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(74) Képviselő:

SBGK Szabadalmi Ügyvivői Iroda, Budapest(54) **Adeno-asszociált vírus (AAV) kládok, szekvenciák, az azokat tartalmazó vektorok és alkalmazásaik**

Az európai szabadalom ellen, megadásának az Európai Szabadalmi Közlönyben való meghirdetésétől számított kilenc hónapon belül, felszólalást lehet benyújtani az Európai Szabadalmi Hivatalnál. (Európai Szabadalmi Egyezmény 99. cikk(1))

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(54) **Adeno-associated virus (AAV) clades, sequences, vectors containing same, and uses thereof**

Claden und Sequenzen von adeno-assoziiertem Virus (AAV), diese enthaltende Vektoren und ihre Verwendungen

Variantes des virus associés aux adenovirus (AAV), séquences, vecteurs les contenant, et leur utilisation

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- **GRIMM D ET AL: "FROM VIRUS EVOLUTION TO VECTOR REVOLUTION: USE OF NATURALLY OCCURRING SEROTYPES OF ADENO-ASSOCIATED VIRUS (AAV) AS NOVEL VECTORS FOR HUMAN GENE THERAPY", CURRENT GENE THERAPY, vol. 3, no. 4, August 2003 (2003-08), pages 281-304, XP009040225, ISSN: 1566-5232**

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Remarks:

The complete document including Reference Tables and the Sequence Listing can be downloaded from the EPO website

Description

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

5 **[0001]** This application contains work supported by grants NIDDK P30 DK47757 and NHLBI P01 HL59407 from the National Institutes of Health (NIH). The US government may have certain rights in this invention.

BACKGROUND OF THE INVENTION

10 **[0002]** 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
15 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.

[0003] 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).

20 **[0004]** 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.

[0005] 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
25 but not those of the present invention.

[0006] What is desirable are AAV-based constructs for delivery of heterologous molecules.

SUMMARY OF THE INVENTION

30 **[0007]** 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.

[0008] In one aspect, the invention provides an adeno-associated virus (AAV) comprising at least an AAV capsid comprising amino acids 1 to 734 of SEQ ID NO: 186 (AAVhu.53) or SEQ ID NO: 187 (hu.55), or SEQ ID NO: 188 (hu.54),
35 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.

[0009] In another aspect, the invention provides an isolated adeno-associated virus capsid protein selected from the group consisting of: vp 1 capsid protein having the sequence of amino acids 1 to 734, SEQ ID NO: 186, SEQ ID NO: 187 or SEQ ID NO: 188; vp2 capsid protein having the sequence of amino acids 138 to 734, SEQ ID NO: 186, SEQ ID
40 NO: 187 or SEQ ID NO: 188; and vp3 capsid protein having the sequence of amino acids 204 to 734, SEQ ID NO: 186, SEQ ID NO: 187 or SEQ ID NO: 18. The invention also extends to nucleic acid molecules comprising nucleic acid sequences encoding such proteins.

[0010] In a further alternative 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
45 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 of the invention as described above.

[0011] The present invention also provides host cells comprising the claimed AAVs, as well as compositions containing the AAVs and uses therefor. Advantageously, these compositions are particularly well suited for use in compositions
50 requiring readministration of AAV vectors for therapeutic or prophylactic purposes.

[0012] These and other aspects of the invention will be readily apparent from the following detailed description of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

55 **[0013]**

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

[0014] 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.

[0015] 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.

[0016] 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.

[0017] 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.

[0018] 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.

[0019] 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.

[0020] 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).

[0021] 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.

[0022] 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.

[0023] As defined herein, to form serotype 9, antibodies generated to a selected AAV capsid must not be cross-reactive with any of AAV 1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7 or AAV8.

[0024] 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

[0025] 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.

[0026] The Neighbor-Joining algorithm has been described extensively in the literature. See, e.g., M. Nei and S. Kumar, *Molecular Evolution and Phylogenetics* (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.

[0027] 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.

[0028] 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.

[0029] 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).

[0030] 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.

[0031] 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.

[0032] 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):

[0033] 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]; and 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].

[0034] 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.

[0035] 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):

[0036] 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].

[0037] 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.

[0038] 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)

[0039] 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].

[0040] 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.

[0041] 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)

[0042] 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]. The invention further includes modified cy. 5 [SEQ ID NO: 227]; modified rh.13 [SEQ ID NO: 228]; and modified rh. 37 [SEQ ID NO: 229].

[0043] 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.

[0044] 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)

[0045] 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)].

[0046] 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].

[0047] 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 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.

[0048] 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)

[0049] 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

[0050] 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.

[0051] 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].

[0052] 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

[0053] The invention provides the AAVs, isolated capsid proteins, nucleic acids, methods of generation, transfected host cells, compositions and uses, as defined in the claims, which are characterized by capsids of AAVhu.53, AAVhu.55 and AAVhu.54. 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.

[0054] 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;

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;

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;

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;

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. AY530554], 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. AY530558]; 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. AY530564]; 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. AY530570]; 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;

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.

[0055] 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.

[0056] 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 P19 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.

[0057] The capsids of the invention can be readily utilized in a variety of vector systems and host cells. They 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.

[0058] 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.

[0059] Suitable fragments can be determined using the information provided herein.

[0060] 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.

[0061] These and other embodiments and advantages of the invention are described in more detail below.

A. AAV Serotype 9/hu14 Sequences

[0062] 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

[0063] The AAV9 nucleic acid sequences include the DNA sequences of SEQ ID NO: 3, which consists of 2211 nucleotides.

[0064] 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.

[0065] 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.

[0066] 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.

[0067] 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.

[0068] 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 vp 1 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

[0069] 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 invention is not limited to novel AAV amino acid sequences, peptides and proteins expressed from the novel AAV nucleic acid sequences of the invention, 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.

[0070] 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 and are not a limitation of the present invention.

[0071] 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.

[0072] 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 capsids.

[0073] 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; aa 447-477; aa 495-602; aa 660-669; and aa 707-723. 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; aa 133-165; 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 AAV capsids.

[0074] Still other desirable AAV9/HU.14 proteins include the rep proteins include rep68/78 and rep40/52.

[0075] 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.

[0076] 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, Friezner-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.

[0077] 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

[0078] The invention encompasses novel AAV capsid sequences of which are free of DNA and/or cellular material with which these viruses are associated in nature. To avoid repeating all of the AAV capsids discussed herein, reference is made throughout this and the following sections to the hu.14/AAV9 capsid. However, it should be appreciated that the other AAV capsid sequences can be used in a similar manner.

[0079] 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.

[0080] 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.

[0081] 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.

[0082] 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.

[0083] 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).

[0084] 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.

[0085] In one aspect, the invention provides a method of generating a recombinant adeno-associated virus (AAV) as claimed in claim 11.

[0086] 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.

[0087] 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.

[0088] 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 and one of the other AAV sequences described herein. 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

[0089] 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

[0090] 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.

[0091] 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.

[0092] 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.

[0093] 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.

[0094] 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.

[0095] 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

[0096] 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.

[0097] 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.

[0098] 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 metallothionein (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.

[0099] 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.

[0100] 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), Arbuthnot 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.

[0101] 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].

[0102] 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

[0103] 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.

[0104] 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

[0105] 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.

[0106] 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.

[0107] 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.

[0108] 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.

[0109] 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.

[0110] 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.

[0111] 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.

[0112] 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.

[0113] 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.

[0114] In another embodiment of this invention, the *rep* or *cap* protein may be provided stably by a host cell.

C. The Helper Functions

[0115] 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.

[0116] 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.

[0117] 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

[0118] 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.

[0119] 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 AAV9 *cap* sequences described herein.

[0120] 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.

[0121] 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).

[0122] 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.

[0123] 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 vectors 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.

[0124] 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

[0125] 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 from a single AAV can be utilized. Alternatively, 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

[0126] Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

[0127] In one desirable embodiment, the invention enables AAV-mediated delivery of a transgene to a host.

[0128] 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.

[0129] 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.

[0130] 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 example, 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 examples, 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 examples, 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.

[0131] 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.

[0132] 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.

[0133] 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.

[0134] 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.

[0135] 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

[0136] 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 heregluin/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.

[0137] 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.

[0138] 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.

[0139] 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)).

[0140] 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.

[0141] 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].

[0142] 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.

[0143] 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).

[0144] 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)].

[0145] 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.

[0146] 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.

[0147] 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.

[0148] 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.

[0149] 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

[0150] 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.

[0151] 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 calcivirus family. The calcivirus 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 encephalitis, blue tongue). The retrovirus family includes the sub-family oncorovirinae 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 (BKV and JC virus) and the sub-family papillomavirus (associated with cancers or malignant progression of papilloma). The adenovirus family includes viruses (EX, AD7, AD7, O.B.) which cause respiratory disease and/or enteritis. The parvovirus family includes feline parvovirus (feline enteritis), feline panleucopenia virus, canine parvovirus, and porcine parvovirus. The herpesvirus family includes the sub-family alphaherpesvirinae, which encompasses the genera simplexvirus (HSV-I, HSV-II), 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.

[0152] 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; erysiplothrax rhusiopathiae; *Corynebacterium diphtheriae* (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.

[0153] 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), *Ricinus 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 (*Richettsia 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.

[0154] 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.

[0155] 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 example, 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.

[0156] 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.

[0157] The following examples illustrate several aspects and embodiments of the invention.

EXAMPLE 1 - Computational analysis of primate AAV sequences

A. Collection of primate tissues

[0158] 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

[0159] 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

[0160] 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 MEGA™ 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.

[0161] 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.

[0162] 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)].

[0163] 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.

[0164] 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)				

(continued)

Classification of the number of sources (sequences) per species and per clade or clone

	Human	Rhesus	Cyno	Baboon	Chimp	Pigtail
<u>Clade/representative</u>						
AAV5						
Ch.5					1(1)	
Rh.8		2(2)				

[0165] 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.

[0166] 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

[0167] 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).

[0168] 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 USA 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

[0169] 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).

[0170] 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

[0171] 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.

[0172] 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*

[0173] 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 USA 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*

[0174] 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).

[0175] 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.

[0176] 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.

[0177] 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

[0178] 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.

[0179] 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

[0180] 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.

[0181] 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.

[0182] 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.

[0183] 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

[0184] 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.

[0185] 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.

[0186] 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.

[0187] 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

[0188] 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

[0189] 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

[0190] 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.

[0191] 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 naïve 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 μ g/ml) ten weeks after injection and has sustained at 1.3-1.5 μ g/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

[0192] 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.

[0193] 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.

[0194] 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.

[0195] The AAVrh.43 vector demonstrated gene transfer efficiency that was close to AAV9 but at least 5 fold higher than AAV 1. 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

[0196] 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.

[0197] 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 - Human AAV based vectors in mouse models for liver and lung-directed gene transfer

[0198] 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).

[0199] 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

[0200] 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.

Claims

1. An adeno-associated virus (AAV) comprising at least an AAV capsid comprising amino acids 1 to 734 of SEQ ID NO: 186 (AAVhu.53) or SEQ ID NO: 187 (hu.55), or SEQ ID NO: 188 (hu.54), 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.
2. An AAV according to claim 1, wherein said capsid is encoded by the nucleic acid sequence of SEQ ID NO: 176 (hu.53).
3. An AAV according to claim 1, wherein said capsid is encoded by the nucleic acid sequence of SEQ ID NO: 177 (hu.54).
4. An AAV according to claim 1, wherein said capsid is encoded by the nucleic acid sequence of SEQ ID NO: 178 (hu.55).
5. The AAV according to any one of claims 1 to 4 wherein the inverted terminal repeats are from an AAV heterologous to the AAV providing the capsid protein.
6. An isolated adeno-associated virus capsid protein selected from the group consisting of:
 - vp1 capsid protein having the sequence of amino acids 1 to 734 of SEQ ID NO: 186, SEQ ID NO: 187 or SEQ ID NO: 188;
 - vp2 capsid protein having the sequence of amino acids 138 to 734 of SEQ ID NO: 186, SEQ ID NO: 187 or SEQ ID NO: 188; and
 - vp3 capsid protein having the sequence of amino acids 204 to 734 of SEQ ID NO: 186, SEQ ID NO: 187 or SEQ ID NO: 188.
7. A nucleic acid molecule comprising a nucleic acid sequence encoding a protein according to claim 6.
8. A nucleic acid molecule according to claim 7, wherein said nucleic acid sequence is selected from the group consisting of:
 - vp1 having the sequence of nt 1 to 2206 of SEQ ID NO: 176;
 - vp2 having the sequence of nt 411 to 2206 of SEQ ID NO: 176; and
 - vp3 having the sequence of nt 609 to 2206 of SEQ ID NO: 176.
9. A nucleic acid molecule according to claim 7 or 8, wherein said nucleic acid molecule further comprises an AAV sequence encoding a functional AAV rep protein.
10. A nucleic acid molecule according to any of claims 7 to 9, wherein said molecule is a plasmid.
11. 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 according to any of claims 7 to 10.
12. An isolated host cell comprising an adeno-associated virus according to any of claims 1 to 5 or a nucleic acid molecule according to any of claims 7 to 10.
13. A composition comprising an AAV according to any of claims 1 to 5 or a nucleic acid molecule according to any of claims 7 to 10 and a physiologically compatible carrier.
14. Use of an AAV according to any of claims 1 to 5 in the manufacture of a medicament for delivering a molecule to a cell.
15. An AAV according to any of claims 1 to 5, for use in delivering a molecule to a cell.

Patentansprüche

1. Adenoassoziiertes Virus (AAV), umfassend wenigstens ein AAV-Kapsid, umfassend Aminosäuren 1 bis 734 von SEQ ID NO:186 (AAVhu.53) oder SEQ ID NO:187 (hu.55), oder SEQ ID NO:188 (hu.54), wobei das AAV ferner Folgendes umfasst: ein Minigen mit sich gegenläufig wiederholenden AAV-Endsequenzen und ein heterologes Gen, wirkverbunden mit regulatorischen Sequenzen, die dessen Expressierung in einer Wirtszelle steuern.
2. AAV nach Anspruch 1, wobei durch die Nukleinsäuresequenz von SEQ ID NO:176 (hu.53) für das Kapsid codiert wird.
3. AAV nach Anspruch 1, wobei durch die Nukleinsäuresequenz von SEQ ID NO:177 (hu.54) für das Kapsid codiert wird.
4. AAV nach Anspruch 1, wobei durch die Nukleinsäuresequenz von SEQ ID NO:178 (hu.55) für das Kapsid codiert wird.
5. AAV nach einem der Ansprüche 1 bis 4, wobei die sich gegenläufig wiederholenden Endsequenzen von einem AAV stammen, das heterolog zu dem AAV ist, das das Kapsidprotein bereitstellt.
6. Isoliertes Kapsidprotein eines adenoassoziierten Virus, ausgewählt aus der Gruppe bestehend aus:
 - vp1-Kapsidprotein mit der Sequenz von Aminosäuren 1 bis 734 von SEQ ID NO:186, SEQ ID NO:187 oder SEQ ID NO:188;
 - vp2-Kapsidprotein mit der Sequenz von Aminosäuren 138 bis 734 von SEQ ID NO:186, SEQ ID NO:187 oder SEQ ID NO:188; und
 - vp3-Kapsidprotein mit der Sequenz von Aminosäuren 204 bis 734 von SEQ ID NO:186, SEQ ID NO:187 oder SEQ ID NO:188.
7. Nukleinsäuremolekül, umfassend eine Nukleinsäuresequenz, die für ein Protein nach Anspruch 6 codiert.
8. Nukleinsäuremolekül nach Anspruch 7, wobei die Nukleinsäuresequenz ausgewählt ist aus der Gruppe bestehend aus:
 - vp1 mit der Sequenz von nt 1 bis 2206 von SEQ ID NO:176;
 - vp2 mit der Sequenz von nt 411 bis 2206 von SEQ ID NO:176; und
 - vp3 mit der Sequenz von nt 609 bis 2206 von SEQ ID NO:176.
9. Nukleinsäuremolekül nach Anspruch 7 oder 8, wobei das Nukleinsäuremolekül ferner eine AAV-Sequenz umfasst, die für ein funktionelles AAV-rep-Protein codiert.
10. Nukleinsäuremolekül nach einem der Ansprüche 7 bis 9, wobei das Molekül ein Plasmid ist.
11. Verfahren zum Erzeugen eines rekombinanten adenoassoziierten Virus (AAV), umfassend ein AAV-Kapsid, umfassend die Schritte des Kultivierens einer Wirtszelle, Folgendes enthaltend: (a) ein Molekül, das für ein AAV-Kapsidprotein codiert; (b) ein funktionelles rep-Gen; (c) ein Minigen, umfassend sich gegenläufig wiederholende AAV-Endsequenzen (ITR) und ein Transgen; und (d) ausreichende Helferfunktionen, um ein Verpacken des Minigens in das AAV-Kapsidprotein zu ermöglichen, wobei die Wirtszelle ein Nukleinsäuremolekül nach einem der Ansprüche 7 bis 10 umfasst.
12. Isolierte Wirtszelle, umfassend ein adenoassoziiertes Virus nach einem der Ansprüche 1 bis 5 oder ein Nukleinsäuremolekül nach einem der Ansprüche 7 bis 10.
13. Zusammensetzung, umfassend ein AAV nach einem der Ansprüche 1 bis 5 oder ein Nukleinsäuremolekül nach einem der Ansprüche 7 bis 10 und einen physiologisch unbedenklichen Träger.
14. Gebrauch eines AAV nach einem der Ansprüche 1 bis 5 beim Erzeugen eines Medikaments zum Liefern eines Moleküls an eine Zelle.
15. AAV nach einem der Ansprüche 1 bis 5 für den Gebrauch beim Liefern eines Moleküls an eine Zelle.

Revendications

- 5 1. Virus adéno-associé (AAV) comprenant au moins une capsid AAV comprenant les acides aminés 1 à 734 de SEQ ID NO : 186 (AAVhu.53) ou SEQ ID NO : 187 (hu.55), ou SEQ ID NO : 188 (hu.54), dans lequel l'AAV comprend en outre un minigène ayant des répétitions terminales inversées d'AAV et un gène hétérologue lié de façon fonctionnelle à des séquences régulatrices qui dirigent son expression dans une cellule hôte.
- 10 2. AAV selon la revendication 1, dans lequel ladite capsid est codée par la séquence d'acide nucléique SEQ ID NO : 176 (hu.53).
3. AAV selon la revendication 1, dans lequel ladite capsid est codée par la séquence d'acide nucléique SEQ ID NO : 177 (hu.54).
- 15 4. AAV selon la revendication 1, dans lequel ladite capsid est codée par la séquence d'acide nucléique SEQ ID NO : 178 (hu.55).
5. AAV selon l'une quelconque des revendications 1 à 4 dans lequel les répétitions terminales inversées sont issues d'un AAV hétérologue à l'AAV fournissant la protéine de capsid.
- 20 6. Protéine de capsid de virus adéno-associé isolée sélectionnée parmi le groupe constitué de :
protéine de capsid vp1 ayant la séquence en acides aminés 1 à 734 de SEQ ID NO : 186, SEQ ID NO : 187 ou SEQ ID NO : 188 ;
protéine de capsid vp2 ayant la séquence en acides aminés 138 à 734 de SEQ ID NO : 186, SEQ ID NO : 187 ou SEQ ID NO : 188 ; et
25 protéine de capsid vp3 ayant la séquence en acides aminés 204 à 734 de SEQ ID NO : 186, SEQ ID NO : 187 ou SEQ ID NO : 188.
- 30 7. Molécule d'acide nucléique comprenant une séquence d'acide nucléique codant une protéine selon la revendication 6.
8. Molécule d'acide nucléique selon la revendication 7, dans laquelle ladite séquence d'acide nucléique est sélectionnée parmi le groupe constitué de :
35 vp 1 ayant la séquence en nt 1 à 2206 de SEQ ID NO : 176 ;
vp 2 ayant la séquence en nt 411 à 2206 de SEQ ID NO : 176 ; et
vp31 ayant la séquence en nt 609 à 2206 de SEQ ID NO : 176.
- 40 9. Molécule d'acide nucléique selon la revendication 7 ou 8, dans laquelle ladite molécule d'acide nucléique comprend en outre une séquence AAV codant une protéine rep de AAV fonctionnelle.
10. Molécule d'acide nucléique selon l'une quelconque des revendications 7 à 9, dans laquelle ladite molécule est un plasmide.
- 45 11. Méthode pour générer un virus adéno-associé (AAV) recombinant comprenant une capsid AAV comprenant les étapes de cultiver une cellule hôte contenant :
(a) une molécule codant une protéine de capsid d'AAV ; (b) un gène rep fonctionnel ; (c) un minigène comprenant des répétitions terminales inversées (ITRs) d'AAV et un transgène ; et (d) des fonctions auxiliaires suffisantes
50 pour permettre l'empaquetage du minigène à l'intérieur de la protéine de capsid d'AAV, dans laquelle ladite cellule hôte comprend une molécule d'acide nucléique selon l'une quelconque des revendications 7 à 10.
12. Cellule hôte isolée comprenant un virus adéno-associé selon l'une quelconque des revendications 1 à 5 ou une molécule d'acide nucléique selon l'une quelconque des revendications 7 à 10.
- 55 13. Composition comprenant un AAV selon l'une quelconque des revendications 1 à 5 ou une molécule d'acide nucléique selon l'une quelconque des revendications 7 à 10 et un véhicule physiologiquement compatible.

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14. Utilisation d'un AAV selon l'une quelconque des revendications 1 à 5 dans la fabrication d'un médicament pour délivrer une molécule à une cellule.
15. AAV selon l'une quelconque des revendications 1 à 5, pour son utilisation dans la délivrance d'une molécule à une cellule.

