE
hu.34-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.47-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.29-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.63-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.56-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.57-B 613 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.35-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.58-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.28-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.51-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.19-B 614 QGPIWAKIPHDTDGHFHPSPILVGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.49-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.52-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.13-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
AAV2-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.20-B 614 QGPIWAKIPHDTDGHFHPSPPMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.24-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.64-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.27-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.21-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE
hu.22-B 614 QGPIWAKIPHDTDGHFHPSPLMGGFGLKHPPPPQILIKNTVPANPSTTSSAAKFAFASITQYSTGQVSVEIE

FIG. 22

hu.23-B 614 RGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQILIKNTVPANPSTTFSSAKFASFIQYSTGQVSVEIE
 hu.7-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.61-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 rh.56-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.9-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.54-C 613 RGPWAKI PHADGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.53-C 613 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.60-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.55-C 613 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.2-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.1-C 614 QGPWAKI PHTDGHFHPSPLTGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.18-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.3-C 615 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKSTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.29-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.15-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.16-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.11-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.10-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 hu.4-C 614 QGPWAKI PHTDGHFHPSPLMGGFGLKHPPPQIMIKNTVPANPTNFSSAKFASFIQYSTGQVSVEIE
 rh.54-D 616 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPANPEVFTPAKFASFIQYSTGQVSVEIE
 rh.48-D 616 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPANPEVFTPAKFASFIQYSTGQVSVEIE
 rh.55-D 616 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPANPEVFTPAKFASFIQYSTGQVSVEIE
 rh.62-D 616 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPANPEVFTPAKFASFIQYSTGQVSVEIE
 AAV7-D 616 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPANPEVFTPAKFASFIQYSTGQVSVEIE
 rh.52-E 617 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPADPPTAFNQAKLNSFIQYSTGQVSVEIE
 rh.51-E 617 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPADPPTAFNQAKLNSFIQYSTGQVSVEIE
 hu.39-E 617 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPADPPTAFNQAKLNSFIAQYSTGQVSVEIE
 rh.53-E 617 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPADPPTAFNQAKLNSFIQYSTGQVSVEIE
 hu.37-E 617 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPADPPTFSQAKLASFIQYSTGQVSVEIE
 rh.43-E 615 QGPWAKI PHTDGNFHPSPLMGGFGLKHPPPQILIKNTVPADPPTTFNQSKLNSFIQYSTGQVSVEIE

FIG. 2AA

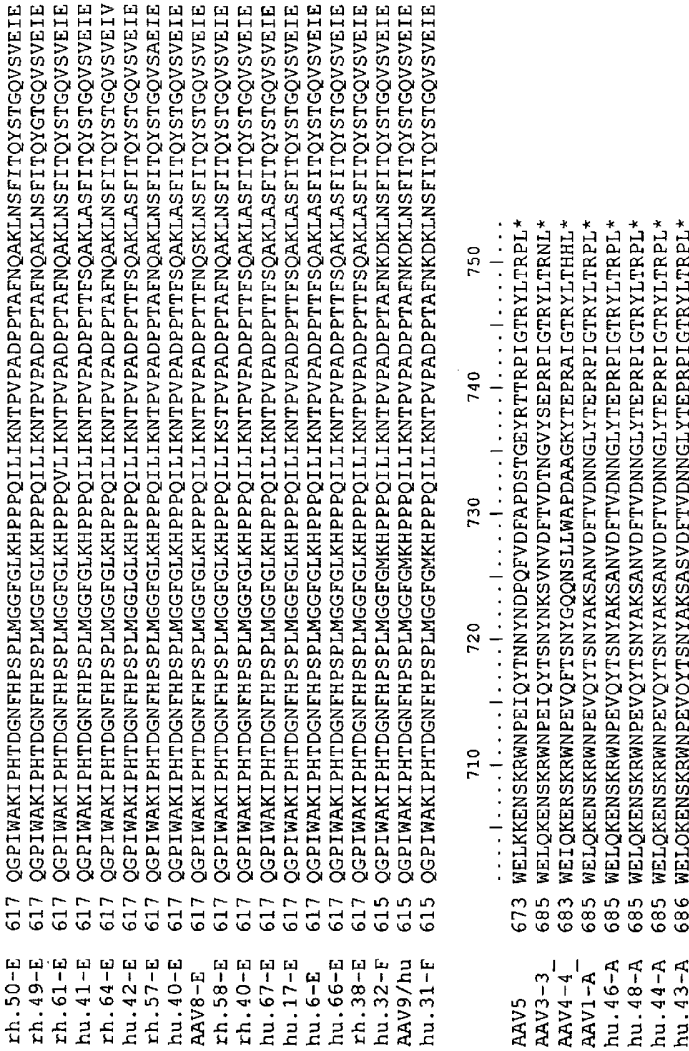


FIG. 2AB

AAV6-A 685 WELOKENSKRWNPEVQYTSNYAKSANVDFTVDNNGLYTEPRPIGTRYLTRNL*
hu.34-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.47-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.29-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.63-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.56-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.45-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.57-B 683 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.35-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.58-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.28-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.51-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.19-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.49-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.52-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.13-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
AAV2-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.20-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.24-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.64-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.27-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.21-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.23-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.22-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.23-B 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.61-C 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
rh.56-C 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.9-C 684 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.54-C 683 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.53-C 683 WELOKENSKRWNPEIQYTSNYKSNVNDFTVDTNGVYSEPRPIGTRYLTRNL*

FIG. 2AC

hu.60-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.55-C	683	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.2-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.1-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.18-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.3-C	685	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.25-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.15-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.16-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.11-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.10-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.4-C	684	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.54-D	686	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.48-D	686	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.55-D	686	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.62-D	686	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
AAV7-D	686	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.52-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.51-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.39-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.53-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.37-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.43-E	685	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.50-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.49-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.61-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.41-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.64-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
hu.42-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*
rh.57-E	687	WELQKENS	KRWNP	EIOYTSN	YKSNV	NVDF	TVDTNG	VYSE	PRPIG	TRYLTRNL*

FIG. 2AD

hu.40-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	AVNTEGTYSEPR	PIGTRYLTRNL*
AAV8-E	687	WELQENSKRWNP	EQYTSNYYKSTSVDF	AVNTEGVYSEPR	PIGTRYLTRNL*
rh.58-E	687	WELQENSKCWN	PEIQYTSNYYKSTNVDF	AVNTEGVYSEPR	PIGTRYLTRNL*
rh.40-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	AVNSEGTYSSEPR	PIGTRYLTRNL*
hu.67-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	AVNTEGTYSEPR	PIGTRYLTRNL*
hu.17-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	TVDN	GVYSEPRPIGTRYLTRNL*
hu.6-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	AVNTEGTYSEPR	PIGTRYLTRNL*
hu.66-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	AVNTEGTYSEPR	PIGTRYLTRNL*
rh.38-E	687	WELQENSKRWNP	EQYTSNYYKSTNVDF	AVNTEGTYSEPR	PIGTRYLTRNL*
hu.32-F	685	WELQENSKRWNP	EQYTSNYYKSNVFE	AVNTEGVYSEPR	PIGTRYLTRNL*
AAV9/hu	685	WELQENSKRWNP	EQYTSNYYKSNVFE	AVNTEGVYSEPR	PIGTRYLTRNL*
hu.31-F	685	WELQENSKRWNP	EQYTSNYYKSNVFE	AVNTEGVYSEPR	PIGTRYLTRNL*

FIG. 2AE

hu.27-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.21-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.22-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.23-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.7-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.61-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
rh.56-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.9-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.54-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.53-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.60-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.55-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.2-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.1-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.18-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.3-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.25-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.15-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.16-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.11-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.10-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
hu.4-C	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACTCTCTCTGAAGGAATTAAGACAGTGGTGG
rh.54-D	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
rh.48-D	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
rh.55-D	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
rh.62-D	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
AAV7-D	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
rh.52-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
rh.51-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG
hu.39-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACACCTCTCTGAGGGCATTCGCCGAGTGGTGG

FIG. 3B

[illegible]

FIG. 3C

hu. 48-A	71	ACTTGAACCTGGAGCCCGAAGCCCAAGCAACAGCAAAAGCAGGACGACGCGCCGGGTCTTGCT
hu. 44-A	71	AGCTCAGACCTGGCCACACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 43-A	71	ACCTGAACCTGGAGCCCGAAGCCCAAGCAACAGCAAAAGCAGGACGACGCGCCGGGTCTTGCT
AAV6-A	71	ACTTGAACCTGGAGCCCGAAGCCCAAGCAACAGCAAAAGCAGGACGACGCGCCGGGTCTTGCT
hu. 34-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 47-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 29-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 63-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 56-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 45-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 57-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 35-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 58-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 28-B	71	AACTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 51-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 19-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 49-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 52-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 13-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
AAV2-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 20-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 24-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 64-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 27-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 21-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 22-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 23-B	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 7-C	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
hu. 61-C	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT
rh. 56-C	71	AGCTCAAACTGGCCACACCAAGCCCGCAGAGCGGCATTAAGGACGACGAGGGGTCTTGCT

FIG. 3D

hu. 9-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGAGCGGCATCAGGACAAACAGCAGGGGCTTTGTGCT
hu. 54-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 53-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 50-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 55-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 2-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 1-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 18-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 3-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 25-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 15-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 16-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 11-C	71	AGCTCAAACTGGGCCACACCAACCAAGCCGACAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
hu. 10-C	71	AGCTCAAACTGGGCCACACCAACCAAGCTCGCAGAGCGGCATAAGGACGACAGCAGGGGCTTTGTGCT
rh. 54-D	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 48-D	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 55-D	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 62-D	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
AAV7-D	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 52-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 51-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 39-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 53-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 37-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 43-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 50-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 49-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 61-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT
rh. 41-E	71	AGCTGAAACTTGGAGCCCGAAACCCAAAGCCAAACGACGAAAGCAGACGCGCCGGGGCTTGGTGCT

FIG. 3E

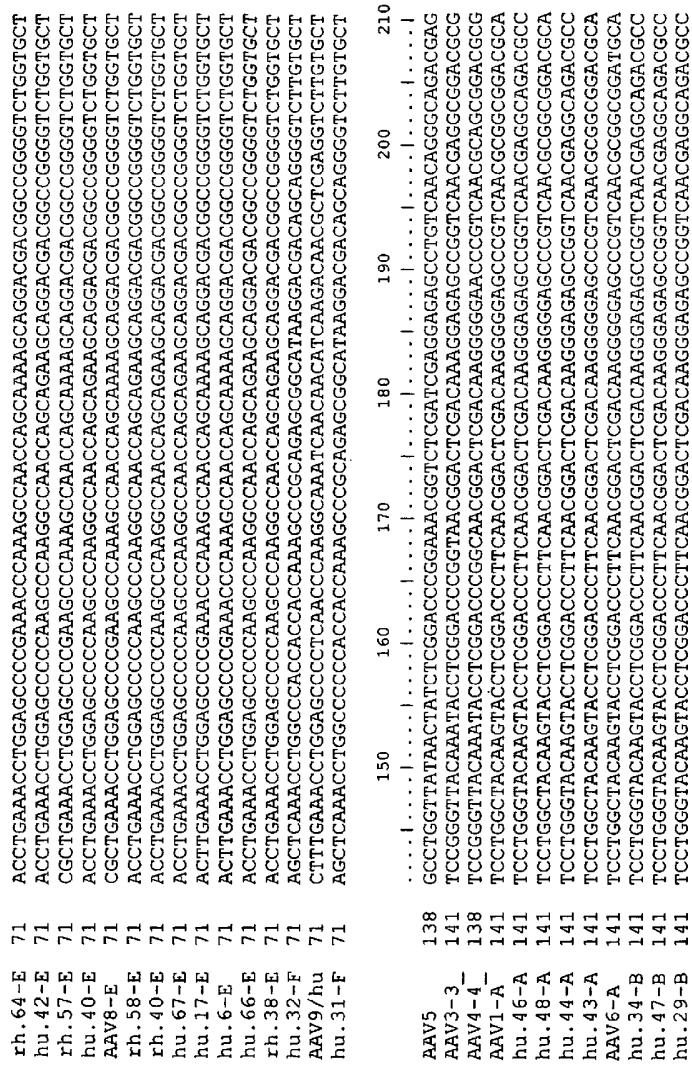


FIG. 3F

hu. 63-B	141	TCCTGGGTACAAGTACCTTGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 56-B	141	TCCTGGTACAAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 45-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 57-B	138	TCCTGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 35-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 58-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 28-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 51-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 19-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 49-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 52-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 13-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
AAV2-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 20-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 24-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 64-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 27-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 21-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 22-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 23-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 7-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 61-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
xh. 56-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 9-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 54-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 53-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 60-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 55-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 2-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC
hu. 1-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGAGAGCCGGTCAACGAGGCAGACGCC

FIG. 36

hu. 18-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 3-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 25-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 15-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 16-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 11-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 10-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 4-C	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 54-D	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 48-D	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 55-D	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 62-D	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
AAV7-D	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 52-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 51-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 39-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 53-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 37-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 43-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 50-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 49-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 61-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 41-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 64-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 42-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 57-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
hu. 40-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
AAV8-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 58-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC
rh. 40-E	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGCAAGGGAGAGCCGGTCAACGAGGACAGAGCC

FIG. 3H

hu. 67-E	141	TCTTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAATGCGGCGGAGCGCA
hu. 17-E	141	TCCTGGCTGCAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGCGGAGCGCA
hu. 6-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGCGGAGCGCA
hu. 66-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGCGGAGCGCA
rh. 38-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGCGGAGCGCA
hu. 32-F	141	TCCTGGGTACAAGTACCTCGGACCCCGGCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGAGAGCGCG
AAV9/hu	141	TCGGGTACAAGTACCTTGGACCCCGGCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGAGAGCGCG
hu. 31-F	141	TCCTGGGTACAAGTACCTCGGACCCCGGCAACGGACTCGACAAAGGGGAGCCCGTCAAGCGAGAGCGCG
AAV5	208	
AAV3-3	211	GTGCGCGGAGAGCAGACATCTCGTACAACGAGCAGCTTGAGGGGGGAGACAAACCCCTACCTCAAGTACA
AAV4-4	208	GCAGCCCTCGAACACAGCAAGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
AAV1-A	211	GCAGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 46-A	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 48-A	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 44-A	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 43-A	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
AAV6-A	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 34-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 47-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 29-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 63-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 56-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 45-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 57-B	208	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 35-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA
hu. 58-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACG
hu. 28-B	211	GCGGCCCTCGAGCAGCAAGGCTTAGGACCCAGCAGCTCAAGGCGGGTACAAACCCCTACCTCAAGTACA

FIG. 31

hu.51-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.19-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.49-B	211	GCGGCCCTCGAGTACGACAAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.52-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.13-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
AAV2-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.20-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.24-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.64-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.27-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.21-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.22-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.23-B	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.7-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.61-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
rh.56-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.9-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.54-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.53-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.60-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.55-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.2-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.1-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.18-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.3-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.25-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.15-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.16-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.11-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA
hu.10-C	211	GCGGCCCTCGAGCAGCAGCAAGGCTTACGACCGGCGAGCTCGACAGCGGAGACACCCCGTACCTCAAGTACA

FIG. 3J

hu. 4-C	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCGACAGGGGAGACAACCCGTACCTCAAGTACA
rh. 54-D	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 48-D	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 55-D	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 62-D	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
AAV7-D	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 52-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 51-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 39-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 53-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 37-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 43-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 50-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 49-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 61-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 41-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 64-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 42-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 57-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 40-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
AAV8-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 58-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 40-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 67-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 17-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 6-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 66-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
rh. 38-E	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
hu. 32-F	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA
AAV9/hu	211	GCGGCCCTCGAGCAGCAGCAAGGCCTAGCAGCCGGCAGCTCAAGAGGGGTGACAATCCGTACCTGCGGGTATA

