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(54) Titre : VARIANTES DES VIRUS ASSOCIES AUX ADENOVIRUS (AAV), SEQUENCES, VECTEURS LES
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(54) Title: ADENO-ASSOCIATED VIRUS (AAV) CLADES, SEQUENCES, VECTORS CONTAINING SAME, AND USES
THEREFOR

(57) **Abrégé/Abstract:**

Sequences of 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.



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

(57) Abstract: Sequences of 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.



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DEMANDES OU BREVETS VOLUMINEUX

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JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
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THIS IS VOLUME __1__ OF __3__

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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; rh.14, rh.16, rh.17, rh.12, rh.18, rh.21 (formerly termed 41.10); rh.25 (formerly termed 41.15; GenBank accession AY530557); rh.2; rh.31; cy.3; cy.5; rh.13; cy.4; cy.6; rh.22; rh.19; rh.35; rh.37; rh.36; rh.23; rh.8; and ch.5 [US Published Patent Application No. 2003/0138772 A1 (Jul 24,
 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 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
 25 130.4/hu.48 (SEQ ID NO: 78); 3.1/hu.9 (SEQ ID No: 58); 16.8/hu.10 (SEQ ID No: 56); 16.12/hu.11 (SEQ ID No: 57); 145.1/hu.53 (SEQ ID No: 176); 145.6/hu.55 (SEQ ID No: 178); 145.5/hu.54 (SEQ ID No: 177); 7.3/hu.7 (SEQ ID No: 55); 52/hu.19 (SEQ ID No: 62); 33.4/hu.15 (SEQ ID No: 50); 33.8/hu.16 (SEQ ID No: 51); 58.2/hu.25 (SEQ ID No: 49); 161.10/hu.60 (SEQ ID No: 170); H-5/hu.3 (SEQ ID No: 44); H-1/hu.1 (SEQ ID No:

46); 161.6/hu.61 (SEQ ID No: 174); hu.31 (SEQ ID No: 1); hu.32 (SEQ ID No: 2); hu.46 (SEQ ID NO: 82); hu.34 (SEQ ID NO: 72); hu.47 (SEQ ID NO: 77); hu.63 (SEQ ID NO: 204); hu.56 (SEQ ID NO: 205); hu.45 (SEQ ID NO: 76); hu.57 (SEQ ID NO: 206); hu.35 (SEQ ID NO: 73); hu.58 (SEQ ID NO: 207); hu.51 (SEQ ID NO: 208); hu.49 (SEQ ID NO: 209); hu.52 (SEQ ID NO: 210); hu.13 (SEQ ID NO: 71); hu.64 (SEQ ID NO: 212); rh.56 (SEQ ID NO: 54); hu.2 (SEQ ID NO: 48); hu.18 (SEQ ID NO: 52); hu.4 (SEQ ID NO: 47); and hu.67 (SEQ ID NO: 215). These sequences are also reproduced in the 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.

5 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
10 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
15 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.

20 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
25 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
30 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.

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. AY530606]; modified hu. 43 [SEQ ID NO:236]; 128.3/hu. 44 [SEQ ID Nos: 81 and 158; GenBank Accession No. AY530607] and 130.4/hu.48 [SEQ ID NO: 78 and 157; GenBank Accession No. AY530611]; from the Clade A;
- 52/hu.19 [SEQ ID NOs: 62 and 133; GenBank Accession No. AY530584], 52.1/hu.20 [SEQ ID NOs: 63 and 134; GenBank Accession No. AY530586], 54.5/hu.23 [SEQ ID Nos: 60 and 137; GenBank Accession No. AY530589], 54.2/hu.22 [SEQ ID Nos: 67 and 138; GenBank Accession No. AY530588], 54.7/hu.24 [SEQ ID Nos: 66 and 136; GenBank Accession No. AY530590], 54.1/hu.21 [SEQ ID Nos: 65 and 135; GenBank Accession No. AY530587], 54.4R/hu.27 [SEQ ID Nos: 64 and 140; GenBank Accession No. AY530592]; 46.2/hu.28 [SEQ ID Nos: 68 and 130; GenBank Accession No. AY530593]; 46.6/hu.29 [SEQ ID Nos: 69 and 132; GenBank Accession No. AY530594]; modified hu. 29 [SEQ ID NO: 225]; 172.1/hu.63 [SEQ ID NO: 171 and 195]; and 140.2/hu.52 (SEQ ID NO: 167 and 191; from Clade B;
- 3.1/hu.9 [SEQ ID Nos: 58 and 155; GenBank Accession No. AY530626]; 16.8/hu.10 [SEQ ID Nos: 56 and 156; GenBank Accession No. AY530576]; 16.12/hu.11 [SEQ ID Nos: 57 and 153; GenBank Accession No. AY530577]; 145.1/hu.53 [SEQ ID Nos: 176 and 186; GenBank Accession No. AY530615]; 145.6/hu.55 [SEQ ID Nos: 178 and 187; GenBank Accession No. AY530617]; 145.5/hu.54 [SEQ ID Nos: 177 and 188; GenBank Accession No. AY530616]; 7.3/hu.7 [SEQ ID Nos: 55 and 150; GenBank Accession No. AY530628]; modified hu. 7 [SEQ ID NO: 226]; hu.18 [SEQ ID Nos: 52 and 149; GenBank Accession No. AY530583]; 33.4/hu.15 [SEQ ID Nos: 50 and 147; GenBank Accession No. AY530580]; 33.8/hu.16 [SEQ ID Nos: 51 and 148; GenBank Accession No. AY530581]; 58.2/hu.25 [SEQ ID Nos: 49 and 146; GenBank Accession No. AY530591]; 161.10/hu.60 [SEQ ID Nos: 170 and 184; GenBank Accession No. AY530622]; H-5/hu.3 [SEQ ID Nos: 44 and 145; GenBank Accession No. AY530595]; H-1/hu.1 [SEQ ID Nos: 46 and 144; GenBank Accession No. AY530575]; and 161.6/hu.61 [SEQ ID Nos: 174 and 185; GenBank Accession No. AY530623] from Clade C;

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

30.10/pi.1 [SEQ ID NOs:28 and 93; GenBank Accession No. AY53055], 30.12/pi.2 [SEQ ID NOs:30 and 95; GenBank Accession No. 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.

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.

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.

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

III. Production of rAAV with Novel AAV Capsids

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.

5 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
10 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.

20 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,
25 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.
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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 enzyme linked immunosorbent assay (ELISA), radioimmunoassay (RIA) and immunohistochemistry. For example, where the marker sequence is the LacZ gene, the presence of the vector carrying the signal is detected by assays for beta-galactosidase activity. Where the transgene is green fluorescent protein or luciferase, the vector carrying the signal may be measured visually by color or light production in a luminometer.

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

The transgene may be used to correct or ameliorate gene deficiencies, which may include deficiencies in which normal genes are expressed at less than normal levels or deficiencies in which the functional gene product is not expressed. Alternatively, the transgene may provide a product to a cell which is not natively expressed in the cell type or in the host. A preferred type of transgene sequence encodes a therapeutic protein or polypeptide which is expressed in a host cell. The invention further includes using multiple transgenes. In certain situations, a different transgene may be used to encode each subunit of a protein, or to encode different peptides or proteins. This is desirable when the size of the DNA encoding the protein subunit is large, *e.g.*, for an immunoglobulin, the platelet-derived growth factor, or a dystrophin protein. In order for the cell to produce the multi-subunit protein, a cell is infected with the recombinant virus containing each of the different subunits. Alternatively, different subunits of a protein may be encoded by the same transgene. In this case, a single transgene includes

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

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

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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

developmentally, or in a tissue-specific manner, or in response to specific transcriptional stimuli. In a further embodiment, other native expression control elements, such as enhancer elements, polyadenylation sites or Kozak consensus sequences may also be used to mimic the native expression.

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

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

30 The combination of the transgene, promoter/enhancer, and 5' and 3' AAV ITRs is referred to as a "minigene" for ease of reference herein. Provided

with the teachings of this invention, the design of such a minigene can be made by resort to conventional techniques.

3. Delivery of the Minigene to a Packaging Host Cell

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
5 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).

10 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.

15 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
20 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,
25 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
30 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 responsible for foot and mouth diseases, primarily in non-human animals. Within the picornavirus family of viruses, target antigens include the VP1, VP2, VP3, VP4, and VPG. Other viral families include the astroviruses and the calcivirus family. The calcivirus family encompasses the Norwalk group of viruses, which are an important causative agent of epidemic gastroenteritis. Still another viral family desirable for use in targeting antigens for inducing immune responses in humans and non-human animals is the togavirus family, which includes the genera alphavirus, which include Sindbis viruses, Ross River virus, and Venezuelan, Eastern & Western Equine encephalitis, and rubivirus, including Rubella virus. The flaviviridae family includes dengue, yellow fever, Japanese encephalitis, St. Louis encephalitis and tick borne encephalitis viruses. Other target antigens may be generated from the Hepatitis C or the coronavirus family, which includes a number of non-human viruses such as infectious bronchitis virus (poultry), porcine transmissible gastroenteric virus (pig), porcine hemagglutinin encephalomyelitis virus (pig), feline infectious peritonitis virus (cat), feline enteric coronavirus (cat), canine coronavirus (dog), and human respiratory coronaviruses, which may cause the common cold and/or non-A, B or C hepatitis, and which include the putative cause of sudden acute respiratory syndrome (SARS). Within the coronavirus family, target antigens include the E1 (also called M or matrix protein), E2 (also called S or Spike protein), E3 (also called HE or hemagglutinin-esterase) glycoprotein (not present in all coronaviruses), or N (nucleocapsid). Still other antigens may be targeted against the arterivirus family and the rhabdovirus family. The rhabdovirus family includes the genera vesiculovirus (*e.g.*, Vesicular Stomatitis Virus), and the general lyssavirus (*e.g.*, rabies). Within the rhabdovirus family, suitable antigens may be derived from the G protein or the N protein. The family filoviridae, which includes hemorrhagic fever viruses such as Marburg and Ebola virus may be a suitable source of antigens. The paramyxovirus family includes parainfluenza Virus Type 1, parainfluenza Virus Type 3, bovine parainfluenza Virus Type 3, rubulavirus (mumps virus, parainfluenza Virus Type 2, parainfluenza virus Type 4, Newcastle disease virus (chickens), rinderpest, morbillivirus, which includes measles and

canine distemper, and pneumovirus, which includes respiratory syncytial virus. The influenza virus is classified within the family orthomyxovirus and is a suitable source of antigen (*e.g.*, the HA protein, the N1 protein). The bunyavirus family includes the genera bunyavirus (California encephalitis, La Crosse), phlebovirus (Rift Valley Fever),

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 burnetti* (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 cynomologus 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 monophylic 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 monophylic 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 – cynomologus 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.

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

B. *In Vivo*

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

A1AT > 10,000 ng/ml; Muscle: 0 = A1AT < 100 ng/ml, 1 = A1AT 100-1000 ng/ml, 2 = A1AT 1000-10,000 ng/ml, 3 = A1AT > 10,000 ng/ml).

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

30

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 (WPRES). A 10-fold lower dose (1×10^{10} GC/mouse) of AAV2/8 vector generated normal level of cFIX and aPTT time. In University of North Carolina (UNC) hemophilia B dogs, it was previously demonstrated that administration of an AAV2/8 vector into a dog previously treated with an AAV2 vector was successful; cFIX expression peaked at 10 $\mu\text{g/ml}$ 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
- 25
- 30

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

EXAMPLE 7 – 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 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 administered to 4 – 6 week old C57BL/6 mouse intramuscularly. Serum samples were collected from animals at day 28 post vector infusion for the human alpha 1 anti-trypsin (hA1AT) assay.

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

10 All publications cited in this specification are incorporated herein by reference. While the invention has been described with reference to particularly preferred embodiments, it will be appreciated that modifications can be made without departing from the spirit of the invention.

DEMANDES OU BREVETS VOLUMINEUX

**LA PRÉSENTE PARTIE DE CETTE DEMANDE OU CE BREVETS
COMPREND PLUS D'UN TOME.**

CECI EST LE TOME __1__ DE __3__

NOTE: Pour les tomes additionels, veuillez contacter le Bureau Canadien des Brevets.

JUMBO APPLICATIONS / PATENTS

**THIS SECTION OF THE APPLICATION / PATENT CONTAINS MORE
THAN ONE VOLUME.**

THIS IS VOLUME __1__ OF __3__

NOTE: For additional volumes please contact the Canadian Patent Office.

CLAIMS:

1. An adeno-associated virus (AAV) clade comprising at least three AAV members, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.
2. The AAV clade according to claim 1, wherein the clade is selected from the group consisting of Clade E comprising as a member AAV8, Clade D comprising as a member AAV7, Clade F comprising as a member AAV9, Clade B comprising as a member AAV2, and Clade C comprising as a member H2.
3. The clade according to claim 1, wherein one or more of said AAV members is a non-naturally occurring AAV.
4. The clade according to claim 1, wherein two or more of said AAV members are naturally occurring AAV.
5. An adeno-associated virus (AAV) clade E comprising AAV8 and at least two additional AAV members, wherein each member of said AAV clade as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.
6. The AAV Clade E according to claim 5, wherein one or more of said AAV members has a capsid with an amino acid identity of at least 85% with the capsid of AAV8, SEQ ID NO: 183.
7. The AAV Clade E according to claim 5, wherein said clade comprises at least AAV8 SEQ ID NO:183, 43.1/rh.2; rh. 4; rh.8; 44.2/rh.10; rh. 25; 29.3/bb.1; 29.5/bb.2; 30.10/pi.1 (SEQ ID NOs:28 and 93), 30.12/pi.2 (SEQ ID NOs:30 and 95), 30.19/pi.3 (SEQ ID NOs:29 and 94), LG-4/rh.38 (SEQ ID Nos: 7 and 86); LG-10/rh.40

(SEQ ID Nos: 14 and 92); N721-8/rh.43 (SEQ ID Nos: 43 and 163); 1-8/rh.49 (SEQ ID NOs: 25 and 103); 2-4/rh.50 (SEQ ID Nos: 23 and 108); 2-5/rh.51 (SEQ ID Nos: 22 and 104); 3-9/rh.52 (SEQ ID Nos: 18 and 96); 3-11/rh.53 (SEQ ID NOs: 17 and 97); 5-3/rh.57 (SEQ ID Nos: 26 and 105); 5-22/rh.58 (SEQ ID Nos: 27 and 58); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NOs: 21 and 107); 4-8/rh.64 (SEQ ID Nos: 15 and 99); modified rh. 64 (SEQ ID NO: 233); 3.1/hu.6 (SEQ ID NO: 5 and 84); 33.12/hu.17 (SEQ ID NO:4 and 83); 106.1/hu.37 (SEQ ID Nos: 10 and 88); LG-9/hu.39 (SEQ ID Nos: 24 and 102); 114.3/hu. 40 (SEQ ID Nos: 11 and 87); 127.2/hu.41 (SEQ ID NO:6 and 91); 127.5/hu.42 (SEQ ID Nos: 8 and 85); hu. 66 (SEQ ID NOs: 173 and 197); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NOs: 174 and 198).

8. An AAV of clade E according to claim 5, provided that none of the AAV of said clade comprises a capsid of AAV8, 43.1/rh.2; rh. 4; rh.8; 44.2/rh.10; rh. 25; 29.3/bb.1; or 29.5/bb.2

9. The AAV of claim 8 selected from the group consisting of 30.10/pi.1 (SEQ ID NOs:28 and 93), 30.12/pi.2 (SEQ ID NOs:30 and 95), 30.19/pi.3 (SEQ ID NOs:29 and 94), LG-4/rh.38 (SEQ ID Nos: 7 and 86); LG-10/rh.40 (SEQ ID Nos: 14 and 92); N721-8/rh.43 (SEQ ID Nos: 43 and 163); 1-8/rh.49 (SEQ ID NOs: 25 and 103); 2-4/rh.50 (SEQ ID Nos: 23 and 108); 2-5/rh.51 (SEQ ID Nos: 22 and 104); 3-9/rh.52 (SEQ ID Nos: 18 and 96); 3-11/rh.53 (SEQ ID NOs: 17 and 97); 5-3/rh.57 (SEQ ID Nos: 26 and 105); 5-22/rh.58 (SEQ ID Nos: 27 and 58); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NOs: 21 and 107); 4-8/rh.64 (SEQ ID Nos: 15 and 99); modified rh. 64 (SEQ ID NO: 233); 3.1/hu.6 (SEQ ID NO: 5 and 84); 33.12/hu.17 (SEQ ID NO:4 and 83); 106.1/hu.37 (SEQ ID Nos: 10 and 88); LG-9/hu.39 (SEQ ID Nos: 24 and 102); 114.3/hu. 40 (SEQ ID Nos: 11 and 87); 127.2/hu.41 (SEQ ID NO:6 and 91); 127.5/hu.42 (SEQ ID Nos: 8 and 85); hu. 66 (SEQ ID NOs: 173 and 197); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NOs: 174 and 198).

10. An adeno-associated virus (AAV) clade D comprising AAV7 and least two additional AAV members, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap

value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

11. The AAV clade D according to claim 10, wherein said clade comprises at least AAV sources: AAV7; cy.2; cy.3; cy.4; cy.5; cy.6; rh.13; rh.37; rh. 36; rh.35; 2-15/rh.62 (SEQ ID Nos: 33 and 114); 1-7/rh.48 (SEQ ID Nos: 32 and 115); 4-9/rh.54 (SEQ ID Nos: 40 and 116); and 4-19/rh.55 (SEQ ID Nos: 37 and 117) modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229).

12. An AAV of the AAV clade D according to claim 10, provided that none of the AAV of said clade comprises a capsid of AAV7 SEQ ID NOs: 180 and 181; AAV7; cy.2; cy.3; cy.4; cy.5; cy.6; rh.13; rh.37; rh. 36; rh.35.

13. The AAV of claim 12 selected from the group consisting of 2-15/ rh.62 (SEQ ID Nos: 33 and 114); 1-7/rh.48 (SEQ ID Nos: 32 and 115); 4-9/rh.54 (SEQ ID Nos: 40 and 116); and 4-19/rh.55 (SEQ ID Nos: 37 and 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229).

14. An adeno-associated virus (AAV) clade B comprising AAV2 and least two additional AAV members, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

15. The AAV clade B according to claim 14, wherein said clade comprises at least AAV: AAV2, 52/hu.19 (SEQ ID NOs: 62 and 133), 52.1/hu.20 (SEQ ID NOs: 63 and 134), 54.5/hu.23 (SEQ ID Nos: 60 and 137), 54.2/hu.22 (SEQ ID Nos: 67 and 138), 54.7/hu.24 (SEQ ID Nos: 66 and 136), 54.1/hu.21 (SEQ ID Nos: 65 and 135), 54.4R/hu.27 (SEQ ID Nos: 64 and 140); 46.2/hu.28 (SEQ ID Nos: 68 and 130); 46.6/hu.29 (SEQ ID Nos: 69 and 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 171 and 195); 172.2/hu. 64 (SEQ ID NO: 172 and 196); 24.5/hu.13 (SEQ ID NO: 71 and 129); 145.6/hu.56 (SEQ ID NO: 168 and 192); hu.57 (SEQ ID Nos: 169

and 193); 136.1/hu.49 (SEQ ID NO: 165 and 189); 156.1/hu.58 (SEQ ID NO: 179 and 194); 72.2/hu.34 (SEQ ID NO: 72 and 125); 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); 140.1/hu.51 (SEQ ID NO: 161 and 190); and 140.2/hu.52 (SEQ ID NO: 167 and 191).

16. A member AAV of the AAV clade B according to claim 14, provided that none of the AAV of said clade comprises a capsid of AAV2.

17. The member AAV of claim 16 selected from the group consisting of 52/hu.19 (SEQ ID NOs: 62 and 133), 52.1/hu.20 (SEQ ID NOs: 63 and 134), 54.5/hu.23 (SEQ ID Nos: 60 and 137), 54.2/hu.22 (SEQ ID Nos: 67 and 138), 54.7/hu.24 (SEQ ID Nos: 66 and 136), 54.1/hu.21 (SEQ ID Nos: 65 and 135), 54.4R/hu.27 (SEQ ID Nos: 64 and 140); 46.2/hu.28 (SEQ ID Nos: 68 and 130); 46.6/hu.29 (SEQ ID Nos: 69 and 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 171 and 195); 172.2/hu. 64 (SEQ ID NO: 172 and 196); 24.5/hu.13 (SEQ ID NO: 71 and 129); 145.6/hu.56 (SEQ ID NO: 168 and 192); hu.57 (SEQ ID Nos: 169 and 193); 136.1/hu.49 (SEQ ID NO: 165 and 189); 156.1/hu.58 (SEQ ID NO: 179 and 194); 72.2/hu.34 (SEQ ID NO: 72 and 125); 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); 140.1/hu.51 (SEQ ID NO: 161 and 190); and 140.2/hu.52 (SEQ ID NO: 167 and 191).

18. An adeno-associated virus (AAV) clade A comprising AAV1, AAV6 and at least one additional member AAV, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

19. The AAV clade A according to claim 18, wherein said clade comprises at least AAV: AAV1; AAV6; 128.1/hu. 43; 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).

20. A member AAV of the AAV clade A according to claim 19, provided that none of the AAV of said clade comprises a capsid of AAV1 or AAV6.

21. The member AAV of claim 19 selected from the group consisting of 128.1/hu. 43; 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).

22. An adeno-associated virus (AAV) clade C comprising A3.1/ch.5; H-6/hu.4; H-2/hu.2 and at least one further member AAV, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

23. The AAV clade C according to claim 21 wherein said clade comprises at least AAV: H-6/hu.4; H-2/hu.2; 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); hu.18 (SEQ ID NOs: 52 and 149); H-1/hu.1 (SEQ ID Nos: 46 and 144); and 161.6/hu.61 (SEQ ID Nos: 174 and 185).

24. A member AAV of clade C according to claim 21, provided that none of the AAV of said clade comprises a capsid of A3.1/ch.5; H-6/hu.4; or H-2/hu.2.

25. The member AAV according to claim 24, wherein the AAV is selected from the group consisting 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); hu.18 (SEQ ID NOs: 52 and 149); and 161.6/hu.61 (SEQ ID Nos: 174 and 185).

26. An adeno-associated virus (AAV) clade F comprising AAV9 and at least further two member AAV, wherein each member of said AAV clade is phylogenetically related as determined using a Neighbor-Joining heuristic by a bootstrap value of at least 75 % per 1000 isolates and a Poisson correction distance measurement of no more than 0.05.

27. The AAV clade F according to claim 26 wherein said clade comprises at least AAV hu.14/AAV9 (SEQ ID Nos: 3 and 123), hu.31 (SEQ ID NOs:1 and 121) and hu.32 (SEQ ID Nos: 2 and 122).

28. A member AAV of the AAV clade F according to claim 26.

29. The member AAV according to claim 28, wherein the AAV is selected from the group consisting of hu.14/AAV9 (SEQ ID Nos: 3 and 123), hu.31 (SEQ ID NOs:1 and 121) and hu.32 (SEQ ID Nos: 2 and 122).

30. An adeno-associated virus (AAV) of serotype 9 comprising an AAV capsid and a heterologous molecule for delivery to a cell,
wherein the AAV capsid 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.

31. The AAV according to claim 30, wherein said virus has the nucleic acid sequence of SEQ ID NO: 3.

32. The AAV according to claim 30, wherein said AAV further comprises a minigene having AAV inverted terminal repeats and the heterologous gene operably linked to regulatory sequences which direct its expression in a host cell.

33. A protein comprising an AAV9/HU.14 protein or a fragment thereof selected from the group consisting of:

(a) an AAV9/HU.14 capsid protein or fragment thereof, selected from the group consisting of:

vp1 capsid protein, amino acids (aa) 1 to 736, SEQ ID NO:123;

vp2 capsid protein, aa 138 to 736, SEQ ID NO: 123 ;

vp3 capsid protein, aa 203 to 736, SEQ ID NO: 123;

a fragment encompassing hypervariable region (HVR)1 through 12 or a smaller fragment thereof selected the group consisting of: aa 146 to 152; aa 182 to 187; aa 262 to 264; aa 263 to 266; aa 263 to 266; aa 381 to 383; 383 to 385; aa 450 to 474; aa 451 to 475; aa 490 to 495; aa 491 to 496; aa500 to 504; aa 501 to 505; aa 514 to 522; aa 533 to 554; aa 534 to 555; aa 581 to 594; aa 583 to 596; aa 658 to 667; aa 660 to 669; and aa 705 to 719; aa 707 to 723;

aa 24 to 42, aa 25 to 28; aa 81 to 85; aa133 to 165; aa 134 to 165; aa 137 to 143; aa 154 to 156; aa 194 to 208; aa 261 to 274; aa 262 to 274; aa 171 to 173; aa 185 to 198; aa 413 to 417; aa 449 to 478; aa 494 to 525; aa 534 to 571; aa 581 to 601; aa 660 to 671; aa 709 to 723; and

aa 1 to 184, aa 199 to 259; aa 274 to 446; aa 603 to 659; aa 670 to 706; aa 724 to 736; aa 185 to 198; aa 260 to 273; aa447 to 477; aa495 to 602; aa603 to 659; aa 660 to 669; and aa707 to 723, wherein the amino acid numbers are those of the AAV2 capsid, SEQ ID NO:4 and corresponding regions in the capsid of AAV9/HU.14, SEQ ID NO:123.

34. An artificial adeno-associated virus (AAV) capsid protein comprising one or more of the AAV9/HU.14 capsid protein fragments according to claim 33a.

35. A recombinant adeno-associated virus (AAV) comprising an artificial capsid according to claim 34.

36. A molecule comprising a nucleic acid sequence encoding a protein according to claim 34.
37. The molecule according to claim 36, wherein said nucleic acid sequence is selected from the group consisting of:
vp1, nt 1 to 2211;
vp2, nt 2532 to 2211; and
vp 3, nt 2730 to 2211;
wherein the nucleotides numbers are of AAV9/HU.14, SEQ ID NO: 3.
38. The molecule according to claim 37, wherein said molecule comprises an AAV sequence encoding an AAV capsid protein and a functional AAV rep protein.
39. The molecule according to claim 37, wherein said molecule is a plasmid.
40. 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 molecule according to claim 37.
41. A host cell transfected with an adeno-associated virus according to claim 30.
42. A host cell transfected with a molecule according to claim 33.
43. A composition comprising an AAV according to claim 30 and a physiologically compatible carrier.

44. A composition comprising a molecule according to claim 36 and a physiologically compatible carrier.

45. A method of delivering a transgene to a cell, said method comprising the step of contacting the cell with an AAV according to claim 30, wherein said rAAV comprises the transgene.

46. A non-naturally occurring adeno-associated virus (AAV) comprising an AAV capsid having an amino acid sequence selected from the group consisting of:

30.10/pi.1 (SEQ ID NO: 93), 30.12/pi.2 (SEQ ID NO: 95), 30.19/pi.3 (SEQ ID NO: 94), LG-4/rh.38 (SEQ ID No: 86); LG-10/rh.40 (SEQ ID No: 92); N721-8/rh.43 (SEQ ID No: 163); 1-8/rh.49 (SEQ ID NO: 103); 2-4/rh.50 (SEQ ID No: 108); 2-5/rh.51 (SEQ ID No: 104); 3-9/rh.52 (SEQ ID No: 96); 3-11/rh.53 (SEQ ID NO: 97); 5-3/rh.57 (SEQ ID No: 105); 5-22/rh.58 (SEQ ID No: 58); 2-3/rh.61 (SEQ ID NO: 107); 4-8/rh.64 (SEQ ID No: 99); 3.1/hu.6 (SEQ ID NO: 84); 33.12/hu.17 (SEQ ID NO: 83); 106.1/hu.37 (SEQ ID No: 88); LG-9/hu.39 (SEQ ID No: 102); 114.3/hu. 40 (SEQ ID No: 87); 127.2/hu.41 (SEQ ID NO: 91); 127.5/hu.42 (SEQ ID No: 85); hu. 66 (SEQ ID NO: 197); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NO: 198) from Clade E;

2-15/ rh.62 (SEQ ID No: 114); 1-7/rh.48 (SEQ ID No: 115); 4-9/rh.54 (SEQ ID No: 116); and 4-19/rh.55 (SEQ ID No: 117); 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; 52/hu.19 (SEQ ID NO: 133), 52.1/hu.20 (SEQ ID NO: 134), 54.5/hu.23 (SEQ ID No: 137), 54.2/hu.22 (SEQ ID No: 138), 54.7/hu.24 (SEQ ID No: 136), 54.1/hu.21 (SEQ ID No: 135), 54.4R/hu.27 (SEQ ID No: 140); 46.2/hu.28 (SEQ ID No: 130); 46.6/hu.29 (SEQ ID No: 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 195); 172.2/hu. 64 (SEQ ID NO: 196); 24.5/hu.13 (SEQ ID NO: 129); 145.6/hu.56 (SEQ ID NO: 192); hu.57 (SEQ ID No: 193); 136.1/hu.49 (SEQ ID NO: 189); 156.1/hu.58 (SEQ ID NO: 194); 72.2/hu.34 (SEQ ID NO: 125); 72.3/hu.35 (SEQ ID NO: 164); 129.1/hu.45 (SEQ ID NO: 127); 130.1/hu.47 (SEQ ID NO: 128); 140.1/hu.51 (SEQ ID NO: 190); and 140.2/hu.52 (SEQ ID NO: 191) from clade B;

128.1/hu. 43 (SEQ ID Nos: 160); modified hu. 43 (SEQ ID NO: 236);
128.3/hu. 44 (SEQ ID Nos: 158); hu.46 (SEQ ID NO: 159); modified hu.46 (SEQ ID
NO: 224); and 130.4/hu.48 (SEQ ID NO: 157) from Clade A;

3.1/hu.9 (SEQ ID Nos: 155); 16.8/hu.10 (SEQ ID Nos: 156); 16.12/hu.11
(SEQ ID Nos: 153); 145.1/hu.53 (SEQ ID No: 186); 145.6/hu.55 (SEQ ID No: 187);
145.5/hu.54 (SEQ ID No: 188); 7.3/hu.7 (SEQ ID No: 150); modified hu. 7 (SEQ ID NO:
226); 33.4/hu.15 (SEQ ID No: 147); 33.8/hu.16 (SEQ ID No: 148); 58.2/hu.25 (SEQ ID
No: 146); 161.10/hu.60 (SEQ ID No: 184); H-5/hu.3 (SEQ ID No: 145); H-1/hu.1 (SEQ
ID No: 144); hu.18 (SEQ ID NOs: 52 and 149); and 161.6/hu.61 (SEQ ID No: 185) from
Clade C;

hu.31 (SEQ ID NO: 121) and hu.32 (SEQ ID No: 122) from Clade F; and
rh.59 (SEQ ID NO: 110) and rh.60 (SEQ ID NO: 120);
or a unique, functional fragment thereof.

