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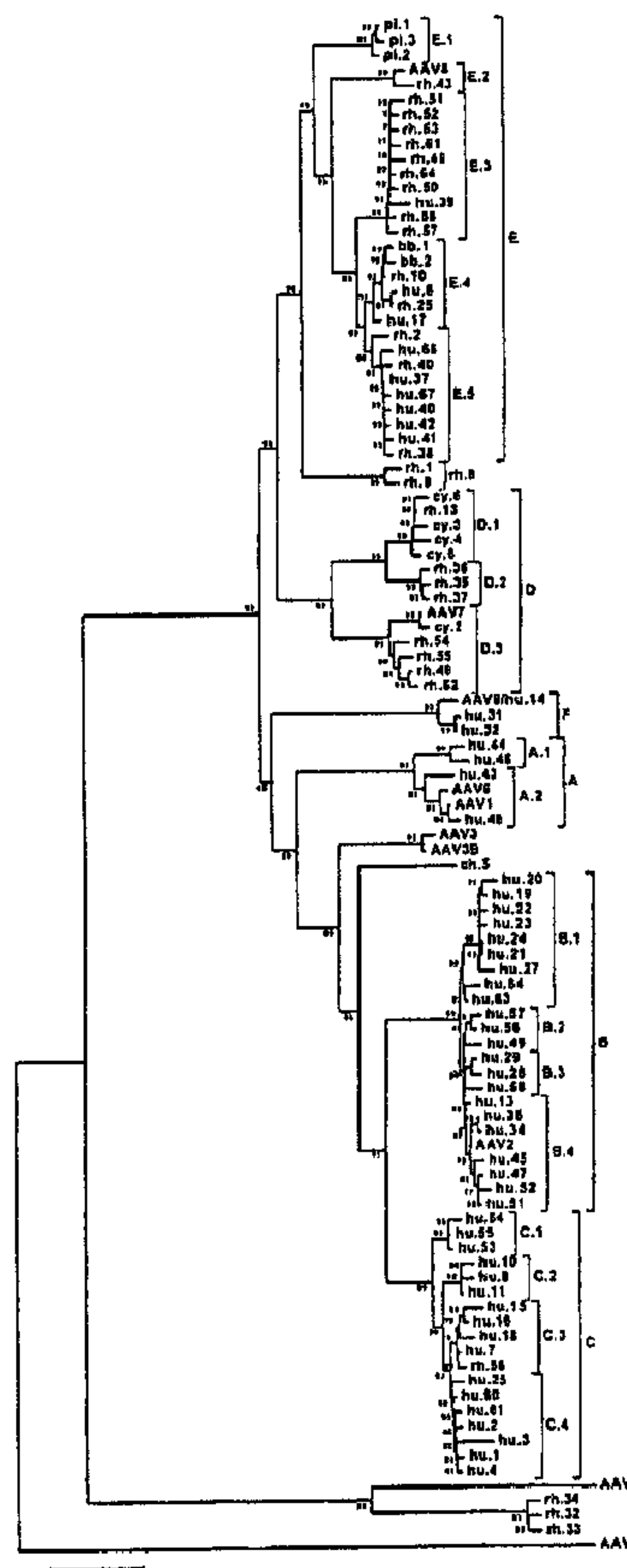
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(54) **Titre : VARIANTES DES VIRUS ASSOCIES AUX ADENOVIRUS (AAV), SEQUENCES, VECTEURS LES CONTENANT, ET LEUR UTILISATION**

(54) **Title:** ADENO-ASSOCIATED VIRUS (AAV) CLADES, SEQUENCES, VECTORS CONTAINING SAME, AND USES THEREFOR



(57) Abrégé/Abstract:

Sequences of novel adeno-associated virus capsids and vectors and host cells containing these sequences are provided. Also described are methods of using such host cells and vectors in production of rAAV particles. AAV-mediated delivery of therapeutic and immunogenic genes using the vectors of the invention is also provided.

ABSTRACT

Sequences of novel adeno-associated virus capsids and vectors and host cells containing these sequences are provided. Also described are methods of using such host cells and vectors in production of rAAV particles. AAV-mediated delivery of therapeutic and immunogenic genes using the vectors of the invention is also provided.

ADENO-ASSOCIATED VIRUS (AAV) CLADES, SEQUENCES, VECTORS CONTAINING SAME, AND USES THEREFOR

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

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BACKGROUND OF THE INVENTION

10 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
15 host chromosomes and an infectious phase in which, following either adenovirus or herpes simplex virus infection, the integrated genomes are subsequently rescued, replicated, and packaged into infectious viruses. The properties of non-pathogenicity, broad host range of infectivity, including non-dividing cells, and potential site-specific chromosomal integration make AAV an attractive tool for gene transfer.

20 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).

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

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

SUMMARY OF THE INVENTION

The present invention provides “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.

In one aspect, the invention provides an AAV clade having at least three AAV members which are phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % (based on 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. Suitably, the AAV clade is composed of AAV sequences useful in generating vectors.

The present invention further provides a human AAV serotype previously unknown, designated herein as clone 28.4/hu.14, or alternatively, AAV serotype 9. Thus, in another aspect, the invention provides an AAV of serotype 9 composed of AAV capsid which is serologically related to a capsid of the sequence of amino acids 1 to 736 of SEQ ID NO: 123 and serologically distinct from a capsid protein of any of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7 or AAV8.

Vectors constructed with capsid of this huAAV9 have exhibited gene transfer efficacies similar to AAV8 in liver, superior to AAV1 in muscle and 200 fold higher than AAV 5 in lung. Further, this novel human AAV serotype shares less than 85% sequence identity to previously described AAV1 through AAV8 and is not cross-neutralized by any of these AAVs.

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

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

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a tree showing the phylogenic 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.

5 Figs. 2A-2AE are an alignment of the amino acid sequences of AAV vp1 capsid proteins of the invention, 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-
10 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 of the invention include hu.14/AAV9 [SEQ ID NO:123]; hu.17 [SEQ ID NO: 83], hu. 6
15 [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-
20 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
25 [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];
30 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
5 Sequence Listing, which is incorporated by reference herein.

Figs. 3A- 3CN are an alignment of the nucleic acid sequences of AAV vp1 capsid
proteins of the invention, 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
10 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; rh14, rh.16, rh.17, rh.12,
rh.18, rh.21 (formerly termed 41.10); rh.25 (formerly termed 41.15; GenBank accession
AY530557); rh2; 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,
15 2003)]. The nucleic acid sequences of the invention 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
20 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
25 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:
30 178); 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 Sequence Listing, which is incorporated by reference herein.

Figs. 4A – 4D provide an evaluation of gene transfer efficiency of novel 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 95 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

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. One way in which the present invention overcomes this problem is by providing clades of AAV, which are useful for selecting phylogenetically related, or where desired for a selected regimen, phylogenetically distinct, AAV and for predicting function. The invention further provides novel AAV viruses.

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.

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.

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.

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.

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
5 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.

Alignments are performed using any of a variety of publicly or commercially
10 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
15 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
20 parameters (a word size of 6 and the NOPAM factor for the scoring matrix) as provided in GCG Version 6.1, herein incorporated by reference. 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
25 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).

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.

5 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%
10 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.

15 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. In one embodiment, the present invention provides an AAV capsid of a novel serotype, identified herein, as human AAV serotype 9.

20 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.

25

I. Clades

In one aspect, the invention provides clades of AAV. 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
30 correction distance measurement of no more than 0.05, based on alignment of the AAV vp1 amino acid sequence.

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
 5 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.

While the clades defined herein are based primarily upon naturally occurring
 10 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
 15 than 0.05, based on alignment of the AAV vp1 amino acid sequence.

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
 20 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.

25 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).

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.
 30 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.

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.

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.

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

In another aspect, the invention provides Clade A, which 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 novel 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]. The invention further provides a modified hu. 43 capsid [SEQ ID NO:236] and a modified hu. 46 capsid [SEQ ID NO:224].

In one embodiment, 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.

In another embodiment, the invention provides novel AAV of Clade A, provided that none of the novel AAV comprises 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):

In another embodiment, the invention provides a Clade B.

5 This clade is characterized by containing, at a minimum, the previously described AAV2 and novel AAV of the invention 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
10 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
15 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
20 ID NO: 167 and 191; GenBank Accession No. AY530614].

In one embodiment, 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.

25 In another embodiment, the invention provides novel AAV of Clade B, provided that none of the AAV has 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],
30 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].

10 C. Clade C (AAV2-AAV3 Hybrid Clade)

In another aspect, the invention provides Clade C, which 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 novel 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].

In one embodiment, 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.

In another embodiment, the invention provides novel AAV of Clade C (the AAV2-AAV3 hybrid clade), provided that none of the novel AAV comprises 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:
 5 174 and 185].

D. Clade D (AAV7 clade)

In another embodiment, the invention provides Clade D. This clade 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
 10 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 novel AAV sequences, including, without
 15 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].

In one embodiment, one or more of the members of this clade has a capsid
 20 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.

In another embodiment, the invention provides novel AAV of Clade D,
 provided that none of the novel AAV comprises a capsid of any of cy.2; cy.3; cy.4; cy.5;
 25 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)

30 In one aspect, the invention provides Clade E. This clade 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)].

Further, the clade novel 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],
 5 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
 10 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
 15 rh. 2 [SEQ ID NO: 231]; modified rh. 58 [SEQ ID NO: 232]; modified rh. 64 [SEQ ID NO: 233].

In one embodiment, 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
 20 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.

In another embodiment, the invention provides novel AAV of Clade E, provided that none of the novel AAV comprises a capsid of any of AAV8. rh.8:
 25 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
 30 [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)

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

In one embodiment, 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.

In another embodiment, the invention provides novel AAV of Clade F, which include, 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].

The AAV clades of the invention 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

The invention provides the nucleic acid sequences and amino acids of a novel AAV serotype, which is termed interchangeably herein as clone hu.14/28.4 and huAAV9. These sequences are useful for constructing vectors that are highly efficient in transduction of liver, muscle and lung. This novel AAV and its sequences are also useful for a variety of other purposes. These sequences are being submitted with GenBank and have been assigned the accession numbers identified herein.

The invention further provides the nucleic acid sequences and amino acid sequences of a number of novel AAV. Many of these sequence include those described above as members of a clade, as summarized below.

128.1/hu. 43 [SEQ ID Nos: 80 and 160 GenBank Accession No.
 5 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],
 10 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
 15 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
 20 [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
 25 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];
 30 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. AY530555], 30.12/pi.2 [SEQ ID NOs:30 and 95; GenBank Accession No. AY 530554], 30.19/pi.3 [SEQ ID NOs:29 and 94; GenBank Accession No. AY530555], LG-4/rh.38 [SEQ ID Nos: 7 and 86; GenBank Accession No. AY 530558]; LG-10/rh.40 [SEQ ID Nos: 14 and 92; GenBank Accession No. AY530559]; N721-8/rh.43 [SEQ ID Nos: 43 and 163; GenBank Accession No. AY530560]; 1-8/rh.49 [SEQ ID NOs: 25 and 103; GenBank Accession No. AY530561]; 2-4/rh.50 [SEQ ID Nos: 23 and 108; GenBank Accession No. AY530563]; 2-5/rh.51 [SEQ ID Nos: 22 and 104; GenBank Accession No. 530564]; 3-9/rh.52 [SEQ ID Nos: 18 and 96; GenBank Accession No. AY530565]; 3-11/rh.53 [SEQ ID Nos: 17 and 97; GenBank Accession No. AY530566]; 5-3/rh.57 [SEQ ID Nos: 26 and 105; GenBank Accession No. AY530569]; 5-22/rh.58 [SEQ ID Nos: 27 and 58; GenBank Accession No. 530570]; modified rh. 58 [SEQ ID NO: 232]; 2-3/rh.61 [SEQ ID Nos: 21 and 107; GenBank Accession No. AY530572]; 4-8/rh.64 [SEQ ID Nos: 15 and 99; GenBank Accession No. AY530574]; modified rh. 64 [SEQ ID NO: 233]; 3.1/hu.6 [SEQ ID NO: 5 and 84; GenBank Accession No. AY530621]; 33.12/hu.17 [SEQ ID NO:4 and 83; GenBank Accession No. AY530582]; 106.1/hu.37 [SEQ ID Nos: 10 and 88; GenBank Accession No. AY530600]; LG-9/hu.39 [SEQ ID Nos: 24 and 102; GenBank Accession No. AY530601]; 114.3/hu. 40 [SEQ ID Nos: 11 and 87; GenBank Accession No. AY530603]; 127.2/hu.41 [SEQ ID NO:6 and 91; GenBank Accession No. AY530604]; 127.5/hu.42 [SEQ ID Nos: 8 and 85; GenBank Accession No. AY530605]; and hu. 66 [SEQ ID NOs: 173 and 197; GenBank Accession No. AY530626]; and hu.67 [SEQ ID NOs: 174 and 198; GenBank Accession No. AY530627]; and modified rh.2 [SEQ ID NO:231]; from Clade E;

30 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.

In addition, the present invention provides 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], which are outside the definition of the clades described above.

5 Also provided are fragments of the AAV sequences of the invention. 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
10 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
15 (TRS). Still other suitable fragments will be readily apparent to those of skill in the art.

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

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.

25 Suitable fragments can be determined using the information provided herein.

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
30 vectors, as well as other viral vectors. The rAAV vectors of the invention are particularly advantageous in rAAV readministration and repeat gene therapy.

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

A. AAV Serotype 9/hu14 Sequences

The invention provides the nucleic acid sequences and amino acids of a novel AAV, which is termed interchangeable herein as clone hu.14 (formerly termed 28.4) and huAAV9. As defined herein, novel 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

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

The nucleic acid sequences of the invention 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 of the invention 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.

Further included in this invention 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.

Also included within the invention 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.

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

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 a novel AAV sequence of the invention (*e.g.*, a fragment of a vp1 capsid protein) in combination with heterologous sequences which may be obtained from another AAV serotype (known or novel), non-contiguous portions of the same AAV serotype, from a non-AAV viral source, or from a non-viral source. An artificial AAV serotype may be, without limitation, a chimeric AAV capsid, a recombinant AAV capsid, or a "humanized" AAV capsid.

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

The invention further provides proteins and fragments thereof which are encoded by the hu.14/AAV9 nucleic acids of the invention, and hu.14/AAV9 proteins and fragments which are generated by other methods. As used herein, these proteins include the assembled capsid. The invention further encompasses AAV serotypes generated using sequences of the novel AAV serotype of the invention, 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.

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.

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.

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 novel 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 novel AAV capsids of the invention.

Still other desirable fragments of the AAV9/HU.14 capsid protein include amino acids 1 to 184 of SEQ ID NO: 123, amino acids 199 to 259; amino acids 274 to 446; amino acids 603 to 659; amino acids 670 to 706; amino acids 724 to 736 of

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

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

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.

15 The invention further provides 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 novel sequences identified according to the method of the invention. This technique is also useful for isolating inverted terminal repeat (ITRs) of the novel AAV9/HU.14 serotype, based upon the novel AAV capsid and rep sequences provided herein.

25 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.

30 III. Production of rAAV with Novel AAV Capsids

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

repeating all of the novel AAV capsids provided herein, reference is made throughout this and the following sections to the hu.14/AAV9 capsid. However, it should be appreciated that the other novel AAV capsid sequences of the invention can be used in a similar manner.

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

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

 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
15 (*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
20 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.

 In one embodiment, the vectors of the invention contain, *inter alia*, sequences encoding an AAV capsid of the invention or a fragment thereof. In another embodiment,
25 the vectors of the invention contain, at a minimum, sequences encoding an AAV rep protein or a fragment thereof. 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
30 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.

Thus, in one embodiment, 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).

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.

In one aspect, the invention provides a method of generating a recombinant adeno-associated virus (AAV) having an AAV serotype 9 capsid, or a portion thereof. Such a method involves culturing a host cell which contains a nucleic acid sequence encoding an AAV serotype 9 capsid protein, or fragment thereof, as defined herein; a

functional rep gene; a minigene composed of, at a minimum, AAV inverted terminal repeats (ITRs) and a transgene; and sufficient helper functions to permit packaging of the minigene into the AAV9/HU.14 capsid protein.

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.

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.

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 novel AAV sequences of the invention. 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

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

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.

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.

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
 5 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
 10 luminometer.

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
 15 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.

20 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
 25 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
 30 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

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.

Examples of constitutive promoters include, without
 5 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
 10 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
 15 other systems have been described and can be readily selected by one of skill in the art. Examples of inducible promoters regulated by exogenously supplied compounds, include, the zinc-inducible sheep metallothioneine (MT) promoter, the dexamethasone (Dex)-inducible mouse mammary tumor virus (MMTV) promoter, the T7 polymerase promoter system [International Patent Publication No. WO 98/10088]; the ecdysone insect
 20 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
 25 (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.

In another embodiment, the native promoter for the
 30 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

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

The minigene can be carried on any suitable vector, *e.g.*, a
 5 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
 10 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
 15 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
 20 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.

Generally, when delivering the vector comprising the minigene by
 25 transfection, the vector is delivered in an amount from about 5 µg to about 100 µg DNA, about 10 µg to about 50 µg 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.

30 B. Rep and Cap Sequences

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.

10 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
15 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.

In another embodiment, the host cell stably contains the *rep*
20 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
25 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.

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
30 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.

Optionally, the *rep* and/or *cap* sequences may be supplied on a
 5 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.

Preferably, the promoter used in this construct may be any of the
 10 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.

In another preferred embodiment, the promoter for *rep* is an
 inducible promoter, such as are discussed above in connection with the transgene
 15 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.

20 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
 25 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
 30 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.

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.

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

C. The Helper Functions

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.

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.

5 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.

10 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

15 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

20 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

 The host cell itself may be selected from any biological organism, including prokaryotic (*e.g.*, bacterial) cells, and eukaryotic cells, including, insect cells,

25 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

30 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.

One host cell useful in the present invention is a host cell stably transformed with the sequences encoding *rep* and *cap*, and which is transfected with the adenovirus E1, E2a, and E4ORF6 DNA and a construct carrying the minigene as described above. Stable *rep* and/or *cap* expressing cell lines, such as B-50 (International Patent Application Publication No. WO 99/15685), or those described in US Patent No. 5,658,785, may also be similarly employed. Another desirable host cell contains the minimum adenoviral DNA which is sufficient to express E4 ORF6. Yet other cell lines can be constructed using the novel AAV9 *cap* sequences of the invention.

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.

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).

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.

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.

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

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, *e.g.*, hu.14/AAV9 [SEQ ID NO: 123] can be utilized. In another embodiment, a full-length capsid may be generated which contains one or more fragments of the novel AAV capsid of the invention fused in frame with sequences from another selected AAV, or from heterologous (*i.e.*, non-contiguous) portions of the same AAV. For example, a rAAV may contain one or more of the novel 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

In another aspect, the present invention provides a method for delivery of a transgene to a host which involves transfecting or infecting a selected host cell with a recombinant viral vector generated with the AAV9/HU.14 sequences (or functional
 5 fragments thereof) of the invention. Methods for delivery are well known to those of skill in the art and are not a limitation of the present invention.

In one desirable embodiment, the invention provides a method for AAV-mediated delivery of a transgene to a host. This method involves transfecting or infecting a selected host cell with a recombinant viral vector containing a selected transgene under
 10 the control of sequences that direct expression thereof and AAV9 capsid proteins.

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*
 15 *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.

In one aspect of this method, the delivery of vector with AAV capsid
 20 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
 25 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.

Optionally, multiple rAAV vectors can be used to deliver large transgenes
 30 or multiple transgenes by co-administration of rAAV vectors concatamerize *in vivo* to form a single vector genome. In such an embodiment, a first AAV may carry an expression cassette which expresses a single transgene (or a subunit thereof) and a second

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

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.

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.

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.

5 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
10 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
15 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.

20 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.

25 B. Therapeutic Transgenes

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
30 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

5 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

10 tyrosine hydroxylase.

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

15 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,

20 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.

Still other useful gene products include any one of the receptors for the

25 hormones, growth factors, cytokines, lymphokines, regulatory proteins and immune system proteins. The invention encompasses 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 gene products such as members of

30 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
 5 winged helix proteins.

Other useful gene products include, carbamoyl synthetase I, ornithine transcarbamylase, arginosuccinate synthetase, arginosuccinate lyase, arginase, fumarylacetate hydrolase, phenylalanine hydroxylase, alpha-1 antitrypsin, glucose-6-phosphatase, porphobilinogen deaminase, cystathione beta-synthase, branched chain
 10 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
 15 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)).

20 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
 25 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
 30 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.

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].

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.

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).

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).

Furthermore, the invention is not limited to human Factor VIII. Indeed, it is intended that the present invention encompass 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.

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.

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.

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
 5 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
 10 polypeptides which are found at higher levels in tumor cells including the polypeptide recognized by monoclonal antibody 17-1A and folate binding polypeptides.

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
 15 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
 20 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

Suitably, the AAV vectors of the invention avoid the generation of
 25 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
 30 vector can be put into degenerating tissue.

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 apthoviruses, which are
 5 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
 10 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
 15 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
 20 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
 25 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
 30 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 NI protein). The bunyavirus family includes the genera bunyavirus (California encephalitis, La Crosse), phlebovirus (Rift Valley Fever),
5 hantavirus (pneumonia is a hantavirus fever virus), nairovirus (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, Lebombo
10 (humans), equine encephalosis, blue tongue). The retrovirus family includes the sub-family oncorivirinal which encompasses such human and veterinary diseases as feline leukemia virus, HTLV I and HTLV II, lentivirinal (which includes HIV, simian immunodeficiency virus, feline immunodeficiency virus, equine infectious anemia virus, and spumavirinal). The papovavirus family includes the sub-family polyomaviruses
15 (BKU and JCU viruses) and the sub-family papillomavirus (associated with cancers or malignant progression of papilloma). The adenovirus family includes viruses (EX, AD7, ARD, O.B.) which cause respiratory disease and/or enteritis. The parvovirus family includes feline parvovirus (feline enteritis), feline panleucopeniavirus, canine parvovirus, and porcine parvovirus. The herpesvirus family includes the sub-family
20 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
25 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
30 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.

The present invention may also encompass immunogens which are useful

5 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

10 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

15 moniliformis and spirillum; Gram-positive bacilli include listeria monocytogenes; erysipelothrix rhusiopathiae; *Corynebacterium diphtheria* (diphtheria); cholera; *B. anthracis* (anthrax); donovanosis (granuloma inguinale); and bartonellosis. Diseases caused by pathogenic anaerobic bacteria include tetanus; botulism (*Clostridium botulinum* and its toxin); *Clostridium perfringens* and its epsilon toxin; other clostridia;

20 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;

25 sporotrichosis; paracoccidioidomycosis, petriellidiosis, torulopsosis, mycetoma and chromomycosis; and dermatophytosis. Rickettsial infections include Typhus fever, Rocky Mountain spotted fever, Q fever (*Coxiella burnetti*), and Rickettsialpox. Examples of mycoplasma and chlamydial infections include: mycoplasma pneumoniae; lymphogranuloma venereum; psittacosis; and perinatal chlamydial infections.

30 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.

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* (meloidosis), *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.

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
 5 encodes at least one of these polypeptides will elicit an immune response that will target T cells involved in scleroderma.

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
 10 AAV sources. In one embodiment, the rAAV and the cells are mixed *ex vivo*; the infected cells are cultured using conventional methodologies; and the transduced cells are re-infused into the patient.

These compositions are particularly well suited to gene delivery for therapeutic purposes and for immunization, including inducing protective immunity.
 15 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
 20 isolated, as desired. Suitable techniques for transfection, cell culturing, purification, and isolation are known to those of skill in the art.

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

25

EXAMPLE 1 - Computational analysis of primate AAV sequences

A. *Collection of primate tissues*

Sources of nonhuman primate tissues were described previously [N. Muzyczka, K. I. Berns, in *Fields Virology* D. M. Knipe, P. M. Howley, Eds. (Lippincott
 30 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
 5 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*

Total cellular DNAs were extracted from human and nonhuman primate
 10 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
 15 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)
 20 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.

25 C. *Analysis of AAV sequences*

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.
 30 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.

5 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
10 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
15 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
20 sequences with their parental sources were considered the criterion for recombination.

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
25 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)].

The phylogenetic analyses were repeated excluding the clones that were
30 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.

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

Table 1

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

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

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.

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.

5 **EXAMPLE 2 - Serological analysis of novel human AAVs**

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
10 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).

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
15 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
20 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
25 [(G. P. Gao *et al.*, *Proc Natl Acad Sci U S A* **99**, 11854-9 (Sep 3, 2002)).

Table 2
Serologic evaluation of novel AAV vectors

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

5 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).

10 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.

15

EXAMPLE 3 - Evaluation of primate AAVs as gene transfer vectors

20 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.

5 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*

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
10 AAVCMVEGFP vectors was measured in 84-31 cells that were seeded in a 96 well plate and infected with pseudotyped AAVCMVEGFP vectors at an MOI of 1×10^4 GC per cell. AAV vectors were pseudotyped with capsids of AAVs 1, 2, 5, 7, 8 and 6 other novel AAVs (Ch.5, Rh.34, Cy5, rh.20, Rh.8 and AAV9) using the technique described in G. Gao *et al.*, *Proc Natl Acad Sci U S A* **99**, 11854-9 (Sep 3, 2002). Relative EGFP
15 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*

For *in vivo* studies, human α -antitrypsin (A1AT) was selected as a
20 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
25 (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,
30 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).

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.

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.

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

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.

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

5

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.

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.

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
5 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
10 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
15 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.

The presence of latent AAVs widely disseminated throughout human and nonhuman primates and their apparent predisposition to recombine and to cross species
20 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
25 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)].

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

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.

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 C57Bl/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.

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.

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

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

- 5 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

- 10 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.

- 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 $\mu\text{g/ml}$) 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 Caroline (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 $\mu\text{g/ml}$ 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 $\mu\text{g/ml}$) ten weeks after injection and has sustained at 1.3-1.5 $\mu\text{g/ml}$, 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
- 15
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25
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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
5 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
10 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.
15 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.

20

EXAMPLE 7 – Novel Rh.43 Vectors of Invention

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

Novel AAVrh.43, which belongs to Clade E by phylogenetic analysis
25 vector was compared to AAV8 and novel 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
30 animals at day 28 post vector infusion for the human alpha 1 anti-trypsin (hA1AT) assay.

