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Patent

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Coke Moya Smead

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If the application for this patent was filed on or after June 8, 1995, the term of this patent begins on the date on which this patent issues and ends twenty years from the filing date of the application or, if the application contains a specific reference to an earlier filed application or applications under 35 U.S.C. 120, 121, 365(c), or 386(c), twenty years from the filing date of the earliest such application (“the twenty-year term”), subject to the payment of maintenance fees as provided by 35 U.S.C. 41(b), and any extension as provided by 35 U.S.C. 154(b) or 156 or any disclaimer under 35 U.S.C. 253.

If this application was filed prior to June 8, 1995, the term of this patent begins on the date on which this patent issues and ends on the later of seventeen years from the date of the grant of this patent or the twenty-year term set forth above for patents resulting from applications filed on or after June 8, 1995, subject to the payment of maintenance fees as provided by 35 U.S.C. 41(b) and any extension as provided by 35 U.S.C. 156 or any disclaimer under 35 U.S.C. 253.



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(12) **United States Patent**
Sabeti et al.(10) **Patent No.:** **US 12,410,447 B2**(45) **Date of Patent:** **Sep. 9, 2025**(54) **ENGINEERED MUSCLE TARGETING COMPOSITIONS**(2013.01); *C12N 2800/80* (2013.01); *C12N 2810/405* (2013.01); *C12N 2810/6027* (2013.01); *C12N 2830/008* (2013.01)(71) Applicants: **The Broad Institute, Inc.**, Cambridge, MA (US); **President and Fellows of Harvard College**, Cambridge, MA (US); **Massachusetts Institute of Technology**, Cambridge, MA (US)(58) **Field of Classification Search**CPC .. C07K 14/005; C07K 14/47; C07K 2319/01; C07K 7/06; C07K 14/4716
See application file for complete search history.(72) Inventors: **Pardis Sabeti**, Cambridge, MA (US); **Mohammadsharif Tabebordbar**, Cambridge, MA (US); **Simon Ye**, Cambridge, MA (US)

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Primary Examiner — Barry A Chestnut(74) *Attorney, Agent, or Firm* — F. Brent Nix, Esq.; Johnson, Marcou, Isaacs & Nix, LLC; Christopher D. Southgate

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ABSTRACT

Described herein are targeting moieties that can be capable of specifically targeting muscle cells and can include an n-mer motif. In some embodiments, the n-mer motif contains an RGD motif. Also described herein are vector systems, particles, polypeptides that can encode and/or contain one or more targeting moieties. Also described herein are methods of delivering a cargo to a cell, such as a muscle cell, using one or more of the targeting moieties described herein.

30 Claims, 36 Drawing Sheets**Specification includes a Sequence Listing.**

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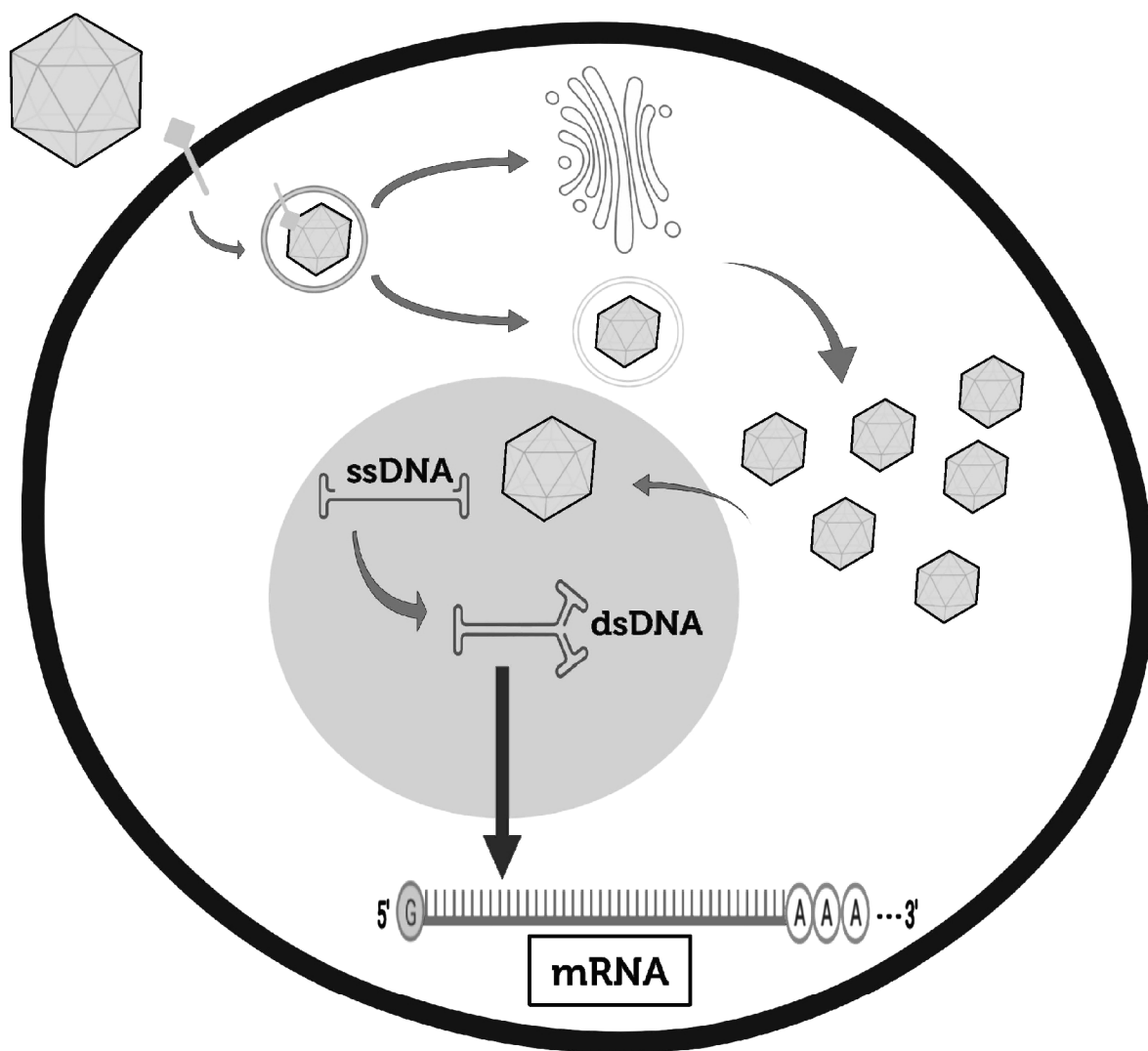
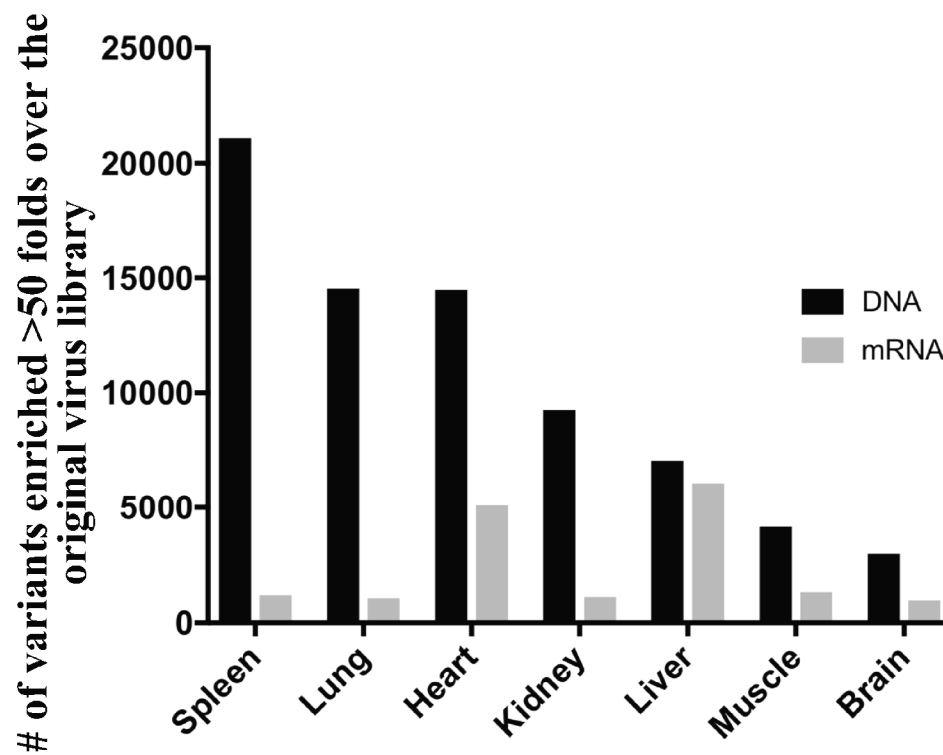
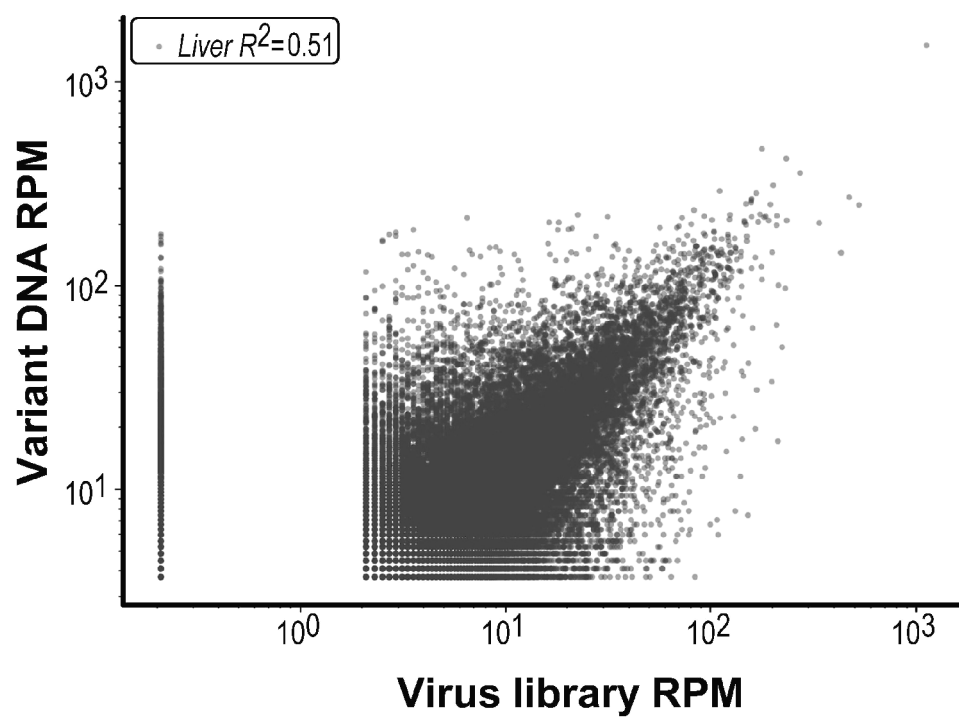
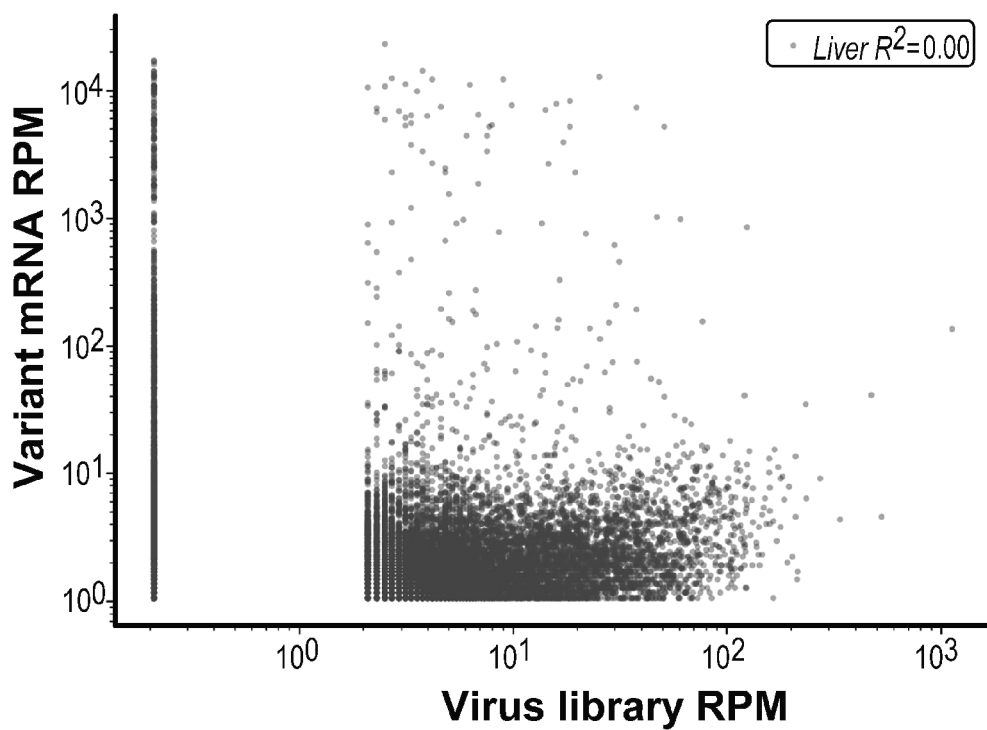


FIG. 1

**FIG. 2**

**FIG. 3A****FIG. 3B**

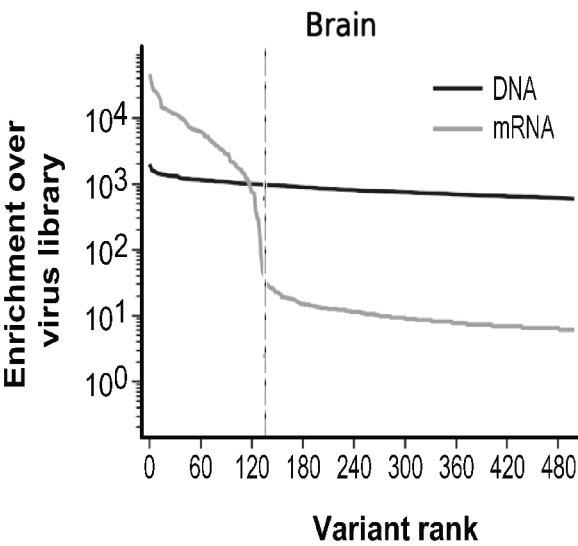


FIG. 4A

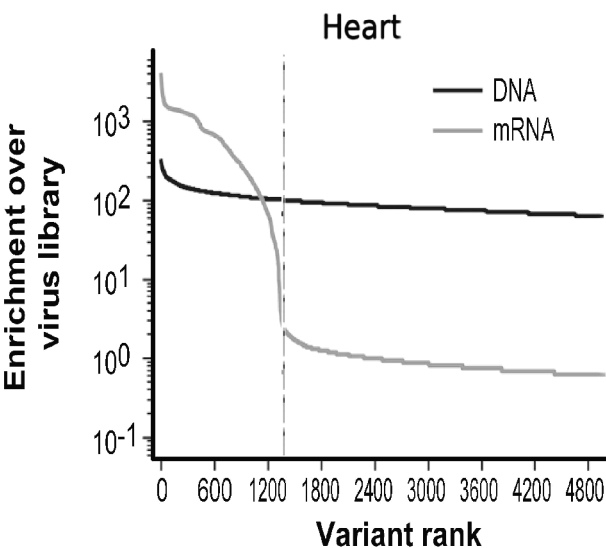


FIG. 4B

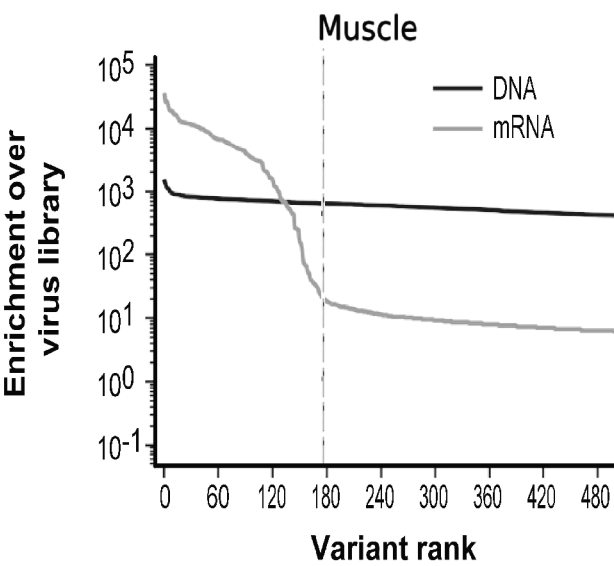
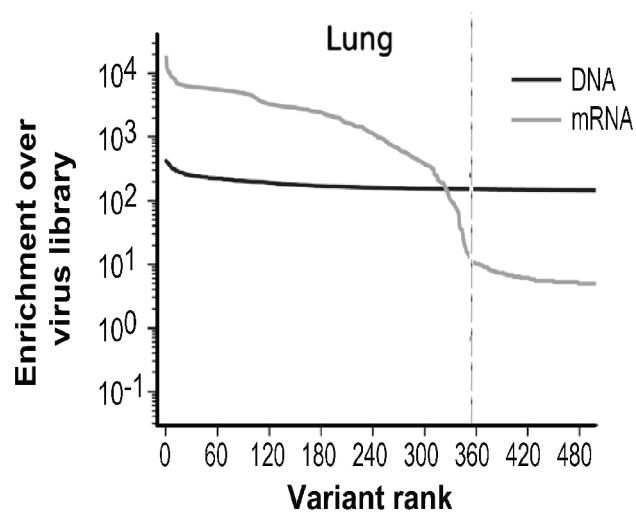
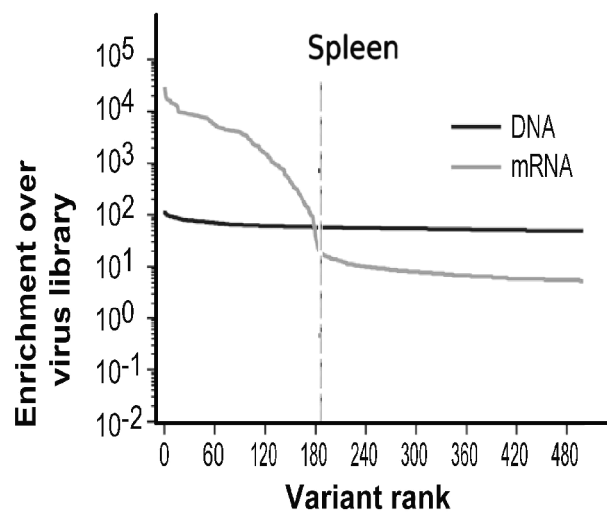
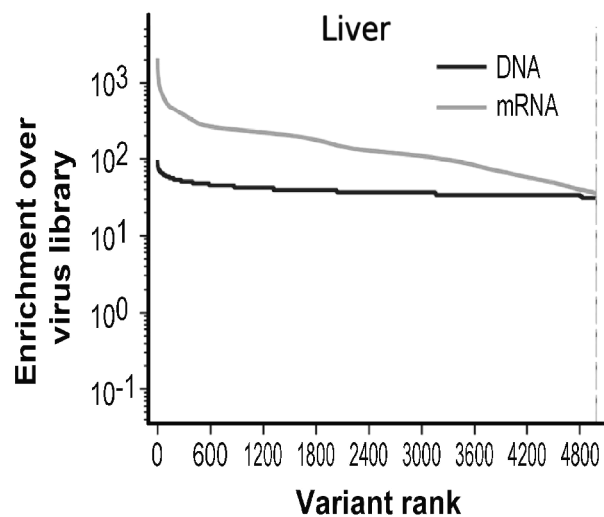
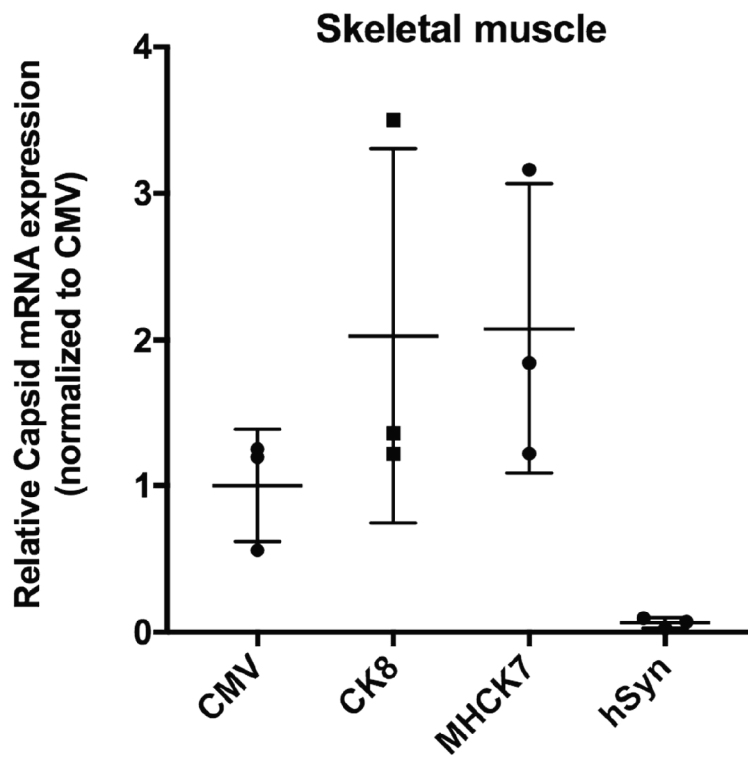
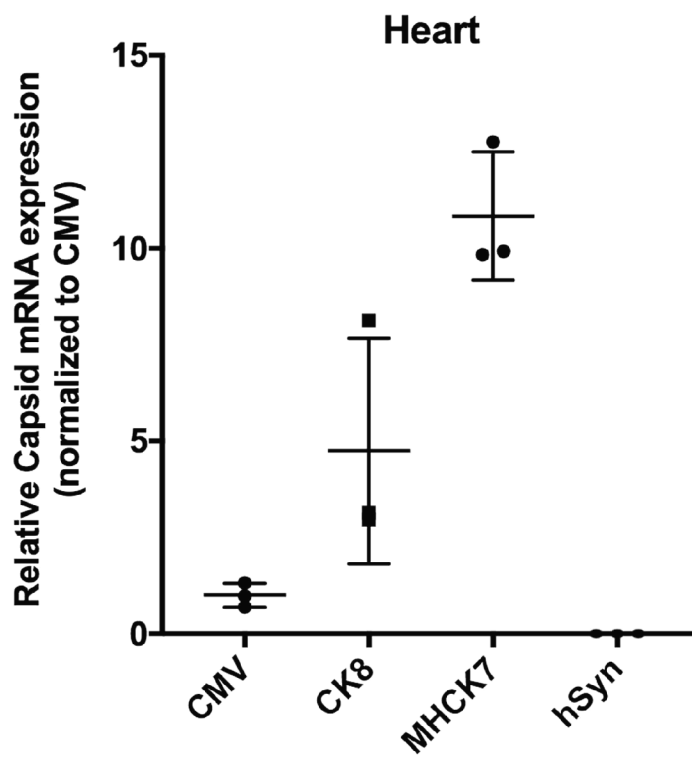
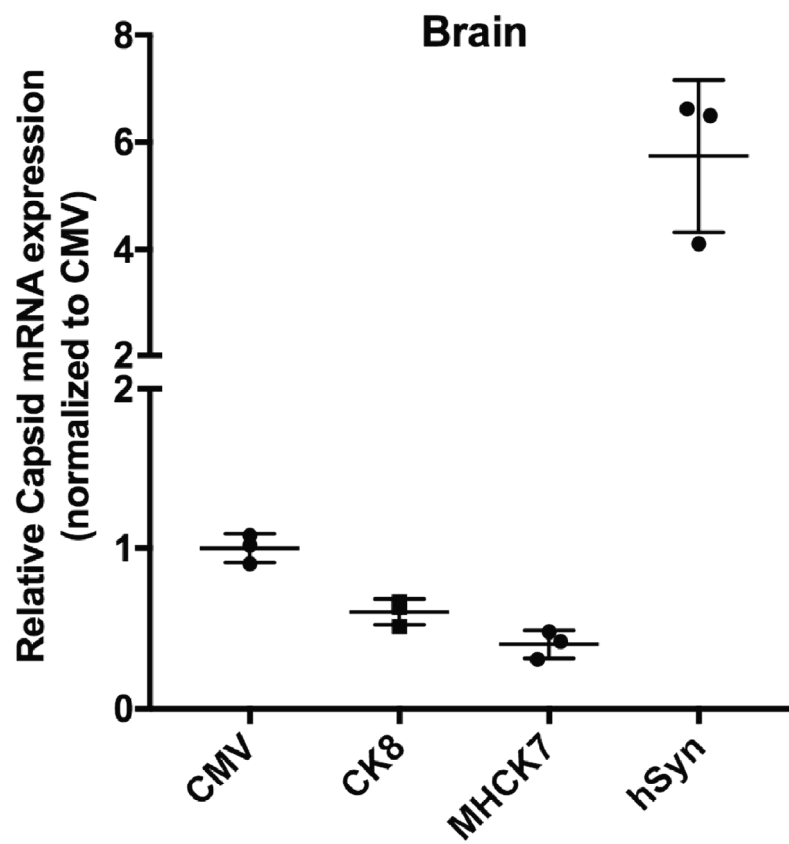
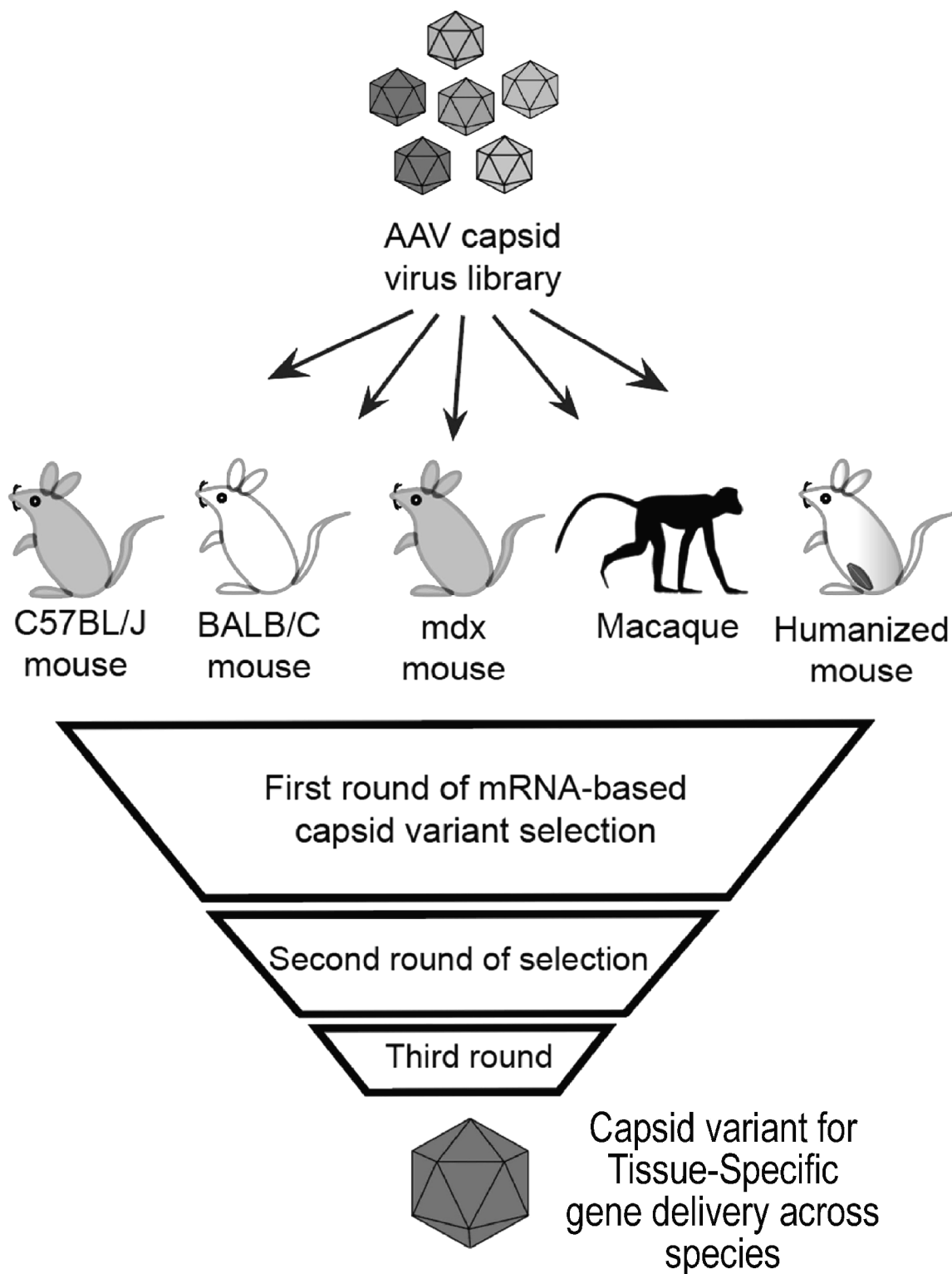