47. The AAV according to claim 46, wherein the fragment is selected
from the group consisting of:

a fragment encompassing hypervariable region (HVR)1 through
12 or a smaller fragment thereof selected the group consisting of: aa 146 to 152; aa 182 to
187; aa 262 to 264; aa 263 to 266; aa 263 to 266; aa 381 to 383; 383 to 385; aa 450 to
474; aa 451 to 475; aa 490 to 495; aa 491 to 496; aa500 to 504; aa 501 to 505; aa 514 to
522; aa 533 to 554; aa 534 to 555; aa 581 to 594; aa 583 to 596; aa 658 to 667; aa 660 to
669; and aa 705 to 719; aa 707 to 723;

aa 24 to 42, aa 25 to 28; aa 81 to 85; aa133 to 165; aa 134 to 165;
aa 137 to 143; aa 154 to 156; aa 194 to 208; aa 261 to 274; aa 262 to 274; aa 171 to 173;
aa 185 to 198; aa 413 to 417; aa 449 to 478; aa 494 to 525; aa 534 to 571; aa 581 to 601;
aa 660 to 671; aa 709 to 723; and

aa 1 to 184, aa 199 to 259; aa 274 to 446; aa 603 to 659; aa 670 to
706; aa 724 to 736; aa 185 to 198; aa 260 to 273; aa447 to 477; aa495 to 602; aa603 to
659; aa 660 to 669; and aa707 to 723,

wherein the amino acid numbers are those of the AAV2 capsid,
SEQ ID NO:4 and corresponding regions in the capsid of 30.10/pi.1 (SEQ ID NO: 93),
30.12/pi.2 (SEQ ID NO: 95), 30.19/pi.3 (SEQ ID NO: 94), LG-4/rh.38 (SEQ ID No: 86);

LG-10/rh.40 (SEQ ID No: 92); N721-8/rh.43 (SEQ ID No: 163); 1-8/rh.49 (SEQ ID NO: 103); 2-4/rh.50 (SEQ ID No: 108); 2-5/rh.51 (SEQ ID No: 104); 3-9/rh.52 (SEQ ID No: 96); 3-11/rh.53 (SEQ ID NO: 97); 5-3/rh.57 (SEQ ID No: 105); 5-22/rh.58 (SEQ ID No: 58); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NO: 107); 4-8/rh.64 (SEQ ID No: 99); modified rh. 64 (SEQ ID NO: 233); 3.1/hu.6 (SEQ ID NO: 84); 33.12/hu.17 (SEQ ID NO: 83); 106.1/hu.37 (SEQ ID No: 88); LG-9/hu.39 (SEQ ID No: 102); 114.3/hu. 40 (SEQ ID No: 87); 127.2/hu.41 (SEQ ID NO: 91); 127.5/hu.42 (SEQ ID No: 85); hu. 66 (SEQ ID NO: 197); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NO: 198) from clade E;

2-15/ rh.62 (SEQ ID No: 114); 1-7/rh.48 (SEQ ID No: 115); 4-9/rh.54 (SEQ ID No: 116); and 4-19/rh.55 (SEQ ID No: 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229) from clade D; 52/hu.19 (SEQ ID NO: 133), 52.1/hu.20 (SEQ ID NO: 134), 54.5/hu.23 (SEQ ID No: 137), 54.2/hu.22 (SEQ ID No: 138), 54.7/hu.24 (SEQ ID No: 136), 54.1/hu.21 (SEQ ID No: 135), 54.4R/hu.27 (SEQ ID No: 140); 46.2/hu.28 (SEQ ID No: 130); 46.6/hu.29 (SEQ ID No: 132); modified hu. 29 (SEQ ID NO: 225); 172.1/hu.63 (SEQ ID NO: 195); 172.2/hu. 64 (SEQ ID NO: 196); 24.5/hu.13 (SEQ ID NO: 129); 145.6/hu.56 (SEQ ID NO: 192); hu.57 (SEQ ID No: 193); 136.1/hu.49 (SEQ ID NO: 189); 156.1/hu.58 (SEQ ID NO: 194); 72.2/hu.34 (SEQ ID NO: 125); 72.3/hu.35 (SEQ ID NO: 164); 129.1/hu.45 (SEQ ID NO: 127); 130.1/hu.47 (SEQ ID NO: 128); 140.1/hu.51 (SEQ ID NO: 190); and 140.2/hu.52 (SEQ ID NO: 191) from clade B;

128.1/hu. 43 (SEQ ID Nos: 160); modified hu. 43 (SEQ ID NO: 236); 128.3/hu. 44 (SEQ ID Nos: 158); hu.46 (SEQ ID NO: 159); modified hu. 46 (SEQ ID NO: 224); and 130.4/hu.48 (SEQ ID NO: 157) from Clade A;

3.1/hu.9 (SEQ ID Nos: 155); 16.8/hu.10 (SEQ ID Nos: 156); 16.12/hu.11 (SEQ ID Nos: 153); 145.1/hu.53 (SEQ ID No: 186); 145.6/hu.55 (SEQ ID No: 187); 145.5/hu.54 (SEQ ID No: 188); 7.3/hu.7 (SEQ ID No: 150); modified hu. 7 ([SEQ ID NO: 226); 33.4/hu.15 (SEQ ID No: 147); 33.8/hu.16 (SEQ ID No: 148); 58.2/hu.25 (SEQ ID No: 146); 161.10/hu.60 (SEQ ID No: 184); H-5/hu.3 (SEQ ID No: 145); H-1/hu.1 (SEQ ID No: 144); hu.18 (SEQ ID NO: 149) and 161.6/hu.61 (SEQ ID No: 185) from Clade C;

hu.31 (SEQ ID NO: 121) and hu.32 (SEQ ID No: 122) from Clade F; and

rh.59 (SEQ ID NO: 110) and rh.60 (SEQ ID NO: 120),.

48. An artificial adeno-associated virus (AAV) capsid protein comprising one or more of the AAV capsid protein fragments according to claim 47a.

49. A recombinant adeno-associated virus (AAV) comprising an artificial capsid according to claim 48.

50. A molecule comprising a heterologous nucleic acid sequence encoding an AAV capsid protein, wherein said nucleic acid sequence is selected from the group consisting of:

30.10/pi.1 (SEQ ID NO: 28), 30.12/pi.2 (SEQ ID NO: 30), 30.19/pi.3 (SEQ ID NO: 29), 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); modified rh. 58 (SEQ ID NO: 232); 2-3/rh.61 (SEQ ID NO: 21); 4-8/rh.64 (SEQ ID No: 15); 3.1/hu.6 (SEQ ID NO: 5); 33.12/hu.17 (SEQ ID NO:4); 106.1/hu.37 (SEQ ID No: 10); LG-9/hu.39 (SEQ ID No: 24); 114.3/hu. 40 (SEQ ID No: 11); 127.2/hu.41 (SEQ ID NO:6); 127.5/hu.42 (SEQ ID No: 8); hu. 66 (SEQ ID NO: 173); modified rh.2 (SEQ ID NO:231); and hu.67 (SEQ ID NO: 174) from Clade E;

2-15/ rh.62 (SEQ ID No: 33); 1-7/rh.48 (SEQ ID No: 32); 4-9/rh.54 (SEQ ID No: 40); and 4-19/rh.55 (SEQ ID Nos: 37 and 117); modified cy. 5 (SEQ ID NO: 227); modified rh.13 (SEQ ID NO: 228); and modified rh. 37 (SEQ ID NO: 229) from Clade D;

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 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); modified hu. 29 (SEQ ID NO: 225); from Clade B;

128.1/hu. 43 (SEQ ID No: 80); 128.3/hu. 44 (SEQ ID No: 81); hu.46 (SEQ ID NOs: 82) and 130.4/hu.48 (SEQ ID NO: 78) from Clade A;

3.1/hu.9 (SEQ ID No: 58); 16.8/hu.10 (SEQ ID No: 56); 16.12/hu.11 (SEQ ID No: 57); 145.1/hu.53 (SEQ ID No: 176); 145.6/hu.55 (SEQ ID No: 178); 145.5/hu.54 (SEQ ID No: 177); 7.3/hu.7 (SEQ ID No: 55); modified hu.7 (SEQ ID NO: 226); 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); hu.18 (SEQ ID NO: 149); H-1/hu.1 (SEQ ID No: 46); and 161.6/hu.61 (SEQ ID No: 174) from Clade C;

hu.14/AAV9 (SEQ ID No: 3), hu.31 (SEQ ID NO:1)and hu.32 (SEQ ID No: 2) from Clade F;

rh.59 (SEQ ID NO: 49) and rh.60 (SEQ ID NO: 31);

or a unique, functional fragment thereof.

51. The molecule according to claim 50, wherein said molecule comprises an AAV sequence encoding an AAV capsid protein and a functional AAV rep protein.

52. The molecule according to claim 50, wherein said molecule is a plasmid.

53. 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 molecule according to claim 50.

54. A host cell transfected with an adeno-associated virus according to claim 30.

55. A host cell transfected with a molecule according to claim 50.

56. A composition comprising an AAV according to claim 47 and a physiologically compatible carrier.

57. A composition comprising a molecule according to claim 50 and a physiologically compatible carrier.

58. A method of delivering a transgene to a cell, said method comprising the step of contacting the cell with an AAV according to claim 47, wherein said rAAV comprises the transgene.

1/125

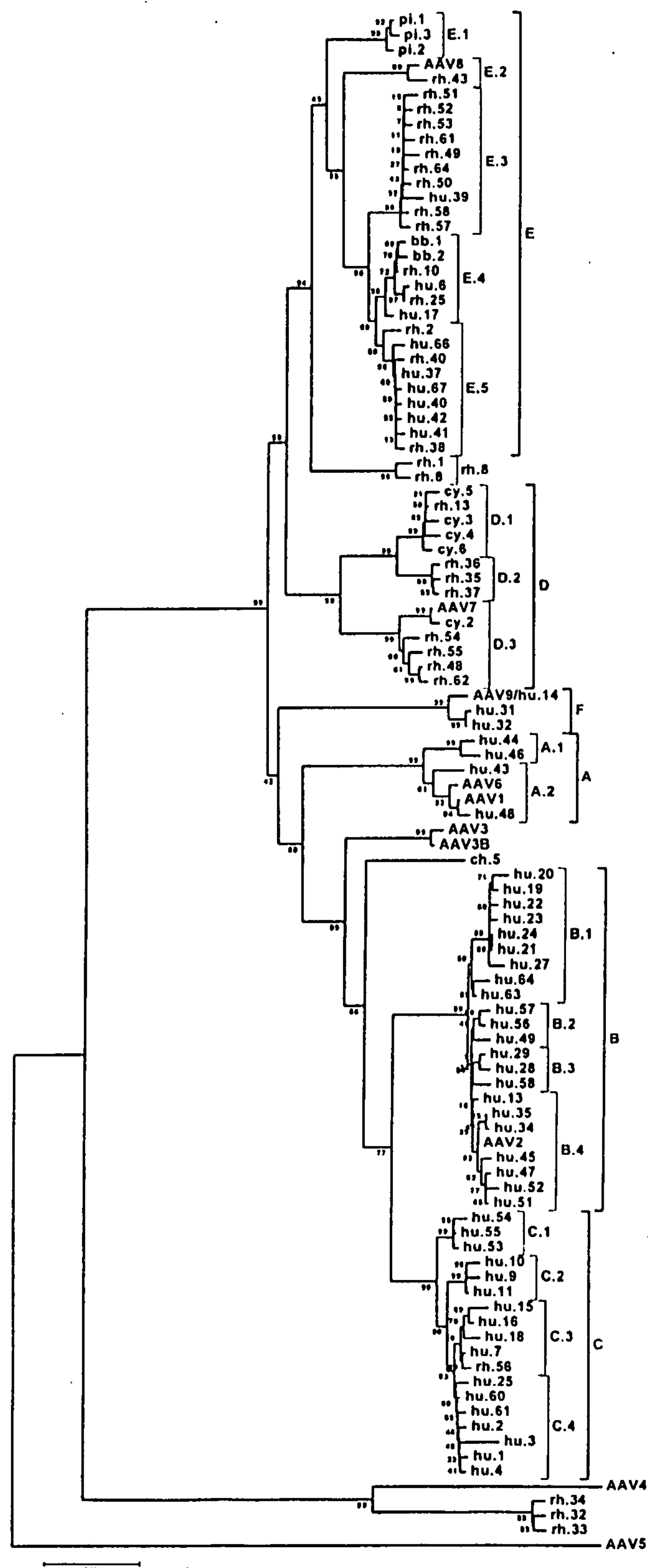


FIG. 1

2/125

	10	20	30	40	50	60	70
AAV5	1						
AAV3-3	1	MSFVDHPPDWLEE-VGEGLREFLGLGAGPPKPKPNQHQDQARGLVLPGYNYLGPNGGLDRGEPVNRAD					
AAV4-4	1	MAADGYLPDWLEDNLSEGIREFWWALKPGVPQPKANQHQDNRRGLVLPGYKYLGPNGGLDKGEPVNEAD					
AAV1-A	1	-MTDGYLPDWLEDNLSEGVREWWALQPGAPKPKANQHQDNARGLVLPGYKYLGPNGGLDKGEPVNAADA					
hu. 46-A	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA					
hu. 48-A	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 44-A	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 43-A	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA					
AAV6-A	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA					
hu. 34-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 47-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 29-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 63-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 56-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 45-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 57-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 35-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 58-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 28-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 51-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 19-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 49-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 52-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 13-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
AAV2-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 20-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 24-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					
hu. 64-B	1	MAADGYLPDWLEDNLSEGIREFWDLKPGAPKPKANQKQDDGRGLVLPGYKYLGPENGLDKGEPVNEADA					

FIG. 2A

3/125

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	MAADGYPPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 1-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 18-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 3-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 25-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDGSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 15-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLYKGEPVDEADA
hu. 16-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLYKGEPVNEADA
hu. 11-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHQDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 10-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKLAERHQDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
hu. 4-C	1	MAADGYLPDWLEDTLSEGIQWQWKLKPGPPPPKPAERHKDDSRGLVLPGYKYLGPENGLDKGEPVNEADA
rh. 54-D	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 48-D	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 55-D	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 62-D	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
AAV7-D	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDNGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 52-E	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA
rh. 51-E	1	MVADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQGDGRGLVLPGYKYLGPENGLDKGEPVNAADA
hu. 39-E	1	MAADGYLPDWLEDNLSEGIREWWDLKP GAPKPKANQQKQDDGRGLVLPGYKYLGPENGLDKGEPVNAADA

rh. 53-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 37-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 43-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 50-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 49-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 61-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 41-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 64-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 42-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 57-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 40-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
AAV8-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 58-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 40-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 67-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLLGYKYLGPFNGLDKGEPVNAADA
hu. 17-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGCKYLGPFNGLDKGEPVNAADA
hu. 6-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 66-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
rh. 38-E 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPFNGLDKGEPVNAADA
hu. 32-F 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQKQDDGRGLVLPGYKYLGPNGNGLDKGEPVNAADA
AAV9/hu 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQHQNARGLVLPGYKYLGPNGNGLDKGEPVNAADA
hu. 31-F 1 MAADGYLPDWLEDNLSEGIREWWDLKPAPKPKANQQHQNARGLVLPGYKYLGPNGNGLDKGEPVNAADA

80 90 100 110 120 130 140
.....|.....|.....|.....|.....|.....|.....|.....|.....|
AAV5 70 VAREHDI SYNEQLEAGDNPYLKYNHADAEEFQEKLADDTSEFGGNLGKAVFQAKKRVLEPFG-LVEEGAKTA
AAV3-3 71 AALEHDKAYDQQLKAGDNPYLKYNHADAEEFQERLQEDTSEFGGNLGRAVFQAKKRILEPLG-LVEEAAKTA
AAV4-4 70 AALEHDKAYDQQLKAGDNPYLKYNHADAEEFQORLQEDTSEFGGNLGRAVFQAKKRVLEPLG-LVEQAGETA
AAV1-A 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEEFQERLQEDTSEFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 46-A 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSEFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA

hu. 48-A 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 44-A 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAETA
hu. 43-A 71 AALEHDKAYDQQLKAGDNPYPRYNHADAEFQERLQEDTPFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
AAV6-A 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPFG-LVEEGAKTA
hu. 34-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 47-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVGEPPVKTA
hu. 29-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 63-B 71 AALEHDKAYDRQLDSGDNPYPKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 56-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 45-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 57-B 70 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 35-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 58-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 28-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLS-LVEEPPVKTA
hu. 51-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVGEPPVKTA
hu. 19-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 49-B 71 AALEYDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 52-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVGEPPVKTA
hu. 13-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
AAV2-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 20-B 71 AALEHDKAYDRQLDSGDNPYLKYNHVDAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLG-LVEEPPVCAA
hu. 24-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLG-LVEEPPVKTA
hu. 64-B 71 AALEHDKAYDRQLDGGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
hu. 27-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLG-LVEEPPVKTA
hu. 21-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLG-LVEEPPVKTA
hu. 22-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLG-LVEEPPVKTA
hu. 23-B 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRILEPLG-LVEEPPVKTA
hu. 7-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEGPPVKTA
hu. 61-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA
rh. 56-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPPVKTA

hu. 9-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 54-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 53-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 60-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 55-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 2-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 1-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 18-C 71 AALEHDKAYDRQLES GDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 3-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 25-C 71 AALEHDKAYDRQLNSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 15-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 16-C 71 AALEHDKAYDRQLDSGDNPYLKYNHAGAAEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 11-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 10-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
hu. 4-C 71 AALEHDKAYDRQLDSGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEPVKTA
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
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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

rh. 64-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 42-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 57-E 71 AALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 40-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
AAV8-E 71 AALEHDKAYDQQLQAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 58-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
rh. 40-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 67-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 17-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 6-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
hu. 66-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEGAKTA
rh. 38-E 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 32-F 71 AALEHDKAYDQQLKAGDNPYLRYNHADAEFQERLQEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
AAV9/hu 71 AALEHDKAYDQQLKAGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA
hu. 31-F 71 AALEHDKAYDQQLKAGDNPYLKYNHADAEEFQERLKEDTSFGGNLGRAVFQAKKRVLEPLG-LVEEAAKTA

	150	160	170	180	190	200	210
							
AAV5	139	PTGKRIDDHFP	-----KRKKARTEEDSKPSTSSDAEAGPSGSQQLQIPAQPASSLGADTMSAGG				
AAV3-3	140	PGKKGAVDQSPQ	-EPDSSSGVGKSGKQPARKKRLNFGQTDSESVDP-PQPLGEPAPAPTSLGSNTMASGG				
AAV4-4	139	PGKKRPLIESPQ	-QPDSSSTGIGKKGKQPAKKKLVFEDETGAGDGP---PEGSTSGAMS--DDSEMRAAA				
AAV1-A	140	PGKKRPVEQSPQ	-EPDSSSGIGKTGQQPAKKRLNFGQTDSESVDP-PQPLGEPAPATPAAVGPTTMSAGG				
hu. 46-A	140	PGKKRPVEQSPQ	-EPDSPSGIGKTGQQPAKKRLNFGQTDSESVDP-PQPLGEPAPATPAAVGPTTMSAGG				
hu. 48-A	140	PGKKRPVEQSPQ	-EPDSSSGIGKTGQQPAKKRLNFGQTDSESVDP-PQPLGEPAPATPAAVGPTTMSAGG				
hu. 44-A	140	PGKKRPVEQSPQ	-GPDSSSGIGKTGQQPAKKRLNFGQTDSESVDP-PQPLGEPAPATPAAVGPTTMSAGG				
hu. 43-A	140	PGKKRPVEPSPQ	RSPDSSSTGIGKKGQQPAKKRLNFGQTDSESVDP-PQPIGEPAPATPAAVGPTTMAAGG				
AAV6-A	140	PGKKRPVEQSPQ	-EPDSSSGIGKTGQQPAKKRLNFGQTDSESVDP-PQPLGEPAPATPAAVGPTTMSAGG				
hu. 34-B	140	PGKKRPVEHSPV	-EPDSSSGTGKAGQQPARKKRLNFGQTDADSVDP-PQPLGQPPAAPSGLGTNTMATGS				
hu. 47-B	140	PGKKRPVEHSPV	-EPDSSSGTGKAGQQPARKKRLNFGQTDADSVDP-PQPLGQPPAAPSGLGTNTMATGS				
hu. 29-B	140	PGKKRPVEHSPA	-EPDSSSGTGKSGNQPARKKRLNFGQTDSDSVDP-PQPLGQPPAAPSGLGTNTMATGS				

hu. 63-B 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPSGLGTNTMATGS
hu. 56-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGNQPARKRLNFGQTDGADSVDP-PQPLGQPPASPSGLGTNTMATGS
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hu. 35-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPSGLGTNTMATGS
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AAV2-B 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPSGLGTNTMATGS
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hu. 61-C 140 PGKKRPVEHPPV-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPSGLGSSTTMATGS
rh. 56-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPSGLGSSTTMATGS
hu. 9-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGHQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPTSLGSSTTMATGS
hu. 54-C 140 PGKKRPVEHSPA-EPDSSSGTGKAGQQPARKRLNFGQTDGADSVDP-PQPLGQPPAAPTSLGSSTTMATGS
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hu.18-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTDADSVDP-PQPLGQPPAAPSGLGSTTMASGS
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hu.4-C 140 PGKKRPVEHSPV-EPDSSSGTGKAGQQPARKRLNFGQTDADSVDP-PQPLGQPPAAPSGLGSTTMATGS
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rh.48-D 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
rh.55-D 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
rh.62-D 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
AAV7-D 140 PAKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPLGEPAPAPSSVSGSTVAAGG
rh.52-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.51-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.39-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGRTGDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.53-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.37-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPAKKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
rh.43-E 140 PGKKRPVEQSPQ-EPDSSSGIGKKGQQPARKRLNFGQTDSESVDP-PQPLGEPAPAPSGVGPNTMAAGG
rh.50-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPAGKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.49-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.61-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.41-E 140 PGKKRPVEPPQSPDSSTGIGKKGQQPAKKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
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hu.42-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPAKKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
rh.57-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
hu.40-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPAKKRLSFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG
AAV8-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPLGEPAPAPSGVGPNTMAAGG
rh.58-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPARKRLNFGQTDSESVDP-PQPIGEPAPAPSSVSGSTMAAGG
rh.40-E 140 PGKKRPVEPSQSPDSSTGIGKKGQQPAKKRLNFGQTDSESVDP-PQPIGEPAGPSGLSGTMAAGG

hu. 67-E	140	PGKKRPVEPSPQRS	PDSS	TGIGKKGQQ	PAKKRLN	FGQTGD	SESPD	-PQ	IGEPPAGPSGLSG	TMAAGG		
hu. 17-E	140	PGKKRPVEPSPQRS	PDSS	TGIGKTGQQ	PAKKRLN	FGQTGD	SESPD	-PQ	IGEPPAGPSGLSG	TMAAGG		
hu. 6-E	140	PGKKRPVEPSPQRS	PDSS	TGIGKTGQQ	PAKKRLN	FGQTGD	SESPD	-PQ	IGEPPAGPSGLSG	TMAAGG		
hu. 66-E	140	PGKKRPVEPSPQRS	PDSS	AGIGKKGQQ	PAKKRLN	FGQTGD	SESPD	-PQ	IGEPPAGPSGLSG	TMAAGG		
rh. 38-E	140	PGKKRPVEPSPQRS	PDSS	TGIGKKGQR	PAKKRLN	FGQTGD	SESPD	-PQ	IGEPPAGPSGLSG	TMAAGG		
hu. 32-F	140	PGKKRPVEQSPQ	-EPD	SSAGIGKSGSQ	PAKKKLN	FGQTGD	TESVPD	-PQ	IGEPPAAPSGVGS	LTMASGG		
AAV9/hu	140	PGKKRPVEQSPQ	-EPD	SSAGIGKSGAQ	PAKKRLN	FGQTGD	TESVPD	-PQ	IGEPPAAPSGVGS	LTMASGG		
hu. 31-F	140	PGKKRPVEQSPQ	-EPD	SSAGIGKSGSQ	PAKKKLN	FGQTGD	TESVPD	-PQ	IGEPPAAPSGVGS	LTMASGG		
AAV5	198	GGPLGDN	NQ	GADGVGN	ASGDWH	CDSTW	MGDRV	TKSTR	TWVLP	SYNNHQYREIKS-GSVDGS	NANAYFGY	
AAV3-3	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	SQWL	GDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
AAV4-4	202	GGA	AVEGGQ	GADGVGN	ASGDWH	CDSTW	SEGHV	TTSTR	TWVLP	TYNNHLYKRLG----	ESLQSN	TYNGF
AAV1-A	208	GAPMAD	NNEGAD	GVGNASGN	WHCD	STW	LGDRV	ITSTR	TWALPT	YNNHLYKQISS-ASTGAS	NDNHYFGY	
hu. 46-A	208	GAPMAD	NNEGAD	GVGNASGN	WHCD	STW	LGDRV	ITSTR	TWALPT	YNNHLYKQISS-ASTGAS	NDNHYFGY	
hu. 48-A	208	GAPMAD	NNEGAD	GVGNASGN	WHCD	STW	LGDRV	ITSTR	TWALPT	YNNHLYKQISS-TSTGAS	NDNHYFGY	
hu. 44-A	208	GAPMAD	NNEGAD	GVGNASGN	WHCD	STW	LGDRV	ITSTR	TWALPT	YNNHLYKQISS-ASTGAS	NDNHYFGY	
hu. 43-A	209	GAPMAD	NNEGAD	GVGNASGN	WHCD	STW	LGDRV	ITSTR	TWALPT	YNNHLYKQISS-ASTGAS	NDNHYFGY	
AAV6-A	208	GAPMAD	NNEGAD	GVGNASGN	WHCD	STW	LGDRV	ITSTR	TWALPT	YNNHLYKQISS-ASTGAS	NDNHYFGY	
hu. 34-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 47-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDSHYFGY	
hu. 29-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 63-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 56-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 45-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 57-B	207	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 35-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 58-B	208	GAPMAD	ND	GADGVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	
hu. 28-B	208	GAPMAD	NNEGAD	GVGNSSGN	WHCD	STW	MGDRV	ITSTR	TWALPT	YNNHLYKQIS--SQSGAS	NDNHYFGY	

hu. 51-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 19-B 208 GAPMADNNEGADGVGNSSGNWYCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 49-B 208 GAPMADNNEGADGVGNSSGSWHCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 52-B 208 GAPMADNNEGADGVGNSSGNRHRCDSTWMGDRVITSTRTWALPTYNNHLYRQIS--SQSGASNDNHYFGY
hu. 13-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
AAV2-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
hu. 20-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
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hu. 27-B 208 GAPMADNNEGADGVGNSSGNWHCDSTWMGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
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hu. 9-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGC
hu. 54-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY
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hu. 10-C 208 GAPMADNNEGADGVGNSSGNWHCDSQWLGDRVITSTRTWALPTYNNHLYKQIS--SQSGASNDNHYFGY

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14/125

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15/125

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rh. 38-E 279 STPWGYFDENRHFHCHFSPRDWQRLINNNWGFRPKRLSEKLFNIQVKEVTQNEGKTIANNLTSTIQVFTD
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hu. 31-F 278 STPWGYFDENRHFHCHFSPRDWQRLINNNWGFRPKRLSEKLFNIQVKEVTQNEGKTIANNLTSTVQVFTD

360 370 380 390 400 410 420
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16/125

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17/125

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 hu. 2-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 hu. 1-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 hu. 18-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 hu. 3-C 347 SEYQLPYVPGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 hu. 25-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSPFYCLEYFPSQMLRTGNNFQFS
 hu. 15-C 346 SGYQLPYVLGLAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 hu. 16-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 hu. 11-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFTFS
 hu. 10-C 346 SEYQLPYVLGSAHQGCLPPFPADVFTVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNLTFS
 hu. 4-C 346 SEYQLPYVLGSAHQGCLPPFPADVFMVPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFS
 rh. 54-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQVLRGTGNNFTFS
 rh. 48-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFS
 rh. 55-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFTFS
 rh. 62-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNND---SQSVGRSSFYCLEYFPSQMLRTGNNFTFS
 AAV7-D 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQSVGRSSFYCLEYFPSQMLRTGNNFEFS
 rh. 52-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTPNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
 rh. 51-E 349 SEYQLPYVLGSAHQGCQPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
 hu. 39-E 349 SEYQPPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
 rh. 53-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
 hu. 37-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFEFS
 rh. 43-E 348 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFQFT
 rh. 50-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGYLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFS
 rh. 49-E 349 SEYQLPYVLGSAHQGCLPPFPADVFMIPQYGNLTLNNG---SQAVGRSSFYCLEYFPSQMLRTGNNFSFS

rh. 61-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS	430	440	450	460	470	480	490
hu. 41-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS							
rh. 64-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS	406	YNFEEVPPFHSSFAPSQNLFKLANPLVDQYLYRFVSTN-----	NTGGVQFNKNLAGRYANTYKNWFPGP				
hu. 42-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	413	YTFEDVPPFHSSYAHSQSLDRLMNPLIDQYLYLNRTOGTSGTTNQSRLLFSQAGPQMSLSQARNWLPGP					
rh. 57-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFSFS	407	YSFEKVPPFHSSMYAHSQSLDRLMNPLIDQYLWGLQSTTTGTTLNAGTATTNFTKLRPTNFSNFKKNWLPGP					
hu. 40-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	414	YTFEEVPPFHSSYAHSQSLDRLMNPLIDQYLYLNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
AAV8-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	414	YTFEEVPLHSSCAHSQSLDRLMNPLIDQYLYLNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
rh. 58-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	414	YTFEEVPPFHSSYAHSQSLDRLMNPLIDQYLYLNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
rh. 40-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	414	YTFEEVPPFHSSYAHSQSLDRLMNPLIDQYLYLNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
hu. 67-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	414	YTFEEVPPFHSSYAHSQSLDRLMNPLIDQYLYPNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
hu. 17-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	415	YTFEEVPLHSSYAHSQSLDRLMNPLIVQYLYLNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
hu. 6-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	414	YTFEDVPPFHSSYAHSQSLDRLMNPLIDQYLYLNRTO-NQSGSAQNKDLLFSRGSFAGMSVQPKNWLPGP					
hu. 66-E	349	SEYQLPYVLGSAHQGCLPPFPADVFMI PQYGYLTLNNG---	SQAVGRSSFYCLEYFPSQMLRTGNNFEFS	413	YTFEDVPPFHSSYAHSQSLGRLMNPLIDQYLYLSRTN-TPSGTTTQSRLOFSQAGASDIRDQSRNWLPGP					
rh. 38-E	348	SDYQLPYVLGSAHEGCLPPFPADVFMI PQYGYLTLNDG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFS							
hu. 32-F	348	SDYQLPYVLGSAHEGCLPPFPADVFMI PQYGYLTLNDG---	SQAVGRSSFYCLEYFPSQMLRTGNNFQFS							
AAV9/hu	348	SDYQLPYVLGSAHEGCLPPFPADVFMI PQYGYLTLNDG---	GQAVGRSSFYCLEYFPSQMLRTGNNFQFS							
hu. 31-F										

hu. 47-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 29-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 63-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 56-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 45-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 57-B 412 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 35-B 413 YTFEDVPEFHSSYAHSQSLGRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 58-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 28-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 51-B 413 YTFEDVPEFHSGYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 19-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 49-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 52-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 13-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
AAV2-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 20-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 24-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 64-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLVDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 27-B 413 YTFEDVPEFHSSYAHGQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDVRDQSRNWLPGP
hu. 21-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 22-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 23-B 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLSTTN-TPSGTTTQSRLLQFSQAGASDIRDQSRNWLPGP
hu. 7-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-SNSGTLQQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 61-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-TNSGTLQQSRLLQFSQAGPTNMSLQAKNWLPGP
rh. 56-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-SNSGTLQQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 9-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-SNSGTLQQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 54-C 413 YTFEDVPEFHSSYAHSQGLDRMLMNPLIDQYLYLNKTQ-TASGT-QQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 53-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-TASGT-QQSRLLQFSQAGPTSMSLQAKNWLPGP
hu. 60-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLVDQYLYLNKTQ-TNSGTLQQSRLLQFSQAGPTNMSLQAKNWLPGP
hu. 55-C 413 YTFEDVPEFHSSYAHSQSLDRMLMNPLIDQYLYLNKTQ-TASGT-QQSRLLQFSQAGPTSMSLQAKNWLPGP