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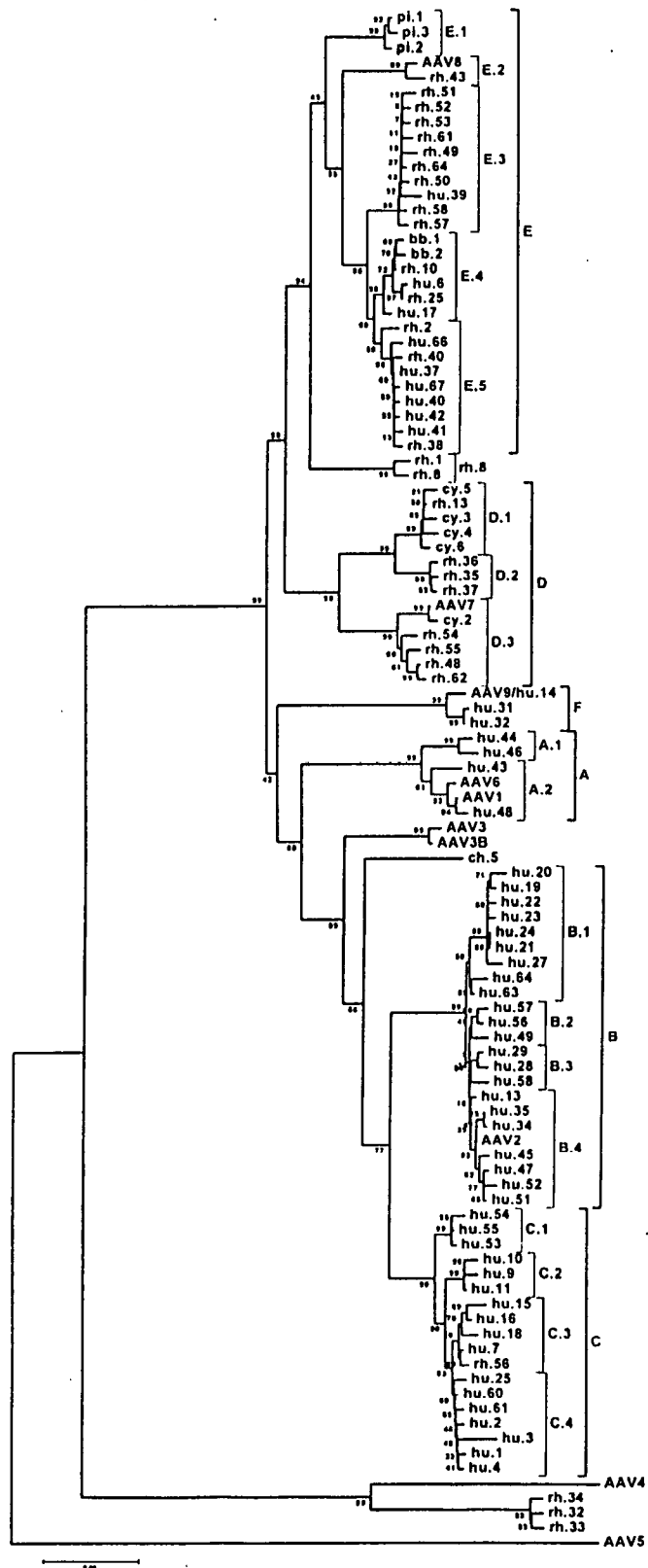


FIG. 1

	10	20	30	40	50	60	70
							
AAV5	1	MSFVDHPPDWLEE-VGEGLREFLGLAAGPPKPKPNQHQDQARGLVLPGYNYLGPNGGLDRGEPVNEADA					
AAV3-3	1	MAADGYLPDWLEDNLSEGIREWAWLKPGVQPKANQHQDNRRLGLVLPGYKYLPGNGLDKGEPVNEADA					
AAV4-4	1	-MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQHQDNARGLVLPGYKYLPGNGLDKGEPVNEADA					
AAV1-A	1	MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQKQDDGRLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.46-A	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.48-A	1	MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQKQDDGRLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.44-A	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.43-A	1	MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQKQDDGRLVLPGYKYLPGFNGGLDKGEPVNEADA					
AAV6-A	1	MAADGYLPDWLEDNLSEGIREWWDLPKPGAPKPKANQKQDDGRLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.34-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.47-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.29-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.63-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.56-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.45-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.57-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.35-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.58-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.28-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.51-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.19-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.49-B	1	MAADGYLPDWLKDTLSEGIQWKKLPGPPPKPAERHKDDSGGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.52-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.13-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
AAV2-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.20-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYRYLPGFNGGLDKGEPVNEADA					
hu.24-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					
hu.64-B	1	MAADGYLPDWLEDTLSEGIQWKKLPGPPPKPAERHKDDSRGLVLPGYKYLPGFNGGLDKGEPVNEADA					

FIG. 2A

hu. 27-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 21-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 22-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 23-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 7-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 61-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
rh. 56-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 9-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHQDNSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 54-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 53-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 60-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 55-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 2-C	1	MAADGYPPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 1-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 18-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 3-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 25-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDGSRLVLPGYKYLGFNGLDKGEPVNEADA
hu. 15-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLYKGEVPVDEADA
hu. 16-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLYKGEVPVNEADA
hu. 11-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHQDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 10-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKLAERHQDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
hu. 4-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGFNGLDKGEPVNEADA
rh. 54-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
rh. 48-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
rh. 55-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
rh. 62-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
AAV7-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
rh. 52-E	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
rh. 51-E	1	MVADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA
hu. 39-E	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKDDGRGLVLPGYKYLGFNGLDKGEPVNAADA

FIG. 2B

rh. 53-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 37-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 43-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 50-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 49-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 61-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 41-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 64-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 42-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 57-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 40-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
AAV8-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 58-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 40-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 67-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 17-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGCKYLG	PFENGLDKGEPV	NAADA	
hu. 6-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 66-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
rh. 38-E	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDGRGLVLP	PGYKYLGP	FENGLDKGEPV	NAADA	
hu. 32-F	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDSRGLVLP	PGYKYLGP	GNGLDKGEPV	NAADA	
AAV9/hu	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPQPKANQ	QHQNARGLVLP	PGYKYLGP	GNGLDKGEPV	NAADA	
hu. 31-F	1	MAADGYLPDWLEDNLSEGI	REWDLKPGAPKPKANQ	QKQDDSRGLVLP	PGYKYLGP	GNGLDKGEPV	NAADA	
AAV5	70	VAREHDI	SYNEQLEAGDNPYLKYN	HADAEFQEK	LADDTSFG	GNLGKAVFQAK	KRVLEPG-LVEEGA	AKTA
AAV3-3	71	AALEHDKAYDQQLKAGDNP	YLKYNHADAEFQER	LQEDTSFG	GNLGRAVVFQAK	KRILEPLG-LVEE	AAKTA	
AAV4-4	70	AALEHDKAYDQQLKAGDNP	YLKYNHADAEFQER	LQEDTSFG	GNLGRAVVFQAK	KRVLEPLG-LVEQ	AGETA	
AAV1-A	71	AALEHDKAYDQQLKAGDNP	YLRYNHADAEFQER	LQEDTSFG	GNLGRAVVFQAK	KRVLEPLG-LVEE	GA	AKTA
hu. 46-A	71	AALEHDKAYDRQLSDGDN	PYLKYNHADAEFQER	LKEDTSFG	GNLGRAVVFQAK	KRVLEPLG-LVEE	GA	AKTA

FIG. 2C

hu. 48-A	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	AEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 44-A	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAETA
hu. 43-A	71	AALEHDKAYDQQLKAGDNPYPRYNHADA	AEFQERLQEDTFFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
AAV6-A	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	AEFQERLQEDTSFGGNLGRAVFQAKKRVLEPFG-LVEEGAKTA
hu. 34-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 47-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVGEPPVKT
hu. 29-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 63-B	71	AALEHDKAYDRQLDSGDNPYPKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 56-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 45-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 57-B	70	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 35-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 58-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 28-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLS-LVEEPPVKT
hu. 51-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVGEPPVKT
hu. 19-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 49-B	71	AALEYDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 52-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVGEPPVKT
hu. 13-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
AAV2-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 20-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 24-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 64-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 27-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 21-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 22-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 23-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 7-C	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
hu. 61-C	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT
rh. 56-C	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKT

FIG. 2D

hu. 9-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 54-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 53-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 60-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 55-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 2-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 1-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 18-C	71	AALEHDKAYDRQLESGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 3-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLRPGIRK	VPVKA
hu. 25-C	71	AALEHDKAYDRQLNSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 15-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVGE	VPVKA
hu. 16-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHAGA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 11-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 10-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
hu. 4-C	71	AALEHDKAYDRQLDSGDNPYLYKYNHADA	AEFQERL	KEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	VPVKA
rh. 54-D	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	AAKTA
rh. 48-D	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	AAKTA
rh. 55-D	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 62-D	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LAEE	AAKTA
AAV7-D	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 52-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 51-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
hu. 39-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 53-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
hu. 37-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	AAKTA
rh. 43-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 50-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 49-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
rh. 61-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-LVEE	GAKTA
hu. 41-E	71	AALEHDKAYDQQLKAGDNPLYLYKYNHADA	AEFQERL	QEDTSFGGNLGRAV	QAKKRVLEPLG-PVEE	AAKTA

FIG. 2E

rh. 64-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA	150	160	170	180	190	200	210
hu. 42-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA							
rh. 57-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA	139	140	139	140	140	140	140
hu. 40-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA	PTGKRIDDHFP----	EPDSSSGVGKSGKQPARKRLNFGQTGDSVPD-PQPLGEPPAAPTSLGSNTMASGG	PGKKRPLIESPQ-QPDSSTGIGKKGKQPAKKKLVFEDETGAGDGP----	PEGSTSGAMS--DDSEMRAAA	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG
AAV8-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA	140	140	140	140	140	140	140
rh. 58-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA	PGKKRPVEQSPQ-GPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-GPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-GPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-GPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQTGDSVPD-PQPLGEPPATPAAVGPTTMSAGG	PGKKRPVEHSPV-EPDSSSGTGKAGQQPAKKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGTNTMATGS
rh. 40-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA	140	140	140	140	140	140	140
hu. 67-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA	PGKKRPVEHSPV-EPDSSSGTGKAGQQPAKKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGTNTMATGS	PGKKRPVEHSPV-EPDSSSGTGKAGQQPAKKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGTNTMATGS	PGKKRPVEHSPA-EPDSSSGTGKSGNQPAKKRLNFGQTGDSDSVPD-PQPLGQPPAAPSGLGTNTMATGS				
hu. 17-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA							
hu. 6-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA							
hu. 66-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA							
rh. 38-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA							
hu. 32-F	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA							
AAV9/hu	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA							
hu. 31-F	71	AALEHDKAYDQQLKAGDNPYLRYNHADADEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA							

FIG. 2F

hu. 63-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 56-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 45-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 57-B 139 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 35-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 58-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 28-B 140 PGKKRPVEHSPA-EPDSSSGTGKSGNQPARKRLNFGQTGDSDSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 51-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 19-B 140 PGEKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTASGS
 hu. 49-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 52-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 13-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTASGS
 AAV2-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 20-B 140 PGEKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTASGS
 hu. 24-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PRPLGQPPAAPSGLGNTMTASGS
 hu. 64-B 140 PGKKRPVEHSLA-EPDSSSGTGKAGQQPARRRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTATGS
 hu. 27-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTASGS
 hu. 21-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PRPLGQPPAAPSGLGNTMTASGS
 hu. 22-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTASGS
 hu. 23-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGNTMTASGS
 hu. 7-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
 hu. 61-C 140 PGKKRPVEHPPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
 rh. 56-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
 hu. 9-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTLSGSTTMATGS
 hu. 54-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTLSGSTTMATGS
 hu. 53-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLRQPPAAPSTLSGSTTMATGS
 hu. 60-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
 hu. 55-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTLSGSTTMATGS
 hu. 2-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQRPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
 hu. 1-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS

FIG. 2G

hu.18-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLSTTMASGS
 hu.3-C 141 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLSTTMATGS
 hu.25-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLSTTMATGS
 hu.15-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLSTTMATGS
 hu.16-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLSTTMATGS
 hu.11-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTLSTTMATGS
 hu.10-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTLSTTMATGS
 hu.4-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLSTTMATGS
 rh.54-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 rh.48-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 rh.55-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.62-D 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 AAV7-D 140 PAKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.52-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.51-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 hu.39-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGRTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.53-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 hu.37-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 rh.43-E 140 PGKKRPVEQSPQ-EPDSSSGTGKAGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSGVGPNTMAAGG
 rh.50-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.49-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.61-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 hu.41-E 140 PGKKRPVEPPQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 rh.64-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 hu.42-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 rh.57-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 hu.40-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLSFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG
 AAV8-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSGVGPNTMAAGG
 rh.58-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPSSVSGTMAAGG
 rh.40-E 140 PGKKRPVEPSQRSPPDSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAGPSGLSGTMAAGG

FIG. 2H

hu. 67-E	140	PGKKRPVEPSPQSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVDP-PQPIGEPPAGPSGLSGTMAAGG	220	230	240	250	260	270	280
hu. 17-E	140	PGKKRPVEPSPQSPDSSTGIGKTGQQPAKKRLNFGQTGDSESVDP-PQPIGEPPAGPSGLSGTMAAGG							
hu. 6-E	140	PGKKRPVEPSPQSPDSSTGIGKTGQQPAKKRLNFGQTGDSESVDP-PQPIGEPPAGPSGLSGTMAAGG							
hu. 66-E	140	PGKKRPVEPSPQSPDSSTGIGKKGQQPAKKRLNFGQTGDSESVDP-PQPIGEPPAGPSGLSGTMAAGG							
rh. 38-E	140	PGKKRPVEPSPQSPDSSTGIGKKGQRPAAKRLNFGQTGDSESVDP-PQPIGEPPAGPSGLSGTMAAGG							
hu. 32-F	140	PGKKRPVEQSPQ-EPDSSAGIGKSGSQPAKKKLNFGQTGDTESVDP-PQPIGEPPAAPSGLSLTMASGG							
AAV9/hu	140	PGKKRPVEQSPQ-EPDSSAGIGKSGAQPAKKRLNFGQTGDTESVDP-PQPIGEPPAAPSGLSLTMASGG							
hu. 31-F	140	PGKKRPVEQSPQ-EPDSSAGIGKSGSQPAKKKLNFGQTGDTESVDP-PQPIGEPPAAPSGLSLTMASGG							
AAV5	198	GGPLGDNNGADGVGNASGDWHCDSTWMDRVVTKSTRTWLPSYNNHLYKQISS-GSVDGSNANAYFGY							
AAV3-3	208	GAPMADNNEGADGVGNSSGNWHCDSQWLGDREVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
AAV4-4	202	GGAAVEGGQADGVGNASGDWHCDSTWSEGHVTTSTRTWLPTYNNHLYKRLG-----ESLQSNTYNGF							
AAV1-A	208	GAPMADNNEGADGVGNASGNWHCDSTWLGDREVITSTRTWTALPTYNNHLYKQISS-ASTGASNDNHYFGY							
hu. 46-A	208	GAPMADNNEGADGVGNASGNWHCDSTWLGDREVITSTRTWTALPTYNNHLYKQISS-ASTGASNDNHYFGY							
hu. 48-A	208	GAPMADNNEGADGVGNASGNWHCDSTWLGDREVITSTRTWTALPTYNNHLYKQISS-ASTGASNDNHYFGY							
hu. 44-A	208	GAPMADNNEGADGVGNASGNWHCDSTWLGDREVITSTRTWTALPTYNNHLYKQISS-TSTGASNDNHYFGY							
hu. 43-A	209	GAPMADNNEGADGVGNASGNWHCDSTWLGDREVITSTRTWTALPTYNNHLYKQISS-ASTGASNDNHYFGY							
AAV6-A	208	GAPMADNNEGADGVGNASGNWHCDSTWLGDREVITSTRTWTALPTYNNHLYKQISS-ASTGASNDNHYFGY							
hu. 34-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDREVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 47-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDREVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 29-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDREVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 63-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDREVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 56-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDRVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 45-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDRVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 57-B	207	GAPMADNNEGADGVGNSSGDWHCDSTWMDRVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 35-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDRVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 58-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDRVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							
hu. 28-B	208	GAPMADNNEGADGVGNSSGNWHCDSTWMDRVITSTRTWTALPTYNNHLYKQISS--SQSGASNDNHYFGY							

FIG. 21

hu. 51-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 19-B 208 GAPMADNNEGADGVGNSSGNWYCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 49-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 52-B 208 GAPMADNNEGADGVGNSSGNRHRCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 13-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 AA2-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 20-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 24-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 64-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 27-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 21-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 22-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 23-B 208 GAPMADNNEGADGVGNSSGNWHCHDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 7-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 61-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 rh. 56-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 9-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGC
 hu. 54-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 53-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 60-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 55-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 2-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 1-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 18-C 208 GAPVADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 3-C 209 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGACNDNHYFGY
 hu. 25-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 15-C 208 GAPVADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 16-C 208 GAPVADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 11-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
 hu. 10-C 208 GAPMADNNEGADGVGNSSGNWHCHDSTWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY

FIG. 2J

hu. 4-C	208	GAPMADNNEGADGVGNSSGNWHCHDSQWLGLDRVITTSTRTWALPTYNNHLYKQISS--SQSGASNDNHYFGY
rh. 54-D	209	GAPMADNNEGADGVGNASGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
rh. 48-D	209	GAPMADNNEGADGVGNASGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
rh. 55-D	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
rh. 62-D	209	GAPMADNNEGADGVGNASGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
AAV7-D	209	GAPMADNNEGADGVGNASGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISS-ETAGSTNDNTYFGY
rh. 52-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 51-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 39-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 53-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 37-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 43-E	208	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGATNDNTYFGY
rh. 50-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 49-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 61-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 41-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 64-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 42-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 57-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 40-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
AAV8-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGATNDNTYFGY
rh. 58-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 40-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 67-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 17-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 6-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 66-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
rh. 38-E	209	GAPMADNNEGADGVGNSSGNWHCHDSWLGLDRVITTSTRTWALPTYNNHLYKQISSNGTSGGSTNDNTYFGY
hu. 32-F	208	GAPVADNNEGADGVGNSSGNWHCHDSQWLGLDRVITTSTRTWALPTYNNHLYKQISSNSTSGSSNDNAYFGY
AAV9/hu	208	GAPVADNNEGADGVGNSSGNWHCHDSQWLGLDRVITTSTRTWALPTYNNHLYKQISSNSTSGSSNDNAYFGY

FIG. 2K

hu.31-F	208	GAPVADNNEGADGVGSSGNHWCDSQWLGDREVITTTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGY	290	300	310	320	330	340	350
									
AAV5	267	STPWGYFDENRFHSHWSPRDWQRLINNNYWGFRPRSLRVKIFNIQVKEVTQDSTTTIANNLSTVQVFTD							
AAV3-3	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKKLSFKLFNIQVRGVTQNDGTTIANNLSTVQVFTD							
AAV4-4	267	STPWGYFDENRFHCHFSPRDWQRLINNNWGMRPKAMRVKIFNIQVKEVTSNGETTVANNLTSTVQIFAD							
AAV1-A	277	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTNDGVTTIANNLTSTVQVFS							
hu.46-A	277	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTNDGVTTIANNLTSTVQVFS							
hu.48-A	277	GTPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVEEVTNDGVTTIANNLTSTVQVFS							
hu.44-A	277	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTNDGVTTIANNLTSTVQVFS							
hu.43-A	278	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTNDGVTTIANNLTSTVQVFS							
AAV6-A	277	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTNDGVTTIANNLTSTVQVFS							
hu.34-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.47-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.29-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.63-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.56-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.45-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.57-B	275	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.35-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.58-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVREVTQNDGTTIANNLSTVQVFTD							
hu.28-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.51-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.19-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.49-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.52-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.13-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
AAV2-B	276	STPWGYFDENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							
hu.20-B	276	STPWGHFDEENRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTQNDGTTIANNLSTVQVFTD							

FIG. 2L

hu. 24-B	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLSFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 64-B	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGSRPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 27-B	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLSFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 21-B	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLSFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 22-B	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLSFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 23-B	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLSFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 7-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 61-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
rh. 56-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 9-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 54-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 53-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 60-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 55-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 2-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 1-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 18-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNSWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 3-C	277	STPWGYFDENRFHCHFS	PRDWQRLINNSWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 25-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 15-C	276	STPWGYFDENRFHCHFS	PRDRQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 16-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 11-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 10-C	276	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
hu. 4-C	276	STPWGYFDENRFHCHFS	PRDWQRLVNNRGERPKRLNFKLFNIQVKEVTQNDGTTTIAN	TLSTVQVFTD
rh. 54-D	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKKLNFKLFNIQVKEVTNDGVTTIAN	TLSTVQVFS
rh. 48-D	278	STPWGYFDENRFHCHFS	PRDWQRLINNSWGERPKKLNFKLFNIQVKEVTNDGVTTIAN	TLSTVQVFS
rh. 55-D	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKKLNFKLFNIQVKEVTNDGVTTIAN	TLSTVQVFS
rh. 62-D	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKKLNFKLFNIQVKEVTGDGVTTIAN	TLSTVQVFS
AAV7-D	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKKLNFKLFNIQVKEVTNDGVTTIAN	TLSTVQVFS
rh. 52-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGERPKRLSFKLFNIQVKEVTQNEGKTIAN	SLSTVQVFTD

FIG. 2M

rh. 51-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 39-E	279	STPWGYLDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLASTIQVFTD
rh. 53-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 37-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 43-E	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 50-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 49-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 61-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 41-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTVANNLTSTIQVFTD
rh. 64-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 42-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 57-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 40-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
AAV8-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 58-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 40-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQDEGT	KTIANNLTSTIQVFTD
hu. 67-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 17-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 6-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 66-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
rh. 38-E	279	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKPFNIQVKEVTQNEGT	KTIANNLTSTIQVFTD
hu. 32-F	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTDNNGV	KTIANNLTSTVQVFTD
AAV9/hu	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTDNNGV	KTIANNLTSTVQVFTD
hu. 31-F	278	STPWGYFDENRFHCHFS	PRDWQRLINNNWGFRPKR	LSFKLFNIQVKEVTDNNGV	KTIANNLTSTVQVFTD
AAV5	337	DDYQLPYVVGNGTEGCL	PAFPQVFTLPQYGYATLNRD	-NTENPTERSFFCLEYF	PSKMLRTGNNEFFT
AAV3-3	346	SEYQLPYVLGSAHQCL	PPFPADVFMVPQYGYLT	LNNG---SQAVGRSSFC	LEYFPSQMLRTGNNFQS
AAV4-4	337	SSYELPYVMDAGQEGSL	PPFPNDVFMVPQYGYCGL	VTGNTSQQTDRN	AFYCLEYFPSQMLRTGNNEFIT

FIG. 2N

AAV1-A	347	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.46-A	347	SEYQLPYVLGSAHQGRLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSSYCLEYFPSQMLRTGNNFTFS
hu.48-A	347	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.44-A	347	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.43-A	348	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
AAV6-A	347	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.34-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNE---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.47-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.29-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.63-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.56-B	346	LEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.45-B	346	SGYQLPYVLGSAHQGCLPPFPADVFMPQYGYPTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.57-B	345	LEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.35-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.58-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.28-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.51-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.19-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.49-B	346	SEYQLPYVPGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.52-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCPEYFPSQMLRTGNNFTFS
hu.13-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
AAV2-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.20-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.24-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.64-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.27-B	346	SGYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.21-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.22-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.23-B	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
hu.7-C	346	SEYQLPYVLGSAHQGCLPPFPADVFMPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFS

FIG. 20

hu.61-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 rh.56-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.9-C 346 SEYPLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFTFS
 hu.54-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.53-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.60-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.55-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.2-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.1-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.18-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.3-C 347 SEYQLPYVPGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.25-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSPFYCYEYFPPSQMLRTGNNFQFS
 hu.15-C 346 SGYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.16-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 hu.11-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFTFS
 hu.10-C 346 SEYQLPYVLGSAHQGCLPPFPADVFTVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNLTFS
 hu.4-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFS
 rh.54-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYEYFPPSQVLRGTGNNFTFS
 rh.48-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYEYFPPSQMLRTGNNFTFS
 rh.55-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYEYFPPSQMLRTGNNFTFS
 rh.62-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNND---SQSVGRSSFYCYEYFPPSQMLRTGNNFTFS
 AAV7-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYEYFPPSQMLRTGNNFEFS
 rh.52-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTPNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFSFS
 rh.51-E 349 SEYQLPYVLGSAHQGCCPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFSFS
 hu.39-E 349 SEYQPPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFSFS
 rh.53-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFSFS
 hu.37-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFEFS
 rh.43-E 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFQFT
 rh.50-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFSFS
 rh.49-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGNLTLNNG---SQAVGRSSFYCYEYFPPSQMLRTGNNFSFS

FIG. 2P

rh. 61-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
hu. 41-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
rh. 64-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
hu. 42-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
rh. 57-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
hu. 40-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNSEFS
AAV8-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFT
rh. 58-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
rh. 40-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
hu. 67-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
hu. 17-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
hu. 6-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
hu. 66-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
rh. 38-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
hu. 32-F	348	SDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
AAV9/hu	348	SDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
hu. 31-F	348	SDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDG---	GQAVGRSSFYCLEYFPSQMLRTGNNFQFS

AAV5	406		YNFEEVPFHSSFAPSQNLFKLANPLVDQYLYRFVSTN-----NTGGVQFNKNLAGRYANTYKNWFPGP
AAV3-3	413	YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYLNRQTGTTSGTTNQSRLLFSQAGPQSMQLQARNWLPGP	
AAV4-4	407	YSFEKVPFHSSYAHSQSLDRLMNPLIDQYLYLNRQTGTTGTLNAGTATTNFTKLRPNTFSNFKKNWLPGP	
AAV1-A	414	YTFEEVPFHSSYAHSQSLDRLMNPLIDQYLYLNRQT-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGP	
hu. 46-A	414	YTFEEVPLHSSCAHSQSLDRLMNPLIDQYLYLNRQT-NQSGSAQNRDLLFSRGSPAGMSVQPKNWLPGP	
hu. 48-A	414	YTFEEVPFHSSYAHSQSLDRLMNPLIDQYLYLNRQT-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGP	
hu. 44-A	414	YTFEEVPFHSSYAHSQSLDRLMNPLIDQYLYPNRQT-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGP	
hu. 43-A	415	YTFEEVPLHSSYAHSQSLDRLMNPLIVQYLYLNRQT-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGP	
AAV6-A	414	YTFEDVPFHSSYAHSQSLDRLMNPLIDQYLYLNRQT-NQSGSAQNKDLLFSRGSPAGMSVQPKNWLPGP	
hu. 34-B	413	YTFEDVPFHSSYAHSQSLGRMLMNPLIDQYLYLSRTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP	

FIG. 20

hu. 47-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 29-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 63-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 56-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 45-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 57-B	412	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 35-B	413	YTFEDVPFHSSYAHSQSLGRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 58-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 28-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 51-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 19-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 49-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 52-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 13-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
AAV2-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 20-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 24-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 64-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLVDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 27-B	413	YTFEDVPFHSSYAHGQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDVRDQSRNWLPGP
hu. 21-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 22-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 23-B	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLSTTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 7-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLNKTQ-SNSGTLQSRLLFSQAGPTMSLSLQAKNWLPGP
hu. 61-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLNKTQ-TNSGTLQSRLLFSQAGPTMSLSLQAKNWLPGP
rh. 56-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLNKTQ-SNSGALQSRLLFSQAGPTMSLSLQAKNWLPGP
hu. 9-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLNRTQ-SNSGTLQSRLLFSQAGPTMSLSLQAKNWLPGP
hu. 54-C	413	YTFEDVPFHSSYAHSQGLDRMLNPLIDQYLYLNRTQ-TASGT-QQSRLLFSQAGPTMSLSLQAKNWLPGP
hu. 53-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLNRTQ-TASGT-QQSRLLFSQAGPTMSLSLQAKNWLPGP
hu. 60-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLVDQYLYLNKTQ-TNSGTLQSRLLFSQAGPTMSLSLQAKNWLPGP
hu. 55-C	413	YTFEDVPFHSSYAHSQSLDRMLNPLIDQYLYLNRTQ-TASGT-QQSRLLFSQAGPTMSLSLQAKNWLPGP