The data indicated that the novel 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.

Novel AAV9 and AAVrh.43 based vectors of the invention were compared to AAV1 and AAV2-based vector. The vectors were injected at a dose of
 5 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.

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

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

15 A novel rh.43-based vector of the invention 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.

20 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 lease 100 fold more efficient than AAV5 in the mouse model.

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

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
 30 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).

- 5 Serum AIT 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 .

What is claimed is:

1. A recombinant adeno-associated virus (AAV) comprising an AAV hu.37 capsid which comprises a vp2 protein having the sequence of amino acids 138 to 738 of SEQ ID NO: 88, the AAV further comprising 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. A recombinant AAV comprising an AAV hu.37 capsid which comprises a vp1 protein having the sequence of amino acids 1 to 738 of SEQ ID NO: 88, the AAV further comprising a minigene having AAV inverted terminal repeats and a heterologous gene operably linked to regulatory sequences which direct its expression in a host cell.
3. The recombinant AAV according to claim 1 or 2, wherein the AAV hu.37 capsid has a vp1 protein having an amino acid sequence comprising amino acids 1 to 738 of SEQ ID NO: 88.
4. The recombinant AAV according to claim 3, wherein said capsid is encoded by the nucleic acid sequence of SEQ ID NO: 10.
5. The recombinant AAV according to any one of claims 2 to 4 wherein the inverted terminal repeats are from an AAV heterologous to the AAVhu.37 providing the capsid protein.
6. An isolated capsid protein comprising a hu.37 adeno-associated virus (AAVhu.37) capsid protein selected from the group consisting of:
 - vp1 capsid protein, amino acids (aa) 1 to 738, SEQ ID NO:88; and
 - vp2 capsid protein, aa 138 to 738, SEQ ID NO: 88.

7. A method of generating a recombinant adeno-associated virus (AAV) comprising an AAV capsid comprising the steps of culturing a host cell containing: (a) a molecule encoding an AAV capsid protein; (b) a functional rep gene; (c) a minigene comprising AAV inverted terminal repeats (ITRs) and a transgene; and (d) sufficient helper functions to permit packaging of the minigene into the AAV capsid protein, wherein said host cell comprises a nucleic acid molecule selected from the group consisting of:

vp1, nt 1 to 2217 of SEQ ID NO: 10; and
vp2, nt 411 to 2217 of SEQ ID NO: 10.

8. The method according to claim 7, wherein said molecule comprises an AAV sequence encoding an AAV capsid protein and a functional AAV rep protein.

9. The method according to claim 7 or claim 8, wherein said molecule is a plasmid.

10. A composition comprising the recombinant AAV according to any of claims 1 to 5 and a pharmaceutical carrier.

11. The recombinant AAV according to any of claims 1 to 5 for delivering a molecule to a cell.

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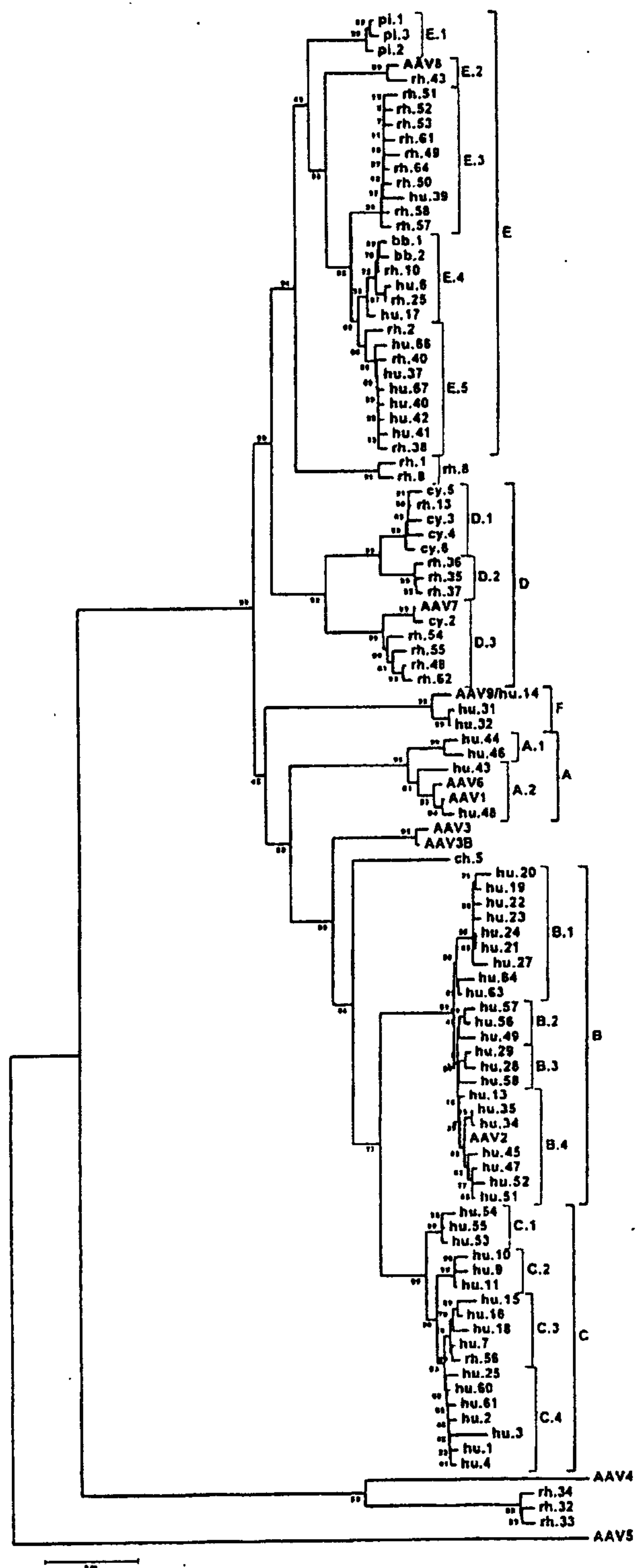


FIG. 1

[illegible]

FIG. 2A

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hu. 27-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 21-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 22-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 23-B	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 7-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 61-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
rh. 56-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 9-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHQDNSRGLVLPGYKYLGPSNGLDKGEPVNEADA
hu. 54-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 53-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 60-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 55-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 2-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 1-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 18-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 3-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 25-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDGSRLVLPGYKYLGPENGLDKGEPVNEADA
hu. 15-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLYKGEVPDEADA
hu. 16-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLYKGEVPNEADA
hu. 11-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKLAERHQDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 10-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 4-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
rh. 54-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 48-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 55-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 62-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
AAV7-D	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 52-E	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 51-E	1	MVADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
hu. 39-E	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA

FIG. 2B

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rh. 53-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA	80	90	100	110	120	130	140
hu. 37-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 43-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 50-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 49-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 61-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 41-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 64-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 42-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 57-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 40-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
AAV8-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 58-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 40-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 67-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLLGYKYLGPFNGLDKGEPVNAADA							
hu. 17-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGCKYLGPFNGLDKGEPVNAADA							
hu. 6-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 66-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
rh. 38-E	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 32-F	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
AAV9/hu	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
hu. 31-F	1	MAADGYLPDWLEDNLSEGI	REWWDLKPGAPKPKANQQKQDD	GRGLVLPGYKYLGPFNGLDKGEPVNAADA							
AAV5	70	VAREHDISYNEQLEAGDNP	YLKYNHADAEEQEK	LADDTSF	GGNLGKAVFQAKKRVLE	PG-LVEEGAKTA					
AAV3-3	71	AALEHDKAYDQQLKAGDNP	YLKYNHADAEEQERLQ	EDTSF	GGNLGRAVFQAKKRILE	PLG-LVEEAAKTA					
AAV4-4	70	AALEHDKAYDQQLKAGDNP	YLKYNHADAEEQERLQ	EDTSF	GGNLGRAVFQAKKRVLE	PLG-LVEQAGETA					
AAV1-A	71	AALEHDKAYDQQLKAGDNP	YLKYNHADAEEQERLQ	EDTSF	GGNLGRAVFQAKKRVLE	PLG-LVEEGAKTA					
hu. 46-A	71	AALEHDKAYDRQLDSDNP	YLKYNHADAEEQERL	KEDTSF	GGNLGRAVFQAKKRVLE	PLG-LVEEGAKTA					

FIG. 2C

hu. 48-A	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	AEFQERLQEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEGAKTA
hu. 44-A	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEGAETA
hu. 43-A	71	AALEHDKAYDQQLKAGDNPYPRYNHADA	AEFQERLQEDTFFGGNLGRAVFQAKKR	VLEPLG-LVEEAAKTA
AAV6-A	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	AEFQERLQEDTSFGGNLGRAVFQAKKR	VLEPFG-LVEEGAKTA
hu. 34-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 47-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVGEPPVKA
hu. 29-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 63-B	71	AALEHDKAYDRQLDSGDNPYPKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 56-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 45-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 57-B	70	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 35-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 58-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 28-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLS-LVEEPPVKA
hu. 51-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVGEPPVKA
hu. 19-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 49-B	71	AALEYDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 52-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVGEPPVKA
hu. 13-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
AAV2-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 20-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 24-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 64-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 27-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 21-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 22-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 23-B	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
hu. 7-C	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEGPPVKA
hu. 61-C	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA
rh. 56-C	71	AALEHDKAYDRQLDSGDNPYLKYNHADA	AEFQERLKEDTSFGGNLGRAVFQAKKR	VLEPLG-LVEEPPVKA

hu. 9-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 54-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 53-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 60-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 55-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 2-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 1-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 18-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 3-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 25-C 71 AALEHDKAYDRQLNSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 15-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 16-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 11-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 10-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 4-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
rh. 54-D 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 48-D 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 55-D 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 62-D 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LAEAAKTA
AAV7-D 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 52-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 51-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 39-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 53-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 37-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 43-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 50-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 49-E 71 AALEHDKAYDQQLKAGDNPHLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 61-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 41-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-PVEEAAKTA

FIG. 2E

rh. 64-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 42-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 57-E	71	AALEHDKAYDQQLQAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 40-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
AAV8-E	71	AALEHDKAYDQQLQAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 58-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 40-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 67-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 17-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 6-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 66-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 38-E	71	AALEHDKAYDQQLKAGDNPYLRYNHADA	EFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 32-F	71	AALEHDKAYDQQLKAGDNPYLKYNHADA	EFQERLKEDTSFGGNLGRAVFQAKKRLLEPLG-LVEEAAKTA
AAV9/hu	71	AALEHDKAYDQQLKAGDNPYLKYNHADA	EFQERLKEDTSFGGNLGRAVFQAKKRLLEPLG-LVEEAAKTA
hu. 31-F	71	AALEHDKAYDQQLKAGDNPYLKYNHADA	EFQERLKEDTSFGGNLGRAVFQAKKRLLEPLG-LVEEAAKTA

	150	160	170	180	190	200	210
AAV5							
AAV3-3	139	PTGKRIDDHF	-----KRKKARTEEDSKPSTSSDAEAGPSGSQLQIPAQPASSLGADTMSAGG				
AAV4-4	140	PGKKGAVDQSPQ-EPDSSSGVGKSGKQPAKRLNFGQ	TGDSVPD-PQPLGEPAAAPTSLGSNTMASGG				
AAV1-A	139	PGKKRPLIESPQ-QPDSSGTGIGKKKGKQPAKKKLVFEDET	GAGDGP---PEGSTSGAMS--DDSEMRAAA				
hu. 46-A	140	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQ	TGDSVPD-PQPLGEPATPAAVGPTTMSAGG				
hu. 48-A	140	PGKKRPVEQSPQ-EPDSPSGIGKTGQQPAKKRLNFGQ	TGDSVPD-PQPLGEPATPAAVGPTTMSAGG				
hu. 44-A	140	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQ	TGDSVPD-PQPLGEPATPAAVGPTTMSAGG				
hu. 43-A	140	PGKKRPVEPSPQ-RSPDSSGTGIGKKGQQPAKKRLNFGQ	TGDSVPD-PQPIGEPAGPSGLSGTMAAGG				
AAV6-A	140	PGKKRPVEQSPQ-EPDSSSGIGKTGQQPAKKRLNFGQ	TGDSVPD-PQPLGEPATPAAVGPTTMSAGG				
hu. 34-B	140	PGKKRPVEHSPV-EPDSSSGTGKAGQQPAKRLNFGQ	TGADSVDP-PQPLGQPPAAPSGLGTNTMATGS				
hu. 47-B	140	PGKKRPVEHSPV-EPDSSSGTGKAGQQPAKRLNFGQ	TGADSVDP-PQPLGQPPAAPSGLGTNTMATGS				
hu. 29-B	140	PGKKRPVEHSPA-EPDSSSGTGKSGNQPAKRLNFGQ	TGSDSVDP-PQPLGQPPAAPSGLGTNTMATGS				

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

FIG. 2G

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hu.18-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMASGS
hu.3-C 141 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
hu.25-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
hu.15-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
hu.16-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
hu.11-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTSLGSTTMATGS
hu.10-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSTSLGSTTMATGS
hu.4-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTGDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
rh.54-D 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPAGPSGLSGTMAAGG
rh.48-D 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG
rh.55-D 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.62-D 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG
AAV7-D 140 PAKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPAPSSVSGSTVAAGG
rh.52-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.51-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.39-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGRTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.53-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.37-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG
rh.43-E 140 PGKKRPVEQSPQ-EPDSSSGTGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPAPSGVGPNTMAAGG
rh.50-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPAGKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.49-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPAPSSVSGSTMAAGG
rh.61-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.41-E 140 PGKKRPVEPPQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG
rh.64-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.42-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG
rh.57-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.40-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG
AAV8-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPLGEPAPAPSGVGPNTMAAGG
rh.58-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.40-E 140 PGKKRPVEPSQSPDSSSTGIGKKGQQPARKRLNFGQTGDSESVDP-PQPIGEPAPAGPSGLSGTMAAGG

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hu. 67-E 140 PGKKRPVEPSPQSPDSSTGIGKKGQQPAKKRLNFGQTGDSESPD-PQPIGEPAGPSGLSGGTMAAGG
hu. 17-E 140 PGKKRPVEPSPQSPDSSTGIGKTGQQPAKKRLNFGQTGDSESPD-PQPIGEPAGPSGLSGGTMAAGG
hu. 6-E 140 PGKKRPVEPSPQSPDSSTGIGKTGQQPAKKRLNFGQTGDSESPD-PQPIGEPAGPSGLSGGTMAAGG
hu. 66-E 140 PGKKRPVEPSPQSPDSSAGIGKKGQQPAKKRLNFGQTGDSESPD-PQPIGEPAGPSGLSGGTMAAGG
rh. 38-E 140 PGKKRPVEPSPQSPDSSTGIGKKGQORPAKKRLNFGQTGDSESPD-PQPIGEPAGPSGLSGGTMAAGG
hu. 32-F 140 PGKKRPVEQSPQ-EPDSSAGIGKSGSQPAKKKLNFGQTGDTESPD-PQPIGEPAPAGVGSGLTMAAGG
AAV9/hu 140 PGKKRPVEQSPQ-EPDSSAGIGKSGAQPAKKRLNFGQTGDTESPD-PQPIGEPAPAGVGSGLTMAAGG
hu. 31-F 140 PGKKRPVEQSPQ-EPDSSAGIGKSGSQPAKKKLNFGQTGDTESPD-PQPIGEPAPAGVGSGLTMAAGG

AAV5 198 GGPLGDNNGADGVGNASGDWHCDSTWMGDRVVTCKSTRTWLPSYNNHQYREIKS-GSVDGSNANAYFGY
AAV3-3 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGD RVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
AAV4-4 202 GGAAVEGGQADGVGNASGDWHCDSTWSEGHVTTTSTRTWLPTYNNHLYKRLG----ESLQSNYNGF
AAV1-A 208 GAPMADNNEGADGVGNASGNWHCDSTWLGD RVI TTSTRTWALPTYNNHLYKQISS-ASTGASNDNHYFGY
hu. 46-A 208 GAPMADNNEGADGVGNASGNWHCDSTWLGD RVI TTSTRTWALPTYNNHLYKQISS-ASTGASNDNHYFGY
hu. 48-A 208 GAPMADNNEGADGVGNASGNWHCDSTWLGD RVI TTSTRTWALPTYNNHLYKQISS-TSTGASNDNHYFGY
hu. 44-A 208 GAPMADNNEGADGVGNASGNWHCDSTWLGD RVI TTSTRTWALPTYNNHLYKQISS-ASTGASNDNHYFGY
hu. 43-A 209 GAPMADNNEGADGVGNASGNWHCDSTWLGD RVI TTSTRTWALPTYNNHLYKQISS-ASTGASNDNHYFGY
AAV6-A 208 GAPMADNNEGADGVGNASGNWHCDSTWLGD RVI TTSTRTWALPTYNNHLYKQISS-ASTGASNDNHYFGY
hu. 34-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 47-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDSHYFGY
hu. 29-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 63-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 56-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 45-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 57-B 207 GAPMADNNEGADGVGNSSGDWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 35-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 58-B 208 GAPMADNNDGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 28-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVI TTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY

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hu. 51-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 19-B 208 GAPMADNNEGADGVGNSSGNWYCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 49-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 52-B 208 GAPMADNNEGADGVGNSSGNRHCDSTWMGDRVITTTSTRTWALPTYNNHLYRQIS--SQSGASNDNHYFGY
hu. 13-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
AAV2-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 20-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 24-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 64-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYRQIS--SQSGASNDNHYFGY
hu. 27-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 21-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 22-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 23-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITTTSTRTWALPTCENNHLKQIS--SQSGASNDNHYFGY
hu. 7-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 61-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
rh. 56-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWAQPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 9-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGC
hu. 54-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 53-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 60-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 55-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 2-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 1-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 18-C 208 GAPVADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 3-C 209 GAPMADNNEGADGVGNSSGNWHCDSQWLDLDRVIATSTRTWALPTYNNHLYKQIS--SQSGACNDNHYFGY
hu. 25-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 15-C 208 GAPVADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 16-C 208 GAPVADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 11-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 10-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY

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hu.4-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQISS--SQSGASNDNHYFGY
 rh.54-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
 rh.48-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
 rh.55-D 209 GAPMADNNEGADGVGSSSGNWHCDSTRLGDRVITTTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
 rh.62-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISS-QSAGSTNDNVYFGY
 AAV7-D 209 GAPMADNNEGADGVGNASGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISS-ETAGSTNDNTYFGY
 rh.52-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.51-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.39-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.53-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.37-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.43-E 208 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGATNDNTYFGY
 rh.50-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.49-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.61-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.41-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.64-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.42-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.57-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.40-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 AAV8-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGATNDNTYFGY
 rh.58-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.40-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.67-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.17-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.6-E 209 GAPMADNNEGADGVGSSSGNWHCDSAWLGDRVITTTSTRPWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.66-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 rh.38-E 209 GAPMADNNEGADGVGSSSGNWHCDSTWLGDRVITTTSTRTWALPTYNNHLYKQISNGTSGGSTNDNTYFGY
 hu.32-F 208 GAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGY
 AAV9/hu 208 GAPVADNNEGADGVGSSSGNWHCDSQWLGDRVITTTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGY

FIG. 2K

hu.31-F 208 GAPVADNNEGADGVGSSSGNWHCDSQLGDRVITTTSTRTWALPTYNNHLYKQISNSTSGSSNDNAYFGY
AAV5 267 STPWGYFDENRFSHWSPRDWQRLINNNWGERPRSLRVKIFNIQVKEVTQDSTTTIANNNLTSTVQVFTD
AAV3-3 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKKLSFKLFNIQVRGVTQNDGTTIANNNLTSTVQVFTD
AAV4-4 267 STPWGYFDENRFHCHFSPRDWQRLINNNWGMRPKAMRVKIFNIQVKEVTTSNGETTVANNLTSTVQIFAD
AAV1-A 277 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTTNDGVTTIANNLTSTVQVFS
hu.46-A 277 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTTNDGVTTIANNLTSTVQVFS
hu.48-A 277 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTTNDGVTTIANNLTSTVQVFS
hu.44-A 277 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVEEVTTNDGVTTIANNLTSTVQVFS
hu.43-A 277 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTTNDGVTTIANNLTSTVQVFS
AAV6-A 277 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTTNDGVTTIANNLTSTVQVFS
hu.34-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.47-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.29-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.63-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.56-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.45-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.57-B 275 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.35-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.58-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVREVTQNDGTTIANNNLTSTVQVFTD
hu.28-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.51-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.19-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLSEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.49-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.52-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.13-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
AAV2-B 276 STPWGYFDENRFHCHFSPRDWQRLINNNWGERPKRLNEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD
hu.20-B 276 STPWGHFDENRFHCHFSPRDWQRLINNNWGERPKRLSEKLFNIQVKEVTQNDGTTIANNNLTSTVQVFTD

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hu. 24-B	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 64-B	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 27-B	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 21-B	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 22-B	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 23-B	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 7-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 61-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
rh. 56-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 9-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 54-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 53-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 60-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 55-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 2-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 1-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 18-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 3-C	277	STPWGYFDFENRFHCHFS	PRDWQRLINNSWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 25-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 15-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 16-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 11-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 10-C	276	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
hu. 4-C	276	STPWGYFDFENRFHCHFS	PRDWQRLVNNNRGERPKRLSEKLENI	QVKEVTQNDGTTTIANNLSTVQVFTD
rh. 54-D	278	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTNDGVTTIANNLSTVQVFS
rh. 48-D	278	STPWGYFDFENRFHCHFS	PRDWQRLINNSWGERPKRLSEKLENI	QVKEVTNDGVTTIANNLSTVQVFS
rh. 55-D	278	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTNDGVTTIANNLSTVQVFS
rh. 62-D	278	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTNDGVTTIANNLSTVQVFS
AAV7-D	278	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTNDGVTTIANNLSTVQVFS
rh. 52-E	279	STPWGYFDFENRFHCHFS	PRDWQRLINNNWGERPKRLSEKLENI	QVKEVTQNEGTKTIANSLSTVQVFTD

FIG. 2M

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rh. 51-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 39-E 279 STPWGYLDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 53-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 37-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 43-E 278 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 50-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 49-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 61-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 41-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 64-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTVANNLTSTIQVFTD
hu. 42-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 57-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 40-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
AAV8-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 58-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
rh. 40-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQDEGTKTIANNLTSTIQVFTD
hu. 67-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 17-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 6-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 66-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTEETIANNLTSTIQVFTD
rh. 38-E 279 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQNEGTKTIANNLTSTIQVFTD
hu. 32-F 278 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQDNNGVKTIANNLTSTVQVFTD
AAV9/hu 278 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQDNNGVKTIANNLTSTVQVFTD
hu. 31-F 278 STPWGYFDFNRFHCHFSPRDWQRLINNNWGFPRKRLSEFKLFNIQVKEVTQDNNGVKTIANNLTSTVQVFTD

AAV5 337 DDYQLPYVVGNGTEGCLPAFPQVFTLPQYGYATLNRD-NTENPTERSSEFFCLEYFPSKMLRTGNFFEFT
AAV3-3 346 SEYQLPYVLGSAHQCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFCLEYFPSQMLRTGNNFQFS
AAV4-4 337 SSYELPYVMDAQEGSLPPFPNDVFMVPQYGYCGLVTGNTSQQTDRNAFYCLEYFPSQMLRTGNFFEIT

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AAV1-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.46-A 347 SEYQLPYVLGSAHQGRLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.48-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.44-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.43-A 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
AAV6-A 347 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.34-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNE---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.47-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.29-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLGYFSPQMLRTGNNFTFS
hu.63-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.56-B 346 LEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.45-B 346 SGYQLPYVLGSAHQGCLPPFPADVFMVPQYGYPTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.57-B 345 LEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.35-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.58-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.28-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.51-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.19-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.49-B 346 SEYQLPYVPGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.52-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCPYFSPQMLRTGNNFTFS
hu.13-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
AAV2-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.20-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.24-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.64-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.27-B 346 SGYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.21-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.22-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.23-B 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS
hu.7-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFSPQMLRTGNNFTFS

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hu. 61-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
rh. 56-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 9-C 346 SEYPLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFTFS
hu. 54-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 53-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 60-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 55-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 2-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 1-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 18-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 3-C 347 SEYQLPYVPGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 25-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSPFYCYCLEYFPSQMLRTGNNFQFS
hu. 15-C 346 SGYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 16-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
hu. 11-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFTFS
hu. 10-C 346 SEYQLPYVLGSAHQGCLPPFPADVFTVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNLTFS
hu. 4-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFS
rh. 54-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYCLEYFPSQVLRGTGNNFTFS
rh. 48-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYCLEYFPSQMLRTGNNFTFS
rh. 55-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYCLEYFPSQMLRTGNNFTFS
rh. 62-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNND---SQSVGRSSFYCYCLEYFPSQMLRTGNNFTFS
AAV7-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCYCLEYFPSQMLRTGNNFEFS
rh. 52-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTPNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFSFS
rh. 51-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFSFS
hu. 39-E 349 SEYQPPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFSFS
rh. 53-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFSFS
hu. 37-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFEFS
rh. 43-E 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFQFT
rh. 50-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFSFS
rh. 49-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGNLTLNNG---SQAVGRSSFYCYCLEYFPSQMLRTGNNFSFS

FHG. 2P

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rh. 61-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSES
hu. 41-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
rh. 64-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSES
hu. 42-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
rh. 57-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSES
hu. 40-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNSEFS
AAV8-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFT
rh. 58-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSES
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