hu.2-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.1-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.18-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-SNSGTLQQSRLLFSQAGPTSMSLQAKNWLPGP
hu.3-C 414 YTFEDVPFHSSYAHCQSLDRMLMNPLIDQYLYYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.25-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
hu.15-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-SNSGTLQQSRLLFSQAGPTSMSLQAKNWLPGP
hu.16-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-SNSGTLQQSRLLFSQAGPTSMSLQAKNWLPGP
hu.11-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-SNSGTLQQSRLLFSQAGPTSMSLQAKNWLPGP
hu.10-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-SNSGTLQQSRLLFSQAGPTSMSLQAKNWLPGP
hu.4-C 413 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYYLNKTQ-TNSGTLQQSRLLFSQAGPTNMSLQAKNWLPGP
rh.54-D 415 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLARTQSNPGGTSGNRELQFYQGGPSTMAEQAKNWLPGP
rh.48-D 415 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLARTQSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
rh.55-D 415 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLARTQSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
rh.62-D 415 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLARTQSNAGGTAGNRELQFYQGGPTTMAEQAKNWLPGP
AAV7-D 415 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLARTQSNPGGTAGNRELQFYQGGPSTMAEQAKNWLPGP
rh.52-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
rh.51-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
hu.39-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
rh.53-E 416 YTFEDVPFHSSYVHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
hu.37-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTQGTQQLLSSQAGPANMSAQAKNWLPGP
rh.43-E 415 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQT-TGGTANTQTLLGFSQGGPNTMANQAKNWLPGP
rh.50-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLVDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
rh.49-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
rh.61-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
hu.41-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTQGTQQLLSSQAGPANMSAQAKNWLPGP
rh.64-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
hu.42-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTQGTQQLLSSQAGPANMSAQAKNWLPGP
rh.57-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTAGTQQLLSSQAGPSNMSAQARNWLPGP
hu.40-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQS-TGGTQGTQQLLSSQAGPANMSAQAKNWLPGP
AAV8-E 416 YTFEDVPFHSSYAHSQSLDRMLMNPLIDQYLYLSRTQT-TGGTANTQTLLGFSQGGPNTMANQAKNWLPGP

rh. 58-E	416	YTFEDVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSRTQS-TGGTAGTQQLLFSQAGPSNMSAQARNWLPGP
rh. 40-E	416	YTFEDVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSRTQS-TGGTQGTQQLLFSQAGPANMSARAKNWLPGP
hu. 67-E	416	YTFEDVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSRTQS-TGGTQGTQQLLFSQAGPANMSAQAKNWLPGP
hu. 17-E	416	YQFEDVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKNWLPGP
hu. 6-E	416	YQFEDVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSRTQS-TGGTAGTQQLLFSQAGPNNMSAQAKNWLPGP
hu. 66-E	416	YTFEDVPFHSSCA	HSQSSDR	LMNPLIDQ	LYLSRTRS-TGGTQGTQQLLFSQAGPANMSAQAKNWLPGP
rh. 38-E	416	YTFEDVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSRTQS-TGGTQGTQQLLFSQAGPANMSAQAKNWLPGP
hu. 32-F	415	YEFENVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSKTINGSG--QNQQTCLKFSVAGPSNMAVQGRNYIPGP
AAV9/hu	415	YEFENVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSKTINGSG--QNQQTCLKFSVAGPSNMAVQGRNYIPGP
hu. 31-F	415	YEFENVPFHSSY	AHSQSLDR	LMNPLIDQ	LYLSKTINGSG--QNQQTCLKFSVAGPSNMAVQGRNYIPGP
AAV5	469	MGR	TQGNLGS	GVN-----RASVSAFATNRMELEGASYQVPPQPNMGMTNNLQGSNTYALENTMIFNSQP	
AAV3-3	483	CYRQQRVSKT	ANDN-----NNSFPWTAASKYHLNGRDSL	VNPGPAMASHKDDEEKFFPMHGNLIFGKEG	
AAV4-4	477	SIKQQGF	SKTANQNYKI	PATGSDSLIKYETHSTLDGRWSALT	PGPPMATAGPADSKFS-NSQLIFAGPKQ
AAV1-A	483	CYRQQRVSKT	KTDN-----NNSNFTWTGASKYNLNGRESI	INPGTAMASHKDDEDKFFPMSGVMI FGKES	
hu. 46-A	483	CYRQQRVSKT	KTDN-----NNSNFTWTGASKYNLNGRESI	INPGTAMASHKDDEDKFFPMSGVMI FGKES	
hu. 48-A	483	CYRQQRVSKT	KTDN-----NNSNFTWTGASKYNLNGRESI	INPGTAVASHKDDEDKFFPMSGVMI FGKES	
hu. 44-A	483	CYRQQRVSKT	KTDN-----NNSNFTWTGASKYNLNGRESI	INPGTAMASHKDDEDKFFPMSGVMI FGKES	
hu. 43-A	484	CYRQQRVSKT	KTDN-----NNSNFTWTGASKYNLNGRESI	INPGTAMASHKDDEDKFFPMSGVMI FGKES	
AAV6-A	483	CYRQQRVSKT	KTDN-----NNSNFTWTGASKYNLNGRESI	INPGTAMASHKDDEDKFFPMSGVMI FGKES	
hu. 34-B	482	CYRQQRVSKT	SADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDEEKFFPQSGVLI FGKQG	
hu. 47-B	482	CYRQQRVSKT	SADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDNEEKFFPQSGVLI FGKQG	
hu. 29-B	482	CYRQQRVSKT	SADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDEEKFFPQSGVLI FGKQG	
hu. 63-B	482	CYRQQRVSKT	SADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDEEKFFPQSGVLI FGKQD	
hu. 56-B	482	CYRQQRVSKT	AADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDEEKFFPQSGVLI FGKQG	
hu. 45-B	482	CYRQQRVSKT	SADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAVASHKDDEEKFFPQSGVLI FGKQG	
hu. 57-B	481	CYRQQRVSKT	AADN-----NNGEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDEEKFFPQSGVLI FGKQG	
hu. 35-B	482	CYRQQRVSKT	SADN-----NNSEYSWTGATKYHLNGRDSL	VNPGPAMASHKDDEEKFFPQSGVLI FGKQG	

22/125

hu. 58-B 482 CYRQQRVSKTSADN-----NNSEYSWIGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPQSGVLI FGKQG
hu. 28-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPQSGVLI FGKQG
hu. 51-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDNEEKEFFPQSGVLI FGKQG
hu. 19-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 49-B 482 CYRQQRVSKTAADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPQSGVLI FGKQG
hu. 52-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDNEEKEFFPQSGVLI FGKQG
hu. 13-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPQSGVLI FGKQG
AAV2-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPQSGVLI FGKQG
hu. 20-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 24-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 64-B 482 CYRQQRVSKTSADN-----NNSEYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPQSGVLI FGKQD
hu. 27-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 21-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 22-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 23-B 482 CYRQQRVSKTAADN-----NNSDYSWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEYFPQSGVLI FGKQD
hu. 7-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 61-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
rh. 56-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 9-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 54-C 481 CYRQQRLSKQANDN-----NNSNFPWTGATKYHLNGGDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKEG
hu. 53-C 481 CYRQQRLSKQANDN-----NNSNFPWTGATKYLYLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKEG
hu. 60-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 55-C 481 CYRQQRLSKQANDN-----NNSNFPWTGATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKEG
hu. 2-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 1-C 482 CYRQQRLSKQANGN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 18-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 3-C 483 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 25-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 15-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG
hu. 16-C 482 CYRQQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPNPGPAMASHKDDDEEKEFFPMHGTLI FGKQG

23/125

hu.11-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYRLNGRDSLVPGPAMASHKDDDEEKEFFPMHGTLIFGKQG
hu.10-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPGPAMASHKDDDEEKEFFPMHGTLIFGKQG
hu.4-C 482 CYRQRLSKQANDN-----NNSNFPWTAATKYHLNGRDSLVPGPAMASHKDDDEEKEFFPMHGTLIFGKQG
rh.54-D 485 CFRQQRVSKTLDQN-----NNSNEFAWTGATKYHLNGRNSLVPGVAMATHKDDDEDRFFPSSGVLIFGKQG
rh.48-D 485 CFRQQRVSKTLDQN-----NNSNEFAWTGATKYHLNGRNSLVPGVAMATHKDDDEERFFPSSGVLIFGKQG
rh.55-D 485 CFRQRRVSKTLDQN-----NNSNEFAWTGATKYHLNGRNSLVPGVAMATHKDDDEERFFPSSGVLIFGKQG
rh.62-D 485 CFRQQRVSKTLDQN-----NNSNEFAWTGATKYHLNGRNSLVPGVAMATHKDDDEERFFPSSGVLIFGKQG
AAV7-D 485 CFRQQRVSKTLDQN-----NNSNEFAWTGATKYHLNGRNSLVPGVAMATHKDDDEDRFFPSSGVLIFGKQG
rh.52-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh.51-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu.39-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh.53-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu.37-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh.43-E 484 CYRQQRVSTTSGQN-----NNSNEFAWTAGTKYHLNGRNSLANPGIAMATHKDDDEERFFPVTG-SCFWQQN
rh.50-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh.49-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh.61-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu.41-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh.64-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu.42-E 485 CYRQQRVSTTLSQS-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh.57-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
hu.40-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
AAV8-E 485 CYRQQRVSTTSGQN-----NNSNEFAWTAGTKYHLNGRNSLANPGIAMATHKDDDEERFFPSNGILIFGKQN
rh.58-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATNKDDDEDRFFPSSGILMFGKQG
rh.40-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu.67-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu.17-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu.6-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
hu.66-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG
rh.38-E 485 CYRQQRVSTTLSQN-----NNSNEFAWTGATKYHLNGRDSLVPGVAMATHKDDDEERFFPSSGVLMFGKQG

hu.32-F 483 SYRQQRVSTTVTQN-----NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG
AAV9/hu 483 SYRQQRVSTTVTQN-----NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG
hu.31-F 483 SYRQQRVSTTVTQN-----NNSEFAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQG

570 580 590 600 610 620 630

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AAV5 534 ANPGTTATYLEGNMLITSESETQPVNRVAYNVGGQMATNNQSSTTAPATGTYNLQEI VPGSVWMERDVYL
AAV3-3- 548 T--TASNAELD-NVMITDEEEIRTTNPVATEQYGTVANNLQSSNTAPTGTGNHQGALPGMVWQDRDVYL
AAV4-4- 546 N--GNTATVPG-TLIFTSEEELAATNATDMDMGNLPGGDQSSNSNLP TVDRLTALGAVPGMVWQNRDIYY
AAV1-A- 548 A--GASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPA TGDVHAMGALPGMVWQDRDVYL
hu.46-A 548 A--GASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPA TGDVHAMGALPGMVWQDRDVYL
hu.48-A 548 A--GASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPA TGDVHAMGALPGMVWQDRDVYL
hu.44-A 548 A--GASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPA TGDVHAMGALPGMVWQDRDVYL
hu.43-A 549 A--GASNTALD-NVMITDEEEIKATNPVATERFGTVAVNFQSSSTDPA TGDVHAMGALPGMVWQDRDVYL
AAV6-A 548 A--GASNTALD-NVMITDEEEIKATNPVATERFGTVAVNLQSSSTDPA TGDVHVMGALPGMVWQDRDVYL
hu.34-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu.47-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu.29-B 547 P--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATADVNTQGVLPGMVWQDRDVYL
hu.63-B 547 S--GKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.56-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.45-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATADVNTQGVLPGMVWQDRDVYL
hu.57-B 546 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTRAATSDVNTQGVLPGMVWQDRDVYL
hu.35-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu.58-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATADVNTQGVLPGMVWQDRDVYL
hu.28-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATADVNTQGVLPGMVWQDRDVYL
hu.51-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu.19-B 547 S--GKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu.49-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQSGNTQAATADVNTQGVLPGMVWQDRDVHL
hu.52-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu.13-B 547 S--EKTNV DIE-KVMITDEEEIRTTNPVATEQYGSVSTNLQGGNTQAATADVNTQGVLPGMVWQDRDVYL

AAV2-B 547 S--EKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQRGNRQAATADVNTQGVLPGMVWQDRDVYL
hu. 20-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 24-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 64-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 27-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPAAATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 21-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 22-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 23-B 547 S--GKTNV DIE-KVMI TDEEEI RTTNPVATEQYGSVSTNLQSGNTQAATSDVNTQGVLPGMVWQDRDVYL
hu. 7-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 61-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
rh. 56-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 9-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 54-C 546 T--NATNAELE-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTAASTETVNVNHQGALPGMVWQDRDVYL
hu. 53-C 546 T--NATNAELE-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTAASTETVNVNHQGALPGMVWQDRDVYL
hu. 60-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 55-C 546 T--NATNAELE-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTAASTETVNVNHQGALPGMVWQDRDVYL
hu. 2-C 547 T--NANDADLD-NVMI TDEEEI RATNPVATEQYGYVSNNLQNSNTGPTTGTNVNRQGALPGMVWQDRDVYL
hu. 1-C 547 T--NANDADLD-NVMI TDEEEI RATNPVATEQYGYVSNNLQNSNTGPTTGTNVNRQGALPGMVWQDRDVYL
hu. 18-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 3-C 548 T--NANDADLD-NVMI TDEEEI RPTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 25-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 15-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 16-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 11-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
hu. 10-C 547 T--NANDADLD-NVMI TDEEEI RTTNPVATEQYGYVSNNLQNSNTGPTTGTNVNHQGALPGMVWQDRDVYL
rh. 54-D 550 A--TN-KTTLE-NVLM TNEEEI RPTNPVATEEYGI VSSNLQAANTAAQTQVNVNNGALPGMVWQNRDVYL
rh. 48-D 550 A--AN-KTTLE-NVLM TNEEEI RPTNPVATEEYGT VSSNLQAANTAAQTQVNVNNGALPGMVWQNRDVYL
rh. 55-D 550 A--AN-KTTLE-NVLM TNEEEI RPTNPVATEEYGT VSSNLQAANTAAQTQVNVNNGALPGMVWQNRDVYL
rh. 62-D 550 A--AN-KTTLE-NVLM TNEEEI RPTNPVATEEYGT VSSNLQAANTAAQTQVNVNNGALPGMVWQNRDVYL

AAV7-D	550	A--TN-KTTL	EEIRPTNPVATEEY	GIVSSNLQAANTAAQTQV	VNNQGALPGMVWQNRDVYL	700
rh. 52-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
rh. 51-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 39-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPTIVGAVNSQGALPGMVWQNRDVYL	
rh. 53-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 37-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
rh. 43-E	548	A--ARDNADYS	-DVMLTSEEE	IKTTNPVATEEYGIVADNLQ	QQNTAPQIGTVNSQGALPGMVWQNRDVYL	
rh. 50-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
rh. 49-E	550	A--GKDNMGYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
rh. 61-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQDTAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 41-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
rh. 64-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 42-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
rh. 57-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 40-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
AAV8-E	550	A--ARDNADYS	-DVMLTSEEE	IKTTNPVATEEYGIVADNLQ	QQNTAPQIGTVNSQGALPGMVWQNRDVYL	
rh. 58-E	550	A--GKDNVDYS	-NVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNTAPIVGAVNSQGALPGMVWQNRDVYL	
rh. 40-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QANTGTGPIVGNVNSQGALPGMVWQNRDVYL	
hu. 67-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
hu. 17-E	550	A--GKDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNAAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 6-E	550	A--GKDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QQNAAPIVGAVNSQGALPGMVWQNRDVYL	
hu. 66-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
rh. 38-E	550	A--GRDNVDYS	-SVMLTSEEE	IKTTNPVATEQYGVVADNLQ	QNTGTGPIVGNVNSQGALPGMVWQNRDVYL	
hu. 32-F	548	T--GRDNVDAD	-KVMITNEEE	IKTTNPVATESYGQVATNHQ	SAQAQTGWVQNQGI LPGMVWQDRDVYL	
AAV9/hu	548	T--GRDNVDAD	-KVMITNEEE	IKTTNPVATESYGQVATNHQ	SAQAQTGWVQNQGI LPGMVWQDRDVYL	
hu. 31-F	548	T--GRDNVDAD	-KVMITNEEE	IKTTNPVATESYGQVATNHQ	SAQAQTGWVQNQGI LPGMVWQDRDVYL	

27/125

AAV3-3- 615 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQIMIKNTPVPANPPTTFSPAKFASFITQYSTGQVSVEIE
AAV4-4- 613 QGPIWAKIPHDTGHEHPSPLIGGFGLKHPPPPQIFIKNTPVPANPATTFSSTPVNSFITQYSTGQVSQID
AAV1-A- 615 QGPIWAKIPHDTGHEHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu. 46-A 615 QGPIWAKIPHDTGHEHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSAGQVSVEIE
hu. 48-A 615 QGPIWAKIPHDTGHEHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu. 44-A 615 QGPIWAKIPHDTGHEHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu. 43-A 616 QGPIWAKIPHDTGHEHPSPLMGGFGLKNPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
AAV6-A 615 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPPAEFSATKFASFITQYSTGQVSVEIE
hu. 34-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 47-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 29-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 63-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 56-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 45-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 57-B 613 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 35-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 58-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGRVSVEIE
hu. 28-B 614 QGPTWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 51-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 19-B 614 QGPIWAKIPHDTGHEHPSPLVGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 49-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 52-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 13-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
AAV2-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 20-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 24-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 64-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 27-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 21-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE
hu. 22-B 614 QGPIWAKIPHDTGHEHPSPLMGGFGLKHPPPPQILIKNTPVPANPSTTFSAAKFASFITQYSTGQVSVEIE

28/125

hu. 23-B 614 RGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQILIKNTVPANPSTTFSAAKFAFIFTQYSTGQVSVEIE
 hu. 7-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 61-C 614 QGPIWAKIPHTDGHFHPSPVLVGGFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 rh. 56-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 9-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 54-C 613 RGPIWAKIPHADGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 53-C 613 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 60-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 55-C 613 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 2-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 1-C 614 QGPIWAKIPHTDGHFHPSPLTGGFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 18-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSSKFAFIFTQYSTGQVSVEIE
 hu. 3-C 615 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKSTVPANPPTNFSSAKFASSITQYSTGQVSVEIE
 hu. 25-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 15-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 16-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 11-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 10-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 hu. 4-C 614 QGPIWAKIPHTDGHFHPSPMLMGFFGLKHPPPPQIMIKNTVPANPPTNFSSAKFAFIFTQYSTGQVSVEIE
 rh. 54-D 616 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPANPPEVFTPAKFAFIFTQYSTGQVSVEIE
 rh. 48-D 616 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPANPPEVFTPAKFAFIFTQYSTGQVSVEIE
 rh. 55-D 616 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPANPPEVFTPAKFAFIFTQYSTGQVSVEIE
 rh. 62-D 616 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPANPPEVFTPAKFAFIFTQYSTGQVSVEIE
 AAV7-D 616 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPANPPEVFTPAKFAFIFTQYSTGQVSVEIE
 rh. 52-E 617 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPADPPTAFNQAKLNSFIFTQYSTGQVSVEIE
 rh. 51-E 617 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPADPPTAFNQAKLNSFIFTQYSTGQVSVEIE
 hu. 39-E 617 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPADPPTAFNQAKLNSFIAQYSTGQVSVEIE
 rh. 53-E 617 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPADPPTAFNQAKLNSFIFTQYSTGQVSVEIE
 hu. 37-E 617 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPADPPTTFSQAKLASFIFTQYSTGQVSVEIE
 rh. 43-E 615 QGPIWAKIPHTDGNFHPSPMLMGFFGLKHPPPPQILIKNTVPADPPTTFNQSKLNSFIFTQYSTGQVSVEIE

FIG. 2AA

29/125

rh. 50-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	Q	A	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
rh. 49-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	Q	A	K	L	N	S	F	I	T	Q	Y	G	T	G	Q	V	S	V	E	I	E
rh. 61-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQV	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	Q	A	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 41-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
rh. 64-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	Q	A	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 42-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
rh. 57-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	Q	A	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	A	E	I	E
hu. 40-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
AAV8-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	N	Q	S	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
rh. 58-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	S	T	P	V	P	A	D	P	P	T	A	F	N	Q	A	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
rh. 40-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 67-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 17-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 6-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 66-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
rh. 38-E	617	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 32-F	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	T	F	S	Q	A	K	L	A	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
AAV9/hu	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	K	D	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E
hu. 31-F	615	QGPIWAKIPH	TDGNFHPSP	LMGGFGLKH	PPPPQI	L	I	K	N	T	P	V	P	A	D	P	P	T	A	F	N	K	D	K	L	N	S	F	I	T	Q	Y	S	T	G	Q	V	S	V	E	I	E

		710		720		730		740		750
										
AAV5	673	WELKKENSKR	WNPEIQY	TNNYNDPQ	FVDFAPD	STGEYR	TRPIG	TRYLTRPL*		
AAV3-3	685	WELQKENSKR	WNPEIQY	TSNYNKS	VNVDF	TVDTNG	VYSEPR	PIGTRYLTRNL*		
AAV4-4	683	WEIQERSKR	WNPEVQ	TSNYGQQ	NSLLWAP	DAAGKY	TEPR	IGTRYLTRHL*		
AAV1-A	685	WELQKENSKR	WNPEVQ	TSNYAKS	ANVDF	TVDNNG	LYTEPR	IGTRYLTRPL*		
hu. 46-A	685	WELQKENSKR	WNPEVQ	TSNYAKS	ANVDF	TVDNNG	LYTEPR	IGTRYLTRPL*		
hu. 48-A	685	WELQKENSKR	WNPEVQ	TSNYAKS	ANVDF	TVDNNG	LYTEPR	IGTRYLTRPL*		
hu. 44-A	685	WELQKENSKR	WNPEVQ	TSNYAKS	ANVDF	TVDNNG	LYTEPR	IGTRYLTRPL*		
hu. 43-A	686	WELQKENSKR	WNPEVQ	TSNYAKS	ASVDF	TVDNNG	LYTEPR	IGTRYLTRPL*		

FIG. 2AB

30/125

AAV6-A 685 WELQENSKRWNPEVQYTSNYAKSANVDFTTVDNNGLYTEPRPIGTRYLTRPL*
 hu.34-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.47-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.29-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.63-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.56-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.45-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.57-B 683 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.35-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.58-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.28-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.51-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.19-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.49-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.52-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.13-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 AAV2-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.20-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGARYLTRNL*
 hu.24-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.64-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.27-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.21-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.22-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.23-B 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.7-C 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.61-C 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 rh.56-C 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.9-C 684 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPCPIGTRYLTRNL*
 hu.54-C 683 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*
 hu.53-C 683 WELQENSKRWNPEIQYTSNYNKSXNVDFTTVDNTNGVYSEPRPIGTRYLTRNL*

FIG. 2AC

31/125

hu. 60-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 55-C 683 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 2-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 1-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 18-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYPTRNL*
hu. 3-C 685 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 25-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNNGVYSEPRPIGTRYLTRNL*
hu. 15-C 684 WELQEDSKRWNPEIQYTSNYNKPVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 16-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 11-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 10-C 684 WELRKENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
hu. 4-C 684 WELQENSKRWNPEIQYTSNYNKSVNVDFTVDTNGVYSEPRPIGTRYLTRNL*
rh. 54-D 686 WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh. 48-D 686 WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh. 55-D 686 WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh. 62-D 686 WELQENSKRWNPEIQYTSNFDKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
AAV7-D 686 WELQENSKRWNPEIQYTSNFEKQGTGVDFAVDSQGVYSEPRPIGTRYLTRNL*
rh. 52-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 51-E 687 WEPQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
hu. 39-E 687 WELQENSKRWNPEIQYTSNYYKSTNADFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 53-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYPTRNL*
hu. 37-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 43-E 685 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 50-E 687 WELQENSKRWSPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 49-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 61-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
hu. 41-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 64-E 687 WELQENSKRRNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
hu. 42-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh. 57-E 687 WELQENSKRWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*

FIG. 2AD

32/125

hu.40-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
AAV8-E	687	WELQKENS	KRWNPEIQYTSNYYKSTSVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh.58-E	687	WELQKENS	KCWNPEIQYTSNYYKSTNVDFAVNTEGVYSEPRPIGTRYLTRNL*
rh.40-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNSEGTYSEPRPIGTRYLTRNL*
hu.67-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.17-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.6-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.66-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
rh.38-E	687	WELQKENS	KRWNPEIQYTSNYYKSTNVDFAVNTEGTYSEPRPIGTRYLTRNL*
hu.32-F	685	WELQKENS	KRWNPEIQYTSNYYKSNVDFAVNTEGTYSEPRPIGTRYLTRNL*
AAV9/hu	685	WELQKENS	KRWNPEIQYTSNYYKSNVDFAVNTEGVYSEPRPIGTRYLTRNL*
hu.31-F	685	WELQKENS	KRWNPEIQYTSNYYKSNVDFAVNTEGVYSEPRPIGTRYLTRNL*

FIG. 2AE

33/125

	10	20	30	40	50	60	70
							
AAV5	1	ATGTC	TTTGT	GATC	ACCC	CTCC	AGATT
AAV3-3	1	ATGGC	TGCT	GACG	GTAT	CTTCC	AGATT
AAV4-4	1	---	ATG	ACTG	ACG	GTAC	CTTCC
AAV1-A	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 46-A	1	ATGGC	TGCC	GACG	GTAT	CTTCC	AGATT
hu. 48-A	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 44-A	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 43-A	1	ATGGC	TGCT	GACG	GTAT	CTTCC	AGATT
AAV6-A	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 34-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 47-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 29-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 63-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 56-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 45-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 57-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 35-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 58-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 28-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 51-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 19-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 49-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 52-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 13-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
AAV2-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 20-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 24-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT
hu. 64-B	1	ATGGC	TGCC	GATG	GTAT	CTTCC	AGATT

34/125

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

rh. 53-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 37-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 43-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 50-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 49-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 61-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 41-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 64-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 42-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 57-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 40-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
AAV8-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 58-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 40-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 67-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 17-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 6-E 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 66-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
rh. 38-E 1 ATGGCTGCTGACGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
hu. 32-F 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAGGGCATTCGCGAGTGGTGGG
AAV9/hu 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTTAGTGAAGGAATTCGCGAGTGGTGGG
hu. 31-F 1 ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAACCTCTCTGAAGGAATAAGACAGTGGTGGG

80 90 100 110 120 130 140
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
GCCTTGAAGCGGGCCACCGAAACCAACCCAAATCAGCAGCATCAAGATCAAGCCCGTGGTCTTTGTGCT
CTCTGAAACCTGGAGTCCCTCAACCCAAAGCGAAACCAACACCCAGGACAACCGTCGGGGTCTTTGTGCT
CGCTGCAACCTGGAGCCCCCTAAACCCAAAGGCAAAATCAACAACATCAGGACAACGCTCGGGGTCTTTGTGCT
ACTTGAAACCTGGAGCCCCCGAAGCCCCAAAGCCAGCAAAAGCAGGACGCGCGGGGTCTGTGCTGCT
AGCTCAAACCTGGCCCCACCCACCAAGCCCCGAGCGGCATAAGGACGACAGCGGTCTTTGTGCT

36/125

hu. 48-A	71	ACTTGAACCTGGAGCCCCGAAAGCCCAAGCCAAAGCCAGCAAAAGCAGGACGAGCGCGGGTCTGGTGCT
hu. 44-A	71	AGCTCAGACCTGGCCCCACACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 43-A	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGCCACAGAGCAAGCAGGACGACGCGCGGGTCTGGTGCT
AAV6-A	71	ACTTGAAACCTGGAGCCCCGAAACCCAAAGCCAAACCAAGCAGGACGACGCGCGGGTCTGGTGCT
hu. 34-B	71	AGTCAAACCTGGCCCCACCAACCAAGAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 47-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 29-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 63-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 56-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 45-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 57-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 35-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 58-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 28-B	71	AACTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 51-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 19-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 49-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 52-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 13-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
AAV2-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 20-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 24-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 64-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 27-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 21-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 22-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 23-B	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 7-C	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
hu. 61-C	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT
rh. 56-C	71	AGTCAAACCTGGCCCCACCAACCAAGCCCGCAGAGCGGCATAAGGACGACAGCAGGGTCTTGTGCT

37/125

hu. 9-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATCAGGACAACAGCAGGGGTCTTGTGCT
hu. 54-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 53-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 60-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 55-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 2-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 1-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 18-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 3-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 25-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 15-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 16-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 11-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
hu. 10-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCTCGAGAGCGGCATCAGGACGACAGCAGGGGTCTTGTGCT
hu. 4-C	71	AGCTCAAAACCTGGCCCCACCAACCAAAAGCCCCGAGAGCGGCATAAGGACGACAGCAGGGGTCTTGTGCT
rh. 54-D	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 48-D	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 55-D	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 62-D	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
AAV7-D	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 52-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 51-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
hu. 39-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 53-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
hu. 37-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 43-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 50-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 49-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
rh. 61-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT
hu. 41-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAAGCAGCAGAGCAGGACGAGCCGGGTCTGGTGCT

38/125

rh. 64-E	71	ACCTGAAACCTGGAGCCCCGAAACCCAAAGCCAAACAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT	150	160	170	180	190	200	210
hu. 42-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGAGCAGGACGAGCCGGGGTCTGGTGCT							
rh. 57-E	71	CGCTGAAACCTGGAGCCCCGAAAGCCCAAGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
hu. 40-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
AAV8-E	71	CGCTGAAACCTGGAGCCCCGAAAGCCCAAGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
rh. 58-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
rh. 40-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
hu. 67-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
hu. 17-E	71	ACTTGAAACCTGGAGCCCCGAAACCCCAAGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
hu. 6-E	71	ACTTGAAACCTGGAGCCCCGAAACCCCAAGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
hu. 66-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
rh. 38-E	71	ACCTGAAACCTGGAGCCCCCAAGCCCAAGGCCAAACAGCAGCAAAAGCAGGACGAGCCGGGGTCTGGTGCT							
hu. 32-F	71	AGCTCAACCTGGCCCCACCAACCCAAAGCCCGCAGAGCGGCATAAGGACGACAGAGGGGTCTTGTGCT							
AAV9/hu	71	CTTTGAAACCTGGAGCCCCCTCAACCCAAAGGCCAAATCAACAACATCAAGACAACGCTCGAGGTCTTGTGCT							
hu. 31-F	71	AGCTCAACCTGGCCCCCACCAACCCAAAGCCCGCAGAGCGGCATAAGGACGACAGAGGGGTCTTGTGCT							
AAV5	138	GCCTGGTTATAACTATCTCGGACCCCGGAAACGGTCTCGATCGAGGAGAGCCTGTCAACAGGGCAGACGAG							
AAV3-3	141	TCCGGGTTACAAATACCTCGGACCCCGGTAACGGACTCGACAAAGGAGAGCCGGTCAACGAGGCGGACGCG							
AAV4-4	138	TCCGGGTTACAAATACCTCGGACCCCGGCAACGGACTCGACAAAGGGGAACCCGTCAACGAGCGGACGCG							
AAV1-A	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGCCCGTCAACGCGGCGACGCA							
hu. 46-A	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGAGGACGAGCC							
hu. 48-A	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGCGGCGACGCA							
hu. 44-A	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGAGGACGAGCC							
hu. 43-A	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGCGGCGACGCA							
AAV6-A	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGCGGCGATGCA							
hu. 34-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGAGGACGAGCC							
hu. 47-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGAGGACGAGCC							
hu. 29-B	141	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAAGGGGAGAGCCCGTCAACGAGGACGAGCC							