FIG. 2R

hu.2-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.1-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.18-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-SNSGTLQQSRLLFSQAGPTSMQAKNWLPGP
hu.3-C	414	YTFEDVPFHSSYAHQCQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.25-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.15-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-SNSGTLQQSRLLFSQAGPTSMQAKNWLPGP
hu.16-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-SNSGTLQQSRLLFSQAGPTSMQAKNWLPGP
hu.11-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-SNSGTLQQSRLLFSQAGPTSMQAKNWLPGP
hu.10-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-SNSGTLQQSRLLFSQAGPTSMQAKNWLPGP
hu.4-C	413	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.54-D	415	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.48-D	415	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.55-D	415	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.62-D	415	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
AAV7-D	415	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.52-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.51-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.39-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.53-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.37-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.43-E	415	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.50-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.49-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.61-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.41-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.64-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.42-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.57-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.40-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
AAV8-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP

FIG. 28

rh.58-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTAGTQQLLFSQAGPSNMSAQARNWLP	PGP
rh.40-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTQGTQQLLFSQAGPANMSARAKNWL	PGP
hu.67-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTQGTQQLLFSQAGPANMSAQAKNWL	PGP
hu.17-E	416	YQFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKNWL	PGP
hu.6-E	416	YQFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKNWL	PGP
hu.66-E	416	YTFEDVPFHSSCAHSQSSDRMLMNP	LIDQYLYLSRTRS-TGGTQGTQQLLFSQAGPANMSAQAKNWL	PGP
rh.38-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTQGTQQLLFSQAGPANMSAQAKNWL	PGP
hu.32-F	415	YEFENVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSKTINGSG--QNQQTLLKFSVAGPSNMAVQGRN	YIPGP
AAV9/hu	415	YEFENVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSKTINGSG--QNQQTLLKFSVAGPSNMAVQGRN	YIPGP
hu.31-F	415	YEFENVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSKTINGSG--QNQQTLLKFSVAGPSNMAVQGRN	YIPGP

		500	510	520	530	540	550	560
								
AAV5	469	MGR	TQGNL	GSVN----	RASV	SAFAT	TNRME	LEGASYQVPPQPN
AAV3-3	483	CYR	QRLSK	TANDN-----	NNSN	FPWTA	ASKYHLN	GRDSLVP
AAV4-4	477	SIK	QGF	SKTANQNYKIPAT	GSDSL	IKYETH	STLDGR	WSALT
AAV1-A	483	CYR	QQRV	SKTKTDN-----	NNSN	FTWTG	ASKYN	LNGRESI
hu.46-A	483	CYR	QQRV	SKTKTDN-----	NNSN	FTWTG	ASKYN	LNGRESI
hu.48-A	483	CYR	QQRV	SKTKTDN-----	NNSN	FTWTG	ASKYN	LNGRESI
hu.44-A	483	CYR	QQRV	SKTKTDN-----	NNSN	FTWTG	ASKYN	LNGRESI
hu.43-A	484	CYR	QQRV	SKTKTDN-----	NNSN	FTWTG	ASKYN	LNGRESI
AAV6-A	483	CYR	QQRV	SKTKTDN-----	NNSN	FTWTG	ASKYN	LNGRESI
hu.34-B	482	CYR	QQRV	SKTSADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP
hu.47-B	482	CYR	QQRV	SKTSADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP
hu.29-B	482	CYR	QQRV	SKTSADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP
hu.63-B	482	CYR	QQRV	SKTSADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP
hu.56-B	482	CYR	QQRV	SKTAAADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP
hu.45-B	482	CYR	QQRV	SKTSADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP
hu.57-B	481	CYR	QQRV	SKTAAADN-----	NNGE	YSWTG	ATKYHLN	GRDSLVP
hu.35-B	482	CYR	QQRV	SKTSADN-----	NNSE	YSWTG	ATKYHLN	GRDSLVP

FIG. 27

hu.58-B 482 CYRQQRVSKTSADN-----NNSEYSWIGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 hu.28-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 hu.51-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 hu.19-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.49-B 482 CYRQQRVSKTAADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 hu.52-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 hu.13-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 AAV2-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQG
 hu.20-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.24-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.64-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.27-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.21-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.22-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.23-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPQSGVLIIFGKQD
 hu.7-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.61-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 rh.56-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.9-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.54-C 481 CYRQQRLSKQANDN-----NNSNFPWTGATKYHLNNGDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKEG
 hu.53-C 481 CYRQQRLSKQANDN-----NNSNFPWTGATKYHLNNGDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKEG
 hu.60-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.55-C 481 CYRQQRLSKQANDN-----NNSNFPWTGATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKEG
 hu.2-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.1-C 482 CYRQQRLSKQANGN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.18-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.3-C 483 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.25-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.15-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG
 hu.16-C 482 CYRQQRLSKQANDN-----NNSNFPWTAAATKYHLNGRDLSLVNPGPAMASHKDDDEKFFFPMHGTLIFGKQG

FIG. 2U

hu. 11-C	482	CYRQRLSKQANDN-----NNSNFPWTAATKYRLNGRDSLVPNPGPAMASHKDDDEKEFFPMHGTLI FGKQG
hu. 10-C	482	CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEKEFFPMHGTLI FGKQG
hu. 4-C	482	CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEKEFFPMHGTLI FGKQG
rh. 54-D	485	CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLI FGKTG
rh. 48-D	485	CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLI FGKTG
rh. 55-D	485	CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLI FGKTG
rh. 62-D	485	CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLI FGKTG
AAV7-D	485	CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLI FGKTG
rh. 52-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh. 51-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu. 39-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh. 53-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu. 37-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh. 43-E	484	CYRQQRVSTTTGQN-----NNSNFAWTAGTKYHLNGRNSLANPGIAMATHKDDDEERFFPVTG-SCFWQQN
rh. 50-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh. 49-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh. 61-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu. 41-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh. 64-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu. 42-E	485	CYRQQRVSTTLSQS-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh. 57-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu. 40-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
AAV8-E	485	CYRQQRVSTTTGQN-----NNSNFAWTAGTKYHLNGRNSLANPGIAMATHKDDDEERFFPSNGILIFGKQN
rh. 58-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh. 40-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu. 67-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu. 17-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu. 6-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu. 66-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh. 38-E	485	CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPGVAMATHKDDDEERFFPSSGVLMFGKQG

FIG. 2V

hu.32-F	483	SYRQQRVSTTVTQN-----NNSEFAWP	GASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG	570	580	590	600	610	620	630
AAV9/hu	483	SYRQQRVSTTVTQN-----NNSEFAWP	GASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG							
hu.31-F	483	SYRQQRVSTTVTQN-----NNSEFAWP	GASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG							
										
AAV5	534	ANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEI	VPGSVWMERDVYL							
AAV3-3	548	T--TASNAELD-NVMITDEEEI	RTTNPVATEQYGTVANLQSSNTAPTGTGNHQGALPGMVWQDRDVYL							
AAV4-4	546	N--GNTATVPG-TLIFTSEEE	LAATNATDMDWGNLPGDQNSNLP	TVDRLTALGAVPGMVWQN	RDIIY					
AAV1-A	548	A--GASNTALD-NVMITDEEEI	KATNPVATERFGTVAVNFQSSSTD	PATG	DVHAMGALPGMVWQDRDVYL					
hu.46-A	548	A--GASNTALD-NVMITDEEEI	KATNPVATERFGTVAVNFQSSSTD	PATG	DVHAMGALPGMVWQDRDVYL					
hu.48-A	548	A--GASNTALD-NVMITDEEEI	KATNPVATERFGTVAVNFQSSSTD	PATG	DVHAMGALPGMVWQDRDVYL					
hu.44-A	548	A--GASNTALD-NVMITDEEEI	KATNPVATERFGTVAVNFQSSSTD	PATG	DVHAMGALPGMVWQDRDVYL					
hu.43-A	549	A--GASNTALD-NVMITDEEEI	KATNPVATERFGTVAVNFQSSSTD	PATG	DVHAMGALPGMVWQDRDVYL					
AAV6-A	548	A--GASNTALD-NVMITDEEEI	KATNPVATERFGTVAVNLQSSSTD	PATG	DVHVMGALPGMVWQDRDVYL					
hu.34-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQRGNRQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.47-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQRGNRQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.29-B	547	P--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.63-B	547	S--GKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATSD	VNTQGVLP	GMVWQDRDVYL				
hu.56-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATSD	VNTQGVLP	GMVWQDRDVYL				
hu.45-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.57-B	546	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTRAATSD	VNTQGVLP	GMVWQDRDVYL				
hu.35-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNRQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.58-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.28-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.51-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNRQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.19-B	547	S--GKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATSD	VNTQGVLP	GMVWQDRDVYL				
hu.49-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNTQAATA	DVNTQGVLP	GMVWQDRDVHL				
hu.52-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQSGNRQAATA	DVNTQGVLP	GMVWQDRDVYL				
hu.13-B	547	S--EKTNV	DIE-KVMITDEEEI	RTTNPVATEQYGSVSTNLQGGNTQAATA	DVNTQGVLP	GMVWQDRDVYL				

FIG. 2W

AAV2-B	547	S--EKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQRGN	RQAAT	ADVNT	QGVLP	GMVWQ	DRDVYL
hu.20-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.24-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.64-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.27-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.21-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.22-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.23-B	547	S--GKTNV	DIE-KVMI	TDEEEI	RTTNP	VATEQY	GSVSTN	LQSGN	TQAAT	SDVNT	QGVLP	GMVWQ	DRDVYL
hu.7-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.61-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
rh.56-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.9-C	547	T--NAND	ADLD-HVMI	TDEEEI	RTTNP	VATEQY	GNVSN	NLQNS	TGPTT	EN	VNHQ	GALP	GMVWQ
hu.54-C	546	T--NATNA	ELE-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TAA	STET	VNHQ	GALP	GMVWQ
hu.53-C	546	T--NATNA	ELE-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TAA	STET	VNHQ	GALP	GMVWQ
hu.60-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.55-C	546	T--NATNA	ELE-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TAA	STET	VNHQ	GALP	GMVWQ
hu.2-C	547	T--NAND	ADLD-NVMI	TDEEEI	IRATNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNRQ	GALP	GMVWQ
hu.1-C	547	T--NAND	ADLD-NVMI	TDEEEI	IRATNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.18-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.3-C	548	T--NAND	ADLD-NVMI	TDEEEI	IRPTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.25-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.15-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.16-C	547	T--NAND	ADLD-NVMI	TDEEEI	RTTNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
hu.11-C	547	T--NAND	ADLD-HVMI	TDEEEI	RTTNP	VATEQY	GNVSN	NLQNS	TGPTT	EN	VNHQ	GALP	GMVWQ
hu.10-C	547	T--NAND	ADLD-HVMI	TDEEEI	RTTNP	VATEQY	GNVSN	NLQNS	TGPTT	EN	VNHQ	GALP	GMVWQ
hu.4-C	547	T--NAND	ADLD-NVMI	TDEEEI	IRATNP	VATEQY	GYVSN	NLQNS	TGPTT	GT	VNHQ	GALP	GMVWQ
rh.54-D	550	A--TN-K	TTL-NVLM	TNEEEI	IRPTNP	VATEEY	GVSSN	LQA	ANTAA	QTV	VNNQ	GALP	GMVWQ
rh.48-D	550	A--AN-K	TTL-NVLM	TNEEEI	IRPTNP	VATEEY	GVSSN	LQA	ANTAA	QTV	VNNQ	GALP	GMVWQ
rh.55-D	550	A--AN-K	TTL-NVLM	TNEEEI	IRPTNP	VATEEY	GVSSN	LQA	ANTAA	QTV	VNNQ	GALP	GMVWQ
rh.62-D	550	A--AN-K	TTL-NVLM	TNEEEI	IRPTNP	VATEEY	GVSSN	LQA	ANTAA	QTV	VNNQ	GALP	GMVWQ

FIG. 2X

[illegible]

FIG. 2Y

AAV3-3_	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSVEIE
AAV4-4_	613	QGPIWAKIPHTDGHFHPSPPLIGFGLKHPPPPQIFIKNTPVPANPATTFSSTPVNSFITQYSTGQVSQID
AAV1-A_	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu.46-A	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu.48-A	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu.44-A	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu.43-A	616	QGPIWAKIPHTDGHFHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
AAV6-A	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu.34-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.47-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.29-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.63-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.56-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.45-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.57-B	613	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.35-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.58-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGRVSVEIE
hu.28-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.51-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.19-B	614	QGPIWAKIPHTDGHFHPSPLVGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.49-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.52-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.13-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
AAV2-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.20-B	614	QGPIWAKIPHTDGHFHPSPMPMGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.24-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.64-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.27-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.21-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu.22-B	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE

FIG. 22

hu. 23-B	614	RGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 7-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 61-C	614	QGPIWAKIPHTDGHFHPSPLVGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
rh. 56-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 9-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 54-C	613	RGPIWAKIPHADGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 53-C	613	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 60-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 55-C	613	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 2-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 1-C	614	QGPIWAKIPHTDGHFHPSPLTGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 18-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 3-C	615	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKSTVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 25-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 15-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 16-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 11-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
hu. 10-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNYSSAKFASFITQYSTGQVSVEIE
hu. 4-C	614	QGPIWAKIPHTDGHFHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTNFSSAKFASFITQYSTGQVSVEIE
rh. 54-D	616	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPANPPEVTPAKFASFITQYSTGQVSVEIE
rh. 48-D	616	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPANPPEVTPAKFASFITQYSTGQVSVEIE
rh. 55-D	616	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPANPPEVTPAKFASFITQYSTGQVSVEIE
rh. 62-D	616	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPANPPEVTPAKFASFITQYSTGQVSVEIE
AAV7-D	616	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPANPPEVTPAKFASFITQYSTGQVSVEIE
rh. 52-E	617	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPADPPTAFNQAKLNSFITQYSTGQVSVEIE
rh. 51-E	617	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPADPPTAFNQAKLNSFITQYSTGQVSVEIE
hu. 39-E	617	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPADPPTAFNQAKLNSFIAQYSTGQVSVEIE
rh. 53-E	617	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPADPPTAFNQAKLNSFITQYSTGQVSVEIE
hu. 37-E	617	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPADPPTTFSQAKLASFITQYSTGQVSVEIE
rh. 43-E	615	QGPIWAKIPHTDGNFHPSPLMGGFGLKHPPPPQILIKNTPVPADPPTTFNQSKLNSFITQYSTGQVSVEIE

FIG. 2AA

rh.50-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNQAKLNS	FITQYSTGQ	VSVEIE
rh.49-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNQAKLNS	FITQYSTGQ	VSVEIE
rh.61-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNQAKLNS	FITQYSTGQ	VSVEIE
hu.41-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
rh.64-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNQAKLNS	FITQYSTGQ	VSVEIV
hu.42-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
rh.57-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNQAKLNS	FITQYSTGQ	VSVEIE
hu.40-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
AAV8-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQSKLNS	FITQYSTGQ	VSVEIE
rh.58-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	STVPADPPT	AFNQAKLNS	FITQYSTGQ	VSVEIE
rh.40-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
hu.67-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
hu.17-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
hu.6-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
hu.66-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
rh.38-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	TFNQAKLAS	FITQYSTGQ	VSVEIE
hu.32-F	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNCKLNS	FITQYSTGQ	VSVEIE
AAV9/hu	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNCKLNS	FITQYSTGQ	VSVEIE
hu.31-F	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQILIK	NTVPADPPT	AFNCKLNS	FITQYSTGQ	VSVEIE

AAV5	673	WELKENS	KRWNPEI	QYTN	NYNDPQ	VDFAPD	STGEYR	TRPIG	TRYLTRPL*
AAV3-3-	685	WELQENS	KRWNPEI	QYTS	NYNKS	VNVDF	TVDTNG	VYSEPR	PIGTRYLTRNL*
AAV4-4-	683	WEIQERS	KRWNPEV	QFTS	NYGQQ	NSLLW	APDAAG	KYTEPR	AIIGTRYLTRHL*
AAV1-A-	685	WELQENS	KRWNPEV	QYTS	NYAKS	ANVDF	TVDNNG	LYTEPR	PIGTRYLTRPL*
hu.46-A	685	WELQENS	KRWNPEV	QYTS	NYAKS	ANVDF	TVDNNG	LYTEPR	PIGTRYLTRPL*
hu.48-A	685	WELQENS	KRWNPEV	QYTS	NYAKS	ANVDF	TVDNNG	LYTEPR	PIGTRYLTRPL*
hu.44-A	685	WELQENS	KRWNPEV	QYTS	NYAKS	ANVDF	TVDNNG	LYTEPR	PIGTRYLTRPL*
hu.43-A	686	WELQENS	KRWNPEV	QYTS	NYAKS	ASVDF	TVDNNG	LYTEPR	PIGTRYLTRPL*

FIG. 2AB

AAV6-A	685	WELQKENS	KRWNPE	IQYTSN	YAKSAN	VDF	TV	DN	NG	LY	TE	PR	PI	G	TR	Y	L	R	P	L	*
hu.34-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.47-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.29-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.63-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.56-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.45-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.57-B	683	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.35-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.58-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.28-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.51-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.19-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.49-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.52-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.13-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
AAV2-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.20-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	AR	Y	L	R	N	L	*	
hu.24-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.64-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.27-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.21-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.22-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.23-B	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.7-C	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.61-C	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
rh.56-C	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.9-C	684	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.54-C	683	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	
hu.53-C	683	WELQKENS	KRWNPE	IQYTSN	YNKSVN	VDF	TV	DN	GV	SE	PR	PI	G	TR	Y	L	R	N	L	*	

FIG. 2AC

hu.60-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.55-C	683	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.2-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.1-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.18-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.3-C	685	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.25-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.15-C	684	WELQEDSKRWNPEIQYTSNYNKPXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.16-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.11-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.10-C	684	WELRQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
hu.4-C	684	WELQENSKRWNPEIQYTSNYNKSXVNDFTVDTNGVYSEPRPIGTRYLTRNL*
rh.54-D	686	WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.48-D	686	WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.55-D	686	WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.62-D	686	WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
AAV7-D	686	WELQENSKRWNPEIQYTSNFEKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.52-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.51-E	687	WEPQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
hu.39-E	687	WELQENSKRWNPEIQYTSNYKSTNADFAVTEGVYSEPRPIGTRYLTRNL*
rh.53-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
hu.37-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.43-E	685	WELQENSKRWNPEIQYTSNYKSTSVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.50-E	687	WELQENSKRWSPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.49-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.61-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
hu.41-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.64-E	687	WELQENSKRRNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
hu.42-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*
rh.57-E	687	WELQENSKRWNPEIQYTSNYKSTNVDFAVTEGVYSEPRPIGTRYLTRNL*

FIG. 2AD

hu.40-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGTYSEPRPIG	TRYLTRNL*
AAV8-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTSVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
rh.58-E	687	WELQKENS	KCWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
rh.40-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
hu.67-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
hu.17-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
hu.6-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
hu.66-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
rh.38-E	687	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
hu.32-F	685	WELQKENS	KRWNPEI	QYTSNYYKSTNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
AAV9/hu	685	WELQKENS	KRWNPEI	QYTSNYYKSNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*
hu.31-F	685	WELQKENS	KRWNPEI	QYTSNYYKSNVDF	AVNTEGVYSEPRPIG	TRYLTRNL*

FIG. 2AE

		10	20	30	40	50	60	70
AAV5	1							
AAV3-3	1	ATGCTCTTTGTTGATCACCCCTCCAGATGGTTGGAAGAA--GTGTTGAAGGTCTTCGCGAGTTTGTG						
AAV4-4	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTTCTGAAGGCATTCTGAGTGGTGGG						
AAV1-A	1	---ATGACTGACGGTTACCTTCCAGATTGGCTAGAGGACAACCTCTCTGAAGCGTTCCGAGAGTGGTGGG						
hu.46-A	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG						
hu.48-A	1	ATGGCTGCCGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.44-A	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG						
hu.43-A	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
AAV6-A	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG						
hu.34-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG						
hu.47-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.29-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.63-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.56-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.45-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.57-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.35-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.58-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.28-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.51-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.19-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.49-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCAAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.52-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.13-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
AAV2-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.20-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.24-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						
hu.64-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAAGGAATAAGACAGTGGTGA						

FIG. 3A

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

FIG. 3B

rh. 53-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG	80	90	100	110	120	130	140
hu. 37-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
rh. 43-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG	GCCTTGAA	68					
rh. 50-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG	CTCTGAA	71					
rh. 49-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG	CGCTGCA	68					
rh. 61-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG	ACTTGAA	71					
hu. 41-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG	AGCTCAA	71					
rh. 64-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 42-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
rh. 57-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 40-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
AAV8-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
rh. 58-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
rh. 40-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 67-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 17-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 6-E	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 66-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
rh. 38-E	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
hu. 32-F	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
AAV9/hu	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTTAGTGAAGGAATTCGCGAGTGGTGGG							
hu. 31-F	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCAATTCGCGAGTGGTGGG							
AAV5	68								
AAV3-3	71	GCCTTGAA							
AAV4-4	68	CTCTGAA							
AAV1-A	71	CGCTGCA							
hu. 46-A	71	ACTTGAA							
		AGCTCAA							

FIG. 3C

70

hu. 9-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATCAGGACAAACAGACAGGGGTCTTGTGCT
hu. 54-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 53-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 60-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 55-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 2-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 1-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 18-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 3-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 25-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 15-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 16-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACACAGACAGGGGTCTTGTGCT
hu. 11-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATCAGGACGACAGACAGGGGTCTTGTGCT
hu. 10-C	71	AGTCAAACCTGGCCACCAACCAACAAAGTCTGCAGAGCGGGCATCAGGACGACAGACAGGGGTCTTGTGCT
hu. 4-C	71	AGTCAAACCTGGCCACCAACCAACAAAGCCCCGAGAGCGGGCATAAAGACGACAGACAGGGGTCTTGTGCT
rh. 54-D	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAACGACAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 48-D	71	ACCTGAAACCTGGAGCCCCCAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 55-D	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 62-D	71	ACCTGAAACCTGGAGCCCCCAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
AAV7-D	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 52-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 51-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
hu. 39-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 53-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
hu. 37-E	71	ACCTGAAACCTGGAGCCCCCAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 43-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 50-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 49-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
rh. 61-E	71	ACCTGAAACCTGGAGCCCCGAAACCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT
hu. 41-E	71	ACCTGAAACCTGGAGCCCCCAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGCGCGGGGTCTGGTGCT

FIG. 3E

72

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

FIG. 3G

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

FIG. 3H

hu. 67-E	141	TCTTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAATGCGGCGGACGCA	220	230	240	250	260	270	280
hu. 17-E	141	TCCTGGCTGCAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCA							
hu. 6-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCA							
hu. 66-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCA							
rh. 38-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGGCGGACGCA							
hu. 32-F	141	TCCTGGGTACAAGTACCTCGGACCCCGCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGAGCAGACGCG							
AAV9/hu	141	TCCGGGTTACAAATACCTTGAGACCCCGCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGAGCAGACGCG							
hu. 31-F	141	TCCTGGGTACAAGTACCTCGGACCCCGCAACGGACTCGACAAGGGGGAGCCCGTCAACGCGAGCAGACGCG							
									
AAV5	208	GTGCGCGAGAGCACGACATCTCGTACAACGAGCAGCTTGAGGCGGGAGACAACCCCTACCTCAAGTACA							
AAV3-3-	211	GCAGCCCTCGAACACGACAAAGCTTACGACCAGCAGCTCAAGGCCGTGACAACCCGTACCTCAAGTACA							
AAV4-4-	208	GCAGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCAAGGCCGTGACAACCCCTACCTCAAGTACA							
AAV1-A-	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCAAGGCCGTGACAATCCGTACCTGCGGTATA							
hu. 46-A	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 48-A	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCAAGGCCGTGACAATCCGTACCTGCGGTATA							
hu. 44-A	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 43-A	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCAAGGCCGTGACAATCCGTACCCCGGGTATA							
AAV6-A	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCAAGGCCGTGACAATCCGTACCTGCGGTATA							
hu. 34-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 47-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 29-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 63-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCCCAAGTACA							
hu. 56-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 45-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 57-B	208	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 35-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							
hu. 58-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACG							
hu. 28-B	211	GCGGCCCTCGAGCACGACAAAGCCCTACGACCAGCAGCTCGACAGGGAGACAACCCGTACCTCAAGTACA							

