CLAIMS

1. A recombinant adeno-associated virus (rAAV) which comprises an AAVhu68 capsid and a vector genome in the AAVhu68 capsid, wherein:

(A) the vector genome comprises a nucleic acid molecule comprising AAV inverted terminal repeat sequences (ITRs) and between the ITRs a non-AAV nucleic acid sequence encoding a product operably linked to sequences which direct expression of the product in a mammalian target cell; and

(B) the AAVhu68 capsid comprises AAVhu68 vp1 proteins, AAVhu68 vp2 proteins, and AAVhu68 vp3 proteins produced from a nucleic acid sequence encoding the amino acid sequence of SEQ ID NO: 2, wherein the AAVhu68vp1 proteins comprise a glutamic acid at position 67 and a valine at position 157 and the AAVhu68vp2 proteins comprise a valine at position 157 based on the numbering of SEQ ID NO: 2.

2. The rAAV according to claim 1, wherein the AAVhu68 capsid comprises subpopulations of AAVhu68 vp1, AAVhu68 vp2 and AAVhu68 vp3 proteins, wherein the subpopulations of the AAVhu68 vp1, AAVhu68 vp2 and AAV hu68 vp3 proteins comprise at least 50% to 100% deamidated asparagines (N) in asparagine - glycine pairs at each of positions 57, 329, 452, 512, relative to the amino acids in SEQ ID NO: 2, wherein the deamidated asparagines are deamidated to aspartic acid, isoaspartic acid, an interconverting aspartic acid/isoaspartic acid pair, or combinations thereof, as determined using mass spectrometry.

3. A recombinant adeno-associated virus (rAAV) which comprises an AAVhu68 capsid and a vector genome in the AAVhu68 capsid, wherein:

(A) the vector genome comprises a nucleic acid molecule comprising AAV inverted terminal repeat sequences (ITRs) and between the ITRs a non-AAV nucleic acid sequence encoding a product operably linked to sequences which direct expression of the product in a mammalian target cell; and

(B) the AAVhu68 capsid comprises heterogenous populations of AAVhu68 vp1, AAVhu68 vp2 and AAVhu68 vp3 proteins,

wherein the AAVhu68 vp1 proteins are amino acids 1 to 736 of SEQ ID NO: 2 (vp1) which comprise a glutamic acid at position 67 and a valine at position 157 and further comprise subpopulations of vp1 proteins comprising modified amino acids based on the amino acids positions in SEQ ID NO: 2,

wherein the AAVhu68 vp2 proteins are amino acids 138 to 736 of SEQ ID NO: 2 (vp2) which comprise a valine at position 157 and further comprise subpopulations of vp2 proteins comprising modified amino acids based on the amino acid positions in SEQ ID NO: 2, and

wherein the AAVhu68 vp3 proteins are amino acids 203 to 736 of SEQ ID NO: 2 (vp3), which comprise subpopulations of vp3 proteins comprising modified amino acids based on the amino acid positions in SEQ ID NO: 2,

wherein the subpopulations of the AAVhu68 vp1, AAVhu68 vp2 and AAV hu68 vp3 proteins comprise at least 50% to 100% deamidated asparagines (N) in asparagine - glycine pairs at each of positions 57, 329, 452, 512, relative to the amino acids in SEQ ID NO: 2, wherein the deamidated asparagines are deamidated to aspartic acid, isoaspartic acid, an interconverting aspartic acid/isoaspartic acid pair, or combinations thereof, as determined using mass spectrometry.

4. The rAAV according to claim 2 or claim 3, wherein the subpopulations of AAVhu68 vp1, vp2 and vp3 proteins further comprise:

(i) one or more modifications selected from: acetylated lysine, phosphorylated serine and/or threonine, isomerized aspartic acid, deamidated glutamines, oxidated tryptophan and/or methionine, or an amidated amino acid as determined using mass spectrometry; and/or

(ii) 1 % to 40% deamidation of asparagines at one or more of positions N94, N113, N252, N253, Q259, N270, N303, N304, N305, N319, N328, N336, N409, N410, N477, N515, N598, Q599, N628, N651, N663, N709, or combinations thereof, based on the numbering of SEQ ID NO: 2, as determined using mass spectrometry.

5. The rAAV according to any one of claims 2 to 4, wherein the AAVhu68 capsid subpopulations of AAVhu68 vp1, vp2 and vp3 capsid proteins further comprise

(a) at least 65% of asparagines (N) in asparagine - glycine pairs located at positions 57 of the vp1 proteins are deamidated, as determined using mass spectrometry, based on the numbering of SEQ ID NO:2; and/or

(b) at least 75% of N in asparagine - glycine pairs in position 329 of the vp1, vp2 and vp3 proteins are deamidated, as determined using mass spectrometry, based on the residue numbering of the amino acid sequence of SEQ ID NO: 2; and/or

(c) at least 50% of N in asparagine - glycine pairs in position 452 of the vp1, vp2 and vp3 proteins are deamidated, as determined using mass spectrometry, based on the residue numbering of the amino acid sequence of SEQ ID NO: 2; and/or

(d) at least 75% of N in asparagine - glycine pairs in position 512 of the vp1, vp2 and vp3 proteins are deamidated, as determined using mass spectrometry, based on the residue numbering of the amino acid sequence of SEQ ID NO: 2.

6. The rAAV according to any one of claims 1 to 5, wherein the AAVhu68 capsid comprises:

(a) a subpopulation of vp1 proteins in which 75% to 100% of the N at position 57 of the vp1 proteins are deamidated, as determined using mass spectrometry; and/or

(b) subpopulations of vp1 proteins, vp2 proteins, and/or vp3 proteins in which 75% to 100% of the N at position 329, based on the numbering of SEQ ID NO:2, are deamidated as determined using mass spectrometry; and/or

(c) subpopulations of vp1 proteins, vp2 proteins, and/or vp3 proteins in which 75% to 100% of the N at position 452, based on the numbering of SEQ ID NO:2, are deamidated as determined using mass spectrometry; and/or

(d) subpopulations of vp1 proteins, vp2 proteins, and/or vp3 proteins in which 75% to 100% of the N at position 512, based on the numbering of SEQ ID NO:2, are deamidated as determined using mass spectrometry.

7. The rAAV according to any one of claims 1 to 6, wherein the nucleic acid sequence encoding the vp1 proteins is SEQ ID NO: 1, or a sequence at least 80% to at least 99% identical to SEQ ID NO: 1 which encodes the amino acid sequence of SEQ ID NO:2; optionally wherein the nucleic acid sequence is at least 80% to 97% identical to SEQ ID NO: 1.

8. A composition comprising a mixed population of recombinant adeno-associated virus hu68 (rAAVhu68), wherein each of the rAAVhu68 is independently selected from an rAAV according to any one of claims 1 to 7.

9. The rAAV according to any one of claims 1 to 7, or the composition according to claim 8, wherein the AAV ITR sequences are a 5' ITR and a 3' ITR from an AAV source other than AAVhu68.

10. The composition according to any one of claims 8 or 9, wherein the composition is formulated for

(i) intrathecal delivery and the vector genome comprises a nucleic acid sequence encoding a product for delivery to the central nervous system;

(ii) intravenous delivery; or

(iii) intranasal or intramuscular delivery.