FIG. 3F

39/125

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	TCCTGGGTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGAGAGCCGGTCAACGAGGCAGACGCC
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

40/125

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

hu. 67-E	141	TCTTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAATGCGGCGGACGCA	220	230	240	250	260	270	280
hu. 17-E	141	TCCTGGCTGCAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGCGGACGCA							
hu. 6-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGCGGACGCA							
hu. 66-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGCGGACGCA							
rh. 38-E	141	TCCTGGCTACAAGTACCTCGGACCCCTTCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGGCGGACGCA							
hu. 32-F	141	TCCTGGGTACAAGTACCTCGGACCCCGGCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGAGCAGACGCG							
AAV9/hu	141	TCCGGGTACAATAACCTTGGACCCCGGCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGAGCAGACGCG							
hu. 31-F	141	TCCTGGGTACAAGTACCTCGGACCCCGGCAACGGACTCGACAAGGGGAGCCCCGTCAACGCGAGCAGACGCG							
AAV5	208	GTGCGCGGAGAGCAGACATCTCGTACAACGAGCAGCTTGAGGCGGGAGACAAACCCCTACCTCAAGTACA							
AAV3-3-	211	GCAGCCCTCGAACACGACAAAGCTTACGACCAGCAGCTCAAGGCCGGTGACAAACCCCGTACCTCAAGTACA							
AAV4-4-	208	GCAGCCCTCGAGCACGACAAGGCTACGACCAGCAGCTCAAGGCCGGTGACAAACCCCTACCTCAAGTACA							
AAV1-A	211	GCGGCCCTCGAGCACGACAAGGCTACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCCGTATA							
hu. 46-A	211	GCGGCCCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 48-A	211	GCGGCCCTCGAGCACGACAAGGCTACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCCGTATA							
hu. 44-A	211	GCGGCCCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 43-A	211	GCGGCCCTCGAGCACGACAAGGCTACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCCCGGTATA							
AAV6-A	211	GCGGCCCTCGAGCACGACAAGGCTACGACCAGCAGCTCAAAGCGGGTGACAATCCGTACCTGCCGTATA							
hu. 34-B	211	GCGGCCCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 47-B	211	GCGGCCCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 29-B	211	GCGGCCCTCGAGCACGACAAGGCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 63-B	211	GCGGCCCTCGAGCACGACAAGGCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCCCAAGTACA							
hu. 56-B	211	GCGGCCCTCGAGCACGACAAGGCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 45-B	211	GCGGCCCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 57-B	208	GCGGCCCTCGAGCACGACAAGGCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 35-B	211	GCGGCCCTCGAGCACGACAAGCCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							
hu. 58-B	211	GCGGCCCTCGAGCACGACAAGGCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACG							
hu. 28-B	211	GCGGCCCTCGAGCACGACAAGGCTACGACCGGCAGCTCGACAGCGGAGACAACCCGTACCTCAAGTACA							

42/125

hu. 51-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 19-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 49-B 211 GCGGCCCTCGAGTACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 52-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 13-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 AAV2-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 20-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 24-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGATAACCCGTACCTCAAAGTACA
 hu. 64-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACGGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 27-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 21-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGATAACCCGTACCTCAAAGTACA
 hu. 22-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 23-B 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 7-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 61-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 rh. 56-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 9-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 54-C 211 GCGGCTCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 53-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 60-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 55-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 2-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 1-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 18-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGAAAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 3-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 25-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCAACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 15-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 16-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 11-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA
 hu. 10-C 211 GCGGCCCTCGAGCACGACAAAGCCCTACGACCCGGCAGCTCGACAGCGGAGACAAACCCGTACCTCAAAGTACA

43/125

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

44/125

hu.31-F	211	GCGGCCCTCGAGCACGACAAGGCCTACGACCAGCAGCTCAAGGCCGGAGACAACCCGTACCTCAAGTACA	290	300	310	320	330	340	350
									
AAV5	278	ACCACGGGACGCCGAGTTTCAGGAGAAAGCTCGCCGACGACACATCCTTCGGGGGAAACCTCGGAAAGGC							
AAV3-3	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTTCAAGAAGATACGTCTTTTGGGGGCAACCTTGGCAGAGC							
AAV4-4	278	ACCACGCCGACGCCGAGTTTCAGCAGCGGCTTCAGGGCGACACATCGTTTGGGGGCAACCTCGGCAGAGC							
AAV1-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC							
hu.46-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGGGC							
hu.48-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC							
hu.44-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC							
hu.43-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGCCCTTTTGGGGGCAACCTCGGGCGAGC							
AAV6-A	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC							
hu.34-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC							
hu.47-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC							
hu.29-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC							
hu.63-B	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGGCAACCTCGGACGAGC							
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							

45/125

hu. 24-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 64-B	281	ACCACGCCGACGCGGAGTTCCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 27-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 21-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAGGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 22-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGGAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 23-B	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 7-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 61-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
rh. 56-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 9-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 54-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 53-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 60-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 55-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 2-C	281	ACCACGCCGACGACAGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 1-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 18-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 3-C	281	ACCACGCCGACGACAGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 25-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 15-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 16-C	281	ACCACGCCGCGGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 11-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 10-C	281	ACCACGCCGACGCGGAGTTTCAGGAGCGTCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
hu. 4-C	281	ACCACGCCGACGACAGAGTTTCAGGAGCGCCTTAAAGAAGATACGTCTTTTGGGGCAACCTCGGACGAGC
rh. 54-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGCGGAGC
rh. 48-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGCGGAGC
rh. 55-D	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGCGGAGC
rh. 62-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGCGGAGC
AAV7-D	281	ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGCGGAGC
rh. 52-E	281	ATCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGCAACCTCGGCGGAGC

rh. 51-E 281 ATACGCCGACGCCGAGCTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 39-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 53-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 37-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 43-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 50-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 49-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 61-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 41-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTACAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 64-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 42-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 57-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 40-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
AAV8-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 58-E 281 ATACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 40-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 67-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 17-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 6-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 66-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTGCAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
rh. 38-E 281 ACCACGCCGACGCCGAGTTTCAGGAGCGTCTACAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 32-F 281 ACCACGCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
AAV9/hu 281 ACCACGCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC
hu. 31-F 281 ACCACGCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTCTTTTGGGGGCAACCTCGGGCGAGC

360 370 380 390 400 410 420
.....|.....|.....|.....|.....|.....|.....|.....|.....|
AAV5 348 AGTCTTTCAGGCCCAAGAAAAGGGTTCTCGAACCTTTTGGC---CTGGTTGAAGAGGGTGCTAAGACGGCC
AAV3-3 351 AGTCTTTCAGGCCCAAAAGAGGATCCTTGAGCCTCTTGGT---CTGGTTGAGGAAGCAGCTAAACGGCT
AAV4-4 348 AGTCTTTCAGGCCCAAAAGAGGGTTCTTGAACCTCTTGGT---CTGGTTGAGCAAGCGGGTGAGACGGCT

47/125

AAV1-A 351 AGTCTTCCAGGCCAAGAACGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTAAGACGGCT
 hu.46-A 351 AGTCTTCCAGGCCAAGAACGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTAAGACGGCT
 hu.48-A 351 AGTCTTCCAGGCCAAGAACGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTAAGACGGCT
 hu.44-A 351 AGTCTTCCAGGCCAAGAACGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGGCGCTGAGACGGCT
 hu.43-A 351 AGTCTTCCAGGCCAAGAACGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
 AAV6-A 351 AGTCTTCCAGGCCAAGAACGGGTTCTCGAACCTTTTGGT---CTGGTTGAGGAAGGTGCTAAGACGGCT
 hu.34-B 351 AGTCTTCCAGGCCAAGAACGGGTACTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.47-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTGAACCTCTGGC---CTGGTTGGGGAACCTGTTAAGACGGCT
 hu.29-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTGGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
 hu.63-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.56-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.45-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.57-B 348 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.35-B 351 AGTCTTCCAGGCCAAGAACGGGTACTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.58-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
 hu.28-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTGGAACCTCTGAGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
 hu.51-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGGGGAACCTGTCAAGACGGCT
 hu.19-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.49-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.52-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGGGGAACCTGTTAAGACGGCT
 hu.13-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT
 AAV2-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.20-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.24-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.64-B 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.27-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.21-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.22-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.23-B 351 AGTCTTCCAGGCCAAGAACGGATTCTTGAACCTCTGGC---CTGGTTGAGGAACCTGTTAAGACGGCT
 hu.7-C 351 AGTCTTCCAGGCCAAGAACGGGTTCTTGAACCTCTGGC---CTGGTTGAGGAGCCTGTTAAGACGGCT

48/125

hu. 61-C 351 AGTCTTCCAGGCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAACGGCT
 rh. 56-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 9-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 54-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 53-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 60-C 351 AGTCTTCCAGGCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAACGGCT
 hu. 55-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 2-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 1-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 18-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAACGGCT
 hu. 3-C 351 AGTCTTCCAGGCGAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 25-C 351 AGTCTTCCAGGCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAACGGCT
 hu. 15-C 351 AGTCTTCCAGGCGCAAAAAGAGGGTTCTTGAACCTCTGGGC---TTGGTTGGGAGCCTGTAAAACGGCT
 hu. 16-C 351 AGTCTTCCAGGCGCAAAAAGAGGGTTCTTGAACCTCTGGGC---TTGGTTGAGGAACCTGTAAAACGGCT
 hu. 11-C 351 AGTCTTCCAGGCGCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 10-C 351 AGTCTTCCAGGCGCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 hu. 4-C 351 AGTCTTCCAGGCGCAAAAAGAGGGTTCTTGAACCTCTGGGC---CTGGTTGAGGAACCTGTAAAGACGGCT
 rh. 54-D 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
 rh. 48-D 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
 rh. 55-D 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 rh. 62-D 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGCTGAGGAAGCTGCTAAGACGGCT
 AAV7-D 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 rh. 52-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 rh. 51-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 hu. 39-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 rh. 53-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 hu. 37-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCTGCTAAGACGGCT
 rh. 43-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 rh. 50-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT
 rh. 49-E 351 AGTCTTCCAGGCGCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTAAGACGGCT

49/125

rh. 61-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 hu. 41-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CCGGTTGAGGAAGCTGCTAAGACGGCT
 rh. 64-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 hu. 42-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 rh. 57-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 hu. 40-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 AAV8-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 rh. 58-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTGCTAAGACGGCT
 rh. 40-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTGCTAAGACGGCT
 hu. 67-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTGCTAAGACGGCT
 hu. 17-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 hu. 6-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 hu. 66-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTGCTAAGACGGCT
 rh. 38-E 351 AGTCTTCCAGGCCAAGAAGCGGGTTCTCGAACCTCTCGGT---CTGGTTGAGGAAGCGCTGCTAAGACGGCT
 hu. 32-F 351 AGTCTTCCAGGCCAAGAAGAGAGGCTTCTTGAACCTCTTGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 AAV9/hu 351 AGTCTTCCAGGCCAAGAAGAGAGGCTTCTTGAACCTCTTGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT
 hu. 31-F 351 AGTCTTCCAGGCCAAGAAGAGAGGCTTCTTGAACCTCTTGGT---CTGGTTGAGGAAGCGCGCTAAGACGGCT

430 440 450 460 470 480 490
|....|....|....|....|....|....|....|....|....|....|....|....|
 AAV5 415 CCTACCGGAAGCGGATAGACGACCACCTTCCA-----
 AAV3-3 418 CCTGGAAGAAGGGGCTGTAGATCAGTCTCCTCAG---GAACCGGACTCATCTGGTGTGGCAAAAT
 AAV4-4 415 CCTGGAAGAAGAGACCGTTGATTGAATCCCCCAG---CAGCCCAGACTCTCCACGGGTATCGGCAAAA
 AAV1-A 418 CCTGGAAGAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCTCTCGGGCATCGGCAAGA
 hu. 46-A 418 CCTGGAAGAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCTCTCGGGCATCGGCAAGA
 hu. 48-A 418 CCTGGAAGAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCTCTCGGGCATCGGCAAGA
 hu. 44-A 418 CCTGGAAGAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GGGCCAGACTCTCTCGGGCATCGGCAAGA
 hu. 43-A 418 CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCTCCACGGGCTCGGCAAGA
 AAV6-A 418 CCTGGAAGAAGAAACGTCCGGTAGAGCAGTCGCCACAA---GAGCCAGACTCTCTCGGGCATCGGCAAGA
 hu. 34-B 418 CCGGGAAAAAAGAGCCGGTAGAGCACTCTCTGTG---GAGCCAGACTCTCTCGGGAAACCGGAAAGG

50/125

hu. 47-B 418 CCGGGA AAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAGG
 hu. 29-B 418 CCGGGA AAAAAGAGCCGGTAGAGCACTCTCCTGTCA---GAGCCAGATTCTCCTCCGGAACCTGGAAAAGT
 hu. 63-B 418 CCGGGA AAAAAGAGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 56-B 418 CCGGGA AAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 45-B 418 CCGGGA AAAAAGAGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 57-B 415 CCGGGA AAAAAGAGCCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 35-B 418 CCGGGA AAAAAGAGCCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 58-B 418 CCGGGA AAAAAGAGCCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 28-B 418 CCGGGA AAAAAGAGCCCGGTAGAGCACTCTCCCGCA---GAGCCAGATTCTCCTCCGGAACCTGGAAAAGT
 hu. 51-B 418 CCAGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 19-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 49-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACAGGAAAAG
 hu. 52-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 13-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 AAV2-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 20-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 24-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 64-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCTGTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 27-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 21-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 22-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 23-B 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 7-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 61-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 rh. 56-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 9-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 54-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 53-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 60-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGTG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG
 hu. 55-C 418 CCGGGA AAAAAGAGGCCGGTAGAGCACTCTCCTGCG---GAGCCAGACTCCTCCTCGGGAAACCGGAAAAG

51/125

hu.2-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.1-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.18-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.3-C 421 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.25-C 418 CCGGAAAAAAGAGACCGGTAGAGCACTCTCCTGCG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.15-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.16-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.11-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.10-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 hu.4-C 418 CCGGAAAAAAGAGCCGGTAGAGCACTCTCCTGTG--GAGCCAGACTCCTCCTCGGGAAACCGGAAAAAG
 rh.54-D 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.48-D 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.55-D 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.62-D 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 AAV7-D 418 CCTGCAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.52-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.51-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 hu.39-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.53-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 hu.37-E 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.43-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCAGTCACTCAGCGTTCCCGGACTCCTCCTCGGGCAATCGGCAAGA
 rh.50-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.49-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.61-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 hu.41-E 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.64-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 hu.42-E 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 rh.57-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 hu.40-E 418 CCTGGAAAGAAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCGGACTCCTCCACGGGCAATCGGCAAGA
 AAV8-E 418 CCTGGAAAGAAAGAGACCGGTAGAGCCATCACTCAGCGTTCTCCAGACTCCTCTACGGGCAATCGGCAAGA

rh. 58-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA	500	510	520	530	540	550	560
rh. 40-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 67-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 17-E	418	CCTGGAAGAAGAGACCGGTAGAGCCATCACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA							
hu. 6-E	418	CCTGGAAGAAGAGACCGGTAGAGCCATCACCCAGCGTTCTCCAGACTCCTCTACGGGCATCGGCAAGA							
hu. 66-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCGCGGCATCGGCAAGA							
rh. 38-E	418	CCTGGAAGAAGAGACCGGTAGAACCGTCACTCAGCGTTCCCCCGACTCCTCCACGGGCATCGGCAAGA							
hu. 32-F	418	CCTGGAAGAAGAGAGCCCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
AAV9/hu	418	CCTGGAAGAAGAGAGCCCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
hu. 31-F	418	CCTGGAAGAAGAGAGCCCTGTAGAGCAGTCTCCTCAG--GAACCGGACTCCTCCGCGGTATTGGCAAAT							
AAV5	452	GAAAGAAGGCTCGGACCGAAGAGGACTCCAAGCCTTCCACCTCGTCAGACGCCGAAGCTGGACCCAGCGG							
AAV3-3	485	CGGGCAACAGCCTGCCAGAAAAGACTAAATTTCCGTCAAGTGGAGACTCAGAGTCAGTCCCAGAC--							
AAV4-4	482	AAGGCAAGCAGCCGGCTAAAAGAGCTCGTTTTCGAAGACGAAACTGGAGCAGGCGACGCC-----							
AAV1-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 46-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 48-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGCCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 44-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAT--							
hu. 43-A	488	AAGGCCAGCAGCCCGCTAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--							
AAV6-A	485	CAGGCCAGCAGCCCGCTAAAAGAGACTCAATTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--							
hu. 34-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 47-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 29-B	485	CGGGCAACCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACTCAGACTCCGTACCTGAC--							
hu. 63-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 56-B	485	CGGGCAACCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 45-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							
hu. 57-B	482	CGGGCAACCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--							
hu. 35-B	485	CGGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--							

53/125

hu. 58-B 485 CCGGCAACCAGCCTGCAAGAAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 28-B 485 CCGGCAACCAGCCTGCAAGAAAAGAGATTGAATTTCCGGTCAGACTGGAGACTCAGACTCCGTACCTGAC--
hu. 51-B 485 CCGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 19-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGCCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 49-B 485 CCGGCCAGCAGCCTGCCGAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 52-B 485 CCGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 13-B 485 CCGGCCAGCAGCCTGCAAGAAAAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
AAV2-B 485 CCGGCCAGCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 20-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 24-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 64-B 485 CCGGCCAGCAGCCTGCAAGAAAGGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 27-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 21-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 22-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 23-B 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCAGTACCTGAC--
hu. 7-C 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 61-C 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
rh. 56-C 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 9-C 485 CCGGCCATCAGCCTGCGAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 54-C 485 CCGGCCAGCAGCCTGCAAGAAAAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 53-C 485 CCGGCCAGCAGCCTGCAAGAAAAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 60-C 485 CCGGCCAGCAGCCTGCAAGAAAAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 55-C 485 CCGGCCAGCAGCCTGCAAGAAAAGACTGAATTTCCGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 2-C 485 CCGGCCAGCGGCCTGCAAGAAAAGACTTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 1-C 485 CCGGCCAGCAGCCTGCAAGAAAAGACTTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 18-C 485 CCGGCCAGCAGCCTGCGAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 3-C 488 CCGGCCAGCAGCCTGCAAGAAAAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 25-C 485 CCGGCCAGCAGCCTGCAAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 15-C 485 CCGGCAACCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
hu. 16-C 485 CCGGCAACCAGCCTGCAAGAAAAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--

hu.11-C 485 CGGGCCATCAGCCCTGCGAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
 hu.10-C 485 CGGGCCATCAGCCCTGCGAGAAAAGAGATTGAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
 hu.4-C 485 CGGGCCAGCAGCCCTGCAAGAAAAGATTAAATTTTGGTCAGACTGGAGACGCAGACTCCGTACCTGAC--
 rh.54-D 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.48-D 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.55-D 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.62-D 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 AAV7-D 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.52-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.51-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.39-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.53-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.37-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.43-E 485 AAGGCCAACAGCCCCGCTAGAAAAGAGACTCAATTTGGCCAGACTGGCGACTCAGAGTCAGTCCAGAC--
 rh.50-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.49-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.61-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.41-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.64-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.42-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.57-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAATTTCCGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.40-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAGCTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 AAV8-E 488 AAGGCCAACAGCCCCGCTAGAAAAGAGACTCAATTTGGTCAGACTGGCGACTCAGAGTCAGTCCAGAC--
 rh.58-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGGCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.40-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.67-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 hu.17-E 488 CAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAACTTTGGGCAGACTGGCGACTCAGAGTCAGTGCCCGAC--
 hu.6-E 488 CAGGCCAGCAGCCCCGCTAGAAAAGAGACTCAACTTTGGGCAGACTGGCGACTCAGAGTCAGTGCCCGAC--
 hu.66-E 488 AAGGCCAGCAGCCCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--
 rh.38-E 488 AAGGCCAGCGGCCGCTAGAAAAGAGACTGAACTTTGGTCAGACTGGCGACTCAGAGTCAGTCCCCGAC--

55/125

hu. 32-F	485	CGGGTTACAGCCCGCTAAAAAGAAACTCAATTTTCGGTCAGACTGGCGACACAGAGTCAGTCCCCGAC--	570	580	590	600	610	620	630
AAV9/hu	485	CGGGTGACAGCCCGCTAAAAAGAGACTCAATTTTCGGTCAGACTGGCGACACAGAGTCAGTCCCCGAC--							
hu. 31-F	485	CGGGTTACAGCCCGCTAAAAAGAAACTCAATTTTCGGTCAGACTGGCGACACAGAGTCAGTCCCCGAC--							
AAV5	522								
AAV3-3	552	ATCCCAGCAGCTGCAAAATCCCAGGCCCAACCAGCCCTCAAGTTTGGGAGCTGATACAAATGTCTGCGGGAGGT							
AAV4-4	552	-CCTCAACCTCTCGGAGAACCAACAGAGCCCCACAAAGTTTGGGATCTAATACAAATGGCTTCAGGCGGT							
AAV1-A	546	-----CCTGAGGGATCAACTTCCGGAGCCATGTCT-----GATGACAGTGAGATGGTGCAGCAGCT							
hu. 46-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAAATGGCTTCAGGCGGT							
hu. 48-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAAATGGCTTCAGGCGGT							
hu. 44-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAAATGGCTTCAGGCGGT							
hu. 43-A	555	-CCTCAACCAATCGGAGAACCAACAGAGCCCTCTGCTGTGGATCTGGTACAAATGGCTGCAGGCGGT							
AAV6-A	552	-CCACAACCTCTCGGAGAACCTCCAGCAACCCCGCTGCTGTGGGACCTACTACAAATGGCTTCAGGCGGT							
hu. 34-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 47-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 29-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 63-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 56-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 45-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 57-B	549	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 35-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 58-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 28-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 51-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 19-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 49-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 52-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							
hu. 13-B	552	-CCCCAGCCTCTCGGACAGCCACCAAGCAGCCCTCTGCTGTGGAACTAATACGATGGCTACAGGCAGT							

56/125

AAV2-B	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT
hu. 20-B	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTTCAGGCAGT
hu. 24-B	552	-CCCCGGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTTCAGGCAGT
hu. 64-B	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTACAGGCAGT
hu. 27-B	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTTCAGGCAGT
hu. 21-B	552	-CCCCGGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTTCAGGCAGT
hu. 22-B	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTTCAGGCAGT
hu. 23-B	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGAACCTAATACGATGGCTTCAGGCAGT
hu. 7-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 61-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
rh. 56-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 9-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCACAAGTTTGGATCTACTACAATGGCTACAGGCAGT
hu. 54-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCACAAGTTTGGATCTACTACAATGGCTACAGGCAGT
hu. 53-C	552	-CCCAGCCTCTCAGACAGCCACAGCAGCCCCCACAAGTTTGGATCTACTACAATGGCTACAGGCAGT
hu. 60-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 55-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCACAAGTTTGGATCTACTACAATGGCTACAGGCAGT
hu. 2-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 1-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 18-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 3-C	555	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 25-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 15-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 16-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
hu. 11-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCACAAGTTTGGATCTACTACAATGGCTACAGGCAGT
hu. 10-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCACAAGTTTGGATCTACTACAATGGCTACAGGCAGT
hu. 4-C	552	-CCCAGCCTCTCGGACAGCCACAGCAGCCCCCTCTGGTCTGGGATCTACTACAATGGCTACAGGCAGT
rh. 54-D	555	-CCTCAACCTCTCGGAGAACCAACAGCAGGCCCTCTGGTCTGGGATCTGGTACAATGGCTGCAGGCGGT
rh. 48-D	555	-CCTCAACCTCTCGGAGAACCAACAGCAGGCCCTCTGGTCTGGGATCTGGTACAATGGCTGCAGGCGGT
rh. 55-D	555	-CCTCAACCTATCGGAGAACCTCCAGCAGGCCCTCTAGTGTGGATCTGGTACAATGGCTGCAGGCGGT
rh. 62-D	555	-CCTCAACCAATCGGAGAGCCACAGCAGGCCCTCTGGTCTGGGATCTGGTACAATGGCTGCAGGCGGT

57/125

AAV7-D	555	-CCTCAACCTCTCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAGTGGCTGCAGGCGGT	640	650	660	670	680	690	700
rh. 52-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 51-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 39-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 53-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 37-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 43-E	552	-CCTCAACCTCTCGGAGAACTCCAGCAGCGCCCTCTGGTGTGGGATCTAATACAAATGGCTGCAGGCGGT							
rh. 50-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 49-E	555	-CCTCAACTTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 61-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 41-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 64-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 42-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 57-E	555	-CCTCAACCTATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 40-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
AAV8-E	555	-CCTCAACCTCTCGGAGAACTCCAGCAGCGCCCTCTGGTGTGGGATCTAATACAAATGGCTGCAGGCGGT							
rh. 58-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTAGTGTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 40-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 67-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 17-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 6-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 66-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
rh. 38-E	555	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCTGGTCTGGGATCTGGTACAAATGGCTGCAGGCGGT							
hu. 32-F	552	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCAGGTGTGGGATCTCTTACAAATGGCTTCAGGTGGT							
AAV9/hu	552	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCAGGTGTGGGATCTCTTACAAATGGCTTCAGGTGGT							
hu. 31-F	552	-CCTCAACCAATCGGAGAACTCCAGCAGCGCCCTCAGGTGTGGGATCTCTTACAAATGGCTTCAGGTGGT							
AAV5	592	 GGCGGCCCATTTGGCGGACAAATAACCAAGGTGCCGATGGAGTGGGCAATGCCCTCGGGAGATTGGCATTTGCG							

58/125

AAV3-3- 622 GGCGACCAATGGCAGACAAATAACGAGGGTGCCGATGGAGTGGGTAATTCTCAGGAAATTGGCATTGCG
 AAV4-4- 604 GGCGAGCTGCAGTCGAGGCGGACAAAGGTGCTCCGATGGAGTGGGTAATGCCCTCGGCTGATTGGCATTGCG
 AAV1-A- 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 46-A 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 48-A 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 44-A 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 43-A 625 GGCGTCCAAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 AAV6-A 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 34-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 47-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 29-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 63-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 56-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 45-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 57-B 619 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAGATTGGCATTGCG
 hu. 35-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 58-B 622 GGCGACCAATGGCAGACAAATAACGATGGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 28-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 51-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 19-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGTATTGCG
 hu. 49-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 52-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 13-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 AAV2-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 20-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 24-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 64-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 27-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 21-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG
 hu. 22-B 622 GGCGACCAATGGCAGACAAATAACGAAGCGCCGACGAGTGGGTAATGCCCTCAGGAAATTGGCATTGCG

59/125

hu.23-B	622	GGCGACCAATGGCAGACAATAACGAGGGCGCCGACGGAGTGGGTAATTCCCTCGGGAAATTGGCATTTGCG
hu.7-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.61-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCGGGAAATTGGCATTTGCG
rh.56-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCTTCAGGAAATTGGCATTTGCG
hu.9-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.54-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.53-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.60-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCGGGAAATTGGCATTTGCG
hu.55-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.2-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.1-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.18-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.3-C	625	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.25-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.15-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.16-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.11-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.10-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
hu.4-C	622	GGCGACCAATGGCAGACAATAACGAGGGTGCCGATGGAGTGGGTAATTCCCTCAGGAAATTGGCATTTGCG
rh.54-D	625	GGCGTCCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.48-D	625	GGCGACCAATGGCTGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.55-D	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.62-D	625	GGCGACCAATGGCTGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
AAV7-D	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.52-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.51-E	625	GGCGGCCCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
hu.39-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.53-E	625	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
hu.37-E	625	GGCGTCCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG
rh.43-E	622	GGCGACCAATGGCAGACAATAACGAAGGCGCCGACGGAGTGGGTAATGCCCTCAGGAAATTGGCATTTGCG

FIG. 3AA

60/125

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

FIG. 3AB

61/125

AAV6-A	692	ATTCCACATGGCTGGGCGACAGAGTCATCACCAGCACCCGAACATGGGCCTTGCCACCTATAACAA
hu. 34-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 47-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 29-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 63-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCTCTGCCACCTACAACAA
hu. 56-B	692	ATTCCACATGGATGGGCGACAGAGTCGTCAACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 45-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 57-B	689	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 35-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 58-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCTCTGCCACCTACAACAA
hu. 28-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 51-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 19-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 49-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCTCTGCCACCTACAACAA
hu. 52-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 13-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
AAV2-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 20-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 24-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 64-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCTCTGCCACCTACAACAA
hu. 27-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 21-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 22-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 23-B	692	ATTCCACATGGATGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
hu. 7-C	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 61-C	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAGCACCCGCACCTGGGCCCTGCCACCTACAACAA
rh. 56-C	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCAGCCACCTACAACAA
hu. 9-C	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 54-C	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
hu. 53-C	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA

62/125

hu. 60-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCAGCACCCGACCTGGGCCCTGCCACCTACAACAA
 hu. 55-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
 hu. 2-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACATACAACAA
 hu. 1-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACATACAACAA
 hu. 18-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
 hu. 3-C 695 ATCCCAATGGCTGGCGACAGAGTCATCGCCACACAGCACCCGAACCTGGGCCCTGCCACATACAACAA
 hu. 25-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCACAAGCACTCGAACCTGGGCCCTGCCACCTACAACAA
 hu. 15-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCTCTGCCACCTACAATAA
 hu. 16-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCTCTGCCACCTACAACAA
 hu. 11-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
 hu. 10-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA
 hu. 4-C 692 ATCCCAATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCACATACAACAA
 rh. 54-D 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCTTTGCCCACCTACAACAA
 rh. 48-D 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCTTTGCCCACCTACAACAA
 rh. 55-D 695 ATCCACACGGCTGGCGACAGAGTCATCACCACAGCACCCGGAACCTGGGCTTTGCCCACCTACAACAA
 rh. 62-D 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCTTTGCCCACCTACAACAA
 AAV7-D 695 ATCCACATGGCTGGCGACAGAGTCATTACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 52-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 51-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 hu. 39-E 695 ATCCACATGGCTGGCGACAGAGTTATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 53-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 hu. 37-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 43-E 692 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 50-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 49-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 61-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 hu. 41-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 64-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 hu. 42-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA
 rh. 57-E 695 ATCCACATGGCTGGCGACAGAGTCATCACCACAGCACCCGAACCTGGGCCCTGCCCACCTACAACAA