FIG. 31

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

FIG. 3J

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

FIG. 3K

hu.31-F	211	GCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAGGCCGGAGACAACCCGTACCTCAAGTACA	290	300	310	320	330	340	350
AAV5	278								
AAV3-3	281	ACCACGGGACGCCGAGTTTCAGGAGAAAGCTCGCCGACGACACATCCTTCGGGGGAAACCTCGGAAAGGC							
AAV4-4	278	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTTCAAGAAGATACGTCCTTTTGGGGCAACCTTGGCAGAGC							
AAV1-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCCTTTTGGGGCAACCTCGGCGGAGC							
hu.46-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGCGGGC							
hu.48-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCCTTTTGGGGCAACCTCGGCGGAGC							
hu.44-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGCGGAGC							
hu.43-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGCTTTTGGGGCAACCTCGGCGGAGC							
AAV6-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCCTTTTGGGGCAACCTCGGCGGAGC							
hu.34-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.47-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.29-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.63-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.56-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.45-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.57-B	278	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.35-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.58-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.28-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.51-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.19-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.49-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.52-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.13-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
AAV2-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							
hu.20-B	281	ACCACGTCGACGCCGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCCTTTTGGGGCAACCTCGGACGAGC							

FIG. 3L

hu. 24-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 64-B	281	ACCACGCCGACGCGGAGTTCCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 27-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 21-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 22-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGGAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 23-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 7-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 61-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
rh. 56-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 9-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 54-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 53-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 60-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 55-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 2-C	281	ACCACGCCGACGCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 1-C	281	ACCACGCCGACGCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 18-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 3-C	281	ACCACGCCGACGCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 25-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 15-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 16-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 11-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 10-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 4-C	281	ACCACGCCGACGCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
rh. 54-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 48-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 55-D	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 62-D	281	ACCACGCCGACGCCGAGTTCCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
AAV7-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 52-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC

FIG. 3M

rh. 51-E	281	ATCACGCCGACGCCGAGCTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC	360	370	380	390	400	410	420
hu. 39-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 53-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 37-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 43-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 50-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 49-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 61-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 41-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 64-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 42-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 57-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 40-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
AAV8-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 58-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 40-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 67-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 17-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 6-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 66-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
rh. 38-E	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 32-F	281	ACCACGCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
AAV9/hu	281	ACCACGCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
hu. 31-F	281	ACCACGCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC							
AAV5	348								
AAV3-3	351	AGTCTTTCAGGCCAAGAAAAGGGTTCTCGAACCTTTTGGC---CTGGTTGAAGAGGGTGCTAAGACGGCC							
AAV4-4	348	AGTCTTTCAGGCCAAGAAAAGAGGATCCTTGAGCCTCTTGGT---CTGGTTGAGCAAGCGGGTGAGACGGCT							

FIG. 3N

AAV1-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu.46-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu.48-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTAAGACGGCT
hu.44-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGGCTGAGACGGCT
hu.43-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
AAV6-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTTTTGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
hu.34-B	351	AGTCTTCCAGGCCGAAAAAGAGGGTACTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.47-B	351	AGTCTTCCAGGCCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGGGGAACCTGTTAAGACGGCT
hu.29-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
hu.63-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.56-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.45-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.57-B	348	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.35-B	351	AGTCTTCCAGGCCAAAAAGAGGGTACTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.58-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
hu.28-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGAGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
hu.51-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGGGGAACCTGTTAAGACGGCT
hu.19-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.49-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.52-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGGGGAACCTGTTAAGACGGCT
hu.13-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAAACGGCT
AAV2-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.20-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGCGGCT
hu.24-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.64-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.27-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.21-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.22-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.23-B	351	AGTCTTCCAGGCCAAAAAGAGGATTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.7-C	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT

FIG. 30

hu. 61-C	351	AGTCTTCCAGGCAAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTATAAACGGCT
rh. 56-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 9-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 54-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 53-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 60-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTATAAACGGCT
hu. 55-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 2-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 1-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 18-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTATAAACGGCT
hu. 3-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTATAAACGGCT
hu. 25-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTATAAACGGCT
hu. 15-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---TTGGTTGGGAGCCTGTATAAACGGCT
hu. 16-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---TTGGTTGAGGAGCCTGTATAAACGGCT
hu. 11-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTAAAGACGGCT
hu. 10-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAAACCTGTATAAACGGCT
hu. 4-C	351	AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTAAAGACGGCT
rh. 54-D	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCTGCTAAGACGGCT
rh. 48-D	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCTGCTAAGACGGCT
rh. 55-D	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
rh. 62-D	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGCTGAGGAAAGCTGCTAAGACGGCT
AAV7-D	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
rh. 52-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
rh. 51-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
hu. 39-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
rh. 53-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
hu. 37-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCTGCTAAGACGGCT
rh. 43-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
rh. 50-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT
rh. 49-E	351	AGTCTTCCAGGCGAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAAGCGCTAAGACGGCT

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---	CTGGTTGAGGAAGCTGCTAAGACGGCT
AAV8-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCGGCTAAGACGGCT
rh. 58-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCTGCTAAGACGGCT
rh. 40-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCTGCTAAGACGGCT
hu. 67-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCTGCTAAGACGGCT
hu. 17-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 6-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 66-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCTGCTAAGACGGCT
rh. 38-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCTGCTAAGACGGCT
hu. 32-F	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCGGCTAAGACGGCT
AAV9/hu	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCGGCTAAGACGGCT
hu. 31-F	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---	CTGGTTGAGGAAGCGGCTAAGACGGCT
AAV5	415		
AAV3-3	418	CCTACCGGAAAGCGGATAGACGACCACTTTCCA-----	GAACCGGACTCATCTGGTGTGGCAAAAT
AAV4-4	415	CCTGGAAAGAAAGAGACCGTTGATTGAATCCCCCAG---	CAGCCCAGACTCCTCCACGGGTATCGGCAAAA
AAV1-A	418	CCTGGAAAGAAACGTCGGGTAGAGCAGTCGCCACAA---	GAGCCAGACTCCTCCTCGGGCATCGGCAAGA
hu. 46-A	418	CCTGGAAAGAAACGTCGGGTAGAGCAGTCGCCACAA---	GAGCCAGACTCCCCCTCGGGCATCGGCAAGA
hu. 48-A	418	CCTGGAAAGAAACGTCGGGTAGAGCAGTCGCCACAA---	GAGCCAGACTCCTCCTCGGGCATCGGCAAGA
hu. 44-A	418	CCTGGAAAGAAACGTCGGGTAGAGCAGTCGCCACAA---	GGGCCAGACTCCTCCTCGGGCATCGGCAAGA
hu. 43-A	418	CCTGGAAAGAAAGACCGGTAGAACCGTCACCTCAGCGTT	CCCCCGACTCCTCCACGGGCATCGGCAAGA
AAV6-A	418	CCTGGAAAGAAACGTCGGGTAGAGCAGTCGCCACAA---	GAGCCAGACTCCTCCTCGGGCATCGGCAAGA
hu. 34-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---	GAGCCAGACTCCTCCTCGGGAAACCGGAAAGG

FIG. 30

hu. 47-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 29-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCA---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAGT
hu. 63-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 56-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 45-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 57-B	415	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 35-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 58-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 28-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCGCA---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAGT
hu. 51-B	418	CCAGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 19-B	418	CCGGGAGAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 49-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACAGGAAAAAG
hu. 52-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 13-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
AAV2-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 20-B	418	CCGGGAGAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 24-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 64-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCTTGG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 27-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 21-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 22-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 23-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 7-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 61-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
rh. 56-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 9-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 54-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 53-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 60-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 55-C	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG

FIG. 3R

hu. 2-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 1-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 18-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 3-C	421	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 25-C	418	CCGGAAAAAAGAGACCAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 15-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 16-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 11-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 10-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
hu. 4-C	418	CCGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAAG
rh. 54-D	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 48-D	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 55-D	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 62-D	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
AAV7-D	418	CCTGCAAGAAGAGACCAGCCGGTAGAGCCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 52-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 51-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
hu. 39-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 53-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
hu. 37-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 43-E	418	CCTGGAAGAAGAGACCAGTAGAGCAGTCAACCCAA---GAAACAGACTCCTCCTCGGGCATCGGCAAGA
rh. 50-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 49-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 61-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
hu. 41-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGCCACCTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 64-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
hu. 42-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
rh. 57-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCGTCAACACAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
hu. 40-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA
AAV8-E	418	CCTGGAAGAAGAGACCAGCCGGTAGAGCCATCAACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA

FIG. 3S

rh. 58-E	418	CCTGGAAAGAGACCGGTAGAACCGTCACCTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA	500	510	520	530	540	550	560
rh. 40-E	418	CCTGGAAAGAGACCGGTAGAACCGTCACCTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 67-E	418	CCTGGAAAGAGACCGGTAGAACCGTCACCTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 17-E	418	CCTGGAAAGAGACCGGTAGAGCCATCACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA							
hu. 6-E	418	CCTGGAAAGAGACCGGTAGAGCCATCACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA							
hu. 66-E	418	CCTGGAAAGAGACCGGTAGAACCGTCACCTCAGCGTTCCCCGACTCCTCCGCGGCATCGGCAAGA							
rh. 38-E	418	CCTGGAAAGAGACCGGTAGAACCGTCACCTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 32-F	418	CCTGGAAAGAGAGGCCCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
AAV9/hu	418	CCTGGAAAGAGAGGCCCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
hu. 31-F	418	CCTGGAAAGAGAGGCCCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
AAV5	452	GAAGAAGGCTCGGACCGAAGAGGACTCCAAGCCTTCCACCTCGTCAGACGCCGAAGCTGGACCCAGCGG							
AAV3-3	485	CGGCAAAACAGCCTGCCAGAAAAGACTAAATTTGGGTACAGACTGGAGACTCAGAGTCAGTCCCAGAC--							
AAV4-4	482	AAGCAAGCAGCCGGCTAAAAGAGCTCGTTTTCGAAGACGAACTGGAGCAGCGACGGACCC----							
AAV1-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 46-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 48-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 44-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 43-A	488	AAGGCCAGCAGCCCGCTAAAAGAGACTGAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--							
AAV6-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--							
hu. 34-B	485	CGGCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 47-B	485	CGGCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 29-B	485	CGGCCAACCAAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACTCAGACTCCGTACCTGAC--							
hu. 63-B	485	CGGCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 56-B	485	CGGCCAACCAAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 45-B	485	CGGCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 57-B	482	CGGCCAACCAAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 35-B	485	CGGCCAGCAGCCTGCAAGAAAAGATTGAATTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							

FIG. 3F

hu. 58-B	485	CGGGCAACCGCCTGCAAGAAAAGAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 28-B	485	CGGGCAACCGCCTGCAAGAAAAGAGATTGAATTTTCGGTCAGACTGGAGACTCAGACTCCGTACCTGAC--
hu. 51-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 19-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGCCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 49-B	485	CGGGCCAGCAGCCTGCGAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 52-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 13-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
AAV2-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 20-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 24-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 64-B	485	CGGGCCAGCAGCCTGCAAGAAAGGAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 27-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 21-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 22-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 23-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 7-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 61-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
rh. 56-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 9-C	485	CGGGCCATCAGCCTGCGAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 54-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 53-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 60-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 55-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 2-C	485	CGGGCCAGCGGCCTGCAAGAAAAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 1-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 18-C	485	CGGGCCAGCAGCCTGCGAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 3-C	488	CGGGCCAGCAGCCTGCAAGAAAAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 25-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 15-C	485	CGGGCAACCGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 16-C	485	CGGGCAACCGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--

FIG. 3U

hu.11-C	485	CGGGCCATCAGCCTGCGAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.10-C	485	CGGGCCATCAGCCTGCGAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.4-C	485	CGGGCCAGCAGCCTGCAAGAAAAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
rh.54-D	488	AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.48-D	488	AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.55-D	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.62-D	488	AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
AAV7-D	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.52-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.51-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.39-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCGAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.53-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.37-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.43-E	485	AAGGCCAACAGCCCCGCCAGAAAAGAGACTCAATTTTGGCCAGACTGGCGACTCAGAGTCAGTCCAGAC--
rh.50-E	488	AAGGCCAGCAGCCCCGCCGGAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.49-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.61-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.41-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.64-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.42-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.57-E	488	AAGGCCAGCAGCCCCGCCAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.40-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAGCTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
AAV8-E	488	AAGGCCAACAGCCCCGCCAGAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCAGAC--
rh.58-E	488	AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.40-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.67-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.17-E	488	CAGGCCAGCAGCCCCGCCGAAAAGAGACTCAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.6-E	488	CAGGCCAGCAGCCCCGCCGAAAAGAGACTCAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu.66-E	488	AAGGCCAGCAGCCCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh.38-E	488	AAGGCCAGCGGGCCGCTAAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--

FIG. 3V

hu.32-F	485	CGGGTTCACAGCCCGCTAAAAAGAAACTCAATTTCCGGTCAGACTGGCGACACAGAGTCAGTCCCCGAC--	570	580	590	600	610	620	630
AAV9/hu	485	CGGGTGCACAGCCCGCTAAAAAGAGACTCAATTTCCGGTCAGACTGGCGACACAGAGTCAGTCCCCGAC--							
hu.31-F	485	CGGGTTCACAGCCCGCTAAAAAGAAACTCAATTTCCGGTCAGACTGGCGACACAGAGTCAGTCCCCGAC--							
									
AAV5	522	ATCCACAGCAGCTGCAAAATCCACAGCCCAACCCAGCCTCAAGTTTGGGAGCTGATACAAATGTCTGCGGGAGGT							
AAV3-3	552	-CCTCAACCTCTCGGAGAACCCACAGCAGCCCCCACAAGTTTGGGATCTAATACAAATGGCTTCAGGCGGT							
AAV4-4	546	-----CCTGAGGGATCAACTTCCGGAGCCATGTCT-----GATGACAGTGAGATGCCCTTCAGGCGGT							
AAV1-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGACCTACTACAAATGGCTTCAGGCGGT							
hu.46-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGACCTACTACAAATGGCTTCAGGCGGT							
hu.48-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGACCTACTACAAATGGCTTCAGGCGGT							
hu.44-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGACCTACTACAAATGGCTTCAGGCGGT							
hu.43-A	555	-CCTCAACCAATCGGAGAACCCACAGCAGGCCCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
AAV6-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGACCTACTACAAATGGCTTCAGGCGGT							
hu.34-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.47-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.29-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.63-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.56-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGTCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.45-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.57-B	549	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.35-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.58-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.28-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.51-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.19-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTTCAGGCAGT							
hu.49-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.52-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTACAGGCAGT							
hu.13-B	552	-CCCAGCCTCTCGGACAGCCACCCAGCAGCCCCCTCTGGTCTGGGAACTAATACGATGGCTTCAGGCAGT							

FIG. 3W

AAV2-B	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTACAGGCAGT
hu.20-B	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTTACAGGCAGT
hu.24-B	552	-CCCCGGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTTACAGGCAGT
hu.64-B	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTACAGGCAGT
hu.27-B	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTTACAGGCAGT
hu.21-B	552	-CCCCGGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTTACAGGCAGT
hu.22-B	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTTACAGGCAGT
hu.23-B	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGAACTAATACGATGGCTTACAGGCAGT
hu.7-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.61-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
rh.56-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.9-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGATCTACTACAAATGGCTACAGGCAGT
hu.54-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGATCTACTACAAATGGCTACAGGCAGT
hu.53-C	552	-CCCCAGCCCTCTCAGACAGCCACACAGCAGCCCCCTCTGGATCTACTACAAATGGCTACAGGCAGT
hu.60-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.55-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGATCTACTACAAATGGCTACAGGCAGT
hu.2-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.1-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.18-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTTACAGGCAGT
hu.3-C	555	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.25-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.15-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.16-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
hu.11-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGATCTACTACAAATGGCTACAGGCAGT
hu.10-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGATCTACTACAAATGGCTACAGGCAGT
hu.4-C	552	-CCCCAGCCCTCTCGGACAGCCACACAGCAGCCCCCTCTGGTCTGTGGATCTACTACAAATGGCTACAGGCAGT
rh.54-D	555	-CCTCAACCTCTCGGAGAACCCACACAGCAGGCCCTCTGGTCTGTGGATCTGGTACAAATGGCTGCAGGCCGT
rh.48-D	555	-CCTCAACCAATCGGAGAACCCACACAGCAGGCCCTCTGGTCTGTGGATCTGGTACAAATGGCTGCAGGCCGT
rh.55-D	555	-CCTCAACCTATCGGAGAACCTCCAGCAGGCCCTCTAGTGTGGATCTGGTACAAATGGCTGCAGGCCGT
rh.62-D	555	-CCTCAACCAATCGGAGAGCCACACAGCAGGCCCTCTGGTCTGTGGATCTGGTACAAATGGCTGCAGGCCGT

FIG. 3X

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AAV3-3	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAATTCCTCAGGAAATTGGCATTGCG
AAV4-4	604	GGCGAGCTGCAGTCGAGGGCGACAAGGTGCCGATGGAGTGGGTAATGCCCTCGGTGATTGGCATTGCG
AAV1-A	622	GGCGACCAATGGCAGACAAATAACGAAAGCGCGCGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu.46-A	622	GGCGACCAATGGCAGACAAATAACGAAAGCGCGCGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu.48-A	622	GGCGACCAATGGCAGACAAATAACGAAAGCGCGCGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu.44-A	622	GGCGACCAATGGCAGACAAATAACGAAAGCGCGCGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu.43-A	625	GGCGTCCAATGGCAGACAAATAACGAAAGCGCGCGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
AAV6-A	622	GGCGACCAATGGCAGACAAATAACGAAAGCGCGCGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu.34-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.47-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.29-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.63-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.56-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.45-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.57-B	619	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAGATTGGCATTGCG
hu.35-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.58-B	622	GGCGACCAATGGCAGACAAATAACGATGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.28-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.51-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.19-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.49-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.52-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.13-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
AAV2-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.20-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.24-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.64-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.27-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.21-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG
hu.22-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCGCGAGTGGTAATTCCTCGGAAATTGGCATTGCG

FIG. 3N

hu. 23-B	622	GGCGACCAATGGCAGACAAATAACGAGGGCGCCGACGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
hu. 7-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 61-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
rh. 56-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 9-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 54-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 53-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 60-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
hu. 55-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 2-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 1-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 18-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 3-C	625	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 25-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 15-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 16-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 11-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 10-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
hu. 4-C	622	GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
rh. 54-D	625	GGCGTCCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
rh. 48-D	625	GGCGACCAATGGCTGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
rh. 55-D	625	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
rh. 62-D	625	GGCGACCAATGGCTGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
AAV7-D	625	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
rh. 52-E	625	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
rh. 51-E	625	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
hu. 39-E	625	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
rh. 53-E	625	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG
hu. 37-E	625	GGCGTCCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCAGGAAATTTGGCATTGCG
rh. 43-E	622	GGCGACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAAATTCCTCGGAAATTTGGCATTGCG

FIG. 3AA

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AAV6-A	692	ATCCACATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACATGGGCCTTGCCACCTATAACAA
hu.34-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.47-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.29-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.63-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.56-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.45-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.57-B	689	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.35-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.58-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.28-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.51-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.19-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.49-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.52-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.13-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
AAV2-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.20-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.24-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.64-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.27-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.21-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.22-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.23-B	692	ATCCACATGGATGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.7-C	692	ATCCCAATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.61-C	692	ATCCCAATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh.56-C	692	ATCCCAATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.9-C	692	ATCCCAATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.54-C	692	ATCCCAATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu.53-C	692	ATCCCAATGGCTGGCGACAGAGTTCATCACCAACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA

FIG. 3AC

hu. 60-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 55-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 2-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACATAACAACAA
hu. 1-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACATAACAACAA
hu. 18-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 3-C	695	ATTTCCCAATGGCTGGACGACAGAGTCA	TGCCACACAGACCCCGAACCTGGGCCCTGCCACATAACAACAA
hu. 25-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACAAAGCACTCGAACCTGGGCCCTGCCACCTACAACAA
hu. 15-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCTCTGCCACCTACAATAA
hu. 16-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCTCTGCCACCTACAACAA
hu. 11-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 10-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 4-C	692	ATTTCCCAATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACATAACAACAA
rh. 54-D	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCTTTGGCCACCTACAACAA
rh. 48-D	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCTTTGGCCACCTACAACAA
rh. 55-D	695	ATTTCCACACGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCTTTGGCCACCTACAACAA
rh. 62-D	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCTTTGGCCACCTACAACAA
AAV7-D	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 52-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 51-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 39-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 53-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 37-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 43-E	692	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 50-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 49-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 61-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 41-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 64-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 42-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA
rh. 57-E	695	ATTTCCACATGGCTGGCGACAGAGTCA	TACCACACAGACCCCGAACCTGGGCCCTGCCACCTACAACAA

FIG. 3AD

hu.40-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
AAV8-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
rh.58-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
rh.40-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
hu.67-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
hu.17-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
hu.6-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
hu.66-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
rh.38-E	695	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
hu.32-F	692	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
AAV9/hu	692	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
hu.31-F	692	ATTCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAAACCTGGGCCCTGCCACCTACAACAA							
AAV5	732								
AAV3-3	762	CCACAGTACCGAGAGATCAAAAGC---GGTCCGTGACGGAAAGCAACGCCAAAGCCTACTTTGGATAC							
AAV4-4	744	CCATCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCTTCAAACGACAAACCCTACTTTGGCTAC							
AAV1-A	762	CCACCTCTACAAGCGACTCGGA-----GAGAGCCTGCAGTCCAAACACCTACAACGGATTCTC							
hu.46-A	762	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
hu.48-A	762	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
hu.44-A	762	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
hu.43-A	765	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
AAV6-A	762	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
hu.34-B	762	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
hu.47-B	762	CCACCTCTACAAGCAAAATCTCCAGT---GCTTCAAACGGGGCCAGCAACGACAAACCCTACTTCGGCTAC							
hu.29-B	762	CCATCTGTACAAGCAAAATATCC-----AGCCAGTCTGGAGCCAGCAACGACAAATCACTACTTTGGCTAC							
hu.63-B	762	CCACCTCTACAAGCAGATTTC-----AGCCAATCAGGAGCCTCAAACGACAAACCCTACTTCGGCTAC							
hu.56-B	762	CCACCTCTACAAGCAGATTTC-----AGCCAATCAGGAGCCTCAAACGACAAACCCTACTTCGGCTAC							
hu.45-B	762	CCACCTCTACAAGCAAAATTTCC-----AGCCAATCAGGAGCCTCGAACGACAAATCACTACTTTGGCTAC							

FIG. 3AE

hu. 57-B	759	CCACCTCTACAAGCAGATTTC-----AGCCAATCAGGAGCCAGCAATGACAACCACTACTTTTGGCTAC
hu. 35-B	762	CCACCTCTACAAGCAAAATTTC-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTTGGCTAC
hu. 58-B	762	CCATCTGTACAAGCAGATTTC-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 28-B	762	CCATCTGTACAAGCAAAATATCC-----AGCCAGTCTGGAGCCAGCAACGACAATCACTACTTTTGGCTAC
hu. 51-B	762	CCACCTCTACAAGCAAAATTTC-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTTGGCTAC
hu. 19-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 49-B	762	CCATCTGTACAAGCAGATCTCC-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 52-B	762	CCACCTCTACAGACAAATTTCC-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTTGGCTAC
hu. 13-B	762	CCATCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
AAV2-B	762	CCACCTCTACAAGCAAAATTTCC-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTTGGCTAC
hu. 20-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 24-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 64-B	762	CCACCTCTACAGGCAGATTTC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 27-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 21-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 22-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 23-B	762	CCATCTGTACAAGCAAAATCTCC-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 7-C	762	CCACCTCTACAAGCAAAATCTCA-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 61-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
rh. 56-C	762	CCACCTCTACAAGCAAAATCTCA-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 9-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCGAACGACAACCACTACTTTTGGCTGC
hu. 54-C	762	CCACCTTTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 53-C	762	CCACCTTTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 60-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 55-C	762	CCACCTTTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 2-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 1-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTTGGCTAC
hu. 18-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTTGGCTAC
hu. 3-C	765	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTGCAACGACAACCACTACTTTTGGCTAC
hu. 25-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTATTTTGGCTAC

FIG. 3Af

hu. 15-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTGGGTAC
hu. 16-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTGGGTAC
hu. 11-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCGAAGCAGACAACCACTACTTTGGGTAC
hu. 10-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCGAAGCAGACAACCACTACTTTGGGTAC
hu. 4-C	762	CCACCTCTACAAGCAAAATCTCC-----AGCCAATCAGGAGCCTCGAAGCAGACAACCACTACTTTGGGTAC
rh. 54-D	765	CCACCTCTACAAGCAAAATCTCCAGT---AGTCAAGCAGGTAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 48-D	765	CCACCTCTACAAGCAAAATCTCCAGT---AGTCAAGCAGGTAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 55-D	765	CCACCTCTACAAGCAAAATCTCCAGT---AGTCAAGCAGGTAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 62-D	765	CCACCTCTACAAGCAAAATCTCCAGT---AGTCAAGCAGGTAGCACCACCAACGACAACCACTACTTTGGGTAC
AAV7-D	765	CCACCTCTACAAGCAAAATCTCCAGT---GAACTGCAGGTAGTACCAACGACAACCACTACTTTGGGTAC
rh. 52-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 51-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 39-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 53-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 37-E	765	CCACCTCTACAAGCAAAATATCCAAATGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 43-E	762	CCACCTCTACAAGCAAAATCTCCAAACGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 50-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 49-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 61-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 41-E	765	CCACCTCTACAAGCAAAATATCCAAATGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 64-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 42-E	765	CCACCTCTACAAGCAAAATATCCAAATGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 57-E	765	CCACCTCTACAAGCAAAACCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 40-E	765	CCACCTCTACAAGCAAAATATCCAAATGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
AAV8-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 58-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACCTCGGAGGCAGCACCACCAACGACAACCACTACTTTGGGTAC
rh. 40-E	765	CCACCTCTACAAGCAAAATATCCAAATGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 67-E	765	CCACCTCTACAAGCAAAATATCCAAATGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 17-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC
hu. 6-E	765	CCACCTCTACAAGCAAAATCTCCAAACGGGACATCGGAGGAGCAGCACCACCAACGACAACCACTACTTTGGGTAC

FIG. 3AG

hu.66-E	765	CCACCTCTACAAGCAAAATATCCAATGGGACATCGGGAGGAAGCACCAACGACAACACCTACTTCGGGTAC	850	860	870	880	890	900	910
rh.38-E	765	CCACCTCTACAAGCAAAATATCCAATGGGACATCGGGAGGAAGCACCAACGACAACACCTACTTCGGGTAC							
hu.32-F	762	TCACCTCTACAAGCAAAATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTACTTCGGGTAC							
AAV9/hu	762	TCACCTCTACAAGCAAAATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTACTTCGGGTAC							
hu.31-F	762	TCACCTCTACAAGCAAAATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGCCTACTTCGGGTAC							
AAV5	799	AGCACCCCTTGGGGGTACTTTGACTTTAAACCGCTTCCACAGCCACTGGAGCCCCCGAGACTGGCAAAGAC							
AAV3-3	826	AGCACCCCTTGGGGGTATTTTGACTTTAAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
AAV4-4	799	TCCACCCCTTGGGGGTACTTTGACTTTCAACCGCTTCCACTGCCACTTCTCACACGTGACTGGCAGCGAC							
AAV1-A	829	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
hu.46-A	829	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
hu.48-A	829	GGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
hu.44-A	829	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
hu.43-A	832	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
AAV6-A	829	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGCGAC							
hu.34-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.47-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.29-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.63-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.56-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGAGAC							
hu.45-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.57-B	823	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAGAGAC							
hu.35-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.58-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.28-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.51-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.19-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							
hu.49-B	826	AGCACCCCTTGGGGGTATTTGACTTTCAACAGATTCACCTGCCACTTCTCACACGTGACTGGCAAAGAC							

FIG. 3AH

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

FIG. 3AI

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

FIG. 3A

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

FIG. 3AK

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

FIG. 3AL

hu. 37-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	990	1000	1010	1020	1030	1040	1050
rh. 43-E	902	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 50-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGGTGCAGGACTCCACCCACCACCATCGCCAAACAACCTCACCTCCACCGTCCAAGTGTTTACGGAC						
rh. 49-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGCAGAACGATGGCAGCAGACTATTGCCAATAACCTTACCGACACGGTTCAAGTGTTTACGGAC						
rh. 61-E	905	CCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGACGTCGAACGGCAGACAAACGGTGGCTAATAACCTTACCGACACGGTTCAAGTCTTTGCGGAC						
hu. 41-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC						
rh. 64-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC						
hu. 42-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC						
rh. 57-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC						
hu. 40-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
AAV8-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 58-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 40-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 67-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 17-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 6-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 66-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 38-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 32-F	902	TCATCAACAACAACTGGGGATTCCGGCCCTAAGCGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
AAV9/hu	902	TCATCAACAACAACTGGGGATTCCGGCCCTAAGCGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 31-F	902	TCATCAACAACAACTGGGGATTCCGGCCCTAAGCGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
AAV5	939	GGTCACGGTGCAGGACTCCACCCACCACCATCGCCAAACAACCTCACCTCCACCGTCCAAGTGTTTACGGAC							
AAV3-3	966	GGTCACGCAGAACGATGGCAGCAGACTATTGCCAATAACCTTACCGACACGGTTCAAGTGTTTACGGAC							
AAV4-4	939	GGTCACGACGTCGAACGGCAGACAAACGGTGGCTAATAACCTTACCGACACGGTTCAAGTCTTTGCGGAC							
AAV1-A	969	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC							
hu. 46-A	969	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC							
hu. 48-A	969	GGTCACGACGGAATGATGGCGTCACAACCATCGCTAATAACCTTACCGACACGGTTCAAGTCTTCTCGGAC							

FIG. 3AM

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

FIG. 3AN

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

FIG. 3A

hu. 42-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC	1060	1070	1080	1090	1100	1110	1120
rh. 57-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTGTTTACGGAC							
hu. 40-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
AAV8-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTGTTTACGGAC							
rh. 58-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
rh. 40-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu. 67-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu. 17-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu. 6-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu. 66-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
rh. 38-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu. 32-F	972	GGTTACGGACAACAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
AAV9/hu	972	GGTTACGGACAACAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu. 31-F	972	GGTTACGGACAACAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
AAV5	1009	GACGACTACCAAGCTGCCCTACGTCGTCGGCAACGGACCCGAGGGATGCCCTGCCGGCCCTTCCCTCCGCAGG							
AAV3-3	1036	TCGGAGTATCAGTCCCGTACGTGCTCGGGTCGGGTCGGCGCACCAAGGTGTCTCCCGCCGTTCACAGCGGACG							
AAV4-4	1009	TCGTCGTACGAACTGCCGTACGTGATGGATGGGGTCAAGAGGGCAGCCTGCCCTCCGTTCGCCAAGCAGC							
AAV1-A	1039	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 46-A	1039	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 48-A	1039	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 44-A	1039	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 43-A	1042	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
AAV6-A	1039	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 34-B	1036	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 47-B	1036	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 29-B	1036	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							
hu. 63-B	1036	TCGGAGTACCAAGCTTCCGTACGTCTCGGCTCTGGGCACCAAGGGCTGCCCTCCCTCCGTTCGCCGGGACG							

FIG. 3AP

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

FIG. 3AQ

hu. 3-C	1039	TCGGAGTACCAGCTCCCGTACGTCCCGGGGCTCGGGCGCATCAAGGATGCCTCCCGCCGTTTCCAGCGGACG
hu. 25-C	1036	TCGGAGTACCAGCTCCCGTACGTCTCTCGGCTCGGGCGCATCAAGGATGCCTCCCGCCGTTTCCAGCGGACG
hu. 15-C	1036	TCGGGGTACCAGCTCCCGTACGTCTCTCGGCTTGCGGCATCAAGGATGCCTCCCGCCGTTTCCAGCAGACG
hu. 16-C	1036	TCGGAGTACCAGCTCCCGTACGTCTCTCGGCTCGGGCGCATCAAGGATGCCTCCCGCCGTTTCCAGCAGACG
hu. 11-C	1036	TCGGAGTACCAGCTCCCGTACGTCTCTCGGCTCGGGCGCATCAAGGATGCCTCCCGCCGTTTCCAGCGGACG
hu. 10-C	1036	TCGGAGTACCAGCTCCCGTACGTCTCTCGGCTCGGGCGCATCAAGGATGCCTCCCGCCGTTTCCAGCGGACG
hu. 4-C	1036	TCGGAGTACCAGCTCCCGTACGTCTCTGGGCTCGGGCGCATCAAGGATGCCTCCCGCCGTTTCCAGCGGACG
rh. 54-D	1042	TCGGAGTACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 48-D	1042	TCGGAATACCAGCTGCCCTACGTCTCTCGGCTCCGCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 55-D	1042	TCGGAATACCAGCTGCCCTACGTCTCTCGGCTCCGCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 62-D	1042	TCGGAATACCAGCTGCCCTACGTCTCTCGGCTCCGCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
AAV7-D	1042	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCGCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 52-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 51-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
hu. 39-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 53-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
hu. 37-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 43-E	1042	TCGGAGTACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 50-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 49-E	1045	TCGGAGTACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 61-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
hu. 41-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 64-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
hu. 42-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 57-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
hu. 40-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
AAV8-E	1045	TCGGAGTACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 58-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
rh. 40-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG
hu. 67-E	1045	TCGGAATACCAGCTGCCGTACGTCTCTCGGCTCTGCCACACAGGGCTGCCTGCCCTCCGTTCCCGCGGACG

FIG. 3AR

hu. 17-E	1045	TCGGAATACCAAGCTCCCGTACGTCTCGGCTCTGCGCACCAAGGGCTGCCCGCCTCCGTTCCCGGCGGACG							
hu. 6-E	1045	TCGGAATACCAAGCTCCCGTACGTCTCGGCTCTGCGCACCAAGGGCTGCCCGCCTCCGTTCCCGGCGGACG							
hu. 66-E	1045	TCGGAATACCAAGCTCCCGTACGTCTCGGCTCCGCGCACCAAGGGCTGCCGTCCGTTCCCGGCGGACG							
rh. 38-E	1045	TCGGAATACCAAGCTCCCGTACGTCTCGGCTCCGCGCACCAAGGGCTGCCGTCCGTTCCCGGCGGACG							
hu. 32-F	1042	TCAGACTATCAGCTCCCGTACGTCTCGGCTCCGCGCACCAAGGGCTGCCGTCCCGCCTCCCGGCGGACG							
AAV9/hu	1042	TCAGACTATCAGCTCCCGTACGTCTCGGCTCCGCGCACCAAGGGCTGCCGTCCCGCCTCCCGGCGGACG							
hu. 31-F	1042	TCAGACTATCAGCTCCCGTACGTCTCGGCTCCGCGCACCAAGGGCTGCCGTCCCGCCTCCCGGCGGACG							
			1130	1140	1150	1160	1170	1180	1190
AAV5	1079	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGAC--AACACAGAAATCCACCGAGAG							
AAV3-3-	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGAC--AGTCAAGCGGTGGACG							
AAV4-4-	1079	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGAC--AGTCAAGCGGTGGACG							
AAV1-A-	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC--AGCCAAGCCGTGGGACG							
hu. 46-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC--AGCCAAGCCGTGGGACG							
hu. 48-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC--AGCCAAGCCGTGGGACG							
hu. 44-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC--AGCCAAGCCGTGGGACG							
hu. 43-A	1112	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC--AGCCAAGCCGTGGGACG							
AAV6-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC--AGTCAAGCGAGTAGGACG							
hu. 34-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 47-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 29-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 63-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 56-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 45-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 57-B	1103	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 35-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 58-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 28-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							
hu. 51-B	1106	TCATTACGCTGCCGACGTACGGTTACGGACGCTGAACCGCGG--AGTCAAGCGAGTAGGACG							

FIG. 3A8

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

FIG. 3AT

rh. 54-D	1112	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGACG
rh. 48-D	1112	TCTTCATGATTCCCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTGG
rh. 55-D	1112	TCTTCATGATTCCCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTGG
rh. 62-D	1112	TCTTCATGATTCCCCAGTACGGCTACCTGACTCTGAACAATGAC-----AGCCAATCGGTGGGTGG
AAV7-D	1112	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAATGGC-----AGTCAGTCTGTGGGACG
rh. 52-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 51-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 39-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 53-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 37-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 43-E	1112	TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 50-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 49-E	1115	TCTTCATGATTCCCTCAGTACGGCAACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 61-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 41-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 64-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 42-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 57-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 40-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
AAV8-E	1115	TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 58-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 40-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 67-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 17-E	1115	TCTTCATGATTCCCTCAGTACGGGTACCTGACTCTGAACAACGGC-----AGTCAGGCCGTGGGCCG
hu. 6-E	1115	TCTTCATGATTCCCTCAGTACGGGTACCTGACTCTGAACAACGGC-----AGTCAGGCCGTGGGCCG
hu. 66-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 38-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 32-F	1112	TTTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAAATGATGG-----AGCCAGGCCGTGGGTGG
AAV9/hu	1112	TTTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAAATGATGGA-----AGCCAGGCCGTGGGTGG
hu. 31-F	1112	TTTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAAATGATGGA-----GGCCAGGCCGTGGGTGG

FIG. 3AU

	1200	1210	1220	1230	1240	1250	1260
AAV5							
AAV3-3	1146 GAGCAGCTTCTTGCCCTAGAGTACTTCCCAGCAAGATGCTGAGAACGGGCAACAACCTTTGAGTTTACC						
AAV4-4	1167 CTCATCCCTTTTACTGCCCTGGAGTACTTCCCTTCGCAGATGCTAAGGACTGGAATAAATCCCAATTCAGC						
AAV1-A	1149 AATGCCCTTCTACTGCCCTGGAGTACTTCCCTTCGCAGATGCTGCGGACTGGCAACAACCTTTGAAATTCAG						
hu.46-A	1170 TTCATCCCTTTTACTGCCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC						
hu.48-A	1170 TTCATCCCTTTTACTGCCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC						
hu.44-A	1170 TTCATCCCTTTTACTGCCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC						
hu.43-A	1173 TTCATCCCTTTTACTGCCCTGGAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC						
AAV6-A	1170 GTCATCCCTTTTACTGCCCTGGAATATTTCCCATCGCAGATGCTGAGAACGGGCAATAAATTTACCTTCAGC						
hu.34-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.47-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.29-B	1167 CTCTTCATTTTACTGCCCTAGGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.63-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.56-B	1167 CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGCAACCGGAAACAACCTTTACCTTCAGC						
hu.45-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.57-B	1164 CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC						
hu.35-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.58-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.28-B	1167 CTCTTCATTTTACTGCCCTAGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.51-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.19-B	1167 CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC						
hu.49-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC						
hu.52-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.13-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
AAV2-B	1167 CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC						
hu.20-B	1167 CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC						
hu.24-B	1167 CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC						

FIG. 3AV

hu. 64-B	1167	CTCTTCATTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTACCTTCAGC
hu. 27-B	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTTCTGTAACCGGAAACAACCTTACCTTCAGC
hu. 21-B	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTTCTGTAACCGGAAACAACCTTACCTTCAGC
hu. 22-B	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGACGCTTCTGTAACCGGAAACAACCTTACCTTCAGC
hu. 23-B	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTTCTGTAACCGGAAACAACCTTACCTTCAGC
hu. 7-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTTCTGTAACCGGAAACAACCTTACCTTCAGC
hu. 61-C	1167	CTCTTCATTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
rh. 56-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTTCTGTAACCGGAAACAACCTTTCAGTTCAGC
hu. 9-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTACCTTCAGC
hu. 54-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTACCTTCAGC
hu. 53-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTACCTTCAGC
hu. 60-C	1167	CTCTTCATTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 55-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 2-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 1-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 18-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 3-C	1170	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 25-C	1167	CTCTCCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 15-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 16-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 11-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 10-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 4-C	1167	CTCTTCCTTTTACTGCGCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
rh. 54-D	1173	TTCAATCCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGT
rh. 48-D	1173	TTCCCTCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTCACTTCAGT
rh. 55-D	1173	TTCCCTCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTCACTTCAGT
rh. 62-D	1173	TTCCCTCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTCACTTCAGT
AAV7-D	1173	TTCCCTCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTCACTTCAGT
rh. 52-E	1176	TTCCCTCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTTCAGTTCAGT
rh. 51-E	1176	TTCCCTCTTCTACTGCGCTGGAATACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTTCAGTTCAGT

FIG. 3AW

hu.39-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC	1270	1280	1290	1300	1310	1320	1330
rh.53-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
hu.37-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.43-E	1173	CTCCTCCCTTCTACTGCCCTGGAATACTTTCCCTTCGAGATGCTGAGAACCGGCAACAACACTTCCAGTTTACT							
rh.50-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
rh.49-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
rh.61-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
hu.41-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.64-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
hu.42-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.57-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
hu.40-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
AAV8-E	1176	CTCCTCCCTTCTACTGCCCTGGAATACTTTCCCTTCGAGATGCTGAGAACCGGCAACAACACTTCCAGTTTACT							
rh.58-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACACTTTTCCTTCAGC							
rh.40-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.67-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.17-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTTCCCTCTCAAAATGCGGAGAACGGGCAACAACACTTTGAGTTCAGC							
hu.6-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTTCCCTCTCAAAATGCGGAGAACGGGCAACAACACTTTGAGTTCAGC							
hu.66-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.38-E	1176	TTCCCTCCCTTCTACTGCCCTGGAATATTTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.32-F	1173	TTCGTCCCTTTTACTGCCCTGGAATATTTCCCGTCGCAAAATGCTAAGAACGGGTAACAACACTTCCAGTTCAGC							
AAV9/hu	1173	TTCGTCCCTTTTACTGCCCTGGAATATTTCCCGTCGCAAAATGCTAAGAACGGGTAACAACACTTCCAGTTCAGC							
hu.31-F	1173	TTCGTCCCTTTTACTGCCCTGGAATATTTCCCGTCGCAAAATGCTAAGAACGGGTAACAACACTTCCAGTTCAGC							
AAV5	1216								
AAV3-3	1237	TACAACCTTTGAGGAGGTGCCCTTCCACTCCAGCTTCGCTCCAGTCAGAACCTGTTCAGCTGGCCCAACC							
AAV4-4	1219	TATACCTTCGAGGATGTACCTTTTACACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGCTTGATGAATC							
AAV1-A	1240	TACAGTTTGTGAGGAGGTGCCCTTCCACTCGATGTACGCGCACAGCCAGAGCCCTGGACCGGCTGATGAACC							
		TACACCTTTGAGGAGGTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGCCCTGGACCGGCTGATGAATC							

FIG. 3AX

hu. 46-A	1240	TACACCTTTGAGGAAGTGCCTCTCCACAGCAGCTGCGGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 48-A	1240	TACACCTTTGAGGAAGTGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 44-A	1240	TACACCTTTGAGGAAGTGCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 43-A	1243	TACACCTTTGAGGAAGTGCCTCTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
AAV6-A	1240	TACACCTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 34-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCAGCTACGCGCACAGCCAGAGTCTGGCCGCTCATGAATC
hu. 47-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGCCGCTCATGAATC
hu. 29-B	1237	TACACCTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 63-B	1237	TACACCTTTGAGGACGTTCCTTTCCACAGCAGCTACGCGCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 56-B	1237	TACACTTTTGAAGACGTTCCTTTCCACAGCAGCTACGCTCACAGTCAAAGTCTGGACCGTCTCATGAATC
hu. 45-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 57-B	1234	TACACTTTTGAAGACGTTCCTTTCCACAGCAGCTACGCTCACAGTCAAAGTCTGGACCGTCTCATGAATC
hu. 35-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGCCGCTCTCATGAATC
hu. 58-B	1237	TACACCTTTGAGGATGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 28-B	1237	TACACCTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 51-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCGGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 19-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 49-B	1237	TACACCTTTGAGGATGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 52-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 13-B	1237	TACACCTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
AAV2-B	1237	TACACTTTTGAGGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 20-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 24-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 64-B	1237	TACACCTTTGAGGACGTTCCTTTCCACAGCAGCTACGCGCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 27-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACGGCCAAAGTCTGGACCGTCTCATGAATC
hu. 21-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 22-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 23-B	1237	TACACCTTTGAAGACGTTCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 7-C	1237	TACACCTTTGAAGACGTTCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 61-C	1237	TACACTTTTGAAGACGTGCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC

FIG. 3AY

rh. 56-C	1237	TACACCTTTGAAGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 9-C	1237	TACACCTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAATC
hu. 54-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGGGTTTGGATCGGCTGATGAATC
hu. 53-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 60-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 55-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 2-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 1-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 18-C	1237	TACACCTTTGAAGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 3-C	1240	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 25-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 15-C	1237	TACACCTTTGAAGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 16-C	1237	TACACCTTTGAAGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 11-C	1237	TACACCTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAATC
hu. 10-C	1237	TACACCTTTGAGGACGTTCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAATC
hu. 4-C	1237	TACACCTTTGAAGACGTTGCCCTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
rh. 54-D	1243	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGCCTAGACCGGCTGATGAATC
rh. 48-D	1243	TACACCTTCGAGGACGTTCCCTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
rh. 55-D	1243	TACACCTTCGAGGACGTTCCCTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
rh. 62-D	1243	TACACCTTCGAGGACGTTCCCTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
AAV7-D	1243	TACAGCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
rh. 52-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
rh. 51-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
hu. 39-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
rh. 53-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
hu. 37-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
rh. 43-E	1243	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACCGGCTGATGAATC
rh. 50-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
rh. 49-E	1246	TACACCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC
rh. 61-E	1246	TACCCCTTCGAGGACGTTGCCCTTCCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC

FIG. 3AZ

hu. 41-E	1246	TACACCTTCGAGGACGTGCCTTCCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC	1340	1350	1360	1370	1380	1390	1400
rh. 64-E	1246	TACACTTTCGAGGACGTGCCTTCCACAGCAGCTACGCACACAGCCAGAGTTTGGACAGGCTGATGAATC							
hu. 42-E	1246	TACACCTTCGAGGACGTGCCTTCCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
rh. 57-E	1246	TACACTTTCGAGGACGTGCCTTCCACAGCAGCTACGCACACAGCCAGAGTTTGGACAGGCTGATGAATC							
hu. 40-E	1246	TACACTTTCGAGGACGTGCCTTCCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGCTGATGAATC							
AAV8-E	1246	TACACTTTCGAGGACGTGCCTTCCACAGCAGCTACGCCACAGCCAGAGTTTGGACAGGCTGATGAATC							
rh. 58-E	1246	TACACTTTCGAGGACGTGCCTTCCACAGCAGCTACGCACACAGCCAGAGTTTGGACCGACTGATGAATC							
rh. 40-E	1246	TACACCTTCGAGGACGTGCCTTCCACAGCGGTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
hu. 67-E	1246	TACACCTTCGAGGACGTGCCTTCCACAGCGGTACGCACACAGCCAGAGCTTGGACCGGTGATGAATC							
hu. 17-E	1246	TACAGTTTCGAGGACGTGCCTTTCACAGCAGCTACGGCATAGCCAAAGCCTGGACCGGTGATGAATC							
hu. 6-E	1246	TACAGTTTCGAGGACGTGCCTTTCACAGCAGCTACGGCATAGCCAAAGCCTGGACCGGTGATGAATC							
hu. 66-E	1246	TACACCTTCGAGGACGTGCCTTTCACAGCAGCTACGGCATAGCCAAAGCCTGGACCGGTGATGAATC							
rh. 38-E	1246	TACACCTTCGAGGACGTGCCTTTCACAGCAGCTACGGCATAGCCAAAGCCTGGACCGGTGATGAATC							
hu. 32-F	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCAGAGCCAAAGCCTGGACCGGTGATGAATC							
AAV9/hu	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCAGAGCCAAAGCCTGGACCGGTGATGAATC							
hu. 31-F	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCAGAGCCAAAGCCTGGACCGGTGATGAATC							
AAV5	1286	CGCTGGTGACCAAGTACTTGTACCGCTTCGTGAGCACAAAT	1340	1350	1360	1370	1380	1390	1400
AAV3-3	1307	CTCTTATTGATCAGTATCTGTACTACTGAACAGAACGCAAGGAACAACCTCTGGAACAACCAACCAATC							
AAV4-4	1289	CTCTCATCGACCAAGTACCTGTGGGACTGCAATCGACCAACCCGGAACCCCTGAATGCCGGACTGC							
AAV1-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
hu. 46-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
hu. 48-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
hu. 44-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
hu. 43-A	1313	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
AAV6-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
hu. 34-B	1307	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							
hu. 47-B	1307	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTCCCAAAACAA							