		430	440	450	460	470	480	490
AAV5	406	YNFEEVPEHSSFAPSQNLEKLANPLVDQYLYRFVSTN----	NTGGVQFNKNLAGRYANTYKNWFPGP					
AAV3-3	413	YTFEDVPEHSSYAHSQSLDRIMNPLIDQYLYYLNRTQGTTS	GTTNQSRLLFSQAGPQMSLQARNWLPGP					
AAV4-4	407	YSFEKVPFHSMYAHSQSLDRIMNPLIDQYLYWGLQSTTTG	TTLNAGTATTNFTKLRPTNFSNFKKNWLPGP					
AAV1-A	414	YTFEEVPEHSSYAHSQSLDRIMNPLIDQYLYYLNRTQ-NQ	SGSAQNKDLLFSRGSPAGMSVQPKNWLPGP					
hu. 46-A	414	YTFEEVPLHSSCAHSQSLDRIMNPLIDQYLYYLNRTQ-NQ	SGSAQNKDLLFSRGSPAGMSVQPKNWLPGP					
hu. 48-A	414	YTFEEVPEHSSYAHSQSLDRIMNPLIDQYLYYLNRTQ-NQ	SGSAQNKDLLFSRGSPAGMSVQPKNWLPGP					
hu. 44-A	414	YTFEEVPEHSSYAHSQSLDRIMNPLIDQYLYYPNRTQ-NQ	SGSAQNKDLLFSRGSPAGMSVQPKNWLPGP					
hu. 43-A	415	YTFEEVPLHSSYAHSQSLDRIMNPLIVQYLYYLNRTQ-NQ	SGSAQNKDLLFSRGSPAGMSVQPKNWLPGP					
AAV6-A	414	YTFEDVPEHSSYAHSQSLDRIMNPLIDQYLYYLNRTQ-NQ	SGSAQNKDLLFSRGSPAGMSVQPKNWLPGP					
hu. 34-B	413	YTFEDVPEHSSYAHSQSLGRIMNPLIDQYLYLSRTN-TP	SGTTQSRLLQFSQAGASDIRDQSRNWLPGP					

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hu. 47-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 29-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 63-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 56-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 45-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 57-B 412 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 35-B 413 YTFEDVPFHSSYAHSQSLGRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 58-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 28-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 51-B 413 YTFEDVPFHSGYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 19-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 49-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 52-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 13-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
AAV2-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 20-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 24-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 64-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLVDQYLYLSRTN-TPSGTTTQSRQLQFSQAGASDIRDQSRNWLPGP
hu. 27-B 413 YTFEDVPFHSSYAHGQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTMSRLQFSQAGASDVDRDQSRNWLPGP
hu. 21-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 22-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 23-B 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTN-TPSGTTTMSRLQFSQAGASDIRDQSRNWLPGP
hu. 7-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-SNSGTLQQSRLQFSQAGPTSMSLQAKNWLPGP
hu. 61-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-TNSGTLQQSRLQFSQAGPTSMSLQAKNWLPGP
rh. 56-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-SNSGALQQSRLQFSQAGPTSMSLQAKNWLPGP
hu. 9-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLNRTQ-SNSGTLQQSRLQFSQAGPTSMSLQAKNWLPGP
hu. 54-C 413 YTFEDVPFHSSYAHSQGLDRMLMNPLIDQYLYLNRTQ-TASGT-QQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 53-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLNRTQ-TASGT-QQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 60-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLVDQYLYLNKTQ-TNSGTLQQSRLQFSQAGPTSMSLQAKNWLPGP
hu. 55-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLNRTQ-TASGT-QQSRLLQFSQAGPTSMSLQAKNWLPGP

FIG. 2R

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

rh. 58-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTAGTQQLLFSQAGPSNMSAQARNWLPGP
rh. 40-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTQGTQQLLFSQAGPANMSARAKNWLPGP
hu. 67-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTQGTQQLLFSQAGPANMSAQAKNWLPGP
hu. 17-E	416	YQFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKNWLPGP
hu. 6-E	416	YQFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKNWLPGP
hu. 66-E	416	YTFEDVPFHSSCAHSQSSDRMLMNP	LIDQYLYLSRTRS-TGGTQGTQQLLFSQAGPANMSAQAKNWLPGP
rh. 38-E	416	YTFEDVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSRTQS-TGGTQGTQQLLFSQAGPANMSAQAKNWLPGP
hu. 32-F	415	YEFENVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSKTINGSG--QNQQTLKFSVAGPSNMAVQGRNYIPGP
AAV9/hu	415	YEFENVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSKTINGSG--QNQQTLKFSVAGPSNMAVQGRNYIPGP
hu. 31-F	415	YEFENVPFHSSYAHSQSLDRMLMNP	LIDQYLYLSKTINGSG--QNQQTLKFSVAGPSNMAVQGRNYIPGP

AAV5	469	MGR	TQGWNLGSGVN-----RASVS	AFA	TNRMELEGASYQVPPQPN	GMTNNLQGSNTYALENTMIFNSQP
AAV3-3	483	CYRQQR	LSKTANDN-----NNSNFP	WTAASKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPMHGNLI FGKEG
AAV4-4	477	SIKQ	QGFSTANQYKIPATGSD	SLIKYETHSTLDGRWSALT	TPGPPMATAGPADSKFS-NSQLIFAGPKQ	
AAV1-A	483	CYRQQR	VSCTKTDN-----NNSNFT	WTGASKYNLNGRESI	INPGTAMASHKDDDEKFFPMSGVMI FGKES	
hu. 46-A	483	CYRQQR	VSCTKTDN-----NNSNFT	WTGASKYNLNGRESI	INPGTAMASHKDDDEKFFPMSGVMI FGKES	
hu. 48-A	483	CYRQQR	VSCTKTDN-----NNSNFT	WTGASKYNLNGRESI	INPGTAVASHKDDDEKFFPMSGVMI FGKES	
hu. 44-A	483	CYRQQR	VSCTKTDN-----NNSNFT	WTGASKYNLNGRESI	INPGTAMASHKDDDEKFFPMSGVMI FGKES	
hu. 43-A	484	CYRQQR	VSCTKTDN-----NNSNFT	WTGASKYNLNGRESI	INPGTAMASHKDDDEKFFPMSGVMI FGKES	
AAV6-A	483	CYRQQR	VSCTKTDN-----NNSNFT	WTGASKYNLNGRESI	INPGTAMASHKDDKDKFFPMSGVMI FGKES	
hu. 34-B	482	CYRQQR	VSCTSADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEKFFPQSGVLI FGKQG
hu. 47-B	482	CYRQQR	VSCTSADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDNEEKFFPQSGVLI FGKQG
hu. 29-B	482	CYRQQR	VSCTSADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPQSGVLI FGKQG
hu. 63-B	482	CYRQQR	VSCTSADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPQSGVLI FGKQD
hu. 56-B	482	CYRQQR	VSCTAADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPQSGVLI FGKQG
hu. 45-B	482	CYRQQR	VSCTSADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPQSGVLI FGKQG
hu. 57-B	481	CYRQQR	VSCTAADN-----NNGEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPQSGVLI FGKQG
hu. 35-B	482	CYRQQR	VSCTSADN-----NSEYS	WTGATKYHLN	GRDLSVNP	GPAMASHKDDDEEKFFPQSGVLI FGKQG

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hu. 58-B	482	CYRQQRVSKTSADN-----NNSEYSWIGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
hu. 28-B	482	CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
hu. 51-B	482	CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
hu. 19-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 49-B	482	CYRQQRVSKTAADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
hu. 52-B	482	CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
hu. 13-B	482	CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
AAV2-B	482	CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQG
hu. 20-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 24-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 64-B	482	CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 27-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 21-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 22-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 23-B	482	CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 7-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 61-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
rh. 56-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 9-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 54-C	481	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 53-C	481	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 60-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 55-C	481	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 2-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 1-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 18-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 3-C	483	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 25-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 15-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD
hu. 16-C	482	CYRQQRVSKTAADN-----NNSNFPWTAATKYHLNGRDSL	VNPGPAMASHKDDDEEKFFPQSGVLI	FGKQD

FIG. 2U

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hu. 11-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPAMASHKDDDEEKFFPMHGTLIIFGKQG
 hu. 10-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPAMASHKDDDEEKFFPMHGTLIIFGKQG
 hu. 4-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPAMASHKDDDEEKFFPMHGTLIIFGKQG
 rh. 54-D 485 CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLIFGKTG
 rh. 48-D 485 CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEERFFPSSGVLIFGKTG
 rh. 55-D 485 CFRQRRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEERFFPSSGVLIFGKTG
 rh. 62-D 485 CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEERFFPSSGVLIFGKTG
 AAV7-D 485 CFRQQRVSKTLDQN-----NNSNFAWTGATKYHLNGRNSLVNPGVAMATHKDDDEDRFFPSSGVLIFGKTG
 rh. 52-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 rh. 51-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 hu. 39-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 rh. 53-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNSGVAMATNKDDDEDRFFPSSGILMFGKQG
 hu. 37-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 rh. 43-E 484 CYRQQRVSTTGSQN-----NNSNFAWTAGTKYHLNGRNSLANPGIAMATHKDDDEERFFPVTG-SCFWQQN
 rh. 50-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 rh. 49-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 rh. 61-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 hu. 41-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 rh. 64-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 hu. 42-E 485 CYRQQRVSTTLSQS-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 rh. 57-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 hu. 40-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQN
 AAV8-E 485 CYRQQRVSTTGSQN-----NNSNFAWTAGTKYHLNGRNSLANPGIAMATHKDDDEERFFPSNGILIFGKQN
 rh. 58-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATNKDDDEDRFFPSSGILMFGKQG
 rh. 40-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 hu. 67-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 hu. 17-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 hu. 6-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 hu. 66-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG
 rh. 38-E 485 CYRQQRVSTTLSQN-----NNSNFAWTGATKYHLNGRDSLVPNPAMATHKDDDEERFFPSSGVLIFGKQG

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hu.32-F	483	SYRQQRVSTTVTQN-----NNSEFAWP	GASSWALNGRNSLMNPPG	PAMASHKEGEDRFFPLSGSLIFGKQG
AAV9/hu	483	SYRQQRVSTTVTQN-----NNSEFAWP	GASSWALNGRNSLMNPPG	PAMASHKEGEDRFFPLSGSLIFGKQG
hu.31-F	483	SYRQQRVSTTVTQN-----NNSEFAWP	GASSWALNGRNSLMNPPG	PAMASHKEGEDRFFPLSGSLIFGKQG

		570	580	590	600	610	620	630
								
AAV5	534	ANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQSS	TTAPATGTYNLQEI	VPGSVWMERDVYL				
AAV3-3	548	T--TASNAELD-NVMITDEEEIRTTNPVATEQYGTVAN	NLQSSNTAPT	TGTVNHQGALPGMVWQDRDVYL				
AAV4-4	546	N--GNTATVPG-TLIFTSEEEIAATNATD	TDMWGNLPGGDQSN	SNLPTVDRLTALGAVPGMVWQNRDIYY				
AAV1-A	548	A--GASNTALD-NVMITDEEEIKATNPVATERF	GTVAVNFQSSSD	PDATGVDVHAMGALPGMVWQDRDVYL				
hu.46-A	548	A--GASNTALD-NVMITDEEEIKATNPVATERF	GTVAVNFQSSSD	PDATGVDVHAMGALPGMVWQDRDVYL				
hu.48-A	548	A--GASNTALD-NVMITDEEEIKATNPVATERF	GTVAVNFQSSSD	PDATGVDVHAMGALPGMVWQDRDVYL				
hu.44-A	548	A--GASNTALD-NVMITDEEEIKATNPVATERF	GTVAVNFQSSSD	PDATGVDVHAMGALPGMVWQDRDVYL				
hu.43-A	549	A--GASNTALD-NVMITDEEEIKATNPVATERF	GTVAVNFQSSSD	PDATGVDVHAMGALPGMVWQDRDVYL				
AAV6-A	548	A--GASNTALD-NVMITDEEEIKATNPVATERF	GTVAVNLQSSSD	PDATGVDVHVMGALPGMVWQDRDVYL				
hu.34-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QRGNRQAATADVNTQGVLP	GMVWQDRDVYL			
hu.47-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QRGNRQAATADVNTQGVLP	GMVWQDRDVYL			
hu.29-B	547	P--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATADVNTQGVLP	GMVWQDRDVYL			
hu.63-B	547	S--GKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATSDVNTQGVLP	GMVWQDRDVYL			
hu.56-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATSDVNTQGVLP	GMVWQDRDVYL			
hu.45-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QRGNRQAATADVNTQGVLP	GMVWQDRDVYL			
hu.57-B	546	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTRAATSDVNTQGVLP	GMVWQDRDVYL			
hu.35-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QRGNRQAATADVNTQGVLP	GMVWQDRDVYL			
hu.58-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATADVNTQGVLP	GMVWQDRDVYL			
hu.28-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATADVNTQGVLP	GMVWQDRDVYL			
hu.51-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QRGNRQAATADVNTQGVLP	GMVWQDRDVYL			
hu.19-B	547	S--GKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATSDVNTQGVLP	GMVWQDRDVYL			
hu.49-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QSGNTQAATADVNTQGVLP	GMVWQDRDVHL			
hu.52-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QRGNRQAATADVNTQGVLP	GMVWQDRDVYL			
hu.13-B	547	S--EKTNV	DIE-KVMITDEEEIRTTNPVATEQYGSVSTNL	QGGNTQAATADVNTQGVLP	GMVWQDRDVYL			

FIG. 2W

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AAV2-B 547 S--EKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu.20-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.24-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.64-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.27-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPAATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.21-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.22-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.23-B 547 S--GKTNV DIE--KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.7-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.61-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
rh.56-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.9-C 547 T--NANDADLD--HVMITDEEEIRTTNPVATEQYGNVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.54-C 546 T--NATNAELE--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTAASTETVNHQGALPGMVWQDRDVYL
hu.53-C 546 T--NATNAELE--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTAASTETVNHQGALPGMVWQDRDVYL
hu.60-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.55-C 546 T--NATNAELE--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTAASTETVNHQGALPGMVWQDRDVYL
hu.2-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.1-C 547 T--NANDADLD--NVMITDEEEIRATNPVATEQYGYVSNLQNSNTGPTTGTVNRQGALPGMVWQDRDVYL
hu.18-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.3-C 548 T--NANDADLD--NVMITDEEEIRPTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.25-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.15-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.16-C 547 T--NANDADLD--NVMITDEEEIRTTNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.11-C 547 T--NANDADLD--HVMITDEEEIRTTNPVATEQYGNVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.10-C 547 T--NANDADLD--HVMITDEEEIRTTNPVATEQYGNVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
hu.4-C 547 T--NANDADLD--NVMITDEEEIRATNPVATEQYGYVSNLQNSNTGPTTGTVNHQGALPGMVWQDRDVYL
rh.54-D 550 A--TN-KTTLE--NVLMTNEEEIRPTNPVATEEYGVSSNLQAANTAAQTQVNNQGALPGMVWQNRDVYL
rh.48-D 550 A--AN-KTTLE--NVLMTNEEEIRPTNPVATEEYGVSSNLQAANTAAQTQVNNQGALPGMVWQNRDVYL
rh.55-D 550 A--AN-KTTLE--NVLMTNEEEIRPTNPVATEEYGVSSNLQAANTAAQTQVNNQGALPGMVWQNRDVYL
rh.62-D 550 A--AN-KTTLE--NVLMTNEEEIRPTNPVATEEYGVSSNLQAANTAAQTQVNNQGALPGMVWQNRDVYL

FIG. 2X

AAV5 604 QGPIWAKIPETGAHFHPSAMGGFGLKHPPPMMLIKNTVPGN-ITSFSDVPVSSFFITQYSTGQVTVEME

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AAV3-3 615 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQIMIKNTPVPANPPTTFSPAKFASFIQTYSTGQVSVEIE
 AAV4-4 613 QGPIWAKIPHTDGHFHPSPPLIGFGGLKHPPPPQIFIKNTPVPANPATTFSSTPVNSFITQYSTGQVSQID
 AAV1-A 615 QGPIWAKIPHTDGHFHPSPMLMGFGGLKNPPPPQILIKNTPVPANPPAEFSATKFASFIQTYSTGQVSVEIE
 hu.46-A 615 QGPIWAKIPHTDGHFHPSPMLMGFGGLKNPPPPQILIKNTPVPANPPAEFSATKFASFIQTYSAGQVSVEIE
 hu.48-A 615 QGPIWAKIPHTDGHFHPSPMLMGFGGLKNPPPPQILIKNTPVPANPPAEFSATKFASFIQTYSTGQVSVEIE
 hu.44-A 615 QGPIWAKIPHTDGHFHPSPMLMGFGGLKNPPPPQILIKNTPVPANPPAEFSATKFASFIQTYSTGQVSVEIE
 hu.43-A 616 QGPIWAKIPHTDGHFHPSPMLMGFGGLKNPPPPQILIKNTPVPANPPAEFSATKFASFIQTYSTGQVSVEIE
 AAV6-A 615 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPPAEFSATKFASFIQTYSTGQVSVEIE
 hu.34-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.47-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.29-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.63-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.56-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.45-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.57-B 613 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.35-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.58-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGRVSVEIE
 hu.28-B 614 QGPTWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.51-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.19-B 614 QGPIWAKIPHTDGHFHPSPMLVGGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.49-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.52-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGPKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.13-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 AAV2-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.20-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.24-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.64-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.27-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFVSFIQTYSTGQVSVEIE
 hu.21-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE
 hu.22-B 614 QGPIWAKIPHTDGHFHPSPMLMGFGGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFIQTYSTGQVSVEIE

FIG. 2AA

rh. 50-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTAF	NQAKLNS	FI	TQYSTG	QVSVE	IE
rh. 49-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTAF	NQAKLNS	FI	TQYSTG	QVSVE	IE
rh. 61-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQV	LIKNTVP	ADPPTAF	NQAKLNS	FI	TQYSTG	QVSVE	IE
hu. 41-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
rh. 64-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTAF	NQAKLNS	FI	TQYSTG	QVSVE	I
hu. 42-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
rh. 57-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTAF	NQAKLNS	FI	TQYSTG	QVSAE	IE
hu. 40-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
AAV8-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	TENQSKLNS	FI	TQYSTG	QVSVE	IE
rh. 58-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKSTVP	ADPPTAF	NQAKLNS	FI	TQYSTG	QVSVE	IE
rh. 40-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
hu. 67-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
hu. 17-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
hu. 6-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
hu. 66-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
rh. 38-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPQI	LIKNTVP	ADPPTF	SQAKLAS	FI	TQYSTG	QVSVE	IE
hu. 32-F	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGMK	HPPPQI	LIKNTVP	ADPPTAF	NKDKLNS	FI	TQYSTG	QVSVE	IE
AAV9/hu	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGMK	HPPPQI	LIKNTVP	ADPPTAF	NKDKLNS	FI	TQYSTG	QVSVE	IE
hu. 31-F	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGMK	HPPPQI	LIKNTVP	ADPPTAF	NKDKLNS	FI	TQYSTG	QVSVE	IE
AAV5	673	WELKKENSK	RWNPEIQY	TNNYNDPQ	FVDFAPD	STGEYR	TRPIG	TRYLTRPL	*			
AAV3-3	685	WELQKENS	KRWNPEIQY	TSNKNKSV	NVDFTV	DNGVSE	PRPIG	TRYLTRNL	*			
AAV4-4	683	WEIQKERS	KRWNPEVQ	FTSNYGQ	QNSLLW	APDAAG	KYTEP	RAIGTRYL	THHL*			
AAV1-A	685	WELQKENS	KRWNPEVQY	TSNYAKS	ANVDFT	VDDNNG	LYTEP	PRPIG	TRYLTRPL*			
hu. 46-A	685	WELQKENS	KRWNPEVQY	TSNYAKS	ANVDFT	VDDNNG	LYTEP	PRPIG	TRYLTRPL*			
hu. 48-A	685	WELQKENS	KRWNPEVQY	TSNYAKS	ANVDFT	VDDNNG	LYTEP	PRPIG	TRYLTRPL*			
hu. 44-A	685	WELQKENS	KRWNPEVQY	TSNYAKS	ANVDFT	VDDNNG	LYTEP	PRPIG	TRYLTRPL*			
hu. 43-A	686	WELQKENS	KRWNPEVQY	TSNYAKS	ASVDFT	VDDNNG	LYTEP	PRPIG	TRYLTRPL*			

FIG. 2AB

FIG. 2AC

hu.60-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.55-C 683 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.2-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.1-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.18-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYPTRNL*
hu.3-C 685 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.25-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.15-C 684 WELQKEDS KRWNPEIQYTSN YNKP VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.16-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.11-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.10-C 684 WELR KENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
hu.4-C 684 WELQKENS KRWNPEIQYTSN YNKS VNVDFTVD TNGVYSEPRPIGTRYLTRNL*
rh.54-D 686 WELQKENS KRWNPEIQYTSN FDKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.48-D 686 WELQKENS KRWNPEIQYTSN FDKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.55-D 686 WELQKENS KRWNPEIQYTSN FDKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.62-D 686 WELQKENS KRWNPEIQYTSN FDKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
AAV7-D 686 WELQKENS KRWNPEIQYTSN FEKQTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh.52-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.51-E 687 WEPQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
hu.39-E 687 WELQKENS KRWNPEIQYTSN YKSTNADFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.53-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYPTRNL*
hu.37-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.43-E 685 WELQKENS KRWNPEIQYTSN YKSTSVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.50-E 687 WELQKENS KRWSPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.49-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.61-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
hu.41-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.64-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
hu.42-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*
rh.57-E 687 WELQKENS KRWNPEIQYTSN YKSTNVDFAVNTGEGVYSEPRPIGTRYLTRNL*

FIG. 2AD

hu.40-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
AAV8-E	687	WELQKENS	KRWNPEIQYTSNYYKSTSVDFAVNTEGTYSEPRPIGTRYLTRNL*
rh.58-E	687	WELQKENS	KCWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
rh.40-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNSEGTYSEPRPIGTRYLTRNL*
hu.67-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.17-E	687	WELQKENS	KRWNPEIQYTSNYYKSNVDFVDTNNGVYSEPRPIGTRYLTRNL*
hu.6-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.66-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
rh.38-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.32-F	685	WELQKENS	KRWNPEIQYTSNYYKSNNVEFVAVNTEGTYSEPRPIGTRYLTRNL*
AAV9/hu	685	WELQKENS	KRWNPEIQYTSNYYKSNNVEFVAVNTEGTYSEPRPIGTRYLTRNL*
hu.31-F	685	WELQKENS	KRWNPEIQYTSNYYKSNNVEFVAVNTEGTYSEPRPIGTRYLTRNL*

FIG. 2AE

		10	20	30	40	50	60	70
								
AAV5	1	ATGCTTTTGTGATCACCCCTCCAGATGGTTGGAAGAA--GTTGGTGAAGGTCTTCGCCGAGTTTGTGG						
AAV3-3-	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAAACCTTTCTGAAGGCATTCGTGAGTGGTGGG						
AAV4-4-	1	--ATGACTGACGGTTACCTTCCAGATTGGCTAGAGGACAAACCTCTCTGAAGCGCTTCGAGAGTGGTGGG						
AAV1-A-	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAAACCTCTCTGAGGGCATTCGCCGAGTGGTGGG						
hu.46-A	1	ATGGCTGCCGACGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.48-A	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAAACCTCTCTCTGAGGGCATTCGCCGAGTGGTGGG						
hu.44-A	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.43-A	1	ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAAACCTCTCTCTGAGGGCATTCGCCGAGTGGTGGG						
AAV6-A	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAAACCTCTCTCTGAGGGCATTCGCCGAGTGGTGGG						
hu.34-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTGAAGGAAATAAGACAGCGGTGGGA						
hu.47-B	1	ATGGCTGCCGATGGCTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.29-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.63-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.56-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.45-B	1	ATGGCTGCCGATGGCTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.57-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.35-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGCGGTGGGA						
hu.58-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.28-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.51-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.19-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.49-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCAAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.52-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.13-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
AAV2-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.20-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.24-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						
hu.64-B	1	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACTCTCTCTCTGAAGGAAATAAGACAGTGGTGGGA						

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

	80	90	100	110	120	130	140
AAV5	68		GCCTTGAAAGCGGGCCACCGAAACCCAAATCAGCAGCATCAAGATCAAGCCCGTGGTCTTGTGCT				
AAV3-3	71	CTCTGAAACCTGGAGTCCCTCAACCCAAAGCGAACCAACACCCAGGACAACCGTCGGGGCTCTTGTGCT					
AAV4-4	68	CGCTGCAACCTGGAGCCCCCTAAACCCCAAGGCAATCAACAACATCAGGACAACGCTCGGGGCTCTTGTGCT					
AAV1-A	71	ACTTGAAACCTGGAGCCCCGAGCCCAAGCCAAACAGCAAAAGCAGGACGACGCCGGGCTCTGGTGCT					
hu.46-A	71	AGCTCAAAACCTGGCCCCACCCACCACCAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGTGCT					

FIG. 3C

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hu. 48-A	71	ACTTGAAACCTGGAGCCCCGAAAGCCCAAAGCCAAAGCAGCAAAAGCAGGACGAGCGCCGGGCTCTGGTGCT
hu. 44-A	71	AGCTCAGACCTGGCCCAACCAACCAAGCCCGCAGAGCGGCAATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 43-A	71	ACCTGAAACCTGGAGCCCCAAGCCCAAGCCCAACCAAGCAGCAAGCAGGACGACGCGCCGGGCTCTGGTGCT
AAV6-A	71	ACTTGAAACCTGGAGCCCCGAAACCAAGCCAAAGCAGCAAAAGCAGGACGAGCGCCGGGCTCTGGTGCT
hu. 34-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 47-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 29-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 63-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 56-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 45-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 57-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 35-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 58-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 28-B	71	AACTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 51-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 19-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 49-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 52-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 13-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
AAV2-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 20-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 24-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 64-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 27-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 21-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 22-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 23-B	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 7-C	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
hu. 61-C	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT
rh. 56-C	71	AGCTCAAACCTGGCCCAACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGGCTCTTGCTGCT

FIG. 3E

rh. 64-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAACCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCT	150	160	170	180	190	200	210
hu. 42-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT							
rh. 57-E	71	CGCTGAAACCTGGAGCCCCGAAAGCCCAAGCCCAACCCAGCAAAAGCAGGACGACGGCCGGGGTCTGGTGCT	GCCTGGTTATAACTATCTCGGACCCCGGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGCAGACGAG						
hu. 40-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCGGGTTACAAATACCTCGGACCCCGGTAAACGGACTCGACAAAGGAGAGCCGGTCAACGAGGCGGACGCG						
AAV8-E	71	CGCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCGGGTTACAAATACCTCGGACCCCGGCAACGGACTCGACAAAGGGGAAACCCGTCAACGCAGCGGACCGG						
rh. 58-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
rh. 40-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGAGGACAGCGCC						
hu. 67-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
hu. 17-E	71	ACTTGAAACCTGGAGCCCCGAAACCCAAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
hu. 6-E	71	ACTTGAAACCTGGAGCCCCGAAACCCAAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
hu. 66-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
rh. 38-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGCCGGGGTCTGGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
hu. 32-F	71	AGCTCAAAACCTGGGCCCAACCAAGCCCAAGCCCAACCCAGCAGAAAGCAGGACGACGGGGTCTTGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
AAV9/hu	71	CTTTGAAACCTGGAGCCCCCTCAACCCCAAGGCCAAATCAACAACATCAAGACAACGCTCGAGGTCCTTGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
hu. 31-F	71	AGCTCAAAACCTGGGCCCCCCACCCACCAAGCCCGCAGAGCGGCATAGGACGACAGGAGGTCCTTGTGCT	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA						
AAV5	138								
AAV3-3	141	GCCTGGTTATAACTATCTCGGACCCCGGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGCAGACGAG							
AAV4-4	138	TCCGGGTTACAAATACCTCGGACCCCGGTAAACGGACTCGACAAAGGAGAGCCGGTCAACGAGGCGGACGCG							
AAV1-A	141	TCCGGGTTACAAATACCTCGGACCCCGGCAACGGACTCGACAAAGGGGAAACCCGTCAACGCAGCGGACCGG							
hu. 46-A	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							
hu. 48-A	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGAGGACAGCGCC							
hu. 44-A	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							
hu. 43-A	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							
AAV6-A	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							
hu. 34-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							
hu. 47-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							
hu. 29-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCCGGGACGCA							

FIG. 3F

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

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

hu. 67-E	141	TCTTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAATGCGGGCGGACGCA	220	230	240	250	260	270	280
hu. 17-E	141	TCCCTGGCTGCAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGGACGCA							
hu. 6-E	141	TCCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGGACGCA							
hu. 66-E	141	TCCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGGACGCA							
rh. 38-E	141	TCCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGGACGCA							
hu. 32-F	141	TCCCTGGGTACAAGTACCTCGGACCCCGCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGAGCAGACGCG							
AAV9/hu	141	TCCGGGTACAATAATACCTTGGACCCCGCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGAGCAGACGCG							
hu. 31-F	141	TCCCTGGGTACAAGTACCTCGGACCCCGCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGAGCAGACGCG							
AAV5	208	GTGCGCGGAGAGCAGACATCTCGTACAAACGAGCAGCTTGAGGCGGGAGACAACCCCTACCTCAAGTACA							
AAV3-3	211	GCAGCCCTCGAACAACGAAAGCTTACGACCAGCAGCTCAAGGCCGGTGACAACCCCGTACCTCAAGTACA							
AAV4-4	208	GCAGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCAAGGCCGGTGACAACCCCGTACCTCAAGTACA							
AAV1-A	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCAAGGCCGGTGACAATCCGTACCTGCGGTATA							
hu. 46-A	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 48-A	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCAAGGCCGGTGACAATCCGTACCTGCGGTATA							
hu. 44-A	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCCGTACCTCAAGTACA							
hu. 43-A	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCAAGGCCGGTGACAATCCGTACCCGCGGTATA							
AAV6-A	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCAAGGCCGGTGACAATCCGTACCTGCGGTATA							
hu. 34-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 47-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 29-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 63-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCCCAAGTACA							
hu. 56-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 45-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 57-B	208	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 35-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 58-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACG							
hu. 28-B	211	GCGGCCCTCGAGCAGACAAGGCCCTACGACCAGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							

hu. 51-B 211 GGGCCCTCGAGCACGACAAAGCCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 19-B 211 GGGCCCTCGAGCACGACAAAGCCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 49-B 211 GGGCCCTCGAGTACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 52-B 211 GGGCCCTCGAGCACGACAAAGCCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 13-B 211 GGGCCCTCGAGCACGACAAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
AAV2-B 211 GGGCCCTCGAGCACGACAAAGCCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 20-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 24-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 64-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 27-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 21-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 22-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 23-B 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 7-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 61-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
rh. 56-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 9-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 54-C 211 GGGCTCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 53-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 60-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 55-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 2-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 1-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 18-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGAAAGCGGAGACAACCCGTACCTCAAGTACA
hu. 3-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 25-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCAACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 15-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 16-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 11-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA
hu. 10-C 211 GGGCCCTCGAGCACGACAAGGCTACGACCGGCGAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA

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

FIG. 3K

hu.31-F	211	GCGGCCCTCGAGCACGACAAGGCTACGACCAGCAGCTCAAGGCCGGAGACAACCCGTACCTCAAGTACA
AAV5	278	
AAV3-3	281	ACCACGGGACGCCGAGTTTCAGGAGAAAGCTCGCCGACGACACATCCTTCGGGGGAAACCTCGGAAAGGC
AAV4-4	278	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTTCAAGAAGATACGTCTTTTGGGGGCAACCTTGGCAGAGC
AAV1-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGGCTTCAGGGCGACACATCGTCTTTTGGGGGCAACCTCGGCAGAGC
hu.46-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu.48-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGGC
hu.44-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu.43-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
AAV6-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGCCCTTTTGGGGGCAACCTCGGGCGAGC
hu.34-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu.47-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.29-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.63-B	281	ACCACGCCGACGCCGAGTTCCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.56-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.45-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.57-B	278	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.35-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.58-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.28-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.51-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.19-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.49-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.52-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.13-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
AAV2-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu.20-B	281	ACCACGTCGACGCCGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC

hu. 24-B 281 ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 64-B 281 ACCACGCCGACGCGGAGTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
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 ACCACGCCGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 11-C 281 ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 10-C 281 ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
hu. 4-C 281 ACCACGCCGACGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC
rh. 54-D 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 48-D 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 55-D 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 62-D 281 ACCACGCCGACGCCGAGTTCCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
AAV7-D 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 52-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC

rh. 51-E 281 ATCAGCCGACGCCGAGCTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 39-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 53-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 37-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 43-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 50-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 49-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 61-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 41-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 64-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 42-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 57-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 40-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
AAV8-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 58-E 281 ATCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 40-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 67-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 17-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 6-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 66-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
rh. 38-E 281 ACCAGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 32-F 281 ACCAGCCGACGCCGAGTTTCAGGAGCGGCTCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
AAV9/hu 281 ACCAGCCGACGCCGAGTTCCAGGAGCGGCTCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC
hu. 31-F 281 ACCAGCCGACGCCGAGTTCCAGGAGCGGCTCAAGAAGATACGTCTTTTGGGGCAACCTCGGGCGAGC

360 370 380 390 400 410 420
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
AGTCTTTCAGGCCAAGAAAGGGTCTCGAACCTTTTGGC---CTGGTTGAAGAGGGTGCTAAGACGGCC
AGTCTTCCAGGCCAAGAAAGAGGATCCTTGAGCCCTCTTGGT---CTGGTTGAGGAAGCAGCTAAAACGGCT
AGTCTTCCAGGCCAAGAAAGAGGGTCTTGAACCTCTTGGT---CTGGTTGAGCAAGCGGGTGAGACGGCT

AAV5 348
AAV3-3 351
AAV4-4 348

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AAV1-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTAAGACGGCT
hu.46-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTAAGACGGCT
hu.48-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTAAGACGGCT
hu.44-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTGAGACGGCT
hu.43-A	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
AAV6-A	351	AGTCTTCCAGGCCAAGAAGAGGGTTCTCGAACCTTTTGGT---CTGGTTGAGGAAGGTGCTAAGACGGCT
hu.34-B	351	AGTCTTCCAGGCCGAAAAAGAGGGTACTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.47-B	351	AGTCTTCCAGGCCGAAAAAGAGGGTCTTGAACCTCTGGGC---CTGGTTGGGAACCTGTTAAGACGGCT
hu.29-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTGGAACCTCTGGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
hu.63-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.56-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.45-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.57-B	348	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.35-B	351	AGTCTTCCAGGCCAAAAAGAGGGTACTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.58-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
hu.28-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTGGAACCTCTGAGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
hu.51-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGGGAACCTGTCAAGACGGCT
hu.19-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.49-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.52-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGGGAACCTGTTAAGACGGCT
hu.13-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAGCCTGTTAAACGGCT
AAV2-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.20-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.24-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.64-B	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.27-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.21-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.22-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.23-B	351	AGTCTTCCAGGCCAAAAAGAGGATTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
hu.7-C	351	AGTCTTCCAGGCCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGGACCTGTTAAGACGGCT

FIG. 30

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

FIG. 3P

rh. 61-E	351	AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT--CTGGTTGAGGAAGCGGCTAAGACGGCT	430	440	450	460	470	480	490
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	CCTACCGGAAAGCGGATAGACGACCACCTTTCCA-----							AAAA
AAV4-4	415	CCTGGAAAGAGGGGCTGTAGATCAGTCTCCTCAG---GAACCGGACTCATCTGGTGTGGCAAAAT							
AAV1-A	418	CCTGGAAAGAGAGACCGTTGATTGAATCCCCCAG---CAGCCCCGACTCCTCCACGGGTATCGGCAAAA							
hu. 46-A	418	CCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCCTCCTCGGGCATCGGCAAGA							
hu. 48-A	418	CCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCCCCCTCGGGCATCGGCAAGA							
hu. 44-A	418	CCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GGGCCAGACTCCTCCTCGGGCATCGGCAAGA							
hu. 43-A	418	CCTGGAAAGAGACCGGTAGAACCGTCACCTCAGCGTTCCCCCGACTCCTCCACGGGCTCGGCAAGA							
AAV6-A	418	CCTGGAAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCCTCCTCGGGCATCGGCAAGA							
hu. 34-B	418	CCGGGAAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAGG							

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hu. 47-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAGG
 hu. 29-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCA---GAGCCAGATTCTCCTCCTCGGAACCTGGAAAGT
 hu. 63-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 56-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 45-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 57-B 415 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 35-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 58-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 28-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCCGCA---GAGCCAGATTCTCCTCCTCGGGAACCTGGAAAGT
 hu. 51-B 418 CCAGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 19-B 418 CCGGAGAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 49-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACAGGAAAG
 hu. 52-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 13-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 AAV2-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 20-B 418 CCGGAGAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 24-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 64-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCTTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 27-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 21-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 22-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 23-B 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 7-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 61-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 rh. 56-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 9-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 54-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 53-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 60-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG
 hu. 55-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAG

FIG. 3R

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hu.2-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.1-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.18-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.3-C	421	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.25-C	418	CCGGGAAAAAGAGACC GG TAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.15-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.16-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.11-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.10-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
hu.4-C	418	CCGGGAAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAACCGGAAAAG
rh.54-D	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.48-D	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.55-D	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.62-D	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
AAV7-D	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.52-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.51-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
hu.39-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.53-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
hu.37-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.43-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.50-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.49-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.61-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
hu.41-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.64-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
hu.42-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
rh.57-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
hu.40-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA
AAV8-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCTCAGCGTTCCTCAGCGGCAATCGGCAAGA

rh. 58-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA	500	510	520	530	540	550	560
rh. 40-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 67-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 17-E	418	CCTGGAAGAAGAGACCGGTAGAGCCATCACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA							
hu. 6-E	418	CCTGGAAGAAGAGACCGGTAGAGCCATCACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA							
hu. 66-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCGACTCCTCCGCGGCATCGGCAAGA							
rh. 38-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 32-F	418	CCTGGAAGAAGAGAGCGCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
AAV9/hu	418	CCTGGAAGAAGAGAGCGCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
hu. 31-F	418	CCTGGAAGAAGAGAGCGCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
AAV5	452	GAAAGAAGGCTCGGACCGAAGAGGACTCCAAGCCTTCCACCTCGTCAGACGCCGAAGCTGGACCCAGCGG							
AAV3-3	485	CGGGCAACACAGCCTGCCAGAAAAGACTAAATTTTCGGTCAGACTGGAGACTCAGAGTCAGTCCCAGAC--							
AAV4-4	482	AAGGCAAGCAGCCGGCTAAAAGAAAGCTCGTTTTCGAAGACGAAACTGGAGCAGCGGACGCC-----							
AAV1-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 46-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 48-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGCCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 44-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 43-A	488	AAGGCCAGCAGCCCGCTAAAAGAGACTGAACTTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--							
AAV6-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--							
hu. 34-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 47-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 29-B	485	CGGGCAACCAAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACTCAGACTCCGTACCTGAC--							
hu. 63-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 56-B	485	CGGGCAACCAAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 45-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 57-B	482	CGGGCAACCAAGCCTGCAAGAAAAGATTGAATTTTCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 35-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							

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FIG. 3F

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hu.58-B 485 CGGGCAACCAGCCTGCAAGAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.28-B 485 CGGGCAACCAGCCTGCAAGAAAGAGATTGAATTTCCGGTCAGACTGGAGACTCAGACTCCGTACCTGAC--
hu.51-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.19-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTGGCCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.49-B 485 CGGGCCAGCAGCCTGCGAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.52-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.13-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
AAV2-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.20-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.24-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.64-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.27-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.21-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.22-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.23-B 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu.7-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.61-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
rh.56-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.9-C 485 CGGGCCATCAGCCTGCGAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.54-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.53-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.60-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.55-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.2-C 485 CGGGCCAGCGGCCTGCAAGAAAGAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.1-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.18-C 485 CGGGCCAGCAGCCTGCGAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.3-C 488 CGGGCCAGCAGCCTGCAAGAAAGAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.25-C 485 CGGGCCAGCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.15-C 485 CGGGCAACCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu.16-C 485 CGGGCAACCAGCCTGCAAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--

FIG. 3U

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hu. 11-C	485	CGGGCCATCAGCCTGCGAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 10-C	485	CGGGCCATCAGCCTGCGAGAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 4-C	485	CGGGCCAGCAGCCTGCAAGAAAGATTAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
rh. 54-D	488	AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACTTTGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 48-D	488	AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACTTTGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 55-D	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 62-D	488	AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACTTTGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
AAV7-D	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 52-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 51-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 39-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 53-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 37-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 43-E	485	AAGGCCAACAGCCCGCCAGAAAAAGACTCAATTTTGGCCAGACTGGCGACTCAGAGTCAGTCCAGAC--
rh. 50-E	488	AAGGCCAGCAGCCCGCCGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 49-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 61-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 41-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 64-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 42-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 57-E	488	AAGGCCAGCAGCCCGCCAGAAAGAGACTCAATTTTCGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 40-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAGCTTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
AAV8-E	488	AAGGCCAACAGCCCGCCAGAAAAAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCAGAC--
rh. 58-E	488	AAGGCCAGCAGCCCGCTAGAAAGAGACTGAACTTTGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 40-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 67-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
hu. 17-E	488	CAGGCCAGCAGCCCGCGAAAGAGACTCAACTTTGGCAGACTGGCGACTCAGAGTCAGTGGCCCGAC--
hu. 6-E	488	CAGGCCAGCAGCCCGCGAAAGAGACTCAACTTTGGCAGACTGGCGACTCAGAGTCAGTGGCCCGAC--
hu. 66-E	488	AAGGCCAGCAGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
rh. 38-E	488	AAGGCCAGCGGCCCGCTAAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--

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hu. 32-F	485	CGGGTTACAGCCCGCTAAAGAACTCAATTTCGGTTCAGACTGGCGACACAGAGTCAGTCCCCGAC--	570	580	590	600	610	620	630
AAV9/hu	485	CGGGTGACAGCCCGCTAAAGAACTCAATTTCGGTTCAGACTGGCGACACAGAGTCAGTCCCCGAC--							
hu. 31-F	485	CGGGTTACAGCCCGCTAAAGAACTCAATTTCGGTTCAGACTGGCGACACAGAGTCAGTCCCCGAC--							

AAV5	522	ATCCCAGCAGCTGCAAAATCCCAGCCCAACCAAGCTTTCAGAGCTGATACAATGCTGCGGAGGT	570	580	590	600	610	620	630
AAV3-3	552	-CCTCAACCTCTCGGAGAACCAACAGCAGCCCAAGTTTGGGATCTAATACAATGGCTTCAGGCGGT							
AAV4-4	546	-----CCTGAGGGATCAACTTCGGAGCCATGTCT-----GATGACAGTGAGATGCGTGCAGCAGCT							
AAV1-A	552	-CCACAACTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT							
hu. 46-A	552	-CCACAACTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT							
hu. 48-A	552	-CCACAACTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT							
hu. 44-A	552	-CCACAACTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT							
hu. 43-A	555	-CCTCAACCAATCGGAGAACCAACAGCAGGCCCTCTGGTCTGGGATCTGGTACAATGGCTGCAGGCGGT							
AAV6-A	552	-CCACAACTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAATGGCTTCAGGCGGT							
hu. 34-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 47-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 29-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 63-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 56-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 45-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 57-B	549	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 35-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 58-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 28-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 51-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 19-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 49-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 52-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							
hu. 13-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT							

FIG. 3W

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AAV2-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTACAGGCAGT
hu. 20-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 24-B	552	-CCCCGGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 64-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTACAGGCAGT
hu. 27-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 21-B	552	-CCCCGGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 22-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 23-B	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 7-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 61-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
rh. 56-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 9-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 54-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 53-C	552	-CCCCAGCCTCTCAGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 60-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 55-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 2-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 1-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 18-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 3-C	555	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 25-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 15-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 16-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 11-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 10-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
hu. 4-C	552	-CCCCAGCCTCTCGGACAGCCACCAGCAGCCCCCTCTGGTCTGGGAACATAATACGATGGCTTACAGGCAGT
rh. 54-D	555	-CCTCAACCTCTCGGAGAACCCAGCAGGCCCTCTGGTCTGGGAACATAATGGTACAAATGGCTGCAGCCGGT
rh. 48-D	555	-CCTCAACCTCTCGGAGAACCCAGCAGGCCCTCTGGTCTGGGAACATAATGGTACAAATGGCTGCAGCCGGT
rh. 55-D	555	-CCTCAACCTATCGGAGAACCTCCAGCAGGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGCCGGT
rh. 62-D	555	-CCTCAACCAATCGGAGAGCCACCAGCAGGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGCCGGT

FIG. 3X

AAV5 592 GCGGCCCATTTGGCGACAATAACCAAGTGCAGTGGGCAATGCCCTGGGAGATTGGCATTGCG

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AAV3-3 622 GCGCACCAATGGCAGACAAATAACGAGGTGCCGATGGAGTGGGTAATTCCTCAGGAAATTGGCATTTGCG
 AAV4-4 604 GCGGAGCTGCAGTCGAGGCGGACAAAGGTGCCGATGGAGTGGGTAATGCCCTCGGTGATTGGCATTTGCG
 AAV1-A 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.46-A 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCACTTGGC
 hu.48-A 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.44-A 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.43-A 625 GCGCTCCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 AAV6-A 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.34-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.47-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.29-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.63-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.56-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.45-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.57-B 619 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAGATTGGCATTTGCG
 hu.35-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.58-B 622 GCGCACCAATGGCAGACAAATAACGAATGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.28-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.51-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.19-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGTATTGCG
 hu.49-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.52-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.13-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 AAV2-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.20-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.24-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.64-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.27-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.21-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
 hu.22-B 622 GCGCACCAATGGCAGACAAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG

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hu. 23-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCCGACGGAGTGGGTAATTCCTCGGAAATTGGCATTGCG
hu. 7-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 61-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCGGAAATTGGCATTGCG
rh. 56-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 9-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 54-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 53-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 60-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 55-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 2-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 1-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 18-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 3-C	625	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 25-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 15-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 16-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 11-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 10-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
hu. 4-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGTAATTCCTCAGGAAATTGGCATTGCG
rh. 54-D	625	GGCGTCCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 48-D	625	GGCGACCAATGGCTGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 55-D	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 62-D	625	GGCGACCAATGGCTGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
AAV7-D	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 52-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 51-E	625	GGCGGCGCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu. 39-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 53-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
hu. 37-E	625	GGCGTCCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG
rh. 43-E	622	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGTAATGCCCTCAGGAAATTGGCATTGCG

FIG. 3AA

rh. 50-E	625	GGCGACCAATGGCAGACAATAACGAAGTGCCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	710	720	730	740	750	760	770
rh. 49-E	625	GGCGACCAATGGCAGACAATAACGAAGTGCCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG							
rh. 61-E	625	GGCGACCAATGGCAGACAATAACGAAGTGCCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACGTGGATGGGGACAGAGTCGTACCAAGTCCACCCGAACCTGGGTGCTGCCCAGCTACAACAA						
hu. 41-E	625	GGCGTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCCAATGGCTGGCGACAGAGTCATCACCAACAGCACCAACCTGGGCCCTGCCCACTTACAACAA						
rh. 64-E	625	GGCGACCAATGGCAGACAATAACGAAGTGCCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACCTGGTCTGAGGGCCACGTCACGACCACCAAGAACCTGGGTCTTGCCCACTACAACAA						
hu. 42-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
rh. 57-E	625	GGCGGCCAATGGCAGACAATAACGAAGGTGCCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 40-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
AAV8-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
rh. 58-E	625	GGCGACCAATGGCAGACAATAACGAAGGTGCCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
rh. 40-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 67-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 17-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 6-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 66-E	625	GGGCTCCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCAGGAAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
rh. 38-E	622	GGCGACCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 32-F	622	GGCGACCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
AAV9/hu	622	GGCGACCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						
hu. 31-F	622	GGCGACCAATGGCAGACAATAACGAAGGCGCGACGGAGTGGGTAGTTCTCGGGAATTGGCATTGCG	ATTCCACATGGCTGGCGACAGAGTCATCACCAACAGCACCCGCACCTGGGCCTTGCCCACTACAATAA						

FIG. 3AB

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AAV6-A	692	ATTCCACATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CATGGG	CCTTGCCC	ACCTATA	CAAA
hu. 34-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 47-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 29-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 63-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 56-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 45-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 57-B	689	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 35-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 58-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 28-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 51-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 19-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 49-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 52-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 13-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
AAV2-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 20-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 24-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 64-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 27-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 21-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 22-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 23-B	692	ATTCCACATGGATGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 7-C	692	ATTCCCAATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 61-C	692	ATTCCCAATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
rh. 56-C	692	ATTCCCAATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 9-C	692	ATTCCCAATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 54-C	692	ATTCCCAATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA
hu. 53-C	692	ATTCCCAATGGCTGGCGACAGAGTCA	TACCA	CCAGCACCCGAA	CCTGGG	CCCTGCCC	ACCTATA	CAAA

FIG. 3AC

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hu. 60-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGACCTGGGCCCTG	CCCCACCTACAACAA
hu. 55-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCCCTG	CCCCACCTACAACAA
hu. 2-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCCCTG	CCCCACATACAACAA
hu. 1-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCCCTG	CCCCACATACAACAA
hu. 18-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCCCTG	CCCCACCTACAACAA
hu. 3-C	695	ATTCCCAATGGCTGGGCGACAGAGTCA	TGCCACAGCACCCGAACTGGGCCCTG	CCCCACATACAACAA
hu. 25-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACTCGAACTGGGCCCTG	CCCCACCTACAACAA
hu. 15-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCTCTG	CCCCACCTACAATAA
hu. 16-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCTCTG	CCCCACCTACAACAA
hu. 11-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCCCTG	CCCCACCTACAACAA
hu. 10-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCCCTG	CCCCACCTACAACAA
hu. 4-C	692	ATTCCCAATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTGGGCTTTG	CCCCACCTACAACAA
rh. 54-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 48-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 55-D	695	ATTCCACACGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 62-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
AAV7-D	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 52-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 51-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
hu. 39-E	695	ATTCCACATGGCTGGGCGACAGAGTTA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 53-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
hu. 37-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 43-E	692	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 50-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 49-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 61-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
hu. 41-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 64-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
hu. 42-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA
rh. 57-E	695	ATTCCACATGGCTGGGCGACAGAGTCA	TACCACAGCACCCGAACTTTGGGCTT	TGCCCACCTACAACAA