63/125

hu.40-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA	780	790	800	810	820	830	840
AAV8-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
rh.58-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
rh.40-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
hu.67-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
hu.17-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
hu.6-E	695	ATTCCGATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
hu.66-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
rh.38-E	695	ATTCCACATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
hu.32-F	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
AAV9/hu	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
hu.31-F	692	ATTCCCAATGGCTGGGCGACAGAGTCATCACCAACAGCACCCGAACCTGGGCCCTGCCACCTACAACAA							
AAV5	732								
AAV3-3-	762	CCACCAGTACCGAGAGATCAAAAGC---GGCTCCGTCGACGGGAAGCAACGCCAAGCCCTACTTTGGATAC							
AAV4-4-	762	CCATCTCTACAAGCAAATCTCC-----AGCCAATCAGGAGCTTCAAACGACAAACCACTACTTTGGCTAC							
AAV1-A	744	CCACCTCTACAAGCGACTCGGA-----GAGAGCCTGCAGTCCAAACACCTACAACGGATTTC							
hu.46-A	762	CCACCTCTACAAGCAAATCTCCAGT---GCTTCAACGGGGCCAGCAACGACAAACCACTACTTTCGGCTAC							
hu.48-A	762	CCACCTCTACAAGCAAATCTCCAGT---GCTTCAACGGGGCCAGCAACGACAAACCACTACTTTCGGCTAC							
hu.44-A	762	CCACCTCTACAAGCAAATCTCCAGT---ACTTCAACGGGGCCAGCAACGACAAACCACTACTTTCGGCTAC							
hu.43-A	762	CCACCTCTACAAGCAAATCTCCAGT---GCTTCAACGGGGCCAGCAACGACAAACCACTACTTTCGGCTAC							
AAV6-A	765	CCACCTCTACAAGCAAATCTCCAGT---GCTTCAACGGGGCCAGCAACGACAAACCACTACTTTCGGCTAC							
hu.34-B	762	CCACCTCTACAAGCAAATCTCCAGT---GCTTCAACGGGGCCAGCAACGACAAACCACTACTTTCGGCTAC							
hu.47-B	762	CCACCTCTACAAGCAAATTTCC-----AGCCAATCAGGAGCCTCGAACGACAAATCATACTTTGGCTAC							
hu.29-B	762	CCACCTCTACAAGCAAATTTCC-----AGCCAATCAGGAGCCTCGAACGACAGTCACTACTTTGGCTAC							
hu.63-B	762	CCATCTGTACAAGCAAATATCC-----AGCCAGTCTGGAGCCAGCAACGACAAATCATACTTTGGCTAC							
hu.56-B	762	CCACCTCTACAAGCAGATTTC-----AGCCAATCAGGAGCCTCAAACGACAAACCACTACTTTGGCTAC							
hu.45-B	762	CCACCTCTACAAGCAGATTTC-----AGCCAATCAGGAGCCTCAAACGACAAACCACTACTTTGGCTAC							

FIG. 3AE

64/125

hu. 57-B	759	CCACCTCTACAAGCAGATTTC	-----AGCCAATCAGGAGCCAGCAATGACAACCACCTACTTTTGGCTAC
hu. 35-B	762	CCACCTCTACAACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAAATCACTACTTTTGGCTAC
hu. 58-B	762	CCATCTGTACAAGCAGATTTC	-----AGCCAATCAGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 28-B	762	CCATCTGTACAAGCAAATATCC	-----AGCCAGTCTGGAGCCAGCAACGACAAATCACTACTTTTGGCTAC
hu. 51-B	762	CCACCTCTACAACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAAATCACTACTTTTGGCTAC
hu. 19-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 49-B	762	CCATCTGTACAAGCAGATCTCC	-----AGCCAATCAGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 52-B	762	CCACCTCTACAGACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAAATCACTACTTTTGGCTAC
hu. 13-B	762	CCATCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
AAV2-B	762	CCACCTCTACAACAAATTTC	-----AGCCAATCAGGAGCCTCGAACGACAAATCACTACTTTTGGCTAC
hu. 20-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 24-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 64-B	762	CCACCTCTACAGGCAGATTTC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 27-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 21-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 22-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 23-B	762	CCATCTGTACAAGCAAATCTCC	-----AGCCAGTCTGGAGCCAGCAACGACAAACCACCTACTTTTGGCTAC
hu. 7-C	762	CCACCTCTACAAGCAAATCTCA	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 61-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
rh. 56-C	762	CCACCTCTACAAGCAAATCTCA	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 9-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCGAACGACAAACCACCTACTTTTGGCTGC
hu. 54-C	762	CCACCTTTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 53-C	762	CCACCTTTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 60-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 55-C	762	CCACCTTTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 2-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 1-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 18-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC
hu. 3-C	765	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTGCAACGACAAACCACCTACTTTTGGCTAC
hu. 25-C	762	CCACCTCTACAAGCAAATCTCC	-----AGCCAATCAGGAGCCTCAAACGACAAACCACCTACTTTTGGCTAC

FIG. 3AF

65/125

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--CAGTCAGCAGGTAGCACCAACGACAACGTCCTACTTTCGGCTAC
rh.48-D	765	CCACCTCTACAAGCAAATCTCCAGT--CAGTCAGCAGGTAGCACCAACGACAACGTCCTACTTTCGGCTAC
rh.55-D	765	CCACCTCTACAAGCAAATCTCCAGT--CAGTCAGCAGGTAGCACCAACGACAACGTCCTACTTTCGGCTAC
rh.62-D	765	CCACCTCTACAAGCAAATCTCCAGT--CAGTCAGCAGGTAGCACCAACGACAACGTCCTACTTTCGGCTAC
AAV7-D	765	CCACCTCTACAAGCAAATCTCCAGT--GAAACTGCAGGTAGTACCAACGACAACCACTACTTTCGGCTAC
rh.52-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
rh.51-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
hu.39-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
rh.53-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
hu.37-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
rh.43-E	762	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
rh.50-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
rh.49-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
rh.61-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
hu.41-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
rh.64-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
hu.42-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
rh.57-E	765	CCACCTCTACAAGCAAACCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
hu.40-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
AAV8-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
rh.58-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACCTCGGAGGCAGCACCAACGACAACCACTACTTTCGGCTAC
rh.40-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
hu.67-E	765	CCACCTCTACAAGCAAATATCCAATGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
hu.17-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC
hu.6-E	765	CCACCTCTACAAGCAAATCTCCAACGGGACATCGGAGGAAGCACCAACGACAACCACTACTTTCGGCTAC

FIG. 3A

66/125

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	AGCACCCCTGGGGTACTTTGACTTTAAACCGCTTCCACAGCCACTGGAGCCCCCGAGACTGGCAAAGAC							
AAV4-4	799	AGCACCCCTTGGGGTATTTTGACTTTAAACAGATTCCACTGCCACTTCTCACCCACGTGACTGGCAGCGAC							
AAV1-A	829	TCCACCCCTGGGGTACTTTGACTTTCAACCGCTTCCACTGCCACTTCTCACCCACGTGACTGGCAGCGAC							
hu. 46-A	829	AGCACCCCTGGGGTATTTTGATTTC AACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAGCGAC							
hu. 48-A	829	AGCACCCCTGGGGTATTTTGATTTC AACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAGCGAC							
hu. 44-A	829	GGCACCCCTGGGGTATTTTGATTTC AACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAGCGAC							
hu. 43-A	832	AGCACCCCTGGGGTATTTTGATTTC AACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAGCGAC							
AAV6-A	829	AGCACCCCTGGGGTATTTTGATTTC AACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAGCGAC							
hu. 34-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 47-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 29-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 63-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCGCCACGTGACTGGCAAAGAC							
hu. 56-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCGCCACGTGACTGGCAGAGAC							
hu. 45-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 57-B	823	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCGCCACGTGACTGGCAGAGAC							
hu. 35-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 58-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 28-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 51-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							
hu. 19-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTCTCCCCACGTGACTGGCAAAGAC							
hu. 49-B	826	AGCACCCCTTGGGGTATTTTGACTTCAACAGATTCCACTGCCACTTTTCACCCACGTGACTGGCAAAGAC							

FIG. 3A

67/125

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

FIG. 3A1

68/125

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

FIG. 3A_J

69/125

AAV5	869	
AAV3-3-	896	TCATCAACAACAACTAGGGCTTCAGACCCCGGTCCCTCAGAGTCAAAATCTTCAACATTCAGTCAAAGA
AAV4-4-	869	TCATTAAACAACAACAACTAGGGGATTCGGGCCCAAGAAACTCAGCTTCAAGCTCTTCAACATCCAAGTTAGAGG
AAV1-A-	899	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGGCCATGCGGGTCAAAATCTTCAACATCCAGGTCAAAGGA
hu.46-A	899	TCATCAACAACAACAAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAAGTCAAAGGA
hu.48-A	899	TCATCAACAACAACAAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAAGTCCGAGGA
hu.44-A	899	TCATCAACAACAACAAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAAGTCAAAGGA
hu.43-A	902	TCATCAACAACAACAAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAACTCTTCAACATCCAAAGTCAAAGGA
AAV6-A	899	TCATCAACAACAACAAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAAAGTCAAAGGA
hu.34-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.47-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.29-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.63-B	896	TCATCAACAACAACAAATTTGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.56-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.45-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.57-B	893	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.35-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.58-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.28-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.51-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.19-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAAGCTCTTAAACATTCAGTCAAAGA
hu.49-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAAGCTCTTAAACATTCAGTCAAAGA
hu.52-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAAGCTCTTAAACATTCAGTCAAAGA
hu.13-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAAGCTCTTAAACATTCAGTCAAAGA
AAV2-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAAGCTCTTAAACATTCAGTCAAAGA
hu.20-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.24-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.64-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAACTTCAAGCTCTTAAACATTCAGTCAAAGA
hu.27-B	896	TCATCAACAACAACAACTAGGGGATTCGGGCCCAAGAGACTCAGCTTCAAGCTCTTAAACATTCAGTCAAAGA

FIG. 3AK

70/125

hu. 21-B	896	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 22-B	896	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 23-B	896	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 7-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 61-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
rh. 56-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 9-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 54-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 53-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 60-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 55-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 2-C	896	TCATCAACAACAACTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
hu. 1-C	896	TCATCAACAACAACTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
hu. 18-C	896	TCATCAACAACAGCTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 3-C	899	TCATCAACAGCAACTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
hu. 25-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 15-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 16-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 11-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 10-C	896	TCATCAACAACAACTGGGGATTCCGACCCCAAGAGACTCAACTTCAAGCTCTTTAAACATTCAAGTCAAAGA
hu. 4-C	896	TCGTCAACAACAACCCGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTCTTTAAATATTCAAGTCAAAGA
rh. 54-D	902	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTCTTTCAACATCCAGGTCAAAGGA
rh. 48-D	902	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTGTTCACATCCAGGTCAAAGGA
rh. 55-D	902	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTGTTCACATCCAGGTCAAAGGA
rh. 62-D	902	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAACTTCAAGCTGTTCACATCCAGGTCAAAGGA
AAV7-D	902	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTGCGGTTCAGCTTCAAGCTGTTCACATCCAGGTCAAAGGA
rh. 52-E	905	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA
rh. 51-E	905	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA
hu. 39-E	905	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA
rh. 53-E	905	TCATCAACAACAACCTGGGGATTCCGGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA

FIG. 3AL

71/125

hu. 37-E	905	TCATCAACAACAACTGGGGATTCCGGCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA	990	1000	1010	1020	1030	1040	1050
rh. 43-E	902	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAGGA							
rh. 50-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 49-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 61-E	905	CCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 41-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 64-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 42-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 57-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 40-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
AAV8-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 58-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 40-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 67-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 17-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 6-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAGAGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 66-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
rh. 38-E	905	TCATCAACAACAACTGGGGATTCCGGCCCAAAAGACTCAGCTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 32-F	902	TCATCAACAACAACTGGGGATTCCGGCCCTAAGCGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGA							
AAV9/hu	902	TCATCAACAACAACTGGGGATTCCGGCCCTAAGCGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGA							
hu. 31-F	902	TCATCAACAACAACTGGGGATTCCGGCCCTAAGCGACTCAACTTCAAGCTCTTCAACATCCAGGTCAAAGA							
AAV5	939	GGTCACGGTGCAGGACTCCACACCACCACTCGCCAAACAACCTCACCTCCACCGTCCAAGTGTTCACGGAC							
AAV3-3	966	GGTCACGCAGAACGATGGCAGCAGCAGCTATTGCCAATAAACCCTTACCAGCACGGTTCAAGTGTTCACGGAC							
AAV4-4	939	GGTCACGACGTCGAACGGCGAGACAAACGGTGCGTAATAAACCCTTACCAGCACGGTTCAGATCTTTGCGGAC							
AAV1-A	969	GGTCACGACGAATGATGGCGTCACAACCATCGCTAATAAACCCTTACCAGCACGGTTCAGTCTTCTCGGAC							
hu. 46-A	969	GGTCACGACGAATGATGGCGTCACAACCATCGCTAATAAACCCTTACCAGCACGGTTCAGTCTTCTCGGAC							
hu. 48-A	969	GGTCACGACGAATGATGGCGTCACAACCATCGCTAATAAACCCTTACCAGCACGGTTCAGTCTTCTCGGAC							

FIG. 3AM

72/125

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

FIG. 3AN

73/125

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

FIG. 3AO

hu. 42-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC	1060	1070	1080	1090	1100	1110	1120
rh. 57-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCAGGTGTTTACGGAC							
hu. 40-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
AAV8-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTCACCAGCACCATCCAGGTGTTTACGGAC							
rh. 58-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
rh. 40-E	975	GGTCACGCAGGATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu. 67-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu. 17-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu. 6-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTCTTTACGGAC							
hu. 66-E	975	GGTCACGCAGAAATGAAGGCACCGAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
rh. 38-E	975	GGTCACGCAGAAATGAAGGCACCAAGACCATCGCCAATAACCTTACCAGCACGATTCAGGTATTTACGGAC							
hu. 32-F	972	GGTTACGGACAACAAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGGTCCAGGTCTTCACGGAC							
AAV9/hu	972	GGTTACGGACAACAAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGGTCCAGGTCTTCACGGAC							
hu. 31-F	972	GGTTACGGACAACAAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGGTCCAGGTCTTCACGGAC							
			1060	1070	1080	1090	1100	1110	1120
AAV5	1009								
AAV3-3-	1036	GACGACTACCAGCTGCCCTACGTCTGGCAACGGGACCGAGGGATGCCCTGCCGGCCTTCCCCTCCGCAGG							
AAV4-4-	1009	TCGGAGTATCAGCTCCCGTACGTGCTCGGGTCGGCGCACCAAGGCTGTCTCCCGCCGTTTCCAGCGGACG							
AAV1-A-	1039	TCGTCGTACGAACCTGCCGTACGTGATGGATGCGGGTCAAGAGGGCAGCCTGCCCTCCTTTTCCCAACGACG							
hu. 46-A	1039	TCGGAGTACCAGCTTCCGTACGTCCCTCGGCTCTGCGCACCAAGGGCTGCCCTCCGTTCCCGCGGACG							
hu. 48-A	1039	TCGGAGTACCAGCTTCCGTACGTCCCTCGGCTCTGCGCACCAAGGGCTGCCCTCCGTTCCCGCGGACG							
hu. 44-A	1039	TCGGAGTACCAGCTTCCGTACGTCCCTCGGCTCTGCGCACCAAGGGCTGCCCTCCGTTCCCGCGGACG							
hu. 43-A	1042	TCGGAGTACCAGCTTCCGTACGTCCCTCGGCTCTGCGCACCAAGGGCTGCCCTCCGTTCCCGCGGACG							
AAV6-A	1039	TCGGAGTACCAGTTGCCGTACGTCCCTCGGCTCTGCGCACCAAGGGCTGCCCTCCGTTCCCGCGGACG							
hu. 34-B	1036	TCGGAGTACCAGTCCCCTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCGCCGTTCCAGCAGACG							
hu. 47-B	1036	TCGGAGTACCAGTCCCCTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCGCCGTTCCAGCAGACG							
hu. 29-B	1036	TCGGAGTACCAGTCCCCTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCGCCGTTCCAGCAGACG							
hu. 63-B	1036	TCGGAGTACCAGTCCCCTACGTCCCTCGGCTCGGGCATCAAGGATGCCCTCCGCCGTTCCAGCAGACG							

FIG. 3AP

75/125

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

FIG. 3AQ

76/125

hu. 3-C	1039	TCGGAGTACCAGCTCCCGTACGTCCCGGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 25-C	1036	TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 15-C	1036	TCGGGGTACCAGCTCCCGTACGTCCCTCGGCTTGCGGCATCAAGGATGCCCTCCCGCCGTTTCCAGCAGACG
hu. 16-C	1036	TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCAGACG
hu. 11-C	1036	TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 10-C	1036	TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 4-C	1036	TCGGAGTACCAGCTCCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 54-D	1042	TCGGAGTACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 48-D	1042	TCGGAAATACCAGCTGCCCTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 55-D	1042	TCGGAAATACCAGCTGCCCTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 62-D	1042	TCGGAAATACCAGCTGCCCTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
AAV7-D	1042	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 52-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 51-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 39-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 53-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 37-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 43-E	1042	TCGGAGTACCAGCTGCCGTACGTTCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 50-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 49-E	1045	TCGGAGTACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 61-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 41-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 64-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 42-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 57-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 40-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
AAV8-E	1045	TCGGAGTACCAGCTGCCGTACGTTCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 58-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
rh. 40-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG
hu. 67-E	1045	TCGGAAATACCAGCTGCCGTACGTCCCTCGGCTCGGCGCATCAAGGATGCCCTCCCGCCGTTTCCAGCGGACG

FIG. 3AR

77/125

hu. 17-E	1045	TCGGAATACCAGTCCCGTACGTCCCTCGGCTCTGCCACACAGGGCTGCCCGCCTCCGTTCCCGGGACG	1130	1140	1150	1160	1170	1180	1190
hu. 6-E	1045	TCGGAATACCAGTCCCGTACGTCCCTCGGCTCTGCCACACAGGGCTGCCCGCCTCCGTTCCCGGGACG							
hu. 66-E	1045	TCGGAATACCAGTCCCGTACGTCCCTCGGCTCCCGCACACAGGGCTGCCCTGCCCTCCCGGGACG							
rh. 38-E	1045	TCGGAATACCAGTCCCGTACGTCCCTCGGCTCCCGCACACAGGGCTGCCCTCCCGGGACG							
hu. 32-F	1042	TCAGACTATCAGTCCCGTACGTGCTCGGCTCAGAGGGCTGCCCTCCCGCGTTCCAGCGGACG							
AAV9/hu	1042	TCAGACTATCAGTCCCGTACGTGCTCGGCTCAGAGGGCTGCCCTCCCGCGTTCCAGCGGACG							
hu. 31-F	1042	TCAGACTATCAGTCCCGTACGTGCTCGGCTCAGAGGGCTGCCCTCCCGCGTTCCAGCGGACG							
AAV5	1079	TCTTTACGCTGCCCGCAGTACGGTTACGCGACGCTGAACCGGAC--AACACAGAAATCCACCGAGAG							
AAV3-3-	1106	TCTTCATGGTCCCTCAGTATGGATACCTCACCTGAACAACGGA-----AGTCAAGCGGTGGACG							
AAV4-4-	1079	TCTTTATGGTGCCCGCAGTACGGCTACTGTGACTGGTGAACGCAACACTTCGCAGCAACAGACTGACAG							
AAV1-A-	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC-----AGCCAAGCCGTGGACG							
hu. 46-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC-----AGCCAAGCCGTGGACG							
hu. 48-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC-----AGCCAAGCCGTGGACG							
hu. 44-A	1109	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC-----AGCCAAGCCGTGGACG							
hu. 43-A	1112	TGTTTCATGATTCCGCAATACGGCTACCTGACGCTCAACAATGGC-----AGCCAAGCCGTGGACG							
AAV6-A	1109	TGTTTCATGATTCCGCGAGTACGGCTACCTAACGCTCAACAATGGC-----AGCCAGGCAGTGGACG							
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. 3AS

78/125

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

79/125

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-----AGTCAGGCCGTGGGACG
rh. 51-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 39-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 53-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 37-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 43-E	1112	TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 50-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 49-E	1115	TCTTCATGATTCCCTCAGTACGGCAACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 61-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 41-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 64-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 42-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 57-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
hu. 40-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
AAV8-E	1115	TGTTTCATGATTCCCCAGTACGGCTACCTAACACTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 58-E	1115	TCTTCATGATTCCCTCAGTACGGCTACCTGACTCTCAACAACGGT-----AGTCAGGCCGTGGGACG
rh. 40-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 67-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 17-E	1115	TCTTCATGATTCCCTCAGTACGGGTACCTGACTCTGAACAACGGC-----AGTCAGGCCGTGGGCCG
hu. 6-E	1115	TCTTCATGATTCCCTCAGTACGGGTACCTGACTCTGAACAACGGC-----AGTCAGGCCGTGGGCCG
hu. 66-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
rh. 38-E	1115	TCTTCATGATTCCCCAGTACGGCTACCTTACACTGAACAATGGA-----AGTCAAGCCGTAGGCCG
hu. 32-F	1112	TTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAATGATGGG-----AGCCAGGCCGTGGGTCG
AAV9/hu	1112	TTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAATGATGGA-----AGCCAGGCCGTGGGTCG
hu. 31-F	1112	TTTTCATGATTCCCTCAGTACGGGTATCTGACGCTTAATGATGGA-----GGCCAGGCCGTGGGTCG

80/125

	1200	1210	1220	1230	1240	1250	1260
							
AAV5	1146	GAGCAGCTTCTTCTGCCTAGAGTACTTCC	CAGCAAGATGCTGAGAACGGGCAACAAC	TTTGAGTTTACC			
AAV3-3-	1167	CTCATCCCTTTTACTGCCCTGGAGTACTTCC	CTCGCAGATGCTAAGGACTGGAAATAA	CTTCCAATTTCAGC			
AAV4-4-	1149	AAATGCCCTTCTACTGCCCTGGAGTACTTCC	TTCCGAGATGCTGCGGACTGGCAACA	CTTTGAAATTACG			
AAV1-A-	1170	TTCATCCCTTTTACTGCCCTGGAAATATTTCC	CTCAGATGCTGAGAACGGGCAACA	CTTTACCTTCAGC			
hu.46-A	1170	TTCATCCCTTTTACTGCCCTGGAAATATTTCC	CTCAGATGCTGAGAACGGGCAACA	CTTTACCTTCAGC			
hu.48-A	1170	TTCATCCCTTTTACTGCCCTGGAAATATTTCC	CTCAGATGCTGAGAACGGGCAACA	CTTTACCTTCAGC			
hu.44-A	1170	TTCATCCCTTTTACTGCCCTGGAAATATTTCC	CTCAGATGCTGAGAACGGGCAACA	CTTTACCTTCAGC			
hu.43-A	1173	TTCATCCCTTTTACTGCCCTGGAAATATTTCC	CTCAGATGCTGAGAACGGGCAACA	CTTTACCTTCAGC			
AAV6-A	1170	GTCAATCCCTTTTACTGCCCTGGAAATATTTCC	ATCGCAGATGCTGAGAACGGGCAATA	TAACCTTTACCTTCAGC			
hu.34-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.47-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.29-B	1167	CTCTTCAATTTTACTGCCCTAGGGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.63-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.56-B	1167	CTCTTCCCTTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.45-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.57-B	1164	CTCTTCCCTTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.35-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.58-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.28-B	1167	CTCTTCAATTTTACTGCCCTAGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.51-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.19-B	1167	CTCTTCCCTTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.49-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.52-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.13-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
AAV2-B	1167	CTCTTCAATTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.20-B	1167	CTCTTCCCTTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			
hu.24-B	1167	CTCTTCCCTTTTACTGCCCTGGAGTACTTTC	CTCAGATGCTGCCGTACCGGAAACA	AACTTTACCTTCAGC			

FIG. 3AV

81/125

hu. 64-B	1167	CTCTTCATTTTACTGCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTACCTTCAGC
hu. 27-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC
hu. 21-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC
hu. 22-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGACGCTTCGTACCGGAAACAACCTTTACCTTCAGC
hu. 23-B	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACCGGAAACAACCTTTACCTTCAGC
hu. 7-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 61-C	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
rh. 56-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTTCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 9-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 54-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 53-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 60-C	1167	CTCTTCATTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACCGGAAACAACCTTTCAGTTCAGC
hu. 55-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 2-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 1-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 18-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 3-C	1170	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 25-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 15-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 16-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 11-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 10-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
hu. 4-C	1167	CTCTTCCTTTTACTGCCCTGGAGTACTTTCCTTCTCAGATGCTGCGTACTGGAAACAACCTTTCAGTTCAGC
rh. 54-D	1173	TTCAATCCTTCTACTGCCCTGGAATACTTCCCTTCTCAGGTGCTGAGAACGGGTAAACAACCTTCACCTTCAGT
rh. 48-D	1173	TTCCCTCTTCTACTGCCCTGGAATATTTCCCTTCTCAGAACGGGTAAACAACCTTCACCTTCAGC
rh. 55-D	1173	TTCCCTCTTCTACTGCCCTGGAATATTTCCCTTCTCAGAACGGGTAAACAACCTTCACCTTCAGC
rh. 62-D	1173	TTCCCTCTTCTACTGCCCTGGAATATTTCCCTTCTCAGAACGGGTAAACAACCTTCACCTTCAGC
AAV7-D	1173	TTCCCTCTTCTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTTCAGTTCAGC
rh. 52-E	1176	TTCCCTCTTCTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTTCAGTTCAGC
rh. 51-E	1176	TTCCCTCTTCTACTGCCCTGGAGTACTTCCCTTCTCAGATGCTGAGAACGGGTAAACAACCTTTCAGTTCAGC

FIG. 3AW

82/125

hu. 39-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC	1270	1280	1290	1300	1310	1320	1330
rh. 53-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
hu. 37-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
rh. 43-E	1173	CTCCCTCCCTTCTACTGCCCTGGAAATACTTTCCCTTCCGAGATGCTGAGAACCCGGCAACAAC							
rh. 50-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
rh. 49-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
rh. 61-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
hu. 41-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
rh. 64-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
hu. 42-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
rh. 57-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
hu. 40-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
AAV8-E	1176	CTCCCTCCCTTCTACTGCCCTGGAAATACTTTCCCTTCCGAGATGCTGAGAACCCGGCAACAAC							
rh. 58-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTCCCCCTCTCAGATGCTGAGAACGGGCAACAAC							
rh. 40-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
hu. 67-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
hu. 17-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
hu. 6-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTTCCCTTCTCAAAATGCTGCCGAGAACGGGCAACAAC							
hu. 66-E	1176	TTCCCTCCCTTCTACTGCCCTGGAGTACTTTCCCTTCTCAAAATGCTGCCGAGAACGGGCAACAAC							
rh. 38-E	1176	TTCCCTCCCTTCTACTGCCCTGGAAATATTTTCCATCTCAAAATGCTGCCAACTGGAAACAATTTTGAATTCAGC							
hu. 32-F	1173	TTCGTCCCTTTTACTGCCCTGGAAATATTTTCCCGTCCGAAATGCTAAGAACGGGTAACAAC							
AAV9/hu	1173	TTCGTCCCTTTTACTGCCCTGGAAATATTTTCCCGTCCGAAATGCTAAGAACGGGTAACAAC							
hu. 31-F	1173	TTCGTCCCTTTTACTGCCCTGGAAATATTTTCCCGTCCGAAATGCTAAGAACGGGTAACAAC							
AAV5	1216								
AAV3-3	1237	TACAACCTTTGAGGAGGTGCCCTTCCACTCCAGCTTCGCTCCCAGTCAGAACCTGTTCAAGCTGGCCAAACC							
AAV4-4	1219	TATACCTTCGAGGATGTACCTTTTTCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGCTTGATGAATC							
AAV1-A	1240	TACAGTTTGGAGAGGTGCCCTTTTCCACTCGATGTACGCCACAGCCAGAGCCTGGACCGGCTGATGAACC							
		TACACCTTTGAGGAAGTGCCTTTTCCACAGCAGCTACGCCGACAGCCAGAGCCTGGACCGGCTGATGAATC							

FIG. 3AX

83/125

hu. 46-A 1240 TACACCTTTGAGGAAGTGCCCTCTCCACAGCAGCTGCGCGCACAGCCAGAGCCCTGGACCGGCTGATGAATC
hu. 48-A 1240 TACACCTTTGAGGAAGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCCTGGACCGGCTGATGAATC
hu. 44-A 1240 TACACCTTTGAGGAAGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCCTGGACCGGCTGATGAATC
hu. 43-A 1243 TACACCTTTGAGGAAGTGCCCTCTCCACAGCAGCTACGCGCACAGCCAGAGCCCTGGACCGGCTGATGAATC
AAV6-A 1240 TACACCTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCGCACAGCCAGAGCCCTGGACCGGCTGATGAATC
hu. 34-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGGCCGCTCATGAATC
hu. 47-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 29-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 63-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 56-B 1237 TACACTTTTGAAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGTCAAAGTCTGGACCGTCTCATGAATC
hu. 45-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 57-B 1234 TACACTTTTGAAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGTCAAAGTCTGGACCGTCTCATGAATC
hu. 35-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGGCCGCTCATGAATC
hu. 58-B 1237 TACACCTTTGAGGATGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 28-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 51-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCGGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 19-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 49-B 1237 TACACCTTTGAGGATGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 52-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
hu. 13-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
AAV2-B 1237 TACACTTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 20-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 24-B 1237 TACACCTTTGAAGACGTTCCCTTTCCATAGCAGCTACGCTCACAGCCAAAGTCTGGACCGTCTCATGAATC
hu. 64-B 1237 TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGACCGTCTCATGAATC
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 TACACTTTTGAAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAATC

FIG. 3AY

rh. 56-C	1237	TACACCTTTGAAGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 9-C	1237	TACACCTTTGAGGACGTTCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGACCGGCTGATGAAATC
hu. 54-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGGGTTTGGATCGGCTGATGAAATC
hu. 53-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAAATC
hu. 60-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 55-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTTTGGATCGGCTGATGAAATC
hu. 2-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 1-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 18-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 3-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 25-C	1240	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGTCCACTGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 15-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 16-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 11-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 10-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
hu. 4-C	1237	TACACTTTTGAAGACGTGCCCTTTCCACAGCAGCTACGCTCACAGCCAGAGTCTGGATCGGCTGATGAAATC
rh. 54-D	1243	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGCCTAGACCGGCTGATGAAATC
rh. 48-D	1243	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAAATC
rh. 55-D	1243	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAAATC
rh. 62-D	1243	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAAATC
AAV7-D	1243	TACAGCTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGCCTGGACCGGCTGATGAAATC
rh. 52-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC
rh. 51-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC
hu. 39-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC
rh. 53-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC
hu. 37-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACCGACTGATGAAATC
rh. 43-E	1243	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACCGGCTGATGAAATC
rh. 50-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC
rh. 49-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC
rh. 61-E	1246	TACACTTTCGAGGACGTGCCCTTTCCACAGCAGCTACGCTACGCGCACAGCCAGAGTCTGGACAGGCTGATGAAATC

85/125

hu. 41-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
rh. 64-E	1246	TACACTTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC							
hu. 42-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
rh. 57-E	1246	TACACTTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC							
hu. 40-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
AAV8-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCCCACAGCCAGAGCTTGGACCGGCTGATGAATC							
rh. 58-E	1246	TACACTTTCGAGGACGTGCCCTTTCACAGCAGCTACGCGCACAGCCAGAGTTTGGACAGGCTGATGAATC							
rh. 40-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
hu. 67-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
hu. 17-E	1246	TACCAGTTTGAGGACGTGCCCTTTCACAGCAGCTACGCGCATAGCCAAAGCCTGGACCGGCTGATGAACC							
hu. 6-E	1246	TACCAGTTTGAGGACGTGCCCTTTCACAGCAGCTACGCGCATAGCCAAAGCCTGGACCGGCTGATGAACC							
hu. 66-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTCGGACCGACTGATGAATC							
rh. 38-E	1246	TACACCTTCGAGGACGTGCCCTTTCACAGCAGCTACGCACACAGCCAGAGCTTGGACCGACTGATGAATC							
hu. 32-F	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATC							
AAV9/hu	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATC							
hu. 31-F	1243	TACGAGTTTGAGAACGTACCTTTCATAGCAGCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATC							
			1340	1350	1360	1370	1380	1390	1400
									