FIG. 3K

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hu.31-F 211 GCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAGGCGCGGAGACAACCCGTACCTCAAGTACA
          290      300      310      320      330      340      350
AAV5      278 ACCAGCGGACGCGGAGTTTCAGGAGAGCTCGCCGACGACATCCTTCGGGGGAAACCTCGGAAGGC
          281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTTGGGACGAGC
AAV3-3    281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTTGGGACGAGC
AAV4-4-   278 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGCGGCTTCAGGCGACATCGCTTGGGGCAACCTCGGACGAGC
AAV1-A    281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTCGGCGGAGC
hu.46-A   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGCGGAGC
hu.48-A   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTCGGCGGAGC
hu.44-A   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTCGGCGGAGC
hu.43-A   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTCGGCGGAGC
AAV6-A    281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAAGATACGTCCTTGGGGGCAACCTCGGCGGAGC
hu.34-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.47-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.29-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.63-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.56-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.45-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.57-B   278 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.35-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.58-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.28-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.51-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.19-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.49-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.52-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.13-B   281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
AAV2-B    281 ACCAGCGGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC
hu.20-B   281 ACCAGGTGACGCGGAGTTTCAGGAGAGCTTCAGGAGCGCTTAAGAAGATACGTCCTTGGGGGCAACCTCGGACGAGC

```

FIG. 3L

hu. 24-B 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 64-B 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 27-B 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 21-B 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 22-B 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 23-B 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 7-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 61-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 rh. 56-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 9-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 54-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 53-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 60-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 55-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 2-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 1-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 18-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 3-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 25-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 15-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 16-C 281 ACCAGCCGCGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 11-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 10-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 hu. 4-C 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 rh. 54-D 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 rh. 48-D 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 rh. 55-D 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 rh. 62-D 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 AAV7-D 281 ACCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC
 rh. 52-E 281 ATCAGCCGACGCGGAGTTTCAGGAGCGCTTAAAGAGATACGTCCTTTTGGGGCAACCTCGGACGAGC

FIG. 3M

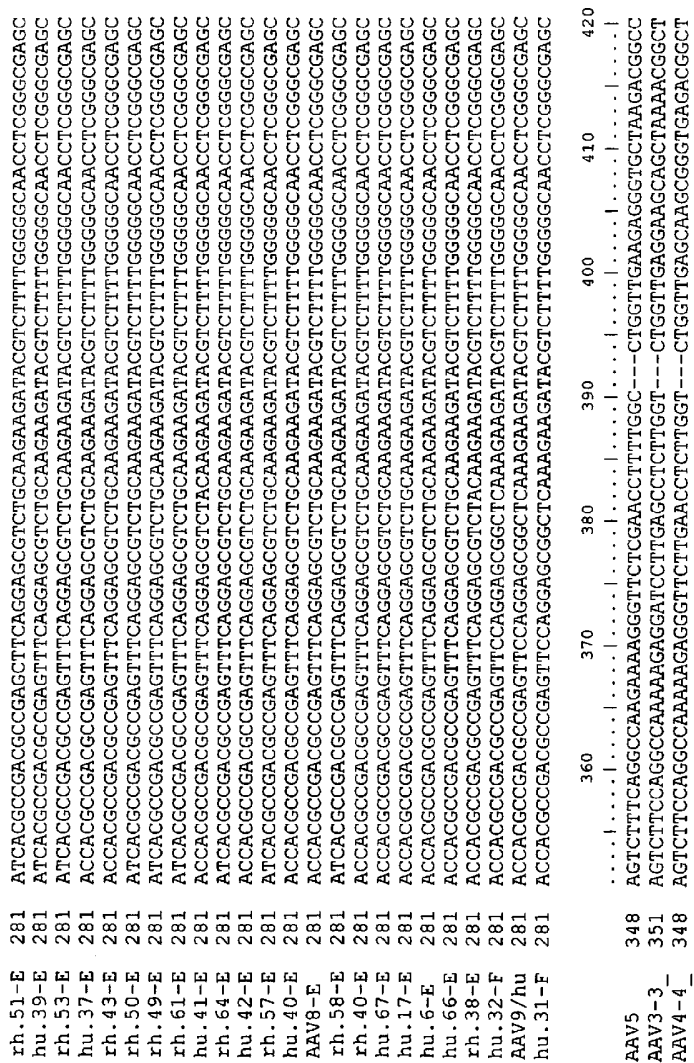


FIG. 3N

AAV1-A	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 46-A	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 48-A	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 44-A	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 43-A	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
AAV6-A	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 34-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 47-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 29-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 63-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 56-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 45-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 57-B	348	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 35-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 58-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 28-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 51-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 19-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 49-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 52-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 13-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
AAV2-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 20-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 24-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 64-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 27-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 21-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 22-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 23-B	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
hu. 7-C	351	AGTCTTCCAGGCCAAGAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT

FIG. 30

hu. 61-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 56-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 9-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 54-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 53-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 60-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 55-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 2-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 1-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 18-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 3-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 25-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 15-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 16-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 11-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 10-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 4-C 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 54-D 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 48-D 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 55-D 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 62-D 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 AAV7-D 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 52-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 51-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 39-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 53-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 hu. 37-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 43-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 50-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT
 rh. 49-E 351 AGTCTTCCAGGCGCAAAAAGAGAGGGTTCTTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAACGGCT

FIG. 3P

rh. 61-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 41-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CCGGTTGAGGAAGCTGCTAAGACGGCT
rh. 64-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 42-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
rh. 57-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 40-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
AAV8-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
rh. 58-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
rh. 40-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 67-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 17-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 6-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 66-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
rh. 38-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 32-F	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
AAV9/hu	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 31-F	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
....		
AAV5	415	CCTACCGGAAAGCGGATAGACGACCACTTTCCA-----GACCGGACTCATCTGTGTTGGCAAT
AAV3-3	418	CCTGGAAGAAGGGGCTGTAGATCAGTCTCTAG-----CAGCCGACTCTCCACGGGTATCGCAAAA
AAV4-4	415	CCTGGAAGAAGAGACCGTTGATTGAATCCCCCAG-----CAGCCGACTCTCCACGGGTATCGCAAAA
AAV1-A	418	CCTGGAAGAAGACGTCGGGTAGAGCAGTCCGACAA---GAGCCAGACTCTCTCGGGCATCGCAAGA
hu. 46-A	418	CCTGGAAGAAGACGTCGGGTAGAGCAGTCCGACAA---GAGCCAGACTCTCTCGGGCATCGCAAGA
hu. 48-A	418	CCTGGAAGAAGACGTCGGGTAGAGCAGTCCGACAA---GAGCCAGACTCTCTCGGGCATCGCAAGA
hu. 44-A	418	CCTGGAAGAAGACGTCGGGTAGAGCAGTCCGACAA---GGCCAGACTCTCTCGGGCATCGCAAGA
hu. 43-A	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCAGACTCTCTCCACGGGCATCGCAAGA
AAV6-A	418	CCTGGAAGAAGACGTCGGGTAGAGCAGTCCGACAA---GAGCCAGACTCTCTCTCGGGCATCGCAAGA
hu. 34-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAAACCGGAAAGG

FIG. 30

hu. 47-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAGG
 hu. 29-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGCA---GAGCCAGACTCTCTCTCGGGAACCGGAAAGT
 hu. 63-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 56-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 45-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 57-B 415 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 35-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 58-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 28-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGCA---GAGCCAGACTCTCTCTCGGGAACCGGAAAGT
 hu. 51-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 19-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 49-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 52-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 13-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 AAV2-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 20-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 24-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 27-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 21-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 22-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 23-B 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 7-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 61-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 rh. 56-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 9-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 54-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 53-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 60-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG
 hu. 55-C 418 CCGGGAAGAGAGGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGAACCGGAAAG

FIG. 3R

hu.2-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.1-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.18-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.3-C	421	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.25-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.15-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.16-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.11-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.10-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
hu.4-C	418	CCGGGAAAAAGAGCGCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCTCGGGACCGGAAAAAG
rh.54-D	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.48-D	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.55-D	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.62-D	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
AAV7-D	418	CCTGCAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.52-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.51-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
hu.39-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.53-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
hu.37-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.43-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.50-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.49-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.61-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
hu.41-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.64-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
hu.42-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
rh.57-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
hu.40-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA
AAV8-E	418	CCTGGAAAGAGAGACCGGTAGAGCGGTACCTCAGCGTTCCCGGACTCTCCACGGGCAATCGGCAAGA

FIG. 35

rh. 58-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
rh. 40-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
hu. 67-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
hu. 17-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
hu. 6-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
hu. 66-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
rh. 38-E	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
rh. 32-F	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
AAV9/hu	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
hu. 31-F	418	CCTGGAAGAGACCGGTAGAACCGTCACCTACGCGTTCCCGGACTCCTCCACGGGATCGGCAAGA
AAV5	452	GAAGAAGGCTCGGACCGAAGAGGACTCCAGCCTTCCCTCAGACGCGGAGCTGGACCCGAGCGG
AAV3-3	485	CGGCAACAGCCTGCCAGAAAAGACTAAATTCGGTCAGACTGGAGACTCAGAGTCAGTCCCGAC--
AAV4-4	482	AAGCAAGCAGCCGCTAAAGAGAGCTCGTTTCGAAACGAACTGGAGGAGGACGACCC----
AAV1-A	485	CAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAT--
hu. 46-A	485	CAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAT--
hu. 48-A	485	CAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAT--
hu. 44-A	485	CAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAT--
hu. 43-A	488	AAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAC--
AAV6-A	485	CAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAC--
hu. 34-B	485	CAGGCCAGCAGCCCGCTAAAGAGAGACTCAATTTGGTCAGACTGGGCACTCAGAGTCAGTCCCGAC--
hu. 47-B	485	CGGCCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--
hu. 29-B	485	CGGCCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--
hu. 63-B	485	CGGCCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--
hu. 56-B	485	CGGCAACAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--
hu. 45-B	485	CGGCCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--
hu. 57-B	482	CGGCAACAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--
hu. 35-B	485	CGGCCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGAGACTCAGTACCTGAC--

FIG. 31

hu. 58-B 485 CGGGCAACCCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 28-B 485 CGGGCAACCCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACTCCGTTACCTGAC--
 hu. 51-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 19-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 49-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 52-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 13-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 AAV2-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 20-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 24-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 64-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 27-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 21-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 22-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 23-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 7-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 61-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 rh. 56-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 9-C 485 CGGGCCATCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 54-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 53-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 60-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 55-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 2-C 485 CGGGCCAGCGGCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 1-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 18-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 3-C 488 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 25-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 15-C 485 CGGGCAACCCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--
 hu. 16-C 485 CGGGCAACCCAGCCTGCAAGAAAGAGATTGAATTTGGTTCAGACTGGAGACGGCAGACTCCGTTACCTGAC--

FIG. 3U

hu.11-C 485 CGGCCATCAGCCTGCGAGAAAGAGATTGATTTTGGTCAGACTGGAGCGCAGACTCCGTACCTGAC--
 hu.10-C 485 CGGCCATCAGCCTGCGAGAAAGAGATTGATTTTGGTCAGACTGGAGCGCAGACTCCGTACCTGAC--
 hu.4-C 485 CGGCCAGCAGCCTGCGAGAAAGAGATTGATTTTGGTCAGACTGGAGCGCAGACTCCGTACCTGAC--
 rh.54-D 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.48-D 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.55-D 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.62-D 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 AAV7-D 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.52-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.51-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.39-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.53-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.37-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.43-E 485 AAGGCCAACAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.50-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.49-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.61-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.41-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.64-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.42-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.57-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.40-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 AAV8-E 488 AAGGCCAACAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.58-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.40-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.67-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.17-E 488 CAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.6-E 488 CAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 hu.66-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--
 rh.38-E 488 AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACCTTTGGGAGACTGGGAGCTCAGAGTCAGTCCCGGAC--

FIG. 3V

hu.32-F	485	CGGGTTACAGCCCGCTAAAGAAGAACTCAATTTTCGGTCAGACTGGGCACACAGAGTCAGTCCCGGAC---
AAV9/hu	485	CGGGTGCACAGCCCGCTAAAGAAGAACTCAATTTTCGGTCAGACTGGGCACACAGAGTCAGTCCCGGAC---
hu.31-F	485	CGGGTTACAGCCCGCTAAAGAAGAACTCAATTTTCGGTCAGACTGGGCACACAGAGTCAGTCCCGGAC---
AAV5	522	
AAV3-3	552	ATCCAGAGCTGCAATCCAGCCCAACAGCCTCAAGTTTGGGAGCTGATACAAATGTCTGCGGAGGT
AAV4-4	552	-CCTCAACTCTCGGAGAACACACAGCAGCCGCCACAATTTGGGATCTAATACAATGGCTTCAGGCGGT
AAV1-A	546	-----CCTGAGGGATCAACTTCGGAGCCATGCT-----GATGACAGTGAGATGGCTGCGCAGAGT
hu.46-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT
hu.48-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT
hu.44-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT
hu.43-A	555	-CCTCAACCAATCGGAGAACACACAGCAGCCCGCTGCTGTGGGATCTGGTACAAATGGCTGCAGGCGGT
AAV6-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT
hu.34-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.47-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.29-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.63-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.56-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.45-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.57-B	549	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.35-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.58-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.28-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.51-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.19-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.49-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.52-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT
hu.13-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCGCTCTGCTCTGGGAACTAATACGATGGCTTACAGGCAGT

FIG. 3W