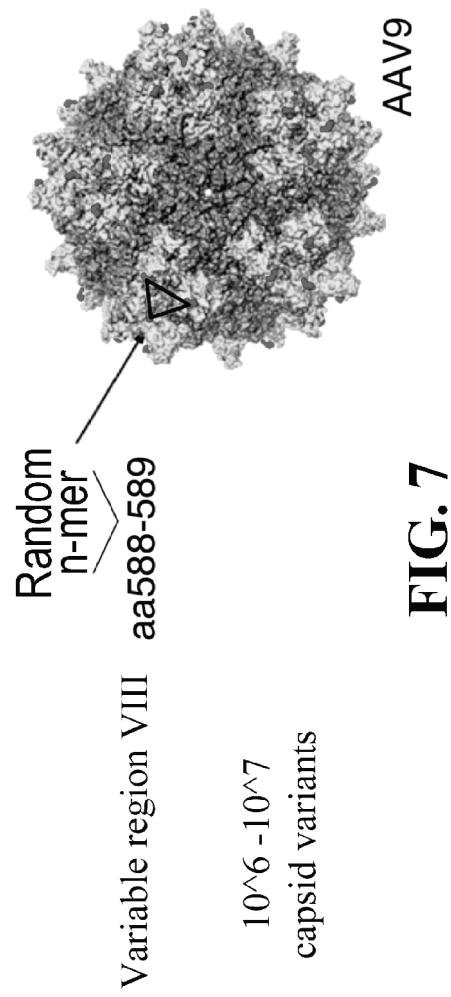
FIG. 4C

**FIG. 4D****FIG. 4E****FIG. 4F**

**FIG. 5A****FIG. 5B**

**FIG. 5C**

**FIG. 6**



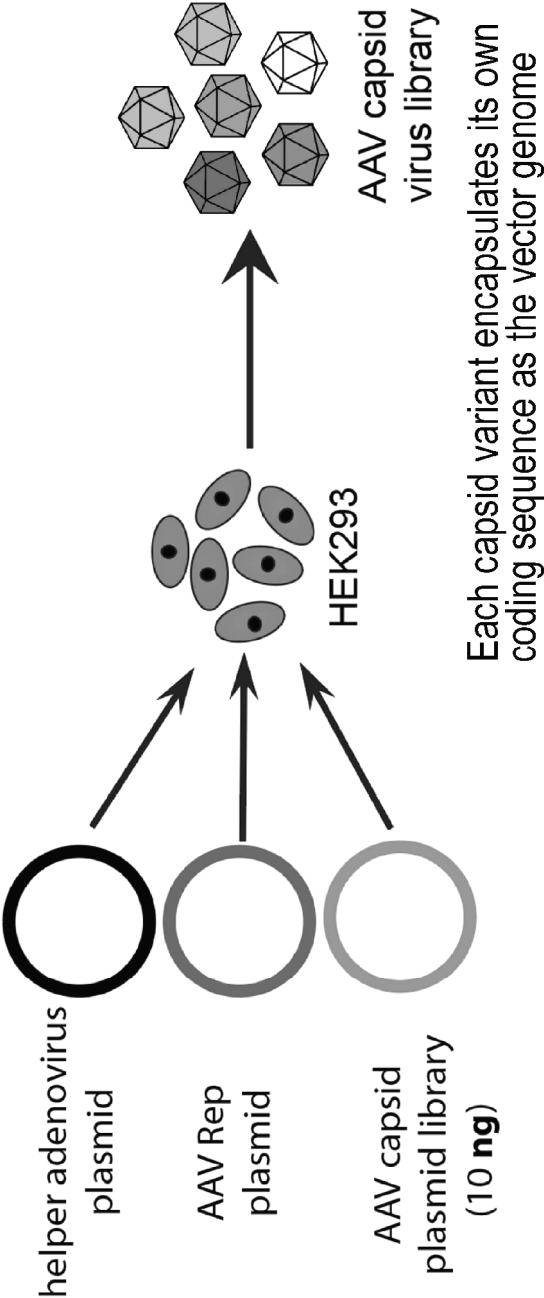


FIG. 8

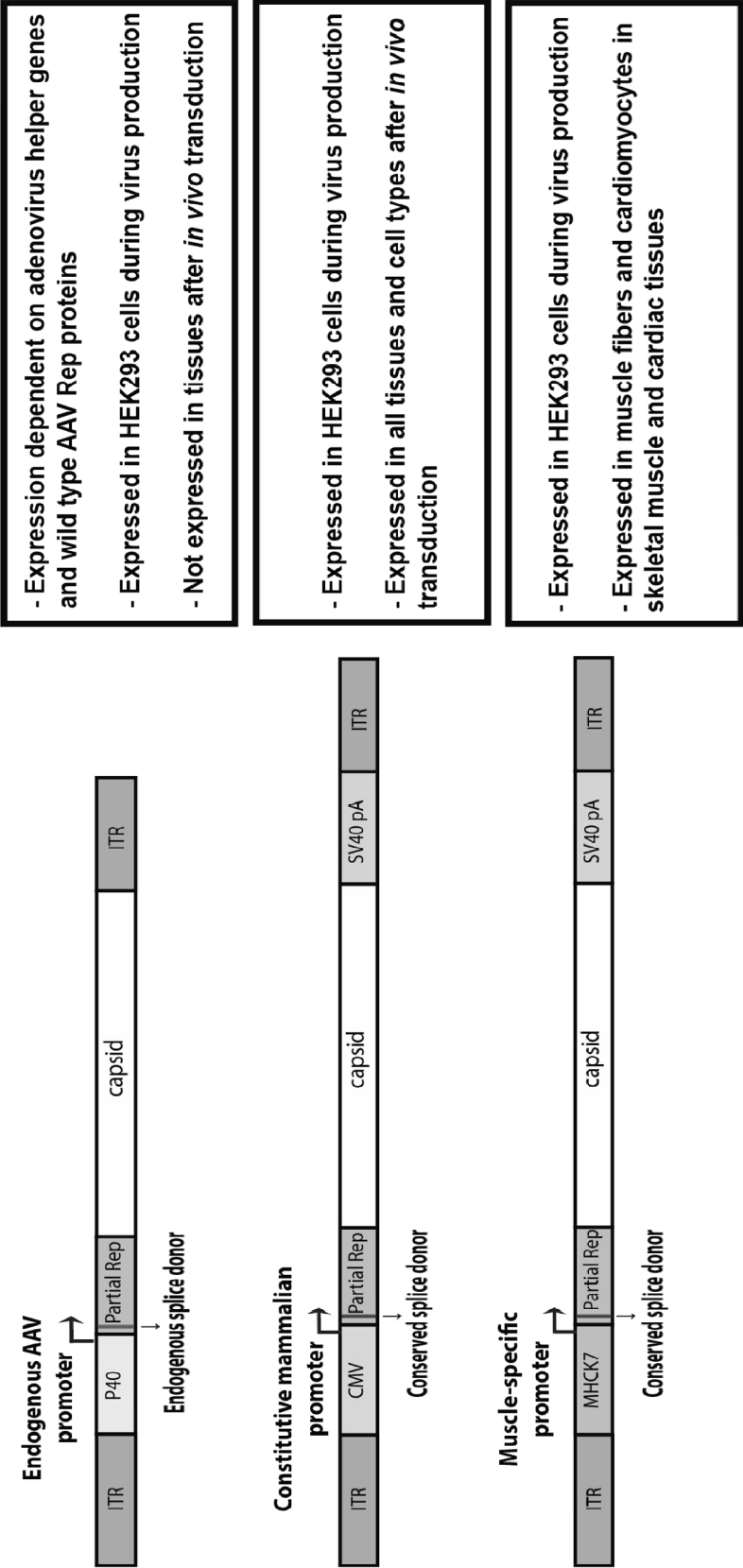
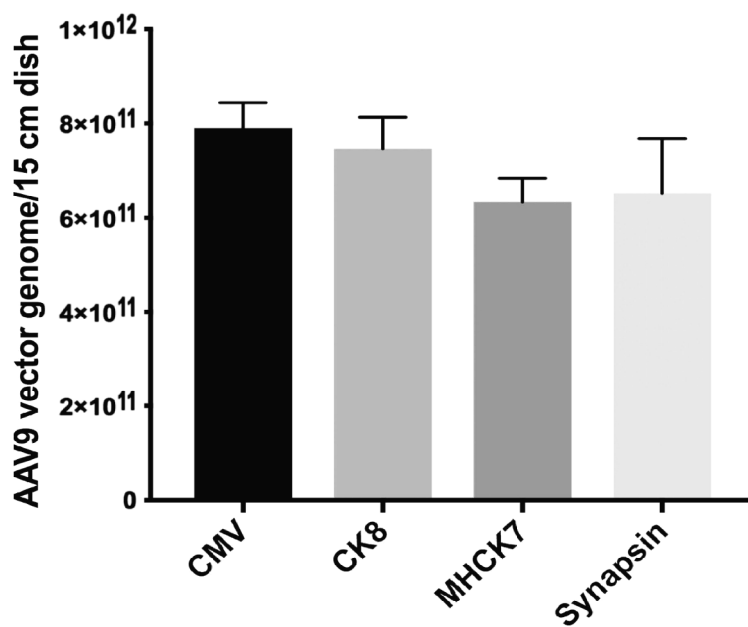
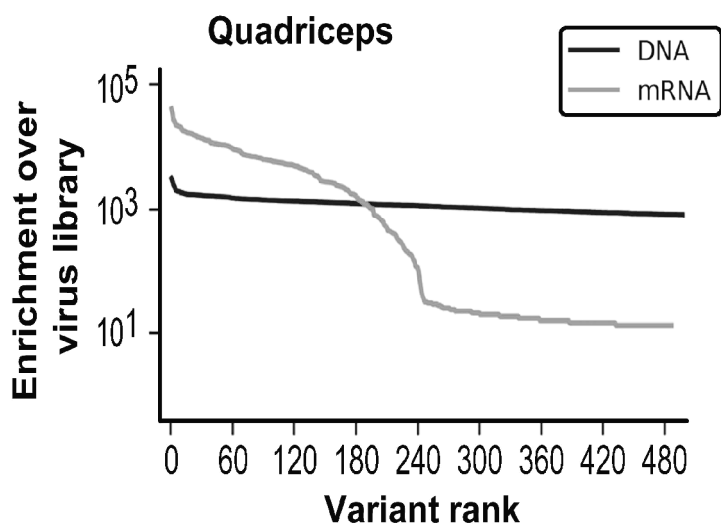
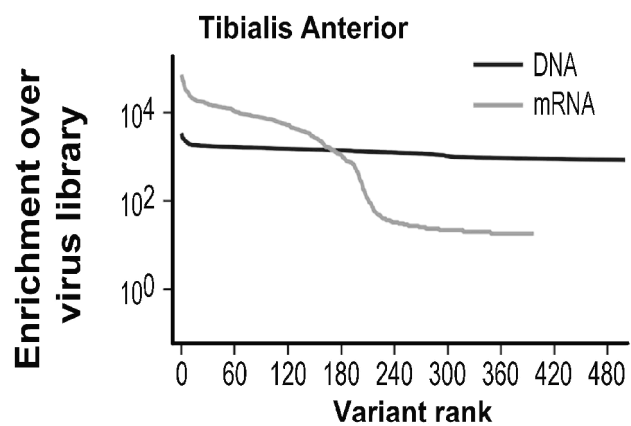
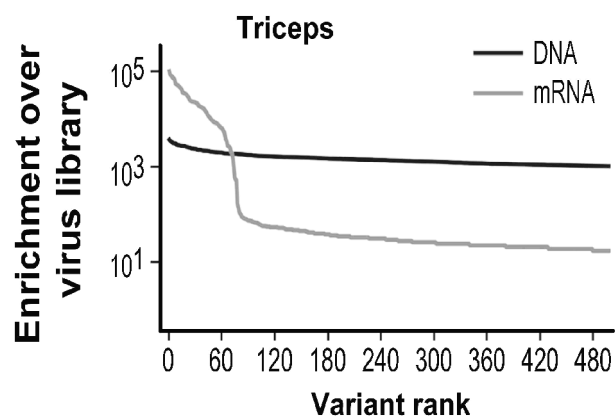
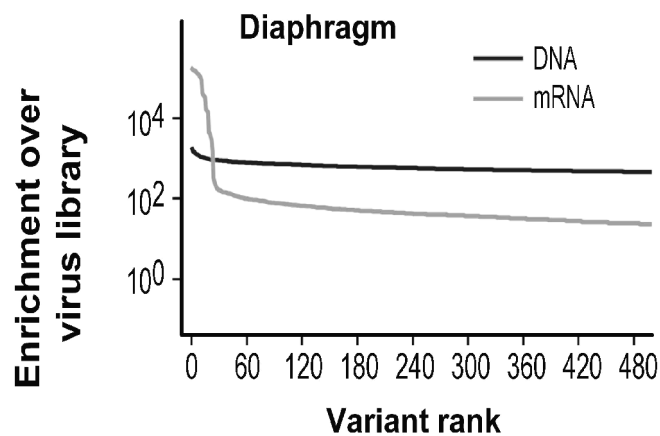
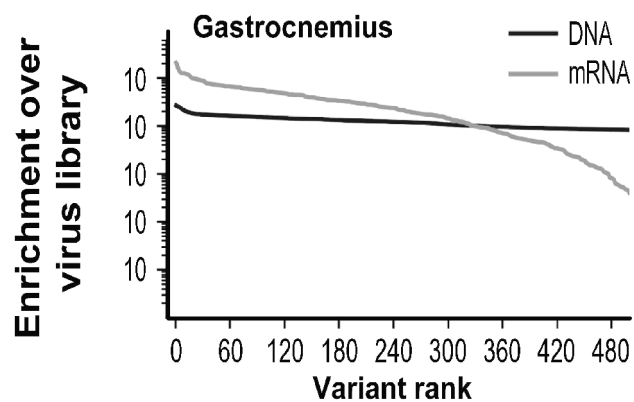
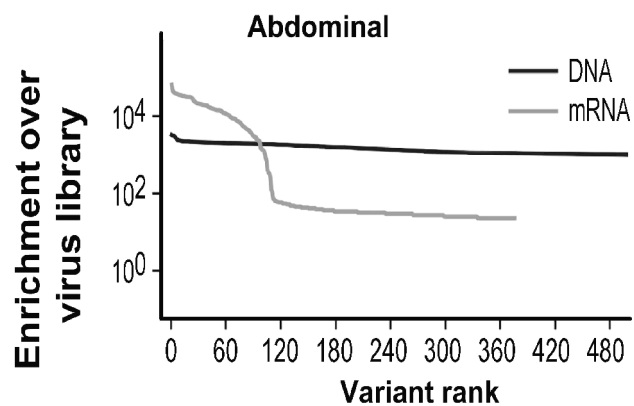
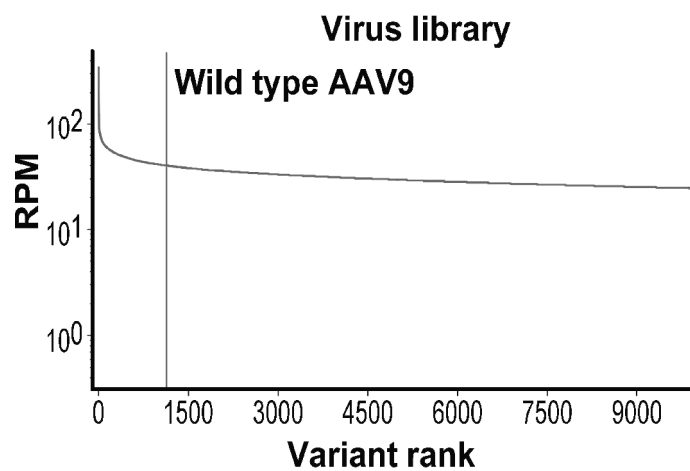
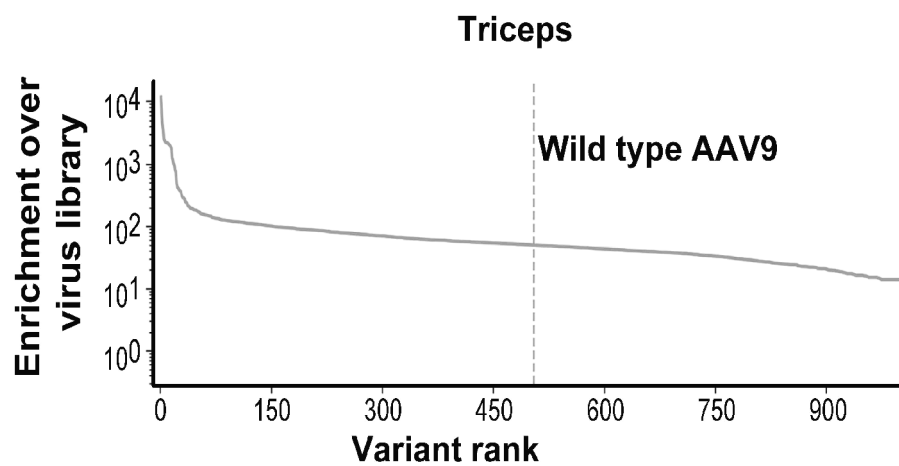
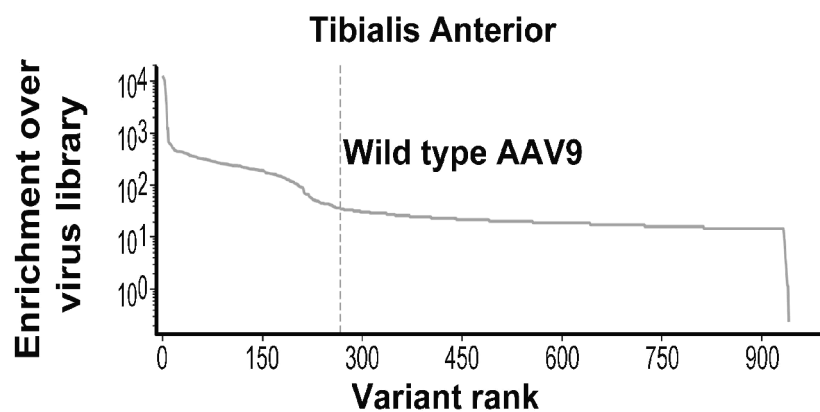
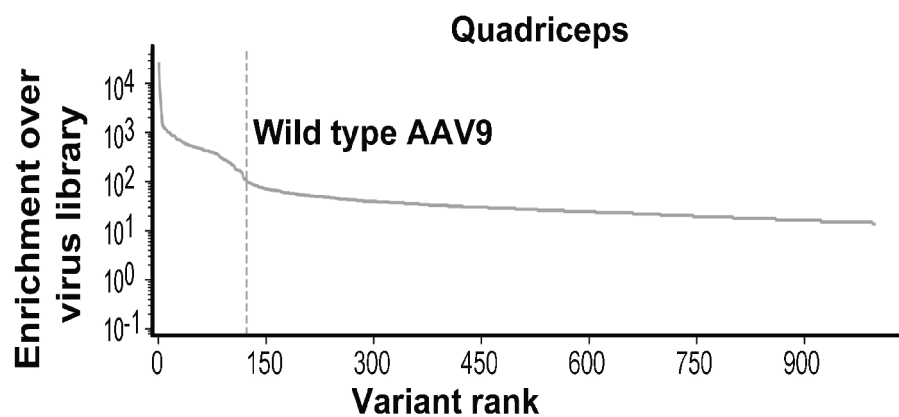


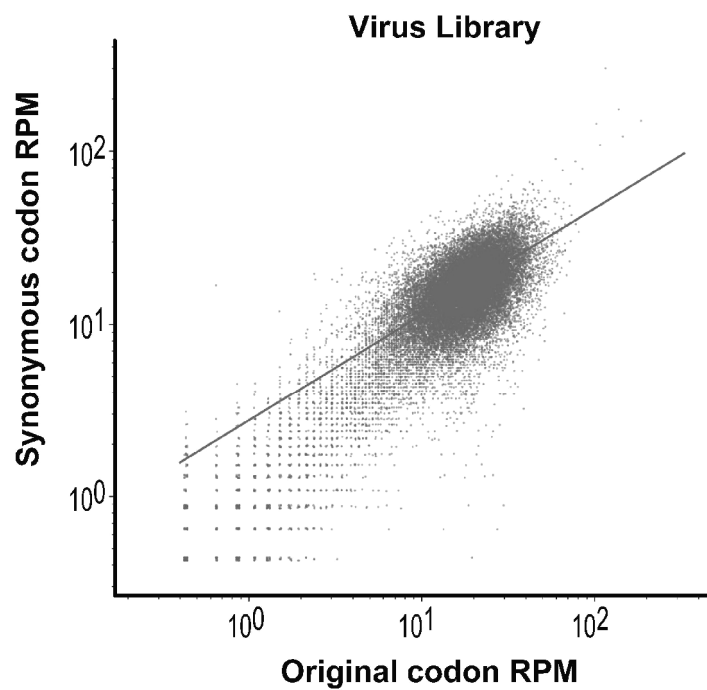
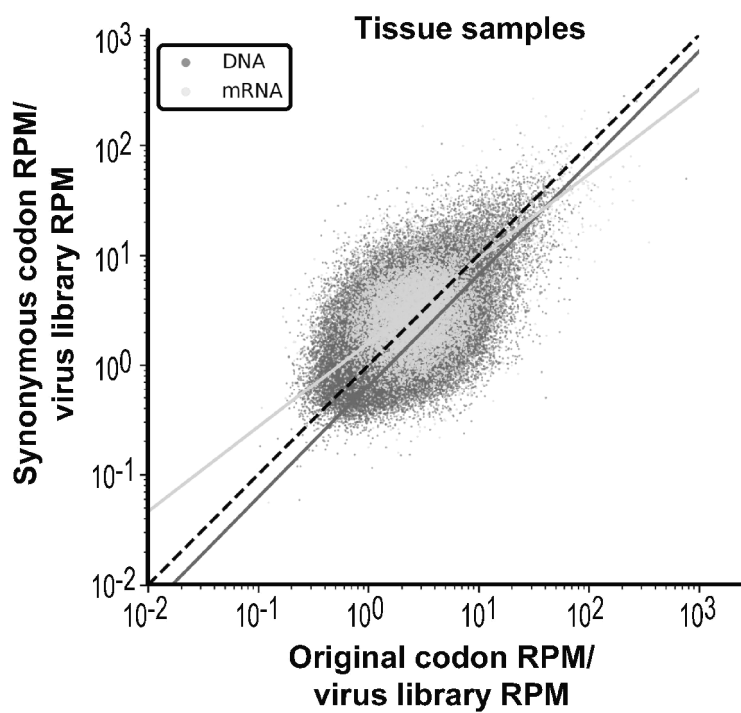
FIG. 9