FIG. 3BA

hu. 29-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 63-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 56-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 45-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGTGGAAACCAACACGCAGTC
hu. 57-B	1304	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 35-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGTGGAAACCAACACGCAGTC
hu. 58-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 28-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 51-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGTGGAAACCAACACGCAGTC
hu. 19-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 49-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 52-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGTGGAAACCAACACGCAGTC
hu. 13-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
AAV2-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGTGGAAACCAACACGCAGTC
hu. 20-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 24-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 64-B	1307	CTCTCGTCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCAGTC
hu. 27-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 21-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 22-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 23-B	1307	CTCTCATCGACCCAGTACCTGTATTACTTTGAGCAGAAACAAC---ACTCCAAGCGGAACCAACACGCATGTC
hu. 7-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTGAAACAAAACACAA---TCAAATAGTGGAACTCTTCAGCAGTC
hu. 61-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTGAAACAAAGACACAA---ACAAATAGTGGAACTCTTCAGCAGTC
rh. 56-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTGAAACAAAACACAA---TCAAATAGTGGAGCTCTTCAGCAGTC
hu. 9-C	1307	CTCTGATCGACCCAGTATCTATATCTGAAACAGGACACAA---TCAAATAGTGGAACTCTTCAGCAGTC
hu. 54-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTAAACAGAAACACAA---ACAGCTAGTGGAACT---CAGCAGTC
hu. 53-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTAAACAGAAACACAA---ACAGCTAGTGGAACT---CAGCAGTC
hu. 60-C	1307	CTCTGGTCGACCCAGTACCTGTATTATCTGAAACAAAGACACAA---ACAAATAGTGGAACTCTTCAGCAGTC
hu. 55-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTAAACAGAAACACAA---ACAGCTAGTGGAACT---CAGCAGTC
hu. 2-C	1307	CTCTGATCGACCCAGTACCTGTATTATCTGAAACAAAGACACAA---ACAAATAGTGGAACTCTTCAGCAGTC

FIG. 3BB

hu. 1-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
hu. 18-C	1307	CTCTGATCGACCGAGTACCTATATATCTGAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 3-C	1310	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
hu. 25-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
hu. 15-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 16-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 11-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 10-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACTCTTTCAGCAGTC
hu. 4-C	1307	CTCTGATCGACCGAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACTCTTTCAGCAGTC
rh. 54-D	1313	CCCTCATCGACCGAGTACCTGTATTACCTGGCTAGAACACAGAGTAACCCAGGAGGCACATCTGGCAATCG
rh. 48-D	1313	CTCTTATCGACCGAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGCAGAGGCACAGCTGGCAATCG
rh. 55-D	1313	CTCTTATCGACCGAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGCAGAGGCACAGCTGGCAATCG
rh. 62-D	1313	CTCTTATCGACCGAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGCAGAGGCACAGCTGGCAATCG
AAV7-D	1313	CCCTCATCGACCGAGTACCTGTATTACCTGGCCAGAACACAGAGTAACCCAGGAGGCACAGCTGGCAATCG
rh. 52-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
rh. 51-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
hu. 39-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
rh. 53-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
hu. 37-E	1316	CTCTCATCGACCGAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
rh. 43-E	1313	CTCTGATTGACCGAGTACCTGTACTACTTGTCTCGGACTCAAAACA---ACAGGAGGCACGGCAATAACGCA
rh. 50-E	1316	CTCTCGTCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
rh. 49-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
rh. 61-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
hu. 41-E	1316	CTCTCATCGACCGAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
rh. 64-E	1316	CTCTCATCGACCGAGTACCTGTACTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
hu. 42-E	1316	CTCTCATCGACCGAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
rh. 57-E	1316	CTCTCATCGACCGAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA
hu. 40-E	1316	CTCTCATCGACCGAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
AAV8-E	1316	CTCTGATTGACCGAGTACCTGTACTACTTGTCTCGGACTCAAAACA---ACAGGAGGCACGGCAATAACGCA
rh. 58-E	1316	CTCTCATCGACCGAGTACCTGTACTACTACCTGTCAAGAACCCAGTCT---ACGGGAGGCACAGCGGGGAACCCA

FIG. 3BC

rh. 40-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC---	1410	1420	1430	1440	1450	1460	1470
hu. 67-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCAGTCC---							
hu. 17-E	1316	CCCTCATCGACCACTACCTGTACTACTCTCGGACTCAGTCC---							
hu. 6-E	1316	CCCTCATCGACCACTACCTGTACTACTCTCGGACTCAGTCC---							
hu. 66-E	1316	CTCTCATCGACCACTACCTGTACTACTTATCCAGAACTCGGTCC---							
rh. 38-E	1316	CTCTCATCGACCACTACCTGCACACTTATCCAGAACTCAGTCC---							
hu. 32-F	1313	CACATCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAACGGTCTGGA-----							
AAV9/hu	1313	CACATCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAACGGTCTGGA-----							
hu. 31-F	1313	CACTCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAACGGTCTGGA-----							
AAV5	1335	CGGAGTCCAGTTCACACAGAACTGGCCGGGAGATACGCCAACACCTACAAAACCTGGTTC							
AAV3-3	1377	ACGGCTGCTTTTAGCCAGGCTGGGCTCAGTCTATGTCTTTCAGGCCAGAAAATGGCTACCTGGGCCC							
AAV4-4	1359	CACCACCAACTTTACCAAGCTGGGCTACCAACTTTTCCAACTTTAAAAAAGAACTGGCTGCCCCGGCCT							
AAV1-A	1377	GGACTTGCTGTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCCAAAACCTGGCTACCTGGACCC							
hu. 46-A	1377	GGACTTGCTGTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCCAAAACCTGGCTACCTGGACCC							
hu. 48-A	1377	GGACTTGCTGTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCCAAAACCTGGCTACCTGGACCC							
hu. 44-A	1377	GGACTTGCTGTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCCAAAACCTGGCTACCTGGACCC							
hu. 43-A	1380	GGACTTGCTGTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCCAAAACCTGGCTACCTGGACCC							
AAV6-A	1377	GGACTTGCTGTTAGCCGCTGGGTCTCCAGCTGGCATGTCTGTTTCAGCCCCAAAACCTGGCTACCTGGACCC							
hu. 34-B	1374	AAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 47-B	1374	AAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 29-B	1374	CAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 63-B	1374	AAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 56-B	1374	CAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 45-B	1374	AAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 57-B	1371	CAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 35-B	1374	AAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGACCACTAGGAACTGGCTTCCTGGACCC							
hu. 58-B	1374	CAGGCTTCAGTTTCTCAGGCCGAGCGAGTGACATTCGGGATCAGTCTAGGAACTGGCTTCCTGGACCC							

FIG. 3BD

hu.28-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAGTGACATTTCAGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.51-B	1374	AAGGCTTCAGTTTTTCTCAGGCCGGAGCGAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.19-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.49-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.52-B	1374	AAGGCTTCAGTTTTTCTCAGGCCGGAGCGAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.13-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
AAV2-B	1374	AAGGCTTCAGTTTTTCTCAGGCCGGAGCGAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.20-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.24-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.64-B	1374	AAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.27-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.21-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.22-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.23-B	1374	CAGGCTTCAGTTTTTCTCAGGCCGGAGCGAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.7-C	1374	TCGGCTACTGTTTAGTCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.61-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCACCAACATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
rh.56-C	1374	TCGGCTACTGTTTAGTCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.9-C	1374	TAGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.54-C	1371	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCC
hu.53-C	1371	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCC
hu.60-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.55-C	1371	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCC
hu.2-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.1-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.18-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.3-C	1377	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.25-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.15-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.16-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT
hu.11-C	1374	TAGGCTACTGTTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGCTGGCTACCTGGACCT

FIG. 3BE

hu. 10-C	1374	TAGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAAAGTGGCTGCCTGGACCT
hu. 4-C	1374	TCGGCTACTGTTTAGCCAAAGCTGGACCAACCAACATGTCTCTTCAAGCTAAAAAAGTGGCTGCCTGGACCT
rh. 54-D	1383	GGAAGTGCAGTTTTACCAGGCGGGCCTTCCACCATGGCCGACCAAGCCAAAGAACTGGTTACCTGGACCT
rh. 48-D	1383	GGAAGTGCAGTTTTATCAGGGCGGGCCTACCACCATGGCCGACCAAGCCAAAGAACTGGCTGCCTGGACCT
rh. 55-D	1383	GGAAGTGCAGTTTTATCAGGGCGGGCCTACCACCATGGCCGACCAAGCCAAAGAACTGGCTGCCTGGACCT
rh. 62-D	1383	GGAAGTGCAGTTTTATCAGGGCGGGCCTACCACCATGGCCGACCAAGCCAAAGAACTGGCTGCCTGGACCT
AAV7-D	1383	GGAAGTGCAGTTTTACCAGGCGGGCCTTCAACTATGGCCGACCAAGCCAAAGAACTGGTTACCTGGACCT
rh. 52-E	1383	GCAGTTGCTGCTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
rh. 51-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
hu. 39-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
rh. 53-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
hu. 37-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 43-E	1380	GACTCTGGGCTTCAGCCAAAGTGGGCTAATACAATGGCCAATCAGGCAAGAAACTGGCTGCCAGGACCC
rh. 50-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
rh. 49-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
rh. 61-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
hu. 41-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 64-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
hu. 42-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 57-E	1383	GCAGTTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
hu. 40-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
AAV8-E	1383	GACTCTGGGCTTCAGCCAAAGTGGGCTAATACAATGGCCAATCAGGCAAGAAACTGGCTGCCAGGACCC
rh. 58-E	1383	GCAGCTGCTGTTTTCTCAGGCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCTGGACCC
rh. 40-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCGGGCTAGGCTAAGAACTGGCTACCTGGACCT
hu. 67-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu. 17-E	1383	GCAGTTGCTATTTCTCAGGCGGGCCTAATAACATGTGGCTCAGGCCAGAAACTGGCTACCCGGGCC
hu. 6-E	1383	GCAGTTGCTATTTCTCAGGCGGGCCTAATAACATGTGGCTCAGGCCAGAAACTGGCTACCCGGGCC
hu. 66-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 38-E	1383	GCAATTGTTATTTCTCAAAGCTGGGCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu. 32-F	1377	AACGCTAAAAATTCAGCGTGGCCGACCCAGCAACATGGCTGTCCAGGGAAGAAACTACATACCTGGACCC

FIG. 3BF

AAV9/hu	1377	AACGCTAAATTCAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC	1480	1490	1500	1510	1520	1530	1540
hu.31-F	1377	AACGCTAAATTCAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC							
AAV5	1405	ATGGGCCGAACCCAGGGCTGGAACCTGGGCTCCGGGTCAAC							
AAV3-3	1447	TGCTACCGGCAACAGAGACTTCAAGACTGCTAACGACAAC							CGGCCAGTGTCA
AAV4-4	1429	TCAATCAAGCAGCAGGGCTTCTCAAAGACTGCCAATCAAACTACAAGATCCCTGCCACCGGGTCAGACA							AACAACAGTAACT
AAV1-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAACAGACAAC							AACAACAGCAATT
hu.46-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAACAGACAAC							AACAACAGCAATT
hu.48-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAACAGACAAC							AACAACAGCAATT
hu.44-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAACAGACAAC							AACAACAGCAATT
hu.43-A	1450	TGTTATCGGCAGCAGCGCGTTTCTAAACAAACAGACAAC							AACAACAGCAATT
AAV6-A	1447	TGTTACCGGCAGCAGCGCGTTTCTAAACAAACAGACAAC							AACAACAGCAACT
hu.34-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.47-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.29-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.63-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.56-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.45-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.57-B	1441	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACGGTGAAT
hu.35-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.58-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.28-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.51-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.19-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.49-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.52-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
hu.13-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT
AAV2-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTGCGGATAAC							AACAACAGTGAAT

FIG. 3BG

hu.20-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACAGCTGCGGACAAC	-----AACAAACAGTGATT
hu.24-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACAGCTGCGGACAAC	-----AACAAACAGTGATT
hu.64-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACATCTGCGGATAAC	-----AACAAACAGTGAAT
hu.27-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACAGCTGCGGACAAC	-----AACAAACAGTGATT
hu.21-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACAGCTGCGGACAAC	-----AACAAACAGTGATT
hu.22-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACAGCTGCGGACAAC	-----AACAAACAGTGATT
hu.23-B	1444	TGTTACCGCCAGCAGCGAGTATCAAAGACAGCTGCGGACAAC	-----AACAAACAGTGATT
hu.7-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.61-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
rh.56-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.9-C	1444	TGCTACAGACAGCAGCGTCTTTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.54-C	1441	TGTTATCGCCAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.53-C	1441	TGTTATCGCCAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.60-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.55-C	1441	TGTTATCGCCAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.2-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAACGACAAC	-----AACAAACAGCAACT
hu.1-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAACGACAAC	-----AACAAACAGCAACT
hu.18-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.3-C	1447	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAACGACAAT	-----AACAACTGCAACT
hu.25-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.15-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.16-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.11-C	1444	TGCTACAGACAGCAGCGTCTTTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.10-C	1444	TGCTACAGACAGCAGCGTCTTTCAAAGCAGGCAACGACAAC	-----AACAAACAGCAACT
hu.4-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAACGACAAC	-----AACAAACAGCAACT
rh.54-D	1453	TGCTTCGGCAACAAAGAGTTTCCAAAACACTGGATCAAAAAC	-----AACAAACAGCAACT
rh.48-D	1453	TGCTTCGGCAACAAAGAGTCTCCAAGACGCTGGATCAAAAAC	-----AACAAACAGCAACT
rh.55-D	1453	TGCTTCGGCAACGAAGAGTCTCCAAGACGCTGGATCAAAAAC	-----AACAAACAGCAACT
rh.62-D	1453	TGCTTCGGCAACAAAGAGTCTCCAAGACGCTGGATCAAAAAC	-----AACAAACAGCAACT
AAV7-D	1453	TGCTTCGGCAACAAAGAGTCTCCAAAAACGCTGGATCAAAAAC	-----AACAAACAGCAACT

FIG. 3BH

rh. 52-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC	1550	1560	1570	1580	1590	1600	1610
rh. 51-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 39-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
rh. 53-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 37-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
rh. 43-E	1450	TGTTACCGCCAAACAACGCGTCTCAACGACAACCGGGCAAAAC							
rh. 50-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
rh. 49-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
rh. 61-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 41-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
rh. 64-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 42-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
rh. 57-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 40-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
AAV8-E	1453	TGTTACCGCCAAACAACGCGTCTCAACGACAACCGGGCAAAAC							
rh. 58-E	1453	TGCTACAGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
rh. 40-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
hu. 67-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
hu. 17-E	1453	TGCTACCGGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 6-E	1453	TGCTACCGGACAGCAGCGGTCTCCACGACACTGTGCGAAAAAC							
hu. 66-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
rh. 38-E	1453	TGCTACCGGACAGCAGCGGTCTTACGACACTGTGCGAAAAAC							
hu. 32-F	1447	AGTACCGGACAAACAACGTGTCTCAACCACTGTGACTCAAAAC							
AAV9/hu	1447	AGTACCGGACAAACAACGTGTCTCAACCACTGTGACTCAAAAC							
hu. 31-F	1447	AGTACCGGACAAACAACGTGTCTCAACCACTGTGACTCAAAAC							
AAV5	1460	GCGCCTTCGCCACGACCAATAGGATGGAGCTCGAGGCGCGAGTTACCAAGGTGCCCGCCGACGCCGAAACGG							
AAV3-3	1502	TTCCCTGGACAGCGGCCAGCAAAATATCATCTCAATGGCCCGCGACTCGCTGGTGAATCCAGGACCGACGCTAT							

FIG. 3BI

AAV4-4	1499	GTCTCATCAAAATACGAGACGCACAGCACTCTGGACGGAAGATGGAGTGCCCTGACCCCCGGACCTCCAAAT
AAV1-A	1502	TTACCTGGACTGGTGTCTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCACTGCTAT
hu.46-A	1502	TTACCTGGACTGGTGTCTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCACTGCTAT
hu.48-A	1502	TTACCTGGACTGGTGTCTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCACTGCTAT
hu.44-A	1502	TTACCTGGACTGGTGTCTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCACTGCTAT
hu.43-A	1505	TTACCTGGACTGGTGTCTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCACTGCTAT
AAV6-A	1502	TTACCTGGACTGGTGTCTCAAAATATAACCTTAATGGCGTGAATCTATAATCAACCCCTGGCACTGCTAT
hu.34-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.47-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.29-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.63-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTTAATGGAAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.56-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.45-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.57-B	1496	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.35-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.58-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.28-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.51-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.19-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT
hu.49-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.52-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.13-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
AAV2-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.20-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT
hu.24-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT
hu.64-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTTAATGGAAGAGACTCTCTGTGAATCCGGGCCCGGCCAT
hu.27-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT
hu.21-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT
hu.22-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT
hu.23-B	1499	ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGAATCCGGGCCCGAGCTAT

FIG. 3BJ

hu. 7-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCACCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 61-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
rh. 56-C	1499	TTCCCTGGACTGCGGCTACAAAAGTACCACTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 9-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 54-C	1496	TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCGGAGACTCTTTGGTGAACCCGGGCCCGGCCAT
hu. 53-C	1496	TTCCCTGGACTGGAGCTACCAAGTACTACCTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGGCCAT
hu. 60-C	1499	TTCCCTGGACTGCAGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 55-C	1496	TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGGCCAT
hu. 2-C	1499	TTCCCTGGACTGCAGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 1-C	1499	TTCCCTGGACTGCAGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 18-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 3-C	1502	TTCCCTGGACTGCAGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 25-C	1499	TTCCCTGGACTGCAGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 15-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 16-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 11-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCGTCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 10-C	1499	TTCCCTGGACTGCGGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 4-C	1499	TTCCCTGGACTGCAGCTACAAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
rh. 54-D	1508	TTGCTTGGACTGGTGCCACCAAATATCACCTGAACGGCAGAAACTCATTTGGTGAATCCTGGTGTGCCCCAT
rh. 48-D	1508	TTGCTTGGACTGGTGCCACCAAATATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTGCCCCAT
rh. 55-D	1508	TTGCTTGGACTGGTGCCACCAAATATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTGCCCCAT
rh. 62-D	1508	TTGCTTGGACTGGTGCCACCAAATATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTGCCCCAT
AAV7-D	1508	TTGCTTGGACTGGTGCCACCAAATATCACCTGAACGGCAGAAACTCGTTGGTTAATCCCGGTGTGCCCCAT
rh. 52-E	1508	TTGCTTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCCCCAT
rh. 51-E	1508	TTGCTTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCCCCAT
hu. 39-E	1508	TTGCTTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCCCCAT
rh. 53-E	1508	TTGCTTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCCCCAT
hu. 37-E	1508	TTGCTTGGACTGGTGCCACCAAATATCACCTGAACGGAGAGACTCTTTGGTAAATCCCGGTGTGCCCCAT
rh. 43-E	1505	TTGCTTGGACTGGTGCCACCAAATATACCATCTGAATGGAAGAAATTCATTTGGTAAATCCTGGCATCGCTAT
rh. 50-E	1508	TTGCTTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCCCCAT

FIG. 3BK

rh. 49-E	1508	TTGCCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCGCCAT	1620	1630	1640	1650	1660	1670	1680
rh. 61-E	1508	TTGCCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCGCCAT							
hu. 41-E	1508	TTGCTTGGACTGGTGCCACCAATATCACCTGAACGGAAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
rh. 64-E	1508	TTGCCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCCGGTGTCGCCAT							
hu. 42-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGAAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
rh. 57-E	1508	TTGCCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCCGGTGTCGCCAT							
hu. 40-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGAAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
AAV8-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAATGGAAGAAATTCATTTGGTAAATCCCGGTGTCGCCAT							
rh. 58-E	1508	TTGCCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCCGGTGTCGCCAT							
rh. 40-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGCAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
hu. 67-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGCAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
hu. 17-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGCAGAGACTCTCTGGTGAATCCCGGTGTCGCCAT							
hu. 6-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAATGGAAGAAATTCATTTGGTAAATCCCGGTGTCGCCAT							
hu. 66-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGCAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
rh. 38-E	1508	TTGCCCTGGACTGGTGCCACCAATATCACCTGAACGGCAGAGACTCTTGGTAAATCCCGGTGTCGCCAT							
hu. 32-F	1502	TTGCTTGGCCTGGAGCTTCTTCTTGGGCTCTCAATGGACGTAATAGCTTGAATCCTGGACCTGCTAT							
AAV9/hu	1502	TTGCTTGGCCTGGAGCTTCTTCTTGGGCTCTCAATGGACGTAATAGCTTGAATCCTGGACCTGCTAT							
hu. 31-F	1502	TTGCTTGGCCTGGAGCTTCTTCTTGGGCTCTCAATGGACGTAATAGCTTGAATCCTGGACCTGCTAT							
AAV5	1530	CATGACCAACAACCTCCAGGGCAGCAACACCTATGCCCTGGAGAACACTATGATCTTCAACAGCCAGCCG							
AAV3-3	1572	GGCCAGTCACAAGGACGATGAAGAAAATTTTCCCTATGCACGGCAATCTAATATTTGGCAAAGAAGGG							
AAV4-4	1569	GGCCACGGCTGGACCTGCGGACAGCAAGTTCAGC--AACAGCCAGCTCATCTTGGGGGCGCTAAACAG							
AAV1-A	1572	GGCTTCACACAAAGACGACGAAGACAAAGTCTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 46-A	1572	GGCTTCACACAAAGACGACGAAGACAAAGTCTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 48-A	1572	GGCTTCACACAAAGACGACGAAGACAAAGTCTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 44-A	1572	GGCTTCACACAAAGACGACGAAGACAAAGTCTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 43-A	1575	GGCTTCACACAAAGACGACGAAGACAAAGTCTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
AAV6-A	1572	GGCTTCACACAAAGACGACGAAGACAAAGTCTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							

FIG. 3BL

hu. 34-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 47-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 29-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTATCTTTGGGAAGCAAGGC
 hu. 63-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 56-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 45-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 57-B 1566 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 35-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 58-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGGA
 hu. 28-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTATCTTTGGGAAGCAAGGC
 hu. 51-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 19-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 49-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 52-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 13-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 AAV2-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGGAAGCAAGGC
 hu. 20-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 24-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 64-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 27-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 21-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 22-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 23-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAAATATTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGAC
 hu. 7-C 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGAAAAACAAGGA
 hu. 61-C 1569 GGCAAGCCACAAGGATGACGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGTAACAAGGA
 rh. 56-C 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGTAACAAGGA
 hu. 9-C 1569 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGTAACAAGGA
 hu. 54-C 1566 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGTAACAAGGA
 hu. 53-C 1566 GGCAAGCCACAAGGACGATGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGTAACAAGGA
 hu. 60-C 1569 GGCAAGCCACAAGGATGACGAAGAAAAAGTTTTTCTCAGAGCGGGGTTCTCATCTTTGGTAACAAGGA

FIG. 3BM

hu. 55-C 1566 GGCCAGGCCACAAGGACGATGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTAATATTTGGTAAAGAAGGA
 hu. 2-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 1-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 18-C 1569 GGCCAGGCCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 3-C 1572 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 25-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 15-C 1569 GGCCAGGCCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 16-C 1569 GGCCAGGCCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 11-C 1569 GGCCAGGCCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 10-C 1569 GGCCAGGCCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 hu. 4-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAAACCCCTGATATTTGGTAAACAAGGA
 rh. 54-D 1578 GGCAACTCACAAAGGACGACGAGGACCGCTTTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAAAAGCTGGA
 rh. 48-D 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCTTCGAGCGGAGTCCCTGATTTTGGAAAAAAGCTGGA
 rh. 55-D 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCTTCGAGCGGAGTCCCTGATTTTGGAAAAAAGCTGGA
 rh. 62-D 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCTTCGAGCGGAGTCCCTGATTTTGGAAAAAAGCTGGA
 AAV7-D 1578 GGCAACTCACAAAGGACGACGAGGACCGCTTTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAAAAGCTGGA
 rh. 52-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 rh. 51-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 hu. 39-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 rh. 53-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 hu. 37-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCCCTCATGTTCGGAAAAACAGGGT
 rh. 43-E 1575 GGCAACACACAAGGACGACGAGGACCGCTTTTCCAGTAACGGGA--TCCTGTTTTGGCAACAAAAT
 rh. 50-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 rh. 49-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 rh. 61-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 hu. 41-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCCCTCATGTTTGGAAAAACAGGGT
 rh. 64-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 hu. 42-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCCCTCATGTTTGGAAAAACAGGGT
 rh. 57-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTCATGTTTGGCAAGCAGGGA
 hu. 40-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCCCTCATGTTTGGAAAAACAGGGT