AAV2-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 20-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 24-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 64-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 27-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 21-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 22-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 23-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT
hu. 7-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 61-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
rh. 56-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 9-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 54-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 53-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 60-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 55-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 2-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 1-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 18-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 3-C	555	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 25-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 15-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 16-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 11-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 10-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 4-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
rh. 54-D	555	-CCTCAACCTCTCGGAGAACCCAGCAGCCCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT
rh. 48-D	555	-CCTCAACCTCTCGGAGAACCCAGCAGCCCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT
rh. 55-D	555	-CCTCAACCTCTCGGAGAACCCAGCAGCCCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT
rh. 62-D	555	-CCTCAACCTCTCGGAGAACCCAGCAGCCCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT

FIG. 3X

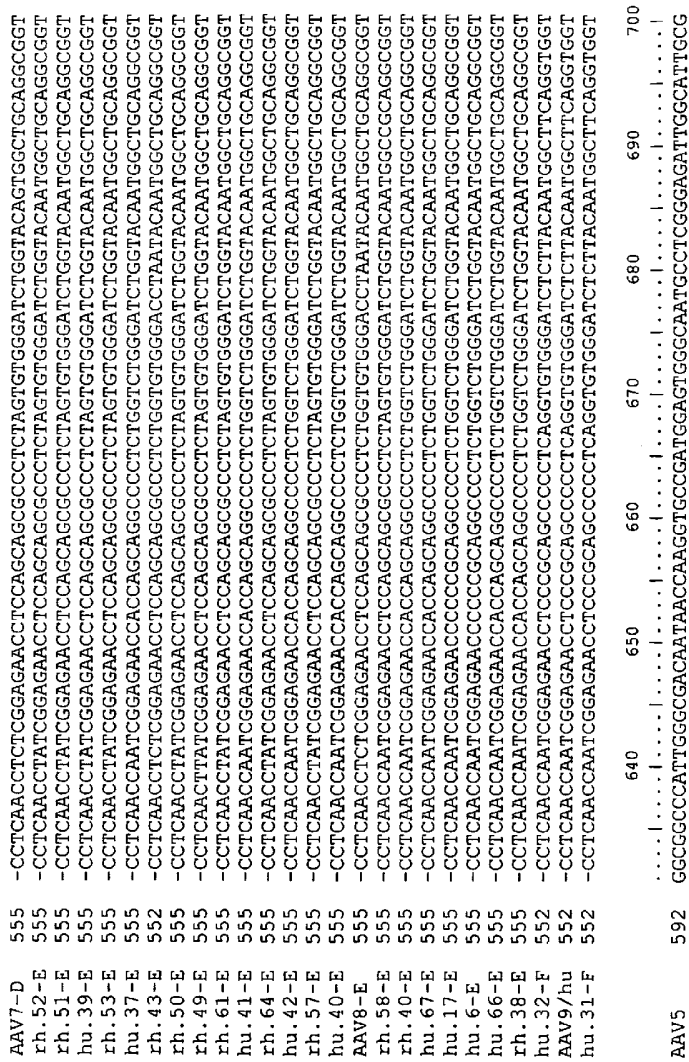


FIG. 3V

AAV3-3	622	GGCGACCAATGGCAGACAATAACGAGGGTCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
AAV4-4	604	GGCGAGCTGCAGTCGAGGGCGGACAAAGGCGCGATGGAGTGGTAATTCCTCGGGTGAATTGGCATTGCG
AAV1-A	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.46-A	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.48-A	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.44-A	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.43-A	625	GGCGTCCCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
AAV6-A	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.34-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.47-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.29-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.63-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.56-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.45-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.57-B	619	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.35-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.58-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.28-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.51-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.19-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.49-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.52-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.13-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
AAV2-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.20-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.24-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.64-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.27-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.21-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu.22-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG

FIG. 32

hu. 23-B	622	GGCGACCAATGGCAGACAAATAACGAGGGGCGCGACGGAGTGGGTAATCTCTCGGAAATTTGGCATTGCG
hu. 7-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 61-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 56-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 9-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 54-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 53-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 60-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 55-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 2-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 1-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 18-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 3-C	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 25-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 15-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 16-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 11-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 10-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 4-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 54-D	625	GGCGTCCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 48-D	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 55-D	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 62-D	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
AAV7-D	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 52-E	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 51-E	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 39-E	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 53-E	625	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
hu. 37-E	625	GGCGTCCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG
rh. 43-E	622	GGCGACCAATGGCAGACAAATAACGAGGGTGGCGATGGAGTGGGTAATCTCTCAGGAAATTTGGCATTGCG

FIG. 3AA

rh. 50-E	625	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	710
rh. 49-E	625	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	720
rh. 61-E	625	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	730
hu. 41-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	740
rh. 64-E	625	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	750
hu. 42-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	760
rh. 57-E	625	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	770
hu. 40-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
AAV8-E	625	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
rh. 58-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
hu. 67-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
hu. 17-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
hu. 6-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
hu. 66-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
rh. 38-E	625	GGCGTCCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
hu. 32-F	622	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
AAV9/hu	622	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
hu. 31-F	622	GGCGCACCAATGGCAGACAAATAACGAGGTGCCGACGGAGTGGTAGTTCTCTCGGGAAATTGGCATTTGCG	
AAV5	662		
AAV3-3	692	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	
AAV4-4	674	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	
AAV1-A	692	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	
hu. 46-A	692	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	
hu. 48-A	692	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	
hu. 44-A	692	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	
hu. 43-A	695	ATTCACATGGGTGGGGACAGAGTCTACCACTCCACCCAGACACCACTGGGTCTGCCCACTACACAA	

FIG. 3AB

AAV6--A	692	ATTCCACATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACATGGGCTT	GGCCACCTATAACAA
hu. 34-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 47-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 29-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 63-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 56-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 45-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 57-B	689	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 35-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 58-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 28-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 51-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 19-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 49-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 52-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 13-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
AAV2-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 24-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 64-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 27-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 21-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 22-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 23-B	692	ATTCCACATGGATGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 7-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 61-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
rh. 56-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 9-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 54-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA
hu. 53-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCCACAGCAGCCCGAACCTGGGCTT	GGCCACCTATAACAA

FIG. 3AC

hu. 60-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCCGGACCTGGGCGCTGCCACCTACACAA
hu. 55-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCCGGACCTGGGCGCTGCCACCTACACAA
hu. 2-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCCGGACCTGGGCGCTGCCACCTACACAA
hu. 1-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCCGGACCTGGGCGCTGCCACCTACACAA
hu. 18-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCCGGACCTGGGCGCTGCCACCTACACAA
hu. 3-C	695	ATTCCCAATGGCTGGGCGACAGAGTCA	TCCGACACAGACCTGGGCGCTGCCACCTACACAA
hu. 25-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 15-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 16-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 11-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 10-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 4-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 54-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 48-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 55-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 62-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
AAV7-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 52-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 51-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 39-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 53-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 37-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 43-E	692	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 50-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 49-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 61-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 41-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 64-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
hu. 42-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA
rh. 57-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACACACAGACACCTGGGCGCTGCCACCTACACAA

FIG. 3AD

hu.40-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
AAV8-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
rh.58-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
rh.40-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
hu.67-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
hu.17-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
hu.6-E	695	ATTCCGATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
hu.66-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
rh.38-E	695	ATTCCACATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
hu.32-F	692	ATTCCCAATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
AAV9/hu	692	ATTCCCAATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
hu.31-F	692	ATTCCCAATGGCTGGGACACAGAGTCATACACACAGACCCCAACCTGGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
AAV5	732	CCACAGTACCGAGAGATCAAAAGC---GGCTCGTCGACGGAGCAACGCCCAACGCTACTTTGGATAC	780	790	800	810	820	830	840
AAV3-3	762	CCATCTCTACAAAGCAATCTCC-----AGCCAATCAGAGCTTCAACGACCAACCACTACTTTGGCTAC	780	790	800	810	820	830	840
AAV4-4	744	CCACCTCTACAAAGCGACTCGGA-----GAGAGCTTCAGTCCAAACACCTACAACGGATTTC	780	790	800	810	820	830	840
AAV1-A	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.46-A	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.48-A	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.44-A	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.43-A	765	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
AAV6-A	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.34-B	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.47-B	762	CCACCTCTACAAAGCAATCTCCAGT---GTTCAACGGGGGCGAGCAACGACCAACCTACTTCGGCTAC	780	790	800	810	820	830	840
hu.29-B	762	CCATCTGTACAAAGCAATATCC-----AGCCAGTCTGGAGCGAGCAACGACCAATCCTACTTTGGCTAC	780	790	800	810	820	830	840
hu.63-B	762	CCACCTCTACAAAGCAGATTTCG-----AGCCAAATCAGGAGCCTCAACGACCAACCTACTTTGGCTAC	780	790	800	810	820	830	840
hu.56-B	762	CCACCTCTACAAAGCAGATTTCG-----AGCCAAATCAGGAGCCTCAACGACCAACCTACTTTGGCTAC	780	790	800	810	820	830	840
hu.45-B	762	CCACCTCTACAAAGCAGATTTCG-----AGCCAAATCAGGAGCCTCAACGACCAATCCTACTTTGGCTAC	780	790	800	810	820	830	840

FIG. 3AE

hu. 57-B	759	CCACCTCTACAAGCAGATTTC	-----AGCCAATCAGAGGCCAGCAATGACAACCACTACTTTGGCTAC
hu. 35-B	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTGAAAGCAATCACTACTTTGGCTAC
hu. 58-B	762	CCATCTGTACAAGCAGATTTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 28-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 51-B	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTGAAAGCAATCACTACTTTGGCTAC
hu. 19-B	762	CCATCTGTACAAGCAGATTTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 49-B	762	CCATCTGTACAAGCAGATTTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 52-B	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTGAAAGCAATCACTACTTTGGCTAC
hu. 13-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
AAV2-B	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTGAAAGCAATCACTACTTTGGCTAC
hu. 20-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 24-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 64-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 27-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 21-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 22-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 23-B	762	CCATCTGTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 7-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 61-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
rh. 56-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 9-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 54-C	762	CCACCTTTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 53-C	762	CCACCTTTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 60-C	762	CCACCTTTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 55-C	762	CCACCTTTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 2-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 1-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCAGCAACGACAACTACTTTGGCTAC
hu. 18-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 3-C	765	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC
hu. 25-C	762	CCACCTCTACAAGCAAAATTC	-----AGCCAATCAGAGGCCCTCAAACGACAACTACTTTGGCTAC

FIG. 3AF

hu. 15-C	762	CCACCTCTACAGCAAAATCTCC-----AGCCAAATCAGGAGCCTCAAACGCAACCACTACTTTGGCTAC
hu. 16-C	762	CCACCTCTACAGCAAAATCTCC-----AGCCAAATCAGGAGCCTCAAACGCAACCACTACTTTGGCTAC
hu. 11-C	762	CCACCTCTACAGCAAAATCTCC-----AGCCAAATCAGGAGCCTCAAACGCAACCACTACTTTGGCTAC
hu. 10-C	762	CCACCTCTACAGCAAAATCTCC-----AGCCAAATCAGGAGCCTCAAACGCAACCACTACTTTGGCTAC
hu. 4-C	762	CCACCTCTACAGCAAAATCTCC-----AGCCAAATCAGGAGCCTCAAACGCAACCACTACTTTGGCTAC
rh. 54-D	765	CCACCTCTACAGCAAAATCTCCAGT---CAGTCAGCAGGTAGCAACCAACGCACTACTTTGGCTAC
rh. 48-D	765	CCACCTCTACAGCAAAATCTCCAGT---CAGTCAGCAGGTAGCAACCAACGCACTACTTTGGCTAC
rh. 48-D	765	CCACCTCTACAGCAAAATCTCCAGT---CAGTCAGCAGGTAGCAACCAACGCACTACTTTGGCTAC
rh. 55-D	765	CCACCTCTACAGCAAAATCTCCAGT---CAGTCAGCAGGTAGCAACCAACGCACTACTTTGGCTAC
rh. 62-D	765	CCACCTCTACAGCAAAATCTCCAGT---CAGTCAGCAGGTAGCAACCAACGCACTACTTTGGCTAC
AAV7-D	765	CCACCTCTACAGCAAAATCTCCAGT---GAAACTTCAGGTAGTACCAACGCAACCACTACTTTGGCTAC
rh. 52-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 51-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 39-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 53-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
hu. 37-E	765	CCACCTCTACAGCAAAATCTCCAAATGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
rh. 43-E	762	CCACCTCTACAGCAAAATCTCCAACGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
rh. 49-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 49-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 61-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
hu. 41-E	765	CCACCTCTACAGCAAAATCTCCAAATGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
rh. 64-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 42-E	765	CCACCTCTACAGCAAAATCTCCAAATGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
rh. 57-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
hu. 40-E	765	CCACCTCTACAGCAAAATCTCCAAATGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
AAV8-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
rh. 58-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACCTCGGGAGCAGCAACCAACCACTACTTTGGCTAC
rh. 40-E	765	CCACCTCTACAGCAAAATCTCCAAATGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
rh. 67-E	765	CCACCTCTACAGCAAAATCTCCAAATGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
hu. 17-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC
hu. 16-E	765	CCACCTCTACAGCAAAATCTCCAACGGGACATCGGGAGGAGCCACCAACCACTACTTTGGCTAC

FIG. 3AG

765	hu. 66-E	CGACCTCTACAAGCAAAATATCCAATGGGACATCGGAGGAAGAGCAACCAAGCAACAACCTACTTGGGTAC	850	860	870	880	890	900	910
765	rh. 38-E	CGACCTCTACAAGCAAAATATCCAATGGGACATCGGAGGAAGAGCAACCAAGCAACAACCTACTTGGGTAC							
762	hu. 32-F	CGACCTCTACAAGCAAAATCTCCACAGCACAATCTGGAGGATCTTCAAATGACACCGCTACTTTCGGGTAC							
762	AAV9/hu	TCACCTCTACAAGCAAAATCTCCACAGCACAATCTGGAGGATCTTCAAATGACACCGCTACTTTCGGGTAC							
762	hu. 31-F	TCACCTCTACAAGCAAAATCTCCACAGCACAATCTGGAGGATCTTCAAATGACACCGCTACTTTCGGGTAC							
799	AAV5	AGCACCCCTCGGGGTACTTTGACTTTTAAACCGCTTCACAGCCACTGGAGCCCGCGAGACTGGCAAGAC							
826	AAV3-3	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
799	AAV4-4	TCCACCCCTCGGGGTACTTTGACTTTTAAACCGCTTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
829	AAV1-A	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
829	hu. 46-A	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
829	hu. 48-A	GGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
829	hu. 44-A	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
832	hu. 43-A	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
829	AAV6-A	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 34-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 47-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 29-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 63-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 56-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 45-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
823	hu. 57-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 35-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 58-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 28-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 51-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 19-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							
826	hu. 49-B	AGCACCCCTCGGGGTACTTTGACTTTTAAACAGATTCACATGCCACTTTCACACAGTACTGGCAGCAGAC							

FIG. 3AH

hu. 52-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 13-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
AAV2-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 20-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 24-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 64-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 27-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 21-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 22-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 23-B	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 7-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 61-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
rh. 56-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 9-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 54-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 53-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 60-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 55-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 2-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 1-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 18-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 3-C	829	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 25-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 15-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 16-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 11-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 10-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