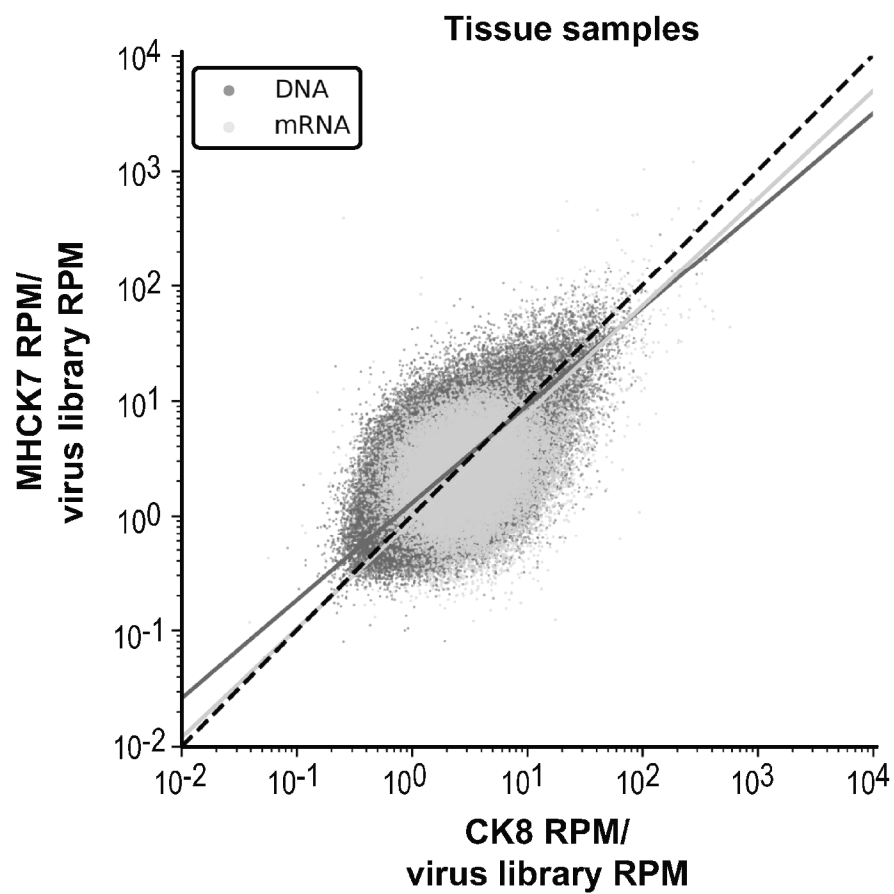
**FIG. 10****FIG. 11A**

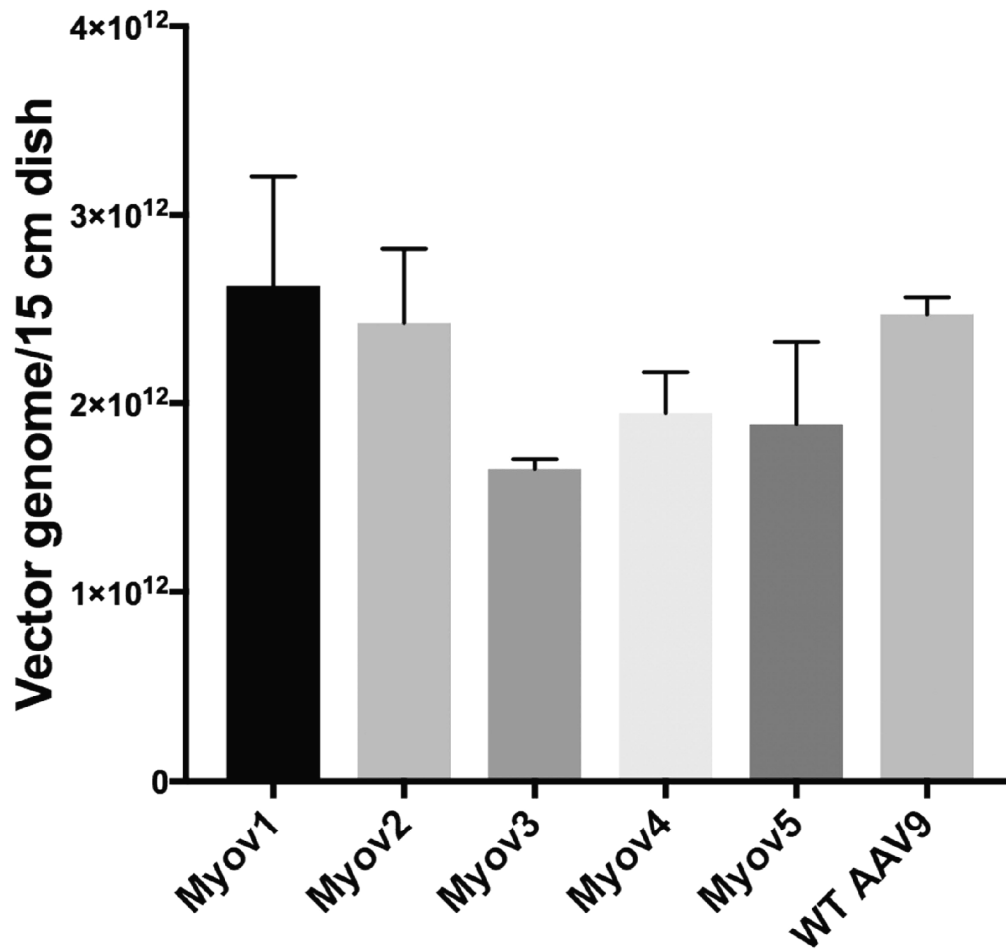
**FIG. 11B****FIG. 11C****FIG. 11D**

**FIG. 11E****FIG. 11F****FIG. 12A**

**FIG. 12B****FIG. 12C****FIG. 12D**

**FIG. 13A****FIG. 13B**

**FIG. 14**

**FIG. 15**

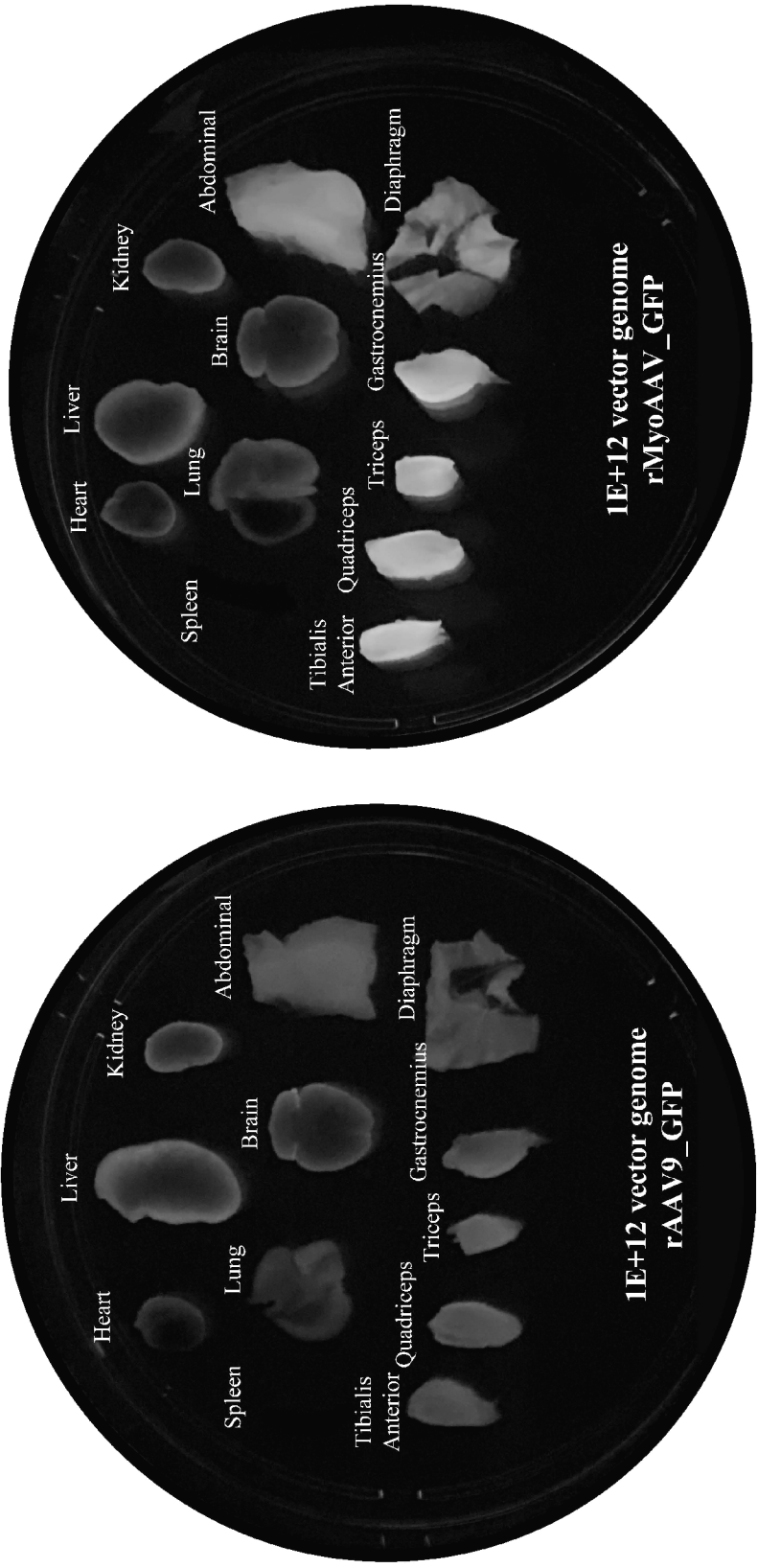


FIG. 16

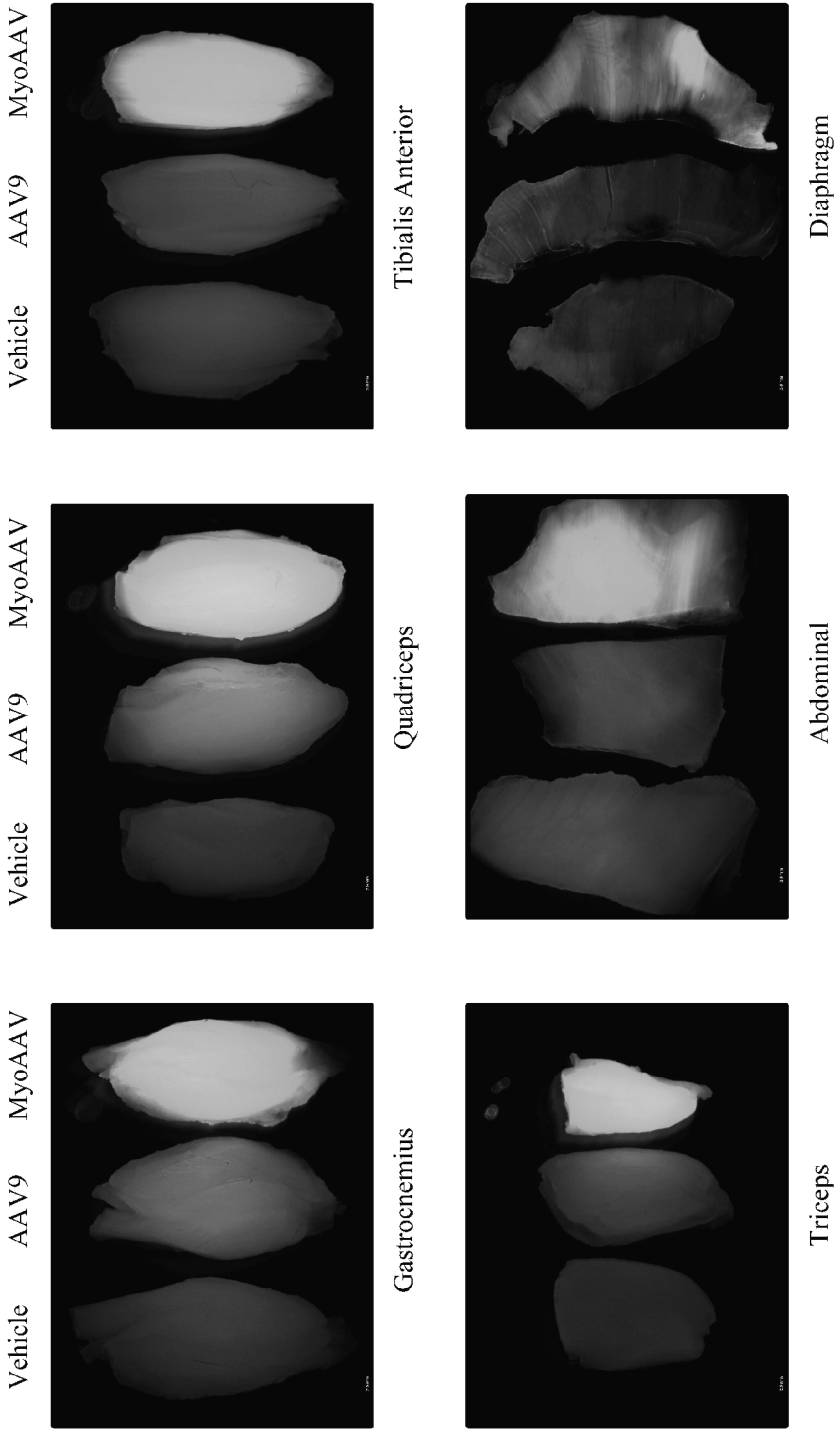


FIG. 17

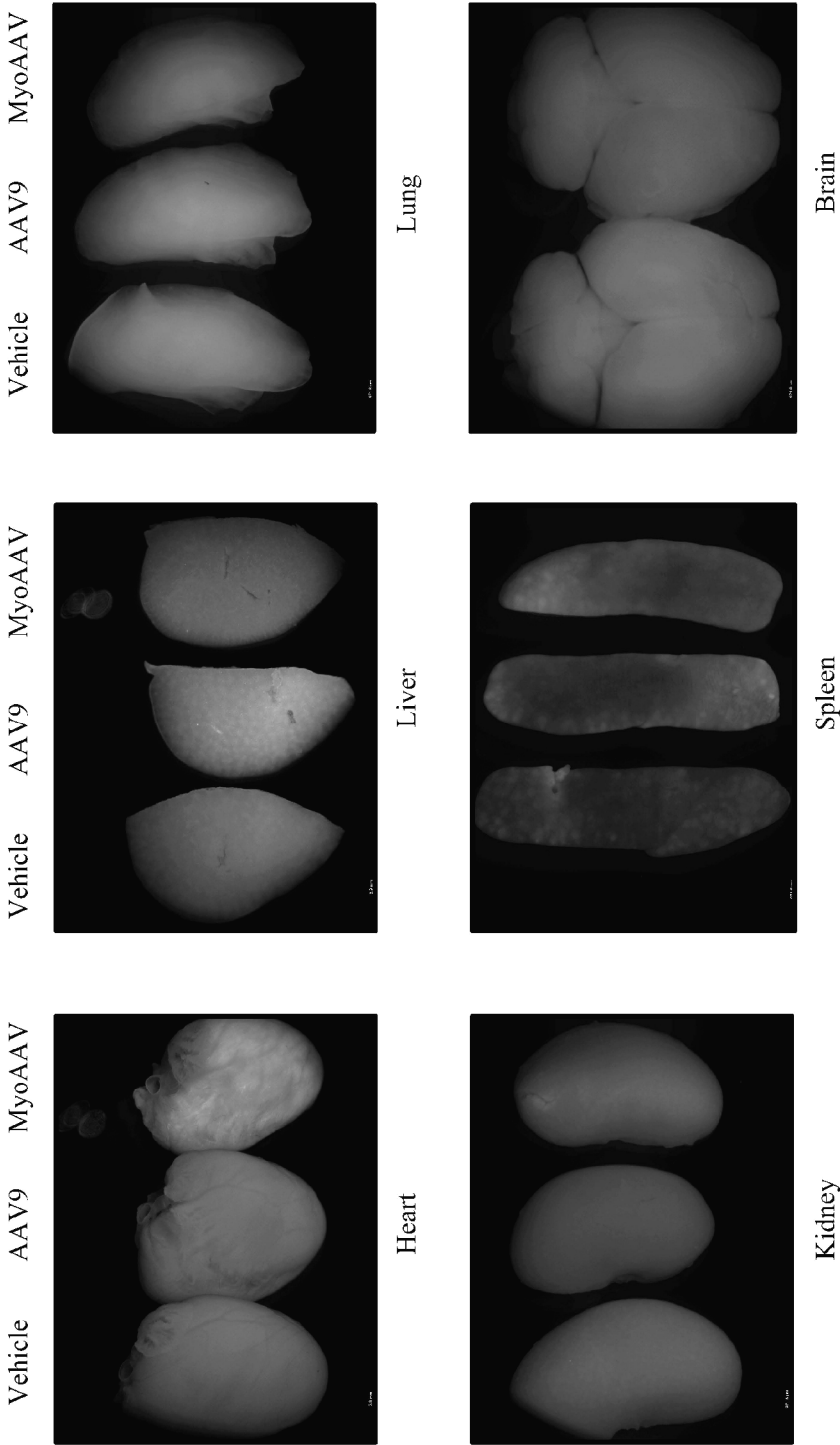


FIG. 18

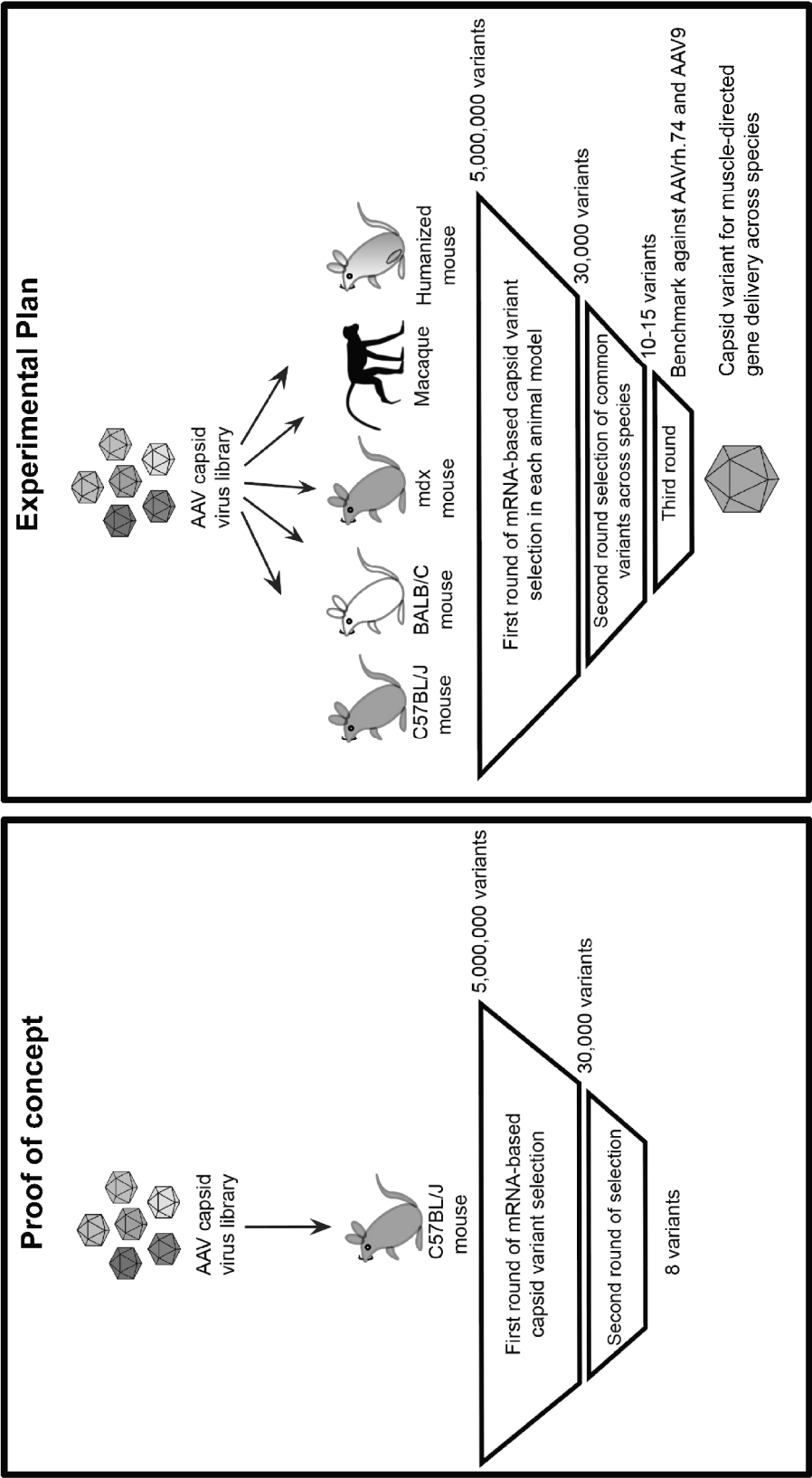


FIG. 19

Mouse strain	Tissue type	First 3 amino acids	Rank
C57BL/6J	Diaphragm	RGD	2
C57BL/6J	Gastrocnemius	RGD	2
C57BL/6J	Quadriceps	RGD	1
C57BL/6J	Tibialis Anterior	RGD	3
C57BL/6J	Triceps	RGD	12
C57BL/6J	Heart	RGD	8
C57BL/6J	Liver	RGD	245
C57BL/6J	Brain	RGD	2312

FIG. 20A

Mouse strain	Tissue type	First 3 amino acids	Rank
BALB/cJ	Diaphragm	RGD	9
BALB/cJ	Gastrocnemius	RGD	2
BALB/cJ	Quadriceps	RGD	18
BALB/cJ	Tibialis Anterior	RGD	10
BALB/cJ	Triceps	RGD	4
BALB/cJ	Heart	RGD	4
BALB/cJ	Liver	RGD	883
BALB/cJ	Brain	RGD	1266

FIG. 20B

Mouse strain	Tissue type	First 3 amino acids	Rank
mdx	Diaphragm	RGD	6
mdx	Gastrocnemius	RGD	1
mdx	Quadriceps	RGD	1
mdx	Tibialis Anterior	RGD	1
mdx	Triceps	RGD	1
mdx	Heart	RGD	25
mdx	Liver	RGD	166
mdx	Brain	RGD	1584

FIG. 20C

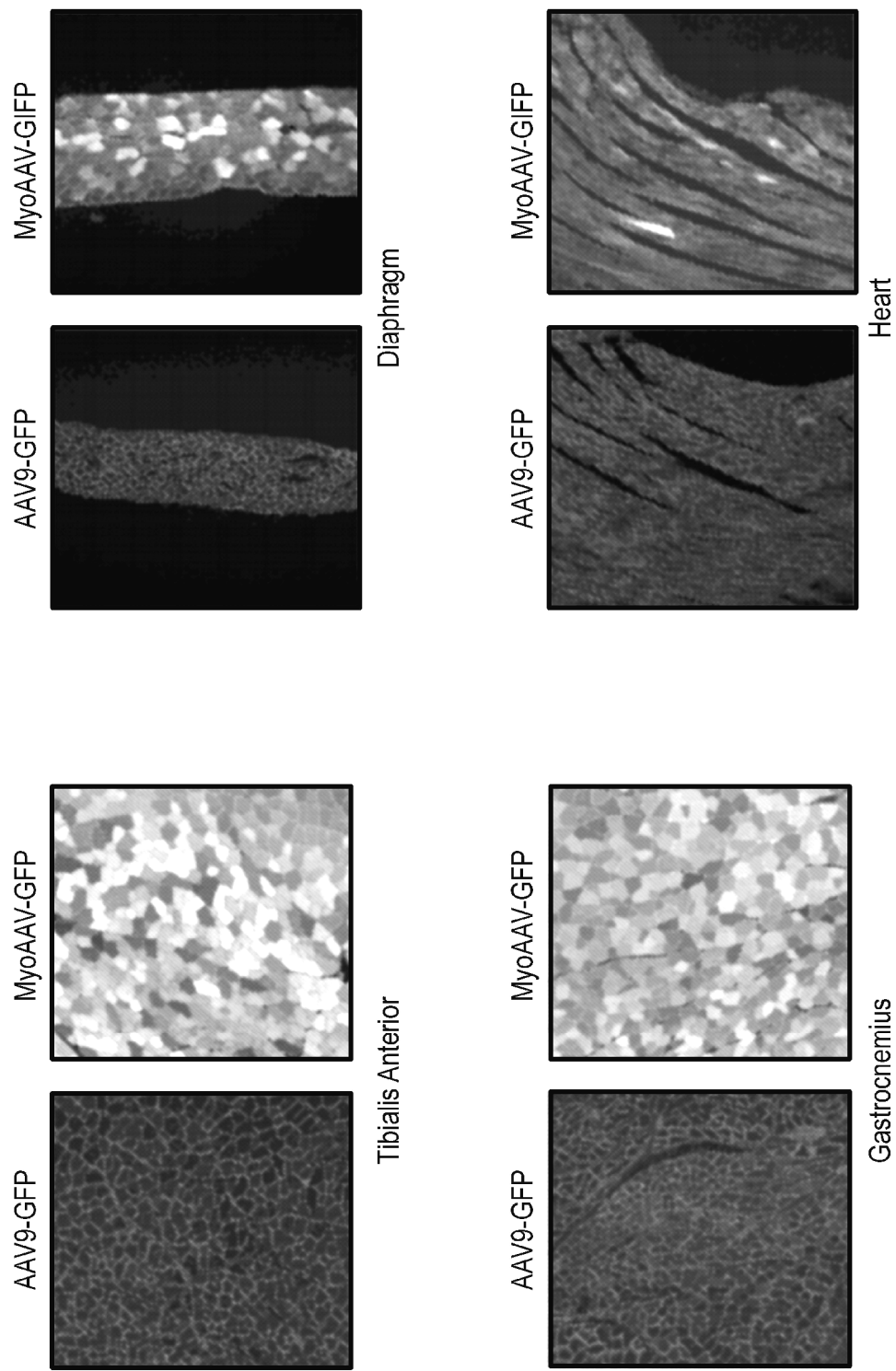
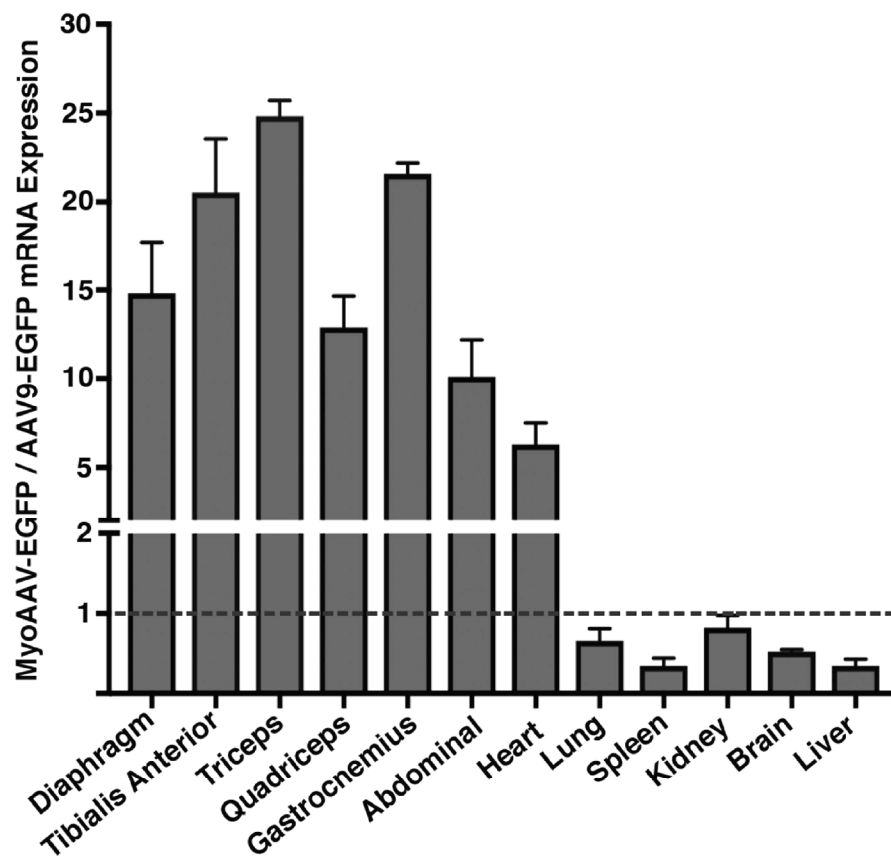