FIG. 3BN

AAV8-E	1578	GGCAACACACAAGACGACGAGGAGCGTTT	1690	1700	1710	1720	1730	1740	1750
rh. 58-E	1578	GGCAACCAACAAGGACGACGAGGACCGCTT							
rh. 40-E	1578	GGCAACGCATAAGGACGACGAGGAACGTTT							
hu. 67-E	1578	GGCAACCCACAAGGACGACGAGGAACGCTT							
hu. 17-E	1578	GGCAACGCACAAGGACGACGAGAGCGATTTT							
hu. 6-E	1578	GGCAACGCACAAGGACGACGAGAGCGATTTT							
hu. 66-E	1578	GGCAACCCACAAGGACGACGAGGAACGCTT							
rh. 38-E	1578	GGCAACCCACAAGGACGACGAGGAACGCTT							
hu. 32-F	1572	GGCCAGCCACAAGAAAGGAGAGGACCGTTT							
AAV9/hu	1572	GGCCAGCCACAAGAAAGGAGAGGACCGTTT							
hu. 31-F	1572	GGCCAGCCACAAGAAAGGAGAGGACCGTTT							
AAV5	1600	GCGAACCCGGCCACCACCGCCACGTACCT							
AAV3-3	1642	ACA-----ACGGCAAGTAACGCAGAAATT							
AAV4-4	1636	AAC-----GGCAACACGGCCACCGTACC							
AAV1-A	1642	GCC-----GGAGCTTCAAACACTGCATT							
hu. 46-A	1642	GCC-----GGAGCTTCAAACACTGCATT							
hu. 48-A	1642	GCC-----GGAGCTTCAAAGCACTGCATT							
hu. 44-A	1642	GCC-----GGAGCTTCAAACACTGCATT							
hu. 43-A	1645	GCC-----GGAGCTTCAAACACTGCATT							
AAV6-A	1642	GCC-----GGAGCTTCAAACACTGCATT							
hu. 34-B	1639	TCA-----GAGAAAACAAATGTGGACATT							
hu. 47-B	1639	TCA-----GAGAAAACAAATGTGGACATT							
hu. 29-B	1639	CCA-----GAGAAAACAAATGTGGATATT							
hu. 63-B	1639	TCG-----GAGAAAACTAATGTGGACATT							
hu. 56-B	1639	TCA-----GAGAAAACAAATGTGGACATT							
hu. 45-B	1639	TCA-----GAGAAAACAAATGTGGACATT							
hu. 57-B	1636	TCA-----GAGAAAACAAATGTGGACATT							

FIG. 3B0

hu. 35-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 hu. 58-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGAA
 hu. 28-B 1639 TCA-----GAGAAAACAAATGTGGATATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 hu. 51-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 hu. 19-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 49-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGAA
 hu. 52-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 hu. 13-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 AAV2-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 hu. 20-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 24-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 64-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTCATGATTACAGACGAAGAGGAAATCAGGA
 hu. 27-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 21-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 22-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 23-B 1639 TCG-----GGAAAACTAATGTGGACATTGAA---AAGGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu. 7-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCTATGATTACAGATGAAGAAGAAATCCGCA
 hu. 61-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
 rh. 56-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCTATGATTACAGATGAAGAAGAAATCCGCA
 hu. 9-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG---CATGTTATGATTACAGATGAAGAAGAAATCAGGA
 hu. 54-C 1636 ACA-----AATGCTAACCAACGCGGAATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
 hu. 53-C 1636 ACA-----AATGCTACCAACGCGGAATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
 hu. 60-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
 hu. 55-C 1636 ACA-----AATGCTACCAACGCGGAATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
 hu. 2-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGG
 hu. 1-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGG
 hu. 18-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCTATGATTACAGATGAAGAAGAAATCCGCA
 hu. 3-C 1642 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGC
 hu. 25-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
 hu. 15-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCTATGATTACAGATGAAGAAGAAATCCGCA

FIG. 3BP

hu. 16-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCTATGATTACAGATGAAGAAAGAAATCCGCA
 hu. 11-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG---CATGTTATGATTACAGATTACAGATGAAGAAAGAAATCAGGA
 hu. 10-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG---CATGTTATGATTACAGATTACAGATGAAGAAAGAAATCAGGA
 hu. 4-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCTATGATTACAGATTACAGATGAAGAAAGAAATCAGGG
 rh. 54-D 1648 GCA-----ACCAAC---AAGACTACATTGGAA---AACGTGTTAATGACAAATGAAGAAAGAAATTCGTC
 rh. 48-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGTGTTAATGACAAATGAAGAGGAAATTCGTC
 rh. 55-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGTGTTAATGACAAATGAAGAGGAAATTCGTC
 rh. 62-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGTGTTAATGACAAATGAAGAGGAAATTCGTC
 AAV7-D 1648 GCA-----ACTAAC---AAAACATACATTGGAA---AATGTGTTAATGACAAATGAAGAAAGAAATTCGTC
 rh. 52-E 1648 GCT-----GGAAGAGACAACTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 51-E 1648 GCT-----GGAAGAGACAACTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 39-E 1648 GCT-----GGAAGAGACAACTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 53-E 1648 GCT-----GGAAGAGACAACTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 37-E 1648 GCT-----GGAAGAGACAACTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 43-E 1642 GCT-----GCCAGAGACAACTGGGATTACAGC---GATGTCTATGCTACCCAGCGAGGAAAGAAATCAAAA
 rh. 50-E 1648 GCT-----GGAAGAGACAACTGGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 49-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 61-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 41-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 64-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 42-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 57-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 40-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 AAV8-E 1648 GCT-----GCCAGAGACAACTGGGATTACAGC---GATGTCTATGCTACCCAGCGAGGAAAGAAATCAAAA
 rh. 58-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 rh. 40-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 67-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 17-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 6-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA
 hu. 66-E 1648 GCT-----GGAAGAGACAACTGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAAGAAATCAAGA

FIG. 3BQ

rh.38-E	1648	GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCAAGCAAGAAATAAAA	1760	1770	1780	1790	1800	1810	1820
hu.32-F	1642	ACT-----GGAAGAGACAACGTGGATCGGAC---AAAGTCATGATAAACCACGAAGAAATAAAA							
AAV9/hu	1642	ACT-----GGAAGAGACAACGTGGATCGGAC---AAAGTCATGATAAACCACGAAGAAATAAAA							
hu.31-F	1642	ACT-----GGAAGAGACAACGTGGATCGGAC---AAAGTCATGATAAACCACGAAGAAATAAAA							
AAV5	1670	CGGTGAACCGCGTGGCGTACAACGTCGGCGGGCAGATGGCCACCAACCAAGAGCTCCACCACTGCCCC							
AAV3-3	1703	CCACCAATCCTGTGGCAACAGAGCAGTATGGAACCTGTGGCAATAAATTCAGAGCTCAAATACAGCTCC							
AAV4-4	1697	CCACCAACGCCACCGATACGGACATGTGGGGCAACCTACCTGGCGGTGACCAAGAGCAACAGCAACCTGCC							
AAV1-A	1703	CCACTAACCCCTGTGGCCACCGAAAGATTTGGACCCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACCC							
hu.46-A	1703	CCACTAACCCCTGTGGCCACCGAAAGATTTGGACCCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACCC							
hu.48-A	1703	CCACTAACCCCTGTGGCCACCGAAAGATTTGGACCCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACCC							
hu.44-A	1703	CCACTAACCCCTGTGGCCACCGAAAGATTTGGACCCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACCC							
hu.43-A	1706	CCACTAACCCCTGTGGCCACCGAAAGATTTGGACCCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACCC							
AAV6-A	1703	CCACTAACCCCTGTGGCCACCGAAAGATTTGGACCCGTGGCAGTCAATTTCCAGAGCAGCAGCAGACCC							
hu.34-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC							
hu.47-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC							
hu.29-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.63-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.56-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.45-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.57-B	1697	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.35-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.58-B	1700	CCACCAATCCCGTGGCCACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.28-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.51-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.19-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.49-B	1700	CCACCAATCCCGTGGCCACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							
hu.52-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACACAAGC							

FIG. 3BR

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rh. 62-D	1706	CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTTAGCAGCAAAACCTGCAGGCGGGCTAAACACTGCAGC
AAV7-D	1706	CTACTAATCCTGTAGCCACGGAAGAAATACGGGATAGTCAGCAGCAAACTTACAAGCGGCTAAATACTGCAGC
rh. 52-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 51-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 39-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 53-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 37-E	1709	CCACTAACCCCGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
rh. 43-E	1703	CCACTAACCCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATAAATTTGCAGCAGCAAAACACGGCTCC
rh. 50-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 49-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 61-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 41-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
rh. 64-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 42-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
rh. 57-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 40-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
AAV8-E	1709	CCACTAACCCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATAAATTTGCAGCAGCAAAACACCGCTCC
rh. 58-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 40-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
hu. 67-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
hu. 17-E	1709	CCACCAACCCAGTGGCCACAGAACAGTACGGCGTGGTGGCCGATAACCTGCAACAGCAAAACCGCGCTCC
hu. 6-E	1709	CCACCAACCCAGTGGCCACAGAACAGTACGGCGTGGTGGCCGATAACCTGCAACAGCAAAACCGCGCTCC
hu. 66-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
rh. 38-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGTGGTGGCTGACAACTTGACGAAACCAATACAGGGCC
hu. 32-F	1703	CTACTAACCCCGTAGCAACGGAGTCCTATGGACAAAGTGGCCACAAACCAACAGAGTGCCCAAGCACAGGC
AAV9/hu	1703	CTACTAACCCCGTAGCAACGGAGTCCTATGGACAAAGTGGCCACAAACCAACAGAGTGCCCAAGCACAGGC
hu. 31-F	1703	CTACTAACCCCGTAGCAACGGAGTCCTATGGACAAAGTGGCCACAAACCAACAGAGTGCCCAAGCACAGGC

AAV5 1740 CGGACCCGGCACGTACAACCTCCAGGAAATCGTCCCCGGCAGCGTGTGGATGGAGAGGGACGTGTACCTC
 AAV3-3 1773 CACGACTGGAAGTGTCAATCATCAGGGGCGCTTACCTGGCATGGTGTGGCAAGATCGTGACGTGTACCTT
 AAV4-4 1767 GACCGTGGACAGACTGACAGCCTTGGAGCCGTGCTGGAATGGTCTGGCAAAACAGAGACATTTACTAC
 AAV1-A 1773 TCGACCCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.46-A 1773 TCGACCCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.48-A 1773 TCGACCCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.44-A 1773 TCGACCCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.43-A 1776 TCGACCCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 AAV6-A 1773 TCGACCCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.34-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTT
 hu.47-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.29-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu.63-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.56-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.45-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.57-B 1767 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu.35-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.58-B 1770 ATCTACTGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.28-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.51-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.19-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTG
 hu.49-B 1770 AGTACTGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.52-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.13-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 AAV2-B 1770 AGTACCCGCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.20-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.24-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.64-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.27-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.21-B 1770 AGTACCTCAGATGTCAACACACACAAAGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG

FIG. 3BU

hu.22-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.23-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.7-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGCATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.61-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 rh.56-C 1770 AACTACTGGAACTGTCAATCACCGAGGAGCGTTACCTGGCATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.9-C 1770 AACTACAGAAAATGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.54-C 1767 AAGTACTGAAACTGTGAATCACCAAGGAGCATTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.53-C 1767 AAGTACTGAAACTGTGAATCACCAAGGAGCATTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.60-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.55-C 1767 AAGTACTGAAACTGTGAATCACCAAGGAGCATTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.2-C 1770 AACTACTGGAACTGTCAATCGCCAAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.1-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.18-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.3-C 1773 AACTACAGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.25-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGATGTACCTT
 hu.15-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.16-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.11-C 1770 AACTACAGAAAATGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.10-C 1770 AACTACAGAAAATGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.4-C 1770 AACTACTGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 rh.54-D 1776 CCAGACACAAAGTTGTCAACAAACCAAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACCTG
 rh.48-D 1776 CCAGACACAAAGTTGTCAACAAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAAACCCGGACGTGTACCTG
 rh.55-D 1776 CCAGACACAAAGTTGTCAACAAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAAACCCGGACGTGTACCTG
 rh.62-D 1776 CCAGACACAAAGTTGTCAACAAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAAACCCGGACGTGTACCTG
 AAV7-D 1776 CCAGACACAAAGTTGTCAACAAACCAAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACCTG
 rh.52-E 1779 TATTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACTTG
 rh.51-E 1779 TATTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACCTG
 hu.39-E 1779 TACTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACCTG
 rh.53-E 1779 TATTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACCTG
 hu.37-E 1779 TATTGTGGGAAATGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCCGGACGTGTACCTG

FIG. 3BV

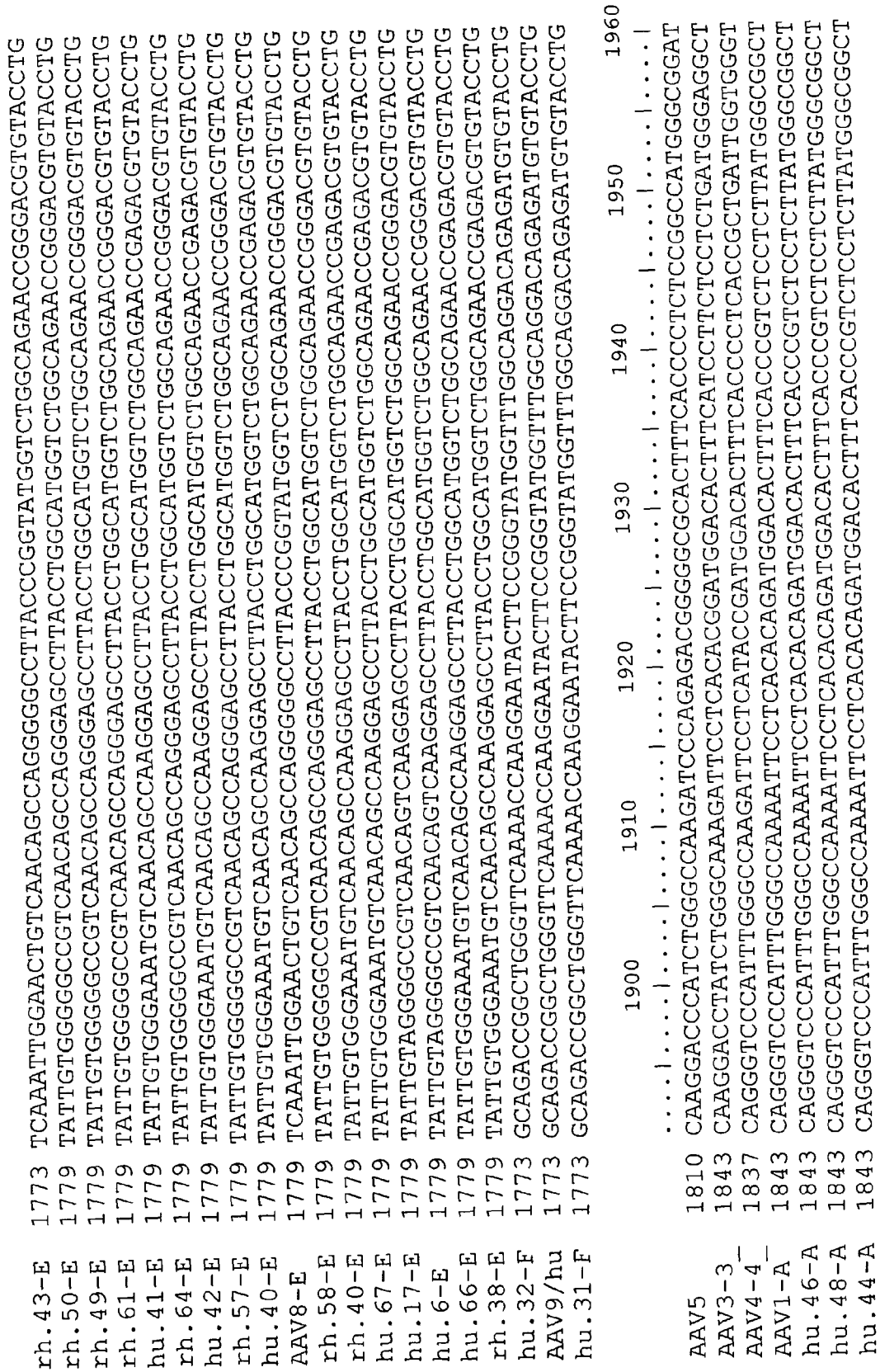


FIG. 3BW

hu.43-A 1846 CAGGGTCCCATTTGGGCCAAAATTCCTCACACAGATGGACACTTTTCAACCCGTCTCCTCTTATGGGCGGCT
 AAV6-A 1843 CAGGGTCCCTATTTGGGCCAAAATTCCTCACACGATGGACACTTTTCAACCCGTCTCCTCTCATGGGCGGCT
 hu.34-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.47-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.29-B 1840 CAGGGGCCCTATTTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.63-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.56-B 1840 CAGGGGCCCATCTGGGCAAAATTCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.45-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.57-B 1837 CAGGGGCCCATCTGGGCAAAAATTCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.35-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.58-B 1840 CAGGGGCCCTATCTGGGCAAAAGATTCCGACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.28-B 1840 CAGGGGCCCTACTTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.51-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.19-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.49-B 1840 CAGGGGCCCTATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.52-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.13-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 AAV2-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGTGGAT
 hu.20-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.24-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.64-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.27-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.21-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.22-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.23-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCCACACACGACGACGACATTTTCAACCCCTCTCCCTCATGGGCGGAT
 hu.7-C 1840 CAGGGACCCCATTTGGGCCAAAGATTCTCACACCGATGGACACTTTTCACTCTCTCCACTGATGGAGGTT
 hu.61-C 1840 CAGGGACCCCATTTGGGCCAAAGATTCTCACACCGATGGACACTTTTCACTCTCTCCACTGATGGAGGTT
 rh.56-C 1840 CAGGGACCCCATTTGGGCCAAAGATTCTCACACCGATGGACACTTTTCACTCTCTCCACTGATGGAGGTT
 hu.9-C 1840 CAGGGACCCCATTTGGGCCAAAGATTCTCACACCGATGGACACTTTTCACTCTCTCCACTGATGGAGGTT
 hu.54-C 1837 CAGGGACCCCATTTGGGCCAAAGATTCTCACGCGGATGGACACTTTTCACTCTCTCCACTGATGGAGGTT

FIG. 3BX

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rh. 57-E	1849	CAGGGTCCTATTGGGCCAAGATTCC	1970	1980	1990	2000	2010	2020	2030
hu. 40-E	1849	CAGGGTCCCATTGGGCCAAGATTCC							
AAV8-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	TCGGACTCAAACACCCACCGCCCATGATGCTCATCAAGAACAACGCGCTGTGCCCGGAAAT---						ATCACCCAG
rh. 58-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1913	TTGGACTGAAACATCCGCCCTCCTCAAATCATGATCAAAAATACTCCGGTACCGGCAAAATCCTCCGACGAC					
rh. 40-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1907	TTGGGCTGAAACACCCGCCCTCCTCAAATTTTATCAAGAACAACCCCGGTACCTGCGAATCCTGCAACGAC					
hu. 67-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1913	TTGGACTCAAGAACCCGCCCTCCTCAGATCCTCATCAAAAACACGCGCTGTTCTGCGAATCCTCCGGCGGA					
hu. 17-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1913	TTGGACTCAAGAACCCGCCCTCCTCAGATCCTCATCAAAAACACGCGCTGTTCTGCGAATCCTCCGGCGGA					
hu. 6-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1913	TTGGACTCAAGAACCCGCCCTCCTCAGATCCTCATCAAAAACACGCGCTGTTCTGCGAATCCTCCGGCGGA					
hu. 66-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1916	TTGGACTCAAGAACCCGCCCTCCTCAGATCCTCATCAAAAACACGCGCTGTTCTGCGAATCCTCCGGCGGA					
rh. 38-E	1849	CAGGGTCCCATTGGGCCAAGATTCC	1913	TTGGACTTAAAGAACCCGCCCTCCTCAGATCCTCATCAAAAACACGCGCTGTTCTGCGAATCCTCCGGCAGA					
hu. 32-F	1843	CAAGGACCCATTGGGCCAAAATTCCT	1910	TCGGACTTAAACACCCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCCAC					
AAV9/hu	1843	CAAGGACCCATTGGGCCAAAATTCCT	1910	TCGGACTTAAACACCCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACTAC					
hu. 31-F	1843	CAAGGACCCATTGGGCCAAAATTCCT	1910	TTGGACTTAAACACCCCTCCACAGATTCTCATTAAGAATAACCCCGGTACCTGCGAATCCTTCGACCCAC					

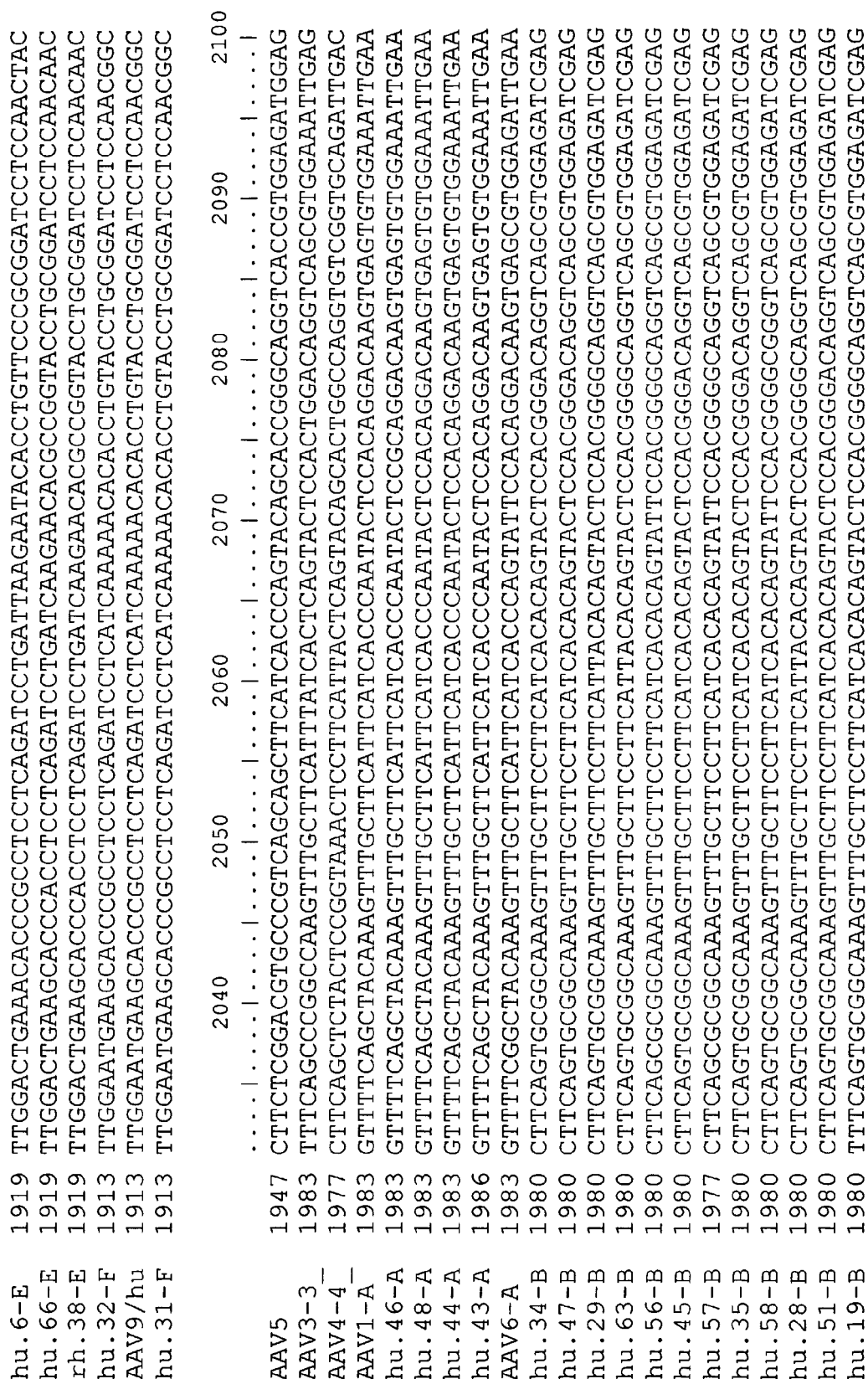
FIG. 3BZ

hu. 45-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 57-B	1907	TTGGACTTAAACACCCCTCCTCCACAGATTCTCATTAAGAATAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 35-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 58-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAAAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 28-B	1910	TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 51-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 19-B	1910	TCGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 49-B	1910	TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCAAAATCCTTCGACCAC
hu. 52-B	1910	TCGGACCTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 13-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
AAV2-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 20-B	1910	TCGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 24-B	1910	TCGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 64-B	1910	TCGGACTTAAACACCCCTCCTCCCGCAGATTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACTAC
hu. 27-B	1910	TCGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 21-B	1910	TCGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 22-B	1910	TCGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 23-B	1910	TTGGACTTAAACACCCCTCCTCCACAATTTCTCATCAAGAACAACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 7-C	1910	TTGGGCTCAAAACACCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 61-C	1910	TTGGACTCAAAACACCCACCTCCTCAAATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
rh. 56-C	1910	TTGGGCTCAAAACACCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 9-C	1910	TTGGACTCAAAACACCCGCTCCTCAAAATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 54-C	1907	TTGGACTCAAAACACCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 53-C	1907	TTGGACTCAAAACACCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 60-C	1910	TTGGACTCAAAACACCCACCTCCTCAAATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 55-C	1907	TTGGACTCAAAACACCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 2-C	1910	TTGGACTCAAAACACCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 1-C	1910	TTGGACTCAAAACACCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCCCACAAA
hu. 18-C	1910	TTGGGCTCAAAACACCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCCTACAAA
hu. 3-C	1913	TTGGACTCAAAACACCCGCTCCTCAGATCATGATCAAAAGCACTCCCGTTCAGCCAAATCCTCCCCACAAA