hu. 4-C	826	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
rh. 54-D	832	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC
rh. 48-D	832	AGCACCCCTTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCACACCGTGACTGGCAAAGAC

FIG. 3AI

rh. 55-D	832	AGACCCCTGGGGTATTTGACTTCAACAGATTCCACTGTCTCTCACCACGTGACTGGCAGCGG	920	930	940	950	960	970	980
rh. 62-D	832	AGACCCCTGGGGTATTTGACTTCAACAGATTCCACTGTCTCTCACCACGTGACTGGCAGCGG							
AAV7-D	832	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 52-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 51-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 39-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 53-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 37-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 43-E	832	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 50-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 49-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 61-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 41-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 64-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 42-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 57-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 40-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
AAV8-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 58-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 40-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 67-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 17-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 6-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 66-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
rh. 38-E	835	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 32-F	832	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
AAV9/hu	832	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							
hu. 31-F	832	AGACCCCTGGGGTATTTGACTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCG							

FIG. 3AJ

AAV5 869 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTCCTCAGAGTCAAAATCTTCAACATTCAGTCAAGG
 AAV3-3 896 TCATTAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 AAV4-4 869 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 AAV1-A 899 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 46-A 899 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 48-A 899 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 44-A 899 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 43-A 902 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 AAV6-A 899 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 34-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 47-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 29-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 63-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 56-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 45-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 57-B 893 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 35-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 58-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 28-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 51-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 19-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 49-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 52-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 13-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 AAV2-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 20-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 24-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 64-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG
 hu. 27-B 896 TCATCAACAACTACTGGGGTTCCGGGTTCCAGACCCCGGTTCCAGAGTCAAGTCTTCAACATTCAGTCAAGG

FIG. 3AK

hu. 21-B	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 22-B	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 23-B	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 7-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 61-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 56-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 9-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 54-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 53-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 60-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 55-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 2-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 1-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 18-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 3-C	899	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 25-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 15-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 16-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 11-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 10-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 4-C	896	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 54-D	902	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 48-D	902	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 55-D	902	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 62-D	902	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
AAV7-D	902	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 52-E	905	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 51-E	905	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
hu. 39-E	905	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA
rh. 53-E	905	TCATCAACAACAACACTGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTTAACAATTCAGTCAAGA

FIG. 3AL

hu. 37-E	905	TCATCAACAACAACCTGGGGATTCCGGCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	990	1000	1010	1020	1030	1040	1050
rh. 43-E	902	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 50-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	GGTCACGGTGCAGGACTCCACACCACTCCGCAACCACTCCACCTCCACGTCGAAGTGTTCAGGGAC						
rh. 49-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	GGTCACGGACGATGGCAGCAGACTATTGCCAATAACCTTACCAGCAGGTTCAAGTGTTCAGGGAC						
rh. 61-E	905	CCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	GGTCACGACGTCGACGCGGAGACACGGTGGCTAATAACCTTACCAGCAGGTTTTCAGATCTTTCGGGAC						
hu. 41-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	GGTCACGACGATGATGGCGTCACACCACTGGCTAATAACCTTACCAGCAGGTTCAAGTCTTTCGGGAC						
rh. 64-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	GGTCACGACGATGATGGCGTCACACCACTGGCTAATAACCTTACCAGCAGGTTCAAGTCTTTCGGGAC						
hu. 42-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 57-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 40-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
AAV8-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 58-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 40-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 67-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 17-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 6-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 66-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 38-E	905	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 32-F	902	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
AAV9/hu	902	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
hu. 31-F	902	TCATCAACAACAACCTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
AAV5	939	GGTCACGGTGCAGGACTCCACACCACTCCGCAACCACTCCACCTCCACGTCGAAGTGTTCAGGGAC							
AAV3-3	966	GGTCACGGACGATGGCAGCAGACTATTGCCAATAACCTTACCAGCAGGTTCAAGTGTTCAGGGAC							
AAV4-4	939	GGTCACGACGTCGACGCGGAGACACGGTGGCTAATAACCTTACCAGCAGGTTTTCAGATCTTTCGGGAC							
AAV1-A	969	GGTCACGACGATGATGGCGTCACACCACTGGCTAATAACCTTACCAGCAGGTTTTCAGTCTTTCGGGAC							
hu. 46-A	969	GGTCACGACGATGATGGCGTCACACCACTGGCTAATAACCTTACCAGCAGGTTTTCAGTCTTTCGGGAC							
hu. 48-A	969	GGTCACGACGATGATGGCGTCACACCACTGGCTAATAACCTTACCAGCAGGTTTTCAGTCTTTCGGGAC							

FIG. 3AM

hu. 44-A	969	GGTCACGACGAATGATGGGTGCACACCATCGCTAATAACCTTACCAGCACGGTTCAGTCTCTCTCGGAC
hu. 43-A	972	GGTCACGACGAATGATGGGTGCACACCATCGCTAATAACCTTACCAGCACGGTTCAGTCTCTCTCGGAC
AAV6-A	969	GGTCACGACGAATGATGGGTGCACACCATCGCTAATAACCTTACCAGCACGGTTCAGTCTCTCTCGGAC
hu. 34-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 47-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 29-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 63-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 56-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 45-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 57-B	963	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 35-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 58-B	966	GGTCACGACGAATGATGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 28-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 51-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 19-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 49-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 52-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 13-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
AAV2-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 20-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 24-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 64-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 27-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 21-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 22-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 23-B	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 7-C	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 61-C	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
rh. 56-C	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC
hu. 9-C	966	GGTCACGACGAATGACGGTACGACGAGATTGCCAATAACCTTACCAGCACGGTTCAGGTGTTTACTGAC

FIG. 3AN

hu. 54-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 53-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 60-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 55-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 2-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 1-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 18-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 3-C	969	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 25-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 15-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 16-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 11-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 10-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
hu. 4-C	966	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGAC
rh. 54-D	972	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTCTGGAC
rh. 48-D	972	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTCTGGAC
rh. 55-D	972	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTCTGGAC
rh. 62-D	972	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTCTGGAC
AAV7-D	972	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTCTGGAC
rh. 52-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 51-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
hu. 39-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 53-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
hu. 37-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 43-E	972	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 50-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 49-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 61-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
hu. 41-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC
rh. 64-E	975	GGTCACGCAGAAATGACCGGTACGACGACGAGTTCGCAATACCTTACCAGCACCGTTTCAGGTCTTTACTGGAC

FIG. 3A0

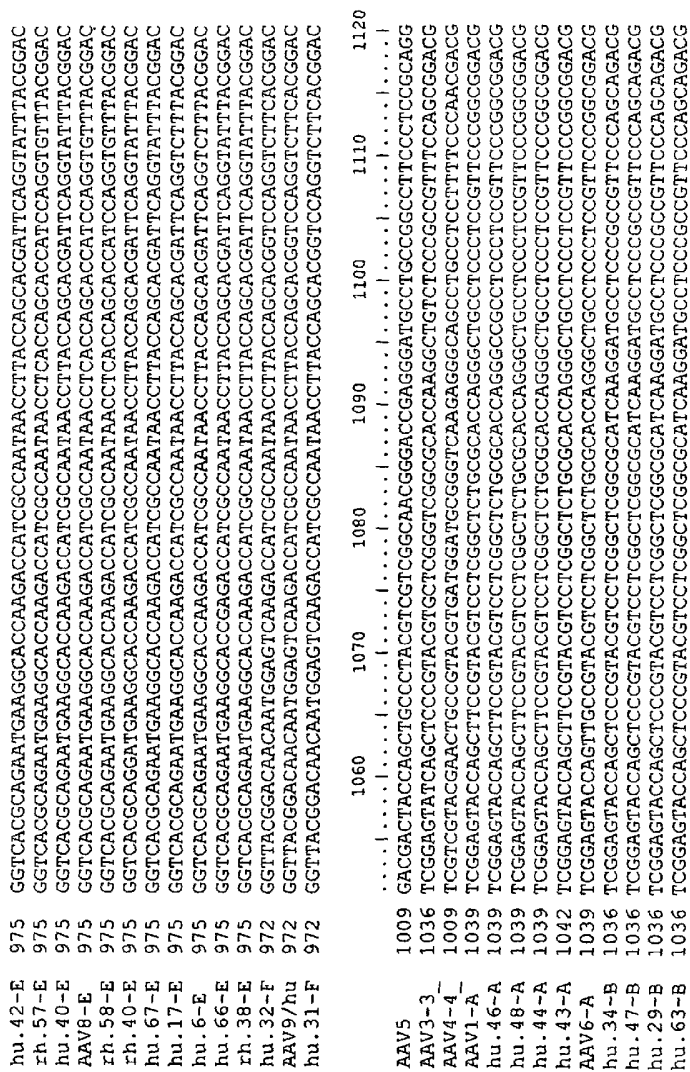


FIG. 3AP

hu.56-B 1036 TTGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.45-B 1036 TCGGGGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.57-B 1033 TTGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.35-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.58-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.28-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.51-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.19-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.49-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.52-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.13-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 AAV2-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.20-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.24-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.64-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.27-B 1036 TCGGGGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.21-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.22-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.23-B 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.7-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.61-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 rh.56-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.9-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.54-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.53-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.60-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.55-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.2-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.1-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG
 hu.18-C 1036 TCGGAGTACCAGCTCCCGTAGCTCCTCGGCTCGGGGCATCAAGGATGCTTCCGCGCTTCCAGCAGACG

FIG. 3AQ

hu..3-C	1039	TCGGAGTACCAGTCCCGTACGTCCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..25-C	1036	TCGGAGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..15-C	1036	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGAGACG
hu..16-C	1036	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGAGACG
hu..11-C	1036	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..10-C	1036	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..4-C	1036	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..54-D	1042	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..48-D	1042	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..55-D	1042	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..62-D	1042	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
AAV7-D	1042	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..52-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..51-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..39-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..53-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..37-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..43-E	1042	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..50-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..49-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..61-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..41-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..64-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..42-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..57-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..40-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
AAV8-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..58-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
rh..40-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG
hu..67-E	1045	TCGGGTACCAGTCCCGTACGTCCCGTCCGGTCCGGGTCCGGATCAAGATGCTCCCGCGTTTCCAGGGACG

FIG. 3AR

hu. 17-E	1045	TCGGAATACAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 6-E	1045	TCGGAATACAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 66-E	1045	TCGGAATACAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
rh. 38-E	1045	TCGGAATACAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 32-F	1042	TCAGACTATCAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
AAV9/hu	1042	TCAGACTATCAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 31-F	1042	TCAGACTATCAGCTCCCGTACGTCCTCGGCTCTGCGACACAGGGTGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
AAV5	1079	TCTTTACGCTGCCGACGTACGTTACGGACGCTGAACGGGAC--AACACAGAAATCCACCCGAGAG	1130	1140	1150	1160	1170	1180	1190
AAV3-3	1106	TCTTCATGGTCCCTCAGTATGGATACCTCACCTGAACACCGA-----AGTCAAGCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
AAV4-4	1079	TCTTTATGGTCCCCAGTACGGTACTGTGGACTGTGACCGGCAACTTCGACGACACACTGACAG	1130	1140	1150	1160	1170	1180	1190
AAV1-A	1109	TGTTCAATCCGCAATACGGTACCTGACGCTCAACAATGGC-----AGCCAGCCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 46-A	1109	TGTTCAATCCGCAATACGGTACCTGACGCTCAACAATGGC-----AGCCAGCCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 48-A	1109	TGTTCAATCCGCAATACGGTACCTGACGCTCAACAATGGC-----AGCCAGCCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 44-A	1109	TGTTCAATCCGCAATACGGTACCTGACGCTCAACAATGGC-----AGCCAGCCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 43-A	1112	TGTTCAATCCGCAATACGGTACCTGACGCTCAACAATGGC-----AGCCAGCCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
AAV6-A	1109	TGTTCAATCCGCAATACGGTACCTGACGCTCAACAATGGC-----AGCCAGCCGTGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 34-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 47-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 29-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 63-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 56-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 45-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 57-B	1103	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 35-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 58-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 28-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 51-B	1106	TCTTCATGGTCCACAGTATGGATACCTCACCTGAACACGAG-----AGTCAGGCGTAGGACG	1130	1140	1150	1160	1170	1180	1190

FIG. 3AS

hu.19-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGC-----AGTCAGGCGGTAGGACG
 hu.49-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.52-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAGCAACGGG-----AGTCAGGCGGTAGGACG
 hu.13-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 AAV2-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.20-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.24-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.64-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.27-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.21-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.22-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.23-B 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.7-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.61-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 rh.56-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.9-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.54-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.53-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.60-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.55-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.2-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.1-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.18-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.3-C 1109 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.25-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.15-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.16-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.11-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.10-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG
 hu.4-C 1106 TCTTCATGGTCCACAGTATGGATACCTCACCCTGAACAACGGG-----AGTCAGGCGGTAGGACG

FIG. 3AT

rh. 54-D	1112	TCTTCATGATTCTCTCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGACG
rh. 48-D	1112	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTGG
rh. 55-D	1112	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTGG
rh. 62-D	1112	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTGG
AAV7-D	1112	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAATGGC-----AGTCAGTCTGTGGGACG