FIG. 21

**FIG. 22**

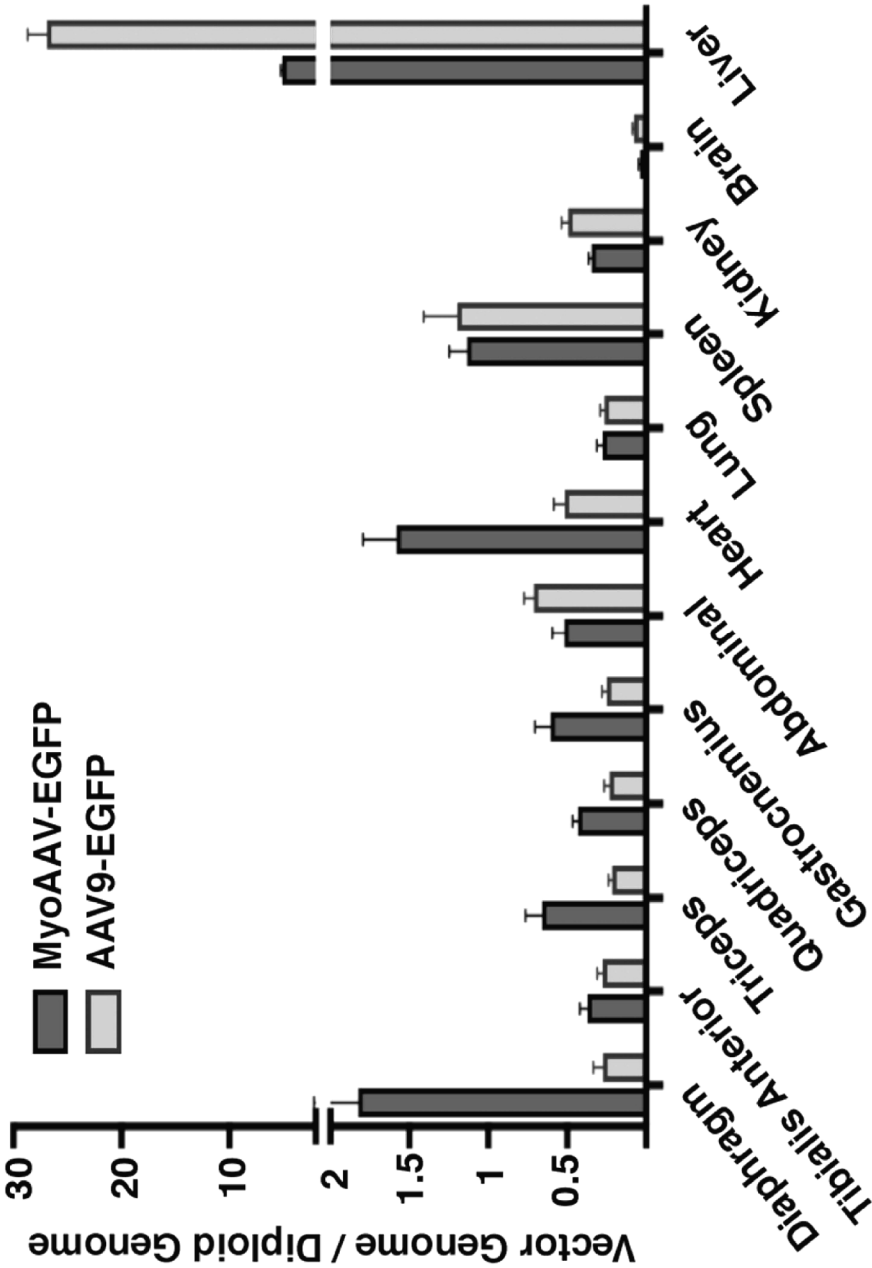


FIG. 23

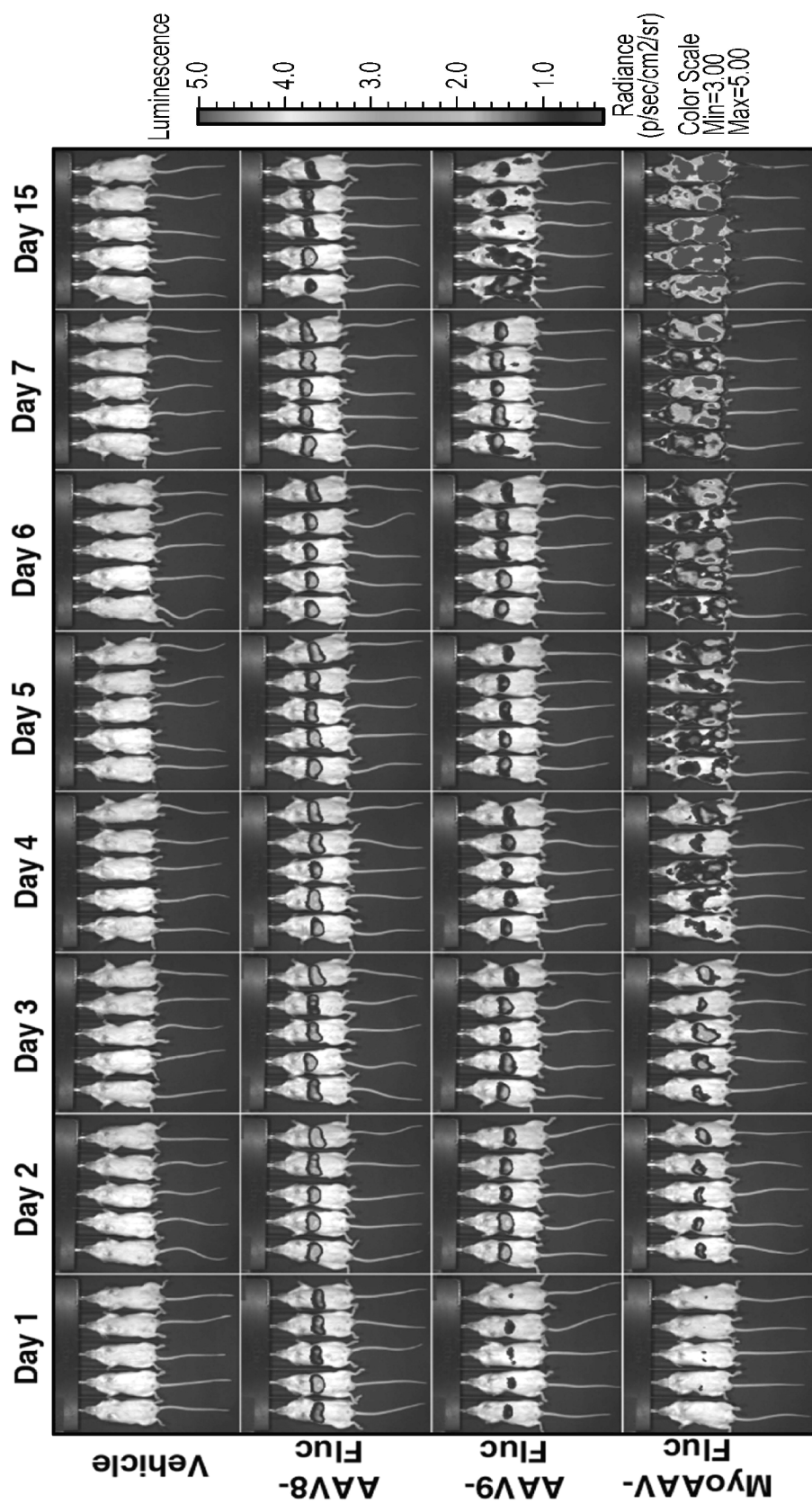


FIG. 24A

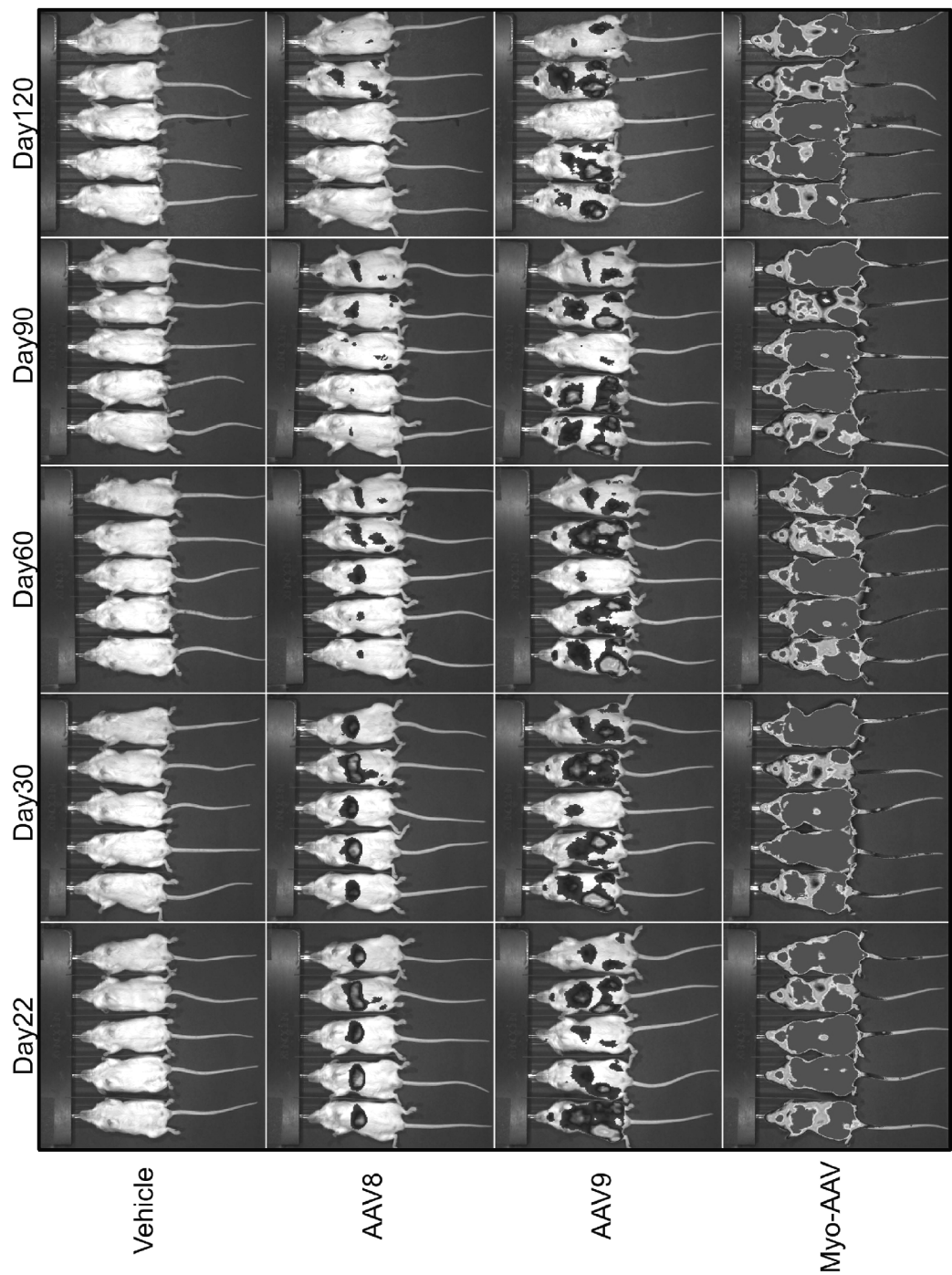


FIG. 24B

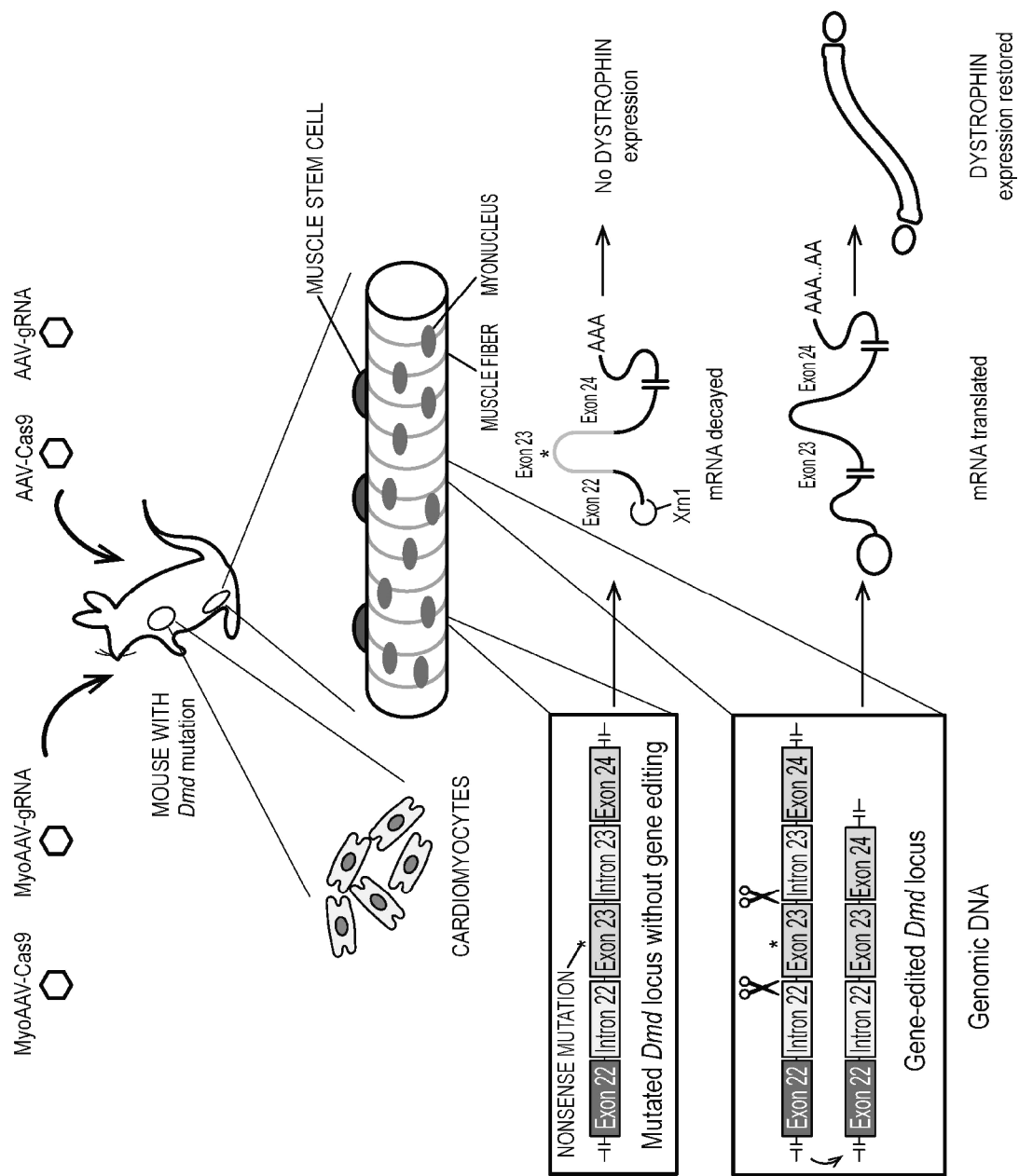


FIG. 25

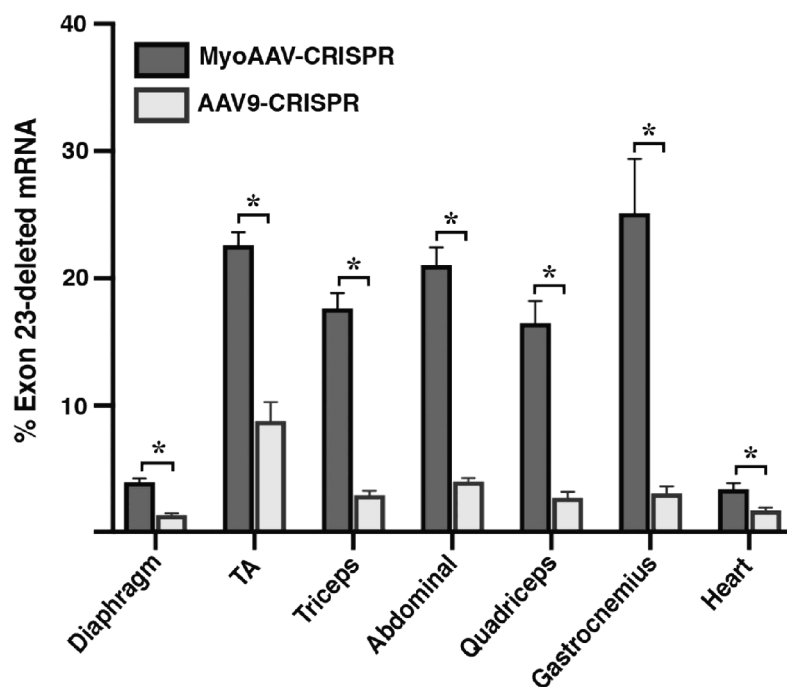


FIG. 26A

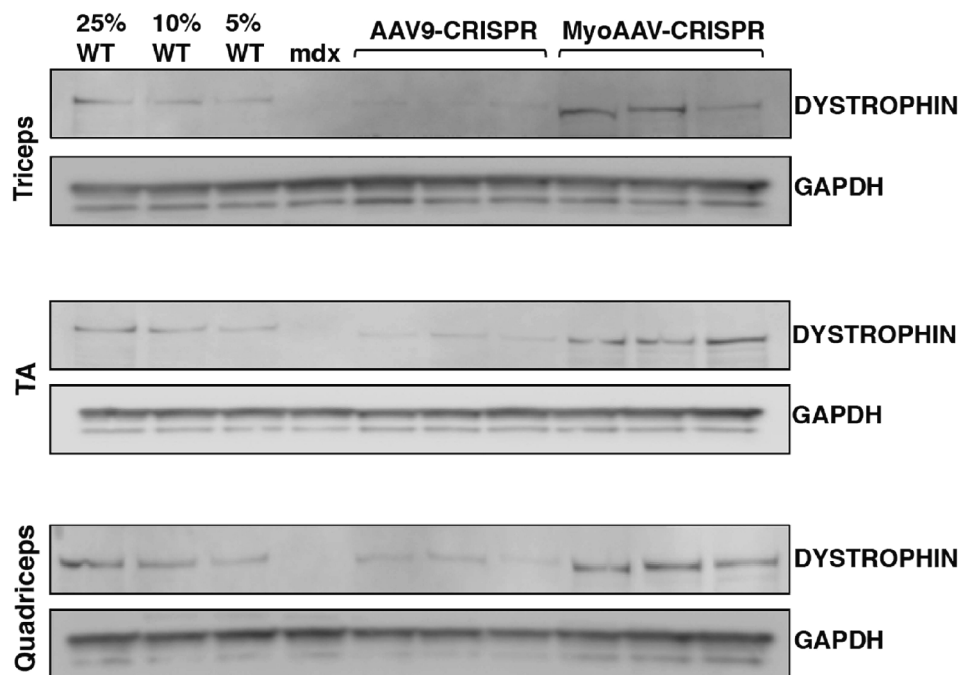


FIG. 26B

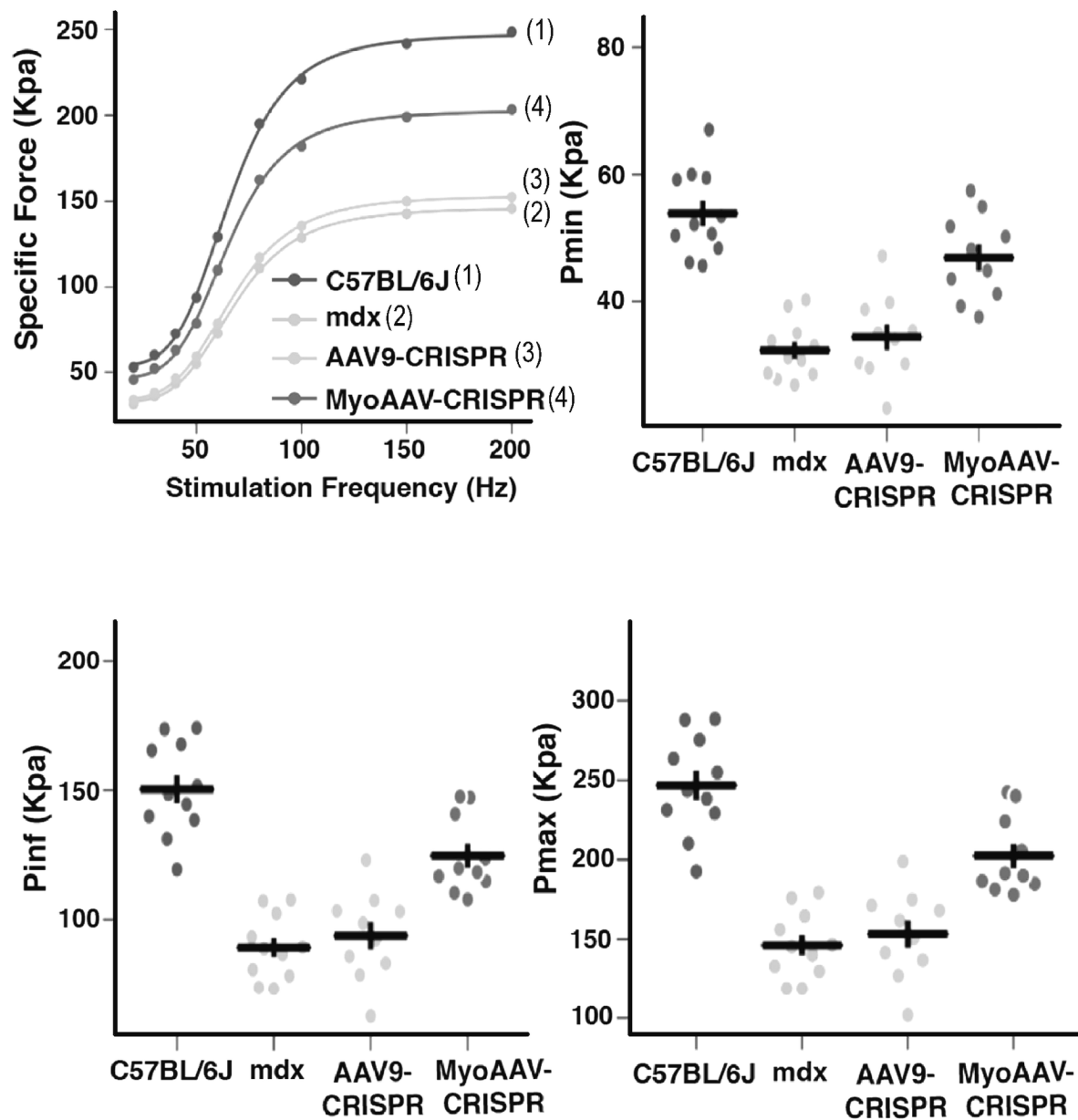


FIG. 26C

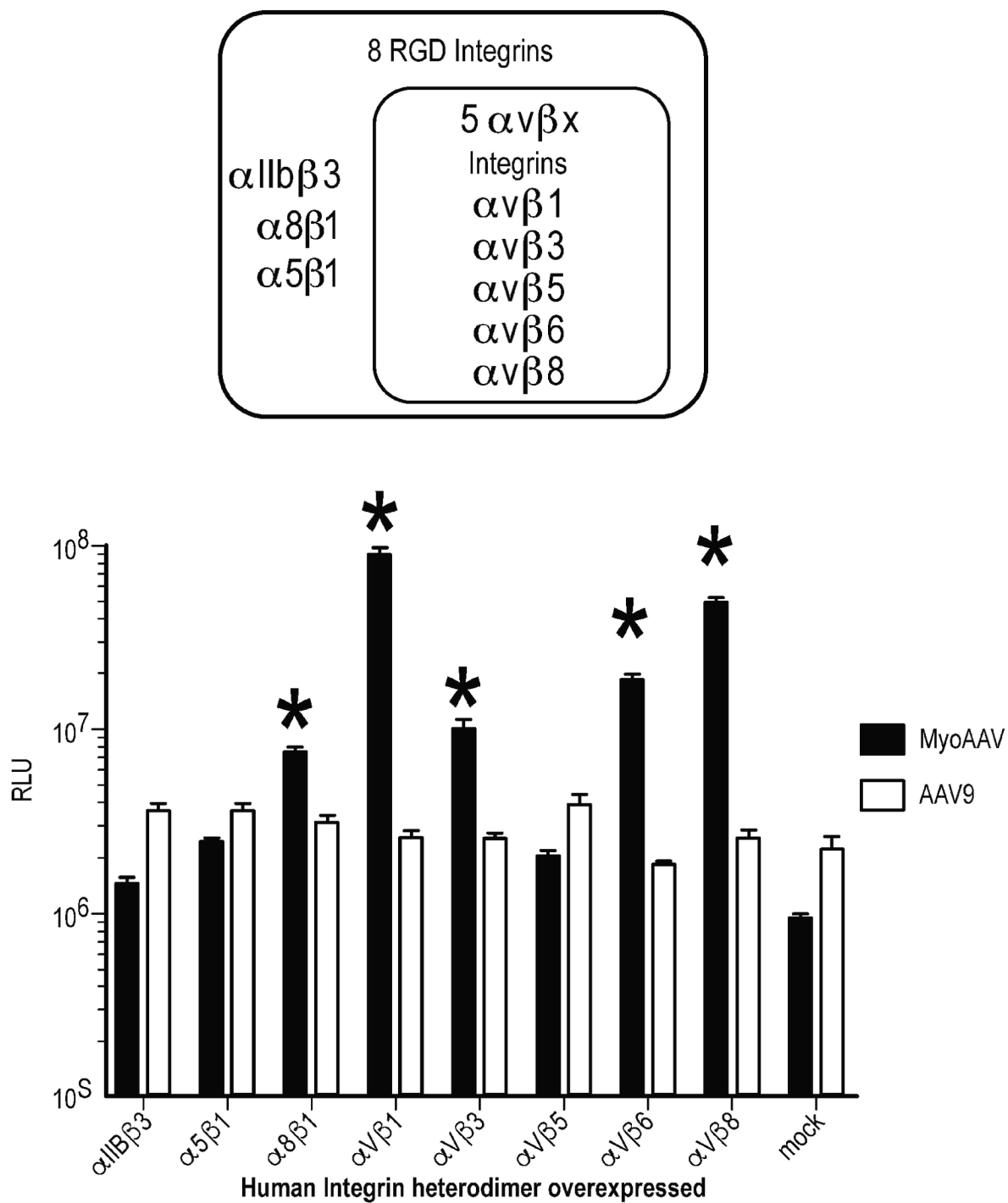


FIG. 27

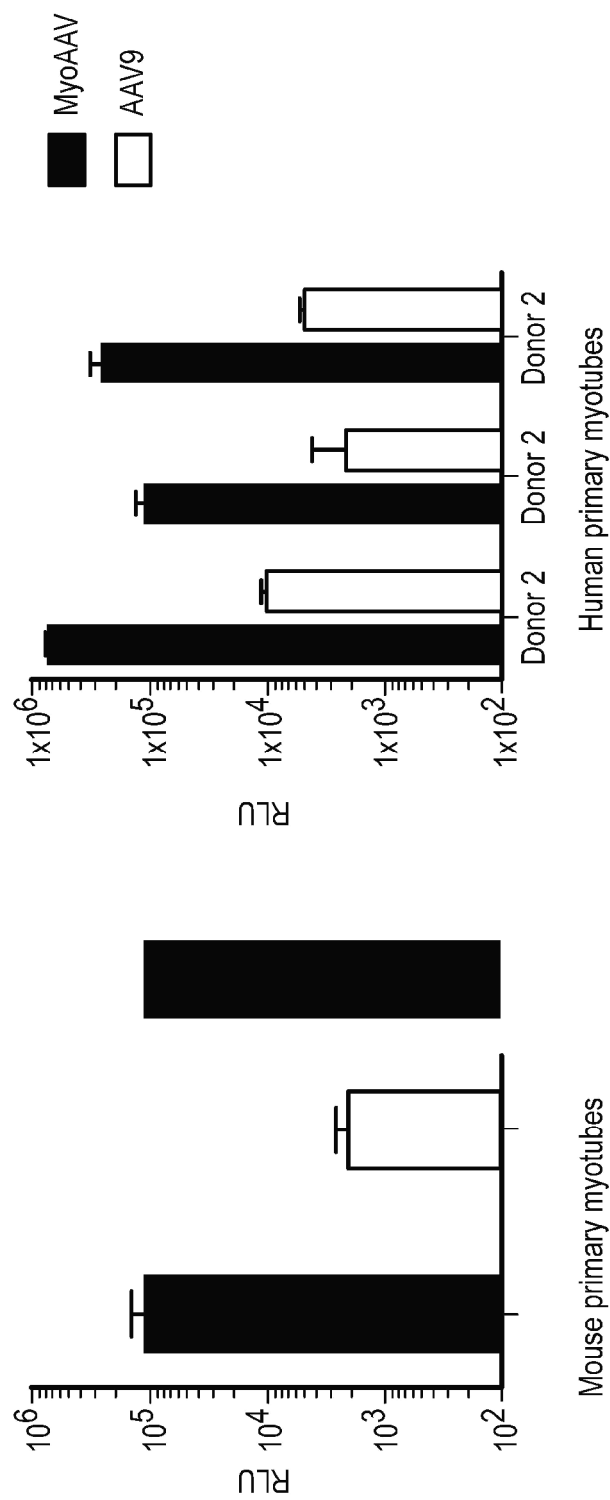
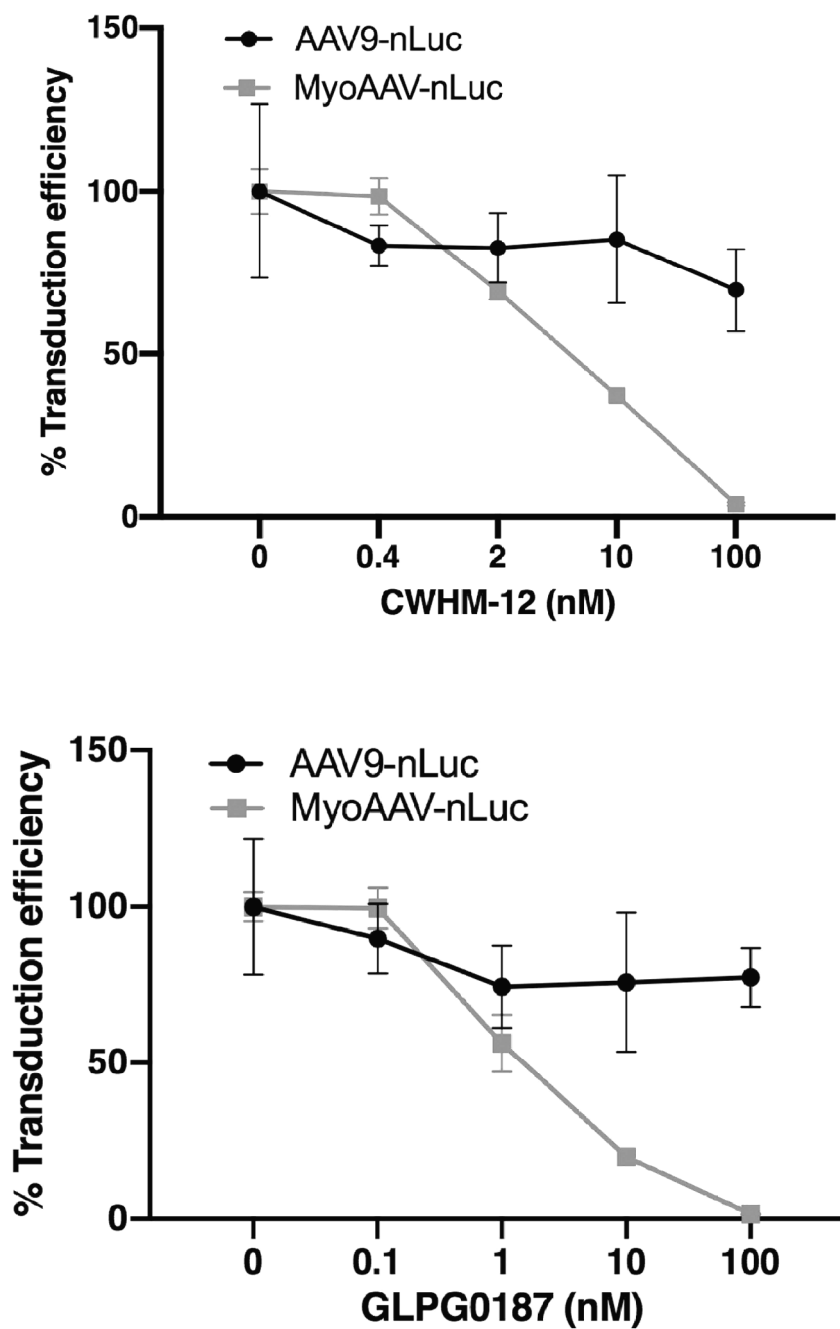
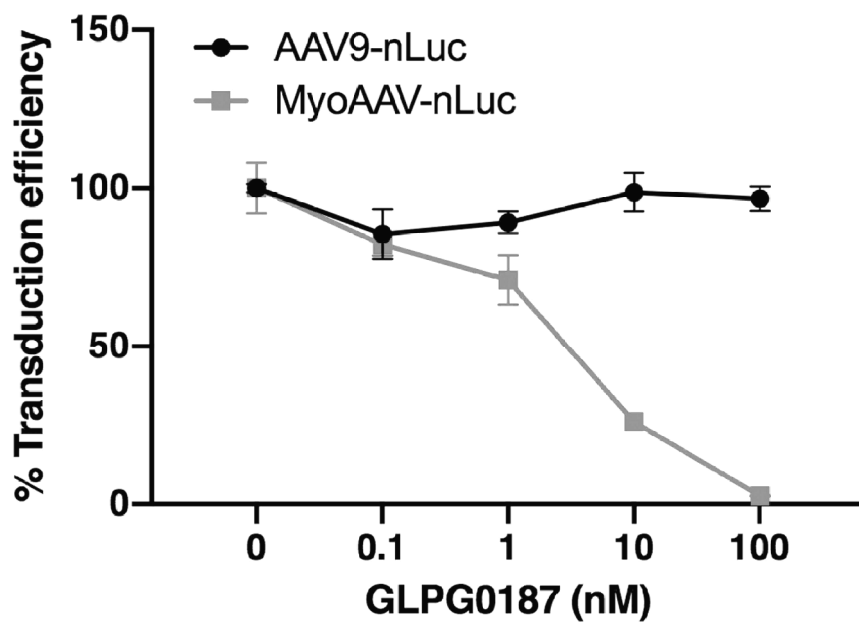
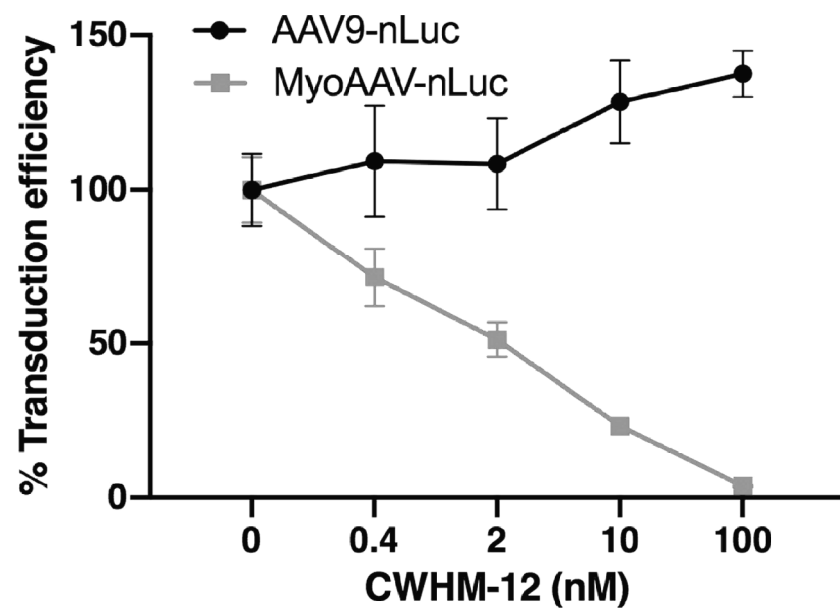


FIG. 28

Human Primary Myotubes**FIG. 29A**

Mouse Primary Myotubes**FIG. 29B**

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**ENGINEERED MUSCLE TARGETING
COMPOSITIONS****CROSS-REFERENCE TO RELATED
APPLICATIONS**

This application is a continuation of U.S. patent application Ser. No. 17/764,509, filed on Mar. 28, 2022, which is the U.S. National Stage Application under 35 U.S.C. § 371 of Patent Cooperation Treaty Application No.: PCT/US2020/056133, filed on Oct. 16, 2020. Patent Cooperation Treaty Application No.: PCT/US2020/056133 claims the benefit of and priority to U.S. Provisional Patent Application Nos. 62/916,207, filed on Oct. 16, 2019; entitled “Engineered Adeno-Associated Virus Capsids”; 62/916,221, filed on Oct. 16, 2019, entitled “Engineered Adeno-Associated Virus Capsids”; 63/018,454, filed on Apr. 30, 2020, entitled “Engineered Adeno-Associated Virus Capsids”; and 63/055,252, filed on Jul. 22, 2020, entitled “Engineered Muscle Targeting Compositions”. The contents of the above-identified applications are hereby fully incorporated herein by reference in their entireties.

SEQUENCE LISTING

The contents of the electronic sequence listing (“BROD-5005US-CON2_ST26.xml”; size is 11,474,790 bytes and it was created on Sep. 24, 2024) is herein incorporated by reference in its entirety.

TECHNICAL FIELD

The subject matter disclosed herein is generally directed to muscle targeting compositions including, but not limited to, recombinant adeno-associated virus (AAV) vectors and systems thereof, compositions, and uses thereof.

BACKGROUND

Recombinant AAVs (rAAVs) are the most commonly used delivery vehicles for gene therapy and gene editing. Nonetheless, rAAVs that contain natural capsid variants have limited cell tropism. Indeed, rAAVs used today mainly infect the liver after systemic delivery. Further, the transduction efficiency of conventional rAAVs in other cell-types, tissues, and organs by these conventional rAAVs with natural capsid variants is limited. Therefore, AAV-mediated polynucleotide delivery for diseased that affect cells, tissues, and organs other than the liver (e.g. nervous system, skeletal muscle, and cardiac muscle) typically requires an injection of a large dose of virus (typically about 1×10^{14} vg/kg), which often results in liver toxicity. Furthermore, because large doses are required when using conventional rAAVs, manufacturing sufficient amounts of a therapeutic rAAV needed to dose adult patients is extremely challenging. Additionally, due to differences in gene expression and physiology, mouse and primate models respond differently to viral capsids. Transduction efficiency of different virus particles varies between different species, and as a result, preclinical studies in mice often do not accurately reflect results in primates, including humans. As such, there exists a need for improved rAAVs for use in the treatment of various genetic diseases.

SUMMARY

Described in certain example embodiments herein are compositions comprising a targeting moiety effective to

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target a muscle cell, wherein the targeting moiety comprises an n-mer motif; and a cargo, wherein the cargo is coupled to or is otherwise associated with the targeting moiety.

In certain example embodiments, the n-mer motif comprises an RGD motif or a non-RGD n-mer motif.

In certain example embodiments, the RGD motif has a formula of $X_m\text{RGDX}_n$, wherein m is 0-4 amino acids, wherein n is 0-15 amino acids, wherein X is any amino acid, and wherein each X amino acid present is independently selected from the others from the group consisting of: any amino acid.

In certain example embodiments, the RGD motif has the formula RGDX_n , wherein n is 4 or 5, wherein X is any amino acid, and wherein each X amino acid present is independently selected from the others from the group consisting of: any amino acid.

In certain example embodiments, the n-mer motif is any one of SEQ ID NO: 13-50, 1277-2493, 3737-4979, 6647-8313, 8314-8502, or 8692-8889.

In certain example embodiments, the targeting moiety comprises a polypeptide, a polynucleotide, a lipid, a polymer, a sugar, or a combination thereof.

In certain example embodiments, the targeting moiety comprises a viral protein.

In certain example embodiments, the viral protein is a capsid protein.

In certain example embodiments, the viral protein is an adeno associated virus (AAV) protein.

In certain example embodiments, the n-mer motif is located between two amino acids of the viral protein such that the n-mer motif is external to a viral capsid of which the viral capsid protein is part.

In certain example embodiments, the n-mer motif is inserted between any two contiguous amino acids between amino acids 262-269, 327-332, 382-386, 452-460, 488-505, 527-539, 545-558, 581-593, 704-714, or any combination thereof in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide.

In certain example embodiments, the n-mer motif is inserted between amino acids 588 and 589 in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide.

In certain example embodiments, the composition is an engineered viral particle.

In certain example embodiments, the engineered viral particle is an engineered AAV viral particle.

In certain example embodiments, the AAV viral particle is an engineered AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV rh.74, or AAV rh.10 viral particle.

In certain example embodiments, the cargo is capable of treating or preventing a muscle disease or disorder.

In certain example embodiments, the muscle disease or disorder is

- a. an auto immune disease;
- b. a cancer;
- c. a muscular dystrophy;
- d. a neuro-muscular disease;
- e. a sugar or glycogen storage disease;
- f. an expanded repeat disease;
- g. a dominant negative disease;
- h. a cardiomyopathy;
- i. a viral disease;
- j. a progeroid disease; or
- k. any combination thereof.

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In certain example embodiments, the cargo is

- a. a morpholino;
- b. a peptide-linked morpholino;
- c. an antisense oligonucleotide;
- d. a PMO, a therapeutic transgene;
- e. a polynucleotide encoding a therapeutic polypeptide or peptide;
- f. a PPMO;
- g. one or more peptides or polypeptides;
- h. one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both;
- i. a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule;
- j. a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein; or
- k. any combination thereof.

In certain example embodiments, the cargo is capable of inducing exon skipping in a gene.

In certain example embodiments, the cargo is capable of inducing exon skipping in a dystrophin gene.

In certain example embodiments, the cargo is a mini- or micro-dystrophin gene.

In certain example embodiments, the mini- or micro-dystrophin gene comprises spectrin-like repeats 1, 1', 2, 3, 16, 17, 20, 21, 22, 23, 24, or any combination thereof, and optionally an nNOS domain, an actin binding domain, one or more hinge regions, a dystroglycan binding domain, or any combination thereof.

In certain example embodiments, the cargo is operably coupled to a muscle specific promoter.

In certain example embodiments, the expanded repeat disease is Huntington's disease, a Myotonic Dystrophy, or Facioscapulohumeral muscular dystrophy (FSHD).

In certain example embodiments, the muscular dystrophy is Duchene muscular dystrophy, Becker Muscular dystrophy, a Limb-Girdle muscular dystrophy, an Emery Dreifuss muscular dystrophy, a myotonic dystrophy, or FSHD.

In certain example embodiments, the myotonic dystrophy is a Type 1 or a Type 2 myotonic dystrophy.

In certain example embodiments, the cardiomyopathy is dilated cardiomyopathy, hypertrophic cardiomyopathy, Duchene muscular dystrophy-associated cardiomyopathy, or Dannon disease.

In certain example embodiments, the sugar or glycogen storage disease is a MPS type III disease or Pompe disease.

In certain example embodiments, the MPS type III disease, is MPS Type IIIA, IIIB, IIIC, or IIID.

In certain example embodiments, the neuro-muscular disease is Charcot-Marie-Tooth disease or Friedreich's Ataxia.

In certain example embodiments, the composition has increased muscle cell potency, muscle cell specificity, reduced immunogenicity, or any combination thereof.

Described in certain example embodiments herein are vector systems comprising a vector comprising: one or more polynucleotides each encoding all or part of one or more targeting moieties effective to target a muscle cell, wherein each targeting moiety comprises one or more n-mer motifs, wherein each n-mer motif an RGD motif or a non-RGD n-mer motif, and wherein each polynucleotide at least encodes one or more of the one or more n-mer motifs; and optionally, a regulatory element operatively coupled to one or more of the one or more polynucleotides.

In certain example embodiments, the RGD motif has a formula of $X_m\text{RGDX}_n$, wherein m is 0-4 amino acids, wherein n is 0-15 amino acids, wherein X is any amino acid,

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and wherein each X amino acid present is independently selected from the others from the group consisting of: any amino acid.

In certain example embodiments, the RGD motif has the formula RGDX_n , wherein n is 4 or 5, wherein X is any amino acid, and wherein each X amino acid present is independently selected from the others from the group consisting of: any amino acid.

In certain example embodiments, the n-mer motif is any one of SEQ ID NO: 13-50, 1277-2493, 3737-4979, 6647-8313, 8314-8502, or 8692-8889.

In certain example embodiments, the vector system further comprises a cargo.

In certain example embodiments, the cargo is a cargo polynucleotide and is optionally coupled to one or more of the one or more polynucleotides encoding the targeting moiety, the regulatory element, or both.

In certain example embodiments, the cargo polynucleotide is present on the same vector or a different vector as the one or more polynucleotides encoding the targeting moiety.

In certain example embodiments, the vector system is capable of producing virus particles that contain the cargo.

In certain example embodiments, the vector system is capable of producing a viral capsid polypeptide comprising one or more of the targeting moieties.

In certain example embodiments, the vector system is capable of producing AAV virus particles.

In certain example embodiments, AAV viral particles are engineered AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV rh.74, or AAV rh.10 viral particle.

In certain example embodiments, the capsid polypeptide is an engineered AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV rh.74, AAV rh.10 capsid polypeptide.

In certain example embodiments, wherein at least one of the one or more polynucleotides encoding the n-mer motif(s) is inserted between two codons corresponding to two amino acids of the viral protein such that at least one of the n-mer motifs is external to the viral capsid.

In certain example embodiments, the two codons correspond to any two contiguous amino acids between amino acids 262-269, 327-332, 382-386, 452-460, 488-505, 527-539, 545-558, 581-593, 704-714, or any combination thereof in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide.