AAV5	1286	CGCTGGTGGACCACTACTTGTAACCGCTTCGTGAGCACAAAT-----AACACTGG							
AAV3-3	1307	CTCTTATTGATCAGTATCTGTACTACCTGAACAGAACGCAAGGAACAACCTCTGGAAACAACCAACCAATC							
AAV4-4	1289	CTCTCATCGACCACTACCTGTGGGACTGCAATCGACCACCAACCTGAATGCCGGGACTGC							
AAV1-A	1310	CTCTCATCGACCAATACTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAACAA							
hu. 46-A	1310	CTCTCATCGACCAATACTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAACAG							
hu. 48-A	1310	CTCTCATCGACCAATACTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAACAA							
hu. 44-A	1310	CTCTCATCGACCAATACTGTATTACCCGAAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAACAA							
hu. 43-A	1313	CTCTCATCGTCCAATACTGTATTACCTGAACAGAACTCAA--AATCAGTCCGGAAGTGCCCAAACAA							
AAV6-A	1310	CTCTCATCGACCACTACCTGTATTACCTGAACAGAACTCAG--AATCAGTCCGGAAGTGCCCAAACAA							
hu. 34-B	1307	CTCTCATCGACCACTACCTGTATTACTTGAGCAGAAACAAC---ACTCCAAGTGGAACCAACGACGATC							
hu. 47-B	1307	CTCTCATCGACCACTACCTGTATTACTTGAGCACAACAAC---ACTCCAAGTGGAACCAACGACGATC							

FIG. 3BA

hu.29-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.63-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.56-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.45-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGTGGAAACCAACACGACGAGTC
 hu.57-B 1304 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCACTACGACGAGTC
 hu.35-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGTGGAAACCAACACGACGAGTC
 hu.58-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.28-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.51-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGTGGAAACCAACACGACGAGTC
 hu.19-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.49-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.52-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGTGGAAACCAACACGACGAGTC
 hu.13-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 AAV2-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGTGGAAACCAACACGACGAGTC
 hu.20-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.24-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.64-B 1307 CTCGTCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGACGAGTC
 hu.27-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.21-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.22-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.23-B 1307 CTCATCGACCGAGTACCTGTATTACTTGAGCAGAAACAAAC---ACTCCAAGCGGAACCAACACGATGTC
 hu.7-C 1307 CTGATCGACCGAGTACCTGTATTACTTGAAACAAACACAA---TCAAATAGTGGAACTCTTCAGCAGTC
 hu.61-C 1307 CTGATCGACCGAGTACCTGTATTACTTGAAACAAAGACACAA---ACAAATAGTGGAACTCTTCAGCAGTC
 rh.56-C 1307 CTGATCGACCGAGTACCTGTATTACTTGAAACAAACACAA---TCAAATAGTGGAGCTCTTCAGCAGTC
 hu.9-C 1307 CTGATCGACCGAGTATCTATATTATCTGAACAGGACACAA---TCAAATAGTGGAACTCTTCAGCAGTC
 hu.54-C 1307 CTGATCGACCGAGTACCTGTATTATCTAAACAGAACACAA---ACAGCTAGTGGAACT---CAGCAGTC
 hu.53-C 1307 CTGATCGACCGAGTACCTGTATTATCTAAACAGAACACAA---ACAGCTAGTGGAACT---CAGCAGTC
 hu.60-C 1307 CTGGTCGACCGAGTACCTGTATTATCTGAACAGACACAA---ACAAATAGTGGAACTCTTCAGCAGTC
 hu.55-C 1307 CTGATCGACCGAGTACCTGTATTATCTAAACAGAACACAA---ACAGCTAGTGGAACT---CAGCAGTC
 hu.2-C 1307 CTGATCGACCGAGTACCTGTATTATCTGAACAGACACAA---ACAAATAGTGGAACTCTTCAGCAGTC

87/125

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 CTCTGATCGACCAGTATCTATATTATCTGAACAGGACACAA--TCAAATAGTGGAACCTCTTCAGCAGTC
 hu.10-C 1307 CTCTGATCGACCAGTATCTATATTATCTGAACAGGACACAA--TCAAATAGTGGAACCTCTTCAGCAGTC
 hu.4-C 1307 CTCTGATCGACCAGTACCTGTATTATCTGAACAAGACACAA--ACAAATAGTGGAACCTCTTCAGCAGTC
 rh.54-D 1313 CCTCATCGACCAGTACCTGTATTACCTGGCTAGAACACAGAGTAACCCAGGAGGCACATCTGGCAATCG
 rh.48-D 1313 CTCTTATCGACCAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGACGAGGACACAGCTGGCAATCG
 rh.55-D 1313 CTCTTATCGACCAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGACGAGGACACAGCTGGCAATCG
 rh.62-D 1313 CTCTTATCGACCAGTACCTGTATTACCTGGCCAGAACACAGAGCAACGACGAGGACACAGCTGGCAATCG
 AAV7-D 1313 CCTCATCGACCAGTACTTGTACTACCTGGCCAGAACACAGAGTAACCCAGGAGGCACAGCTGGCAATCG
 rh.52-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 rh.51-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 hu.39-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 rh.53-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 hu.37-E 1316 CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA
 rh.43-E 1313 CTCTGATTGACCAGTACCTGTACTACTTGTCTCGGACTCAAACA--ACAGGAGGCACGCGGGAACCCA
 rh.50-E 1316 CTCTCGTCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 rh.49-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 rh.61-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 hu.41-E 1316 CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA
 rh.64-E 1316 CTCTCATCGACCAGTACCTGTACTACCTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 hu.42-E 1316 CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA
 rh.57-E 1316 CTCTCATCGACCAGTACCTGTACTACTTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA
 hu.40-E 1316 CTCTCATCGACCAGTACCTGTACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA
 AAV8-E 1316 CTCTGATTGACCAGTACCTGTACTACTTGTCTCGGACTCAAACA--ACAGGAGGCACGCGGGAATACGCA
 rh.58-E 1316 CTCTCATCGACCAGTACCTGTACTACTTGTCAAGAACCCAGTCT--ACGGGAGGCACACAGCGGGAACCCA

FIG. 3B

88/125

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	CTCTCATCGACCAGTACCTGCACACTACTTATCCAGAACTCAGTCC--ACAGGAGGAACTCAAGGTACCCA							
hu. 32-F	1313	CACTCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAACGGTTCTGGA-----CAGAAATCAACA							
AAV9/hu	1313	CACTCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAACGGTTCTGGA-----CAGAAATCAACA							
hu. 31-F	1313	CACTCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAACGGTTCTGGA-----CAGAAATCAACA							
									
AAV5	1335	CGGAGTCCAGTTCAACAAGAACCTGGCCGGAGATACGCCAACACCTACAAAAACTGGTTCCTGGGGCCC							
AAV3-3-	1377	ACGGCTGCTTTTAGCCAGGCTGGGCTCAGTCTATGTCTTTGCAGGCCAGAAATGGCTACCTGGGCC							
AAV4-4-	1359	CACCACCAACTTTACCAAGCTGGGCTACCAACTTTCCAACTTTAAAAAGAACTGGCTGCCCGGGCCT							
AAV1-A	1377	GGACTTGCTGTTAGCCGTTGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC							
hu. 46-A	1377	GGACTTGCTGTTAGCCGTTGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC							
hu. 48-A	1377	GGACTTGCTGTTAGCCGTTGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC							
hu. 44-A	1377	GGACTTGCTGTTAGCCGTTGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC							
hu. 43-A	1380	GGACTTGCTGTTAGCCGTTGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC							
AAV6-A	1377	GGACTTGCTGTTAGCCGTTGGTCTCCAGCTGGCATGTCTGTTCAGCCCAAAAACTGGCTACCTGGACCC							
hu. 34-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 47-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 29-B	1374	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 63-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCAAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 56-B	1374	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 45-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 57-B	1371	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 35-B	1374	AAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGACCCAGTCTAGGAACTGGCTTCCTGGACCC							
hu. 58-B	1374	CAGGCTTCAGTTTCTCAGGCCGGAGCGAGTGACATTCTGGGATCAGTCTAGGAACTGGCTTCCTGGACCC							

89/125

hu.28-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCGAGTGACATTCAGGACCAGTCTAGGAACTGGCTTCCTGGACCC
hu.51-B 1374 AAGGCTTCAGTTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCC
hu.19-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.49-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCC
hu.52-B 1374 AAGGCTTCAGTTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCC
hu.13-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCC
AAV2-B 1374 AAGGCTTCAGTTTTCTCAGGCCGGAGCGAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCC
hu.20-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.24-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.64-B 1374 AAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGGAACTGGCTTCCTGGACCC
hu.27-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACGTTCCGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.21-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.22-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.23-B 1374 CAGGCTTCAGTTTTCTCAGGCCGGAGCAAGTGACATTCGGGACCAGTCTAGAAACTGGCTTCCTGGACCC
hu.7-C 1374 TCGGCTACTGTTAGTCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTACCTGGACCT
hu.61-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCACCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
rh.56-C 1374 TCGGCTACTGTTAGTCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.9-C 1374 TAGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.54-C 1371 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCG
hu.53-C 1371 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCG
hu.60-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.55-C 1371 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCG
hu.2-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.1-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.18-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.3-C 1377 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.25-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.15-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.16-C 1374 TCGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT
hu.11-C 1374 TAGGCTACTGTTAGCCAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGGACCT

90/125

hu. 10-C	1374	TAGGCTACTGTTTAGCCAAAGCTGGACCCACCAGCATGTCTCTTCAAGCTAAAAACTGGCTGCCCTGGACCT
hu. 4-C	1374	TCGGCTACTGTTTAGCCAAAGCTGGACCAACCAACATGTCTCTTCAAGCTAAAAACTGGCTGCCCTGGACCT
rh. 54-D	1383	GGAAGTGCAGTTTTTACCAGGGCGGGCCTTCCACCATGGCCGAACAAGCCAAAGAACTGGTTACCTGGACCT
rh. 48-D	1383	GGAAGTGCAGTTTTTATCAGGGCGGGCCTACCACCATGGCCGAACAAGCCAAAACTGGCTGCCCTGGACCT
rh. 55-D	1383	GGAAGTGCAGTTTTTATCAGGGCGGGCCTACCACCATGGCCGAACAAGCCAAAACTGGCTGCCCTGGACCT
rh. 62-D	1383	GGAAGTGCAGTTTTTATCAGGGCGGGCCTACCACCATGGCCGAACAAGCCAAAACTGGCTGCCCTGGACCT
AAV7-D	1383	GGAAGTGCAGTTTTTACCAGGGCGGGCCTTCAACTATGGCCGAACAAGCCAAAGAACTGGTTACCTGGACCT
rh. 52-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh. 51-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu. 39-E	1383	GCAGTTGCTGTCTTCTCGGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh. 53-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu. 37-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 43-E	1380	GACTCTGGGCTTCAGCCAAGGTGGGCCTAATACAAATGGCCAATCAGGCAAGAACTGGCTGCCAGGACCC
rh. 50-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh. 49-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh. 61-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu. 41-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 64-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu. 42-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 57-E	1383	GCAGTTGCTGTCTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
hu. 40-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
AAV8-E	1383	GACTCTGGGCTTCAGCCAAGGTGGGCCTAATACAAATGGCCAATCAGGCAAGAACTGGCTGCCAGGACCC
rh. 58-E	1383	GCAGCTGCTGTTTCTCAGGCCGGGCCTAGCAACATGTGGCTCAGGCCAGAAACTGGCTGCCCTGGACCC
rh. 40-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu. 67-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu. 17-E	1383	GCAGTTGCTATTTTCTCAGGCCGGGCCTAATAACATGTGGCTCAGGCCAAAACTGGCTACCCGGGCC
hu. 6-E	1383	GCAGTTGCTATTTTCTCAGGCCGGGCCTAATAACATGTGGCTCAGGCCAAAACTGGCTACCCGGGCC
hu. 66-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
rh. 38-E	1383	GCAATTGTTATTTTCTCAAGCTGGGCCTGCAAACATGTGGCTCAGGCTAAGAACTGGCTACCTGGACCT
hu. 32-F	1377	AACGCTAAAAATTCAGCGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC

91/125

	1480	1490	1500	1510	1520	1530	1540
AAV9/hu	1377	AACGCTAAAA	TT	CAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC			
hu.31-F	1377	AACGCTAAAA	TT	CAGTGTGGCCGGACCCAGCAACATGGCTGTCCAGGGAAGAACTACATACCTGGACCC			
AAV5	1405	ATGGGCCGAACCCAGGGCTGGAACCTGGGCTCCGGGGTCAAC	-----	CGGCCAGTGTC			
AAV3-3	1447	TGCTACCGGCAACAGAGACTTTC	AAAGACTGCTAACGACAAC	-----	AACAACAGTAACT		
AAV4-4	1429	TCAATCAAGCAGCAGGGCTTCT	C	AAAGACTGCCAATCAAAACTACAAGATCCCTGCCACCGGTCAGACA			
AAV1-A	1447	TGTTATCGGCAGCAGCGCGTTTCT	AA	AAACAGACAAC	-----	AACAACAGCAATT	
hu.46-A	1447	TGTTATCGGCAGCAGCGCGTTTCT	AA	AAACAGACAAC	-----	AACAACAGCAATT	
hu.48-A	1447	TGTTATCGGCAGCAGCGCGTTTCT	AA	AAACAGACAAC	-----	AACAACAGCAATT	
hu.44-A	1447	TGTTATCGGCAGCAGCGCGTTTCT	AA	AAACAGACAAC	-----	AACAACAGCAATT	
hu.43-A	1450	TGTTATCGGCAGCAGCGCGTTTCT	AA	AAACAGACAAC	-----	AACAACAGCAATT	
AAV6-A	1447	TGTTACCGGCAGCAGCGCGTTTCT	AA	AAACAGACAAC	-----	AACAACAGCAACT	
hu.34-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.47-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.29-B	1444	TGTTACCGTCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.63-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.56-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.45-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.57-B	1441	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACGGTGAAT	
hu.35-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.58-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.28-B	1444	TGTTACCGTCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.51-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.19-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.49-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.52-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
hu.13-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	
AAV2-B	1444	TGTTACCGGCAGCAGCGAGTATCA	AA	GACATCTGCGGATAAC	-----	AACAACAGTGAAT	

92/125

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	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.61-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
rh.56-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.9-C	1444	TGCTACAGACAGCAGCGTCTTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.54-C	1441	TGTTATCGCCAGCAGCGTTTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.53-C	1441	TGTTATCGCCAGCAGCGTTTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.60-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.55-C	1441	TGTTATCGCCAGCAGCGTTTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.2-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.1-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAAAACGGAAC	-----AACAAACAGCAAAC
hu.18-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.3-C	1447	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAAAACGACAAT	-----AACAACTGCAAAC
hu.25-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.15-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.16-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.11-C	1444	TGCTACAGACAGCAGCGTCTTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.10-C	1444	TGCTACAGACAGCAGCGTCTTCAAAGCAGGCAAAACGACAAC	-----AACAAACAGCAAAC
hu.4-C	1444	TGCTACAGACAGCAGCGTCTGTCAAAAACAGGCAAAACGACAAC	-----AACAAACAGCAAAC
rh.54-D	1453	TGCTTCCGGCAACAAAGAGTTTCCAAACACTGGATCAAAAC	-----AACAAACAGCAAAC
rh.48-D	1453	TGCTTCCGGCAACAAAGAGTCTCCAAGACGCTGGATCAAAAC	-----AACAAACAGCAAAC
rh.55-D	1453	TGCTTCCGGCAACGAAGAGTCTCCAAGACGCTGGATCAAAAC	-----AACAAACAGCAAAC
rh.62-D	1453	TGCTTCCGGCAACAAAGAGTCTCCAAGACGCTGGATCAAAAC	-----AACAAACAGCAAAC
AAV7-D	1453	TGCTTCCGGCAACAAAGAGTCTCCAAAACGCTGGATCAAAAC	-----AACAAACAGCAAAC

93/125

rh. 52-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT	1550	1560	1570	1580	1590	1600	1610
rh. 51-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 39-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 53-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 37-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 43-E	1450	TGTTACCGCCAACAACGCGTCTCAACGACAACCGGGCAAAAC-----AACAAATAGCAACT							
rh. 50-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 49-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 61-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 41-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 64-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 42-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAGC-----AACACAGCAACT							
rh. 57-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 40-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
AAV8-E	1453	TGTTACCGCCAACAACGCGTCTCAACGACAACCGGGCAAAAC-----AACAAATAGCAACT							
rh. 58-E	1453	TGCTACAGACAGCGCGTCTCCACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 40-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 67-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 17-E	1453	TGCTACCGGACAGCAACGCGTCTCCACGACACTGTGCAAAAT-----AACACAGCAACT							
hu. 6-E	1453	TGCTACCGGACAGCAACGCGTCTCCACGACACTGTGCAAAAT-----AACACAGCAACT							
hu. 66-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
rh. 38-E	1453	TGCTACCGGACAGCGAGTCTCTACGACACTGTGCAAAAC-----AACACAGCAACT							
hu. 32-F	1447	AGCTACCGACAACAACGTGTCTCAACCACACTGTGACTCAAAAC-----AACACAGCGAAT							
AAV9/hu	1447	AGCTACCGACAACAACGTGTCTCAACCACACTGTGACTCAAAAC-----AACACAGCGAAT							
hu. 31-F	1447	AGCTACCGACAACAACGTGTCTCAACCACACTGTGACTCAAAAC-----AACACAGCGAAT							
AAV5	1460								
AAV3-3_	1502	TTCCTTGGACAGCGGCCAGCAAATATCATCTCAATGGCCGCGACTCGCTGGTGAAATCCAGGACCAGCTAT							

94/125

AAV4-4 1499 GTCTCATCAATACGAGACGCACAGCACTCTGGACGGAAGATGGAGTGCCCTGACCCCCGGACCTCCAAT
AAV1-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCAGCTGCTAT
hu.46-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCAGCTGCTAT
hu.48-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCAGCTGCTGT
hu.44-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCAGCTGCTAT
hu.43-A 1505 TTACCTGGACTGGTGCTTCAAAATATAACCTCAATGGCGTGAATCCATCATCAACCCCTGGCAGCTGCTAT
AAV6-A 1502 TTACCTGGACTGGTGCTTCAAAATATAACCTTAATGGCGTGAATCTATAATCAACCCCTGGCAGCTGCTAT
hu.34-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.47-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.29-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.63-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTTAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.56-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.45-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCGT
hu.57-B 1496 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.35-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.58-B 1499 ACTCGTGGATTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAAT
hu.28-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.51-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.19-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.49-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.52-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.13-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
AAV2-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.20-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGCAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.24-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGAGCTAT
hu.64-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTTAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGGCCAT
hu.27-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGAGCTAT
hu.21-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGAGCTAT
hu.22-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGAGCTAT
hu.23-B 1499 ACTCGTGGACTGGAGCTACCAAGTACCACCTCAATGGAAGAGACTCTCTGGTGAATCCGGGCCCGAGCTAT

95/125

hu. 7-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCACCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 61-C	1499	TTCCCTGGACCGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
rh. 56-C	1499	TTCCCTGGACTGCGGCTACAAAGTACACCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 9-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 54-C	1496	TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCGGAGACTCTTTGGTGAACCCGGGCCCGGCCAT
hu. 53-C	1496	TTCCCTGGACTGGAGCTACCAAGTACTACCTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGGCCAT
hu. 60-C	1499	TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 55-C	1496	TTCCCTGGACTGGAGCTACCAAGTACCACTCAATGGCAGAGACTCTTTGGTGAACCCGGGCCCGGCCAT
hu. 2-C	1499	TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 1-C	1499	TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 18-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 3-C	1502	TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 25-C	1499	TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 15-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 16-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 11-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCGTCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 10-C	1499	TTCCCTGGACTGCGGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
hu. 4-C	1499	TTCCCTGGACTGCAGCTACAAAGTATCATCTAAATGCCCGGACTCGTTGGTTAATCCAGGACCAGCTAT
rh. 54-D	1508	TTGCTTGGACTGGTGCCACCAAATATCACCTGAACGGCAGAAACTCATTTGGTGAATCCTGGTGTGCGCCAT
rh. 48-D	1508	TTGCTTGGACTGGTGCCACCAAATACCATCTAAATGGAAGAAATTCAATTTGGTTAATCCCGGTGTGCGCCAT
rh. 55-D	1508	TTGCTTGGACTGGTGCCACCAAATACCATCTAAATGGAAGAAATTCAATTTGGTTAATCCCGGTGTGCGCCAT
rh. 62-D	1508	TTGCTTGGACTGGTGCCACCAAATACCATCTAAATGGAAGAAATTCAATTTGGTTAATCCCGGTGTGCGCCAT
AAV7-D	1508	TTGCTTGGACTGGTGCCACCAAATATCACCTGAACGGCAGAAACTCGTTGGTTAATCCCGGTGTGCGCCAT
rh. 52-E	1508	TTGCCCTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTGTGCGCCAT
rh. 51-E	1508	TTGCCCTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTGTGCGCCAT
hu. 39-E	1508	TTGCCCTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTGTGCGCCAT
rh. 53-E	1508	TTGCCCTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTGTGCGCCAT
hu. 37-E	1508	TTGCTTGGACTGGTGCCACCAAATATCACCTGAACGGAGAGACTCTTTGGTAAATCCCGGTGTGCGCCAT
rh. 43-E	1505	TTGCCCTGGACTGGTGCCACCAAATACCATCTGAATGGAAGAAATTCAATTTGGCTAAATCCTGGCATCGCTAT
rh. 50-E	1508	TTGCCCTGGACTGGTGCCACCAAAGTATCATCTGAACGGCAGAGACTCTCTGGTGAATCCGGCGTGTGCGCCAT

FIG. 3BK

96/125

rh. 49-E	1508	TTGCC	TGACT	GGTGC	CAAGT	ATCAT	CTGAA	CGCAG	AGACT	CTCTG	GTGA	ATCCG	GGCG	TGCC	CA
rh. 61-E	1508	TTGCC	TGACT	GGTGC	CAAGT	ATCAT	CTGAA	CGCAG	AGACT	CTCTG	GTGA	ATCCG	GGCG	TGCC	CA
hu. 41-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCC
rh. 64-E	1508	TTGCC	TGACT	GGTGC	CAAGT	ATCAT	CTGAA	CGCAG	AGACT	CTCTG	GTGA	ATCCG	GGCG	TGCC	CA
hu. 42-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCC
rh. 57-E	1508	TTGCC	TGACT	GGTGC	CAAGT	ATCAT	CTGAA	CGCAG	AGACT	CTCTG	GTGA	ATCCG	GGCG	TGCC	CA
hu. 40-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCC
AAV8-E	1508	TTGCC	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCT
rh. 58-E	1508	TTGCC	TGACT	GGTGC	CAAGT	ATCAT	CTGAA	CGCAG	AGACT	CTCTG	GTGA	ATCCG	GGCG	TGCC	CA
rh. 40-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	TGCT
hu. 67-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCC
hu. 17-E	1508	TTGCT	TGAC	CCGGT	GC	CAAGT	ATCAT	CTGAA	TGGC	AGAG	ACTCT	CTG	GTAA	ATCCG	GGTG
hu. 6-E	1508	TTGCT	TGAC	CCGGT	GC	CAAGT	ATCAT	CTGAA	TGGC	AGAG	ACTCT	CTG	GTAA	ATCCG	GGTG
hu. 66-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCC
rh. 38-E	1508	TTGCT	TGACT	GGTGC	CAAA	TATC	ACCTG	AACG	GAG	AGACT	CTTTG	GTAA	ATCCG	GGTG	CGCC
hu. 32-F	1502	TTGCT	TGGC	CTGG	AGCTT	CTCT	TGGG	CTCT	CAAT	GGAC	GTAA	AGCTT	GAT	GAAT	CTTG
AAV9/hu	1502	TTGCT	TGGC	CTGG	AGCTT	CTCT	TGGG	CTCT	CAAT	GGAC	GTAA	AGCTT	GAT	GAAT	CTTG
hu. 31-F	1502	TTGCT	TGGC	CTGG	AGCTT	CTCT	TGGG	CTCT	CAAT	GGAC	GTAA	AGCTT	GAT	GAAT	CTTG

AAV5	1530		1620	1630	1640	1650	1660	1670	1680				
AAV3-3	1572	GCCAGT	CACAAG	GACGAT	GAAGAA	AAATTT	TCCCTA	TGCACG	CAATCT	AATAT	TTGGCA	AAAGAG	GGG
AAV4-4	1569	GGCACG	GCTGG	ACCTGC	GACAG	CAAGTTC	AGC--	AAACAG	CCAGCT	CATCT	TTGCGG	GGCCTA	AAACAG
AAV1-A	1572	GGCCTC	CACAA	AGACG	ACGA	AGACA	AGTTCT	TCCCAT	GAGCG	GTGTC	ATGAT	TTTGG	AAAAGAG
hu. 46-A	1572	GGCCTC	CACAA	AGACG	ACGA	AGACA	AGTTCT	TCCCAT	GAGCG	GTGTC	ATGAT	TTTGG	AAAAGAG
hu. 48-A	1572	GGCCTC	CACAA	AGACG	ACGA	AGACA	AGTTCT	TCCCAT	GAGCG	GTGTC	ATGAT	TTTGG	AAAAGAG
hu. 44-A	1572	GGCCTC	CACAA	AGACG	ACGA	AGACA	AGTTCT	TCCCAT	GAGCG	GTGTC	ATGAT	TTTGG	AAAAGAG
hu. 43-A	1575	GGCCTC	CACAA	AGACG	ACGA	AGACA	AGTTCT	TCCCAT	GAGCG	GTGTC	ATGAT	TTTGG	AAAAGAG
AAV6-A	1572	GGCCTC	CACAA	AGACG	ACGA	AGACA	AGTTCT	TCCCAT	GAGCG	GTGTC	ATGAT	TTTGG	AAAAGAG

97/125

hu. 34-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 47-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 29-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTTATCTTTGGGAAGCAAGGC
hu. 63-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 56-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 45-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 57-B 1566 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 35-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 58-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGGA
hu. 28-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTTATCTTTGGGAAGCAAGGC
hu. 51-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 19-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 49-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 52-B 1569 GGCAAGCCACAAGGACAAATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 13-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
AAV2-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGGAAGCAAGGC
hu. 20-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 24-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 64-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 27-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCGTCTTTGGAAAACAAGAC
hu. 21-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 22-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 23-B 1569 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCTCAGAGCGGGTTCTCATCTTTGGAAAACAAGAC
hu. 7-C 1569 GGCAAGTCACAAGGACGATGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 61-C 1569 GGCAAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTTATATTTGGTAAACAAGGA
rh. 56-C 1569 GGCAAGTCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 9-C 1569 GGCAAGCCACAAGACGATGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTGATATTTGGTAAACAAGGA
hu. 54-C 1566 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTAATATTTGGTAAAGAAAGGA
hu. 53-C 1566 GGCAAGCCACAAGGACGATGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTAATATTTGGTAAAGAAAGGA
hu. 60-C 1569 GGCAAGTCACAAGGATGACGAAGAAAAGTTTTTCCCCATGCATGGAACCCCTTATATTTGGTAAACAAGGA

98/125

hu. 55-C 1566 GGCCAGCCACAAGGACGATGAAGAAAAGTTTTCCTCATGCATGGAACCCCTAATATTGGTAAAGAAAGGA
 hu. 2-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 1-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 18-C 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 3-C 1572 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 25-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 15-C 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 16-C 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 11-C 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 10-C 1569 GGCCAGCCACAAGACGATGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 hu. 4-C 1569 GGCCAGTCACAAGGATGACGAAGAAAAGTTTTCCTCATGCATGGAACCCCTGATATTGGTAAACAAAGGA
 rh. 54-D 1578 GGCAACTCACAAGGACGACGAGGACCGCTTTTCCCATCCAGCGGAGTCTGATTTTGGAAAACCTGGA
 rh. 48-D 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCTTCGAGCGGAGTCTGATTTTGGAAAACCTGGA
 rh. 55-D 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCTTCGAGCGGAGTCTGATTTTGGAAAACCTGGA
 rh. 62-D 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCTTCGAGCGGAGTCTGATTTTGGAAAACCTGGA
 AAV7-D 1578 GGCAACTCACAAGGACGACGAGGACCGCTTTTCCCATCCAGCGGAGTCTGATTTTGGAAAACCTGGA
 rh. 52-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 rh. 51-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 hu. 39-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 rh. 53-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 hu. 37-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCTGATGTTTCGGAACACAGGGT
 rh. 43-E 1575 GGCAACACACAAGACGACGAGGACCGTTTTCCTCAGTAACGGGA--TCCTGTTTTCGCAACAAAAT
 rh. 50-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 rh. 49-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 rh. 61-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 hu. 41-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCTGATGTTTGGAAAACAGGGT
 rh. 64-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 hu. 42-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCTGATGTTTGGAAAACAGGGT
 rh. 57-E 1578 GGCAACCAACAAGGACGACGAGGACCGCTTCTTCCCATCCAGCGGATCCTCATGTTTGGCAAGCAGGGA
 hu. 40-E 1578 GGCAACCCACAAGGACGACGAGGACCGCTTCTTCCCGTCGAGTGGAGTCTGATGTTTGGAAAACAGGGT

AAV8-E	1578	GGCAACACACAAGACGACGAGGAGCGT	1690	1700	1710	1720	1730	1740	1750
rh. 58-E	1578	GGCAACCAACAAGGACGACGAGGACCGCT							
rh. 40-E	1578	GGCAACGCATAAGGACGACGAGGAACGTT							
hu. 67-E	1578	GGCAACCCACAAGGACGACGAGGAACGCT							
hu. 17-E	1578	GGCAACGCACAAGGACGACGAAGAGCGATT							
hu. 6-E	1578	GGCAACGCACAAGGACGACGAAGAGCGATT							
hu. 66-E	1578	GGCAACCCACAAGGACGACGAGGAACGCT							
rh. 38-E	1578	GGCAACCCACAAGGACGACGAGGAACGCT							
hu. 32-F	1572	GGCCAGCCACAAGAAAGGAGAGGACCGTT							
AAV9/hu	1572	GGCCAGCCACAAGAAAGGAGAGGACCGTT							
hu. 31-F	1572	GGCCAGCCACAAGAAAGGAGAGGACCGTT							
AAV5	1600	GCGAACCCGGGCACCCACCGCCACGTACCT							
AAV3-3-	1642	ACA-----ACGGCAAGTAACGCAGAA							
AAV4-4-	1636	AAC-----GCAACACGGCCACCGTACC							
AAV1-A	1642	GCC-----GGAGCTTCAAAACACTGCA							
hu. 46-A	1642	GCC-----GGAGCTTCAAAACACTGCA							
hu. 48-A	1642	GCC-----GGAGCTTCAAGCACTGCA							
hu. 44-A	1642	GCC-----GGAGCTTCAAAACACTGCA							
hu. 43-A	1645	GCC-----GGAGCTTCAAAACACTGCA							
AAV6-A	1642	GCC-----GGAGCTTCAAAACACTGCA							
hu. 34-B	1639	TCA-----GAGAAACAAATGTGGACAT							
hu. 47-B	1639	TCA-----GAGAAACAAATGTGGACAT							
hu. 29-B	1639	CCA-----GAGAAACAAATGTGGATAT							
hu. 63-B	1639	TCG-----GGAATAACTAATGTGGACAT							
hu. 56-B	1639	TCA-----GAGAAACAAATGTGGACAT							
hu. 45-B	1639	TCA-----GAGAAACAAATGTGGACAT							
hu. 57-B	1636	TCA-----GAGAAACAAATGTGGACAT							