rh. 52-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 51-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 39-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 53-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 37-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 43-E	1112	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 50-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 49-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 61-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 41-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 64-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 42-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 57-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 40-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAGGCCGTAGGCCG
AAV8-E	1115	TGTTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAGGCCGTGGGACG
rh. 58-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 40-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 17-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAGGCCGTGGGACG
hu. 67-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAGGCCGTAGGCCG
hu. 6-E	1115	TCTTCATGATTCCTCAGTACGGCTACCTGACTCTGAACAACGGC-----AGTCAGGCCGTGGGCCG
hu. 66-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAACGGC-----AGTCAGGCCGTGGGCCG
rh. 38-E	1115	TCTTCATGATTCGCCAGTACGGCTACCTGACTCTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 32-F	1112	TTTTTCATGATTCCTCAGTACGGGTATCTGACGCTTAATGATGGG-----AGCCAGGCCGTGGGTGG
AAV9/hu	1112	TTTTTCATGATTCCTCAGTACGGGTATCTGACGCTTAATGATGGA-----AGCCAGGCCGTGGGTGG
hu. 31-F	1112	TTTTTCATGATTCCTCAGTACGGGTATCTGACGCTTAATGATGGA-----GGCCAGGCCGTGGGTGG

FIG. 3AU

	1200	1210	1220	1230	1240	1250	1260
AAV5	1146	GAGCAGCTTCTTCTGCTAGAGTACTTTC	CCAGCAAGATGCTTGAGAACGGGCACAACTTT	GAGTCTT	GAGTTAC		
AAV3-3	1167	CTCATCTTTACTGCTCGAGTACTTCC	TTTCGAGATGCTTGAAGACTTGAATAACTT	TCGAATTCAGC			
AAV4-4	1149	AAATGCTTTTACTGCTCGAGTACTTTC	TTTCGAGATGCTTGGGACTTGGCAACAAC	TTTCAAAATACG			
AAV1-A	1170	TTTATCTTTTACTGCTCGGAATTA	TTCCCTTTCAGATGCTGAGAACGGGCACAACTTT	TACCTTCAGC			
hu. 46-A	1170	TTTATCTCTTTACTGCTCGGAATTA	TTCCCTTTCAGATGCTGAGAACGGGCACAACTTT	TACCTTCAGC			
hu. 48-A	1170	TTTATCTCTTTTACTGCTCGGAATTA	TTCCCTTTCAGATGCTGAGAACGGGCACAACTTT	TACCTTCAGC			
hu. 44-A	1170	TTTATCTCTTTTACTGCTCGGAATTA	TTCCCTTTCAGATGCTGAGAACGGGCACAACTTT	TACCTTCAGC			
hu. 43-A	1173	TTTATCTCTTTTACTGCTCGGAATTA	TTCCCTTTCAGATGCTGAGAACGGGCACAACTTT	TACCTTCAGC			
AAV6-A	1170	GTTCATCTTTTACTGCTCGGAATTA	TTCCCTTTCAGATGCTGAGAACGGGCACAACTTT	TACCTTCAGC			
hu. 34-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 47-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 29-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 29-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 63-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 56-B	1167	CTCTTCCTTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 45-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 57-B	1164	CTCTTCCTTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 35-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 58-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 28-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 51-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 19-B	1167	CTCTTCCTTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 49-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 52-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 13-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
AAV2-B	1167	CTCTTCATTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 20-B	1167	CTCTTCCTTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			
hu. 24-B	1167	CTCTTCCTTTTACTGCTCGAGTACTTTC	TTCTTTCAGATGCTGCGTACCGGAAACAAC	TTTACCTTCAGC			

FIG. 3AV

hu.64-B 1167 CTCTTCATTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.27-B 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.21-B 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.22-B 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.23-B 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.7-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.61-C 1167 CTCTTCATTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.56-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.9-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.54-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.53-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.60-C 1167 CTCTTCATTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTCAATTTCAGC
 hu.55-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.2-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.1-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.18-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.3-C 1170 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.25-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.15-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.16-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.11-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.10-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 hu.4-C 1167 CTCTTCCTTTTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.54-D 1173 TTCATCCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.48-D 1173 TTCCTCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.55-D 1173 TTCCTCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.62-D 1173 TTCCTCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 AAV7-D 1173 TTCCTCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.52-E 1176 TTCCTCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC
 rh.51-E 1176 TTCCTCTTCTACTGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACTTTACCTTCAGC

FIG. 3AW

hu.39-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC	1270	1280	1290	1300	1310	1320	1330
rh.53-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.37-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.43-E	1173	CTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.50-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.49-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.61-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.41-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.64-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.42-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.57-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.40-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
AAV8-E	1176	CTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.58-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.40-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.67-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.17-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.6-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.66-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
rh.38-E	1176	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.32-F	1173	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
AAV9/hu	1173	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
hu.31-F	1173	TTCTCTCTTCTACTGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACATTTTCCTTCAGC							
AAV5	1216	TACAACTTTGAGGAGTGCCTTCCACTCCAGCTTCGCTCCAGTCCAGACCTGTTCAGCTGGCCAAACC							
AAV3-3	1237	TATACCTTCGAGGATGTACCTTTTCACAGAGTACCGTCACAGCCAGAGTTGGATCGGTTGATGAATC							
AAV4-4 ⁻	1219	TACAGTTTGGAGAGTGCCTTTCCACTCGATGTACGGCCACAGCCAGAGCTGGACCGGCTGATGAACC							
AAV1-A ⁻	1240	TACACCTTTGAGGAGTGCCTTTCCACTCGATGTACGGCCACAGCCAGAGCTGGACCGGCTGATGAATC							

FIG. 3AX

hu.46-A 1240 TACACCTTTGAGGAAGTGCCTCTCCACAGCAGCTGCGGCACAGCCAGAGCCTGGACCCGGCTGATGAATC
 hu.48-A 1240 TACACCTTTGAGGAAGTGCCTTTCCACAGCAGCTACGGCGACAGCCAGAGCCTGGACCCGGCTGATGAATC
 hu.44-A 1240 TACACCTTTGAGGAAGTGCCTTTCCACAGCAGCTACGGCGACAGCCAGAGCCTGGACCCGGCTGATGAATC
 hu.43-A 1243 TACACCTTTGAGGAAGTGCCTCTCCACAGCAGCTACGGCGACAGCCAGAGCCTGGACCCGGCTGATGAATC
 AAV6-A 1240 TACACCTTCGAGGACGTCCTTTCCACAGCAGCTACGGCGACAGCCAGAGCCTGGACCCGGCTGATGAATC
 hu.34-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGCCCGTCTCATGAATC
 hu.47-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGCCCGTCTCATGAATC
 hu.29-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.63-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.56-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCAAGTCAAGTCTGGACCCGTCTCATGAATC
 hu.45-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.57-B 1234 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGCCCGTCTCATGAATC
 hu.35-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGCCCGTCTCATGAATC
 hu.58-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.28-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.51-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.19-B 1237 TACACCTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.49-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.52-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.13-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 AAV2-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.20-B 1237 TACACTTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.24-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.64-B 1237 TACACCTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.27-B 1237 TACACCTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.21-B 1237 TACACCTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.22-B 1237 TACACCTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.23-B 1237 TACACCTTTGAGGACGTTCCCTTTCCATAGCAGCTACGGCTCACAGCCAGAGTGGACCCGTCTCATGAATC
 hu.7-C 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGATCGGCTGATGAATC
 hu.61-C 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGGCTCACAGCCAGAGTGGATCGGCTGATGAATC

FIG. 3AY

rh. 56-C 1237 TACACCTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 9-C 1237 TACACCTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
 hu. 54-C 1237 TACACCTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
 hu. 53-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
 hu. 60-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 55-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
 hu. 2-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 1-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 18-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 3-C 1240 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 25-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 15-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 16-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 11-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 10-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 4-C 1237 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 54-D 1243 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 48-D 1243 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 55-D 1243 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 62-D 1243 TACACTTTTGAAGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 AAV7-D 1243 TACAGCTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 52-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 51-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 39-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 53-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 hu. 37-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 43-E 1243 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 50-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 49-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
 rh. 61-E 1246 TACACTTTTCGAGGACGTGCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC

FIG. 3A2

hu. 41-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCACAGCAGAGCTTGGACCCGACTGATGAATC
 rh. 64-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 42-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCACAGCAGAGCTTGGACCCGACTGATGAATC
 rh. 57-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 40-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 AAV8-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 rh. 58-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 rh. 40-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 67-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 17-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 6-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 66-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 rh. 38-E 1246 TACACCTTCGAGGACGTGCTTTCCACAGCAGCTACCCGACAGAGCTTGGACCCGACTGATGAATC
 hu. 32-F 1243 TACGAGTTTGAGAACGTACCTTTCCATAGCAGCTACGCTCAGCCCAAGCTTGGACCCGACTGATGAATC
 AAV9/hu 1243 TACGAGTTTGAGAACGTACCTTTCCATAGCAGCTACGCTCAGCCCAAGCTTGGACCCGACTGATGAATC
 hu. 31-F 1243 TACGAGTTTGAGAACGTACCTTTCCATAGCAGCTACGCTCAGCCCAAGCTTGGACCCGACTGATGAATC

|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
 AAV5 1286 CGCTGTGGACCACTGTTGACCGCTTCGTGAGCAAAAT-----AAACACTGG
 AAV3-3 1307 CTCTTATTGATCAGTATCTGTACTACCTGAACAGAGAGCAAGCAACCTCTGGAACAAACCAACCAATC
 AAV4-4 1289 CTCTCATCGACCACTACCTGTGGGACTGCAATCGACACACCGGAACCACTCTGAATGCCGGGACTGC
 AAV1-A 1310 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA
 hu. 46-A 1310 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAG
 hu. 48-A 1310 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA
 hu. 44-A 1310 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA
 hu. 43-A 1313 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA
 AAV6-A 1310 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA
 hu. 34-B 1307 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA
 hu. 47-B 1307 CTCTCATCGACCACTACCTGTATTAACCTGAACAGAACTCAA---AATCAGTCCGGAAGTSCCCCAAAACAA

FIG. 3BA

hu. 29-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 63-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 56-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 45-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGTGGAAACCAACACCGCAGTCTC
 hu. 57-B 1304 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 35-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGTGGAAACCAACACCGCAGTCTC
 hu. 58-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 28-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 51-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGTGGAAACCAACACCGCAGTCTC
 hu. 19-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 49-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 52-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGTGGAAACCAACACCGCAGTCTC
 hu. 13-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 AA2-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGTGGAAACCAACACCGCAGTCTC
 hu. 20-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 24-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGTGGAAACCAACACCGCAGTCTC
 hu. 64-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 27-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 21-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 22-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 23-B 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACTCCAAGCGGGAACCAACACCGCAGTCTC
 hu. 7-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---TCAATAGTGGAACTCTTCAGCAGTCTC
 hu. 61-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACAATAGTGGAACTCTTCAGCAGTCTC
 rh. 56-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---TCAATAGTGGAGCTCTTCAGCAGTCTC
 hu. 9-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---TCAATAGTGGAACTCTTCAGCAGTCTC
 hu. 54-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACAGCTAGTGGAACT---CAGCAGTCTC
 hu. 53-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACAGCTAGTGGAACT---CAGCAGTCTC
 hu. 60-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACAATAGTGGAACTCTTCAGCAGTCTC
 hu. 55-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACAGCTAGTGGAACT---CAGCAGTCTC
 hu. 2-C 1307 CTCTCATCGACGAGTACCTGTATTACTTGGAGCAGAACAAAC---ACAATAGTGGAACTCTTCAGCAGTCTC

FIG. 3BB

hu. 1-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
hu. 18-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 3-C	1310	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
hu. 25-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
hu. 15-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 16-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 11-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 10-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 4-C	1307	CTCTGATCGACCACTACCTGTATTATCTGAAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
rh. 54-D	1313	CCCTCATCGACCACTACCTGTATTACCTGGCTAGAACACAGAGTACCCAGGAGGACATCTGGCAATCG
rh. 48-D	1313	CTCTTATCGACCACTACCTGTATTACCTGGCTAGAACACAGAGTACCCAGGAGGACATCTGGCAATCG
rh. 55-D	1313	CTCTTATCGACCACTACCTGTATTACCTGGCTAGAACACAGAGTACCCAGGAGGACATCTGGCAATCG
rh. 62-D	1313	CCCTCATCGACCACTACCTGTATTACCTGGCTAGAACACAGAGTACCCAGGAGGACATCTGGCAATCG
AAV7-D	1313	CTCTCATCGACCACTACCTGTATTACCTGGCTAGAACACAGAGTACCCAGGAGGACATCTGGCAATCG
rh. 52-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
rh. 51-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
hu. 39-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
rh. 53-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
hu. 37-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACAGGAGGAACTCAAGGTACCCA
rh. 43-E	1313	CTCTGATCGACCACTACCTGTATTACCTGTCTGGAATCTAAACA---ACAGGAGGCACAGCGGGAAACCCA
rh. 50-E	1316	CTCTCGTCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
rh. 49-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
rh. 61-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
hu. 41-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACAGGAGGAACTCAAGGTACCCA
rh. 64-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
hu. 42-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACAGGAGGAACTCAAGGTACCCA
rh. 57-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA
hu. 40-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACAGGAGGAACTCAAGGTACCCA
AAV8-E	1316	CTCTGATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACAGGAGGACAGCGGCAATACGCA
rh. 58-E	1316	CTCTCATCGACCACTACCTGTATTACCTGTCTAAGAACCCAGTCT---ACGGGAGGCACAGCGGGAAACCCA

FIG. 3BC

rh. 40-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC-----ACAGGAGGAACCTCAAGTACCCA
hu. 67-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC-----ACAGGAGGAACCTCAAGTACCCA
hu. 17-E	1316	CCCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC-----ACGGGAGGTACCGCAGGAATCA
hu. 6-E	1316	CCCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC-----ACGGGAGGTACCGCAGGAATCA
hu. 66-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC-----ACAGGAGGAACCTCAAGTACCCA
rh. 38-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC-----ACAGGAGGAACCTCAAGTACCCA
hu. 32-F	1313	CACATCATCGACCACTACCTGTACTACTTATCCAGAACTTAAAGGTCTTGG-----CAGATCAACA
AAV9/hu	1313	CACATCATCGACCACTACCTGTACTACTTATCCAGAACTTAAAGGTCTTGG-----CAGATCAACA
hu. 31-F	1313	CACATCATCGACCACTACCTGTACTACTTATCCAGAACTTAAAGGTCTTGG-----CAGATCAACA
		1410 1420 1430 1440 1450 1460 1470
		
AAV5	1335	CGGAGTCCAGTTCACAAAGAACCTGGCCGGAGATACGCCAACACCTACAAAACTGGTTCGCCGGGCC
AAV3-3	1377	ACGGCTGCTTTTAGCCAGGCTGGGCCCTCAGTCTATGTCTTTGCGGCCAGAAATGGCTACCTGGGCC
AAV4-4	1359	CACCAACCACTTACCAAGCTGGGCCCTACCAACTTTTCCAACTTTAAAGAAAGAACTGGCTGCCCGGGCTT
AAV1-A	1377	GGACTTGCTGTTTAGCCGTGGTCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 46-A	1377	GGACTTGCTGTTTAGCCGTGGTCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 48-A	1377	GGACTTGCTGTTTAGCCGTGGTCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 44-A	1377	GGACTTGCTGTTTAGCCGTGGTCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 43-A	1380	GGACTTGCTGTTTAGCCGTGGTCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
AAV6-A	1377	GGACTTGCTGTTTAGCCGTGGTCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 34-B	1374	AAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 47-B	1374	AAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 29-B	1374	CAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 63-B	1374	AAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 56-B	1374	CAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 45-B	1374	AAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 57-B	1371	CAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 35-B	1374	AAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC
hu. 58-B	1374	CAGGCTTCAGTTCAGCCCGGGGCTCCAGCTGGCATGCTGTTCAGCCCAAAACTGGCTACCTGGACCC

FIG. 3BD

hu. 28-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCAGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 51-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 19-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 49-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 52-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 13-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 AAV2-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 20-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 24-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 64-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 27-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 21-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 22-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 23-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGAATTCGGGACCAAGTCTAGGAACCTGGCTTCCTGGACCC