FIG. 3CA

hu. 25-C	1910	TTGGACTCAAAACACCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCAGCCAAATCCTCTACAAA
hu. 15-C	1910	TTGGACTCAAAACACCCACCTCCTCAGATCATGATTAAAAACACTCCCGTTCAGCCAAATCCTCTCCACAAA
hu. 16-C	1910	TTGGACTCAAAACACCCACCTCCTCAGATCATGATTAAAAACACTCCCGTTCAGCCAAATCCTCTCCACAAA
hu. 11-C	1910	TTGGACTCAAAACACCCGCTCCTCAAAATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCTCCACAAA
hu. 10-C	1910	TTGGACTCAAAACACCCGCTCCTCAAAATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCTCCACAAA
hu. 4-C	1910	TTGGACTCAAAACACCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCAGCCAAATCCTCTCCACAAA
rh. 54-D	1916	TTGGACTGAAAGCATCCGCTCCTCAGATCCTGATCAAAAACACTCCTGTTCCTGCTAATCCCCGGAGGT
rh. 48-D	1916	TTGGACTGAAAGCATCCGCTCCTCAGATCCTGATCAAAAACACTCCTGTTCCTGCTAATCCCCGGAGGT
rh. 55-D	1916	TTGGACTGAAAGCATCCGCTCCTCAGATCCTGATCAAAAACACTCCTGTTCCTGCTAATCCCCGGAGGT
rh. 62-D	1916	TTGGACTGAAAGCATCCGCTCCTCAGATCCTGATCAAAAACACTCCTGTTCCTGCTAATCCCCGGAGGT
AAV7-D	1916	TTGGACTTAAACATCCGCTCCTCAGATCCTGATCAAGAACACTCCCGTTCCTGCTAATCCTCCGGAGGT
rh. 52-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
rh. 51-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
hu. 39-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
rh. 53-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
hu. 37-E	1919	TTGGACTGAAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
rh. 43-E	1913	TTGGCTTAAACATCCTCCGCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCGACCAAC
rh. 50-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
rh. 49-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
rh. 61-E	1919	TTGGACTTAAACATCCGCTCCTCAGGTCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
hu. 41-E	1919	TTGGACTGAAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
rh. 64-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
hu. 42-E	1919	TTGGACTGAAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
rh. 57-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAACACTCCTGTTCCTGCGGATCCTCCAACAGC
hu. 40-E	1919	TTGGACTGAAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
AAV8-E	1919	TTGGCTTAAACATCCTCCGCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCGACCAAC
rh. 58-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAAGCACTCCTGTTCCTGCGGATCCTCCAACAGC
rh. 40-E	1919	TTGGACTGAAAGCACCACCTCCCAAGATCCTGATCAAGAATACGCGGTACCTGCGGATCCTCCAACGAC
hu. 67-E	1919	TTGGACTGAAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACGAC
hu. 17-E	1919	TTGGACTGAAACACCCGCTCCTCAGATCCTGATTAAAGATACACCTGTTCCTCCGCGGATCCTCCAACACTAC

FIG. 3CB



hu. 49-B 1980 CTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTATTCCACAGGGCAGGTCA GCGTGGAGATCGAG
 hu. 52-B 1980 CTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGACAGGTCA GCGTGGAGATCGAG
 hu. 13-B 1980 CTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 AAV2-B 1980 CTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGACAGGTCA GCGTGGAGATCGAG
 hu. 20-B 1980 TTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 24-B 1980 TTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 64-B 1980 CTTCAGTGC GGCAAAAGTTTGCTTCTTCATTACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 27-B 1980 TTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 21-B 1980 TTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 22-B 1980 TTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 23-B 1980 TTTCAGTGC GGCAAAAGTTTGCTTCTTCATCACACAGTACTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 7-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 61-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 rh. 56-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 9-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATTGAG
 hu. 54-C 1977 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 53-C 1977 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 60-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 55-C 1977 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 2-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 1-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 18-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 3-C 1983 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 25-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 15-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 hu. 16-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTAGAGATCGAG
 hu. 11-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATTGAG
 hu. 10-C 1980 CTACAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATTGAG
 hu. 4-C 1980 CTTCAGTTCTGCCAAAGTTTGCTTCTTCATCACACAGTATTCCACGGGGCAGGTCA GCGTGGAGATCGAG
 rh. 54-D 1986 GTTTACGCCCTGCCAAAGTTTGCTTCTTCATCACACAGTACAGCACCGGCCAGGTCA GCGTGGAGATCGAG

FIG. 3D

rh. 48-D	1986	GTTTACGCCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 55-D	1986	GTTTACGCCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 62-D	1986	GTTTACGCCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
AAV7-D	1986	GTTTACTCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
rh. 52-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 51-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
hu. 39-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCGCGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 53-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
hu. 37-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
rh. 43-E	1983	GTTCAACCAAGTCAAAGCTGAATTCCTTTTCATCACGCAATACAGCACCGGCCAGGTCAAGCTGGAAATGAA
rh. 50-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 49-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 61-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
hu. 41-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
rh. 64-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGTG
hu. 42-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
rh. 57-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
hu. 40-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
AAV8-E	1989	GTTCAACCAAGTCAAAGCTGAATTCCTTTTCATCACGCAATACAGCACCGGCCAGGTCAAGCTGGAAATGAA
rh. 58-E	1989	GTTCAACCAAGGCAAGCTGAATTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
rh. 40-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAGATCGAG
hu. 67-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
hu. 17-E	1989	GTTCAAGTCAAGCCAAAGCTGGCGTCGTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATGAA
hu. 6-E	1989	GTTCAAGTCAAGCCAAAGCTGGCGTCGTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATGAA
hu. 66-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
rh. 38-E	1989	GTTCAAGCCAGGCAAAATGGCTTCCTTTTCATCACGAGTACAGCACCGGCCAGGTCAAGCTGGAAATCGAG
hu. 32-F	1983	TTTCAATAAGGACAAGCTGAATTCCTTTTCATCACCCAGTATTTCTACTGGCCAAAGTCAAGCTGGAGATTGAG
AAV9/hu	1983	GTTCAACAAGGACAAGCTGAATTCCTTTTCATCACCCAGTATTTCTACTGGCCAAAGTCAAGCTGGAGATCGAG
hu. 31-F	1983	TTTCAATAAGGACAAGCTGAATTCCTTTTCATCACCCAGTATTTCTACTGGCCAAAGTCAAGCTGGAGATTGAG

FIG. 3CE

	2110	2120	2130	2140	2150	2160	2170
AAV5							
AAV3-3	2017	TGGGAGCTCAAGAGGAAACTCCAAAGAGGTGGAACCCAGAGATCCAGTACACAAACTACAACGACC					
AAV4-4	2053	TGGGAGCTACAGAAAGAAAACAGCAACCGTTGGAATCCAGAGATTCAGTACACTTCCAACACTACAACAAGT					
AAV1-A	2047	TGGGAGATCCAGAAAGGAGCGGTCCAAACCGCTGGAACCCGAGGTCAGTTTACCTCCAACACTACGGACAGC					
hu.46-A	2053	TGGGAGCTGCAGAAAGAAAACAGCAACCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
hu.48-A	2053	TGGGAGCTGCAGAAAGAAAACAGCAACCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
hu.44-A	2053	TGGGAGCTGCAGAAAGAAAACAGCAACCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
hu.43-A	2056	TGGGAGCTGCAGAAAGAAAACAGCAACCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
AAV6-A	2053	TGGGAGCTGCAGAAAGAAAACAGCAACCGCTGGAATCCCGAAGTGCAGTACATCTAACTATGCAAAAT					
hu.34-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.47-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.29-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.63-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.56-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.45-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.57-B	2047	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.35-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.58-B	2050	TGGGAGCTACAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.28-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.51-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.19-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.49-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.52-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.13-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
AAV2-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.20-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.24-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					
hu.64-B	2050	TGGGAGCTGCAGAAAGGAAAACAGCAACCGCTGGAATCCCGAAGTTCAGTACACTTCCAACACTACAACAAGT					

FIG. 3CF

hu.27-B 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.21-B 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.22-B 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.23-B 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.7-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.61-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.56-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.9-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.54-C 2047 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.53-C 2047 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.60-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.55-C 2047 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.2-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.1-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.18-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.3-C 2053 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.25-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.15-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.16-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.11-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.10-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.4-C 2050 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.54-D 2056 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.48-D 2056 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.55-D 2056 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.62-D 2056 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 AAV7-D 2056 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.52-E 2059 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 rh.51-E 2059 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT
 hu.39-E 2059 TGGGAGCTGCAGAAAGGAGAACAGCAAAACGGCTGGAATCCCGAAATTCAGTACACTTCCAACACTACAACAAAAT

FIG. 3CG

rh. 53-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCAGAGATT	2180	2190	2200	2210	2220	2230	2240
hu. 37-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAACCGCTGGAACCCAGAGATT							
rh. 43-E	2053	TGGGAGCTACAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC	CCCAGTTTGTGGACTTTGCCCCGGACAGCACCCGGGAATACAGAAC	2087					
rh. 50-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC	CTGTTAATGTGGACTTTACTGTAGACACTAATGGTGTATTATAGTGA	2123					
rh. 49-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC	2117	AAACTCTCTGTTGTGGCTCCCGATGCCGCTGGGAAATACACTGAG					
rh. 61-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTG					
hu. 41-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAACCGCTGGAACCCGAGATCC	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTG					
rh. 64-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 42-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAACCGCTGGAACCCGAGATCC							
rh. 57-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 40-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAACCGCTGGAACCCGAGATCC							
AAV8-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
rh. 58-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
rh. 40-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 67-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 17-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 6-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 66-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
rh. 38-E	2059	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 32-F	2053	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
AAV9/hu	2053	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							
hu. 31-F	2053	TGGGAGCTGCAGAGGAGAAACAGCAAGCGCTGGAACCCGAGATCC							

FIG. 3CH

hu. 48-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu. 44-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu. 43-A	2126	CTGCCAGCGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
AAV6-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu. 34-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 47-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 29-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 63-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGGTA
hu. 56-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGGGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 45-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 57-B	2117	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGGGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 35-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 58-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 28-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 51-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 19-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 49-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 52-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 13-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
AAV2-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 20-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCGCCAGATA
hu. 24-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 64-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 27-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 21-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 22-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 23-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 7-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 61-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
rh. 56-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTCAGAGCCTCGCCCCCATTTGGCACCCAGATA

FIG. 3CI

hu. 9-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 54-C	2117	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 53-C	2117	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 60-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 55-C	2117	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 2-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 1-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 18-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 3-C	2123	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 25-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 15-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 16-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 11-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 10-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
hu. 4-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTTGCCCCATTGGCACCCAGATA
rh. 54-D	2126	AGACTGGTGTGGACTTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA
rh. 48-D	2126	AGACTGGTGTGGACTTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA
rh. 55-D	2126	AGACTGGTGTGGACTTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA
rh. 62-D	2126	AGACTGGTGTGGACTTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA
AAV7-D	2126	AGACTGGTGTGGACTTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA
rh. 52-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
rh. 51-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
hu. 39-E	2129	CTACAAATGCGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
rh. 53-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
hu. 37-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA
rh. 43-E	2123	CTACAAAGTGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACCCCGTTA
rh. 50-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
rh. 49-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
rh. 61-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGCACTCGTTA
hu. 41-E	2129	CTACAAATGTGGACTTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCTTGCCCCATTGGTACTCGTTA

FIG. 3CJ

rh. 64-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTAGAGGTGTTTACTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
hu. 42-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 57-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTAGAGGTGTTTACTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
hu. 40-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
AAV8-E	2129	CTACAAAGTGTGGACTTTGCTGTTAATACAGAGGCGTGTACTCTGAACCCCGCCCCCATTTGGCACCCCGTTA
rh. 58-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
rh. 40-E	2129	CTACAAATGTGGACTTTGCTGTCAATTTCTGAGGTACATATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 67-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 17-E	2129	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTTTCTGAGCCTCGCCCCCATTTGGCACCCAGATA
hu. 6-E	2129	CTACAAATGTGGACTTTGCTGTCAATACTGAGGTACTTATTCTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu. 66-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 38-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 32-F	2123	CTAATAATGTTGAATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACCCAGATA
AAV9/hu	2123	CTAATAATGTTGAATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACCCAGATA
hu. 31-F	2123	CTAATAATGTTGAATTTGCTGTTAGTACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACCCAGATA
AAV5	2157	
AAV3-3	2193	CTTACCCGACCCCTT----
AAV4-4	2187	TCTCACACGAACTTG----
AAV1-A	2193	CCTCACCCACACCTGTAA-
hu. 46-A	2193	CCTTACCCGTCCTCCCTGTAA-
hu. 48-A	2193	CCTTACCCGTCCTCCCTGTAA-
hu. 44-A	2193	CCTTACCCGTCCTCCCTGTAA-
hu. 43-A	2196	CCTTACCCGTCCTCCCTGTAA-
AAV6-A	2193	CCTCACCCGTCCTCCCTGTAA-
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-

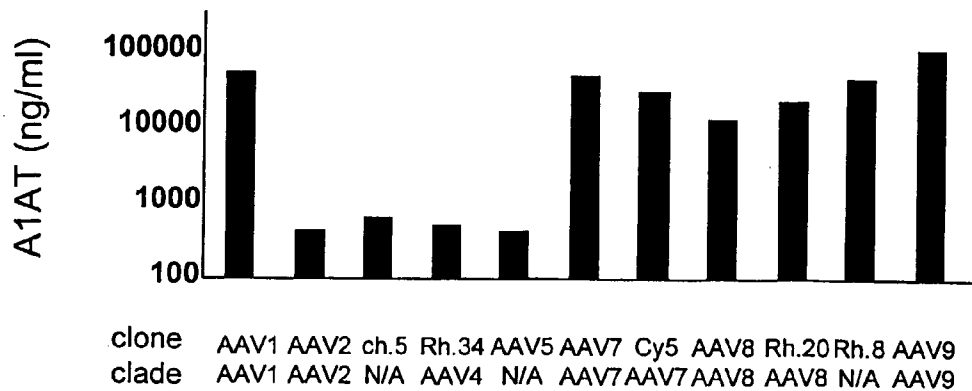
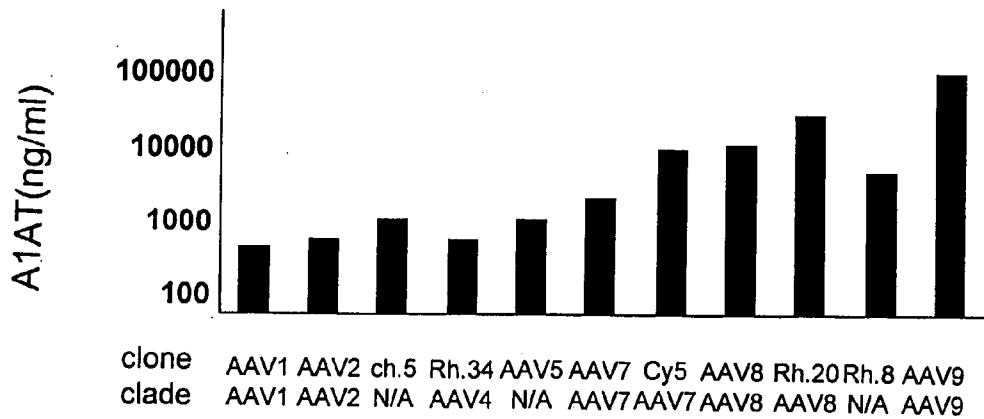
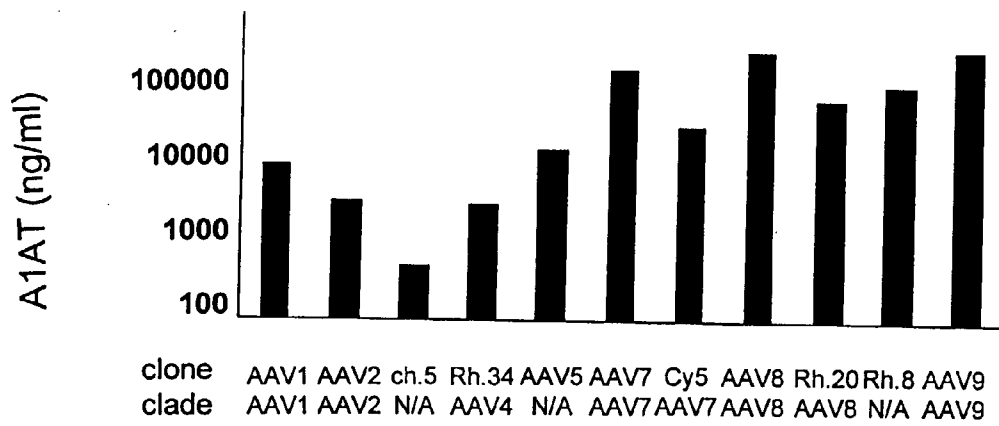
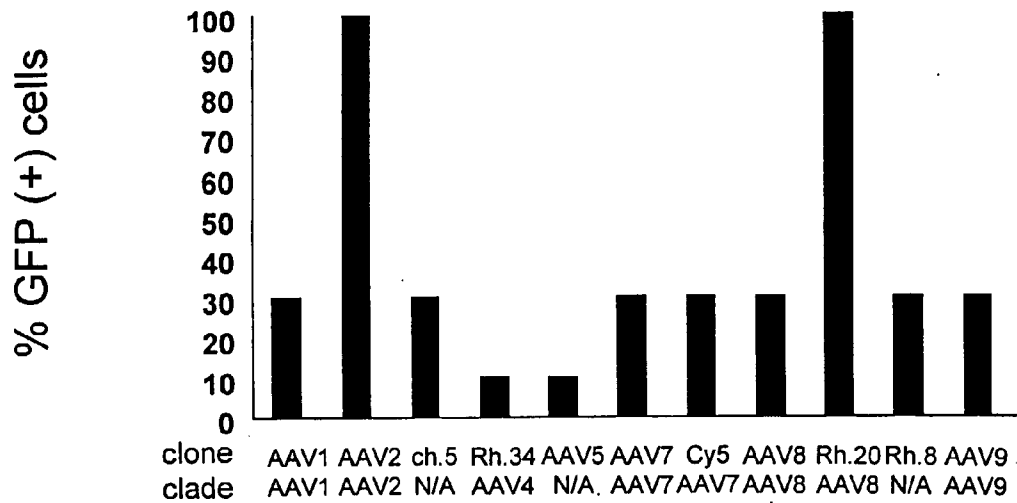
FIG. 3CL

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	CCTCACCCGTAATCTGTAA-
rh.48-D	2196	CCTCACCCGTAATCTGTAA-
rh.55-D	2196	CCTCACCCGTAATCTGTAA-
rh.62-D	2196	CCTCACCCGTAATCTGTAA-
AAV7-D	2196	CCTCACCCGTAATCTGTAA-
rh.52-E	2199	CCTCACCCGTAATCTGTAA-
rh.51-E	2199	CCTCACCCGTAATCTGTAA-
hu.39-E	2199	CCTCACCCGTAATCTGTAA-
rh.53-E	2199	CCCGACCCGTAATCTGTAA-
hu.37-E	2199	CCTCACCCGTAATCTGTAA-
rh.43-E	2193	CCTCACCCGTAATCTGTAA-
rh.50-E	2199	CCTCACCCGTAATCTGTAA-
rh.49-E	2199	CCTCACCCGTAATCTGTAA-
rh.61-E	2199	CCTCACCCGTAATCTGTAA-
hu.41-E	2199	CCTCACCCGTAATCTGTAA-
rh.64-E	2199	CCTCACCCGTAATCTGTAA-
hu.42-E	2199	CCTCACCCGTAATCTGTAA-
rh.57-E	2199	CCTCACCCGTAATCTGTAA-
hu.40-E	2199	CCTCACCCGTAATCTGTAA-
AAV8-E	2199	CCTCACCCGTAATCTGTAA-
rh.58-E	2199	CCTCACCCGTAATCTGTAA-
rh.40-E	2199	TCTGACACGTAATCTGTAA-

FIG. 3CM

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

FIG. 3CN



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Adeno-asszociált vírus (AAV) kládok, szekvenciák, az azokat tartalmazó vektorok és alkalmazásaik

Szabadalmi igénypontok

1. Adeno-asszociált vírus (AAV), mely legalább egy, a 186. számú szekvencia (AAVhu.53), vagy a 187. számú szekvencia (hu.55), vagy a 188. számú szekvencia (hu.54) 1-734. aminosavait tartalmazza, ahol az AAV továbbá AAV invertált terminális ismétlődő szakaszokkal (repeat) rendelkező minigént és egy, egy gazdasejtben kifejeződését irányító szabályozó szekvenciához működőképesen kapcsolt heterológ gént tartalmaz.
2. Az 1. igénypont szerinti AAV, ahol a kapszidot a 176. számú nukleinsav szekvencia (hu.53.) kódolja.
3. Az 1. igénypont szerinti AAV, ahol a kapszidot a 177. számú nukleinsav szekvencia (hu.54.) kódolja.
4. Az 1. igénypont szerinti AAV, ahol a kapszidot a 178. számú nukleinsav szekvencia (hu.55.) kódolja.
5. Az 1-4. igénypontok bármelyike szerinti AAV, ahol AAV invertált terminális ismétlődő szakaszok egy, a kapszid proteint biztosító AAV-re heterológ AAV-ből származnak.
6. Egy izolált adeno-asszociált vírus kapszid protein, mely:
 - a 186. számú, 187. számú vagy 188. számú szekvencia 1-734. aminosavszekvenciájával rendelkező vp1 kapszid protein;
 - a 186. számú, 187. számú vagy 188. számú szekvencia 138-734. aminosavszekvenciájával rendelkező vp2 kapszid protein; és
 - a 186. számú, 187. számú vagy 188. számú szekvencia 204-734. aminosavszekvenciájával rendelkező vp3 kapszid protein közül választott.



7. Egy nukleinsav molekula, mely egy 6. igénypont szerinti proteint kódoló nukleinsav szekvenciát tartalmaz.
8. Egy 7. igénypont szerinti nukleinsav molekula, ahol a nukleinsav szekvencia:
 - a 176. számú szekvencia 1-2206 nt szekvenciával rendelkező vp1;
 - a 176. számú szekvencia 411-2206 nt szekvenciával rendelkező vp2; és
 - a 176. számú szekvencia 609-2206 nt szekvenciával rendelkező vp3 közül választott.
9. Egy 7. vagy 8. igénypont szerinti nukleinsav molekula, ahol a nukleinsav molekula továbbá egy funkcionális AAV rep proteint kódoló AAV szekvenciát tartalmaz.
10. Egy 7-9. igénypontok bármelyike szerinti nukleinsav molekula, ahol a molekula egy plazmid.
11. Eljárás egy AAV kapszidot tartalmazó rekombináns adeno-asszociált vírus (AAV) létrehozására, melynek során egy (a) egy AAV kapszid proteint kódoló molekulát; (b) egy funkcionális rep gént; (c) egy AAV invertált terminális ismétlődő szakaszokat (ITRok) tartalmazó minigént és egy transzgént; és (d) a minigénnek az AAV kapszidba csomagolását lehetővé tevő elegendő segédfunkciókat tartalmazó gazdasejtet tenyésztünk, ahol a gazdasejt egy 7-10. igénypontok bármelyike szerinti nukleinsav molekulát tartalmaz.
12. Egy izolált gazdasejt, mely egy 1-5. igénypontok bármelyike szerinti adeno-asszociált vírust vagy egy 7-10. igénypontok bármelyike szerinti nukleinsav molekulát tartalmaz.
13. Készítmény, mely egy 1-5. igénypontok bármelyike szerinti AAV-t vagy egy 7-10. igénypontok bármelyike szerinti nukleinsav molekulát és egy fiziológiailag elfogadható hordozót tartalmaz.
14. Az 1-5. igénypontok bármelyike szerinti AAV alkalmazása egy molekulának egy sejtbe történő szállítására szolgáló gyógyszer előállításában.
15. Egy 1-5. igénypontok bármelyike szerinti AAV egy molekulának egy sejtbe történő szállításában történő alkalmazásra.