FIG. 3B

100/125

hu.35-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 hu.58-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGAA
 hu.28-B 1639 TCA-----GAGAAAACAAATGTGGATATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 hu.51-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 hu.19-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.49-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGAA
 hu.52-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 hu.13-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 AAV2-B 1639 TCA-----GAGAAAACAAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 hu.20-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.24-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.64-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTCATGATTACAGACGAAGAGGAAATCAGGA
 hu.27-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.21-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.22-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.23-B 1639 TCG-----GGAAAACCTAATGTGGACATTGAA---AAGTTATGATTACAGACGAAGAGGAAATCAGGA
 hu.7-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCATGATTACAGATGAAGAAGAAATCCGCA
 hu.61-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGA
 rh.56-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCATGATTACAGATGAAGAAGAAATCCGCA
 hu.9-C 1639 ACA-----AATGCTAACGACGCGGATTGGAG---CATGTTATGATTACAGATGAAGAAGAAATCAGGA
 hu.54-C 1636 ACA-----AATGCTACCAACGCGGAATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGA
 hu.53-C 1636 ACA-----AATGCTACCAACGCGGAATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGA
 hu.60-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGA
 hu.55-C 1636 ACA-----AATGCTACCAACGCGGAATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGA
 hu.2-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGG
 hu.1-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGG
 hu.18-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCATGATTACAGATGAAGAAGAAATCCGCA
 hu.3-C 1642 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGC
 hu.25-C 1639 ACA-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAGAAATCAGGA
 hu.15-C 1639 ACA-----AATGCTAACGACGCGGATTGGAC---AATGTCATGATTACAGATGAAGAAGAAATCCGCA

101/125

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-----AATGCCAACGACGCGGATTGGAA---AATGTCATGATTACAGATGAAGAAATCAGGG
 rh.54-D 1648 GCA-----ACCAAC---AAGACTACACTTGGAA---AACGTGTTAATGACAAATGAAGAAATTCGTC
 rh.48-D 1648 GCA-----GCTAAT---AAGACTACACTTGGAA---AATGTGTTAATGACAAATGAAGAGGAAATTCGTC
 rh.55-D 1648 GCA-----GCTAAT---AAGACTACACTTGGAA---AATGTGTTAATGACAAATGAAGAGGAAATTCGTC
 rh.62-D 1648 GCA-----GCTAAT---AAGACTACACTTGGAA---AATGTGTTAATGACAAATGAAGAGGAAATTCGTC
 AAV7-D 1648 GCA-----ACTAAC---AAAACCTACACTTGGAA---AATGTGTTAATGACAAATGAAGAAATTCGTC
 rh.52-E 1648 GCT-----GGAAAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 rh.51-E 1648 GCT-----GGAAAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 hu.39-E 1648 GCT-----GGAAAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 rh.53-E 1648 GCT-----GGAAAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 hu.37-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA
 rh.43-E 1642 GCT-----GCCAGAGACAATGCGGATTACAGC---GATGTCATGCTAACCCAGCGGAGGAAATCAAAA
 rh.50-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 rh.49-E 1648 GCT-----GGAAGAAGACAACATGGGCTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 rh.61-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 hu.41-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA
 rh.64-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 hu.42-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA
 rh.57-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 hu.40-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA
 AAV8-E 1648 GCT-----GCCAGAGACAATGCGGATTACAGC---GATGTCATGCTAACCCAGCGGAGGAAATCAAAA
 rh.58-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AACGTGATGCTAACCCAGCGGAGGAAATCAAGA
 rh.40-E 1648 GCT-----GGAAGAGACAATGTGGACTATAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA
 hu.67-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA
 hu.17-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AGCGTTATGCTAACCCAGTGAGGAAATCAAAA
 hu.6-E 1648 GCT-----GGAAGAAGACAACGTTGGACTATAGC---AGCGTTATGCTAACCCAGTGAGGAAATCAAAA
 hu.66-E 1648 GCT-----GGAAGAGACAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGGAGGAAATCAAAA

rh.38-E GCT-----GGAAGAGACAAATGTGGACTACAGC---AGCGTTATGCTAACCCAGCGAAGAAATTAAAA
hu.32-F ACT-----GGAAGAGACAAACGTGGATGCGGAC---AAAGTCATGATAACCAACGAAGAAATTAAAA
AAV9/hu ACT-----GGAAGAGACAAACGTGGATGCGGAC---AAAGTCATGATAACCAACGAAGAAATTAAAA
hu.31-F ACT-----GGAAGAGACAAACGTGGATGCGGAC---AAAGTCATGATAACCAACGAAGAAATTAAAA

	1760	1770	1780	1790	1800	1810	1820
AAV5							
AAV3-3	1670 CGGTGAACCCGCTGGCGTACAACGTCGGCGGCAGATGGCCACCAACCAACAGAGCTCCACCACTGCCCC						
AAV4-4	1703 CCACCAATCCTGTGGCAACAGAGCAGTATGGAACCTGTGGCAATAACTTGCAGAGCTCAAAATACAGCTCC						
AAV1-A	1697 CCACCAACGCCACCGATACGGACATGTGGGGCAACCTACCTGGCGGTGACCAAGCAACAGCAACCTGCC						
hu.46-A	1703 CCACTAACCCCTGTGGCCACCCGAAAGATTTGGGACCCGTGGCAGTCAATTTCAGAGCAGCAGCAGACCC						
hu.48-A	1703 CCACTAACCCCTGTGGCCACCCGAAAGATTTGGGACCCGTGGCAGTCAATTTCAGAGCAGCAGCAGACCC						
hu.44-A	1703 CCACTAACCCCTGTGGCCACCCGAAAGATTTGGGACCCGTGGCAGTCAATTTCAGAGCAGCAGCAGACCC						
hu.43-A	1706 CCACTAACCCCTGTGGCCACCCGAAAGATTTGGGACCCGTGGCAGTCAATTTCAGAGCAGCAGCAGACCC						
AAV6-A	1703 CCACTAACCCCGTGGCCACCCGAAAGATTTGGGACTGTGGCAGTCAATCTCCAGAGCAGCAGCAGACCC						
hu.34-B	1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAAGC						
hu.47-B	1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAAGC						
hu.29-B	1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.63-B	1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.56-B	1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.45-B	1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAAGC						
hu.57-B	1697 CCACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACGAGC						
hu.35-B	1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAAGC						
hu.58-B	1700 CCACCAATCCCGTGGCCACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.28-B	1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.51-B	1700 CAACCAATCCCGTGGCTACGGAGCAGTACGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAAGC						
hu.19-B	1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.49-B	1700 CCACCAATCCCGTGGCCACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAAGC						
hu.52-B	1700 CAACCAATCCCGTGGCTACGGAGCAGTATGGTCTGTATCTACCAACCTCCAGAGAGGCAACAGACAAAGC						

103/125

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 CCACCAATCCCGGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.21-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.22-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCAACCTCCAGAGCGGCAACACACAAGC
 hu.23-B 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTACCTACCTCCAGAGCGGCAACACACAAGC
 hu.7-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.61-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCAAAATAATTGCAAAACTCAAACACTGGTCC
 rh.56-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCAAAATAATTGCAAAACTCAAACACTGGTCC
 hu.9-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTATGGTTCTGTATCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.54-C 1697 CCACCAATCCCGTGGCTACAGAGCAGTACGGAAACGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.53-C 1697 CCACCAATCCCGTGGCTACAGAGCAGTACGGATATGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.60-C 1700 CCACCAATCCCGTGGCTACAGAGCAGTACGGATATGTGTCAAAATAATTGCAAAACTCAAACACTGGTCC
 hu.55-C 1697 CCACCAATCCCGTGGCTACAGAGCAGTACGGATATGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.2-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAAATAATTGCAAAACTCAAACACTGGTCC
 hu.1-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAAATAATTGCAAAACTCAAACACTGGTCC
 hu.18-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGATATGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.3-C 1703 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAAATAATTGCAAAACTCAAACACTGGTCC
 hu.25-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAAATAATTGCAAAACTCAAACACTGGTCC
 hu.15-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGATATGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.16-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGATATGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.11-C 1700 CCACCAATCCCGTGGCTACAGAGCAGTACGGAAACGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.10-C 1700 CCACCAATCCCGTGGCTACAGAGCAGTACGGAAACGTGTCAAAATAATTGCAAAACTCAAATACTGGTCC
 hu.4-C 1700 CCACCAATCCCGTGGCTACGGAGCAGTACGGGACTGTGTCAAAATAATTGCAAAACTCAAACACTGGTCC
 rh.54-D 1706 CTACTAATCCTGTGGCCACAGAGAATACGGGATAGTCAGCAGCAATTTACAGCGGCCAAATACTGCAGC
 rh.48-D 1706 CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTTAGCAGCAACCTGCAGGCGGCTAACACTGCAGC
 rh.55-D 1706 CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTTAGCAGCAACCTGCAGGCGGCTAACACTGCAGC

rh. 62-D	1706	CTACCAACCCGGTAGCCACCGAGGAATACGGGACTGTAGCAGCAACCTGCAGGCGGCTAACACTGCAGC	1830	1840	1850	1860	1870	1880	1890
AAV7-D	1706	CTACTAATCCTGTAGCCACGGAAGAATACGGGATAGTCAGCAGCAACTTACAAGCGGCTAATACTGCAGC							
rh. 52-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
rh. 51-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
hu. 39-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
rh. 53-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
hu. 37-E	1709	CCACTAACCCCGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
rh. 43-E	1703	CCACTAACCCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATAAATCTTGCAGCAGCAAAAACACGGCTCC							
rh. 50-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
rh. 49-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
rh. 61-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
hu. 41-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
rh. 64-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
hu. 42-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
rh. 57-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
hu. 40-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
AAV8-E	1709	CCACTAACCCCTGTGGCTACAGAGGAATACGGTATCGTGGCAGATAAATCTTGCAGCAGCAAAAACACGGCTCC							
rh. 58-E	1709	CCACCAACCCCGTGGCCACAGAACAGTATGGCGTGGTGGCTGATAACCTACAGCAGCAAAAACACCGCTCC							
rh. 40-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAGCCAATACAGGGCC							
hu. 67-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
hu. 17-E	1709	CCACCAACCCAGTGGCCACAGAACAGTACGGGTGGTGGCGATAAATCTTGCAGCAAAACGCGCTCC							
hu. 6-E	1709	CCACCAACCCAGTGGCCACAGAACAGTACGGGTGGTGGCGATAAATCTTGCAGCAAAACGCGCTCC							
hu. 66-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
rh. 38-E	1709	CCACTAACCCCTGTAGCCACAGAACATACGGTGTGGTGGCTGACAACTTGCAGCAAAACCAATACAGGGCC							
hu. 32-F	1703	CTACTAACCCCGTAGCAACGGAGTCCTATGGACAAGTGGCCACAACCAAGTGCCCAAGCACAGGC							
AAV9/hu	1703	CTACTAACCCCGTAGCAACGGAGTCCTATGGACAAGTGGCCACAACCAAGTGCCCAAGCACAGGC							
hu. 31-F	1703	CTACTAACCCCGTAGCAACGGAGTCCTATGGACAAGTGGCCACAACCAAGTGCCCAAGCACAGGC							

FIG. 3BT

105/125

AAV5 1740 CGCGACCGGCACGTACAACCTCCAGGAAATCGTGCCCGGCAGCGTGTGGATGGAGAGGACGTGTACCTC
 AAV3-3 1773 CACGACTGGAACGTCAATCATCAGGGGCCCTTACCTGGCATGGTGTGGCAAGATCGTGACGTGTACCTT
 AAV4-4 1767 GACCGTGGACAGACTGACAGCCCTTGGGAGCCGTGCCCTGGAAATGGTCTGGCAAAACAGAGACATTTACTAC
 AAV1-A 1773 TGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.46-A 1773 TGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.48-A 1773 TGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.44-A 1773 TGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 hu.43-A 1776 TGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGCATGGTGTGGCAAGATAGAGACGTGTACCTG
 AAV6-A 1773 TGCGACCGGAGATGTGCATGCTATGGGAGCATTACCTGGAAATGGTGTGGCAAGACAGAGACGTGTACCTG
 hu.34-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.47-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.29-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAAGACAGAGACGTGTACCTG
 hu.63-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTCCAGGACAGAGACGTGTACCTG
 hu.56-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTCCAGGACAGAGACGTGTACCTG
 hu.45-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTCCAGGACAGAGATGTGTACCTT
 hu.57-B 1767 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.35-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTCCAGGACAGAGATGTGTACCTT
 hu.58-B 1770 ATCTACTGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.28-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAAGACAGAGACGTGTACCTG
 hu.51-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.19-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.49-B 1770 AGCTACTGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGCACCTG
 hu.52-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.13-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 AAV2-B 1770 AGCTACCGCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGATGTGTACCTT
 hu.20-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.24-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.64-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.27-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu.21-B 1770 AGCTACCTCAGATGTCAACACACACAAGGCGTTCTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG

106/125

hu. 22-B 1770 AGTACCTCAGATGTCAACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu. 23-B 1770 AGTACCTCAGATGTCAACACACAAGGCGTTCTTCCAGGCATGGTCTGGCAGGACAGAGACGTGTACCTG
 hu. 7-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGCATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 61-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 rh. 56-C 1770 AACTACTGGAACGTCAATCACCGAGGAGCGTTACCTGGCATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 9-C 1770 AACTACAGAAAAATGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 54-C 1767 AAGTACTGAAACTGTGAATCACCAAGGAGCATTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 53-C 1767 AAGTACTGAAACTGTGAATCACCAAGGAGCATTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 60-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 55-C 1767 AAGTACTGAAACTGTGAATCACCAAGGAGCATTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 2-C 1770 AACTACTGGAACGTCAATCGCCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 1-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 18-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 3-C 1773 AACTACAGGAACTGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 25-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGATGTGTACCTT
 hu. 15-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 16-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 11-C 1770 AACTACAGAAAAATGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 10-C 1770 AACTACAGAAAAATGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 hu. 4-C 1770 AACTACTGGAACGTCAATCACCAAGGAGCGTTACCTGGTATGGTGTGGCAGGATCGAGACGTGTACCTG
 rh. 54-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTG
 rh. 48-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAACCGGGACGTGTACCTG
 rh. 55-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAACCGGGACGTGTACCTG
 rh. 62-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGTATGGTCTGGCAGAACCGGGACGTGTACCTG
 AAV7-D 1776 CCAGACACAAGTTGTCAACAACCAAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTG
 rh. 52-E 1779 TATTGTGGGGCGGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACTTG
 rh. 51-E 1779 TATTGTGGGGCGGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTG
 hu. 39-E 1779 TACTGTGGGGCGGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTG
 rh. 53-E 1779 TATTGTGGGGCGGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTG
 hu. 37-E 1779 TATTGTGGGAAATGTCAACAGCCAGGAGCGTTACCTGGCATGGTCTGGCAGAACCGGGACGTGTACCTG

rh. 43-E 1773 TCAAATTGGAACGTCAACAGCCAGGGGGCCCTTACCCGGTATGGTCTGGCAGAACCGGACGTGTACCTG
rh. 50-E 1779 TATTGTGGGGCCGTCAACAGCCAGGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
rh. 49-E 1779 TATTGTGGGGCCGTCAACAGCCAGGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
rh. 61-E 1779 TATTGTGGGGCCGTCAACAGCCAGGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
hu. 41-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
rh. 64-E 1779 TATTGTGGGGCCGTCAACAGCCAGGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
hu. 42-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
rh. 57-E 1779 TATTGTGGGGCCGTCAACAGCCAGGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
hu. 40-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
AAV8-E 1779 TCAAATTGGAACGTCAACAGCCAGGGGGCCCTTACCCGGTATGGTCTGGCAGAACCGGACGTGTACCTG
rh. 58-E 1779 TATTGTGGGGCCGTCAACAGCCAGGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
rh. 40-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
hu. 67-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
hu. 17-E 1779 TATTGTAGGGGCCGTCAACAGTCAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
hu. 6-E 1779 TATTGTAGGGGCCGTCAACAGTCAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGGACGTGTACCTG
hu. 66-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
rh. 38-E 1779 TATTGTGGGAAATGTCAACAGCCAAAGGAGCCCTTACCTGGCATGGTCTGGCAGAACCGAGACGTGTACCTG
hu. 32-F 1773 GCAGACCGGCTGGGTTCAAAACCAAGGAATACTTCCGGGTATGGTTTGGCAGGACAGAGATGTGTACCTG
AAV9/hu 1773 GCAGACCGGCTGGGTTCAAAACCAAGGAATACTTCCGGGTATGGTTTGGCAGGACAGAGATGTGTACCTG
hu. 31-F 1773 GCAGACCGGCTGGGTTCAAAACCAAGGAATACTTCCGGGTATGGTTTGGCAGGACAGAGATGTGTACCTG

	1900	1910	1920	1930	1940	1950	1960
							
AAV5	1810	CAAGGACCCATCTGGGCCAAGATCCAGAGACGGGGCGCACTTTCACCCCTCTCCGCCATGGCGGAT					
AAV3-3	1843	CAAGGACCTATCTGGGCCAAGATTCTCACACGGATGGACACTTTCATCCTTCTCCTCTGATGGAGGCT					
AAV4-4	1837	CAGGTCCCATTTGGGCCAAGATTCTCATACCGATGGACACTTTCACCCCTCACCCGTGATTTGGTGGT					
AAV1-A	1843	CAGGTCCCATTTGGGCCAAAATTCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGCGGCT					
hu. 46-A	1843	CAGGTCCCATTTGGGCCAAAATTCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGCGGCT					
hu. 48-A	1843	CAGGTCCCATTTGGGCCAAAATTCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGCGGCT					
hu. 44-A	1843	CAGGTCCCATTTGGGCCAAAATTCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGCGGCT					

108/125

hu. 43-A 1846 CAGGGTCCCATTTGGGCCAAAAATTCCTCACACAGATGGACACTTTCACCCGTCTCCTCTTATGGGCGGCT
 AAV6-A 1843 CAGGGTCCATTTGGGCCAAAAATTCCTCACACGGATGGACACTTTCACCCGTCTCCTCTCATGGGCGGCT
 hu. 34-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 47-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 29-B 1840 CAGGGGCCATTTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 63-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 56-B 1840 CAGGGGCCCATCTGGGCAAAATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 45-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 57-B 1837 CAGGGGCCCATCTGGGCAAAATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 35-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 58-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 28-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 51-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 19-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 49-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 52-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 13-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 AAV2-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 20-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGTGGAT
 hu. 24-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 64-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 27-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 21-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 22-B 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 23-B 1840 CGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCCCTCATGGGCGGAT
 hu. 7-C 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCACTGATGGGAGGTT
 hu. 61-C 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCACTGGTGGAGGTT
 rh. 56-C 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCACTGATGGGAGGTT
 hu. 9-C 1840 CAGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCACTGATGGGAGGTT
 hu. 54-C 1837 CGGGGCCCATCTGGGCAAAAGATTCACACACGACGGACATTTTCACCCCTCTCCACTGATGGGAGGTT

FIG. 3BX

109/125

hu. 53-C	1837	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 60-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 55-C	1837	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 2-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 1-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GACGGGAGGT
hu. 18-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGGCACTT	TTCATCCT	TCTCCACT	TAATGGGAGGT
hu. 3-C	1843	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 25-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 15-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	TATGGGAGGT
hu. 16-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	TATGGGAGGT
hu. 11-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 10-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
hu. 4-C	1840	CAGGGACCCATT	TGGGCCAAGATT	CCTCACACCGAT	GGACACTT	TTCATCCT	TCTCCACT	GATGGGAGGT
rh. 54-D	1846	CAGGTCCCAT	CTGGGCCAAAT	TCTCACACAGAC	GGCAACTT	TTCACCCG	TCTCCGCT	GATGGCGGGCT
rh. 48-D	1846	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCCGCT	GATGGCGGGCT
rh. 55-D	1846	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCCGCT	GATGGCGGGCT
rh. 62-D	1846	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCCGCT	GATGGCGGGCT
AAV7-D	1846	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAT	GGCAACTT	TTCACCCG	TCTCCTTT	GATGGCGGGCT
rh. 52-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
rh. 51-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
hu. 39-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
rh. 53-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
hu. 37-E	1849	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCACCG	CTAATGGGAGGAT
rh. 43-E	1843	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCACCG	CTGATGGCGGGCT
rh. 50-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
rh. 49-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
rh. 61-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
hu. 41-E	1849	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCACCG	CTAATGGGAGGAT
rh. 64-E	1849	CAGGTCCCTA	TTGGGCCAAGAT	TCTCACACAGAT	GGCAACTT	TTCACCCG	TCTCCTTT	TAATGGCGGGCT
hu. 42-E	1849	CAGGTCCCAT	CTGGGCCAAGAT	TCTCACACGGAC	GGCAACTT	TTCACCCG	TCTCACCG	CTAATGGGAGGAC

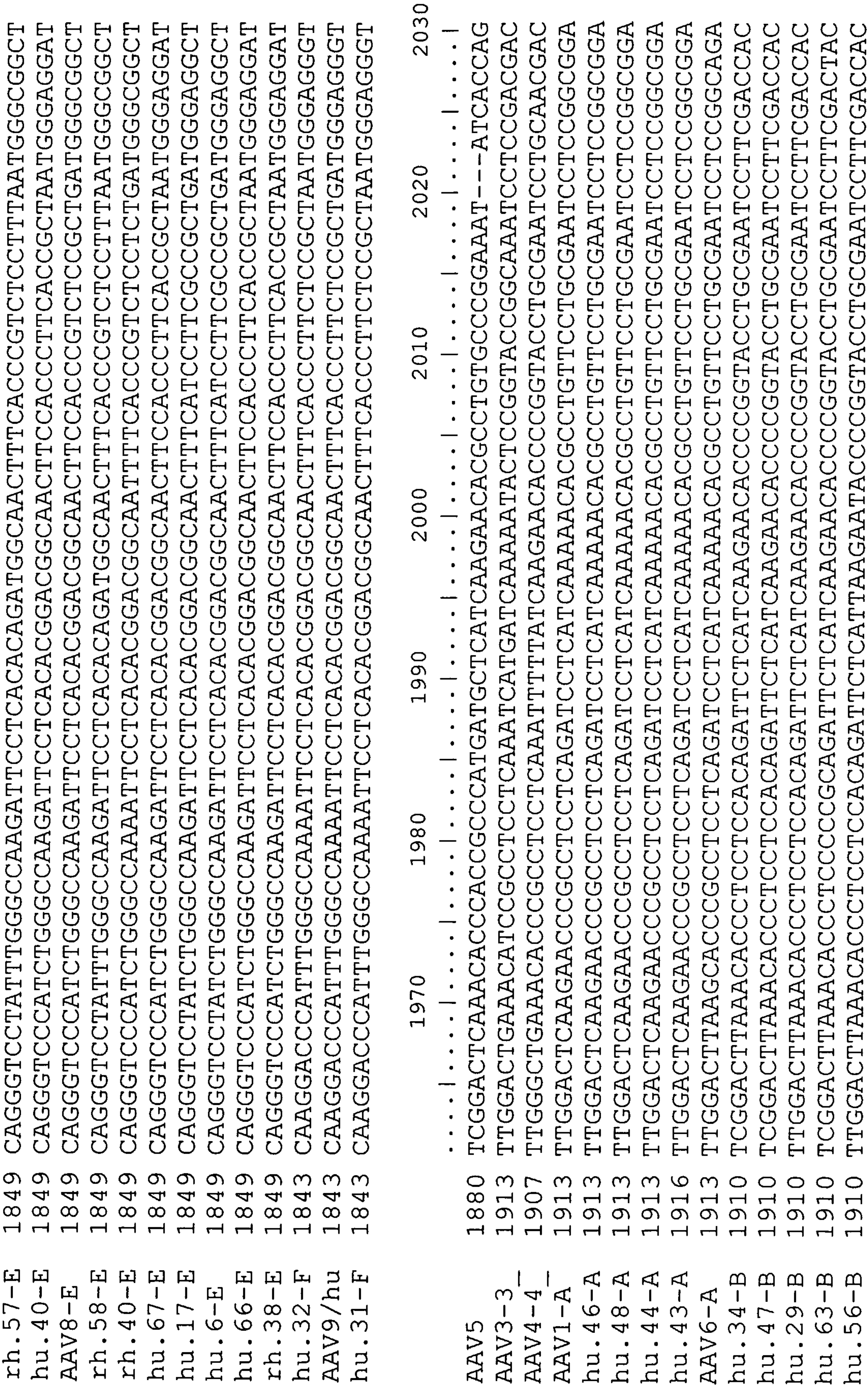


FIG. 3BZ

111/125

hu. 45-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 57-B	1907	TTGGACTTAAACACCCCTCCTCCACAGATTCTCATTAAGAAATACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 35-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 58-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 28-B	1910	TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 51-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 19-B	1910	TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 49-B	1910	TTGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCAAAATCCTTCGACCAC
hu. 52-B	1910	TCGGACCTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 13-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
AAV2-B	1910	TCGGACTTAAACACCCCTCCTCCACAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 20-B	1910	TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 24-B	1910	TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 64-B	1910	TCGGACTTAAACACCCCTCCTCCGCGAGATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACTAC
hu. 27-B	1910	TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 21-B	1910	TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 22-B	1910	TCGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 23-B	1910	TTGGACTTAAACACCCCTCCTCCACAAATTCTCATCAAGAACACCCCGGTACCTGCGAATCCTTCGACCAC
hu. 7-C	1910	TTGGGCTCAAACACCCCGCTCCTCAGATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 61-C	1910	TTGGACTCAAACACCCACCTCCTCAAATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
rh. 56-C	1910	TTGGGCTCAAACACCCCGCTCCTCAGATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 9-C	1910	TTGGACTCAAACACCCCGCTCCTCAAATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 54-C	1907	TTGGACTCAAACACCCCGCTCCTCAGATTATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 53-C	1907	TTGGACTCAAACACCCCGCTCCTCAGATTATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 60-C	1910	TTGGACTCAAACACCCACCTCCTCAAATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 55-C	1907	TTGGACTCAAACACCCCGCTCCTCAGATTATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 2-C	1910	TTGGACTCAAACACCCCGCTCCTCAGATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 1-C	1910	TTGGACTCAAACACCCCGCTCCTCAGATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 18-C	1910	TTGGGCTCAAACACCCCGCTCCTCAGATCATGATCAAAACACTCCCGTTCCAGCCAATCCTCCCACAAA
hu. 3-C	1913	TTGGACTCAAACACCCCGCTCCTCAGATCATGATCAAAAGCACTCCCGTTCCAGCCAATCCTCCCACAAA

FIG. 3CA

112/125

hu.25-C	1910	TTGGACTCAAACACCCGCTCCTCAGATTATGATCAAAACACTCCCCTCCAGCCAAATCCTCCTACAAA
hu.15-C	1910	TTGGACTCAAACACCCACCTCCTCAGATCATGATTAAAAACACTCCCCTCCAGCCAAATCCTCCACAAA
hu.16-C	1910	TTGGACTCAAACACCCACCTCCTCAGATCATGATTAAAAACACTCCCCTCCAGCCAAATCCTCCACAAA
hu.11-C	1910	TTGGACTCAAACACCCGCTCCTCAAAATCATGATCAAAACACTCCCCTCCAGCCAAATCCTCCACAAA
hu.10-C	1910	TTGGACTCAAACACCCGCTCCTCAAAATCATGATCAAAACACTCCCCTCCAGCCAAATCCTCCACAAA
hu.4-C	1910	TTGGACTCAAACACCCGCTCCTCAGATCATGATCAAAACACTCCCCTCCAGCCAAATCCTCCACAAA
rh.54-D	1916	TTGGACTGAAGCATCCGCTCCTCAGATCCTGATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGGT
rh.48-D	1916	TTGGACTGAAGCATCCGCTCCTCAGATCCTGATCAAAACACTCCCCTCCAGCCAAATCCTCCGAGGT
rh.55-D	1916	TTGGACTGAAGCATCCGCTCCTCAGATCCTGATCAAAACACTCCCCTCCAGCCAAATCCTCCGAGGT
rh.62-D	1916	TTGGACTGAAGCATCCGCTCCTCAGATCCTGATCAAAACACTCCCCTCCAGCCAAATCCTCCGAGGT
AAV7-D	1916	TTGGACTTAAACATCCGCTCCTCAGATCCTGATCAAGAACACTCCCCTCCAGCCAAATCCTCCGAGGT
rh.52-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
rh.51-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
hu.39-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
rh.53-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
hu.37-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCACAC
rh.43-E	1913	TTGGCTGAAACATCCTCCGCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCAGC
rh.50-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
rh.49-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
rh.61-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
hu.41-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCACAC
rh.64-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
hu.42-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCACAC
rh.57-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAACACTCCCCTCCAGCCAAATCCTCCACAGC
hu.40-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCACAC
AAV8-E	1919	TTGGCTGAAACATCCTCCGCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCAGCCAC
rh.58-E	1919	TTGGACTTAAACATCCGCTCCTCAGATCCTCATCAAAAGCACTCCTGTTCCCTCCAGCCAAATCCTCCACAGC
rh.40-E	1919	TTGGACTGAAGCACCACCTCCAGATCCTGATCAAGAACATACGCCGCTGACCTCCAGCCAAATCCTCCACAGC
hu.67-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATCAAGAACACGCCGCTGACCTCCAGCCAAATCCTCCACAGC
hu.17-E	1919	TTGGACTGAAGCACCACCTCCTCAGATCCTGATTAAGAAATACACCTGTTCCCGCCGATCCTCCAACTAC

FIG. 3CB

hu.6-E	1919	TTGGACTGAAACACCCGCCCTCCTCAGATCCTGATTAAGAATACACCTGTTCCCGGGATCCTCCAAC	2040	2050	2060	2070	2080	2090	2100
hu.66-E	1919	TTGGACTGAAGCACCCACCTCCTCAGATCCTGATCAAGAACACGCCGGTACCTGCGGATCCTCCAACA							
rh.38-E	1919	TTGGACTGAAGCACCCACCTCCTCAGATCCTGATCAAGAACACGCCGGTACCTGCGGATCCTCCAACA							
hu.32-F	1913	TTGGAATGAAGCACCCGCCCTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGATCCTCCAAC							
AAV9/hu	1913	TTGGAATGAAGCACCCGCCCTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGATCCTCCAAC							
hu.31-F	1913	TTGGAATGAAGCACCCGCCCTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGATCCTCCAAC							
AAV5	1947	CTTCTCGGACGTGCCCGTCAGCAGCTTCATCACCCAGTACAGCACCCGGGCAGGTCACCGTGGAGATGGAG							
AAV3-3'	1983	TTTCAGCCCGGCAAGTTTGCTTCATTATCACTCAGTACTCCACTGGACAGGTCAGCGTGGAATTTGAG							
AAV4-4'	1977	CTTCAGCTCTACTCCGGTAACCTCCTTCACTACTAGTACAGCACTGGCCAGGTGTCGGTGCAGATTTGAC							
AAV1-A'	1983	GTTTTTCAGCTACAAAAGTTTGCTTTCATCATCAACCCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAA							
hu.46-A	1983	GTTTTTCAGCTACAAAAGTTTGCTTTCATCATCAACCCCAATACTCCGCAGGACAAGTGAGTGTGGAAATTGAA							
hu.48-A	1983	GTTTTTCAGCTACAAAAGTTTGCTTTCATCATCAACCCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAA							
hu.44-A	1983	GTTTTTCAGCTACAAAAGTTTGCTTTCATCATCAACCCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAA							
hu.43-A	1986	GTTTTTCAGCTACAAAAGTTTGCTTTCATCATCAACCCCAATACTCCACAGGACAAGTGAGTGTGGAAATTGAA							
AAV6-A	1983	GTTTTTCGGCTACAAAAGTTTGCTTTCATCATCAACCCCAAGTATTCCACAGGACAAGTGAGCGTGGAGATTGAA							
hu.34-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.47-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.29-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.63-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.56-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTATTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.45-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.57-B	1977	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTATTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.35-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.58-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTATTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.28-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.51-B	1980	CTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							
hu.19-B	1980	TTTCAGTGCGGCAAAAGTTTGCTTTCATCATCACACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG							