 hu. 7-C 1374 TCGGCTACTGTTAGTCAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 61-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 rh. 56-C 1374 TCGGCTACTGTTAGTCAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 9-C 1374 TAGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 54-C 1371 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 53-C 1371 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 60-C 1371 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 55-C 1371 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 2-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 1-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 18-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 3-C 1377 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 25-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 15-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 16-C 1374 TCGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT
 hu. 11-C 1374 TAGGCTACTGTTAGCCAAAGCTGGACCCGAGCATGTCTTCAAGCTAAAGTCTGGCTTCCTGGACCT

FIG. 3BE

hu. 10-C 1374 TAGGCTACTGTTTAGCCAAAGCTGGAGCCACAGCATGTCTCTTCAAGCTAAAAACTGGCTGGCTGGACCT
 hu. 4-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGAGCCACAGCATGTCTCTTCAAGCTAAAAACTGGCTGGCTGGACCT
 rh. 54-D 1383 GGAAGCTGAGTTTACAGGGCGGGCTTCCACCATTGGCCGAAACAGCAAGAACTGGTTTACTTGGACCT
 rh. 48-D 1383 GGAAGCTGAGTTTATCAGGGCGGGCTTCCACCATTGGCCGAAACAGCAAGAACTGGTTTACTTGGACCT
 rh. 55-D 1383 GGAAGCTGAGTTTATCAGGGCGGGCTTCCACCATTGGCCGAAACAGCAAGAACTGGTTTACTTGGACCT
 rh. 62-D 1383 GGAAGCTGAGTTTATCAGGGCGGGCTTCCACCATTGGCCGAAACAGCAAGAACTGGTTTACTTGGACCT
 AAV7-D 1383 GGAAGCTGAGTTTATCAGGGCGGGCTTCCACCATTGGCCGAAACAGCAAGAACTGGTTTACTTGGACCT
 rh. 52-E 1383 GCAGTTGCTGTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 rh. 51-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 hu. 39-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 rh. 53-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 hu. 37-E 1383 GCAATTGTTATTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTGGCTGGACCT
 rh. 43-E 1380 GACTCTGGCTTCAGCCCAAGGTGGGCTTAACAATGGCCATGCAAGCTAGGCTAGGCTGGCTGGACCC
 rh. 50-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 rh. 49-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 rh. 61-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 hu. 41-E 1383 GCAATTGTTATTTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 rh. 64-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 hu. 42-E 1383 GCAATTGTTATTTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 rh. 57-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 hu. 40-E 1383 GCAATTGTTATTTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 AAV8-E 1383 GACTCTGGCTTCAGCCCAAGGTGGGCTTAACAATGGCCATGCAAGCTAGGCTAGGCTGGCTGGACCT
 rh. 58-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGCCAGAACTGGCTGGCTGGACCC
 rh. 40-E 1383 GCAATTGTTATTTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 hu. 67-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 hu. 17-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 hu. 6-E 1383 GCAGTTGCTGTTTCTCAGGGCGGGCTTAGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 hu. 66-E 1383 GCAATTGTTATTTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 rh. 38-E 1383 GCAATTGTTATTTTCTCAAGCTGGGGCTGCAACATGTGGCTCAGGGCTAGGCTAGGCTAGGCTGGACCT
 hu. 32-F 1377 AACGCTAAATTCAGCGTGGCGGACCCAGCAACATGGCTGTCCAGGGAGAGAACTACATACCTGGACCC

FIG. 3BF

AAV9/hu 1377 AACGCTAAATTCAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC
 hu.31-F 1377 AACGCTAAATTCAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC

AAV5 1405 ATGGCCGAACCCAGGGCTGGAACCTGGGCTCGGGGTCAAC-----CGGCCAGTGTCA
 AAV3-3 1447 TGCTACCGCAACAGAGACTTTCAAGACTGCTAACGACAAC-----AACACAGTAACT
 AAV4-4 1429 TCAATCAAGCAGCAGGGCTTCTCAAGACTGCCAATCAAACTACAGATCCCTGCCACCGGTGAGACA
 AAV1-A 1447 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGCAATT
 hu.46-A 1447 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGCAATT
 hu.48-A 1447 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGCAATT
 hu.44-A 1447 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGCAATT
 hu.43-A 1450 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGCAATT
 AAV6-A 1447 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGCAATT
 hu.34-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.47-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.29-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.63-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.56-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.45-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.57-B 1441 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.35-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.58-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.28-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.51-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.19-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.49-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.52-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 hu.13-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT
 AAV2-B 1444 TGTATCGGCAGCAGCGCTTCTTAAACAAACAAACAGACAAC-----AACACAGTGAAT

FIG. 3BG

hu..20-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGACAACT-----AACAACTGATGATT
 hu..24-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGACAACT-----AACAACTGATGATT
 hu..64-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGATTAAC-----AACAACTGATGATT
 hu..27-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGACAACT-----AACAACTGATGATT
 hu..21-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGACAACT-----AACAACTGATGATT
 hu..22-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGACAACT-----AACAACTGATGATT
 hu..23-B 1444 TGTACCGCCAGCAGCGAGTATCAAGACAGCTGCGGACAACT-----AACAACTGATGATT
 hu..7-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..61-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 rh..56-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..9-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..54-C 1441 TGTATCGCCAGCAGCGTTTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..53-C 1441 TGTATCGCCAGCAGCGTTTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..60-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..55-C 1441 TGTATCGCCAGCAGCGTTTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..2-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..1-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..18-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..3-C 1447 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..25-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..15-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..16-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..11-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..10-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 hu..4-C 1444 TGTACAGACAGCAGCGTCTGTCAAGAGGCAACAGCAACT-----AACAACTGATGATT
 rh..54-D 1453 TGTTCGGGCAACAAAGAGTTTCCAAACACTGGATCAAACT-----AACAACTGATGATT
 rh..48-D 1453 TGTTCGGGCAACAAAGAGTTTCCAAACACTGGATCAAACT-----AACAACTGATGATT
 rh..55-D 1453 TGTTCGGGCAACAAAGAGTTTCCAAACACTGGATCAAACT-----AACAACTGATGATT
 rh..62-D 1453 TGTTCGGGCAACAAAGAGTTTCCAAACACTGGATCAAACT-----AACAACTGATGATT
 AAV7-D 1453 TGTTCGGGCAACAAAGAGTTTCCAAACACTGGATCAAACT-----AACAACTGATGATT

FIG. 3BH

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rh. 52-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 51-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 39-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 53-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 37-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 43-E 1450 TGTACCGCCAAACAGCGGTCTCAACGCAACCGGCAAAAC-----AACAAATAGCAACT
rh. 50-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 49-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 61-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 41-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 64-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 42-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 57-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 40-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
AAV8-E 1453 TGTACCGCCAAACAGCGGTCTCAACGCAACCGGCAAAAC-----AACAAATAGCAACT
rh. 58-E 1453 TGCTACAGACAGCGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 40-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 67-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 17-E 1453 TGCTACGGGAGCAGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 6-E 1453 TGCTACGGGAGCAGCGGTCTCCACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 66-E 1453 TGCTACGGGAGCAGCGGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
rh. 38-E 1453 TGCTACGGGAGCAGCGAGTCTCTACGACACTGTCGCAAAAC-----AACAAACAGCAACT
hu. 32-F 1447 AGCTACGGACAAACAGGTGTCCTAACCTGTGACTCAAAAC-----AACAAACAGGGAAT
AAV9/hu 1447 AGCTACGGACAAACAGGTGTCCTAACCTGTGACTCAAAAC-----AACAAACAGGGAAT
hu. 31-F 1447 AGCTACGGACAAACAGGTGTCCTAACCTGTGACTCAAAAC-----AACAAACAGGGAAT

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 1550 1560 1570 1580 1590 1600 1610

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AAV5 1460 GGGCCTTCGCCACGACCAATAGGATGGAGCTCGAGGGCGCGAGTTACCGAGTGCCCGCGAGCCGCAACGG
AAV3-3_ 1502 TTCCTTGGACAGCGGCCAGCAATATCATCTCAATGGCGCGACTCGCTGGTGAAATCCAGACCAGCTAT

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FIG. 3BI

AAV4-4_ 1499 GTCTCATCAATACGAGACGACAGCAGCTCTGGACGGAGATGGAGTGGCCCTGACCCCCGACCTCCAAAT
 AAV1-A_ 1502 TTACCTGGACTGGTGGCTTCAAATATAAAGCTCAATGGCGGTGAATCCATCATCAACCTCGACCTGCTAT
 hu. 46-A 1502 TTACCTGGACTGGTGGCTTCAAATATAAAGCTCAATGGCGGTGAATCCATCATCAACCTCGACCTGCTAT
 hu. 48-A 1502 TTACCTGGACTGGTGGCTTCAAATATAAAGCTCAATGGCGGTGAATCCATCATCAACCTCGACCTGCTAT
 hu. 44-A 1502 TTACCTGGACTGGTGGCTTCAAATATAAAGCTCAATGGCGGTGAATCCATCATCAACCTCGACCTGCTAT
 hu. 43-A 1505 TTACCTGGACTGGTGGCTTCAAATATAAAGCTCAATGGCGGTGAATCCATCATCAACCTCGACCTGCTAT
 AAV6-A 1502 TTACCTGGACTGGTGGCTTCAAATATAAAGCTCAATGGCGGTGAATCCATCATCAACCTCGACCTGCTAT
 hu. 34-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 47-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 29-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 63-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 56-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 45-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 57-B 1496 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 35-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 58-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 28-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 51-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 19-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 49-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 52-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 13-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 AAV2-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 20-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 24-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 64-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 27-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 21-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 22-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
 hu. 23-B 1499 ACTCGTGGACTGGAGTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT

FIG. 3Bj

1499	TTCCCTGGACTGCGGTACAAAGTATCACTTAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 7-C
1499	TTCCCTGGACGCGAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 61-C
1499	TTCCCTGGACTGCGGTACAAAGTACCACTTAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	rh. 56-C
1499	TTCCCTGGACTGCGGTACAAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	rh. 9-C
1496	TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCGGAGACTCTTTGGTGAACCCGGGCCCGGCCAT	hu. 54-C
1496	TTCCCTGGACTGGAGCTACCAAGTATCACTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGGCCAT	hu. 53-C
1499	TTCCCTGGACTGCACTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 60-C
1496	TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCCGGGACTCGTGGTTAATCCAGGACCGGCCCAT	hu. 55-C
1499	TTCCCTGGACTGCACTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 2-C
1499	TTCCCTGGACTGAGCTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 1-C
1499	TTCCCTGGACTGCGGTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 18-C
1502	TTCCCTGGACTGAGCTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 3-C
1499	TTCCCTGGACTGAGCTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 25-C
1499	TTCCCTGGACTGCGGTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 15-C
1499	TTCCCTGGACTGCGGTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 16-C
1499	TTCCCTGGACTGCGGTACCAAGTATCGTCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 11-C
1499	TTCCCTGGACTGCGGTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 10-C
1499	TTCCCTGGACTGCACTACCAAGTATCATCTAAATGGCCGGGACTCGTGGTTAATCCAGGACACAGCTAT	hu. 4-C
1508	TTGCTTGGACTGGTGCACCAAAATACCTGAAACGCAGAAACTCTCTGGTGAATCCGGGTGTCGCCAT	rh. 54-D
1508	TTGCTTGGACTGGTGCACCAAAATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTCGCCAT	rh. 48-D
1508	TTGCTTGGACTGGTGCACCAAAATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTCGCCAT	rh. 55-D
1508	TTGCTTGGACTGGTGCACCAAAATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTCGCCAT	rh. 62-D
1508	TTGCTTGGACTGGTGCACCAAAATACCTGAAACGCAGAAACTCGTGGTTAATCCCGGCGTGCGCCAT	AAV7-D
1508	TTGCTTGGACTGGTGCACCAAGTATCATCTGAAACGCAGAGACTCTCTGGTGAATCCGGGCGTGCGCCAT	rh. 52-E
1508	TTGCTTGGACTGGTGCACCAAGTATCATCTGAAACGCAGAGACTCTCTGGTGAATCCGGGCGTGCGCCAT	rh. 51-E
1508	TTGCTTGGACTGGTGCACCAAGTATCATCTGAAACGCAGAGACTCTCTGGTGAATCCGGGCGTGCGCCAT	rh. 39-E
1508	TTGCTTGGACTGGTGCACCAAGTATCATCTGAAACGCAGAGACTCTCTGGTGAATCCGGGCGTGCGCCAT	rh. 53-E
1508	TTGCTTGGACTGGTGCACCAAAATACCTGAAACGCAGAGACTCTTTGGTGAATCCCGGTGTCGCCAT	rh. 37-E
1505	TTGCTTGGACTGCTGGACCAAAATACCATCTGAAATGGAAGAAATTCATTTGGCTTAATCCTGGCATCGCTAT	rh. 43-E
1508	TTGCTTGGACTGGTGCACCAAGTATCATCTGAAACGCAGAGACTCTCTGGTGAATCCGGGCGTGCGCCAT	rh. 50-E

FIG. 3BK

rh. 49-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
rh. 61-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 41-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
rh. 64-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 42-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
rh. 57-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 40-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
AAV8-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
rh. 58-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
rh. 40-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 67-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 17-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 6-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 66-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
rh. 38-E 1508 TTGCTGGACTGGTGCCACCAAGTATCATCTGACGGCAGAGACTCTCTGGTGAATCCGGGCGTGGCCAT
hu. 32-F 1502 TTGCTGGCTGGAGCTTCTTCTGGGCTCTCAATGGAGTAAAGCTTGAATCCTGGACCTGCTAT
AAV9/hu 1502 TTGCTGGCTGGAGCTTCTTCTGGGCTCTCAATGGAGTAAAGCTTGAATCCTGGACCTGCTAT
hu. 31-F 1502 TTGCTGGCTGGAGCTTCTTCTGGGCTCTCAATGGAGTAAAGCTTGAATCCTGGACCTGCTAT

1620 1630 1640 1650 1660 1670 1680
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

AAV5 1530 CATGACCAACACCTCCAGGGCAGCAACACCTATGCCCTGGAGAACACTATGATCTTCAACAGCCAGCCG
AAV3-3 1572 GGCCAGTCACAGGAGATGAAGAAAATTTTCCCTATGCAGGCAATCTAATATTTGGCAAGAGAGG
AAV4-4 1569 GGCCACGGCTGGACCTGGGACAGCAAGTCAGC---PACAGCCAGCTCATCTTTCGGGGCCCTAAACAG
AAV1-A 1572 GGCTTCACACAAAGACGACGAAGTCTTTCCCATGAGCGGTGTCTGATTTTGGAAAAGAGAGC
hu. 46-A 1572 GGCTTCACACAAAGACGACGAAGTCTTTCCCATGAGCGGTGTCTGATTTTGGAAAAGAGAGC
hu. 48-A 1572 GGCTTCACACAAAGACGACGAAGTCTTTCCCATGAGCGGTGTCTGATTTTGGAAAAGAGAGC
hu. 44-A 1572 GGCTTCACACAAAGACGACGAAGTCTTTCCCATGAGCGGTGTCTGATTTTGGAAAAGAGAGC
hu. 43-A 1575 GGCTTCACACAAAGACGACGAAGTCTTTCCCATGAGCGGTGTCTGATTTTGGAAAAGAGAGC
AAV6-A 1572 GGCTTCACACAAAGACGACGAAGTCTTTCCCATGAGCGGTGTCTGATTTTGGAAAAGAGAGC

FIG. 3BL

hu.34-B 1569 GGCAAGCCACAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.47-B 1569 GGCAAGCCACAAAGACATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.29-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.63-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.56-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.45-B 1569 GGCAAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.57-B 1566 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.35-B 1569 GGCAAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.58-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.28-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.51-B 1569 GGCAAGCCCAAAAGACATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.19-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.49-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.52-B 1569 GGCAAGCCCAAAAGACATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.13-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 AAV2-B 1569 GGCAAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.20-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.24-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.64-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.27-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.21-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.22-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.23-B 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCTCAGACGGGGTCTCATCTTTGGGAAGCAAGGC
 hu.7-C 1569 GGCCAGTCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA
 hu.61-C 1569 GGCCAGTCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA
 rh.56-C 1569 GGCCAGTCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA
 hu.9-C 1569 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA
 hu.54-C 1566 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA
 hu.53-C 1566 GGCCAGCCCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA
 hu.60-C 1569 GGCCAGTCAAAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAACCCCTGATATTTGGTAACCAAGGA

FIG. 3BM

hu. 55-C 1566 GGCAGGCCACAGCAGATGAAGAAAGTTTTCCTCCATGCATGGAACCTTAATATTTGGTAAAGAGGA
 hu. 2-C 1569 GGCAGTCAAGATGACGAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 1-C 1569 GGCAGTCAAGATGACGAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 18-C 1569 GGCAGCCCAAGACATGAAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 3-C 1572 GGCAGTCAAGATGACGAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 25-C 1569 GGCAGTCAAGATGACGAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 15-C 1569 GGCAGCCCAAGACATGAAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 16-C 1569 GGCAGCCCAAGACATGAAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 11-C 1569 GGCAGCCCAAGACATGAAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 10-C 1569 GGCAGCCCAAGACATGAAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 hu. 4-C 1569 GGCAGTCAAGATGACGAGAAAGTTTTCCTCCATGCATGGAACCTGATATTTGGTAAACAGGA
 rh. 54-D 1578 GGCAACTCACAAGGACGACGAGACCGCTTTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 48-D 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 55-D 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 62-D 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA
 AAV7-D 1578 GGCAACTCACAAGGACGACGAGACCGCTTTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 52-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 51-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 hu. 39-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 53-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 37-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 43-E 1575 GGCAACCCCAAGGACGACGAGGAGGTTTTCCTCCAGTAACGGGA---TCCGTGTTTGGCAACAAAT
 rh. 50-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 49-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 61-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 hu. 41-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 64-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 hu. 42-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA
 rh. 57-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCATCCAGCGAGTCTGATTTTGGAAAACTGGA
 hu. 40-E 1578 GGCAACCCCAAGGACGACGAGACCGCTTCTTCCCTTCGAGCGAGTCTGATTTTGGAAAACTGGA

FIG. 3BN

AAV8-E	1578	GGCAACACACAAGACGACGAGGAGCGGTTTTCCTCCAGTAGCGGGATCCTGATTTTGGCAAAACAAAAT
rh. 58-E	1578	GGCAACCAACAGGACGACGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
rh. 40-E	1578	GGCAACGATAGGACGACGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
hu. 67-E	1578	GGCAACCAACAGGACGACGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