In certain example embodiments, the two codons correspond to amino acid 588 and 589 in the AAV9 capsid polynucleotide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide.

In certain example embodiments, the vector comprising the one or more polynucleotides each encoding all or part of one or more targeting moieties does not comprise splice regulatory elements.

In certain example embodiments, the vector system further comprises a polynucleotide encoding a viral rep protein.

In certain example embodiments, the viral rep protein is an AAV rep protein.

In certain example embodiments, the polynucleotide encoding the viral rep protein is on the same vector or different vector as the one or more polynucleotides each encoding all or part of one or more targeting moieties.

In certain example embodiments, the viral rep protein is operatively coupled to a regulatory element.

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Described in certain example embodiments herein are polypeptides produced by expressing a vector system as described herein.

In certain example embodiments, the polypeptide is a viral polypeptide.

In certain example embodiments, the viral polypeptide is an AAV polypeptide.

Described in certain example embodiments herein are particles produced by expressing a vector system as described herein.

In certain example embodiments, the particle is a viral particle.

In certain example embodiments, the viral particle is an adeno-associated virus (AAV) particle.

In certain example embodiments, the viral particle has a muscle-specific tropism.

Described in certain example embodiments, a vector system as described herein, a polypeptide as described herein, or a particle as described herein, wherein the cargo is capable of treating or preventing a muscle disease or disorder.

In certain example embodiments, the muscle disease or disorder is

- a. an auto immune disease;
- b. a cancer;
- c. a muscular dystrophy;
- d. a neuro-muscular disease;
- e. a sugar or glycogen storage disease;
- f. an expanded repeat disease;
- g. a dominant negative disease;
- h. a cardiomyopathy;
- i. a viral disease;
- j. a progeroid disease; or
- k. any combination thereof.

In certain example embodiments, the cargo is

- a. a morpholino;
- b. a peptide-linked morpholino;
- c. an antisense oligonucleotide;
- d. a PMO, a therapeutic transgene;
- e. a polynucleotide encoding a therapeutic polypeptide or peptide;
- f. a PPMO;
- g. one or more peptides or polypeptides;
- h. one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both;
- i. a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule;
- j. a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein; or
- k. any combination thereof.

In certain example embodiments, the cargo is capable of inducing exon skipping in a gene.

In certain example embodiments, the cargo is capable of inducing exon skipping in a dystrophin gene.

In certain example embodiments, the cargo is a mini- or micro-dystrophin gene.

In certain example embodiments, the mini- or micro-dystrophin gene comprises spectrin-like repeats 1, 1', 2, 3, 16, 17, 20, 21, 22, 23, 24, or any combination thereof, and optionally an nNOS domain, an actin binding domain, one or more hinge regions, a dystroglycan binding domain, or any combination thereof.

In certain example embodiments, the expanded repeat disease is Huntington's disease, a Myotonic Dystrophy, or Facioscapulohumeral muscular dystrophy (FSHD).

In certain example embodiments, the muscular dystrophy is Duchene muscular dystrophy, Becker Muscular dystro-

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phy, a Limb-Girdle muscular dystrophy, an Emery Dreifuss muscular dystrophy, a myotonic dystrophy, or FSHD.

In certain example embodiments, the myotonic dystrophy is Type 1 or Type 2.

5 In certain example embodiments, the cardiomyopathy is dilated cardiomyopathy, hypertrophic cardiomyopathy, DMD-associated cardiomyopathy, or Dannon disease.

In certain example embodiments, the sugar or glycogen storage disease is a MPS type III disease or Pompe disease.

10 In certain example embodiments, the MPS type III disease, is MPS Type IIIA, IIIB, IIIC, or IIID.

In certain example embodiments, the neuro-muscular disease is Charcot-Marie-Tooth disease or Friedreich's Ataxia.

In certain example embodiments, the polypeptide, the particle, or both have increased muscle cell potency, muscle cell specificity, reduced immunogenicity, or any combination thereof.

A cell comprising:

- a. a composition as described herein;
- b. a vector system as described herein;
- c. a polypeptide as described herein;
- d. a particle as described herein; or
- e. a combination thereof.

25 In certain example embodiments, wherein the cell is prokaryotic.

In certain example embodiments, wherein the cell is eukaryotic.

A pharmaceutical formulation comprising:

- 30 a. a composition as described herein;
- b. a vector system as described herein;
- c. a polypeptide as described herein;
- d. a particle as described herein;
- e. a cell as described herein; or
- 35 f. a combination thereof; and

a pharmaceutically acceptable carrier.

A method comprising:

administering, to a subject in need thereof, a

- a. a composition as described herein;
- b. a vector system as described herein;
- c. a polypeptide as described herein;
- d. a particle as described herein;
- e. a cell as described herein;
- f. a pharmaceutical formulation as described herein; or
- 45 g. a combination thereof.

In certain example embodiments, the subject in need thereof has a muscle disease or disorder.

In certain example embodiments, the muscle disease or disorder is

- 50 a. an auto immune disease;
- b. a cancer;
- c. a muscular dystrophy;
- d. a neuro-muscular disease;
- e. a sugar or glycogen storage disease;
- f. an expanded repeat disease;
- g. a dominant negative disease;
- h. a cardiomyopathy;
- i. a viral disease;
- j. a progeroid disease; or
- 60 k. any combination thereof.

In certain example embodiments, the expanded repeat disease is Huntington's disease, a Myotonic Dystrophy, or Facioscapulohumeral muscular dystrophy (FSHD).

65 In certain example embodiments, the muscular dystrophy is Duchene muscular dystrophy, Becker Muscular dystrophy, a Limb-Girdle muscular dystrophy, an Emery Dreifuss muscular dystrophy, a myotonic dystrophy, or FSHD.

In certain example embodiments, the myotonic dystrophy is Type 1 or Type 2.

In certain example embodiments, the cardiomyopathy is dilated cardiomyopathy, hypertrophic cardiomyopathy, DMD-associated cardiomyopathy, or Dannon disease.

In certain example embodiments, the sugar or glycogen storage disease is a MPS type III disease or Pompe disease.

In certain example embodiments, the MPS type III disease, is MPS Type IIIA, IIIB, IIIC, or IIID.

In certain example embodiments, the neuro-muscular disease is Charcot-Marie-Tooth disease or Friedreich's Ataxia.

These and other embodiments, objects, features, and advantages of the example embodiments will become apparent to those having ordinary skill in the art upon consideration of the following detailed description of illustrated example embodiments.

BRIEF DESCRIPTION OF THE DRAWINGS

An understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention may be utilized, and the accompanying drawings of which:

FIG. 1 demonstrates the adeno-associated virus (AAV) transduction mechanism, which results in production of mRNA from the transgene.

FIG. 2 shows a graph that can demonstrate that mRNA-based selection of AAV variants can be more stringent than DNA-based selection. The virus library was expressed under the control of a CMV promoter.

FIGS. 3A-3B show graphs that can demonstrate a correlation between the virus library and vector genome DNA (FIG. 3A) and mRNA (FIG. 3B) in the liver.

FIGS. 4A-4F show graphs that can demonstrate capsid variants present at the DNA level and expressed at the mRNA level identified in different tissues. For this experiment, the virus library was expressed under the control of a CMV promoter.

FIGS. 5A-5C show graphs that can demonstrate capsid mRNA expression in different tissues under the control of cell-type specific promoters (as noted on x-axis). CMV was included as an exemplary constitutive promoter. CK8 is a muscle-specific promoter. MHCK7 is a muscle-specific promoter. hSyn is a neuron specific promoter. Expression levels from the cell type-specific promoters have been normalized based on expression levels from the constitutive CMV promoter in each tissue.

FIG. 6 shows a schematic demonstrating embodiments of a method of producing and selecting capsid variants for tissue-specific gene delivery across species.

FIG. 7 shows a schematic demonstrating embodiments of generating an AAV capsid variant library, particularly insertion of a random n-mer (n=3-15 amino acids) into a wild-type AAV, e.g. AAV9.

FIG. 8 shows a schematic demonstrating embodiments of generating an AAV capsid variant library, particularly variant AAV particle production. Each capsid variant encapsulates its own coding sequence as the vector genome.

FIG. 9 shows schematic vector maps of representative AAV capsid plasmid library vectors (see e.g. FIG. 8) that can be used in an AAV vector system to generate an AAV capsid variant library.

FIG. 10 shows a graph that can demonstrate the viral titer (calculated as AAV9 vector genome/15 cm dish) produced

by constructs containing different constitutive and cell-type specific mammalian promoters.

FIGS. 11A-11F show graphs that can demonstrate the results obtained after the first round of selection in C57BL/6 mice using a capsid library expressed under the control of the MHCK7 muscle-specific promoter.

FIGS. 12A-12D show graphs that can demonstrate the results obtained after the second round of selection in C57BL/6 mice using a capsid library expressed under the control of the MHCK7 muscle-specific promoter.

FIGS. 13A-13B shows graphs that can demonstrate a correlation between the abundance of variants encoded by synonymous codons.

FIG. 14 shows a graph that can demonstrate a correlation between the abundance of the same variants expressed under the control of two different muscle specific promoters (MHCK7 and CK8).

FIG. 15 shows a graph that can demonstrate muscle-tropic capsid variants that produce rAAV with similar titers to wild-type AAV9 capsid.

FIG. 16 shows images that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 17 shows a panel of images that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-G.

FIG. 18 shows a panel of images that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GF.

FIG. 19 shows a schematic of selection of potent capsid variants for muscle-directed gene delivery across species.

FIGS. 20A-20C show tables that can demonstrate selection in different strains of mice identifies the same variants as the top muscle-tropic hits.

FIG. 21 shows images that can demonstrate a comparison of mouse muscle transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 22 shows graphs that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 23 shows graphs that can demonstrate a comparison of vector genome biodistribution between rAAV9-GFP and rMyoAAV-GFP.

FIGS. 24A-24B show images that can demonstrate faster kinetics of in vivo gene expression in muscle by MyoAAV as compared to AAV9 and AAV8.

FIG. 25 can demonstrate a mechanism of correction of a DMD mutation in model mdx mice by MyoAAV-CRISPR as compared to AAV9-CRISPR.

FIGS. 26A-26C can demonstrate correction of a DMD mutation in model mdx mice with MyoAAV-CRISPR as compared to AAV9-CRISPR.

FIG. 27 can demonstrate that MyoAAV uses integrin heterodimers as the receptor to enter cells.

FIG. 28 shows graphs that can demonstrate that myoAAV can transduce both mouse and human primary myotubes 50-100 times more effectively than AAV9.

FIGS. 29A-29B can demonstrate that integrin alpha V small molecule inhibitors suppress transduction of human primary myotubes by MyoAAV.

The figures herein are for illustrative purposes only and are not necessarily drawn to scale.