FIG. 3C

114/125

hu. 49-B 1980 CTTAGTGGCAAGTTTGCTTCCTTCATCACAGTATCCACAGGGCAGGTCAGCGTGGAGATCGAG
 hu. 52-B 1980 CTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG
 hu. 13-B 1980 CTTAGTGGCAAGTTTGCTTCCTTCATCACAGTATCCACGGGGCAGGTCAGCGTGGAGATCGAG
 AAV2-B 1980 CTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGACAGGTCAGCGTGGAGATCGAG
 hu. 20-B 1980 TTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 24-B 1980 TTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 64-B 1980 CTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 27-B 1980 TTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 21-B 1980 TTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 22-B 1980 TTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 23-B 1980 TTTAGTGGCAAGTTTGCTTCCTTCATCACAGTACTCCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 7-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 61-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 rh. 56-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 9-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 54-C 1977 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 53-C 1977 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 60-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 55-C 1977 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 2-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 1-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 18-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 3-C 1983 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 25-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 15-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 hu. 16-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTAGAGATCGAG
 hu. 11-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATTGAG
 hu. 10-C 1980 CTACAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATTGAG
 hu. 4-C 1980 CTTAGTTCTGCCAAGTTTGCTTCCTTCATCACAGTATTCACGGGGCAGGTCAGCGTGGAGATCGAG
 rh. 54-D 1986 GTTACGCCCTGCCAAGTTTGCTTCCTTCATCACAGTACAGCACCGGCCAGGTCAGCGTGGAGATCGAG

115/125

rh. 48-D 1986 GTTACGCCCTGCCAAGTTTGCTTCTTTCATCACACAGTACAGCACCGCCAGGTCAGCGTGGAGATCGAG
 rh. 55-D 1986 GTTACGCCCTGCCAAGTTTGCTTCTTTCATCACACAGTACAGCACCGCCAGGTCAGCGTGGAGATCGAG
 rh. 62-D 1986 GTTACGCCCTGCCAAGTTTGCTTCTTTCATCACACAGTACAGCACCGCCAGGTCAGCGTGGAGATCGAG
 AAV7-D 1986 GTTACTCCTGCCAAGTTTGCTTCTTTCATCACACAGTACAGCACCGGACAAAGTCAGCGTGGAAATCGAG
 rh. 52-E 1989 GTTCAACCAGGCCAAGCTGAATTCTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 rh. 51-E 1989 GTTCAACCAGGCCAAGCTGAATTCTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 hu. 39-E 1989 GTTCAACCAGGCCAAGCTGAATTCTTTCATCGCGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 rh. 53-E 1989 GTTCAACCAGGCCAAGCTGAATTCTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 hu. 37-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 rh. 43-E 1983 CTTCAACCAGTCAAGCTGAATCTTTTCATCACGCAATACAGCACCGGACAGGTCAGCGTGGAAATTGAA
 rh. 50-E 1989 GTTCAACCAGGCCAAGCTGAATCTTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 rh. 49-E 1989 GTTCAACCAGGCCAAGCTGAATCTTTTCATCACGCAGTACCGGCACCGGACAAAGTCAGCGTGGAGATCGAG
 rh. 61-E 1989 GTTCAACCAGGCCAAGCTGAATCTTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 hu. 41-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 rh. 64-E 1989 GTTCAACCAGGCCAAGCTGAATCTTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGTG
 hu. 42-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 rh. 57-E 1989 GTTCAACCAGGCCAAGCTGAATCTTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGGAGATCGAG
 hu. 40-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 AAV8-E 1989 CTTCAACCAGTCAAGCTGAATCTTTTCATCACGCAATACAGCACCGGACAGGTCAGCGTGGAAATTGAA
 rh. 58-E 1989 GTTCAACCAGGCCAAGCTGAATCTTTTCATCACGCAGTACAGCACCGGACAAAGTCAGCGTGGAGATCGAG
 rh. 40-E 1989 GTTCAGCCAGGCCAATAATTGGCTTCTTTCATCACGCAGTACAGCACCGGCCAGGTCAGCGTGGAGATCGAG
 hu. 67-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 hu. 17-E 1989 CTTCAAGTCAAGCCAAGCTGGCGTCGTTTCATCACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATTGAA
 hu. 6-E 1989 CTTCAAGTCAAGCCAAGCTGGCGTCGTTTCATCACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATTGAA
 hu. 66-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 rh. 38-E 1989 GTTCAGCCAGGCCGAAATTGGCTTCTTTCATTACGCAGTACAGCACCGGACAGGTCAGCGTGGAAATCGAG
 hu. 32-F 1983 TTTCAATAAGGACAAGCTGAATCTTTTCATCACCCAGTATTCTACTGGCCAAAGTCAGCGTGGAGATTGAG
 AAV9/hu 1983 CTTCAACAAGGACAAGCTGAATCTTTTCATCACCCAGTATTCTACTGGCCAAAGTCAGCGTGGAGATCGAG
 hu. 31-F 1983 TTTCAATAAGGACAAGCTGAATCTTTTCATCACCCAGTATTCTACTGGCCAAAGTCAGCGTGGAGATTGAG

	2110	2120	2130	2140	2150	2160	2170
							
AAV5	2017	TGGGAGCTCAAGAAGGAAAAC	TCCAAGAGGTGGAACCCAGAGAT	CCAGTACACAAACA	ACTACAACGACC		
AAV3-3-	2053	TGGGAGCTACAGAAAGAAAAC	AGCAACGTTGGAAATCCAGAGAT	TCAGTACACTTCCA	ACTACAACAAGT		
AAV4-4-	2047	TGGGAGATCCAGAAAGGAGCG	GTCCAAACGCTGGAAATCCCGAGG	TCAGTTTACCTCCA	ACTACGGACAGC		
AAV1-A-	2053	TGGGAGCTGCAGAAAGAAAAC	AGCAAGCGCTGGAAATCCCGAAG	TGCAGTACACATCCA	ATTATGCAAAAT		
hu. 46-A	2053	TGGGAGCTGCAGAAAGAAAAC	AGCAAGCGCTGGAAATCCCGAAG	TGCAGTACACATCCA	ATTATGCAAAAT		
hu. 48-A	2053	TGGGAGCTGCAGAAAGAAAAC	AGCAAGCGCTGGAAATCCCGAAG	TGCAGTACACATCCA	ATTATGCAAAAT		
hu. 44-A	2053	TGGGAGCTGCAGAAAGAAAAC	AGCAAGCGCTGGAAATCCCGAAG	TGCAGTACACATCCA	ATTATGCAAAAT		
hu. 43-A	2056	TGGGAGCTGCAGAAAGAAAAC	AGCAAGCGCTGGAAATCCCGAAG	TGCAGTACACATCCA	ATTATGCAAAAT		
AAV6-A	2053	TGGGAGCTGCAGAAAGAAAAC	AGCAAGCGCTGGAAATCCCGAAG	TGCAGTACATCTAA	CTATGCAAAAT		
hu. 34-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAGT		
hu. 47-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAGT		
hu. 29-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	CCAGTACACTTCCA	ACTACAACAAGT		
hu. 63-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 56-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 45-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 57-B	2047	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 35-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 58-B	2050	TGGGAGCTACAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	CCAGTACACTTCCA	ACTACAACAAT		
hu. 28-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	CCAGTACACTTCCA	ACTACAACAAT		
hu. 51-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 19-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 49-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	CCAGTACACTTCCA	ACTACAACAAT		
hu. 52-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 13-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	CCAGTACACTTCCA	ACTACAACAAT		
AAV2-B	2050	TGGGAGCTGCAGAAAGGAAAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 20-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 24-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAAAT	TCAGTACACTTCCA	ACTACAACAAT		
hu. 64-B	2050	TGGGAGCTGCAGAAAGGAGAAC	AGCAACGCTGGAAATCCCGAGAT	TCAGTACACTTCCA	ACTACAACAAT		

117/125

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

rh. 53-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGCGCTGGAACCCAGAGATTTCAGTATACTTCCAACTACTACAAAT
hu. 37-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACTACTACAAAT
rh. 43-E 2053 TGGGAGCTACAGAAGGAAACAGCAAGCGCTGGAACCCGAGATCCAGTACACCTCCACTACTACAAAT
rh. 50-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGCGCTGGAGCCAGAGATTTCAGTATACTTCCACTACTACAAAT
rh. 49-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGCGCTGGAAACCCAGAGATTTCAGTATACTTCCACTACTACAAAT
rh. 61-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGCGCTGGAAACCCAGAGATTTCAGTATACTTCCACTACTACAAAT
hu. 41-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGTTGGAACCCAGAGATTTCAGTACACTTCAAACCTACTACAAAT
rh. 64-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGCGCGCAGGAAACCCAGAGATTTCAGTATACTTCCACTACTACAAAT
hu. 42-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACCTACTACAAAT
rh. 57-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTATACTTCCACTACTACAAAT
hu. 40-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACCTACTACAAAT
AAV8-E 2059 TGGGAGCTGCAGAAGGAAACAGCAAGCGCTGGAAACCCGAGATCCAGTACACCTCCACTACTACAAAT
rh. 58-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGTGCTGGAAACCCAGAGATTTCAGTATACTTCCACTACTACAAAT
rh. 40-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAAGCGATGGAAACCCAGAAATTTCAGTACACTTCCACTACTACAAAT
hu. 67-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACCTACTACAAAT
hu. 17-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTATACTTCCACTATAACAAAT
hu. 6-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTATACTTCCACTACTACAAAT
hu. 66-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACCTACTACAAAT
rh. 38-E 2059 TGGGAGCTGCAGAAGGAGAAACAGCAACGCTGGAAACCCAGAGATTTCAGTACACTTCAAACCTACTACAAAT
hu. 32-F 2053 TGGGAGCTGCAGAAGGAAACAGCAACGCTGGAAACCCGGAGATCCAGTACACTTCCACTATTACAAAGT
AAV9/hu 2053 TGGGAGCTGCAGAAGGAAACAGCAACGCTGGAAACCCGGAGATCCAGTACACTTCCACTATTACAAAGT
hu. 31-F 2053 TGGGAGCTGCAGAAGGAAACAGCAACGCTGGAAACCCGGAGATCCAGTACACTTCCACTATTACAAAGT

	2180	2190	2200	2210	2220	2230	2240
							
AAV5	2087	CCCA	GT	TTGT	GGACT	TTTG	CCCCGGACAGCACCGGGGAATACAGAAACCACGACCTATCGGAACCCGATA
AAV3-3	2123	CTGT	TAATGT	GGACT	TTTACT	GTAGACACTAATGGTGT	TTTATAGTGAACCTCGCCCTATTGGAACCCGGTA
AAV4-4	2117	AAAA	CTCTCT	GTGT	GGCTCCCGAT	CGCGCTGGGAAATACACT	GAGCCTAGGGCTATCGGTACCCGCTA
AAV1-A	2123	CTGCC	AACGTTGAT	TTTACT	GTGGACAACAAATGGACT	TTTATACTGAGCCTCGCCCAT	TGGCACCCGTTA
hu. 46-A	2123	CTGCC	AACGTTGAT	TTTACT	GTGGACAACAAATGGACT	TTTATACTGAGCCTCGCCCAT	TGGCACCCGTTA

119/125

hu. 48-A 2123 CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCTTA
hu. 44-A 2123 CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCTTA
hu. 43-A 2126 CTGCCAGCGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCTTA
AAV6-A 2123 CTGCCAACGTTGATTTTACTGTGGACAACAATGGACTTTTATACTGAGCCTCGCCCCCATTTGGCACCCTTA
hu. 34-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 47-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 29-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 63-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGTA
hu. 56-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 45-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 57-B 2117 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 35-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 58-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 28-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 51-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 19-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 49-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 52-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 13-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
AAV2-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 20-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 24-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 64-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 27-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 21-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 22-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 23-B 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 7-C 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
hu. 61-C 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA
rh. 56-C 2120 CTGTTAATGTGGACTTTTACTGTGGACACTAATGGCGTGTATTTCAGAGCCTCGCCCCCATTTGGCACCAGATA

120/125

hu. 9-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTTGCCCCATTGGCACCAGATA
hu. 54-C	2117	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 53-C	2117	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 60-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 55-C	2117	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 2-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 1-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 18-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 3-C	2123	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 25-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 15-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 16-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 11-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 10-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
hu. 4-C	2120	CTGTTAATGTGGACTTTACTGTGGACACTAATGGTGTGTATTCTAGAGCCCTCGCCCCATTGGCACCAGATA
rh. 54-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 48-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 55-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 62-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
AAV7-D	2126	AGACTGGTGTGGACTTTGCCGTTGACAGCCAGGGTGTATTCTGAGCCCTCGCCCCATTGGCACTCGTTA
rh. 52-E	2129	CTACAAATGTGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
rh. 51-E	2129	CTACAAATGTGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
hu. 39-E	2129	CTACAAATGCGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
rh. 53-E	2129	CTACAAATGTGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
hu. 37-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGGAACCTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA
rh. 43-E	2123	CTACAAGTGTGGACTTTGCTGTTAAATACAGAAGCGGTGTAATCTGAACCCCGCCCCATTGGCACCCTGTTA
rh. 50-E	2129	CTACAAATGTGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
rh. 49-E	2129	CTACAAATGTGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
rh. 61-E	2129	CTACAAATGTGGACTTTGCTGTTAACTAGAGGTGTTTACTCTGAGCCCTCGCCCCATTGGCACTCGTTA
hu. 41-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGGAACCTATTCTGAGCCCTCGCCCCATTGGTACTCGTTA

rh. 64-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTCTGAGCCCTCGCCCCCATTTGGCACTCGTTA
hu. 42-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGGAACCTTATCTGAGCCCTCGCCCCCATTTGGTACTCGTTA
rh. 57-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTCTGAGCCCTCGCCCCCATTTGGCACTCGTTA
hu. 40-E	2129	CTACAAATGTGGACTTTGCTGTTCAATACAGAGGGAACCTTATCTGAGCCCTCGCCCCCATTTGGTACTCGTTA
AAV8-E	2129	CTACAAAGTGTGGACTTTGCTGTTAATAACAGAGGCGGTGTAATCTGAACCCCGCCCCCATTTGGCACCCCGTTA
rh. 58-E	2129	CTACAAATGTGGACTTTGCTGTTAATACTGAGGGTGTCTGAGCCCTCGCCCCCATTTGGCACTCGTTA
rh. 40-E	2129	CTACAAATGTGGACTTTGCTGTCAATTCTGAGGGTACATATTCAGAGCCCTCGCCCCCATTTGGTACTCGTTA
hu. 67-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGGAACCTTATCTGAGCCCTCGCCCCCATTTGGTACTCGTTA
hu. 17-E	2129	CTGTTAATGTGGACTTTTACTGTGGACACTAATGGTGTGTATTCAGAGCCCTCGCCCCCATTTGGCACCCAGATA
hu. 6-E	2129	CTACAAATGTGGACTTTGCTGTCAATACTGAGGGTACTTATTCAGAGCCCTCGCCCCCATTTGGCACCCCGTTA
hu. 66-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGGAACCTTATCTGAGCCCTCGCCCCCATTTGGTACTCGTTA
rh. 38-E	2129	CTACAAATGTGGACTTTGCTGTCAATACAGAGGGAACCTTATCTGAGCCCTCGCCCCCATTTGGTACTCGTTA
hu. 32-F	2123	CTAATAATGTTGAATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACCCAGATA
AAV9/hu	2123	CTAATAATGTTGAATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACCCAGATA
hu. 31-F	2123	CTAATAATGTTGAATTTGCTGTTAGTACTGAAGGTGTATATAGTGAACCCCGCCCCCATTTGGCACCCAGATA

	2250	2260
AAV5	2157	
AAV3-3	2193	CCTTACCCGACCCCTT----
AAV4-4	2187	TCTCACACGAAACTTG----
AAV1-A	2193	CCTCACCCACCACTGTAA-
hu. 46-A	2193	CCTTACCCGTCCCCTGTAA-
hu. 48-A	2193	CCTTACCCGTCCCCTGTAA-
hu. 44-A	2193	CCTTACCCGTCCCCTGTAA-
hu. 43-A	2196	CCTTACCCGTCCCCTGTAA-
AAV6-A	2193	CCTCACCCGTCCCCTGTAA-
hu. 34-B	2190	CCTGACTCGTAATCTGTAA-
hu. 47-B	2190	CCTGACTCGTAATCTGTAA-
hu. 29-B	2190	CCTGACTCGTAATCTGTAA-

FIG. 3CK

122/125

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. 3CL

123/125

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

FIG. 3CM

124/125

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

125/125

% GFP (+) cells

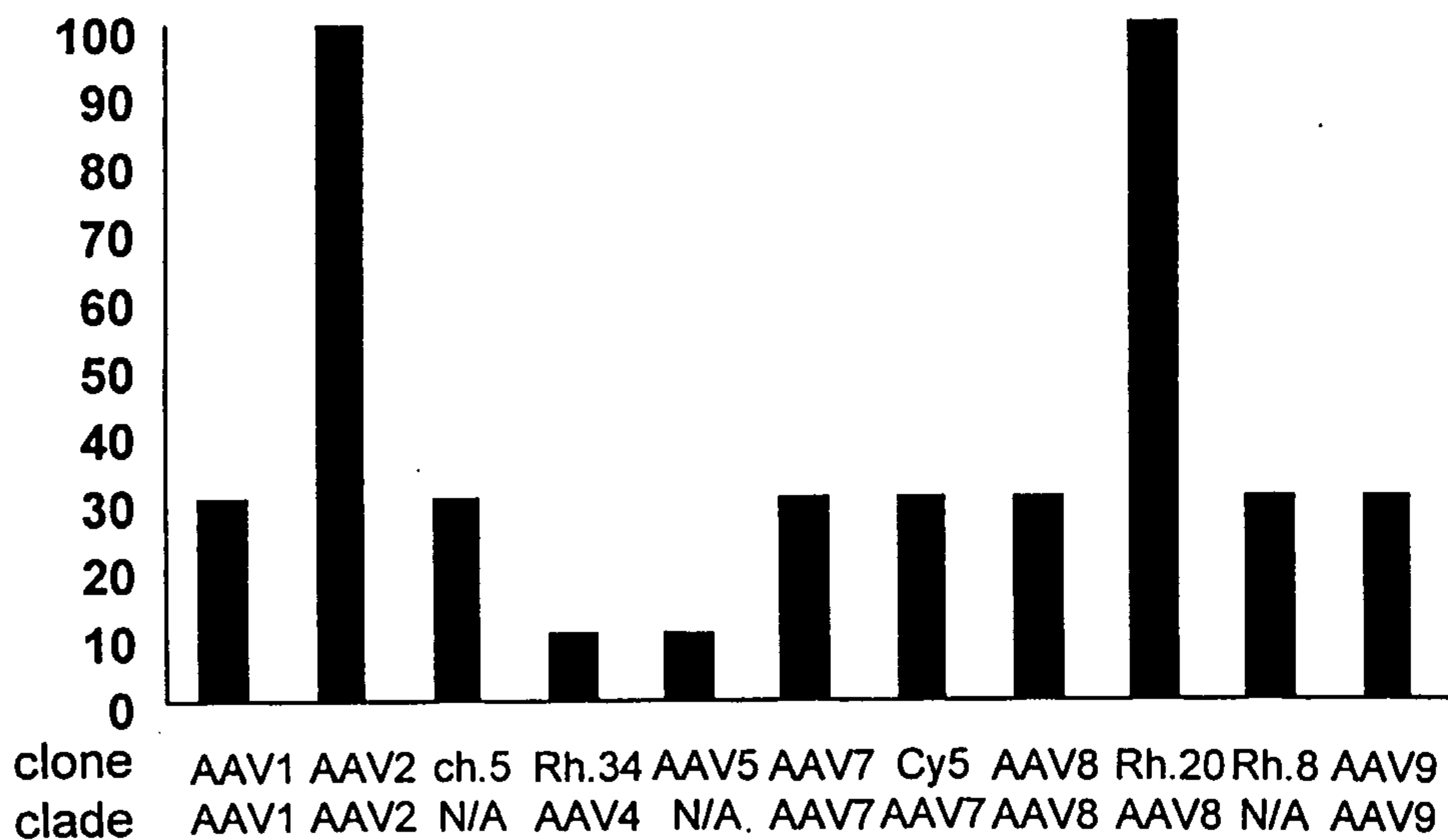


Fig. 4A

In Vitro

A1AT (ng/ml)

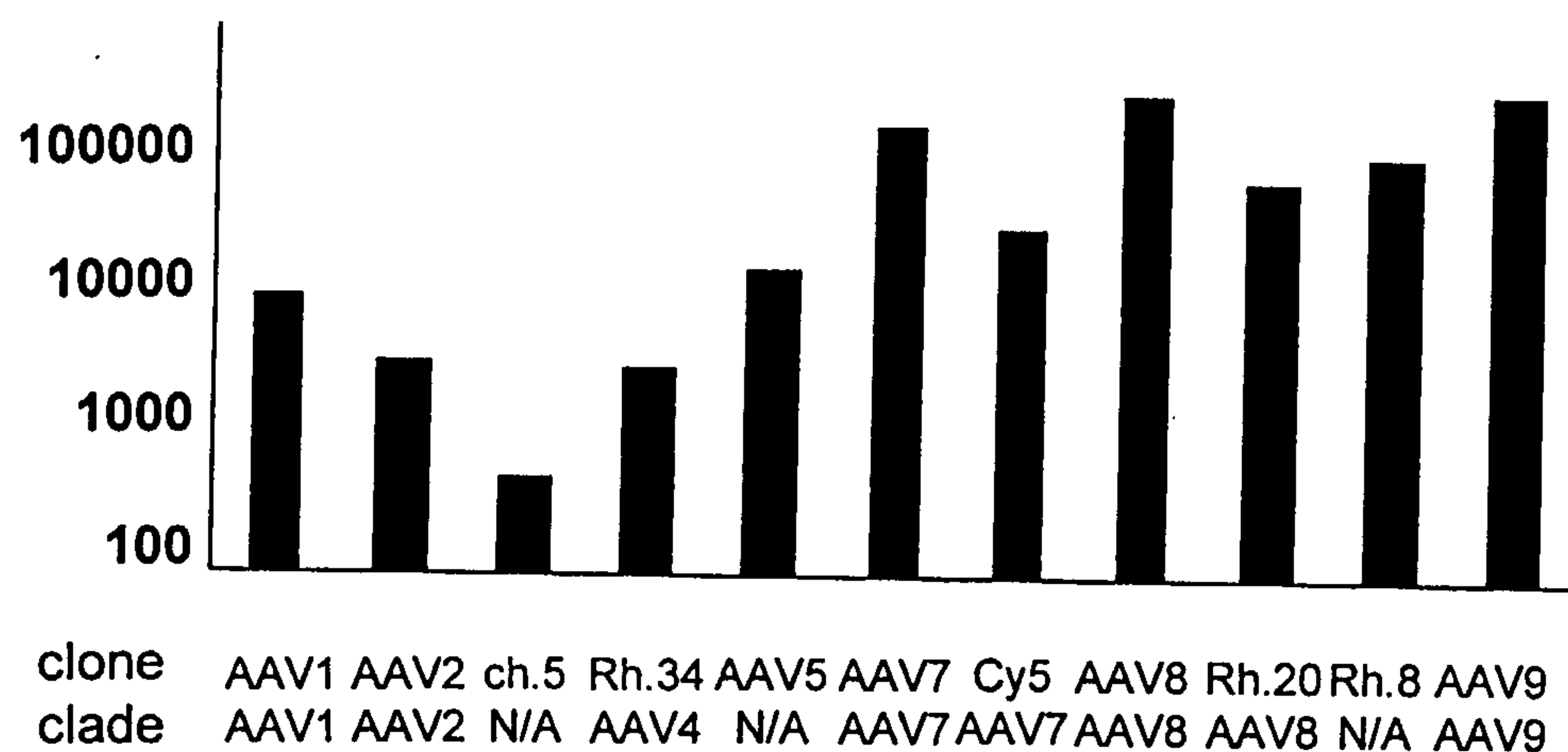


Fig. 4B

Liver

A1AT(ng/ml)

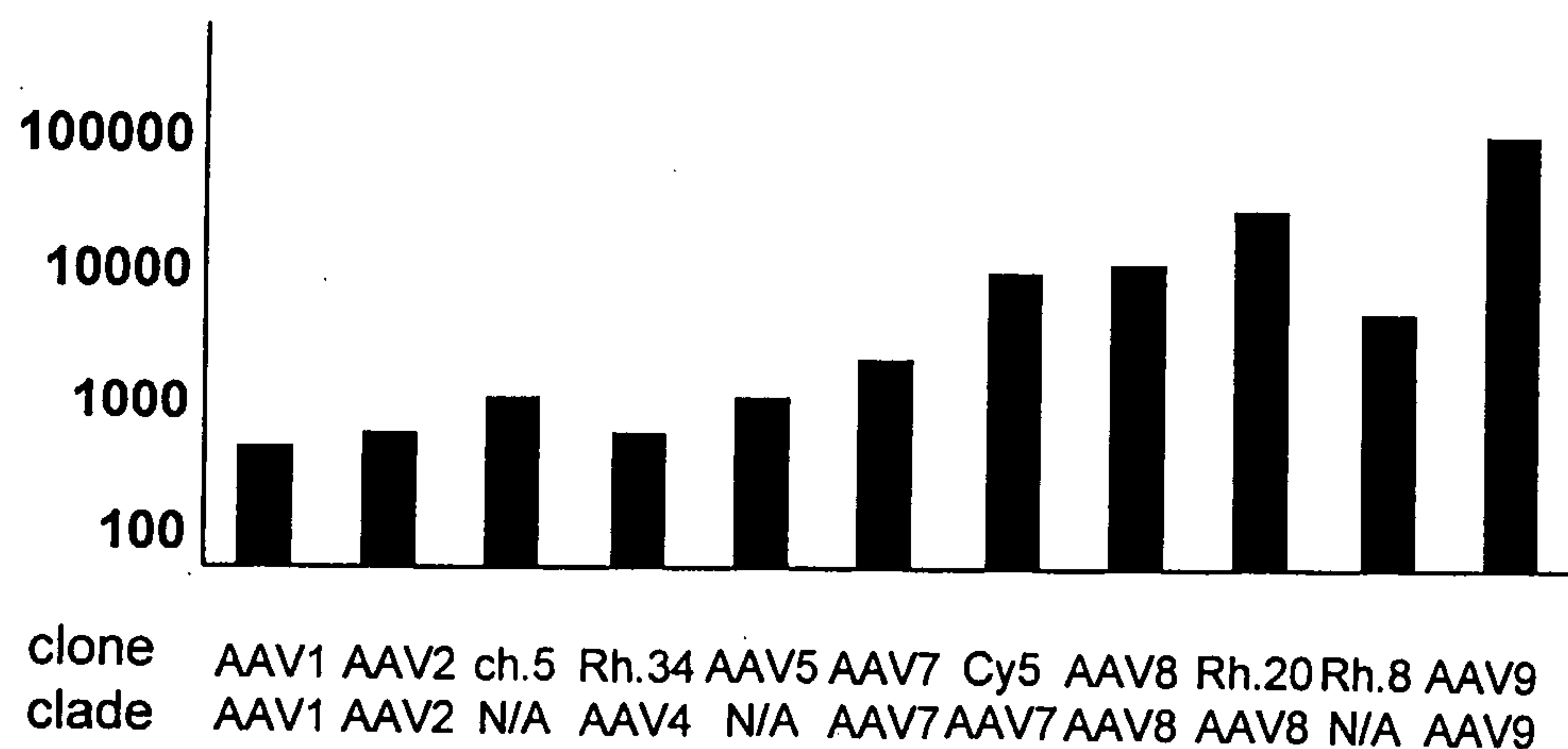


Fig. 4C

Lung

A1AT (ng/ml)

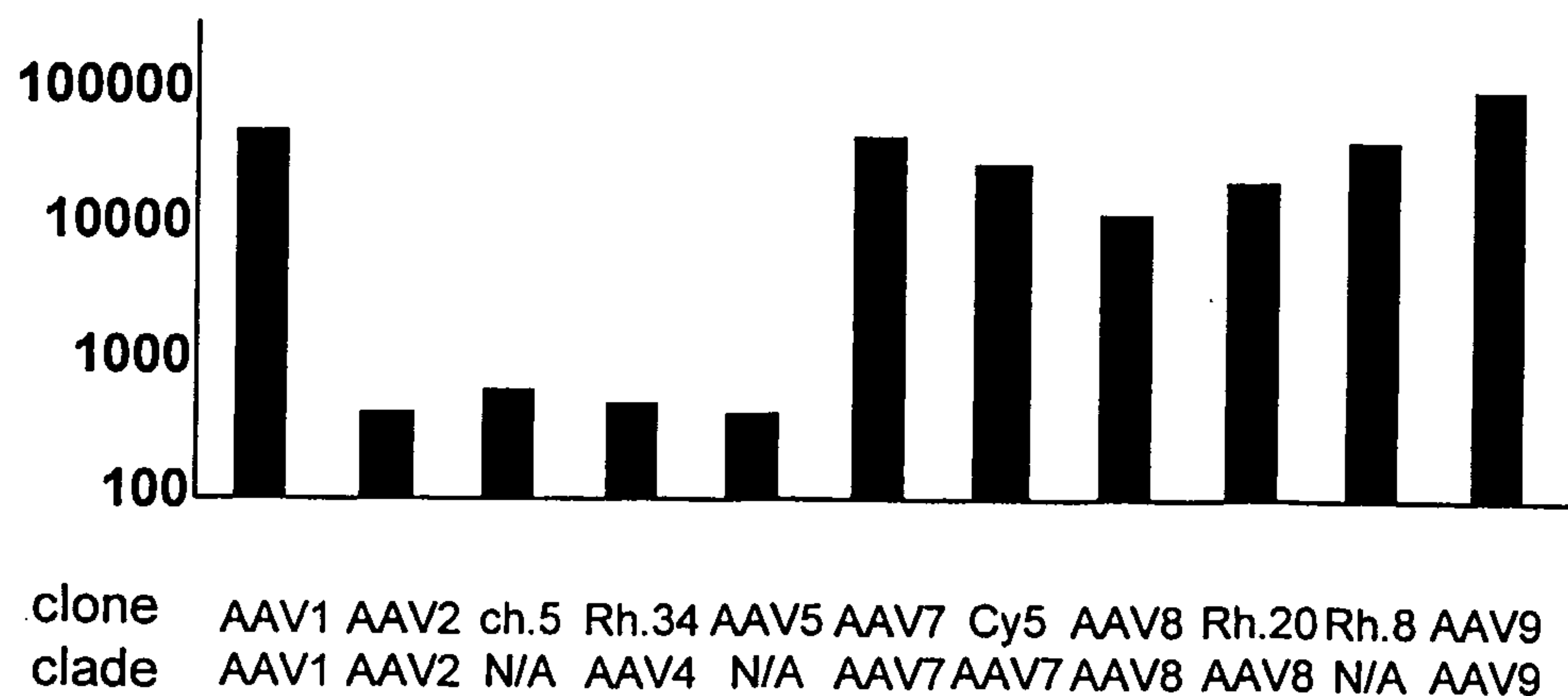


Fig. 4D

Muscle