hu. 17-E	1578	GGCAACGACACAGGACGACGAGGAGCGGTTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
hu. 6-E	1578	GGCAACGACACAGGACGACGAGGAGCGGTTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
hu. 66-E	1578	GGCAACCCACAGGACGACGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
rh. 38-E	1578	GGCAACCCACAGGACGACGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
hu. 32-F	1572	GGCCAGCCACAAAGAGGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
AAV9/hu	1572	GGCCAGCCACAAAGAGGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
hu. 31-F	1572	GGCCAGCCACAAAGAGGAGGAGCGGTTTCCTCCATCCAGCGGATCCTCATGTTTGGCAACGAGGGA
		1690 1700 1710 1720 1730 1740 1750
		
AAV5	1600	GGCAACCCGGCACCCACCGTACCTCGAGGGCAACATGCTCATCACCGCGAGGAGCGGACGCGACG
AAV3-3	1642	ACA-----ACGGCAGTAACGCGAATAGAT--BATGTAATGATTACCGATGAAGAGAGATTCCGTA
AAV4-4	1636	AAC-----GGCAACGCGCCACCGTACCGGG--ACTCTGATCTTCCTCTGAGGAGGAGGCTGGCAG
AAV1-A	1642	GCC-----GGAGCTTCAACACTGCAATTGGAC--AATGTCATGATTACAGACGGAAGAGGAAATTAAG
hu. 46-A	1642	GCC-----GGAGCTTCAACACTGCAATTGGAC--AATGTCATGATTACAGACGGAAGAGGAAATTAAG
hu. 48-A	1642	GCC-----GGAGCTTCAACACTGCAATTGGAC--AATGTCATGATTACAGACGGAAGAGGAAATTAAG
hu. 44-A	1642	GCC-----GGAGCTTCAACACTGCAATTGGAC--AATGTCATGATTACAGACGGAAGAGGAAATTAAG
hu. 43-A	1645	GCC-----GGAGCTTCAACACTGCAATTGGAC--AATGTCATGATTACAGACGGAAGAGGAAATTAAG
AAV6-A	1642	GCC-----GGAGCTTCAACACTGCAATTGGAC--AATGTCATGATTACAGACGGAAGAGGAAATTAAG
hu. 34-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA
hu. 47-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA
hu. 29-B	1639	CCA-----GAGAAACAAATGTGGATATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA
hu. 63-B	1639	TCG-----GAGAAACAAATGTGGACATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA
hu. 56-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA
hu. 45-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA
hu. 57-B	1636	TCA-----GAGAAACAAATGTGGACATTGAA--BAGGTCTGATTACAGACGGAAGAGGAAATCAGGA

FIG. 3B0

hu. 35-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 58-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 28-B	1639	TCA-----GAGAAACAAATGTGGATTTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 51-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 19-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 49-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 52-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 13-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
AAV2-B	1639	TCA-----GAGAAACAAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 20-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 24-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 64-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTCATGATTACAGACGGAAGAGGAATCAGGA
hu. 27-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 21-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 22-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 23-B	1639	TCG-----GGAAAACTAATGTGGACATTGAA-----AAGTTATGATTACAGACGGAAGAGGAATCAGGA
hu. 7-C	1639	ACA-----AATGCTAACGACGCGGATTTGGAC-----AATGTCATGATTACAGATGAAGAGGAATCCGCA
hu. 61-C	1639	ACA-----AATGCTAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCCGCA
rh. 56-C	1639	ACA-----AATGCTAACGACGCGGATTTGGAC-----AATGTCATGATTACAGATGAAGAGGAATCCGCA
hu. 9-C	1639	ACA-----AATGCTAACGACGCGGATTTGGAG-----CATGTTATGATTACAGATGAAGAGGAATCAGGA
hu. 54-C	1636	ACA-----AATGCTAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGA
hu. 53-C	1636	ACA-----AATGCTAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGA
hu. 60-C	1639	ACA-----AATGCCAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGA
hu. 55-C	1636	ACA-----AATGCTAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGA
hu. 2-C	1639	ACA-----AATGCCAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGG
hu. 1-C	1639	ACA-----AATGCCAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGG
hu. 18-C	1639	ACA-----AATGCTAACGACGCGGATTTGGAC-----AATGTCATGATTACAGATGAAGAGGAATCCGCA
hu. 3-C	1642	ACA-----AATGCCAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGC
hu. 25-C	1639	ACA-----AATGCCAACGACGCGGATTTGGAA-----AATGTCATGATTACAGATGAAGAGGAATCAGGA
hu. 15-C	1639	ACA-----AATGCTAACGACGCGGATTTGGAC-----AATGTCATGATTACAGATGAAGAGGAATCCGCA

FIG. 3BP

hu. 16-C 1639 ACA-----AATGCTAACGACGCGGATTTGGAC---AATGTCATGATTACAGATTACAGATGAAGAAGAAATCCGCA
 hu. 11-C 1639 ACA-----AATGCTAACGACGCGGATTTGGAG---CATGTTATGATTACAGATTACAGATGAAGAAGAAATCAGGA
 hu. 10-C 1639 ACA-----AATGCTAACGACGCGGATTTGGAG---CATGTTATGATTACAGATTACAGATGAAGAAGAAATCAGGA
 hu. 4-C 1639 ACA-----AATGCTAACGACGCGGATTTGGAA---AATGTCATGATTACAGATTACAGATGAAGAAGAAATCAGGG
 rh. 54-D 1648 GCA-----ACCAAC---AAGACTACACTGGAA---AACGTTGTTAATGACAAATGAAGAAGAAATTCGTC
 rh. 48-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGCTGTTAATGACAAATGAAGAAGAAATTCGTC
 rh. 55-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGCTGTTAATGACAAATGAAGAAGAAATTCGTC
 rh. 62-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGCTGTTAATGACAAATGAAGAAGAAATTCGTC
 AA7-D 1648 GCA-----ACTAAC---AAACTACACTGGAA---AATGCTGTTAATGACAAATGAAGAAGAAATTCGTC
 rh. 52-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 51-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 39-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 53-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 37-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 43-E 1642 GCT-----GCCAGAGACAATGCCGATTACAGC---GATGTCATGCTACCCAGCGAGGAGAAATCAAAA
 rh. 50-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 49-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 61-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 41-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 64-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 42-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 57-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 40-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 AA8-E 1648 GCT-----GCCAGAGACAATGCCGATTACAGC---GATGTCATGCTACCCAGCGAGGAGAAATCAAAA
 rh. 58-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 rh. 40-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 67-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 17-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 6-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA
 hu. 66-E 1648 GCT-----GGAAAAGACAACTGGACTATAGC---AACCTGATGCTAACCCAGCGAGGAGAAATCAAGA

FIG. 3BQ

[illegible]

FIG. 3BR

hu.13-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGGGGGCAACACACAAGC
 AAV2-B 1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.20-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.24-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.64-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.27-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.21-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.22-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.23-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.7-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.61-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 rh.56-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.9-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.54-C 1697 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.53-C 1697 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.60-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.55-C 1697 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.2-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.1-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.18-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.3-C 1703 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.25-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.15-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.16-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.11-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 hu.4-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACTCGAGAGGGGCAACACACAAGC
 rh.54-D 1706 CTACTAATCCCTGTGGCCACAGAGAATACGGGACTGTAGCAGCAACTCGAGGGGGCTAACACTGCAGC
 rh.48-D 1706 CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTAGCAGCAACTCGAGGGGGCTAACACTGCAGC
 rh.55-D 1706 CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTAGCAGCAACTCGAGGGGGCTAACACTGCAGC

FIG. 3BS

rh. 62-D	1706	CTACCAACCCGGTAGCCACCGAGGAATAGCGGACTGTTAGCAGCAACCTGCAGGGCGGTAACACTGCAGC	1830	1840	1850	1860	1870	1880	1890
AAV7-D	1706	CTACTAATCCITGTAGCCACGGAGAAATAGGGGATAGTACAGAGCACTTACAGGGCTAATATGTCAGC							
rh. 52-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 51-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 39-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 53-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 37-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 43-E	1703	CCACTAACCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATTAACCTTGCGAGCAAAACACCGCTCC							
rh. 50-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 49-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 61-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 41-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 64-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 42-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 57-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 40-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
AAV8-E	1709	CCACTAACCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATAACTTGCAGCAGCAAAACACCGCTCC							
rh. 58-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 40-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 67-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 17-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 6-E	1709	CCACCAACCCCGTGGCCACAGACAGTATGGCTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 66-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
rh. 38-E	1709	CCACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 32-F	1703	CTACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
AAV9/hu	1703	CTACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							
hu. 31-F	1703	CTACTAACCCTGTAGCCACAGAACATACGGTGGTGGCTGATAAACCCTACAGCAGCAAAACACCGCTCC							

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FIG. 3BT

AAV5 1740 CGCGACGGCACGTTACAACTCCAGGAATCGTCCCGGACGCTGTGGATGGAGAGGACGTTGTACCTC
 AAV3-3 1773 CACGACTGGAACTGTCAATCATCAGGGGCGCTTACCTGGCATGGTGTGGCAAGATCGTGTACCTGTACCTT
 AAV4-4 1767 GACCGTGGACAGACTGACAGCCTTGGGAGCCGTGCGCTGGAATGGTCTGGCAAGATGACATTTACTAC
 AAV1-A 1773 TCGACCGGAGATGTGATGCTATGGAGCATTTACCTGGCATGGTGTGGCAGATAGAGAGCGTGTACCTG
 hu. 46-A 1773 TCGACCGGAGATGTGATGCTATGGAGCATTTACCTGGCATGGTGTGGCAGATAGAGAGCGTGTACCTG
 hu. 48-A 1773 TCGACCGGAGATGTGATGCTATGGAGCATTTACCTGGCATGGTGTGGCAGATAGAGAGCGTGTACCTG
 hu. 44-A 1773 TCGACCGGAGATGTGATGCTATGGAGCATTTACCTGGCATGGTGTGGCAGATAGAGAGCGTGTACCTG
 hu. 43-A 1776 TCGACCGGAGATGTGATGCTATGGAGCATTTACCTGGCATGGTGTGGCAGATAGAGAGCGTGTACCTG
 AAV6-A 1773 TCGACCGGAGATGTGATGCTATGGAGCATTTACCTGGCATGGTGTGGCAGATAGAGAGCGTGTACCTG
 hu. 34-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 47-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 29-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 63-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 56-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 45-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 57-B 1767 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 35-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 58-B 1770 ATCTACTGCGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 28-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 51-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 19-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 49-B 1770 AGCTACTGCGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 52-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 13-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 AAV2-B 1770 AGCTACCGGAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu. 20-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 24-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 64-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 27-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu. 21-B 1770 AGCTACCTCAGATGTCAACACACAAAGGCGTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG

FIG. 3BU

hu. 22-B 1770 AGCTACCTCAGATGTCAACACACACACAGGGGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu. 23-B 1770 AGCTACCTCAGATGTCAACACACACACAGGGGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu. 7-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGCATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 61-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGCATGGTGTGGAGGATCGAGACGTGTACCTG
 rh. 56-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGCATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 9-C 1770 AACTACAGAAAATGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 54-C 1767 AAGTACTGAACTGTGAATCACCAGGAGCATTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 53-C 1767 AAGTACTGAACTGTGAATCACCAGGAGCATTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 60-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 55-C 1767 AAGTACTGAACTGTGAATCACCAGGAGCATTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 2-C 1770 AACTACTGGAACTGTCAATCGCCNAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 1-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 18-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 3-C 1773 AACTACAGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 25-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 16-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 11-C 1770 AACTACAGAAAATGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 10-C 1770 AACTACAGAAAATGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 hu. 4-C 1770 AACTACTGGAACTGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 rh. 54-D 1776 CCAGACACAAGTTGTCAACAACCCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 rh. 48-D 1776 CCAGACACAAGTTGTCAACAACCCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 rh. 55-D 1776 CCAGACACAAGTTGTCAACAACCCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 rh. 62-D 1776 CCAGACACAAGTTGTCAACAACCCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 AAV7-D 1776 CCAGACACAAGTTGTCAACAACCCAGGAGCGTTACCTGGTATGGTGTGGAGGATCGAGACGTGTACCTG
 rh. 52-E 1779 TATTGTGGGGCCGTCACAGCCAGGGAGCGTTACCTGGCATGGTGTGGAGAACCCGGGACGTGTACCTG
 rh. 51-E 1779 TATTGTGGGGCCGTCACAGCCAGGGAGCGTTACCTGGCATGGTGTGGAGAACCCGGGACGTGTACCTG
 hu. 39-E 1779 TACTGTGGGGCCGTCACAGCCAGGGAGCGTTACCTGGCATGGTGTGGAGAACCCGGGACGTGTACCTG
 rh. 53-E 1779 TATTGTGGGGCCGTCACAGCCAGGGAGCGTTACCTGGCATGGTGTGGAGAACCCGGGACGTGTACCTG
 hu. 37-E 1779 TATTGTGGAAAATGTCAACAGCCAGGAGCGTTACCTGGCATGGTGTGGAGAACCCGGGACGTGTACCTG

FIG. 3BV

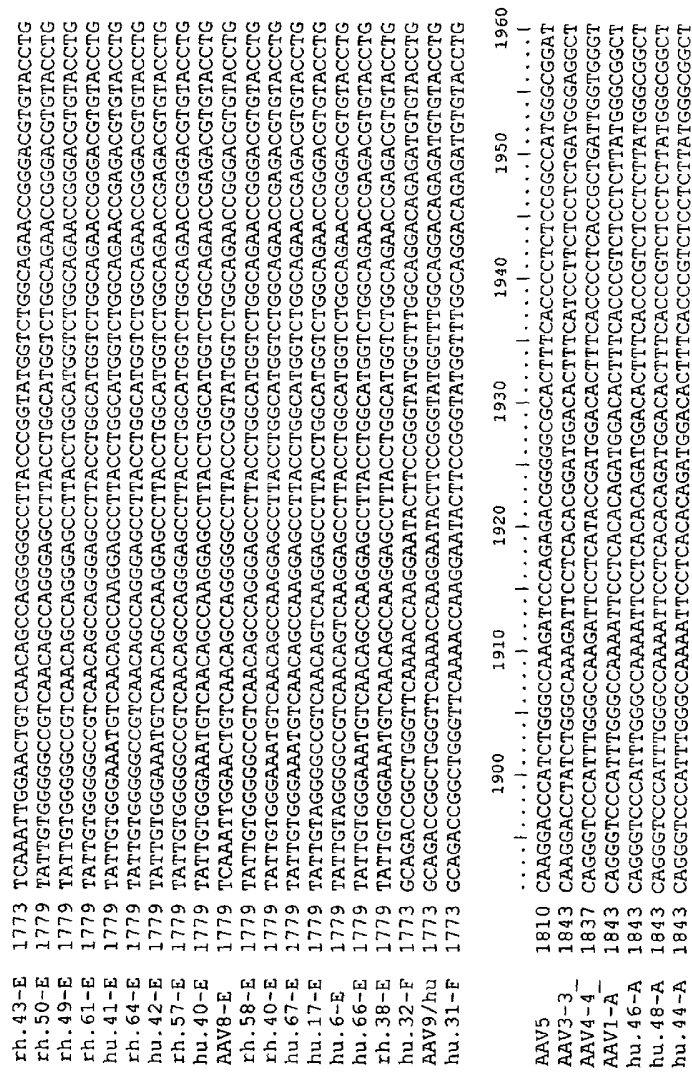


FIG. 3BW

hu. 43-A 1846 CAGGGTCCCATTTGGGCCAAAATTCCTCACACAGATGGACATTTACCCGGTCTCCTCTTATGGGGGGCT
 AAV6-A 1843 CAGGGTCCATTTGGGCCAAAATTCCTCACAGGATGGACATTTACCCGGTCTCCTCTCATATGGGGGGCT
 hu. 34-B 1840 CAGGGGGCCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 47-B 1840 CAGGGGGCCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 29-B 1840 CAGGGGGCCATTTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 63-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 56-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 45-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 57-B 1837 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 35-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 58-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 28-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 51-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 19-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 49-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 52-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 13-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 AAV2-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 20-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 24-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 64-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 27-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 21-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 22-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 23-B 1840 CAGGGGGCCATCTGGGCCAAAGATTCCACACAGGACGGACATTTTACCCCTCTCCCTCATATGGGTGGAT
 hu. 7-C 1840 CAGGGACCCATTTGGGCCAAAGATTCCCTCACACCGATGGACATTTTATCCTTCTCCACTGATGGAGGTT
 hu. 61-C 1840 CAGGGACCCATTTGGGCCAAAGATTCCCTCACACCGATGGACATTTTATCCTTCTCCACTGATGGAGGTT
 rh. 56-C 1840 CAGGGACCCATTTGGGCCAAAGATTCCCTCACACCGATGGACATTTTATCCTTCTCCACTGATGGAGGTT
 hu. 9-C 1840 CAGGGACCCATTTGGGCCAAAGATTCCCTCACACCGATGGACATTTTATCCTTCTCCACTGATGGAGGTT
 hu. 54-C 1837 CAGGGACCCATTTGGGCCAAAGATTCCCTCACACCGATGGACATTTTATCCTTCTCCACTGATGGAGGTT

FIG. 3BX

hu. 53-C 1837 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 60-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 55-C 1837 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 2-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 1-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 18-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 3-C 1843 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 25-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 15-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 16-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 11-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 10-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 4-C 1840 CAGGGACCCATTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 54-D 1846 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 48-D 1846 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 55-D 1846 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 62-D 1846 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 AAV7-D 1846 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 52-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 51-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 39-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 53-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 37-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 43-E 1843 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 50-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 49-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 61-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 41-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 rh. 64-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT
 hu. 42-E 1849 CAGGGTCCCATCTGGGCCAAGATTCTCACACCGATGGACATTTCATCTCTCCACTGATGGAGGTT

FIG. 3BY

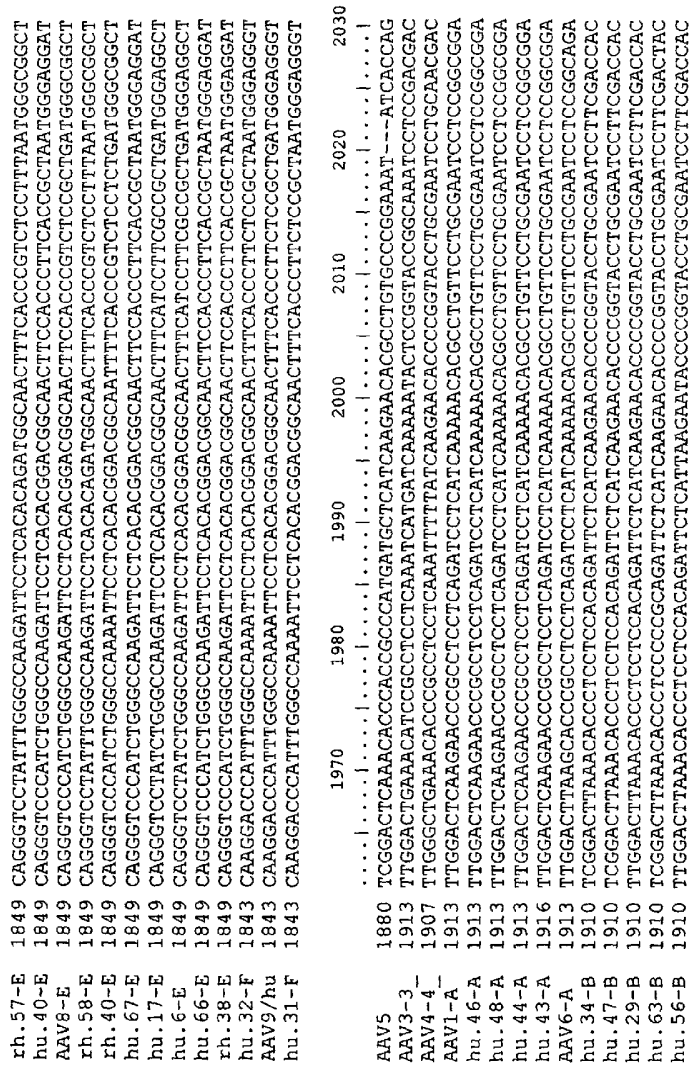


FIG. 3B2

hu.45-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.57-B 1907 TTGGACTTAAACACCCCTCCTCCACAGATTCTCATTAAGATACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.35-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.58-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.28-B 1910 TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.51-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.19-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.49-B 1910 TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.52-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.13-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 AAV2-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.20-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.24-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.64-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.27-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.21-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.22-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.23-B 1910 TTGGACTTAAACACCCCGCTCCTCCACAGATTCTCATCAAGAACACACCCCGGTACCTGGGAATCCTTCGACCAC
 hu.7-C 1910 TTGGCTCAAAACACCCCGCTCCTCAGATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.61-C 1910 TTGGACTCAAAACACCCACCTCCTCAATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 rh.56-C 1910 TTGGCTCAAAACACCCCGCTCCTCAGATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.9-C 1910 TTGGACTCAAAACACCCCGCTCCTCAATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.54-C 1907 TTGGACTCAAAACACCCCGCTCCTCAGATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.53-C 1907 TTGGACTCAAAACACCCCGCTCCTCAGATTATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.60-C 1910 TTGGACTCAAAACACCCACCTCCTCAATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.55-C 1907 TTGGACTCAAAACACCCCGCTCCTCAGATTATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.2-C 1910 TTGGACTCAAAACACCCCGCTCCTCAGATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.1-C 1910 TTGGACTCAAAACACCCCGCTCCTCAGATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.18-C 1910 TTGGCTCAAAACACCCCGCTCCTCAGATCATGATCAAAACACACCTCCGTTCCAGCCAATCCTCCACAAA