FIG. 3D

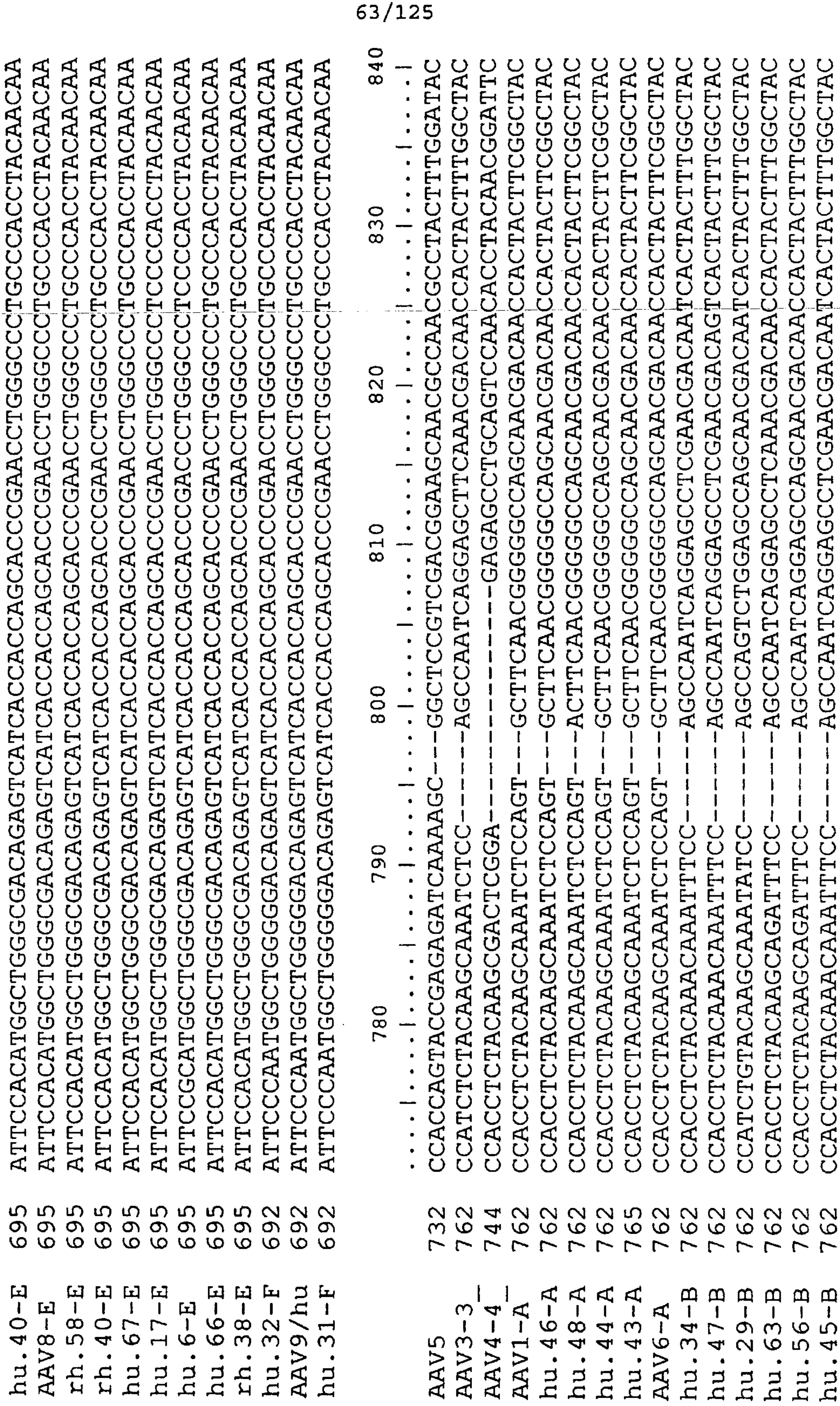


FIG. 3AE

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hu. 57-B	759	CCACCTCTACAAGCAGATTTC	-----AGCCAATCAGGAGCCAGCAATGACAACCACTACTTTGGCTAC
hu. 35-B	762	CCACCTCTACAACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTGGCTAC
hu. 58-B	762	CCATCTGTACAAGCAGATTTC	-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 28-B	762	CCATCTGTACAAGCAAATATCC	-----AGCCAGTCTGGAGCCAGCAACGACAATCACTACTTTGGCTAC
hu. 51-B	762	CCACCTCTACAACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTGGCTAC
hu. 19-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 49-B	762	CCATCTGTACAAGCAGATCTCC	-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 52-B	762	CCACCTCTACAGACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTGGCTAC
hu. 13-B	762	CCATCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTGGCTAC
AAV2-B	762	CCACCTCTACAACAAATTTTC	-----AGCCAATCAGGAGCCTCGAACGACAATCACTACTTTGGCTAC
hu. 20-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 24-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 64-B	762	CCACCTCTACAGGCAGATTTC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 27-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 21-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 22-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 23-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 7-C	762	CCACCTCTACAAGCAAATCTCA	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 61-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
rh. 56-C	762	CCACCTCTACAAGCAAATCTCA	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 9-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCGAACGACAACCACTACTTTGGCTGC
hu. 54-C	762	CCACCTTTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 53-C	762	CCACCTTTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 60-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 55-C	762	CCACCTTTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 2-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 1-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCAGCAACGACAACCACTACTTTGGCTAC
hu. 18-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC
hu. 3-C	765	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTGCAACGACAACCACTACTTTGGCTAC
hu. 25-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAAACGACAACCACTACTTTGGCTAC

FIG. 3AF

hu.15-C	762	CCACCTCTACAAGCAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTGGCTAC
hu.16-C	762	CCACCTCTACAAGCAAATCTCC-----AGCCAATCAGGAGCCTCAAACGACAACCACTACTTTGGCTAC
hu.11-C	762	CCACCTCTACAAGCAAATCTCC-----AGCCAATCAGGAGCCTCGAACGACAACCACTACTTTGGCTAC
hu.10-C	762	CCACCTCTACAAGCAAATCTCC-----AGCCAATCAGGAGCCTCGAACGACAACCACTACTTTGGCTAC
hu.4-C	762	CCACCTCTACAAGCAAATCTCC-----AGCCAATCAGGAGCCTCGAACGACAACCACTACTTTGGCTAC
rh.54-D	765	CCACCTCTACAAGCAAATCTCCAGT---CAGTCAGCAGGTAGCACCAACGACAACCGTCTACTTCGGCTAC
rh.48-D	765	CCACCTCTACAAGCAAATCTCCAGT---CAGTCAGCAGGTAGCACCAACGACAACCGTCTACTTCGGCTAC
rh.55-D	765	CCACCTCTACAAGCAAATCTCCAGT---CAGTCAGCAGGTAGCACCAACGACAACCGTCTACTTCGGCTAC
rh.62-D	765	CCACCTCTACAAGCAAATCTCCAGT---CAGTCAGCAGGTAGCACCAACGACAACCGTCTACTTCGGCTAC
AAV7-D	765	CCACCTCTACAAGCAAATCTCCAGT---GAAACTGCAGGTAGTACCACCAACGACAACCACTACTTCGGCTAC
rh.52-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
rh.51-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
hu.39-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
rh.53-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
hu.37-E	765	CCACCTCTACAAGCAAATCTCCAATGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
rh.43-E	762	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
rh.50-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
rh.49-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
rh.61-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
hu.41-E	765	CCACCTCTACAAGCAAATCTCCAATGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
rh.64-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTTGGCTAC
hu.42-E	765	CCACCTCTACAAGCAAATCTCCAATGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
rh.57-E	765	CCACCTCTACAAGCAAACCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTCGGCTAC
hu.40-E	765	CCACCTCTACAAGCAAATCTCCAATGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
AAV8-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
rh.58-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCGAGCACCAACGACAACCACTACTTCGGCTAC
rh.40-E	765	CCACCTCTACAAGCAAATCTCCAATGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
hu.67-E	765	CCACCTCTACAAGCAAATCTCCAATGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
hu.17-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC
hu.6-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAGCACCAACGACAACCACTACTTCGGCTAC

FIG. 3AG

hu. 66-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGGAGGAAGCACCAACGACAACACCTACTTCGGCTAC	850	860	870	880	890	900	910
rh. 38-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGGAGGAAGCACCAACGACAACACCTACTTCGGCTAC							
hu. 32-F	762	TCACCTCTACAAGCAAATCTCCAACAGCACATCTGGAGGATCTTCAAAATGACAACGCCCTACTTCGGCTAC							
AAV9/hu	762	TCACCTCTACAAGCAAATCTCCAACAGCACATCTGGAGGATCTTCAAAATGACAACGCCCTACTTCGGCTAC							
hu. 31-F	762	TCACCTCTACAAGCAAATCTCCAACAGCACATCTGGAGGATCTTCAAAATGACAACGCCCTACTTCGGCTAC							
AAV5	799								
AAV3-3-	826	AGCACCCCTGGGGGTACTTTGACTTTAAACCGCTTCCACAGCCACTGGAGCCCCCGAGACTGGCAAAGAC							
AAV4-4-	799	AGCACCCCTGGGGGTATTTTGACTTTAAACAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCGAC							
AAV1-A-	829	TCCACCCCTGGGGATACTTTGACTTCAACCGCTTCCACTGCCACTTCTCACCACGTGACTGGCAGCGAC							
hu. 46-A	829	AGCACCCCTGGGGGTATTTTGATTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAC							
hu. 48-A	829	AGCACCCCTGGGGGTATTTTGATTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAC							
hu. 44-A	829	GGCACCCCTGGGGGTATTTTGATTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAC							
hu. 43-A	829	AGCACCCCTGGGGGTATTTTGATTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAC							
AAV6-A	832	AGCACCCCTGGGGGTATTTTGATTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAC							
hu. 34-B	829	AGCACCCCTGGGGGTATTTTGATTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGCGAC							
hu. 47-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 29-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 63-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 56-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGAGAC							
hu. 45-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 57-B	823	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAGAGAC							
hu. 35-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 58-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 28-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 51-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 19-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							
hu. 49-B	826	AGCACCCCTGGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCACGTGACTGGCAAAGAC							

FIG. 3A

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

FIG. 3A1

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

FIG. 3A

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

FIG. 3AK

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hu. 21-B	896	TCATCAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 22-B	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 23-B	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 7-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 61-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
rh. 56-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 9-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 54-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 53-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 60-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 55-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 2-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
hu. 1-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
hu. 18-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 3-C	899	TCATCAACAGCAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
hu. 25-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 15-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 16-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 11-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 10-C	896	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 4-C	896	TCGTCAACAACAACCCGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
rh. 54-D	902	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTCTTTCAACATCCAGTCAAAGGA
rh. 48-D	902	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTGTTCACATCCAGTCAAAGGA
rh. 55-D	902	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTGTTCACATCCAGTCAAAGGA
rh. 62-D	902	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAACTTCAAGCTGTTCACATCCAGTCAAAGGA
AAV7-D	902	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTGCGGTTCAGCTCTTCAACATCCAGTCAAAGGA
rh. 52-E	905	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGTCAAAGGA
rh. 51-E	905	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGTCAAAGGA
hu. 39-E	905	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGTCAAAGGA
rh. 53-E	905	TCATCAACAACAACAACTGGGGATTCCGGCCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGTCAAAGGA

FIG. 3AL

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hu. 37-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	990	1000	1010	1020	1030	1040	1050
rh. 43-E	902	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 50-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 49-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 61-E	905	CCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 41-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 64-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 42-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 57-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 40-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
AAV8-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 58-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 40-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 67-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 17-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 6-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 66-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
rh. 38-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGGA							
hu. 32-F	902	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
AAV9/hu	902	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 31-F	902	TCATCAACAACAACTGGGGATTCCGGCCCAAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
AAV5	939	GGTCACGGTGCAGGACTCCACACCACCATCGCCAAACAACCTCACCTCCACCGTCCCAAGTGTTCACGGAC							
AAV3-3	966	GGTCACGCAGAACGATGGCAGCAGACTATTGCCAATAAACCTTACCAGCAGCGTTCAAGTGTTCACGGAC							
AAV4-4	939	GGTCACGACGTCGAACGGCGAGACAACCGTGGCTAATAACCTTACCAGCAGCGTTCAAGTCTTTCGGGAC							
AAV1-A	969	GGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCAGCGTTCAAGTCTTTCGGGAC							
hu. 46-A	969	GGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCAGCGTTCAAGTCTTTCGGGAC							
hu. 48-A	969	GGTCACGACGAATGATGGCGTCACAACCATCGCTAATAACCTTACCAGCAGCGTTCAAGTCTTTCGGGAC							

FIG. 3AM

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

FIG. 3A

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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. 3A0

hu.42-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTATTTACGGAC	1060	1070	1080	1090	1100	1110	1120
rh.57-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACCATCCAGGTGTTACGGAC							
hu.40-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
AAV8-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACCATCCAGGTGTTACGGAC							
rh.58-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACCATCCAGGTGTTACGGAC							
rh.40-E	975	GGTCACGCAGGATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu.67-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu.17-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu.6-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu.66-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
rh.38-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu.32-F	972	GGTTACGGACAACAATGGAGTCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
AAV9/hu	972	GGTTACGGACAACAATGGAGTCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu.31-F	972	GGTTACGGACAACAATGGAGTCAAGACCATCGCCAAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
AAV5	1009	GACGACTACCAGCTGCCCTACGTCTCGGCAACGGACCGAGGGATGCCCTGCCGGCCTTCCCTCCGCAGG							
AAV3-3	1036	TCGGAGTATCAGCTCCCGTACGTCTCGGGTCTGGGCAACCAAGGCTGTCTCCCGCCGTTCACAGCGGACG							
AAV4-4	1009	TCGTCTGTACGAACCTGCCGTACGTGATGCGGGTCAAGAGGCGAGCTGCCCTCCCTCCCTCCCAACGACG							
AAV1-A	1039	TCGGAGTACCAGCTTCCGTACGTCTCGGCTCTGCGCACCAAGGCTGCCCTCCCTCCCTCCCGCGGACG							
hu.46-A	1039	TCGGAGTACCAGCTTCCGTACGTCTCGGCTCTGCGCACCAAGGCGCGCTCCCTCCCTCCCGCGGACG							
hu.48-A	1039	TCGGAGTACCAGCTTCCGTACGTCTCGGCTCTGCGCACCAAGGCTGCCCTCCCTCCCTCCCGCGGACG							
hu.44-A	1039	TCGGAGTACCAGCTTCCGTACGTCTCGGCTCTGCGCACCAAGGCTGCCCTCCCTCCCTCCCGCGGACG							
hu.43-A	1042	TCGGAGTACCAGCTTCCGTACGTCTCGGCTCTGCGCACCAAGGCTGCCCTCCCTCCCTCCCGCGGACG							
AAV6-A	1039	TCGGAGTACCAGTTGCCGTACGTCTCGGCTCTGCGCACCAAGGCTGCCCTCCCTCCCTCCCGCGGACG							
hu.34-B	1036	TCGGAGTACCAGCTCCCGTACGTCTCGGCTCGGGCGCATCAAGGATGCCCTCCCTCCCTCCCGCGGACG							
hu.47-B	1036	TCGGAGTACCAGCTCCCGTACGTCTCGGCTCGGGCGCATCAAGGATGCCCTCCCGCGGTTCACAGACAGC							
hu.29-B	1036	TCGGAGTACCAGCTCCCGTACGTCTCGGCTCGGGCGCATCAAGGATGCCCTCCCGCGGTTCACAGACAGC							
hu.63-B	1036	TCGGAGTACCAGCTCCCGTACGTCTCGGCTCGGGCGCATCAAGGATGCCCTCCCGCGGTTCACAGACAGC							

FIG. 3AP

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

FIG. 3A0

hu. 3-C 1039 TCGGAGTACCAGCTCCCGTACGTCCCGGGCTCGGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 25-C 1036 TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 15-C 1036 TCGGGGTACCAGCTCCCGTACGTCCCTCGGCTTGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCAGACG
hu. 16-C 1036 TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCAGACG
hu. 11-C 1036 TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 10-C 1036 TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 4-C 1036 TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 54-D 1042 TCGGAGTACCAGCTGCCGTACGTCCCTCGGCTCTGCCACACAGGGCTGCCCTGCCCTCCCGCCGTTTCCAGCGGACG
rh. 48-D 1042 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 55-D 1042 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 62-D 1042 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
AAV7-D 1042 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 52-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 51-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 39-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 53-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 37-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 43-E 1042 TCGGAGTACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 50-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 49-E 1045 TCGGAGTACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 61-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 41-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 64-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 42-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 57-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 40-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
AAV8-E 1045 TCGGAGTACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 58-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 40-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 67-E 1045 TCGGAATACCAGCTGCCGTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG

FIG. 3AR

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hu.17-E	1045	TCGGAATACCAAGTCCCGTACGTCCCTGGGCTCTGCGCACCAAGGGCTGCCCGCCTCCGTTCCCGGGGACG	1130	1140	1150	1160	1170	1180	1190
hu.6-E	1045	TCGGAATACCAAGTCCCGTACGTCCCTGGGCTCTGCGCACCAAGGGCTGCCCGCCTCCGTTCCCGGGGACG							
hu.66-E	1045	TCGGAATACCAAGTCCCGTACGTCCCTGGGCTCCGCGCACCAAGGGCTGCCCTGCCCTCCGTTCCCGGGGACG							
rh.38-E	1045	TCGGAATACCAAGTCCCGTACGTCCCTGGGCTCCGCGCACCAAGGGCTGCCCTGCCCTCCGTTCCCGGGGACG							
hu.32-F	1042	TCAGACTATCAGTCCCGTACGTGCTGGGTCGGCTCAGAGGGCTGCCCTCCGCGCTCCAGCGGACG							
AAV9/hu	1042	TCAGACTATCAGTCCCGTACGTGCTGGGTCGGCTCAGAGGGCTGCCCTCCGCGCTCCAGCGGACG							
hu.31-F	1042	TCAGACTATCAGTCCCGTACGTGCTGGGTCGGCTCAGAGGGCTGCCCTCCGCGCTCCAGCGGACG							
									
AAV5	1079	TCATTACGCTGCCGACGTACGGTTACGCGACGCTGAACCGGAC--AACACAGAAATCCACCGAGAG							
AAV3-3	1106	TCTTCATGGTCCCTCAGTATGATACCTCACCTGAACAACGGA--AGTCAAGCGGTGGGACG							
AAV4-4	1079	TCTTTATGGTGCCCGACGTACGGCTACTGTGGACTGGTGACCGCAACACTTCGCAGCAACAGACTGACAG							
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	TGTTTCATGATTCCGCAATACGGCTACCTAACGCTCAACAATGGC--AGCCAGGCAGTAGGACG							
hu.34-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGAG--AGTCAGGCAGTAGGACG							
hu.47-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.29-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.63-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.56-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.45-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.57-B	1103	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.35-B	1106	TCTTCATGGTACCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.58-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.28-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							
hu.51-B	1106	TCTTCATGGTGCCACAGTATGGATACCTCACCTGAACAACGGG--AGTCAGGCAGTAGGACG							

FIG. 3A5

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

FIG. 3AT

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rh.54-D	1112	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGACG
rh.48-D	1112	TCTTCATGATTCCCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTCG
rh.55-D	1112	TCTTCATGATTCCCCAGTACGGCTACCTGACTCTGAACAATGGC-----AGCCAATCGGTGGGTCG
rh.62-D	1112	TCTTCATGATTCCCCAGTACGGCTACCTGACTCTGAACAATGAC-----AGCCAATCGGTGGGTCG
AAV7-D	1112	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAATGGC-----AGTCAGTCTGTGGGACG
rh.52-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCCCAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.51-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
hu.39-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.53-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
hu.37-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
rh.43-E	1112	TGTTTCATGATTCCCCAGTACGGCTACCTAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.50-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.49-E	1115	TCTTCATGATTCCCTCAGTACGGCAACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.61-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
hu.41-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
rh.64-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
hu.42-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
rh.57-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
hu.40-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
AAV8-E	1115	TGTTTCATGATTCCCCAGTACGGCTACCTAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.58-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCCGTGGGACG
rh.40-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
hu.67-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
hu.17-E	1115	TCTTCATGATTCCCTCAGTACGGGTACCTGACTCTGAACAACGGC-----AGTCAGGCCCGTGGGCCG
hu.6-E	1115	TCTTCATGATTCCCTCAGTACGGGTACCTGACTCTGAACAACGGC-----AGTCAGGCCCGTGGGCCG
hu.66-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
rh.38-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGGCCGTAGGCCG
hu.32-F	1112	TTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAATGATGG-----AGCCAGGCCCGTGGGTCG
AAV9/hu	1112	TTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAATGATGGA-----AGCCAGGCCCGTGGGTCG
hu.31-F	1112	TTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAATGATGGA-----GGCCAGGCCCGTGGGTCG

FIG. 3AU

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	1200	1210	1220	1230	1240	1250	1260
							
AAV5	1146	GAGCAGCTTCTTCTGCTAGAGTACTTCCACGCAAGATGCTGAGAACGGGCAACAACCTTTGAGTTTACC					
AAV3-3	1167	CTCATCCTTTTACTGCCCTGGAGTACTTCCCTTCGCAGATGCTAAGGACTGGAAATAAATTTCCAAATTCAGC					
AAV4-4	1149	AAATGCCCTTCTACTGCCCTGGAGTACTTCCCTTCGCAGATGCTGCGGACTGGCAACAACCTTTGAAATTACG					
AAV1-A	1170	TTCATCCTTTTACTGCCCTGGAAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC					
hu.46-A	1170	TTCATCCTTCTACTGCCCTGGAAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC					
hu.48-A	1170	TTCATCCTTTTACTGCCCTGGAAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC					
hu.44-A	1170	TTCATCCTTTTACTGCCCTGGAAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC					
hu.43-A	1173	TTCATCCTTTTACTGCCCTGGAAATATTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTACCTTCAGC					
AAV6-A	1170	GTCATCCTTTTACTGCCCTGGAAATATTTCCCATCGCAGATGCTGAGAACGGGCAATAAATTTACCTTCAGC					
hu.34-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.47-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.29-B	1167	CTCTTCATTTTACTGCCCTAGGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.63-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.56-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTTCGCACCGGAAACAACCTTTACCTTCAGC					
hu.45-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.57-B	1164	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC					
hu.35-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.58-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.28-B	1167	CTCTTCATTTTACTGCCCTAGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.51-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.19-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC					
hu.49-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC					
hu.52-B	1167	CTCTTCATTTTACTGCCCGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.13-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
AAV2-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC					
hu.20-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC					
hu.24-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC					

FIG. 3AV

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hu. 64-B	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCTACCGGAAACAACATTACCTTCAGC
hu. 27-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 21-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 22-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGACGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 23-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 7-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 61-C	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
rh. 56-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 9-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 54-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 53-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 60-C	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 55-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 2-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 1-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 18-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 3-C	1170	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 25-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 15-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 16-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 11-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 10-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
hu. 4-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACATTACCTTCAGC
rh. 54-D	1173	TTCATCCCTTCTACTGCCCTGGAAATACTTCCCTTCTCAGGTGCTGAGAACGGGTAACAACCTTCACCTTCAGT
rh. 48-D	1173	TTCCCTCTTCTACTGCCCTGGAAATATTTCCCTTCTCAAATGCTGAGAACGGGCAACAACCTTCACCTTCAGC
rh. 55-D	1173	TTCCCTCTTCTACTGCCCTGGAAATATTTCCCTTCTCAAATGCTGAGAACGGGCAACAACCTTCACCTTCAGC
rh. 62-D	1173	TTCCCTCTTCTACTGCCCTGGAAATATTTCCCTTCTCAAATGCTGAGAACGGGCAACAACCTTCACCTTCAGC
AAV7-D	1173	TTCCCTCTTCTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTCAGTTCAGC
rh. 52-E	1176	TTCCCTCTTCTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTCCTTCAGC
rh. 51-E	1176	TTCCCTCTTCTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGAGAACGGGCAACAACCTTTCCTTCAGC

FIG. 3AW

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hu.39-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC	1270	1280	1290	1300	1310	1320	1330
rh.53-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
hu.37-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.43-E	1173	CTCCCTCCCTTCTACTGCGCTGGAAATACTTTCCCTTCCGAGATGCTGAGAACCGGCAACAACCTTCCAGTTTACT							
rh.50-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
rh.49-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
rh.61-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
hu.41-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.64-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
hu.42-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.57-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
hu.40-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTCTGAATTCAGC							
AAV8-E	1176	CTCCCTCCCTTCTACTGCGCTGGAAATACTTTCCCTTCCGAGATGCTGAGAACCGGCAACAACCTTCCAGTTTACT							
rh.58-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTCCCTCTCAGATGCTGAGAACGGGCAACAACCTTTTCCTTCAGC							
rh.40-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.67-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.17-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTTCCCTTCTCAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.6-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTTCCCTTCTCAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.66-E	1176	TTCCCTCCCTTCTACTGCGCTGGAGTACTTTCCCTTCTCAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
rh.38-E	1176	TTCCCTCCCTTCTACTGCGCTGGAAATATTTCCATCTCAAAATGCTGCGAACTGGAACAATTTTGAATTCAGC							
hu.32-F	1173	TTCGTCCCTTTTACTGCGCTGGAAATATTTCCCGTCCGAAATGCTAAGAACGGGTAACAACCTTCCAGTTCAGC							
AAV9/hu	1173	TTCGTCCCTTTTACTGCGCTGGAAATATTTCCCGTCCGAAATGCTAAGAACGGGTAACAACCTTCCAGTTCAGC							
hu.31-F	1173	TTCGTCCCTTTTACTGCGCTGGAAATATTTCCCGTCCGAAATGCTAAGAACGGGTAACAACCTTCCAGTTCAGC							
AAV5	1216	TACAACCTTTGAGGAGGTGCCCTTCCACTCCAGCTTCGCTCCAGTCAGAACCTGTTCAGAGCTGGCCAAACC							
AAV3-3	1237	TATACCTTCGAGGATGTACCTTTTTCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGCTTGATGAATC							
AAV4-4	1219	TACAGTTTTCAGAAAGGTGCCCTTTTCCACTCGATGTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAACC							
AAV1-A	1240	TACACCTTTGAGGAAGTGCCCTTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC							

FIG. 3A

hu. 46-A 1240 TACACCTTTGAGGAAGTGCCCTCTCCACAGCAGCTGCGGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 48-A 1240 TACACCTTTGAGGAAGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 44-A 1240 TACACCTTTGAGGAAGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 43-A 1243 TACACCTTTGAGGAAGTGCCCTCTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
AAV6-A 1240 TACACCTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAATC
hu. 34-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGCCGCTCATGAATC
hu. 47-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 29-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 63-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 56-B 1237 TACACTTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 55-B 1237 TACACTTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGTCAAAGTCTGGACCGTCTCATGAATC
hu. 45-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 57-B 1234 TACACTTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGTCAAAGTCTGGACCGTCTCATGAATC
hu. 35-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGCCCGTCTCATGAATC
hu. 58-B 1237 TACACCTTTGAGGATGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 28-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 51-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCGGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 19-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 49-B 1237 TACACCTTTGAGGATGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 52-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 13-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
AAV2-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 20-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 24-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 64-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGTCTCATGAATC
hu. 27-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACGGCCAAAGTCTGGACCGTCTCATGAATC
hu. 21-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 22-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 23-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 7-C 1237 TACACCTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 61-C 1237 TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC

FIG. 3AY

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rh. 56-C	1237	TACACCTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 9-C	1237	TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAATC
hu. 54-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGGGTTTGGATCGGCTGATGAATC
hu. 53-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 60-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 55-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAATC
hu. 2-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 1-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 18-C	1237	TACACCTTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGCTGAATC
hu. 3-C	1240	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 25-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 15-C	1237	TACACCTTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 16-C	1237	TACACCTTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
hu. 11-C	1237	TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAATC
hu. 10-C	1237	TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAATC
hu. 4-C	1237	TACACTTTTGAAGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
rh. 54-D	1243	TACACCTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC
rh. 48-D	1243	TACACCTTCGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGGCTGATGAATC
rh. 55-D	1243	TACACCTTCGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGGCTGATGAATC
rh. 62-D	1243	TACACCTTCGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGGCTGATGAATC
AAV7-D	1243	TACAGCTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGGCTGATGAATC
rh. 52-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
rh. 51-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
hu. 39-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
rh. 53-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
hu. 37-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
rh. 43-E	1243	TACACCTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGGCTGATGAATC
rh. 50-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
rh. 49-E	1246	TACACTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC
rh. 61-E	1246	TACCTTTTCGAGGACGTTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACAGGCTGATGAATC

FIG. 3A2

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hu. 41-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC	1340	1350	1360	1370	1380	1390	1400
rh. 64-E	1246	TACACTTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC							
hu. 42-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
rh. 57-E	1246	TACACTTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC							
hu. 40-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
AAV8-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGCTTGGACCGGCTGATGAATC							
rh. 58-E	1246	TACACTTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC							
rh. 40-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGCTTGGACCGACTGATGAATC							
hu. 67-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGCTTGGACCGGCTGATGAATC							
hu. 17-E	1246	TACCAGTTTGAGGACGTGCCCTTTCACAGCAGCTACGCGCATAGCCAAAGCCTGGACCGGCTGATGAACC							
hu. 6-E	1246	TACCAGTTTGAGGACGTGCCCTTTCACAGCAGCTACGCGCATAGCCAAAGCCTGGACCGGCTGATGAACC							
hu. 66-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTGCGCACACAGCCAGAGCTCGGACCGACTGATGAATC							
rh. 38-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
hu. 32-F	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATC							
AAV9/hu	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATC							
hu. 31-F	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATC							
									
AAV5	1286	CGCTGGTGGACCACTACTTGTACCGCTTCGTGAGCACAAAT-----AACACTGG							
AAV3-3	1307	CTCTTATTGATCAGTATCTGTACTACCTGAACAGAACGCAAGGAACAACCTCTGGAACAACCAACCAATC							
AAV4-4	1289	CTCTCATCGACCACTACCTGTGGGACTGCAATCGACCAACCACCGGAACCACTGAATGCCGGACTGC							
AAV1-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAAACAA							
hu. 46-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAAACAG							
hu. 48-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAAACAA							
hu. 44-A	1310	CTCTCATCGACCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAAACAA							
hu. 43-A	1313	CTCTCATCGTCCAATACCTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAAACAA							
AAV6-A	1310	CTCTCATCGACCACTACCTGTATTACCTGAACAGAACTCAG--AATCAGTCCGGAAGTGCCCAAAACAA							
hu. 34-B	1307	CTCTCATCGACCACTACCTGTATTACCTGAGCAGAAACAAAC---ACTCCAAGTGAACCAACCAACGAGTC							
hu. 47-B	1307	CTCTCATCGACCACTACCTGTATTACCTGAGCAGAAACAAAC---ACTCCAAGTGAACCAACCAACGAGTC							

FIG. 3BA

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hu.29-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCAACGACGAGTC
hu.63-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCAACGACGAGTC
hu.56-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCAACTACGACGTC
hu.45-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.57-B 1304 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCACTACGACGTC
hu.35-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.58-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCAACGACGAGTC
hu.28-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCAACGACGAGTC
hu.51-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.19-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.49-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGCGGAACCAACGACGAGTC
hu.52-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.13-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
AAV2-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.20-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.24-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.64-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.27-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.21-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.22-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.23-B 1307 CTCATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACTCCAAGTGGAACCAACGACGAGTC
hu.7-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.61-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACAAATAGTGGAACCTCTTCAGCAGTC
rh.56-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.9-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.54-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACAGCTAGTGGAACCT---CAGCAGTC
hu.53-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACAGCTAGTGGAACCT---CAGCAGTC
hu.60-C 1307 CTCGGTCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACAAATAGTGGAACCTCTTCAGCAGTC
hu.55-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACAGCTAGTGGAACCT---CAGCAGTC
hu.2-C 1307 CTCGATCGACCAGTACCTGTATTACTTGAGCAGAACAAAC---ACAAATAGTGGAACCTCTTCAGCAGTC

FIG. 3BB

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hu.1-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACCTCTTCAGCAGTC
hu.18-C	1307	CTCTGATCGACCAGTACCTATATTATCTGAACAAGACACAA---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.3-C	1310	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACCTCTTCAGCAGTC
hu.25-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACCTCTTCAGCAGTC
hu.15-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.16-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.11-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.10-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---TCAAATAGTGGAACCTCTTCAGCAGTC
hu.4-C	1307	CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA---ACAAATAGTGGAACCTCTTCAGCAGTC
rh.54-D	1313	CCCTCATCGACCAGTACCTGTATTACCTGGCTAGAACACAGAGTAACCCAGGAGGCACATCTTGGCAATCG
rh.48-D	1313	CTCTTATCGACCAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGCGAGGAGGCACAGCTGGCAATCG
rh.55-D	1313	CTCTTATCGACCAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGCGAGGAGGCACAGCTGGCAATCG
rh.62-D	1313	CTCTTATCGACCAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGCGAGGAGGCACAGCTGGCAATCG
AAV7-D	1313	CCCTCATCGACCAGTACCTGTACTACCTGGCCAGAACACAGAGTAACCCAGGAGGCACAGCTGGCAATCG
rh.52-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
rh.51-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
hu.39-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
rh.53-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
hu.37-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
rh.43-E	1313	CTCTGATTGACCAGTACCTGTACTACTTGTCTCGGACTCAAAACA---ACAGGAGGCACGGCAATACGCA
rh.50-E	1316	CTCTCGTCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
rh.49-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
rh.61-E	1316	CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA
hu.41-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
rh.64-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCT---ACGGAGGCACAGCGGGAACCCA
hu.42-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
rh.57-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCT---ACGGAGGCACAGCGGGAACCCA
hu.40-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC---ACAGGAGGAACCTCAAGGTACCCA
AAV8-E	1316	CTCTGATTGACCAGTACCTGTACTACTTGTCTCGGACTCAAAACA---ACAGGAGGCACGGCAATACGCA
rh.58-E	1316	CTCTCATCGACCAGTACCTGTACTACTTGTCTCAAGAACCCAGTCT---ACGGAGGCACAGCGGGAACCCA

FIG. 3BC

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rh. 40-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA	1410	1420	1430	1440	1450	1460	1470
hu. 67-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA							
hu. 17-E	1316	CCCTCATCGACCAGTACCTGTACTACTACCTGTCTCGGACTCAGTCC--ACGGGAGGTACCGCAGGAACTCA							
hu. 6-E	1316	CCCTCATCGACCAGTACCTGTACTACTACCTGTCTCGGACTCAGTCC--ACGGGAGGTACCGCAGGAACTCA							
hu. 66-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCGGTCC--ACAGGAGGAACTCAAGGTACCCA							
rh. 38-E	1316	CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA							
hu. 32-F	1313	CACTCATCGACCAATACTTGTAATACTCTCAAGACTATTAAACGGTTCTGGA-----CAGAAATCAACA							
AAV9/hu	1313	CACTCATCGACCAATACTTGTAATACTCTCAAGACTATTAAACGGTTCTGGA-----CAGAAATCAACA							
hu. 31-F	1313	CACTCATCGACCAATACTTGTAATACTCTCAAGACTATTAAACGGTTCTGGA-----CAGAAATCAACA							

AAV5	1335	CGGAGTCCAGTTCAACAAGAACCTGGCCGGGAGATACGCCAACACCTACAAAACCTGGTCCCGGGGCC	
AAV3-3	1377	ACGGCTGCTTTTAGCCAGGCTGGGCTCAGTCTATGTCTTTGCAGGCCAGAAATTGGCTACCTGGGCC	
AAV4-4	1359	CACCACCAACTTTACCAAGCTGCGGCTACCAACTTTTCCAACTTTAAAGAACTGGCTGCCCGGGCCT	
AAV1-A	1377	GGACTTGCTGTTAGCCGCTGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAACCTGGCTACCTGGACCC	
hu. 46-A	1377	GGACTTGCTGTTAGCCGCTGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAACCTGGCTACCTGGACCC	
hu. 48-A	1377	GGACTTGCTGTTAGCCGCTGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAACCTGGCTACCTGGACCC	
hu. 44-A	1377	GGACTTGCTGTTAGCCGCTGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAACCTGGCTACCTGGACCC	
hu. 43-A	1380	GGACTTGCTGTTAGCCGCTGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAACCTGGCTACCTGGACCC	
AAV6-A	1377	GGACTTGCTGTTAGCCGCTGGTCTCCAGCTGGCATGTCTGTTTCAGCCCAAAAACCTGGCTACCTGGACCC	
hu. 34-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 47-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 29-B	1374	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 63-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 56-B	1374	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 45-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 57-B	1371	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 35-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAAGTCTAGGAACTGGCTTCTCTGGACCC	
hu. 58-B	1374	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCGGGATCAGTCTAGGAACTGGCTTCTCTGGACCC	

FIG. 3BD

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hu.28-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTTCAGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.51-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.19-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGAAACCTGGCTTCCTGGACCC
hu.49-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.52-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.13-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
AAV2-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.20-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.24-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.64-B 1374 AAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.27-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.21-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.22-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.23-B 1374 CAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTTCGGGACCAGTCTAGGAACCTGGCTTCCTGGACCC
hu.7-C 1374 TCGGCTACTGTTTAGTCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.61-C 1374 TCGGCTACTGTTTAGCCTAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
rh.56-C 1374 TCGGCTACTGTTTAGTCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.9-C 1374 TAGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.54-C 1371 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.53-C 1371 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.60-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.55-C 1371 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.2-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.1-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.18-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.3-C 1377 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.25-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.15-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.16-C 1374 TCGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT
hu.11-C 1374 TAGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACCTGGCTACCTGGACCT

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hu.10-C	1374	TAGGCTACTGTTTAGCCAAGCTGGACCCACCAAGCATGTCTCTTCAAGCTAAAAACTGGCTGCCCTGGACCT
hu.4-C	1374	TCGGCTACTGTTTAGCCAAGCTGGACCAACCAACATGTCTCTTCAAGCTAAAAACTGGCTGCCCTGGACCT
rh.54-D	1383	GGAACCTGCAGTTTACCAGGGCGGGCCTTCCACCATGGCCGAACAAGCCAAAGAACTGGTTACCTGGACCT
rh.48-D	1383	GGAACCTGCAGTTTATCAGGGCGGGCCTACCACCATGGCCGAACAAGCCAAAGAACTGGCTGCCCTGGACCT
rh.55-D	1383	GGAACCTGCAGTTTATCAGGGCGGGCCTACCACCATGGCCGAACAAGCCAAAGAACTGGCTGCCCTGGACCT
rh.62-D	1383	GGAACCTGCAGTTTATCAGGGCGGGCCTACCACCATGGCCGAACAAGCCAAAGAACTGGCTGCCCTGGACCT
AAV7-D	1383	GGAACCTGCAGTTTACCAGGGCGGGCCTTCAACTATGGCCGAACAAGCCAAAGAACTGGTTACCTGGACCT
rh.52-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh.51-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu.39-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh.53-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu.37-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh.43-E	1380	GACTCTGGGCTTCAGCCCAAGGTGGGCCCTAATACAAATGGCCAATCAGGCAAGAACTGGCTGCCAGGACCC
rh.50-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh.49-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh.61-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu.41-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh.64-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu.42-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh.57-E	1383	GCAGTTGCTGTCTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu.40-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
AAV8-E	1383	GACTCTGGGCTTCAGCCCAAGGTGGGCCCTAATACAAATGGCCAATCAGGCAAGAACTGGCTGCCAGGACCC
rh.58-E	1383	GCAGCTGCTGTTTCTCAGGCCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh.40-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu.67-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu.17-E	1383	GCAGTTGCTATTTTCTCAGGCCCGGGCCTAATAACATGTGGCTCAGGCCAGAAACTGGCTACCCGGGCCC
hu.6-E	1383	GCAGTTGCTATTTTCTCAGGCCCGGGCCTAATAACATGTGGCTCAGGCCAGAAACTGGCTACCCGGGCCC
hu.66-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh.38-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCCTGCAAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu.32-F	1377	AACGCTAAAAATTCAGCGTGGCCCGGACCCAGCAACATGGCTGTCCAGGGAAGAAACTACATACCTGGACCC

FIG. 3B

AAV9/hu	1377	AACGCTAAATTCAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC	1480	1490	1500	1510	1520	1530	1540
hu.31-F	1377	AACGCTAAATTCAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC							
									
AAV5	1405	ATGGGCCGAACCCAGGGCTGGAACCTGGGCTCCGGGGTCAAC-----CGCGCCAGTGTCA							
AAV3-3	1447	TGCTACCGGCAACAGAGACTTTCAAAGACTGCTAACGACAAC-----AACAACAGTAACT							
AAV4-4	1429	TCAATCAAGCAGCAGGGCTTCTCAAAGACTGCCAATCAAACCTACAAGATCCCTGCCACCGGTCAGACA							
AAV1-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAAAACAGACAAC-----AACAACAGCAATT							
hu.46-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAAAACAGACAAC-----AACAACAGCAATT							
hu.48-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAAAACAGACAAC-----AACAACAGCAATT							
hu.44-A	1447	TGTTATCGGCAGCAGCGCGTTTCTAAACAAAAACAGACAAC-----AACAACAGCAATT							
hu.43-A	1450	TGTTATCGGCAGCAGCGCGTTTCTAAACAAAAACAGACAAC-----AACAACAGCAATT							
AAV6-A	1447	TGTTACCGGCAGCAGCGCGTTTCTAAACAAAAACAGACAAC-----AACAACAGCAACT							
hu.34-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.47-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.29-B	1444	TGTTACCGTCAAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.63-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.56-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.45-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.57-B	1441	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACGGTGAAT							
hu.35-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.58-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.28-B	1444	TGTTACCGTCAAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.51-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.19-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.49-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.52-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
hu.13-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							
AAV2-B	1444	TGTTACCGGCAGCAGCGAGTATCAAAGACATCTCGGGATAAC-----AACAACAGTGAAT							

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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	TGTTACCGCCAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 61-C	1444	TGTTACCGCCAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
rh. 56-C	1444	TGTTACCGCCAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 9-C	1444	TGTTACCGCCAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 54-C	1441	TGTTATCGCCAGCAGCGTTTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 53-C	1441	TGTTATCGCCAGCAGCGTTTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 60-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 55-C	1441	TGTTATCGCCAGCAGCGTTTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 2-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 1-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 18-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 3-C	1447	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAT	-----AACAACTGCAACT
hu. 25-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 15-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 16-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 11-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 10-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
hu. 4-C	1444	TGTTACGAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAACT
rh. 54-D	1453	TGTTCCGGCAACAAGAGTTTCCAAACACTGGATCAAAAC	-----AACAAACAGCAACT
rh. 48-D	1453	TGTTCCGGCAACAAGAGTTTCCAAACACTGGATCAAAAC	-----AACAAACAGCAACT
rh. 55-D	1453	TGTTCCGGCAACAAGAGTTTCCAAACACTGGATCAAAAC	-----AACAAACAGCAACT
rh. 62-D	1453	TGTTCCGGCAACAAGAGTTTCCAAACACTGGATCAAAAC	-----AACAAACAGCAACT
AAV7-D	1453	TGTTCCGGCAACAAGAGTTTCCAAACACTGGATCAAAAC	-----AACAAACAGCAACT

FIG. 3BH

rh. 52-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC	1550	1560	1570	1580	1590	1600	1610
rh. 51-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
hu. 39-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC	1460	GCGCCTTCGCCACGACCAATAGGATGGAGCTCGAGGGCGCGAGTTACCAGGTGCCCCCGCAGCCGAACGG					
rh. 53-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC	1502	TTTCCTTGGACAGCGGCCAGCAATAATCATCTCAATGGCCGCGACTCGCTGGTGAATCCAGGACCAGCTAT					
hu. 37-E	1453	TGCTACCGGACGAGCGAGTCTTACGACACTGTCGCAAAC							
rh. 43-E	1450	TGTTACCGCCAACACGCGTCTCAACGACAACCGGGCAAAC							
rh. 50-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
rh. 49-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
rh. 61-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
hu. 41-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
rh. 64-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
hu. 42-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
rh. 57-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
hu. 40-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
AAV8-E	1453	TGTTACCGCCAACACGCGTCTCAACGACAACCGGGCAAAC							
rh. 58-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTCGCAAAC							
rh. 40-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
hu. 67-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
hu. 17-E	1453	TGCTACCGGACGACGCGTCTCCACGACACTGTCGCAAAT							
hu. 6-E	1453	TGCTACCGGACGACGCGTCTCCACGACACTGTCGCAAAT							
hu. 66-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
rh. 38-E	1453	TGCTACCGGACGAGTCTTACGACACTGTCGCAAAC							
hu. 32-F	1447	AGCTACCGACAACACGTGTCTCAACCACTGTGACTCAAAC							
AAV9/hu	1447	AGCTACCGACAACACGTGTCTCAACCACTGTGACTCAAAC							
hu. 31-F	1447	AGCTACCGACAACACGTGTCTCAACCACTGTGACTCAAAC							

FIG. 3B1

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AAV4-4 1499 GTCTCATCAAATACGAGACGCACAGCACTCTGGACGGAAGATGGAGTGCCCTGACCCCCGGACCTCCAAT
AAV1-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAAATCCATCATCAACCTTGGCACTGCTAT
hu.46-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAAATCCATCATCAACCTTGGCACTGCTAT
hu.48-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAAATCCATCATCAACCTTGGCACTGCTAT
hu.44-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAAATCCATCATCAACCTTGGCACTGCTAT
hu.43-A 1505 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAAATCCATCATCAACCTTGGCACTGCTAT
AAV6-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTTAAATGGCGTGAAATCTATAATCAACCTTGGCACTGCTAT
hu.34-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.47-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.29-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.63-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTTAAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.56-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.45-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.57-B 1496 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.35-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.58-B 1499 ACTCGTGGATTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCAAT
hu.28-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.51-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.19-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT
hu.49-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.52-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.13-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
AAV2-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.20-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT
hu.24-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT
hu.64-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTTAAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCGGCCAT
hu.27-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT
hu.21-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT
hu.22-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT
hu.23-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGTGTAATCCGGGCCCCAGCTAT

FIG. 3B

hu. 7-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCACCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 61-C 1499 TTCCCTGGACCGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
rh. 56-C 1499 TTCCCTGGACTGCGGCTACAAAGTACCACTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 9-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 54-C 1496 TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCGGAGACTCTTTGGTGAACCCGGGCCCGCCAT
hu. 53-C 1496 TTCCCTGGACTGGAGCTACCAAGTACTACCTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGCCAT
hu. 60-C 1499 TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 55-C 1496 TTCCCTGGACTGCAGCTACCAAGTACCACTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGCCAT
hu. 2-C 1499 TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 1-C 1499 TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 18-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 3-C 1502 TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 25-C 1499 TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 15-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 16-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 11-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCGTCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 10-C 1499 TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 4-C 1499 TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGGCCGGGACTCGTTGGTTAATCCAGGACCAGCTAT
rh. 54-D 1508 TTGCTTGGACTGGTGCCACCAAAATATCACCTGAACGGCAGAAACTCATTTGGTGAATCCTGGTGCGCCAT
rh. 48-D 1508 TTGCTTGGACTGGTGCCACCAAAATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTCGCCAT
rh. 55-D 1508 TTGCTTGGACTGGTGCCACCAAAATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTCGCCAT
rh. 62-D 1508 TTGCTTGGACTGGTGCCACCAAAATACCATCTAAATGGAAGAAATTCATTTGGTTAATCCCGGTGTCGCCAT
AAV7-D 1508 TTGCTTGGACTGGTGCCACCAAAATATCACCTGAACGGCAGAAACTCGTTGGTTAATCCCGGTGTCGCCAT
rh. 52-E 1508 TTGCTTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTCGCCAT
rh. 51-E 1508 TTGCTTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTCGCCAT
hu. 39-E 1508 TTGCTTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTCGCCAT
rh. 53-E 1508 TTGCTTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTCGCCAT
hu. 37-E 1508 TTGCTTGGACTGGTGCCACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT
rh. 43-E 1505 TTGCTTGGACTGGTGCCACCAAAATACCATCTGAATGGAAGAAATTCATTTGGCTAATCCTGGCATCGCTAT
rh. 50-E 1508 TTGCTTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTCGCCAT

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rh. 49-E	1508	TTGCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCGCCAT	1620	1630	1640	1650	1660	1670	1680
rh. 61-E	1508	TTGCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCGCCAT							
hu. 41-E	1508	TTGCTTGGACTGGTGCCACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT							
rh. 64-E	1508	TTGCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCGCCAT							
hu. 42-E	1508	TTGCTTGGACTGGTGCCACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT							
rh. 57-E	1508	TTGCCTGGACTGGTGCCACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCCGGTGTCGCCAT							
hu. 40-E	1508	TTGCTTGGACTGGTGCCACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT							
AAV8-E	1508	TTGCCTGGACTGGTGGACCAAAATACCATCTGAATGGAAGAAATTCATTTGGCTAATCCTGGCATCGCTAT							
rh. 58-E	1508	TTGCCTGGACTGGTGGACCAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGGCGTCGCCAT							
rh. 40-E	1508	TTGCTTGGACTGGTGGACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCTAT							
hu. 67-E	1508	TTGCTTGGACTGGTGGACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT							
hu. 17-E	1508	TTGCTTGGACCGGTGCCACCAAGTATCATCTGAATGGCAGAGACTCTCTGGTAAATCCCGGTGTCGCTAT							
hu. 6-E	1508	TTGCTTGGACCGGTGCCACCAAGTATCATCTGAATGGCAGAGACTCTCTGGTAAATCCCGGTGTCGCTAT							
hu. 66-E	1508	TTGCTTGGACTGGTGGACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT							
rh. 38-E	1508	TTGCTTGGACTGGTGGACCAAAATATCACCTGAACGGAAAGAGACTCTTTGGTAAATCCCGGTGTCGCCAT							
hu. 32-F	1502	TTGCTTGGCCTGGAGCTTCTTTGGGCTCTCAATGGACGTAATAGCTTGATGAATCCTGGACCTGCTAT							
AAV9/hu	1502	TTGCTTGGCCTGGAGCTTCTTTGGGCTCTCAATGGACGTAATAGCTTGATGAATCCTGGACCTGCTAT							
hu. 31-F	1502	TTGCTTGGCCTGGAGCTTCTTTGGGCTCTCAATGGACGTAATAGCTTGATGAATCCTGGACCTGCTAT							

AAV5	1530								
AAV3-3	1572	CATGACCAACAACCTCCAGGGCAGCAACACCTATGCCCTGGAGAACAATATGATCTTCAACAGCCAGCCG							
AAV4-4	1569	GGCCAGTCACAAGGACGATGAAGAAAATTTTCCCTATGCACGGCAATCTAATATTGGCAAAGAAAGG							
AAV1-A	1572	GGCCACGGCTGGACCTGCGGACAGCAAGTTTCAGC--AACAGCCAGCTCATCTTTGCGGGGCTAAACAG							
hu. 46-A	1572	GGCTCACACAAGACGACGAAAGCAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 48-A	1572	GGCTCACACAAGACGACGAAAGCAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 44-A	1572	GGCTCACACAAGACGACGAAAGCAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
hu. 43-A	1575	GGCTCACACAAGACGACGAAAGCAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							
AAV6-A	1572	GGCTCACACAAGACGACGAAAGCAAGTTCTTTCCCATGAGCGGTGTCATGATTTTGGAAAAGAGAGC							

FIG. 3BL

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hu. 34-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 47-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 29-B 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 63-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 56-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 45-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 57-B 1566 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAAAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 35-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 58-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGGA
hu. 28-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 51-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 19-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 49-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAAAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 52-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 13-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
AAV2-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGGAAGCAAGGC
hu. 20-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 24-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 64-B 1569 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 27-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 21-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 22-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 23-B 1569 GGCCAGCCACAAGGACGATGAAGAAAATAATTTTCCCTCAGAGCGGGTTCATCTTTGGAAAACAAGAC
hu. 7-C 1569 GGCCAGTCACAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTGATAATTTGGTAAACAAGGA
hu. 61-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTTATAATTTGGTAAACAAGGA
rh. 56-C 1569 GGCCAGTCACAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTGATAATTTGGTAAACAAGGA
hu. 9-C 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTGATAATTTGGTAAACAAGGA
hu. 54-C 1566 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTAATAATTTGGTAAAGAAGGA
hu. 53-C 1566 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTAATAATTTGGTAAAGAAGGA
hu. 60-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTTCCCATGCATGGAAACCCCTTATAATTTGGTAAACAAGGA

FIG. 3BM

hu. 55-C 1566 GGCCAGCCACAAGGACGATGAAGAAAGTTTCCCATGCAATGGAACCCCTAATATTTGGTAAAGAGGA
hu. 2-C 1569 GGCCAGTCACAAGGATGACGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 1-C 1569 GGCCAGTCACAAGGATGACGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 18-C 1569 GGCCAGCCACAAGACGATGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 3-C 1572 GGCCAGTCACAAGGATGACGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 25-C 1569 GGCCAGTCACAAGGATGACGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 15-C 1569 GGCCAGCCACAAGACGATGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 16-C 1569 GGCCAGCCACAAGACGATGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 11-C 1569 GGCCAGCCACAAGACGATGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 10-C 1569 GGCCAGCCACAAGACGATGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 4-C 1569 GGCCAGTCACAAGGATGACGAAGAAAGTTTCCCATGCAATGGAACCCCTGATATTTGGTAAACAAGGA
rh. 54-D 1578 GGCAACTCACAAGGACGACGAGGACCGCTTTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAACTGGA
rh. 48-D 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCTTCGAGCGGAGTCCCTGATTTTGGAAAACTGGA
rh. 55-D 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCTTCGAGCGGAGTCCCTGATTTTGGAAAACTGGA
rh. 62-D 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCTTCGAGCGGAGTCCCTGATTTTGGAAAACTGGA
AAV7-D 1578 GGCAACTCACAAGGACGACGAGGACCGCTTTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAACTGGA
rh. 52-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAACTGGA
rh. 51-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAACTGGA
hu. 39-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAACTGGA
rh. 53-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGAAAACTGGA
hu. 37-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCGTGAGTGGAGTCCCTGATGTTTCGAAAAACAGGGT
rh. 43-E 1575 GGCAACACACAAGACGACGAGGAGCGTTTTCCTGTTTGGCAACAAAT
rh. 50-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGCAAGCAGGGA
rh. 49-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGCAAGCAGGGA
rh. 61-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGCAAGCAGGGA
hu. 41-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCGTGAGTGGAGTCCCTGATGTTTGGAAAAACAGGGT
rh. 64-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTGATTTTGGCAAGCAGGGA
hu. 42-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCGTGAGTGGAGTCCCTGATGTTTGGAAAAACAGGGT
rh. 57-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGAGTCCCTGATGTTTGGCAAGCAGGGA
hu. 40-E 1578 GGCAACCCACAAGGACGACGAGGAAACGCTTCTTCCGTGAGTGGAGTCCCTGATGTTTGGAAAAACAGGGT