DETAILED DESCRIPTION OF THE EXAMPLE EMBODIMENTS

General Definitions

Unless defined otherwise, technical and scientific terms used herein have the same meaning as commonly under-

stood by one of ordinary skill in the art to which this disclosure pertains. Definitions of common terms and techniques in molecular biology may be found in *Molecular Cloning: A Laboratory Manual*, 2nd edition (1989) (Sambrook, Fritsch, and Maniatis); *Molecular Cloning: A Laboratory Manual*, 4th edition (2012) (Green and Sambrook); *Current Protocols in Molecular Biology* (1987) (F. M. Ausubel et al. eds.); the series *Methods in Enzymology* (Academic Press, Inc.); *PCR 2: A Practical Approach* (1995) (M. J. MacPherson, B. D. Hames, and G. R. Taylor eds.); *Antibodies, A Laboratory Manual* (1988) (Harlow and Lane, eds.); *Antibodies A Laboratory Manual*, 2nd edition 2013 (E. A. Greenfield ed.); *Animal Cell Culture* (1987) (R. I. Freshney, ed.); Benjamin Lewin, *Genes IX*, published by Jones and Bartlett, 2008 (ISBN 0763752223); Kendrew et al. (eds.), *The Encyclopedia of Molecular Biology*, published by Blackwell Science Ltd., 1994 (ISBN 0632021829); Robert A. Meyers (ed.), *Molecular Biology and Biotechnology: a Comprehensive Desk Reference*, published by VCH Publishers, Inc., 1995 (ISBN 9780471185710); Singleton et al., *Dictionary of Microbiology and Molecular Biology* 2nd ed., J. Wiley & Sons (New York, N.Y. 1994), March, *Advanced Organic Chemistry Reactions, Mechanisms and Structure* 4th ed., John Wiley & Sons (New York, N.Y. 1992); and Marten H. Hofker and Jan van Deursen, *Transgenic Mouse Methods and Protocols*, 2nd edition (2011).

As used herein, the singular forms “a”, “an”, and “the” include both singular and plural referents unless the context clearly dictates otherwise.

The term “optional” or “optionally” means that the subsequent described event, circumstance or substituent may or may not occur, and that the description includes instances where the event or circumstance occurs and instances where it does not.

The recitation of numerical ranges by endpoints includes all numbers and fractions subsumed within the respective ranges, as well as the recited endpoints. It will be further understood that the endpoints of each of the ranges are significant both in relation to the other endpoint, and independently of the other endpoint. It is also understood that there are a number of values disclosed herein, and that each value is also herein disclosed as “about” that particular value in addition to the value itself. For example, if the value “10” is disclosed, then “about 10” is also disclosed. Ranges can be expressed herein as from “about” one particular value, and/or to “about” another particular value. Similarly, when values are expressed as approximations, by use of the antecedent “about,” it will be understood that the particular value forms a further embodiment. For example, if the value “about 10” is disclosed, then “10” is also disclosed.

It is to be understood that such a range format is used for convenience and brevity, and thus, should be interpreted in a flexible manner to include not only the numerical values explicitly recited as the limits of the range, but also to include all the individual numerical values or sub-ranges encompassed within that range as if each numerical value and sub-range is explicitly recited. To illustrate, a numerical range of “about 0.1% to 5%” should be interpreted to include not only the explicitly recited values of about 0.1% to about 5%, but also include individual values (e.g., about 1%, about 2%, about 3%, and about 4%) and the sub-ranges (e.g., about 0.5% to about 1.1%; about 5% to about 2.4%; about 0.5% to about 3.2%, and about 0.5% to about 4.4%, and other possible sub-ranges) within the indicated range.

Where a range is expressed, a further embodiment includes from the one particular value and/or to the other particular value.

Where a range of values is provided, it is understood that each intervening value, to the tenth of the unit of the lower limit unless the context clearly dictates otherwise, between the upper and lower limit of that range and any other stated or intervening value in that stated range, is encompassed within the disclosure. The upper and lower limits of these smaller ranges may independently be included in the smaller ranges and are also encompassed within the disclosure, subject to any specifically excluded limit in the stated range. Where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the disclosure. For example, where the stated range includes one or both of the limits, ranges excluding either or both of those included limits are also included in the disclosure, e.g. the phrase “x to y” includes the range from ‘x’ to ‘y’ as well as the range greater than ‘x’ and less than ‘y’. The range can also be expressed as an upper limit, e.g. ‘about x, y, z, or less’ and should be interpreted to include the specific ranges of ‘about x’, ‘about y’, and ‘about z’ as well as the ranges of ‘less than x’, ‘less than y’, and ‘less than z’. Likewise, the phrase ‘about x, y, z, or greater’ should be interpreted to include the specific ranges of ‘about x’, ‘about y’, and ‘about z’ as well as the ranges of ‘greater than x’, ‘greater than y’, and ‘greater than z’. In addition, the phrase “about ‘x’ to ‘y’”, where ‘x’ and ‘y’ are numerical values, includes “about ‘x’ to about ‘y’”.

The terms “about” or “approximately” as used herein when referring to a measurable value such as a parameter, an amount, a temporal duration, and the like, are meant to encompass variations of and from the specified value, such as variations of $\pm 10\%$ or less, $\pm 5\%$ or less, $\pm 1\%$ or less, and $\pm 0.1\%$ or less of and from the specified value, insofar such variations are appropriate to perform in the disclosed invention. It is to be understood that the value to which the modifier “about” or “approximately” refers is itself also specifically, and preferably, disclosed. As used herein, the terms “about,” “approximate,” “at or about,” and “substantially” can mean that the amount or value in question can be the exact value or a value that provides equivalent results or effects as recited in the claims or taught herein. That is, it is understood that amounts, sizes, formulations, parameters, and other quantities and characteristics are not and need not be exact, but may be approximate and/or larger or smaller, as desired, reflecting tolerances, conversion factors, rounding off, measurement error and the like, and other factors known to those of skill in the art such that equivalent results or effects are obtained. In some circumstances, the value that provides equivalent results or effects cannot be reasonably determined. In general, an amount, size, formulation, parameter or other quantity or characteristic is “about,” “approximate,” or “at or about” whether or not expressly stated to be such. It is understood that where “about,” “approximate,” or “at or about” is used before a quantitative value, the parameter also includes the specific quantitative value itself, unless specifically stated otherwise.

As used herein, a “biological sample” may contain whole cells and/or live cells and/or cell debris. The biological sample may contain (or be derived from) a “bodily fluid”. The present invention encompasses embodiments wherein the bodily fluid is selected from amniotic fluid, aqueous humour, vitreous humour, bile, blood serum, breast milk, cerebrospinal fluid, cerumen (earwax), chyle, chyme, endolymph, perilymph, exudates, feces, female ejaculate, gastric acid, gastric juice, lymph, mucus (including nasal drainage

and phlegm), pericardial fluid, peritoneal fluid, pleural fluid, pus, rheum, saliva, sebum (skin oil), semen, sputum, synovial fluid, sweat, tears, urine, vaginal secretion, vomit and mixtures of one or more thereof. Biological samples include cell cultures, bodily fluids, cell cultures from bodily fluids. Bodily fluids may be obtained from a mammal organism, for example by puncture, or other collecting or sampling procedures.

The terms "subject," "individual," and "patient" are used interchangeably herein to refer to a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are not limited to, murines, simians, humans, farm animals, sport animals, and pets. Tissues, cells and their progeny of a biological entity obtained in vivo or cultured in vitro are also encompassed.

Various embodiments are described hereinafter. It should be noted that the specific embodiments are not intended as an exhaustive description or as a limitation to the broader embodiments discussed herein. One embodiment described in conjunction with a particular embodiment is not necessarily limited to that embodiment and can be practiced with any other embodiment(s). Reference throughout this specification to "one embodiment," "an embodiment," "an example embodiment," means that a particular feature, structure or characteristic described in connection with the embodiment is included in at least one embodiment of the present invention. Thus, appearances of the phrases "in one embodiment," "in an embodiment," or "an example embodiment" in various places throughout this specification are not necessarily all referring to the same embodiment, but may. Furthermore, the particular features, structures or characteristics may be combined in any suitable manner, as would be apparent to a person skilled in the art from this disclosure, in one or more embodiments. Furthermore, while some embodiments described herein include some but not other features included in other embodiments, combinations of features of different embodiments are meant to be within the scope of the invention. For example, in the appended claims, any of the claimed embodiments can be used in any combination.

Reference is made to U.S. Provisional Application No. 62/899,453 and International Application No. PCT/US20/50534.

All publications, published patent documents, and patent applications cited herein are hereby incorporated by reference to the same extent as though each individual publication, published patent document, or patent application was specifically and individually indicated as being incorporated by reference.

Overview

Embodiments disclosed herein provide muscle-specific targeting moieties that can be coupled to or otherwise associated with a cargo. Embodiments disclosed herein provide polypeptides and particles that can incorporate one or more of the muscle-specific targeting moieties. The polypeptides and/or particles can be coupled to, attached to, encapsulate, or otherwise incorporate a cargo, thereby associating the cargo with the targeting moiety(ies).

Embodiments disclosed herein provide muscle-specific targeting moieties that can contain one or more of an n-mer motif as further described herein, an RGD motif as further described herein, or both. In some embodiments, the n-mer motif and/or the RGD motif can confer muscle-specificity of the targeting moiety.

Embodiments disclosed herein provide engineered adeno-associated virus (AAV) capsids that can be engineered to confer cell-specific and/or species-specific tropism to an engineered AAV particle.

Embodiments disclosed herein also provide methods of generating the rAAVs having engineered capsids that can involve systematically directing the generation of diverse libraries of variants of modified surface structures, such as variant capsid proteins. Embodiments of the method of generating rAAVs having engineered capsids can also include stringent selection of capsid variants capable of targeting a specific cell, tissue, and/or organ type. Embodiments of the method of generating rAAVs having engineered capsids can include stringent selection of capsid variants capable of efficient and/or homogenous transduction in at least two or more species.

Embodiments disclosed herein provide vectors and systems thereof capable of producing an engineered AAV described herein.

Embodiments disclosed herein provide cells that can be capable of producing the engineered AAV particles described herein. In some embodiments, the cells include one or more vectors or system thereof described herein.

Embodiments disclosed herein provide engineered AAVs that can include an engineered capsid described herein. In some embodiments, the engineered AAV can include a cargo polynucleotide to be delivered to a cell. In some embodiments, the cargo polynucleotide is a gene modification polynucleotide.

Embodiments disclosed herein provide formulations that can contain an engineered AAV vector or system thereof, an engineered AAV capsid, engineered AAV particles including an engineered AAV capsid described herein, and/or an engineered cell described herein that contains an engineered AAV capsid, and/or an engineered AAV vector or system thereof. In some embodiments, the formulation can also include a pharmaceutically acceptable carrier. The formulations described herein can be delivered to a subject in need thereof or a cell.

Embodiments disclosed herein also provide kits that contain one or more of the one or more of the polypeptides, polynucleotides, vectors, engineered AAV capsids, engineered AAV particles, cells, or other components described herein and combinations thereof and pharmaceutical formulations described herein. In embodiments, one or more of the polypeptides, polynucleotides, vectors, engineered AAV capsids, engineered AAV particles cells, and combinations thereof described herein can be presented as a combination kit.

Embodiments disclosed herein provide methods of using the engineered AAVs having a cell-specific tropism described herein to deliver, for example, a therapeutic polynucleotide to a cell. In this way, the engineered AAVs described herein can be used to treat and/or prevent a disease in a subject in need thereof. Embodiments disclosed herein also provide methods of delivering the engineered AAV capsids, engineered AAV virus particles, engineered AAV vectors or systems thereof and/or formulations thereof to a cell. Also provided herein are methods of treating a subject in need thereof by delivering an engineered AAV particle, engineered AAV capsid, engineered AAV capsid vector or system thereof, an engineered cell, and/or formulation thereof to the subject.

Additional features and advantages of the embodiments engineered AAVs and methods of making and using the engineered AAVs are further described herein.

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Muscle-Specific Targeting Moieties and Compositions Thereof

Described herein are targeting moieties that are capable of specifically targeting, binding, associating with, or otherwise interact specifically with a muscle cell. N-mer motifs are short peptide motifs that can confer cell and/or tissue type-targeting capabilities to another molecule, such as a cargo, to which it is incorporated, coupled to, attached, or otherwise associated with. In one example embodiment, the n-mer motif is incorporated into a viral capsid such that it is expressed on the capsid surface and confers tissue-specific targeting capability to the viral particle to facilitate tissue-specific delivery of viral particle and any optional cargo contained therein. In certain example embodiments, the n-mer motif is about 1-20 amino acids, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 amino acids long. The term n-mer motif encompasses both n-mer motifs that have an RGD motif and those that do not (referred to herein as “non-RGD n-mer motifs”). In some example embodiments, the n-mer motif confers muscle cell/tissue specificity. In some example embodiments, the n-mer motif that confers muscle cell/tissue specificity is an RGD motif. In some example embodiments, the n-mer motif that confers muscle cell/tissue specificity is a non-RGD n-mer motif.

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In some embodiments, the targeting moiety is or includes one or more n-mer motifs, where each of the one or more n-mer motifs is independently selected from an RGD motif or a non-RGD n-mer motif. N-mer motifs, RGD motifs and non-RGD n-mer motifs are described in greater detail elsewhere herein. In some embodiments, the targeting moiety includes more than one n-mer motifs, where each of the more than one n-mer motifs is independently selected from an RGD motif or a non-RGD n-mer motif. In some embodiments, the targeting moiety can include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more n-mer motifs, where each n-mer motif is independently selected from an RGD motif or a non-RGD n-mer motif. In some embodiments, all the n-mer motifs included in the targeting moiety can be the same (i.e. have the same amino acid sequence). In some embodiments where more than one n-mer motif is included, at least two of the n-mer motifs are different from each other (i.e. have a different amino acid sequence). In some embodiments where more than one n-mer motif is included, all the n-mer motifs are different from each other. In some embodiments, each n-mer motif included in the targeting moiety can be any one of those set forth in any of Tables 1-6 and 8-9, which correspond to SEQ ID NOs: 13-50, 1277-2493, 3737-4979, 6647-8313, 8314-8502, or 8692-8889.