 hu.3-C 1913 TTGGACTCAAAACACCCCGCTCCTCAGATCATGATCAAAAGCACCTCCGTTCCAGCCAATCCTCCACAAA

FIG. 3CA

hu.25-C 1910 TTGGACTCAAAACACCCGGCTCCTCAGATTATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.15-C 1910 TTGGACTCAAAACACCCAGCTCCTCAGATCATGATTTAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.16-C 1910 TTGGACTCAAAACACCCAGCTCCTCAGATCATGATTTAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.11-C 1910 TTGGACTCAAAACACCCGGCTCCTCAATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.10-C 1910 TTGGACTCAAAACACCCGGCTCCTCAATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.4-C 1910 TTGGACTCAAAACACCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.54-D 1916 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.48-D 1916 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.55-D 1916 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.62-D 1916 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 AAV7-D 1916 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.52-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.51-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.39-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.53-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.37-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.43-E 1913 TTGGCTGAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.50-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.49-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.61-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.41-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.64-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.42-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.57-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.40-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 AAV8-E 1919 TTGGCTGAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.58-E 1919 TTGGACTTAAACATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 rh.40-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.67-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA
 hu.17-E 1919 TTGGACTGAAGCATCCGGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAAATCCTCTCTACAAA

FIG. 3CB

hu. 6-E	1919	TTGGACTGAAACACCCGCTCCTCAGATCCTGATTAAGAAATACACCTTTCCGCGGATCCTCCAACTAC	2040	2050	2060	2070	2080	2090	2100
hu. 66-E	1919	TTGGACTGAAGCACCCACCTCCTCAGATCCTGATCAAGAACACCCGCTACCTCGGATCCTCCAAACAC							
rh. 38-E	1919	TTGGACTGAAGCACCCACCTCCTCAGATCCTGATCAAGAAACACCCGCTACCTCGGATCCTCCAAACAC							
hu. 32-F	1913	TTGGAATGAAGCACCCGCTCCTCAGATCCTGATCAAAACACACCTGTCTCGGATCCTCCAAACGCG							
AAV9/hu	1913	TTGGAATGAAGCACCCGCTCCTCAGATCCTGATCAAAACACACCTGTCTCGGATCCTCCAAACGCG							
hu. 31-F	1913	TTGGAATGAAGCACCCGCTCCTCAGATCCTGATCAAAACACACCTGTCTCGGATCCTCCAAACGCG							
AAV5	1947	CTTCTCGGACGTGCCGTCAGCAGCTTCATCACCCAGTACAGCACCGGCGAGGTACCCGTGGAGATGGAG							
AAV3-3	1983	TTTCAGCCCGCCAAAGTTTGCTTCATTTACTCAGTACTCCACTGGACAGGTACCGTGGAAATTTGAG							
AAV4-4	1977	CTTCAGCTCTACTCCGGTAACTCCTTCATTTACTCAGTACAGCACTGGCCAGGTGTCGGTCAGATTGAC							
AAV1-A	1983	GTTTTTCAGCTACAAAGTTTGCTTCATTCATCATCCCAATCTCCACAGGACAAAGTGTGGAAATTTGAA							
hu. 46-A	1983	GTTTTTCAGCTACAAAGTTTGCTTCATTCATCATCCCAATCTCCACAGGACAAAGTGTGGAAATTTGAA							
hu. 48-A	1983	GTTTTTCAGCTACAAAGTTTGCTTCATTCATCATCCCAATCTCCACAGGACAAAGTGTGGAAATTTGAA							
hu. 44-A	1983	GTTTTTCAGCTACAAAGTTTGCTTCATTCATCATCCCAATCTCCACAGGACAAAGTGTGGAAATTTGAA							
hu. 43-A	1986	GTTTTTCAGCTACAAAGTTTGCTTCATTCATCATCCCAATCTCCACAGGACAAAGTGTGGAAATTTGAA							
AAV6-A	1983	GTTTTTCAGCTACAAAGTTTGCTTCATTCATCATCCCAATCTCCACAGGACAAAGTGTGGAAATTTGAA							
hu. 34-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 47-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 29-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 63-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 56-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 45-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 57-B	1977	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 35-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 58-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 28-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 51-B	1980	CTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							
hu. 19-B	1980	TTTCAGTGGCGCAAGTTTGCTTCCTTCATCACACAGTACTCCACGGGACAGGTACCGGTGGAGATCGAG							

FIG. 3C

hu. 49-B 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 52-B 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 13-B 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 AAV2-B 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 20-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 24-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 64-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 27-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 21-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 22-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 23-B 1980 TTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 7-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 61-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 rh. 56-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 9-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 54-C 1977 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 53-C 1977 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 60-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 55-C 1977 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 2-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 1-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 18-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 3-C 1983 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 25-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 15-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 16-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 11-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 10-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 hu. 4-C 1980 CTTCAAGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG
 rh. 54-D 1986 GTTTACGCGTGGGCAAGTTGCTTCTTTCATCACACAGTATTCACAGGCGAGGTACGCGTGGAGATCGAG

FIG. 3CD

rh. 48-D 1986 GTTTACGCGTCCCAAGTTTGCTTCTTTCATCACACAGTACAGCACCGGCGAGGTACAGCGTGGAGATCGAG
 rh. 55-D 1986 GTTTAGCGCTGCCAAGTTTGGCTTCTTTCATCACACAGTACAGCACCGGCGAGGTACAGCGTGGAGATCGAG
 rh. 62-D 1986 GTTTACGCGCTCCCAAGTTTGGCTTCTTTCATCACACAGTACAGCACCGGCGAGGTACAGCGTGGAGATCGAG
 AAV7-D 1986 GTTTACTCTGCGCAAGTTTGGCTTCTTTCATCACACAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 rh. 52-E 1989 GTTCAACCGAGGCGCAAGTTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 rh. 51-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 hu. 39-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 rh. 53-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 hu. 37-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 rh. 43-E 1983 CTTCAACCGAGTCAAGCTGAATTTCTTTCATCAGCGAATACAGCACCGGCGAAGTACAGCGTGGAAATCGAA
 rh. 50-E 1989 GTTCAACCGAGGCGCAAGCTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 rh. 49-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 rh. 61-E 1989 GTTCAACCGAGGCGCAAGCTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 hu. 41-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 rh. 64-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGTG
 hu. 42-E 1989 GTTCAACCGAGGCGCAAGCTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 rh. 57-E 1989 GTTCAACCGAGGCGCAAGCTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 hu. 40-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 AAV8-E 1989 CTTCAACCGAGTCAAGCTGAATTTCTTTCATCAGCGAATACAGCACCGGCGAAGTACAGCGTGGAAATCGAA
 rh. 58-E 1989 GTTCAACCGAGGCGCAAGCTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 rh. 40-E 1989 GTTCAACCGAGGCGCAAGTGAATTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 hu. 67-E 1989 GTTCAACCGAGGCGCAAGTGAATTTGGCTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 hu. 17-E 1989 CTTCAACCGAGGCGCAAGTGAATTTGGCTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAA
 hu. 6-E 1989 CTTCAACCGAGGCGCAAGCTGGCTGCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAA
 hu. 66-E 1989 GTTCAACCGAGGCGCAAGTGAATTTGGCTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 rh. 38-E 1989 GTTCAACCGAGGCGCAAGTGAATTTGGCTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAAATCGAG
 hu. 32-F 1983 TTTCAATAGGACAAAGCTGAATCTTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 AAV9/hu 1983 CTTCAACCGAGGACAAAGCTGAATCTTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG
 hu. 31-F 1983 TTTCAATAGGACAAAGCTGAATCTTTCTTTCATCAGCGAGTACAGCACCGGCGAAGTACAGCGTGGAGATCGAG

FIG. 3CE

[illegible]

FIG. 3CF

hu. 27-B 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATCCGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 21-B 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 22-B 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 23-B 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 7-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 61-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 56-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 9-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 54-C 2047 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 53-C 2047 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 60-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 55-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 2-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 1-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 18-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 3-C 2053 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 25-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 15-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 16-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 11-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 10-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 4-C 2050 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 54-D 2056 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 48-D 2056 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 55-D 2056 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 62-D 2056 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 AA7-D 2056 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 52-E 2059 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 rh. 51-E 2059 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT
 hu. 39-E 2059 TGGGAGCTGCAGAGGAGAGACAGCAACCGCTGGAAATTCAGTACACTTCCAACTACACAAAT

FIG. 3CG

rh. 53-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 37-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 43-E	2053	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 50-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 49-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 61-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 41-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 64-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 42-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 57-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 40-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
AAV8-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 58-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 40-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 67-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 17-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 6-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 66-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
rh. 38-E	2059	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 32-F	2053	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
AAV9/hu	2053	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
hu. 31-F	2053	TGGGAGCTGCAGAGGAGGAACAGCAAGCGCTGGAAACCCAGAGATT	2200	2210	2220	2230	2240
AAV5	2087	CCCAAGCTTTGGACTTTGCCCGGACAGACCGGGGAATACAGAACCCAGACCTATCGGAACCCGATA	2210	2220	2230	2240	
AAV3-3	2123	CTGTTAATGTGGACTTTTACTGTAGACACTAATGGTGTATAGTGAACCTCGCCCTATGGAAACCCGTA	2210	2220	2230	2240	
AAV4-4	2117	AAACTCTCTGTTCTGGGCTCCCGATCGGCTGGGAAATACACTGAGCTAGGGCTATCGGTACCCGCTA	2210	2220	2230	2240	
AAV1-A	2123	CTGCCAACGTTGATTTTACTGTGGACAAATGGACTTTATCTGAGCTCGCCCTATGGCAACCCGTTA	2210	2220	2230	2240	
hu. 46-A	2123	CTGCCAACGTTGATTTTACTGTGGACAAATGGACTTTATCTGAGCTCGCCCTATGGCAACCCGTTA	2210	2220	2230	2240	

FIG. 3CH

hu. 48-A 2123 CTGCCAACGTTGATTTTACTGTGGACAAATGGACTTTATCTAGCCTCGCCCATTTGGCACCCGTTA
 hu. 44-A 2123 CTGCCAACGTTGATTTTACTGTGGACAAATGGACTTTATCTAGCCTCGCCCATTTGGCACCCGTTA
 hu. 43-A 2126 CTGCCAGCGTTGATTTTACTGTGGACAAATGGACTTTATCTAGCCTCGCCCATTTGGCACCCGTTA
 AAV6-A 2123 CTGCCAACGTTGATTTTACTGTGGACAAATGGACTTTATCTAGCCTCGCCCATTTGGCACCCGTTA
 hu. 34-B 2120 CTGTTAATGTGGACTTTACTGTGGACAAATGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 47-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 29-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 63-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 56-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGGTTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 45-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 57-B 2117 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGGTTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 35-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 58-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 28-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 51-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 19-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 49-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 52-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 13-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 AAV2-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 20-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 24-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 64-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 27-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 21-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 22-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 23-B 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 7-C 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 hu. 61-C 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGTGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA
 rh. 56-C 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAITGGCGTGTATTCAGAGCCTCGCCCATTTGGCACCCAGATA

FIG. 3CI

hu. 9-C 2120 CTGTTAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 54-C 2117 CTGTTAAATGGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 53-C 2117 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 60-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 55-C 2117 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 2-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 1-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 18-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 3-C 2123 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 25-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 15-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 16-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 11-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 10-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 hu. 4-C 2120 CTGTTAAATGTGGACTTTACTGTGGACACTAAATGGTGTGTATTTCAGAGCCTTGCCTCCCATTTGGCACCAGATA
 rh. 54-D 2126 AGACTGGTGTGGACTTTGCGTTTGACAGCCAGGGTGTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
 rh. 48-D 2126 AGACTGGTGTGGACTTTGCGTTTGACAGCCAGGGTGTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
 rh. 55-D 2126 AGACTGGTGTGGACTTTGCGTTTGACAGCCAGGGTGTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
 rh. 62-D 2126 AGACTGGTGTGGACTTTGCGTTTGACAGCCAGGGTGTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
 AAV7-D 2126 AGACTGGTGTGGACTTTGCGTTTGACAGCCAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 52-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 51-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 hu. 39-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 53-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 hu. 37-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 43-E 2123 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 50-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 49-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 rh. 61-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGCACCAGATA
 hu. 41-E 2129 CTACAAATGTGGACTTTGCTGTTAACTAGAGGGTGTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA

FIG. 3CJ

rh. 64-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTAGGGTGTTTACTCTGAGCCTCGCCCCCATTTGGCAGCTCGTTA
hu. 42-E	2129	CTACAAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 57-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTAGGGTGTTTACTCTGAGCCTCGCCCCCATTTGGCAGCTCGTTA
hu. 40-E	2129	CTACAAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGTACTCGTTA
AAV8-E	2129	CTACAAAGTGTGGACTTTGCTGTTAATACTAGAGAGGGTGTTTACTCTGAGCCTCGCCCCCATTTGGCAGCTCGTTA
rh. 58-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTAGGGTGTTTACTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 40-E	2129	CTACAAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 67-E	2129	CTGTTAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGCAGCAGATA
hu. 17-E	2129	CTGTTAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGCAGCAGATA
hu. 66-E	2129	CTACAAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 38-E	2129	CTACAAATGTGGACTTTGCTGTCATATACAGAGGAACATTATTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 32-F	2123	CTAATAATGTTGAATTTGCTGTTAATACTAGAGGTGTATAGTGAACCCCGCCCCCATTTGGCAGCAGATA
AAV9/hu	2123	CTAATAATGTTGAATTTGCTGTTAATACTAGAGGTGTATAGTGAACCCCGCCCCCATTTGGCAGCAGATA
hu. 31-F	2123	CTAATAATGTTGAATTTGCTGTTAATACTAGAGGTGTATAGTGAACCCCGCCCCCATTTGGCAGCAGATA
		2250 2260
AAV5	2157	
RAV3-3	2193	CCTTACCCGACCCCTT---
AAV4-4	2187	TCTCACAGAACTTG---
RAV1-A	2193	CCTACCCACCACTGTAA-
hu. 46-A	2193	CCTTACCCGTCCTGTAA-
hu. 48-A	2193	CCTTACCCGTCCTGTAA-
hu. 44-A	2193	CCTTACCCGTCCTGTAA-
hu. 43-A	2196	CCTTACCCGTCCTGTAA-
RAV6-A	2193	CCTACCCGTCCTGTAA-
hu. 34-B	2190	CCTGACTCGTAATCTGTAA-
hu. 47-B	2190	CCTGACTCGTAATCTGTAA-
hu. 29-B	2190	CCTGACTCGTAATCTGTAA-

FIG. 3CK

hu.63-B 2190 CCTGACTCGTAATCTGTAA-
hu.56-B 2190 CCTGACTCGTAATCTGTAA-
hu.45-B 2190 CCTGACTCGTAATCTGTAA-
hu.57-B 2187 CCTGACTCGTAATCTGTAA-
hu.35-B 2190 CCTGACTCGTAATCTGTAA-
hu.58-B 2190 CCTGACTCGTAATCTGTAA-
hu.28-B 2190 CCTGACTCGTAATCTGTAA-
hu.51-B 2190 CCTGACTCGTAATCTGTAA-
hu.19-B 2190 CCTGACTCGTAATCTGTAA-
hu.49-B 2190 CCTGACTCGTAATCTGTAA-
hu.52-B 2190 CCTGACTCGTAATCTGTAA-
hu.13-B 2190 CCTGACTCGTAATCTGTAA-
AAV2-B 2190 CCTGACTCGTAATCTGTAA-
hu.20-B 2190 CCTGACTCGTAATCTGTAA-
hu.24-B 2190 CCTGACTCGTAATCTGTAA-
hu.64-B 2190 CCTGACTCGTAATCTGTAA-
hu.27-B 2190 CCTGACTCGTAATCTGTAA-
hu.21-B 2190 CCTGACTCGTAATCTGTAA-
hu.22-B 2190 CCTGACTCGTAATCTGTAA-
hu.23-B 2190 CCTGACTCGTAATCTGTAA-
hu.7-C 2190 CCTGACTCGTAATCTGTAA-
hu.61-C 2190 CCTGACTCGTAATCTGTAA-
rh.56-C 2190 CCTGACTCGTAATCTGTAA-
hu.9-C 2190 CCTGACTCGTAATCTGTAA-
hu.54-C 2187 CCTGACTCGTAATCTGTAA-
hu.53-C 2187 CCTGACTCGTAATCTGTAA-
hu.60-C 2190 CCTGACTCGTAATCTGTAA-
hu.55-C 2187 CCTGACTCGTAATCTGTAA-
hu.2-C 2190 CCTGACTCGTAATCTGTAA-
hu.1-C 2190 CCTGACTCGTAATCTGTAA-

FIG. 3CL

hu.18-C	2190	CCCGACTCGTAATCTGTAA-
hu.3-C	2193	CCTGACTCGTAATCTGTAA-
hu.25-C	2190	CCTGACTCGTAATCTGTAA-
hu.15-C	2190	CCTGACTCGTAATCTGTAA-
hu.16-C	2190	CCTGACTCGTAATCTGTAA-
hu.11-C	2190	CCTGACTCGTAATCTGTAA-
hu.10-C	2190	CCTGACTCGTAATCTGTAA-
hu.4-C	2190	CCTGACTCGTAATCTGTAA-
rh.54-D	2196	CCTCACC CGTAATCTGTAA-
rh.48-D	2196	CCTCACC CGTAATCTGTAA-
rh.55-D	2196	CCTCACC CGTAATCTGTAA-
rh.62-D	2196	CCTCACC CGTAATCTGTAA-
AAV7-D	2196	CCTCACC CGTAATCTGTAA-
rh.52-E	2199	CCTCACC CGTAATCTGTAA-
rh.51-E	2199	CCTCACC CGTAATCTGTAA-
hu.39-E	2199	CCTCACC CGTAATCTGTAA-
rh.53-E	2199	CCCCACC CGTAATCTGTAA-
hu.37-E	2199	CCTCACC CGTAATCTGTAA-
rh.43-E	2193	CCTCACC CGTAATCTGTAA-
rh.50-E	2199	CCTCACC CGTAATCTGTAA-
rh.49-E	2199	CCTCACC CGTAATCTGTAA-
rh.61-E	2199	CCTCACC CGTAATCTGTAA-
hu.41-E	2199	CCTCACC CGTAATCTGTAA-
rh.64-E	2199	CCTCACC CGTAATCTGTAA-
hu.42-E	2199	CCTCACC CGTAATCTGTAA-
rh.57-E	2199	CCTCACC CGTAATCTGTAA-
hu.40-E	2199	CCTCACC CGTAATCTGTAA-
AAV8-E	2199	CCTCACC CGTAATCTGTAA-
rh.58-E	2199	CCTCACC CGTAATCTGTAA-
rh.40-E	2199	TCTGACACGTAATCTGTAA-

FIG. 3CM

hu.67-E	2199	CCTCACCCGGTAATCTGTAA-
hu.17-E	2199	CCTGACTCGTAATCTGTAA-
hu.6-E	2199	CCTCACCCGGTAACCTGTAA-
hu.66-E	2199	CCTCACCCGGTAATCTGTAA-
rh.38-E	2199	CCTCACCCGGTAATCTGTAA-
hu.32-F	2193	CCTGACTCGTAATCTGTAA-
AAV9/hu	2193	CCTGACTCGTAATCTGTAA-
hu.31-F	2193	CCTGACTCGTAATCTGTAA-

FIG. 3CN