FIG. 3B

AAV8-E	1578	GGCAACACAAAGACGACGAGGAGCGT	1690	1700	1710	1720	1730	1740	1750
rh. 58-E	1578	GGCAACCAACAAGACGACGAGGACCGCT							
rh. 40-E	1578	GGCAACGCATAAGACGACGAGGAACGTT							
hu. 67-E	1578	GGCAACCCACAAGACGACGAGGAACGCT							
hu. 17-E	1578	GGCAACGCACAAGACGACGAGAAGCGAT							
hu. 6-E	1578	GGCAACGCACAAGACGACGAGAAGCGAT							
hu. 66-E	1578	GGCAACCCACAAGACGACGAGGAACGCT							
rh. 38-E	1578	GGCAACCCACAAGACGACGAGGAACGCT							
hu. 32-F	1572	GGCCAGCCACAAGAAGGAGAGGACCGTT							
AAV9/hu	1572	GGCCAGCCACAAGAAGGAGAGGACCGTT							
hu. 31-F	1572	GGCCAGCCACAAGAAGGAGAGGACCGTT							
AAV5	1600	GCGAACCCGGCACCCGCCACGTACCTCGAGGGCAACAT							
AAV3-3	1642	ACA-----ACGGCAAGTAACGCAGAA							
AAV4-4	1636	AAC-----GGCAACACGGCCACCGTACCCGGG							
AAV1-A	1642	GCC-----GGAGCTTCAAACACTGCATTGGAC							
hu. 46-A	1642	GCC-----GGAGCTTCAAACACTGCATTGGAC							
hu. 48-A	1642	GCC-----GGAGCTTCAAACACTGCATTGGAC							
hu. 44-A	1642	GCC-----GGAGCTTCAAACACTGCATTGGAC							
hu. 43-A	1645	GCC-----GGAGCTTCAAACACTGCATTGGAC							
AAV6-A	1642	GCC-----GGAGCTTCAAACACTGCATTGGAC							
hu. 34-B	1639	TCA-----GAGAAACAATAATGTGGACATTGAA							
hu. 47-B	1639	TCA-----GAGAAACAATAATGTGGACATTGAA							
hu. 29-B	1639	CCA-----GAGAAACAATAATGTGGATATTGAA							
hu. 63-B	1639	TCG-----GAGAAACAATAATGTGGACATTGAA							
hu. 56-B	1639	TCA-----GAGAAACAATAATGTGGACATTGAA							
hu. 45-B	1639	TCA-----GAGAAACAATAATGTGGACATTGAA							
hu. 57-B	1636	TCA-----GAGAAACAATAATGTGGACATTGAA							

FIG. 3B0

hu.35-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGGA
hu.58-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGAA
hu.28-B 1639 TCA-----GAGAAACAAAATGTGGATATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGGA
hu.51-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGGA
hu.19-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.49-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGAA
hu.52-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGGA
hu.13-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGGA
AAV2-B 1639 TCA-----GAGAAACAAAATGTGGACATTGAA--AAGGTCATGATTACAGACGAAAGAGGAAATCAGGA
hu.20-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.24-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.64-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.27-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.21-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.22-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.23-B 1639 TCG-----GGAAAAACTAATGTGGACATTGAA--AAGGTTATGATTACAGACGAAAGAGGAAATCAGGA
hu.7-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC--AATGTCTATGATTACAGATGAAGAAGAAATCCGCA
hu.61-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
rh.56-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
hu.9-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG--CATGTTATGATTACAGATGAAGAAGAAATCAGGA
hu.54-C 1636 ACA-----AATGCTACCAACGCGGAAATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
hu.53-C 1636 ACA-----AATGCTACCAACGCGGAAATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
hu.60-C 1639 ACA-----AATGCTAACGACGCGGATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
hu.55-C 1636 ACA-----AATGCTACCAACGCGGAAATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
hu.2-C 1639 ACA-----AATGCTAACGACGCGGATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGG
hu.1-C 1639 ACA-----AATGCTAACGACGCGGATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGG
hu.18-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC--AATGTCTATGATTACAGATGAAGAAGAAATCCGCA
hu.3-C 1642 ACA-----AATGCTAACGACGCGGATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGC
hu.25-C 1639 ACA-----AATGCTAACGACGCGGATTGGAA--AATGTCTATGATTACAGATGAAGAAGAAATCAGGA
hu.15-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC--AATGTCTATGATTACAGATGAAGAAGAAATCCGCA

FIG. 3BP

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hu.16-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCATGATTACAGATGAAGAAATCCGCA
hu.11-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG---CATGTTATGATTACAGATGAAGAAATCAGGA
hu.10-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG---CATGTTATGATTACAGATGAAGAAATCAGGA
hu.4-C 1639 ACA-----AATGCTAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAATCAGGG
rh.54-D 1648 GCA-----ACCAAC---AAGACTACACTGGAA---AACGTGTTAATGACAAATGAAGAGAAATTCGTC
rh.48-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGTTAATGACAAATGAAGAGAAATTCGTC
rh.55-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGTTAATGACAAATGAAGAGAAATTCGTC
rh.62-D 1648 GCA-----GCTAAT---AAGACTACACTGGAA---AATGTTAATGACAAATGAAGAGAAATTCGTC
AAV7-D 1648 GCA-----ACTAAC---AAAACACTACATTGGAA---AATGTTAATGACAAATGAAGAGAAATTCGTC
rh.52-E 1648 GCT-----GGAAAAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
rh.51-E 1648 GCT-----GGAAAAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
hu.39-E 1648 GCT-----GGAAAAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
rh.53-E 1648 GCT-----GGAAAAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
hu.37-E 1648 GCT-----GGAAGAGACAAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA
rh.43-E 1642 GCT-----GCCAGAGACAAATGCGGATTACAGC---GATGTCATGCTCACCCAGCGAGGAAATCAATAA
rh.50-E 1648 GCT-----GGAAAAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
rh.49-E 1648 GCT-----GGAAAAGACAACATGGGCTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
rh.61-E 1648 GCT-----GGAAGAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
hu.41-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA
rh.64-E 1648 GCT-----GGAAGAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
hu.42-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA
rh.57-E 1648 GCT-----GGAAGAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
hu.40-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA
AAV8-E 1648 GCT-----GCCAGAGACAATGCGGATTACAGC---GATGTCATGCTCACCCAGCGAGGAAATCAATAA
rh.58-E 1648 GCT-----GGAAGAGACAACGCTGGACTATAGC---AACGTGATGCTAACCCAGCGAGGAAATCAAGA
rh.40-E 1648 GCT-----GGAAGAGACAATGTGGACTATAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA
hu.67-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA
hu.17-E 1648 GCT-----GGAAGAGACAACGCTGGACTATAGC---AGCGTTATGCTAACCCAGTGAGGAAATCAATAA
hu.6-E 1648 GCT-----GGAAGAGACAACGCTGGACTATAGC---AGCGTTATGCTAACCCAGTGAGGAAATCAATAA
hu.66-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAGGAAATTAATAA

FIG. 3BQ

rh. 38-E	1648	GCT-----GGAAGAGACAAATGTGGACTACAGC	---	AGCGTTATGCTAACCAGCGAAGAAATTAAAA
hu. 32-F	1642	ACT-----GGAAGAGACAAACGTGGATGCGGAC	---	AAAGTCATGATAACCAACGAAGAAATTAAAA
AAV9/hu	1642	ACT-----GGAAGAGACAAACGTGGATGCGGAC	---	AAAGTCATGATAACCAACGAAGAAATTAAAA
hu. 31-F	1642	ACT-----GGAAGAGACAAACGTGGATGCGGAC	---	AAAGTCATGATAACCAACGAAGAAATTAAAA
				
AAV5	1670	CGGTGAACCGCGTGGCGTACAACGTCGGCGGCAGATGGCCACCAACCAACAGAGCTCCACCACTGCCCCC		
AAV3-3	1703	CCACCAATCCTGTGGCAACAGAGCAGTATGGAACCTGTGGCAATAAATTAAGTTCAGAGCTCAAATACAGCTCC		
AAV4-4	1697	CCACCAACGCCACCGATACGGACATGTGGGCAACCTACCTGGCGGTGACCAAGCAACAGCAACCTGCC		
AAV1-A	1703	CCACTAACCCCTGTGGCCACCAGAAAGATTGGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCC		
hu. 46-A	1703	CCACTAACCCCTGTGGCCACCAGAAAGATTGGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCC		
hu. 48-A	1703	CCACTAACCCCTGTGGCCACCAGAAAGATTGGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCC		
hu. 44-A	1703	CCACTAACCCCTGTGGCCACCAGAAAGATTGGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCC		
hu. 43-A	1706	CCACTAACCCCTGTGGCCACCAGAAAGATTGGGACCGTGGCAGTCAATTTCCAGAGCAGCAGCACAGACCC		
AAV6-A	1703	CCACTAACCCCGTGGCCACCAGAAAGATTGGGACTGTGGCAGTCAATCTCCAGAGCAGCAGCACAGACCC		
hu. 34-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC		
hu. 47-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC		
hu. 29-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 63-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 56-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 45-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC		
hu. 57-B	1697	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACGAGC		
hu. 35-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC		
hu. 58-B	1700	CCACCAATCCCGTGGCCACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 28-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 51-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTACGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC		
hu. 19-B	1700	CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 49-B	1700	CCACCAATCCCGTGGCCACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC		
hu. 52-B	1700	CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC		

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hu.13-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTGCAGGGCGGCAACACACAAGC
 AAV2-B 1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAGC
 hu.20-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.24-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.64-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.27-B 1700 CCACCAATCCCGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.21-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.22-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.23-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.7-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGATATGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.61-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGATATGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 rh.56-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGATATGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.9-C 1700 CCACCAATCCCTGTGGCTACAGAGCAGTACGGAAACGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.54-C 1697 CCACCAATCCCGTGGCTACAGAGCAGTACGGATATGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.53-C 1697 CCACCAATCCCGTGGCTACAGAGCAGTACGGATATGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.60-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGAACTGTATCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.55-C 1697 CCACCAATCCCGTGGCTACAGAGCAGTACGGATATGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.2-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.1-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.18-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.3-C 1703 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.25-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.15-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.16-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.11-C 1700 CCACCAATCCCTGTGGCTACAGAGCAGTACGGAAACGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.10-C 1700 CCACCAATCCCTGTGGCTACAGAGCAGTACGGAAACGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 hu.4-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAATAAATTTGCAAAACCTCAAATACTGGTCC
 rh.54-D 1706 CTACTAATCCCTGTGGCCACAGAAGAATACGGGATAGTCAGCAGCAATTTACAGCGGCCAATACTGCAGC
 rh.48-D 1706 CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTTAGCAGCAACCTGCAGGGGCTAACACTGCAGC
 rh.55-D 1706 CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTTAGCAGCAACCTGCAGGGGCTAACACTGCAGC

FIG. 3BS

rh. 62-D	1706	CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTTAGCAGCAACCTGCAGGGGCTAACACTGCAGC
AAV7-D	1706	CTACTAATCCTGTAGCCACGGAAGAAATACGGGATAGTCAGCAGCAACTTACAAGCGGCTAATACTACTGCAGC
rh. 52-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 51-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 39-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 53-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 37-E	1709	CCACTAACCCCGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
rh. 43-E	1703	CCACTAACCCCGTAGCCACAGAGGAATACGGTATCGTGGCAGATAAAGTTGCAGCAGCAAAACACGGCTCC
rh. 50-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 49-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 61-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 41-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
rh. 64-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 42-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
rh. 57-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
hu. 40-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
AAV8-E	1709	CCACTAACCCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATAAAGTTGCAGCAGCAAAACACGGCTCC
rh. 58-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAACACCGCTCC
rh. 40-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAGCCAAATACAGGGCC
hu. 67-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
hu. 17-E	1709	CCACCAACCCAGTGGCCACAGAACAGTACGGCTGGTGGCGGATAACCTGCAACAGCAAAACGCCGCTCC
hu. 6-E	1709	CCACCAACCCAGTGGCCACAGAACAGTACGGCTGGTGGCGGATAACCTGCAACAGCAAAACGCCGCTCC
hu. 66-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
rh. 38-E	1709	CCACTAACCCCTGTAGCCACAGAACAAATACGGTGGTGGCTGACAAACTTGCAGCAAAACCAATACAGGGCC
hu. 32-F	1703	CTACTAACCCCGTAGCAACGGAGTCCCTATGGACAAGTGGCCACAACCAACAGAGTGCCCAAGCACAGGC
AAV9/hu	1703	CTACTAACCCCGTAGCAACGGAGTCCCTATGGACAAGTGGCCACAACCAACAGAGTGCCCAAGCACAGGC
hu. 31-F	1703	CTACTAACCCCGTAGCAACGGAGTCCCTATGGACAAGTGGCCACAACCAACAGAGTGCCCAAGCACAGGC

.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|

AAV5 1740 CGCGACCGGCACGTACAACCTCCAGGAAATCGTGCCCGGCAGCGTGTGGATGGAGAGGGACGTGTACCTC
AAV3-3 1773 CACGACTGGAACTGTCAATCATCAGGGGGCCCTTACCTGGCATGGTGTGGCAAGATCGTGACGTGTACCTT
AAV4-4 1767 GACCGTGGACAGACTGACAGCCCTTGGGAGCCGTGCCCTGGAATGGTCTGGCAAAACAGAGACATTTACTAC
AAV1-A 1773 TCGGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
hu. 46-A 1773 TCGGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
hu. 48-A 1773 TCGGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
hu. 44-A 1773 TCGGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
hu. 43-A 1776 TCGGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
AAV6-A 1773 TCGGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
hu. 34-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 47-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 29-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 63-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 56-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 45-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 57-B 1767 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 35-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 58-B 1770 ATCTACTGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 28-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 51-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 19-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 49-B 1770 AGCTACTGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 52-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 13-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
AAV2-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
hu. 20-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 24-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 64-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 27-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
hu. 21-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG

FIG. 3BU

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hu.22-B 1770 AGTACCTCAGATGTCAACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.23-B 1770 AGTACCTCAGATGTCAACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.7-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGCATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.61-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 rh.56-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGCATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.9-C 1770 AACTACAGAAATGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.54-C 1767 AAGTACTGAAACTGTGAATCACCACCAAGGAGCATTAACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.53-C 1767 AAGTACTGAAACTGTGAATCACCACCAAGGAGCATTAACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.60-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.55-C 1767 AAGTACTGAAACTGTGAATCACCACCAAGGAGCATTAACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.2-C 1770 AACTACTGGAACGTCAATCGCCAAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.1-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.18-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.3-C 1773 AACTACAGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.25-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGATGTGTACCTT
 hu.15-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.16-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.11-C 1770 AACTACAGAAATGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.10-C 1770 AACTACAGAAATGTCAATCACCAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu.4-C 1770 AACTACTGGAACGTCAATCACCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 rh.54-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACCTG
 rh.48-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAAACCGGACGTGTACCTG
 rh.55-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAAACCGGACGTGTACCTG
 rh.62-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAAACCGGACGTGTACCTG
 AAV7-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACCTG
 rh.52-E 1779 TATTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACTTG
 rh.51-E 1779 TATTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACCTG
 hu.39-E 1779 TACTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACCTG
 rh.53-E 1779 TATTGTGGGGCCGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACCTG
 hu.37-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCGTTACCTGGCATGGTCTGGCAGAAACCGGACGTGTACCTG

FIG. 3BV

rh. 43-E	1773	TCAAATTGGA	1900	1910	1920	1930	1940	1950	1960
rh. 50-E	1779	TATTGTGGG							
rh. 49-E	1779	TATTGTGGG							
rh. 61-E	1779	TATTGTGGG							
hu. 41-E	1779	TATTGTGGG							
rh. 64-E	1779	TATTGTGGG							
hu. 42-E	1779	TATTGTGGG							
rh. 57-E	1779	TATTGTGGG							
hu. 40-E	1779	TATTGTGGG							
AAV8-E	1779	TCAAATTGGA							
rh. 58-E	1779	TATTGTGGG							
rh. 40-E	1779	TATTGTGGG							
hu. 67-E	1779	TATTGTGGG							
hu. 17-E	1779	TATTGTAGG							
hu. 66-E	1779	TATTGTAGG							
rh. 38-E	1779	TATTGTGGG							
hu. 32-F	1773	GCAGACCGG							
AAV9/hu	1773	GCAGACCGG							
hu. 31-F	1773	GCAGACCGG							
AAV5	1810	CAAGGACCC							
AAV3-3	1843	CAAGGACCC							
AAV4-4	1837	CAGGGTCCC							
AAV1-A	1843	CAGGGTCCC							
hu. 46-A	1843	CAGGGTCCC							
hu. 48-A	1843	CAGGGTCCC							
hu. 44-A	1843	CAGGGTCCC							

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hu. 43-A	1846	CAGGGTCCCATTTGGGCCAAAAATTCCTCACACAGATGGACACTTTCACCCCGTCTCCTCTTATGGGCGGCT
AAV6-A	1843	CAGGGTCCATTTGGGCCAAAAATTCCTCACACGGATGGACACTTTCACCCCGTCTCCTCTCATGGGCGGCT
hu. 34-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 47-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 29-B	1840	CAGGGCCCTATTTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 63-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 56-B	1840	CAGGGCCCATCTGGGCAAAAAATTCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 45-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 57-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 35-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 58-B	1840	CAGGGCCCTATCTGGGCAAAAGATTCCGCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 28-B	1840	CAGGGCCCTACTTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 51-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 19-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 49-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 52-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 13-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
AAV2-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 20-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 24-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 64-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 27-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 21-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 22-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 23-B	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 7-C	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 61-C	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
rh. 56-C	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 9-C	1840	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT
hu. 54-C	1837	CAGGGCCCATCTGGGCAAAAGATTCCACACACGGACGGACATTTTCACCCCTCTCCCTCATGGGTGGAT

FIG. 3BX

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

FIG. 3B4

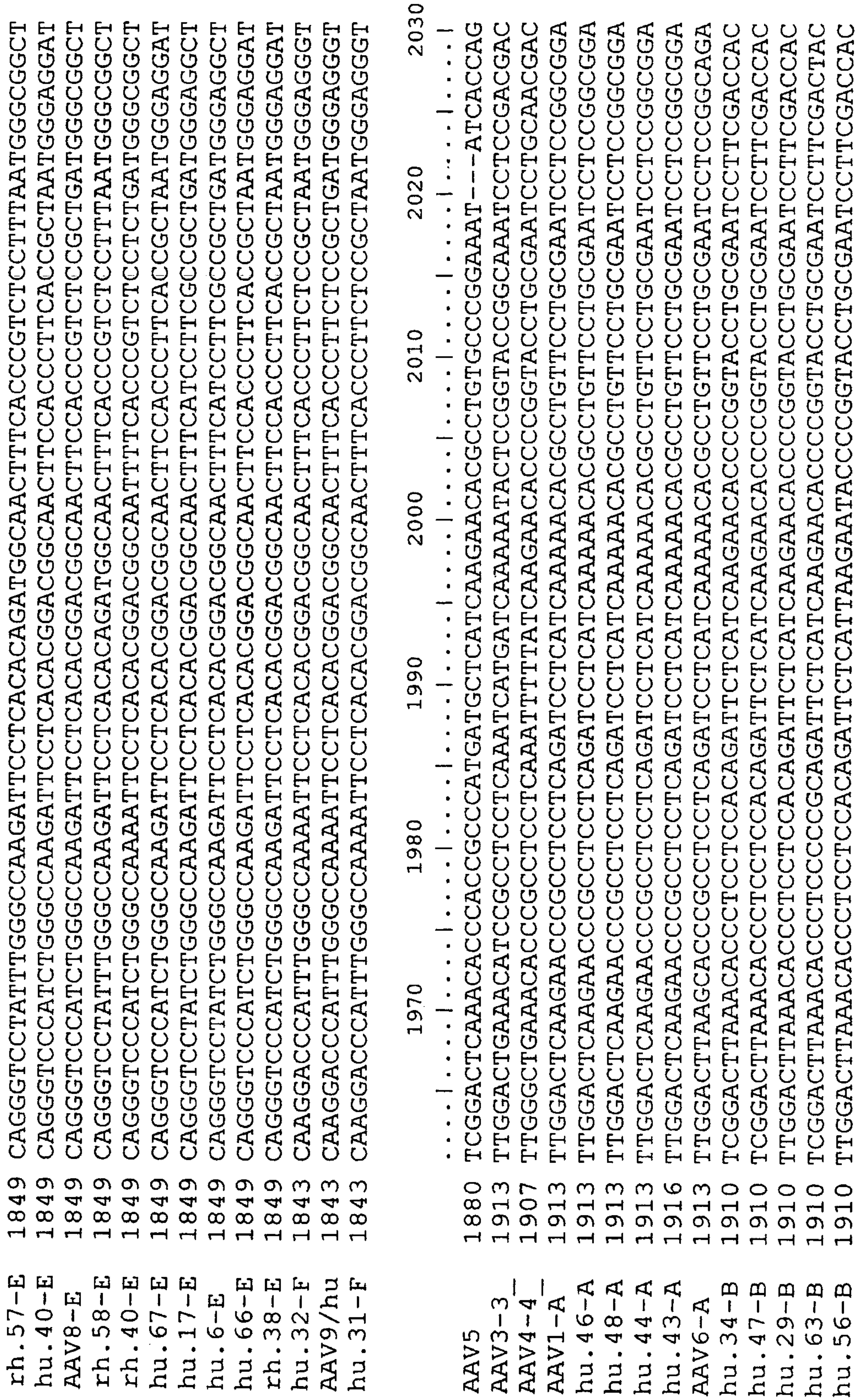


FIG. 3B2

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hu.45-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCGGTACCTGCGAATCCTTCGACCAC
 hu.57-B 1907 TTGGACTTAAACACCCCTCCTCCACAGATTCTCATTAAGAAATACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.35-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.58-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.28-B 1910 TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.51-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.19-B 1910 TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.49-B 1910 TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCAAAATCCTTCGACCAC
 hu.52-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.13-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 AAV2-B 1910 TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.20-B 1910 TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.24-B 1910 TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.64-B 1910 TCGGACTTAAACACCCCTCCTCCCGCAGATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACTAC
 hu.27-B 1910 TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.21-B 1910 TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.22-B 1910 TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.23-B 1910 TTGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAAACACCCCGGTACCTGCGAATCCTTCGACCAC
 hu.7-C 1910 TTGGGCTCAAACACCCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.61-C 1910 TTGGACTCAAACACCCACCTCCTCAAATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 rh.56-C 1910 TTGGGCTCAAACACCCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.9-C 1910 TTGGACTCAAACACCCCGCTCCTCAAATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.54-C 1907 TTGGACTCAAACACCCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.53-C 1907 TTGGACTCAAACACCCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.60-C 1910 TTGGACTCAAACACCCACCTCCTCAAATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.55-C 1907 TTGGACTCAAACACCCCGCTCCTCAGATTATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.2-C 1910 TTGGACTCAAACACCCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.1-C 1910 TTGGACTCAAACACCCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
 hu.18-C 1910 TTGGGCTCAAACACCCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCTACAAA
 hu.3-C 1913 TTGGACTCAAACACCCCGCTCCTCAGATCATGATCAAAAAGCACTCCCGTTCCAGCCAATCCTCCCACAAA

FIG. 3C

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hu.25-C	1910	TTGGACTCAAAACACCCGCCCTCCTCAGATTATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCTACAAA
hu.15-C	1910	TTGGACTCAAAACACCCACCTCCTCAGATCATGATTAAAAACACTCCCGTTCCAGCCAATCCTCCTCACAAA
hu.16-C	1910	TTGGACTCAAAACACCCACCTCCTCAGATCATGATTAAAAACACTCCCGTTCCAGCCAATCCTCCTCACAAA
hu.11-C	1910	TTGGACTCAAAACACCCCGCTCCTCAAAATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCTCACAAA
hu.10-C	1910	TTGGACTCAAAACACCCCGCTCCTCAAAATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCTCACAAA
hu.4-C	1910	TTGGACTCAAAACACCCCGCTCCTCAGATCATGATCAAAAACACTCCCGTTCCAGCCAATCCTCCTCACAAA
rh.54-D	1916	TTGGACTGAAGCATCCGCCCTCCTCAGATCCTGATCAAAAACACTCCTGTTCTGCTAATCCCCCGGAGGT
rh.48-D	1916	TTGGACTGAAGCATCCGCCCTCCTCAGATCCTGATCAAAAACACTCCTGTTCTGCTAATCCCCCGGAGGT
rh.55-D	1916	TTGGACTGAAGCATCCGCCCTCCTCAGATCCTGATCAAAAACACTCCTGTTCTGCTAATCCCCCGGAGGT
rh.62-D	1916	TTGGACTGAAGCATCCGCCCTCCTCAGATCCTGATCAAAAACACTCCTGTTCTGCTAATCCCCCGGAGGT
AAV7-D	1916	TTGGACTTAAACATCCGCCCTCCTCAGATCCTGATCAAGAACACTCCCGTTCCCGCTAATCCTCCGGAGGT
rh.52-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
rh.51-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
hu.39-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
rh.53-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
hu.37-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
rh.43-E	1913	TTGGCCTGAAACATCCTCCGCCCTCAGATCCTGATCAAGAACACGCGCTGTACCTGCGGATCCTCCGACCAC
rh.50-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
rh.49-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
rh.61-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGGTCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
hu.41-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
rh.64-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
hu.42-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
rh.57-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAACACTCCTGTTCTGCGGATCCTCCAACAGC
hu.40-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACAAC
AAV8-E	1919	TTGGCCTGAAACATCCTCCGCCCTCAGATCCTGATCAAGAACACGCGCTGTACCTGCGGATCCTCCGACCAC
rh.58-E	1919	TTGGACTTAAACATCCGCCCTCCTCAGATCCTCATCAAAAAGCACTCCTGTTCTGCGGATCCTCCAACAGC
rh.40-E	1919	TTGGACTGAAGCACCACCTCCTCCAGATCCTGATCAAGAATACGCCGGTACCTGCGGATCCTCCAACGAC
hu.67-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCGGTACCTGCGGATCCTCCAACGAC
hu.17-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATTAAGAATACACCTGTTCCTCCGCGGATCCTCCAACACTAC