TABLE 1

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1	AGGGGTGATCTTTCTACGCCT	60	RGDLSTP	1277	715.366	
2	AGGGGCGACCTGAACCAATAC	61	RGDLNQY	1278	712.149	
3	CGGGGTGATCTTACTACGCCT	62	RGDLTTP	1279	461.536	
4	AGGGGGGATGCGACGGAGCTT	63	RGDATEL	1280	452.77	
5	CGGGGTGATCAGCTTTATCAT	64	RGDQLYH	1281	444.505	
6	AGAGGCGACTTATCCACACCC	65	RGDLSTP	1282	411.692	
7	CGTGGTGATGTGGCGGCTAAG	66	RGDVAAK	1283	371.7	
8	AGAGGAGACTTGACAACCCCA	67	RGDLTTP	1284	361.486	
9	CGGGGTGATCTTAATCAGTAT	68	RGDLNQY	1285	342.712	
10	CGAGGAGACACCATGAGCAAA	69	RGDTMSK	1286	325.632	
11	CGCGGAGACGTAGCCGCCAAA	70	RGDVAAK	1287	315.01	
12	CGGGGGGATACTATGTCTAAG	71	RGDTMSK	1288	309.567	
13	CGGGGTGACGCAACAGAATTG	72	RGDATEL	1289	306.99	
14	GCACGGTCAAACGACTCGGTC	73	ARSNDSV	1290	293.22	
15	CGGGGTGACATGAACAACCTCA	74	RGDMNNS	1291	268.677	
16	ACGATGGGTGCTAATGGTACT	75	TMGANGT	1292	260.853	
17	CCTAATGTTACGCAGTCTTAT	76	PNVTQSY	1293	259.718	
18	CGTTTGGACCTGCAAGTCCAC	77	RLDLQVH	1294	257.65	
19	GGGCTTTCTAAGGCGTCTGAT	78	GLSKASD	1295	255.938	
20	GATCCTGGTCGGACGGGTACG	79	DPGRGTGT	1296	253.325	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
21	TATCGGGGTAGGGAGGATTGG	80	YRGREDW	1297	244.83	
22	AGATACGGAGAATCCATCGAA	81	RYGESIE	1298	231.696	
23	AGTCTGAACAACATGGGATCG	82	SLNNMGS	1299	229.6044	
24	AATAGTGATCAGCGGAATTGG	83	NSDQRNW	1300	229.031	
25	CGTGGTGATATGTCTCGTGAG	84	RGDMSRE	1301	227.081	
26	ATGACTGATGCGAATAGGATT	85	MTDANRI	1302	226.194	
27	GTCTACAACGGCAACGTAGTA	86	VYNGNVV	1303	223.663	
28	CGTGGGGATATGATTAATACG	87	RGDMINT	1304	223.46	
29	AGTGGTCTTTCGCATGGTCAG	88	SGLSHGQ	1305	221.726	
30	ACTGGCCAATTAGTAGGAACC	89	TGQLVGT	1306	221.181	
31	GCTAATTCTATTGGGGTCCG	90	ANSIGGP	1307	220.304	
32	TACAGTCAATCGCTGTCTGAA	91	YSQSLSE	1308	220.02	
33	TATCATAAGTATAGTACGGAT	92	YHKYSTD	1309	217.64	
34	GCTCGTCATGATGAGCATGTG	93	ARHDEHV	1310	217	
35	GCCATAGACTCTATCAAACAA	94	AIDSIKQ	1311	216.071	
36	CGTTTGGACCTGCAAGTCAAC	95	RLDLQVN	1312	215	
37	CGCGGCGACATGATAAACACC	96	RGDMINT	1313	214.271	
38	AGTGTGTTGTCTCAGGCTAAT	97	SVLSQAN	1314	213.907	
39	TTTACGGTGAATCAGGATCTT	98	FTVNQDL	1315	213.78	
40	ACGGATAATGGTCTTCTTG TG	99	TDNGLLV	1316	211.787	
41	TATCAGCAGACTTCTAGTACG	100	YQQTSSST	1317	211.386	
42	ACAGAACAATCTTACTCACGA	101	TEQSYSR	1318	210.762	
43	ATTATGGGGCTTAGTCAGGCT	102	IMGLSQA	1319	208.157	
44	GCTACTGCGCATCAGGATGGT	103	ATAHQDG	1320	207.212	
45	TATAATGCTACTCCTTCGCAG	104	YNATPSQ	1321	206.964	
46	TATACGCAGGGTATTATGAAT	105	YTQGIMN	1322	206.672	
47	GAATCCCTCCCAATCTCTAAA	106	ESLPISK	1323	206.576	
48	GGCACCGTCGTTCCGGGCTCC	107	GTVVPGS	1324	206.111	
49	GGATTAGCTAGTCTACACCTG	108	GLASLHL	1325	204.394	
50	TATATTGTGCGGGTGAGCAG	109	YIAAGEQ	1326	204.24	
51	AACACCTACCCCTTCAACGCC	110	NTYPFNA	1327	203.931	
52	GTTGGTGCGAGTACGGCTTCG	111	VGASTAS	1328	202.92	
53	GGATCCAATACTTAGCAAAC	112	GSNYLAN	1329	202.857	
54	GATACTGGTCGGACGGGTACG	113	DTGRTGT	1330	202.83	
55	AAGCCGAATACGATGAGTGAT	114	KPNTMSD	1331	202.7282	
56	GTAGACAAATCTAGCCCAGTG	115	VDKSSPV	1332	201.849	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
57	AGTTCGGACCCAAAAGGTCAA	116	SSDPKGQ	1333	201.825	
58	TGGCAGACGAATGGTATGCAG	117	WQTNGMQ	1334	201.6943	
59	ACCGGTAGCTTGAACCTCTATG	118	TGSLNSM	1335	201.671	
60	CATTCTAATTCGAGTCAGAAT	119	HSNSSQN	1336	200.954	
61	GGCCGTGACGACCTCACAAAC	120	GRDDLTN	1337	200.911	
62	GATACTTATAAGGGTAAGTGG	121	DTYKGKW	1338	200.7787	
63	TATACGGCGCAGACCGGCTGG	122	YTAQTGW	1339	200	
64	AATCAGGTGGGTGCGTCTGCG	123	NQVGASA	1340	200	
65	ATCGACGTACTGAACGGAAGT	124	IDVLNGS	1341	200	
66	TTTCGGACGGTGTATACTGGT	125	FRTVYTG	1342	200	
67	GGAAACATGGTGACTCCAAAC	126	GNMVTPN	1343	200	
68	GATACTTATAACGGTAAGTGG	127	DTYNGKW	1344	200	
69	ACCATCCAAGACCACATAAAA	128	TIQDHIK	1345	200	
70	GGAGCAAAGGAACCATGGGC	129	GAKGTMG	1346	200	
71	ACGAGGAGCAACTCCGACGAA	130	TRSNSDE	1347	200	
72	GCTACTACTCTTACTGGTGAT	131	ATTLTGD	1348	200	
73	TCATACGGAGGATCTGGCCCC	132	SYGSGSP	1349	198.715	
74	GAAAAATCCGTCGAATCCAAA	133	EKSVESK	1350	196.418	
75	CGAGGCGACACAATGAACTAC	134	RGDTMNY	1351	195.3082	
76	CGGGATCTGGGGCAGACCGGC	135	RDLGQTG	1352	194.34	
77	AGTCCGCAGCTGAGTGTGATG	136	SPQLSVM	1353	194.21	
78	CGAGGAGACAACAGCACACCG	137	RGDNSTP	1354	193.05	
79	CCTATGGCAGGACACCCCCCG	138	PMAGHPP	1355	192.726	
80	ACGGCGTATCAGGCTGGTCTG	139	TAYQAGL	1356	191.778	
81	GTGGTAAACCAAGGAAACCAA	140	VVNQGNQ	1357	191.737	
82	GATAAGACTGAGATGCTGCAG	141	DKTEMLQ	1358	191.13	
83	ACTGTGATGATGAGTACGAGG	142	TVMMSTR	1359	191.063	
84	CAGCAGAATACGCGTTTGCCG	143	QQNTRLP	1360	190.1825	
85	TACCAACACAACCAAGCCAC	144	YQHNQAH	1361	189.595	
86	AATCAGAGTATTAATAATATT	145	NQSINNI	1362	188.654	
87	CGAGGAGACCACAGCACACCG	146	RGDHSTP	1363	187.365	
88	GACTCTACACTTCACTTAAGT	147	DSTLHLS	1364	187.36	
89	GCGAACATAGAAAACACGTCA	148	ANIENTS	1365	187.03	
90	ACAAACGCTGCTCTAGTACCA	149	TNAALVP	1366	185.9743	
91	GGGCAGAAGGAGACTACTGCG	150	GQKETTA	1367	184.457	
92	GAACTTAACACCGCACACGCA	151	ELNTAHA	1368	184.059	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
93	GGTGTTAGTAGTAATTCTGCG	152	GVSSNSA	1369	183.964	
94	AGCACAAACGCGGGACAAAGG	153	STNAGQR	1370	183.571	
95	GAACAACAAAAACAGACAAC	154	EQQKTDN	1371	182.331	
96	GCTGTTGTGAATGAGAATATG	155	AVVNNM	1372	182.3	
97	GGCAGCGTCAGACCAGCGCA	156	GSVSTSA	1373	181.451	
98	GAGTTGGGTAGTCAGCGTATG	157	ELGSQRM	1374	181.36	
99	AGAGGCGACTTATCCACACAC	158	RGDLSTH	1375	181.15	
100	GACCACCAACAAGCCCTAGCT	159	DHQQALA	1376	180.295	
101	AACAGATCTGACGCTCACGAA	160	NRSDAHE	1377	180.265	
102	AATGTTAATGCGCAGAGTAGG	161	NVNAQSR	1378	179.918	
103	ACCCAAGGGAACAACATGGTA	162	TQGNMNV	1379	179.575	
104	ACGGCGCTGAATACGTATCCT	163	TALNTYP	1380	179.568	
105	GTCTCTACATACCTCCTGGCA	164	VSTYLLA	1381	179.172	
106	GGCGGCAACTACAACACAAC	165	GGNYNTT	1382	178.62	
107	AGTAATATTAAGCCGAGATT	166	SNIKPEI	1383	178.567	
108	CCGAGGGTGCATGGTCAGGTT	167	PRVHGQV	1384	178.479	
109	TCTAATTCTAATACTGCTGCT	168	SNSNTAA	1385	178.119	
110	CTTGAGGTGGCGACGAGTCCG	169	LEVATSP	1386	177.75	
111	CACGACGCCGACAAATTAGCT	170	HDADKLA	1387	177.05	
112	GGTGTGTATATTGATGGTCGG	171	GVYIDGR	1388	176.229	
113	TCGATGCAGTCGTATACGATG	172	SMQSYTM	1389	175.538	
114	TCTAAAGGAAACGAACAAATG	173	SKGNEQM	1390	175.311	
115	GGTCGGGATTATGCTATGAGT	174	GRDYAMS	1391	174.17	
116	ACTGATGGTATTTTCAGCCT	175	TDGIFQP	1392	174.014	
117	GGGAGCCCAGTGATAGTAAAC	176	GSPVIVN	1393	173.652	
118	ACATTAACAGACGTTCAACGA	177	TLTDVHR	1394	172.837	
119	AAAAGCGAAGTACCCGCCCGA	178	KSEVPAR	1395	172.72	
120	GTC AACACTGGCGCACTCTTG	179	VNTGALL	1396	172.648	
121	AGTCAGCAGGGITTTACTCTG	180	SQQGFTL	1397	172.124	
122	AATAATAAGTCTGTGCCGGAT	181	NNKSVPD	1398	172.0753	
123	AGTGTGATGGTGGGTACGAAT	182	SVMVGTN	1399	171.86	
124	CGAAACGAAAACACTTACAAC	183	RNENTYN	1400	170.674	
125	CAAGCTAAGTCTATCAATAATC	184	QANLSII	1401	170.5862	
126	CCCGGACGGGACAGCAGAACG	185	PGRDSRT	1402	169.875	
127	TTTCCGGCTAATGGTGGTGCT	186	FPANGGA	1403	169.639	
128	GCTGGTAAGGATCTTAGTAAT	187	AGKDLSN	1404	169.592	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
129	GCACAATTCGAATCAGGCCGA	188	AQFESGR	1405	169.281	
130	GGATACGGCAGTTACAGCAAC	189	GYGSYSN	1406	169.247	
131	ACAATCGTTTCCGCTTACGCC	190	TIVSAYA	1407	168.87	
132	AATGTGAGTCCTAATTGACT	191	NVSPNLT	1408	168.739	
133	AGAGGCGACTTATCAACACCC	192	RGDLSTP	1409	167.66	
134	TTCTTAGAAGGAGTCGCTCAA	193	FLEGVAQ	1410	167.647	
135	GGCTCCGAACGAGGAGAACGA	194	GSEARGER	1411	167.585	
136	TTGAATGTTGGTTCGAGTCTT	195	LNVGSSL	1412	167.104	
137	CGTATTGTGGCTAATGAGCAG	196	RIVANEQ	1413	166.96	
138	CAATCTATCGGCCACCCCGTT	197	QSIGHPV	1414	166.7759	
139	GGTGGTATGTCGGCGCATTCG	198	GGMSAHS	1415	166.775	
140	CATTCTACGAGCTCTATGACG	199	HSTTSMT	1416	166.711	
141	ACTGTAAACGGTACGAACGTA	200	TVNGTNV	1417	166.64	
142	CTTGCGCCTGATAATATTGGG	201	LAPDNIG	1418	166.005	
143	CAAACAGCGACTCTCGTGGCA	202	QTATLVA	1419	165.921	
144	GCATCAGCACCGTCTGAATTC	203	ASAPSEF	1420	165.64	
145	TCGATGGAGGGTCAGCAGCAT	204	SMEGQQH	1421	165.62	
146	CAAGACGTAGGACGCACGAAC	205	QDVGRTN	1422	164.147	
147	GTCTACAACGGCAACGAAGTA	206	VYNGNEV	1423	164.11	
148	GCACAGGCGCAGACAGGCTGG	207	AQAQTGW	1424	163.93	
149	CGGCTGGATCTGACGCATACG	208	RLDLTHT	1425	163.75	
150	GCTGCACACGGCCGCAACAA	209	AAHGREQ	1426	163.577	
151	AGAGGCGACTTATACACACCC	210	RGDLYTP	1427	163.43	
152	GGTATGCAGCAGAGGAGAAG	211	GMQQREK	1428	163.075	
153	CAGACTCAGGCGAGTACTAAT	212	QTQASTN	1429	161.336	
154	CGGGACACCAACGCCCTCGGA	213	RDTNALG	1430	161.225	
155	TCGAGTCAGATTTCTAATAGT	214	SSQISNS	1431	161.063	
156	CAGTCGGTTAATAGTACGAGT	215	QSVNSTS	1432	160.873	
157	GCTCTGGAGAGGGCTCAGTAT	216	ALERAQY	1433	160.837	
158	CATACTGGGCATAGTTCTGTG	217	HTGHSSV	1434	160.068	
159	CGGGGAGACATGACCCGAGCA	218	RGDMTRA	1435	159.605	
160	TTTCAGCGTGATCTTGGGCAT	219	FQRDLGH	1436	159.442	
161	ACAACCGGCGACATAATACGC	220	TTGDIIR	1437	159.11	
162	TCTTTTCAGACGGATCGTGCG	221	SFQTDRA	1438	159.04	
163	CAATCCAGCGACGGCCGAGTG	222	QSSDGRV	1439	158.634	
164	ACTTCTGGGGCTTTGACCCGG	223	TSGALTR	1440	158.32	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
165	AATTCGAATACTGTGAATACG	224	NSNTVNT	1441	157.71	
166	ATCTCCGGTAGTAGCAGTCTA	225	ISGSSSL	1442	157.64	
167	AACGACAAATCAACCAACGTA	226	NDKSTNV	1443	157.594	
168	ATCGTACTTGCTCCACATCG	227	IVLAPTS	1444	157.48	
169	TCAGGCGTCAACTACGGTGTC	228	SGVNYGV	1445	157.321	
170	GTCGGCGCCCAACGGGACCCC	229	VGAQRDP	1446	157.055	
171	ACGGGTATGAATAGTAATAAG	230	TGMNSNK	1447	156.85	
172	ATCGAAGCCTACTCACGAGAC	231	IEAYSRD	1448	156.774	
173	TTACACACAACACTAATGCCC	232	LHTTLMF	1449	156.364	
174	TCTGATAATCATCTGAAGACT	233	SDNHLKT	1450	156.334	
175	CGAAACGAAGACAAAGGAGGA	234	RNEDKGG	1451	156.027	
176	ACGAAGGGTGCTAATGGTACT	235	TKGANGT	1452	155.56	
177	GTCTACAACGGCAACGTAGAA	236	VYNGNVE	1453	155.56	
178	TCAAACAGCGGAGGCAACCAC	237	SNSGGNH	1454	155.294	
179	GTAGCCGCGGGACCAGAAGCG	238	VAAGPEA	1455	154.25	
180	ACGTCTCTTAGTGGTAGTGCG	239	TSLSGSA	1456	153.988	
181	GTTGGCTGCAGAGTAATACT	240	VGLQSNT	1457	153.453	
182	CACACCGCCCACAGCGTGGAC	241	HTAHSVD	1458	153.3866	
183	AACGTGGGAATGAGCTCAACC	242	NVGMSST	1459	153.212	
184	CATGCGGATGTGAATGCTGGG	243	HADVNA	1460	153.21	
185	AAAGCGGACAACTAGTGGAA	244	KAGQLVE	1461	153.178	
186	AGTACTTTTAGTGTGCTGCCT	245	STFSVLP	1462	153.09	
187	CCTCAGTCTCCGAGTCGGGTT	246	PQSPSRV	1463	152.823	
188	CACACCGCCACCCCTAGCAGC	247	HTATLSS	1464	152.8	
189	CTTCCGCGTCATGATCAGTAT	248	LPRHDQY	1465	152.412	
190	CAAGTGAACAACCCACTCACA	249	QVNNPLT	1466	151.574	
191	ACAACAGAAACCGCACGAGGT	250	TTETARG	1467	151.4255	
192	GTTTCATGGGACGTTGACTTAT	251	VHGTLTY	1468	150.654	
193	TATAGTACTGATCTTAGGATG	252	YSTDLRM	1469	150.626	
194	GCACACGCTACCTCAAGCACT	253	AHATSST	1470	150.587	
195	AGGGAGAGTGCTGCTCTGGCG	254	RESAALA	1471	150.506	
196	AAGTACTATAATCAGCAGATT	255	KDTNQOI	1472	150.189	
197	AGTATGCAATCATACCATG	256	SMQSYTM	1473	148.994	
198	ACAGCCTACTCGCCACAGTC	257	TAYSPTV	1474	148.946	
199	GAATCTGCCCAACAAAGAATA	258	ESAHQRI	1475	148.867	
200	AGATACACAACAGCACAAACA	259	RYTTAQQ	1476	148.802	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
201	ACGTCGTGGCGAATGTGAGT	260	TSVANVS	1477	148.731	
202	AGGGATCAGCATACTTCTATT	261	RDQHTSI	1478	148.687	
203	TCTGTTACGTCTTCTGGTCCG	262	SVTSSGP	1479	148.574	
204	GCGGTTGTTCTGAATAGTAAT	263	AVVLNSN	1480	148.476	
205	CCTGGGAATCCGTCTAGTAAT	264	PGNPSSN	1481	147.792	
206	ACGGGGTCTACTACTCAGCTT	265	TGSTTQL	1482	147.767	
207	GCTAATGAGCATAATGTGGGT	266	ANEHNVG	1483	147.569	
208	ATGCAAAGAGAAGCAGCCAAC	267	MQREAAN	1484	147.562	
209	TTAACCGACACAAACACCCGG	268	LTDNTR	1485	147.306	
210	CGAATGACCGAAATATCATAC	269	RMTEISY	1486	146.933	
211	AAAGTGGACATGACCTCCAAA	270	KVDMTSK	1487	146.392	
212	AGAGGAGACTTATCCACACCC	271	RGDLSTP	1488	146.3	
213	CAAGCAAAAGCTAGCACAACT	272	QAKASTT	1489	146.214	
214	CTACCCTCAACAGAACTTTG	273	LPSTETL	1490	145.892	
215	AGTAGTGCGCTTAATGCGTAT	274	SSALNAY	1491	145.667	
216	TCGCTGTATCCTAAGGGGCAG	275	SSDPKGQ	1492	145.644	
217	TTAGACGTGACGAGATGAGA	276	LDVTRMR	1493	145.51	
218	GCGGATGGTGGTGATAAGGGG	277	ADGGDKG	1494	145.45	
219	ATGCTGTCTCAGGTTACGTTG	278	MLSQVTL	1495	145.32	
220	AGTGTTAGTTCTGTGGTGTG	279	SVSSVVL	1496	145.202	
221	ACCGAATCGCAAACCATGAGG	280	TESQTMR	1497	145.0149	
222	TTCGGATCCCAAGAAAACTC	281	FGSQEKL	1498	144.467	
223	ACAGCCGGCGGCGAACGCGCC	282	TAGGERA	1499	144.445	
224	GATCATAGTAAGCAGAGTTCG	283	DHSKQSS	1500	144.0179	
225	ATTGATAGTACTTGAATACG	284	IDSTWNT	1501	143.92	
226	TCGCCTCGCCCCGAACTCCGA	285	SPRPELR	1502	143.362	
227	AGTATTGCGACTGCTACTAGT	286	SIATATS	1503	143.312	
228	GTAATAGGCGGACACGGGACT	287	VIGGHGT	1504	143.136	
229	AGCACCGCCATGTACCCCCAC	288	STAMYPH	1505	142.798	
230	CGGGACTTGAGACCCGTGACG	289	RDLRPVT	1506	142.461	
231	GCTCATCTGACTGATCTTCCG	290	AHLTDLP	1507	142.37	
232	TTTCTGAATAGTACGCAGCTT	291	FLNSTQL	1508	142.276	
233	TTAAACAACAGTGCCACAGTC	292	LNNSATV	1509	142.021	
234	GATCGTCCGAATAATATGACG	293	DRPNNMT	1510	141.945	
235	TCATCGTCAGACTCACCCAGA	294	SSSDSPR	1511	141.849	
236	CGCTTGGACGTTGGAAGCCCG	295	RLDVGSP	1512	141.82	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
237	GCGCAGCAGAGTCTTCATGGT	296	AQQSLHG	1513	141.401	
238	ATGGGGAAGCATGAGGGTCTT	297	MGKHEGL	1514	141.2916	
239	GAGAATGCTCGTGAGGGTGTG	298	ENAREGV	1515	140.87	
240	ACCGTATCTCTCTCGGAAGGC	299	TVSLSEG	1516	140.529	
241	CTTAACACACTAATCGACCGG	300	LNTLIDR	1517	140.256	
242	GAACCTCTCCGTTCGAAACCA	301	ELSVPKP	1518	140.203	
243	AAAGACAAAAACGTATACATA	302	KDKNVYI	1519	140.171	
244	AATGCGAATGGGCCTGTGAGT	303	NANGPVS	1520	140.158	
245	CTTACTACGAATGGTATGCTG	304	LTTNGML	1521	140.147	
246	GCCGGCGAATCTTCACCCACA	305	AGESSTP	1522	139.95	
247	AGTGGGATTGGTACTTATCT	306	SGIGTYS	1523	139.76	
248	GTCAGATCTATGGACGAATTG	307	VRSMDEL	1524	139.74	
249	ATGAACACCGGCTCTTCGAGT	308	MNTGSSS	1525	139.328	
250	GGGGTGACTGTAGGGAGCTT	309	GVTVREL	1526	139.099	
251	CAGATTTTGAATTATAGTGTG	310	QILNYSV	1527	138.991	
252	ATGGCGGGTGAGTATAGGGTT	311	MAGEYRV	1528	138.933	
253	TGGTCGCATGATCGGCCTACT	312	WSHDRPT	1529	138.703	
254	TGCAAAAACAACTCAGAATGC	313	CKNNSEC	1530	138.668	
255	TTGACGACGAATAGTCATTAT	314	LTTNSHY	1531	138.525	
256	ATGCTTGTTTCAGAATACTCCT	315	MLVQNTF	1532	138.3	
257	CGTGGTGCGACTGAGCATGCG	316	RGATEHA	1533	138.186	
258	GCTTCGAATGGGAGTATGGGT	317	ASNGSMG	1534	138.1181	
259	AATAGTTATATCTGTTGGAAG	318	NSYTAGK	1535	137.4033	
260	TCCACCCAAGGAGCATCCTC	319	STQGAIL	1536	137.294	
261	TGGAATACGAATATGGCGATT	320	WNTNMAI	1537	137.17	
262	GTCTCATCGTACGAAAAATA	321	VSSYEKI	1538	137.055	
263	GTGCTGAGTACGGGCGAGCGG	322	VLSTGQR	1539	136.9001	
264	CCTATACCCACGGTTCATCC	323	PIPHGSS	1540	136.523	
265	AACGTGTCACTAACGCAACG	324	NVSLTQT	1541	136.4003	
266	TCTACCATCGGCAACAGCAG	325	STIGNST	1542	136.393	
267	TCTGAGAAGCTGACTGATAAG	326	SEKLTDK	1543	136.36	
268	TCCAAAGACTCGAACATAAGT	327	SKDSNIS	1544	136.166	
269	GCGAATAGTAATCATGAGCGT	328	ANSNHER	1545	136.102	
270	AGGGATACGGGTGATAAGGCT	329	RTGDKA	1546	135.913	
271	AGAACAGACACCCGTCAACC	330	RTDTPST	1547	135.583	
272	CCTACTATGTCGAGTCTGAAT	331	PTMSSLN	1548	135.539	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
273	GATATTACTAATCAGTCGTAT	332	DITNQS	1549	135.473	
274	CTTGTAACCGGAACTGG	333	LVPETW	1550	134.988	
275	GGGACTTCCTTGAAAACCGA	334	GTSLNR	1551	134.981	
276	GCTGCTGGTAATCCTACTCGT	335	AAGNPTR	1552	134.779	
277	CACAACGTCGGCTAGGACAC	336	HNVLGH	1553	134.677	
278	GTATCAACGACAACGGACCGG	337	VSTTDR	1554	134.639	
279	TATTTGTCGTCTGGTAAGATG	338	YLSSGKM	1555	134.553	
280	GATAGTCGGAATGCTGCTTG	339	DSRNAAL	1556	134.213	
281	GTGGAGCGGAATACTGATATG	340	VERNTDM	1557	133.962	
282	ACTGTTGGGAGTAATCTATT	341	TVGSNSI	1558	133.95	
283	GTGCGGTCTGTAATAAGCCG	342	VRSGNKP	1559	133.87	
284	GGCAGTTCGGGGAACAGCGGA	343	GSSGNSG	1560	133.776	
285	TCTACTTCAATAGGAGTGGTA	344	STSIGVV	1561	133.69	
286	CCGAGTCAGAGTAGGTCGCTT	345	PSQRSRL	1562	133.6751	
287	CGGAATGAGAATCTTAATAAT	346	RNENLNN	1563	133.26	
288	TCGTTGGGTAAGAGGGAGGAG	347	SLGKREE	1564	133.032	
289	TCACGCTTGACTCGAGCTCC	348	SRLDSSS	1565	132.783	
290	GATTCGACGTATGTTTGGCT	349	DSTYVLA	1566	132.54	
291	GAGCGTAATCCTATTTCTGAT	350	ERNPISD	1567	132.49	
292	GTTAGCTCCGCCACACGAAA	351	VSSGHTK	1568	132.466	
293	AAGTATACGGAGTCGAATGCG	352	KYTESNA	1569	132.305	
294	AACCGCAACTCAGTTGGGACT	353	NRNSVGT	1570	132.2576	
295	CACGAAAGCCACTACGTGTCA	354	HESHYVS	1571	132.014	
296	ACGACTGGGGGACGGGGATG	355	TTGGTGM	1572	131.954	
297	GCGACTGATAAGATGACTCCT	356	ATDKMTP	1573	131.931	
298	TCCGCGTCTAGCGGCGCTACA	357	SASSGAT	1574	131.886	
299	TCAACCACTACTGGCCACATG	358	STTTGHM	1575	131.581	
300	ATAATAGCATCCTCTACCACG	359	IIASSTT	1576	131.506	
301	GATACTGGGTCTAGGATTGCG	360	DTGSRIA	1577	131.486	
302	TGGGCTGATGATTCGACGCG	361	WADDSQR	1578	131.47	
303	AGGGGTAACACTCTCGAAATG	362	RGNTLEM	1579	131.381	
304	AATCTGCAGGTGAATGCGAAT	363	NLQVNAN	1580	131.172	
305	GCGACGACTCAGCTGATGACT	364	ATTQLMT	1581	130.96	
306	GCTGATACGAATATTATTGTG	365	ADTNIIIV	1582	130.47	
307	GCCATAACAATCACTCAAAAA	366	AITITQK	1583	130.225	
308	GACTCCAACAAAGGAGCGACG	367	DSNKGAT	1584	130.1749	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
309	GGCAACGCTTCCGGAACCCA	368	GNASGNP	1585	129.97	
310	ACGATGGGTGCTAAAGGTACT	369	TMGAKGT	1586	129.92	
311	TATCTGCAGACGGGTACTCTG	370	YLQTGTL	1587	129.907	
312	GCATTACACACCAAGACCTA	371	ALHTKDL	1588	129.846	
313	GTCGACAAAAGCGAAGCCGTC	372	VDKSEAV	1589	129.734	
314	GGGAGGACGGATCTTATGGCG	373	GRTDLMA	1590	129.651	
315	GGCACGGAACCGCGCACTGCA	374	GTEPRTA	1591	129.37	
316	AGAGGCGACATGTACAGAGAA	375	RGDMSRE	1592	129.137	
317	CGGGGGGATACTAAGTCTAAG	376	RGDTKSK	1593	128.94	
318	GGGACATTAGCCTCAATGTCC	377	GTLASMS	1594	128.734	
319	CAGAAGTCTGTGACGTATTCG	378	QKSVTYS	1595	128.602	
320	AGTACGGGGCAGACTCTTGTT	379	STGQTLV	1596	128.1669	
321	TCGCACATAAACATGGGGTCG	380	SHINMGS	1597	128.101	
322	GCGTTGAATGTTACTGGTAAT	381	ALNGTGN	1598	128.045	
323	ACTACGAGTTCGAATCAGCAT	382	TTSSNQH	1599	128.003	
324	AAAAACTACGCAAGCACCGAC	383	KNYASTD	1600	127.84	
325	GAATCCACAAGCAGGACGTAC	384	ESTSRTY	1601	127.765	
326	CCGCGTTCTATTACGGAGTTG	385	PRSITEL	1602	127.623	
327	TACATAGCCGGAGGAGAAAAA	386	YIAGGEK	1603	127.544	
328	ACTAGTAATTATATGCATGAG	387	TSNYMBE	1604	127.522	
329	TTGGATCCTAATAGTACTCGG	388	LDPNSTR	1605	127.175	
330	CACAGTGACATGGGCTCAAGC	389	HSMDGSS	1606	127.01	
331	GACACCGCCAACCGATCCACA	390	DTANRST	1607	127.01	
332	AACGCCGGACACAGCGGTCAA	391	NAGHSGQ	1608	126.611	
333	AGTTTGGGGTCGGATCGTATG	392	SLGSDRM	1609	126.579	
334	GACAACCAACAAGCCCTAGCT	393	DNQQALA	1610	126.49	
335	CCATCCTCAGCGGTTAGCACA	394	PSSAGST	1611	126.201	
336	GACAGGAAAGGTACGACGCA	395	DRKGYDA	1612	126.06	
337	GGAGGAAACCAAAACCTTACT	396	GGNQNLIT	1613	125.7806	
338	GTGAATCTGAATGAGACGGAG	397	VNLNETE	1614	125.719	
339	TCCCCCGGCAACGGGTTGCTA	398	SPGNGLL	1615	125.687	
340	TCTGTCGGGGACCTCACAAA	399	SVGDLTK	1616	125.627	
341	CGATACGAATCCGTCGGACTC	400	RYESVGL	1617	125.54	
342	ACGAGAGAATTGACAAAAAAC	401	TRELTKN	1618	125.47	
343	ACTCCAATAACGGGAACCCT	402	TPTINGNP	1619	125.37	
344	GCGACTGATCAGCGTTCGAGG	403	ATDQRSR	1620	125.26	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
345	GGAACATCGGCAGAATCACGC	404	G TSAESR	1621	125.214	
346	AGGATGCTCTCTACTTTGCCT	405	RMLSTLP	1622	125.088	
347	GGTATCAACTCCTCACACTTC	406	GINSSH F	1623	125.044	
348	AGTAGCTCAACTGAAGGGCAA	407	SSSTEGQ	1624	124.971	
349	GACAAACAACAAACCGGACAA	408	DKQQTGQ	1625	124.923	
350	ACCCAACACCTACCATCCACA	409	TQHLPST	1626	124.773	
351	GGTCTGGGGCAGCCTCAGTTG	410	GLGQPQL	1627	124.752	
352	GTGACTAATGAGAGTCGTGCT	411	VTNESRA	1628	124.728	
353	GGCAACTCGAACTACCGAGAA	412	GNSNYRE	1629	124.482	
354	TGGAATGCTGAGAATAGTAAG	413	WNAENSK	1630	124.373	
355	CCTGGGAGTCAGCGTCAGGAT	414	PGSQRQD	1631	124.325	
356	CATACGTATTCGAGGCTGAT	415	HTYSQAD	1632	124.3	
357	ACTGCCGGCAACCTAAGAAGT	416	TAGNLRS	1633	124.203	
358	GGCAGACACCTTCAATCGGAC	417	GRHLQSD	1634	124.19	
359	AACAACGCACACACCGCCACT	418	NNAHTAT	1635	124.118	
360	AGTACGAGTCAGGAGAATAGG	419	STSQENR	1636	124.0658	
361	AGGGGTGATACTATGAATTAT	420	RGDTMNY	1637	124.04	
362	CCGGTTGCTACTCAGCATGCG	421	PVATQHA	1638	123.9189	
363	GGGCATTTTGAATGCTCCGACT	422	GHLNAPT	1639	123.495	