FIG. 3B

hu. 6-E	1919	TTGGACTGAACACCCGCTCCTCAGATCCTGATTAAAGAAATACACCTGTTCCTCCGGGATCCTCCAAC	2040	2050	2060	2070	2080	2090	2100
hu. 66-E	1919	TTGGACTGAAGCACCCACCTCCTCAGATCCTGATCAAGAACACGCCGGTACCTGCGGATCCTCCAACAAC							
rh. 38-E	1919	TTGGACTGAAGCACCCACCTCCTCAGATCCTGATCAAGAACACGCCGGTACCTGCGGATCCTCCAACAAC							
hu. 32-F	1913	TTGGAATGAAGCACCCGCTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGATCCTCCAACGGC							
AAV9/hu	1913	TTGGAATGAAGCACCCGCTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGATCCTCCAACGGC							
hu. 31-F	1913	TTGGAATGAAGCACCCGCTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGATCCTCCAACGGC							
AAV5	1947	CTTCTCGGACGTGCCCGTCAGCAGCTTCATCACCCAGTACAGCACCCGGGCAGGTCA							
AAV3-3	1983	TTTCAGCCCCGCCAAGTTTGCTTCTATCTACTCAGTACTCCACTGGACAGGTCA							
AAV4-4	1977	CTTCAGCTCTACTCCGGTAAACTCCTTCTACTCAGTACAGCACTGGCCAGGTG							
AAV1-A	1983	GTTTTCAGCTACAAAGTTTGCTTCTATCATCACCCCAATACTCCACAGGACAAG							
hu. 46-A	1983	GTTTTCAGCTACAAAGTTTGCTTCTATCATCACCCCAATACTCCGACGACAAG							
hu. 48-A	1983	GTTTTCAGCTACAAAGTTTGCTTCTATCATCACCCCAATACTCCACAGGACAAG							
hu. 44-A	1983	GTTTTCAGCTACAAAGTTTGCTTCTATCATCACCCCAATACTCCACAGGACAAG							
hu. 43-A	1986	GTTTTCAGCTACAAAGTTTGCTTCTATCATCACCCCAATACTCCACAGGACAAG							
AAV6-A	1983	GTTTTCGGCTACAAAGTTTGCTTCTATCATCACCCCAATACTCCACAGGACAAG							
hu. 34-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 47-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 29-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 63-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 56-B	1980	CTTCAGCGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 45-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 57-B	1977	CTTCAGCGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 35-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 58-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 28-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 51-B	1980	CTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							
hu. 19-B	1980	TTTCAGTGGGCAAAAGTTTGCTTCTTCTATCACACACAGTACTCCACGGGACAG							

FIG. 3C

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

FIG. 3D

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rh. 48-D	1986	GTTTACGCCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCTAGCGTGGAGATCGAG
rh. 55-D	1986	GTTTACGCCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCTAGCGTGGAGATCGAG
rh. 62-D	1986	GTTTACGCCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCTAGCGTGGAGATCGAG
AAV7-D	1986	GTTTACTCCTGCCAAGTTTGCTTCTTTTCATCACACAGTACAGCACCGGCCAGGTCTAGCGTGGAAATCGAG
rh. 52-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCAAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
rh. 51-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCAAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
hu. 39-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
rh. 53-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
hu. 37-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAAATCGAG
rh. 43-E	1983	CTTCAACCAAGTCAAGCTGAACCTTTTCATCACGCAATACAGCACCGGACAGGTCTAGCGTGGAAATCGAA
rh. 50-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
rh. 49-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
rh. 61-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
hu. 41-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGTG
rh. 64-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAAATCGAG
hu. 42-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
rh. 57-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
hu. 40-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAAATCGAG
AAV8-E	1989	CTTCAACCAAGTCAAGCTGAACCTTTTCATCACGCAATACAGCACCGGACAGGTCTAGCGTGGAAATCGAA
rh. 58-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
rh. 40-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAGATCGAG
hu. 67-E	1989	GTTCAACCAAGGCCAAGCTGAATTCTTTTCATCACGCGCAGTACAGCACCGGACAAAGTCTAGCGTGGAAATCGAG
hu. 17-E	1989	CTTCAAGTCAAGCCAAAGCTGGCGTGGTTCATCACGCGCAGTACAGCACCGGACAGGTCTAGCGTGGAAATCGAA
hu. 6-E	1989	CTTCAAGTCAAGCCAAAGCTGGCGTGGTTCATCACGCGCAGTACAGCACCGGACAGGTCTAGCGTGGAAATCGAA
hu. 66-E	1989	GTTCAAGCCAGGCCAAGCTGGCTTCCCTTCATCACGCGCAGTACAGCACCGGACAGGTCTAGCGTGGAAATCGAG
rh. 38-E	1989	GTTCAAGCCAGGCCAAGCTGGCTTCCCTTCATCACGCGCAGTACAGCACCGGACAGGTCTAGCGTGGAAATCGAG
hu. 32-F	1983	TTTCAATAAGGACAAAGCTGAACCTTTTCATCACCCAGTATTTCTACTGGCCAAAGTCTAGCGTGGAGATCGAG
AAV9/hu	1983	CTTCAACAAGGACAAAGCTGAACCTTTTCATCACCCAGTATTTCTACTGGCCAAAGTCTAGCGTGGAGATCGAG
hu. 31-F	1983	TTTCAATAAGGACAAAGCTGAACCTTTTCATCACCCAGTATTTCTACTGGCCAAAGTCTAGCGTGGAGATCGAG

FIG. 3C

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	2110	2120	2130	2140	2150	2160	2170
AAV5							
AAV3-3-	2017	TGGGAGCTCAAGAAGGAAACTCCAAGAGGTGGAACCCAGAGATCCAGTACACAACAACTACAACGACC					
AAV4-4-	2053	TGGGAGCTACAGAAAGAAACAGCAACGTTGGAAATCCAGAGATTCAGTACACTTCCAACCTACAACAAAGT					
AAV1-A-	2047	TGGGAGATCCAGAAAGGAGCGGTCCAAACGCTGGAATCCCGAAGTCCAGTCCAGTTACCTCCAACCTACGGACAGC					
hu.46-A	2053	TGGGAGCTGCAGAAAGAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
hu.48-A	2053	TGGGAGCTGCAGAAAGAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
hu.44-A	2053	TGGGAGCTGCAGAAAGAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
hu.43-A	2056	TGGGAGCTGCAGAAAGAAACAGCAAGCGCTGGAATCCCGAAGTGCAGTACACATCCAATTATGCAAAAT					
AAV6-A	2053	TGGGAGCTGCAGAAAGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACATCTAACTATGCAAAAT					
hu.34-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.47-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.29-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.63-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.56-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.45-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.57-B	2047	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.35-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.58-B	2050	TGGGAGCTACAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.28-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.51-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.19-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.49-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.52-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.13-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
AAV2-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.20-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.24-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					
hu.64-B	2050	TGGGAGCTGCAGAAAGGAAACAGCAACGCTGGAATCCCGAAGTGCAGTACACTTCCAACCTACAACAAAGT					

FIG. 3CF

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

FIG. 3C

rh. 53-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCAGAGATTTCAGTATATACTTCCAACACTACTACAAAT	2180	2190	2200	2210	2220	2230	2240
hu. 37-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACACTACTACAAAT							
rh. 43-E	2053	TGGGAGCTACAGAAAGGAAACAGCAAGCGCTGGAAACCCGAGATCCAGTACACCTCCAACACTACTACAAAT							
rh. 50-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAGCCAGAGATTCAGTATATACTTCCAACACTACTACAAAT							
rh. 49-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCAGAGATTCAGTATATACTTCCAACACTACTACAAAT							
rh. 61-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCAGAGATTCAGTATATACTTCCAACACTACTACAAAT							
hu. 41-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTTGGAAACCCAGAGATTCAGTACACTTCAAACACTACTACAAAT							
rh. 64-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCAGGAAACCCAGAGATTCAGTATATACTTCCAACACTACTACAAAT							
hu. 42-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTCAGTACACTTCAAACACTACTACAAAT							
rh. 57-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCAGAGATTCAGTATATACTTCAAACACTACTACAAAT							
hu. 40-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTCAGTACACTTCAAACACTACTACAAAT							
AAV8-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCGAGATCCAGTACACTTCAAACACTACTACAAAT							
rh. 58-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCGAGATTCAGTATATACTTCAAACACTACTACAAAT							
rh. 40-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGTGTGGAAACCCAGAGATTCAGTATATACTTCAAACACTACTACAAAT							
hu. 67-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGATGGAAACCCAGAAATTCAGTACACTTCAAACACTACTACAAAT							
hu. 17-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTCAGTATATACTTCAAACACTATAACAAAT							
hu. 6-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTCAGTATATACTTCAAACACTACTACAAAT							
hu. 66-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTCAGTATATACTTCAAACACTACTACAAAT							
rh. 38-E	2059	TGGGAGCTGCAGAAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTCAGTACACTTCAAACACTACTACAAAT							
hu. 32-F	2053	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCGAGATCCAGTACACTTCCAACACTATTACAAAGT							
AAV9/hu	2053	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCGAGATCCAGTACACTTCCAACACTATTACAAAGT							
hu. 31-F	2053	TGGGAGCTGCAGAAAGGAGAAACAGCAAGCGCTGGAAACCCGAGATCCAGTACACTTCCAACACTATTACAAAGT							
AAV5	2087	CCCAGTTTGTGGACTTTGCCCCGGACAGCACCGGGGAATACAGAACCCAGACCTATCGGAACCCCGATA							
AAV3-3	2123	CTGTTAATGTGGACTTTACTGTAGACACTAATGGTGTTTATAGTGAACCTCGCCCTATTGGAAACCCGGTA							
AAV4-4	2117	AAAACTCTGTGTGGCTCCCGATCGGGCTGGGAAATACACTGAGCCTAGGGCTATCGGTACCCCGCTA							
AAV1-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA							
hu. 46-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA							

hu.48-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu.44-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu.43-A	2126	CTGCCAGCGTTGATTTTACTGTGGACAACAAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
AAV6-A	2123	CTGCCAACGTTGATTTTACTGTGGACAACAAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCCGTTA
hu.34-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.47-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.29-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.63-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGTA
hu.56-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGGGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.45-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.57-B	2117	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGGGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.35-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.58-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.28-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.51-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.19-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.49-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.52-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.13-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
AAV2-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.20-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCGCCAGATA
hu.24-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.64-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.27-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.21-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.22-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.23-B	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.7-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
hu.61-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA
rh.56-C	2120	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCCAGATA

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hu. 9-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTTGCCCCATTGGCACCAGATA
hu. 54-C	2117	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 53-C	2117	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 60-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 55-C	2117	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 2-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 1-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 18-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 3-C	2123	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 25-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 15-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 16-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 11-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 10-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 4-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCCTCGCCCCATTGGCACCAGATA
rh. 54-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 48-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 55-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 62-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
AAV7-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 52-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 51-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
hu. 39-E	2129	CTACAAATGCGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 53-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
hu. 37-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 43-E	2123	CTACAAAGTGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGCACCCTGTTA
rh. 50-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 49-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 61-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
hu. 41-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA

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rh. 64-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTCTTACTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
hu. 42-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 57-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTCTTACTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
hu. 40-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
AAV8-E	2129	CTACAAGTGTGGACTTTGCTGTTAATACTGAGGGTGTCTTACTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
rh. 58-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTCTTACTCTGAGCCTCGCCCCCATTTGGCACTCGTTA
rh. 40-E	2129	CTACAAATGTGGACTTTGCTGTTCAATCTGAGGGTACATATTCAGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 67-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 17-E	2129	CTGTTAATGTGGACTTTACTGTGGACACATAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACTCGTTA
hu. 6-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGGGTACTTATTTCAGAGCCTCGCCCCCATTTGGCACTCGTTA
hu. 66-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
rh. 38-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGAACTTATTCTGAGCCTCGCCCCCATTTGGTACTCGTTA
hu. 32-F	2123	CTAATAATGTTGAATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACTCGTTA
AAV9/hu	2123	CTAATAATGTTGAATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACTCGTTA
hu. 31-F	2123	CTAATAATGTTGAATTTGCTGTTAGTACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACTCGTTA
AAV5	2157	
AAV3-3	2193	CCTACCCGACCCCTT----
AAV4-4	2187	TCTCACACGAAACTTG----
AAV1-A	2193	CCTACCCACCACTGTAA-
hu. 46-A	2193	CCTACCCGTCCCTGTAA-
hu. 48-A	2193	CCTACCCGTCCCTGTAA-
hu. 44-A	2193	CCTACCCGTCCCTGTAA-
hu. 43-A	2196	CCTACCCGTCCCTGTAA-
AAV6-A	2193	CCTACCCGTCCCTGTAA-
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	CCTGACTCGTAATTTGTAA-
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. 3C

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hu.18-C	2190	CCGACTCGTAATCTGTAA-
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	CCCCACCCGTAATCTGTAA-
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

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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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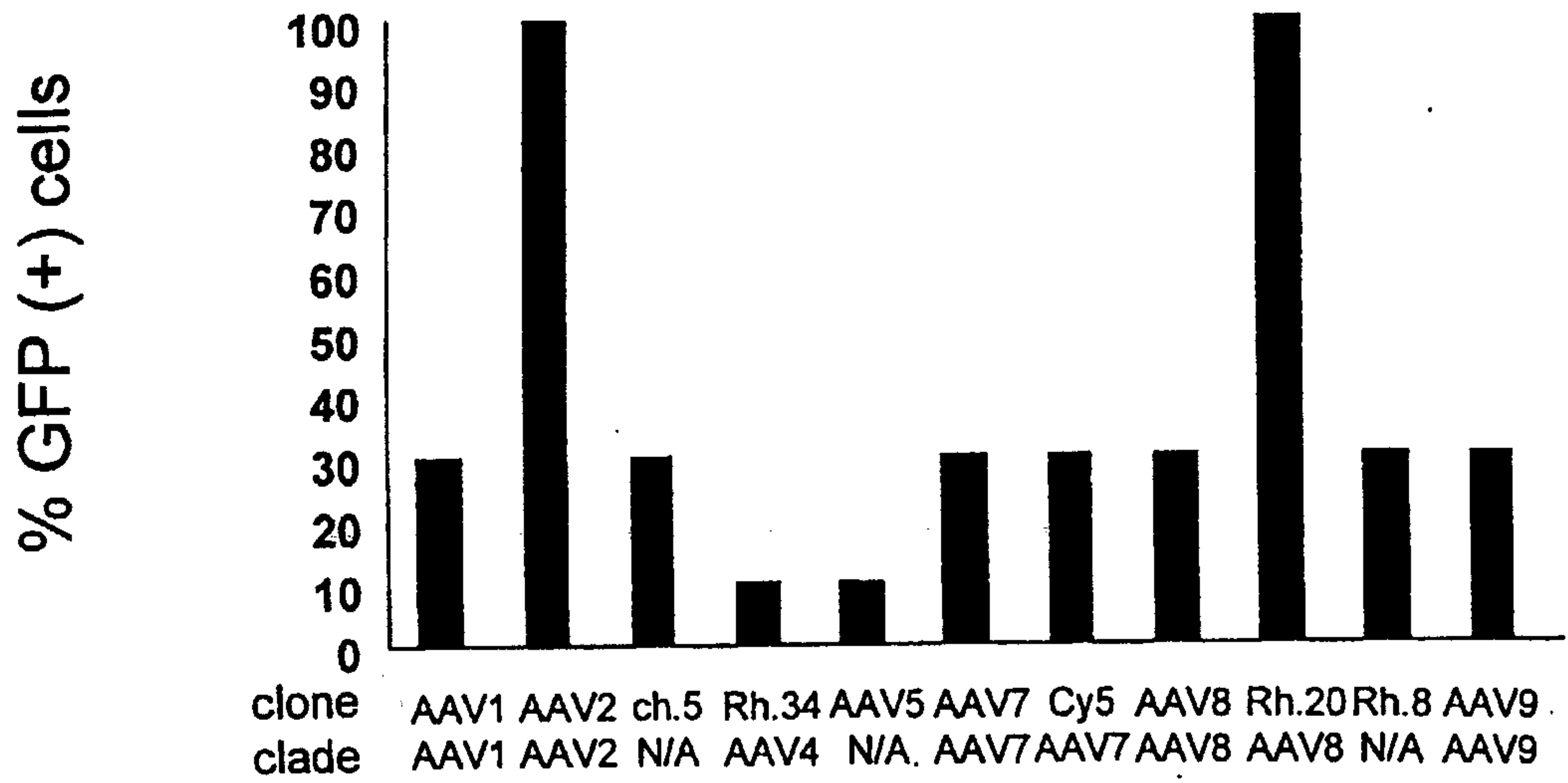


Fig. 4A
In Vitro

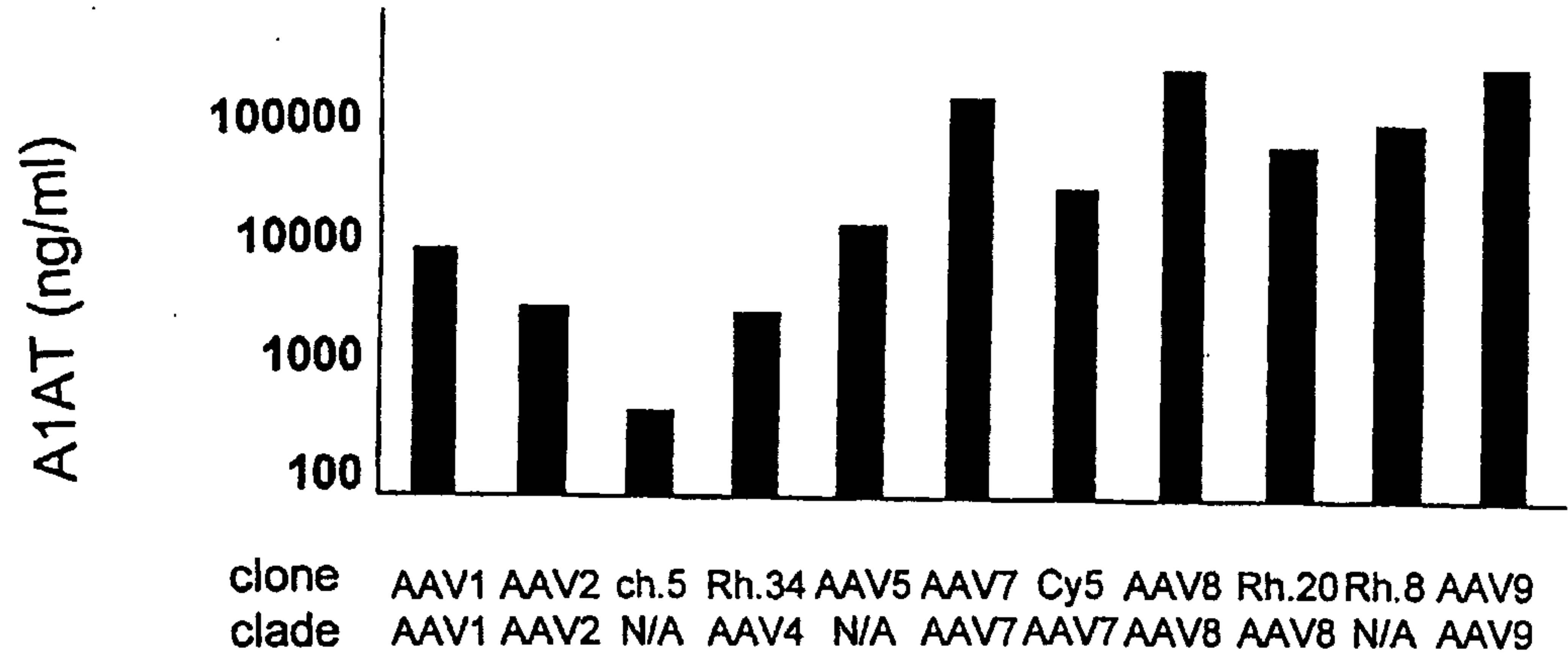


Fig. 4B
Liver

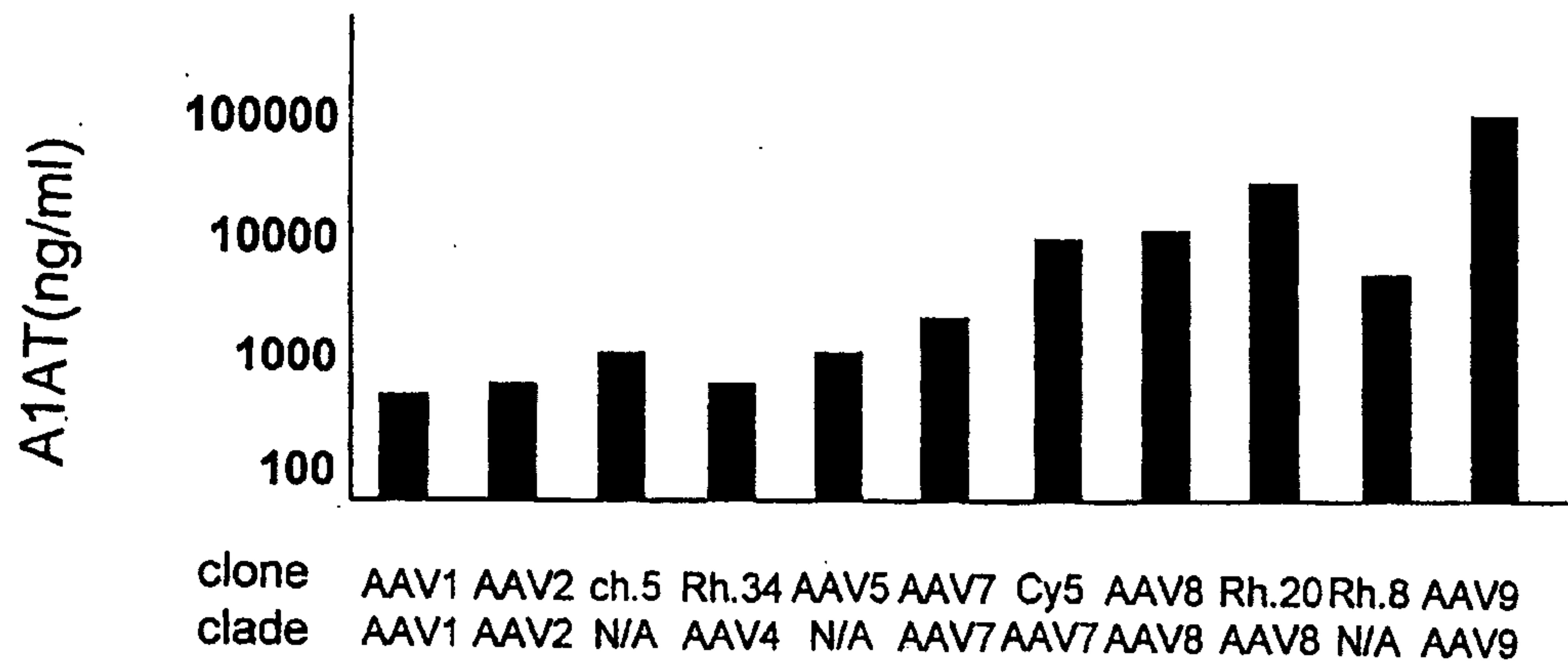


Fig. 4C
Lung

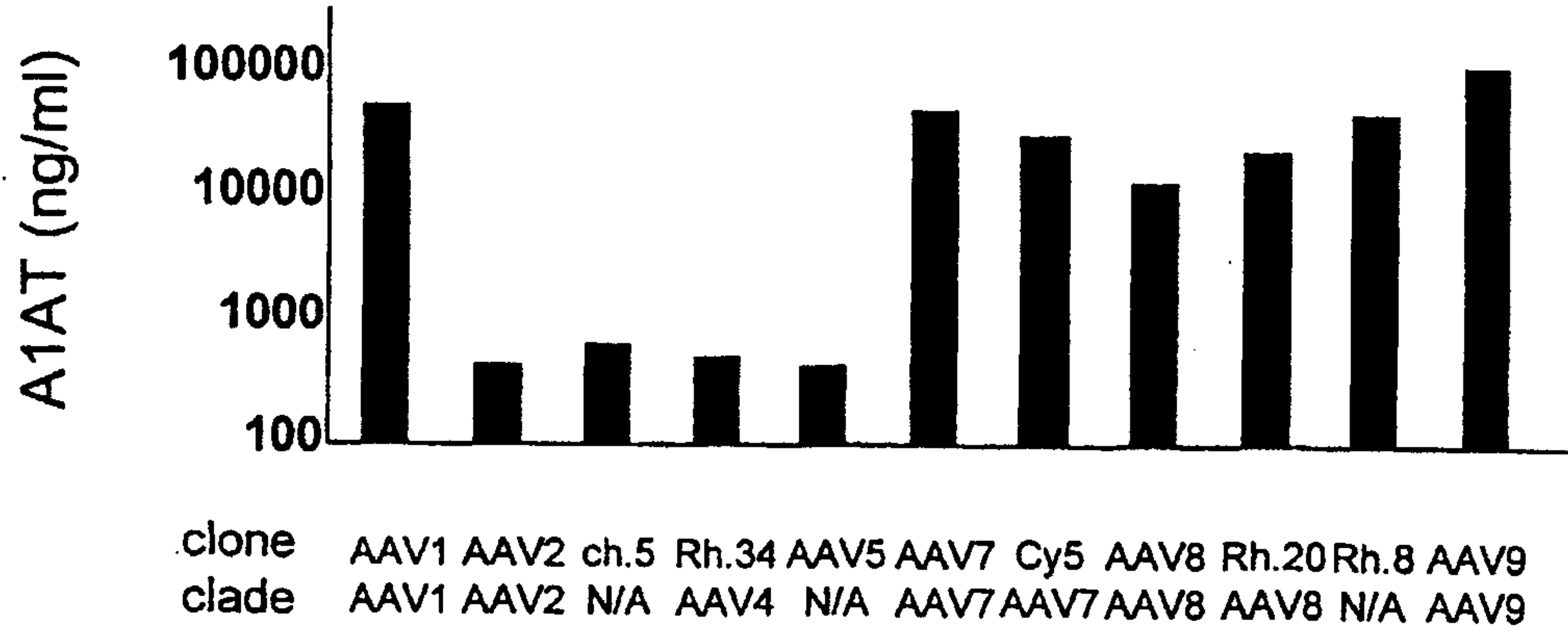


Fig. 4D
Muscle