364	CAAAATATTAACTACTCAGTC	423	QILNYSV	1640	123.4	
365	CAAAACCGCGCTCTGGTGAA	424	QNHASGE	1641	123.372	
366	GGTTTAACAGGGCGGGA ACTA	425	GLTGREL	1642	123.32	
367	GACGTAGCCGTGACTCAACAC	426	DVAVTQH	1643	123.31	
368	GCAACTTACACCGGGCGAACA	427	ATYTGRT	1644	123.292	
369	AAAGAACTACAATGGCAACGA	428	KELQWQR	1645	123.251	
370	GCTAGTTATAGTAGTATGGTG	429	ASYSSMV	1646	123.193	
371	GTTATTAGTCATGGGGCGCTG	430	VISHGAL	1647	123.094	
372	CCTATACACCACGGTTCATCC	431	PIHHGSS	1648	123.09	
373	GTGGATAAGAATCATCCTTTG	432	VDKNHPL	1649	123.04	
374	ACCTCGGGTGACCGGTACACG	433	TSGDRYT	1650	122.844	
375	GGGACAAAAAGCTGGCCTGTC	434	GTKSWPV	1651	122.8432	
376	TACAACGCCACGAATCATTC	435	YNAHESF	1652	122.813	
377	AGAGTCCACGACACTCCTTCA	436	RVHDTPS	1653	122.7503	
378	GCACAAATCGAATCAGGCCGA	437	AQIESGR	1654	122.66	
379	TGGAAGGATAATATGCGGATG	438	WKDNMRM	1655	122.624	
380	ATGCCTAGTGAACACCAGGG	439	MPSEPPG	1656	122.51	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
381	CGTGGTGATTATCCGACGTCG	440	RGDYPTS	1657	122.487	
382	TTTCATAATGAGTCTTATGGG	441	FHNESYG	1658	122.36	
383	TTGAATACGATGATTGATAAG	442	LNTMIDK	1659	122.272	
384	TCCACACTAAGCCAAGGAGCA	443	STLSQGA	1660	122.2662	
385	CCTTTGCACACATACCTCCT	444	PLHNIPP	1661	122.24	
386	GCTTCGTCTACGTTTTTGCCT	445	ASSTFLP	1662	122.24	
387	ATGGAAGGAATGGGACTCGGA	446	MEGMGLG	1663	122.04	
388	AAGGATTATAAGCCGTATGCT	447	KDYKPYA	1664	121.95	
389	AATTTGCAGTCTGGTGTTCAG	448	NLQSGVQ	1665	121.91	
390	ACAACTCTTAGCCAACAAAGC	449	TTLSQQS	1666	121.82	
391	CTTATGTCGTCTACTTCCTCA	450	LMSSTSS	1667	121.536	
392	ACTGGCCAAGGATTCTCGGCA	451	TGQGFSa	1668	121.45	
393	TCTACAATCGGCAACAGCACG	452	STIGNST	1669	121.27	
394	CTGAGGGCGAGTGAGGCTCCG	453	LRASEAP	1670	121.2297	
395	CAGCCTAATAATGGTAATCAT	454	QPNNGNH	1671	121.02	
396	TCGTCAGACGTTACCAGACAA	455	SSDVTRQ	1672	120.98	
397	CGGGGTGACGCAACAGAAATG	456	RGDATeM	1673	120.74	
398	TATAGGGGTAGGGAGGATTGG	457	YRGREDW	1674	120.58	
399	AGCTTGCAACAATCACAATTG	458	SLQQSQL	1675	120.491	
400	AAGCCGACTGCGAATGATTGG	459	KPTANDW	1676	120.3784	
401	CGTCTGACTGATACTATGCAT	460	RLTDTMH	1677	120.35	
402	CTTCATGGGAATTATAGTCCG	461	LHGNYSP	1678	120.346	
403	ATTCCGGTIGGGGCGATGGCT	462	IPVGAMA	1679	120.248	
404	CCGAACACCGCTCAAACCTTC	463	PNTASNF	1680	120.24	
405	ACGAGTAGAGAAGTCAAAGGG	464	TSREVKG	1681	120.171	
406	GACACGTCCTCCGGCAACAGG	465	DTSSGNR	1682	119.94	
407	GAAGCAGTAACAAGTAAATGG	466	EAVTSKW	1683	119.919	
408	CTAATCACAGCCACCACTAAC	467	LITATTN	1684	119.872	
409	GATGGGGTCTGTTCTGGGTATT	468	DGGRSGI	1685	119.847	
410	TTCATGGAAGTCATGAAAAAC	469	FMEVMKN	1686	119.82	
411	TCCTACCAAAACCCACCACCA	470	SYQNPPP	1687	119.701	
412	ACTAATGTGACGTTTAAAGCTT	471	TNVTFKL	1688	119.681	
413	ATTTCTACGCATACGATGACG	472	ISTHTMT	1689	119.64	
414	GAAACCCAAGGAGCAAGATAC	473	ETQGARY	1690	119.591	
415	GCGGCTTATGAGCATGCGCCT	474	AAYEHAP	1691	119.588	
416	TCAACGAACGACCGTGCCTTA	475	STNDRAL	1692	119.57	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
417	TTCACCGAACGCGCACTCCAA	476	FTERALQ	1693	119.423	
418	GTAGCGGGCTTAGTCGACATA	477	VAGLVDI	1694	119.41	
419	AGCTCGGTAACCTTACCTTGCA	478	SSVTNLA	1695	119.38	
420	GATACTACTACTGGTCATCTT	479	DTTGHHL	1696	119.27	
421	ACGCGTAATTTGTCTGAGAGT	480	TRNLSES	1697	118.919	
422	CAGGTGAATGTTGGGCCTGGT	481	QVNVGPG	1698	118.831	
423	AAACAAACGATGTCCGACACA	482	KQTMSDT	1699	118.829	
424	ATGTCGACAACCGCAAAACT	483	MSTTSKT	1700	118.7215	
425	ACTACAATAGGACAAACCAA	484	TTIGTNQ	1701	118.676	
426	GGGACTCTGACGCCGAATCTT	485	GTLPNL	1702	118.622	
427	TTTGATAGTTATAATATTGTG	486	FDSYNIV	1703	118.51	
428	CGTGGTGCGCTGAGCAAGCG	487	RGAPQQA	1704	118.47	
429	ATCGAAAACGTAAACCACTTG	488	IENVNHL	1705	118.42	
430	AGGTCTCTGGAGAGTCAGGCT	489	RSLESQA	1706	118.231	
431	CAGTATACGAGTCTGAGTCCG	490	QYTSLSL	1707	118.006	
432	ACGAAGGGTTATAATGATCTT	491	TKGYNDL	1708	117.876	
433	GTCGCCTCGATGGTACACAAC	492	VASMVHN	1709	117.874	
434	TCCACAACCCACACCTCAGCA	493	STHTSA	1710	117.821	
435	CTTGCGCACCCACAACCAAAC	494	LAHPQPN	1711	117.542	
436	TCGATAAACAACATAGGCGCA	495	SINNIGA	1712	117.538	
437	GCTATAGACTCCATCAAAATG	496	AIDSIKM	1713	117.472	
438	TCTATGTATGGGAGGCTGGG	497	SMYQAG	1714	117.362	
439	GAGTATGCTAATGCTAAGACT	498	EYANAKT	1715	117.351	
440	TATCGGGCTTCGGATGTGGCG	499	YRASDVA	1716	117.348	
441	GTTAGTTTGGAGAGTCGGTTG	500	VSLESRL	1717	117.332	
442	ATTGAGACTAGTTCGCTTCG	501	IETSSRS	1718	117.176	
443	ATGGGAGTGAAACCCGAACAA	502	MGVKPEQ	1719	116.975	
444	GCGCTTCCGTCTCGTGAGCGG	503	ALPSRER	1720	116.914	
445	GGCACCGGATCTTCAGCGCAC	504	GTGSSAH	1721	116.896	
446	CAAACGAACACCAACGACAGA	505	QTNNDNR	1722	116.664	
447	GTATTACACTCTGTATCAGCA	506	VLHSVSA	1723	116.583	
448	CCTTATTCTGCTACTGATCGG	507	PYSATDR	1724	116.577	
449	GCAAACCTCCGATTACACAAC	508	ANGLHNL	1725	116.505	
450	TATGAGAGTACTCATGTTAAT	509	YESTHVN	1726	116.418	
451	AACAACGCACTAGTAGGAAGT	510	NNALVGS	1727	116.34	
452	GGTATCAACTCCTCACACATC	511	GINSSHI	1728	116.28	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
453	AGTATTTCTGATAAGAATCAG	512	SISDKNQ	1729	116.141	
454	GACCACCAACAAGCCCTAGCA	513	DHQQALA	1730	116.13	
455	GACTCTACCAAGCCATGCAA	514	DSTKAMQ	1731	116.116	
456	ACTATTACTAGTCAGTCGGTG	515	TITSQSV	1732	115.95	
457	GGCGCCCGTACAATCTTAGAC	516	GARTILD	1733	115.938	
458	GAGCATAGTCCTACGACTGGT	517	EHSPTTG	1734	115.8995	
459	GGGCTCACAGGATACCCAATG	518	GLTGYPM	1735	115.844	
460	ACGATGGAATCCGGCCGCCAC	519	TMESGRH	1736	115.82	
461	TCTGCGTCGAAAGTGAATAC	520	SASKVEY	1737	115.719	
462	GATAAGTCTAATTATAGTATT	521	DKSNYSI	1738	115.714	
463	TTCAACGAAACTGCCGGCGCA	522	FNETAGR	1739	115.65	
464	CAAAAATCGGAAACCTACACT	523	QKSETYT	1740	115.528	
465	GCACTTACCCGTATGCCTAAC	524	ALTRMPN	1741	115.476	
466	CGTAACGGCTCCGCCCAAAGC	525	RNGSAQS	1742	115.465	
467	GCGAGGGATACGCCTGGGATT	526	ARDTPGI	1743	115.432	
468	ATTGTTAATGCTGAGATTAT	527	IVNAEY	1744	115.31	
469	CGACAAGGCGACTTAAAAGAA	528	RQGDLE	1745	115.3059	
470	CGAAACAACCCATCGCACGAC	529	RNNPSHD	1746	115.224	
471	CTCGCCCACTACTTAAGC	530	LAHNYLS	1747	115.195	
472	AACACCCACAACCTACAAATG	531	NTHNLQM	1748	115.171	
473	CGAGGAGACCACAGCACACAG	532	RGDHSTQ	1749	115.12	
474	CTCCACGGAGTCAGCAGTATA	533	LHGVSSI	1750	115.105	
475	GGTATTAATCATGTGGCGTCT	534	GINHVAS	1751	115.102	
476	ACTGATAAGCTTCAGGGTGTG	535	TDKLQGV	1752	115.062	
477	GGAACCTCCATAGACTACGTA	536	GTSIDYV	1753	115.053	
478	TCGAACACTGCCCCCCCCC	537	SNTAPPP	1754	115.034	
479	ACTGCTAAGAGTTATGGGCCT	538	TAKSYGP	1755	115.006	
480	GACCACCAACAAGCACTAGCT	539	DHQQALA	1756	114.98	
481	ACACAAGTAGTCGCAAGAACA	540	TQVVART	1757	114.9299	
482	AGTCCTCCTAGTACGTCGGGT	541	SPPSTSG	1758	114.816	
483	CCTATGCGAACACCACCGTAC	542	PMRTPPY	1759	114.806	
484	GCTGCTGGTAATACTACTCGT	543	AAGNTTR	1760	114.78	
485	AGAGGCGACTAATCCACACCC	544	RGD*STP	1761	114.78	
486	CTAGCGAAAACGTGCTGCTATC	545	LAKTVAI	1762	114.722	
487	TCTAAATCTGAAAACCTGCAA	546	SKSENLQ	1763	114.59	
488	ACTCAGACGTCGTATGCTACG	547	TQTSYAT	1764	114.505	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
489	ACTGGGGATAGGACTTCGGTG	548	TGDRTSV	1765	114.4766	
490	ATATCGCAAGGCTCGAGCCTC	549	ISQGSSL	1766	114.305	
491	CTTGTTTCAGATGGGAGTGTG	550	LVQMGSV	1767	114.256	
492	TTATCCGCAACATCTACGATG	551	LSATSTM	1768	114.245	
493	CAAAACCACAACGAACTAAAA	552	QNHNELK	1769	114.217	
494	CGTGGTGCGCTGAGCATGCG	553	RGAPCHA	1770	114.09	
495	TCTTCTTTTCGGAAAAGACAAC	554	SSFGKDN	1771	113.982	
496	AACGCTAACGCCGGTGGAAAC	555	NANAGGN	1772	113.958	
497	GATCATCATCTCAGAGTCGT	556	DHHPQSR	1773	113.83	
498	ATGAGGCATGAGGCTCCTCTT	557	MRHEAPL	1774	113.819	
499	AAGGGGATGGTGCTTATGAG	558	KGDGAYE	1775	113.742	
500	CCTATGAATGTTCTGTTG	559	PMNGILL	1776	113.722	
501	AGTAGTGGGGTATGAAGGCG	560	SSGGMKA	1777	113.69	
502	GTGCTGGTTACTCAGAATCAT	561	VLVTQNH	1778	113.631	
503	GAGATTAATAATCGGACTGGT	562	EINNRTG	1779	113.588	
504	TTACCAACAGGCGCTCGCCC	563	LPTGVLP	1780	113.561	
505	GCCTACGGTATCAGAGAAGTG	564	AYGIREV	1781	113.547	
506	TCGACAACTCTATAGGCGCC	565	STNSIGA	1782	113.471	
507	GTGCAGTTGACGCATAATGGG	566	VQLTHNG	1783	113.43	
508	GTTCAAGTTGAGAATGCGAAT	567	VQLENAN	1784	113.43	
509	GGAAAAGCCAACGCGTTCT	568	GKANDGS	1785	113.427	
510	ACCGGGGTTTCGAGAAACCATA	569	TGVRETI	1786	113.41	
511	GGCCTGAACCATGACATCG	570	GLNQITS	1787	113.4	
512	ACGGAGAAGGCGAGTCCTCTG	571	TEKASPL	1788	113.381	
513	TTTCTGGAGGGTGTGCGCAG	572	FLEGVAQ	1789	113.333	
514	ACGAATTATAATATTGGTCCG	573	TNYNIGP	1790	113.318	
515	AGAGGAGACTTGACAACCACA	574	RGDLTTT	1791	113.29	
516	ATGATGAATGTGAGTGGTCAT	575	MMNVSGH	1792	113.09	
517	TCTCAGTCGATTAATGGGCTT	576	SQSINGL	1793	113.084	
518	CTCACGACTTTAACTAACCAC	577	LTTLTNH	1794	113.033	
519	AACTCTGTTCAATCCACCCCA	578	NSVQSTP	1795	113.021	
520	TATAATACGGATCGGACTAAT	579	YNTDRTN	1796	113.001	
521	GAGAAGCCTCAGCATAATAGT	580	EKPQHNS	1797	112.98	
522	ACGATGGCTACAACTTAAGT	581	TMATNLS	1798	112.937	
523	GTGGGGACGCATTTCATTCG	582	VGTHLHS	1799	112.918	
524	GACGCCCACCACTCAAGCAGC	583	DAHSSSS	1800	112.88	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
525	CTTGTGGGACTTTGGTGTAT	584	LVGTLVY	1801	112.853	
526	TATGGTGTGCAGGCGAATAGT	585	YGVQANS	1802	112.806	
527	GTTTTGTCTGATAAGGCGTAT	586	VLSDKAY	1803	112.787	
528	CTTGAGGGTCAGAATAAGACG	587	LEGQNKT	1804	112.731	
529	GAGGTTAGTAATAAATTAT	588	EVSNNNY	1805	112.69	
530	GCCCACCAACAAGCCCTAGCT	589	AHQQALA	1806	112.67	
531	CTTCCGACCACACTCAACCAC	590	LPTTLNH	1807	112.667	
532	TACATAGCAGGTGGTGAACAA	591	YIAGGEQ	1808	112.6513	
533	AATTCTGTACTCTTTATCAG	592	NSGTLYQ	1809	112.609	
534	CGGGGTCTGCCTGATGTTAAT	593	RGLPDVN	1810	112.43	
535	AACCAACAACATATCCCACTCA	594	NQQLSHS	1811	112.375	
536	AATCCTAGTTATGATCATCGG	595	NPSYDHR	1812	112.363	
537	ATAGACAGCGACACCTTCGTA	596	IDSDFV	1813	112.355	
538	ACCGCTTACCTTGC GGGATTA	597	TAYLAGL	1814	112.17	
539	CATAGTAATGTTAGTCTTGAG	598	HSNVSLE	1815	112.162	
540	GGTAATAATTTGAGTTTGTCT	599	GNNLSLS	1816	112.16	
541	GTTATGGATACGATGGGATG	600	VMDTHGM	1817	112.145	
542	GCGTATAATATGTCGTCTGTT	601	AYNMSSV	1818	112.14	
543	ACTAACGCCATCTCTCAAACG	602	TNAISQT	1819	112.063	
544	GCAACACACGCCATGCGCCCA	603	ATHAMRP	1820	112.016	
545	ATGTTAAACAACACAATGATG	604	MLNNTMM	1821	111.939	
546	ATTAGTTCGGGGATTTTGTCTG	605	ISSGILS	1822	111.907	
547	CGCCAAGGCAGCTTGATGATA	606	RQGS LMI	1823	111.83	
548	ACGACTGATAAGGGTATTAAT	607	TTDKGIN	1824	111.818	
549	CACAACCTTAATGACCCAAATA	608	HNLMTQI	1825	111.77	
550	AACCAAAACACCTACGAACTG	609	NQNTYEL	1826	111.756	
551	GCTAACACCGTCACAGAACGA	610	ANTVTER	1827	111.7323	
552	TCTACGCTGCAGACTAATGGT	611	STLQTNG	1828	111.683	
553	CCCAACGAATACAAAGCACCG	612	PNEYKAP	1829	111.646	
554	ATGCAAACACGCTCGGACACA	613	MQTRSDT	1830	111.629	
555	GGAACAGGGTACGCTGGATCA	614	GTGYAGS	1831	111.6183	
556	ATGGGTATGCAGAATACGCAT	615	MGMQNTN	1832	111.599	
557	TCTAGTAAGGAGCGTACATCG	616	SSKERTS	1833	111.57	
558	CGAACGGACACCCCTACACC	617	RTDTPYT	1834	111.562	
559	ACTGCGCTGCGGGATAATAAG	618	TALRDNK	1835	111.51	
560	AGGATGTCTGAGAGTTCGGAT	619	RMSESSD	1836	111.51	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
561	AACCAATCTATAAGCATGGAC	620	NQSISMD	1837	111.491	
562	TCGCTTGGGCATAGTAATAAT	621	SLGHSNN	1838	111.432	
563	CTTAATAGTGTTGGTGCATG	622	LNSGGAM	1839	111.361	
564	AACGAACAATTCGAAAAAGTC	623	NEQFEKV	1840	111.341	
565	ATGATGGCGAATAATATGCAG	624	MMANNMQ	1841	111.28	
566	AGTCGGCGCAAGAACAACCA	625	SRREEQP	1842	111.2512	
567	GCGACTATGACTTCGTCGACG	626	ATMTSST	1843	111.238	
568	CGTGGTTCAGACGGAGGATTG	627	RGSDGGL	1844	111.172	
569	AGTTTGACGCCTAATAATCTT	628	SLTPNNL	1845	111.152	
570	GCTACTCTTTCTCCGCATGCT	629	ATLSPHA	1846	111.132	
571	TATCTGCAGGAGAAGTTTCCT	630	YLQEKFP	1847	111.112	
572	GGCACCGGGTACCCAAACCAA	631	GTGYPNQ	1848	111.111	
573	AATTATCCTTCGGTTCAGGAG	632	NYPSVQE	1849	111.07	
574	ACTGACGCATCGGGTAGATCA	633	TDASGRS	1850	111.017	
575	CGTGTGATTACTGCGGGTGAT	634	RVITAGD	1851	111.009	
576	GTGACTGTGAGTAATAGTCTG	635	VTVSNSL	1852	110.95	
577	TTGTTGACGGCTCCGCATAGG	636	LLTAPHR	1853	110.908	
578	TCAATCGCAAACCATGATA	637	SIANHMI	1854	110.861	
579	ATGCCTTCGAAAGGCGAAGTA	638	MPSKGEV	1855	110.816	
580	AACATGACCAACGAACGGCTC	639	NMTNERL	1856	110.801	
581	TCATTCTCTTCAGGCATAATG	640	SFSSGIM	1857	110.771	
582	CGCGACCGTCAAGACTCGGTA	641	RDRQDSV	1858	110.754	
583	CACGGTGACCGAACAGCTTTA	642	HGDRTAL	1859	110.748	
584	GAAGTACGGGGCAGCGTGCCA	643	EVVGSVP	1860	110.747	
585	CTGATTTGACTGGTAATAAT	644	LISTGNN	1861	110.735	
586	CCAACATCTGGGGACAAACCG	645	PTSGDKP	1862	110.735	
587	AAAGCGGACCACAGTGGGGCA	646	KADHSGA	1863	110.73	
588	CTAAACGACGTCTACCGTAAA	647	LNDVYRK	1864	110.724	
589	AACAGTTTGCAAGCAAGTGCA	648	NSLQASA	1865	110.72	
590	TATCATAATGAGATTATGACG	649	YHNEIMT	1866	110.708	
591	AACAACACCTAAACATCCTA	650	NNTLNIL	1867	110.69	
592	TCTTATGGCAGGGTCTGGAG	651	SYGQGLE	1868	110.684	
593	ATGATAAAAACCAACATGTTG	652	MIKTNML	1869	110.668	
594	ACCGAAGCGGGCCGCCCCCAA	653	TEAGRPQ	1870	110.663	
595	AGGATTGATCAGACTAATGTG	654	RIDQTNV	1871	110.624	
596	GAGGGGCATAATCGTGGTATT	655	EGHNRGI	1872	110.559	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
597	ATGGGGACTGAGTATCGTATG	656	MGTEYRM	1873	110.524	
598	TCGGGTATGAATAGTAATAAG	657	SGMNSNK	1874	110.499	
599	TTGACTAATGATAATAAGTTG	658	LTNDNKL	1875	110.479	
600	TTACACAACCTACCAAGACCGT	659	LHNYQDR	1876	110.438	
601	AAGTCTAATTTGGAGGGTAAG	660	KSNLEGK	1877	110.438	
602	CTTACTGGTCAGAATGCGATT	661	LTGQNAI	1878	110.416	
603	CATACTGTGGGGGCTATGCAT	662	HTVGAMH	1879	110.41	
604	CTCCAACCTGGCTACATCCAC	663	LQLATSH	1880	110.384	
605	AGTCTGAATGGGGTGTGGTT	664	SLNGVLV	1881	110.359	
606	AGTCACAACCAAGTAAACGTA	665	SHNQVNV	1882	110.349	
607	AGTTTGAGTACTGATGTGTTT	666	SLSTDVF	1883	110.261	
608	ATGGTAGGTCGTGCCGAAATC	667	MVGRAEI	1884	110.224	
609	TTGTCTAGTATGAGTACGGAT	668	LSSMSTD	1885	110.204	
610	TCCTACGTACTTCAACACCG	669	SYSTSTP	1886	110.189	
611	TCCGAATTAATGGTCAGACCC	670	SELMVRP	1887	110.0813	
612	TGGAACGGAAACGCCACACAA	671	WNGNATQ	1888	110.039	
613	ATGGATACTGAGCTTTATAGG	672	MDTELYR	1889	109.985	
614	AGGACGAGTCCTGATACGAAT	673	RTSPDTN	1890	109.977	
615	TTCTCAACGCAAGACATAAGC	674	FSTQDIS	1891	109.948	
616	ACGACTGTGCTGGGAATAAT	675	TTVLGNN	1892	109.94	
617	CAGCGTGATGCTGCGTATGCT	676	QRDAAYA	1893	109.927	
618	CACCAAACCGTGGTCCCTACT	677	HQTVVPT	1894	109.8948	
619	TCTAATCCGGGTAATCATAAT	678	SNPGNHN	1895	109.853	
620	TGGGAGACTATGGCTAAGCCT	679	WETMAKP	1896	109.818	
621	GGTCTTTATCAGAATCCTACG	680	GLYQNPT	1897	109.73	
622	CTAATCTTACTAATCATAAT	681	LNLTNHN	1898	109.727	
623	ATGAGTCTCGCCTCCACCCAA	682	MSLASTQ	1899	109.672	
624	ACGTCCCAAACCGTCCGAGTA	683	TSQTVRV	1900	109.654	
625	GGAGCAACGGTCAACACGCGA	684	GATVNTR	1901	109.64	
626	AAAGGGGAAACCTCACC GCA	685	KGGNLTA	1902	109.632	
627	GCGTGGTCTCAAGTCCTGACG	686	AWSQVLT	1903	109.587	
628	GTAGAACACGTAGCCACCAA	687	VEHVAHQ	1904	109.552	
629	CTAATGTCGTCTACTCATCA	688	LMSSYSS	1905	109.546	
630	TCTCTGGGTGGGAATCCGCCT	689	SLGGNPP	1906	109.511	
631	AAGAATGAGAATACGAATTAT	690	KNENTNY	1907	109.5055	
632	ATATTGGACAACCACCGTTTC	691	ILDNHRF	1908	109.489	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
633	AATTCGTCGCATGTTAATTCT	692	NSSHVNS	1909	109.473	
634	CAGGTGCAGCATGAGAGGGTG	693	QVQHERV	1910	109.47	
635	TGGGAGGAACCTGGGAATA	694	LGGTLGI	1911	109.46	
636	ACTCAAGAACGACCACTAATC	695	TQERPLI	1912	109.455	
637	CGTAAGACTGAGGATAGGATG	696	RKTEDRM	1913	109.429	
638	ACCGAACTCACAGCGGGAAC	697	TELTARN	1914	109.398	
639	CGCGGCGACAACACTTACTCC	698	RGDNTYS	1915	109.387	
640	CAGTCTAATACTAATAATAGT	699	QSNTNNS	1916	109.372	
641	GCTTCTTATAGTATTCTGAT	700	ASYSISD	1917	109.309	
642	AGCGAACACCACGCCGGAATA	701	SEHHAGI	1918	109.281	
643	CGTGGTGCGCCAGAGCATGCG	702	RGAPPHA	1919	109.237	
644	AATTTTAGTAGTGGTGATGTT	703	NFSSGDV	1920	109.229	
645	AGTGGCATCAACGCCACCGAC	704	SGINATD	1921	109.22	
646	CGGGCTGATGTTTCTTGGTCT	705	RADVSW	1922	109.213	
647	TGTATGGATGTTGGTAAGGCG	706	CMDVGKA	1923	109.203	
648	GGGGTCGGAGCCACTTCGGTA	707	GVGATSV	1924	109.193	
649	AAAAACAACAACCTCAGACAGT	708	KNNNSDS	1925	109.177	
650	AATGTTGCGATATTGATAGG	709	NVASIDR	1926	109.174	
651	AATAGTGTGAATGGTCTTCTG	710	NSVNGLL	1927	109.154	
652	ACACTAGACCGAAACCAACC	711	TLDRNQT	1928	109.132	
653	GACCAAACTTCGAACGTAGA	712	DQNFERR	1929	109.108	
654	GTCGGTGACAGGAACCTGGTC	713	VGDRNLV	1930	109.062	
655	TTAGAAGTAAACCTGCAACG	714	LEVNLTQ	1931	109.057	
656	ACTAATGGGGGTCGCTTAAT	715	TNGGSLN	1932	109.049	
657	TTCACGCGCACACAGTAACC	716	FTRTPVT	1933	109.033	
658	ACACCGGCGGAAAGCAAAGTT	717	TPAESKV	1934	108.991	
659	TTTCCTTCGCATAATGGGGCG	718	FPSHNGA	1935	108.959	
660	GCCAGGAACGTAATGCTGGGG	719	ARNVMLG	1936	108.958	
661	ACGATTCAGGATCATATTAAG	720	TIQDHIK	1937	108.942	
662	ATTAATTCGTATTTCATGAG	721	INSYLHE	1938	108.918	
663	GCGCATGATGTTACTGTGAAT	722	AHDVTVN	1939	108.918	
664	ACTGTGGGGTTCAGCAGACG	723	TVGVQQT	1940	108.8891	
665	ACAGGTAGTTCAGACAGATTA	724	TGSSDRL	1941	108.887	
666	AATCATGATACTGCTCATGCT	725	NHDTAHA	1942	108.884	
667	GCCGAATCCCACTAGCTAGC	726	AESQLAS	1943	108.8752	
668	GGTAATGCGTATAATACGACT	727	GNAYNTT	1944	108.818	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
669	AATCATCAGGCTGGTACTACT	728	NHQAGTT	1945	108.807	
670	ACGGTAGGAGAAAACCCCGA	729	TVGENHR	1946	108.779	
671	CTAACTACTAAATACCCCTC	730	LTTKIPL	1947	108.773	
672	ACTAATTATCCTGAGGCGAAT	731	TNYPEAN	1948	108.748	
673	AATACTGCTCCGCCGAATCAT	732	NTAPPNH	1949	108.733	
674	GTGCTGAGTACGGGCTGCGG	733	VLSTGLR	1950	108.677	
675	CTCACGTCCCCTCTGCGGGC	734	LTSHSAG	1951	108.648	
676	ATGAATAAGCATGGTGTGCTT	735	MNKHGVL	1952	108.5736	
677	GACCTGACCAGAGCTGCAATA	736	DLTRAAI	1953	108.552	
678	TATATTGTGGATCATGCGAAT	737	YIVDHAN	1954	108.526	
679	AGTGGCCCTGAGAATACGTTG	738	SGPENTL	1955	108.526	
680	CGTTATGGTGATACGGGTATG	739	RYGDTGM	1956	108.512	
681	GATGGTAAGAATAGTTATGCG	740	DGKNSYA	1957	108.451	
682	GAGGCGCATAATCGTGTATT	741	EAHNRVI	1958	108.451	
683	AGTTTGCAGGCTGGTAGGATG	742	SLQAGRM	1959	108.3681	
684	GATGCGAAGGCTCTTACGACT	743	DAKALTT	1960	108.368	
685	ACCGACACCCGAAAAACGAC	744	TDTRKND	1961	108.357	
686	GACTCTTCACACTACTCGACA	745	DSSHYST	1962	108.219	
687	ACAATGCACCTTCCCAACCTG	746	TMHLPNL	1963	108.214	
688	CGAGACGGCTCTACTAAAGTT	747	RDGSTKV	1964	108.207	
689	TCAGGGTACCAATGACAGAA	748	SGYQMTE	1965	108.16	
690	TGCGACTTGTCAATCATGC	749	CDLSQSC	1966	108.133	
691	AGAAACGCGTCAAACGGCGTA	750	RNASNGV	1967	108.044	
692	CAGTCGCAGAATGTGACTCAG	751	QSQNVTV	1968	108.033	
693	GATTCTGCTCCGAGTACTATT	752	DSAPSTI	1969	108.003	
694	AGGTCCGTACCATCACCACAC	753	RSVPSPH	1970	108.001	
695	ATGACGTCTGCGTCTCGTGGT	754	MTSASRG	1971	107.974	
696	GCTCTTGCTAGTCGTCCTATG	755	ALASRPM	1972	107.907	
697	CTAAACCTCTCCAACGACTGG	756	LNLSNDW	1973	107.899	
698	GTTTCTACGGCGCAGAGGCAG	757	VSTAQRQ	1974	107.896	
699	CACGCCGACGTTGGCATGAGC	758	HADVGMS	1975	107.888	
700	GCGGGGGGTTTGCTGTCGCGG	759	AGGLLSR	1976	107.878	
701	CATCTTAGTCAGGCTAATCAT	760	HLSQANH	1977	107.848	
702	GTGCATAATCTACTACTACG	761	VHNPTTT	1978	107.8152	
703	TCTCAGCGGAATCCGGATGAT	762	SQRNPDD	1979	107.784	
704	AGGGAGACTAATAATTTTGGC	763	RETNNFA	1980	107.771	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
705	AATGCGGGGGCTCTTATGGGT	764	NAGALMG	1981	107.764	
706	TTGCCGAAGACTGTGAATATG	765	LPKTVNM	1982	107.738	
707	GCAAGTGACCTACAAATGACG	766	ASDLQMT	1983	107.723	
708	CAAGCCCTGGCCACCACAAAC	767	QALATTN	1984	107.716	
709	CATGAGTCGTCGTGTATCAT	768	HESSGYH	1985	107.696	
710	GGGGTGAATGATCGTGCTAGG	769	GVNDRAR	1986	107.69	
711	CCTCGGGATGCTCTTCGTA	770	PRDALRT	1987	107.673	
712	AACGACTCCTCGTCAATGTCC	771	NDSSSMS	1988	107.641	
713	GAATACAACACGCGCCACGAC	772	EYNTRHD	1989	107.611	
714	GCGTCTCCGCGCATACGTCT	773	ASPAHTS	1990	107.598	
715	CAAAACAGCAACACTCCCTCA	774	QNSNTPS	1991	107.546	
716	TTGGCAAACTAGGGA	775	LAKLGN	1992	107.541	
717	GCTAGTGATAGGCAGTCTGGT	776	ASDRQSG	1993	107.527	
718	TATCAGAATGGTGTCTTCT	777	YQNGVLP	1994	107.5199	
719	AATAAGTTTGGTTATAATCCT	778	NKFGYNP	1995	107.513	
720	AAAAAAACCAACGGAATCCCC	779	KKTNGIP	1996	107.5	
721	GTTAACGACAACCGAGGAAAC	780	VNDNRGN	1997	107.4937	
722	ATGCACACCATAACGGGATCC	781	MHTITGS	1998	107.491	
723	ATTGATGGTGTTGAGAAGCTT	782	IDGVQKL	1999	107.489	
724	GCGCAGGTTAATAATCATGAT	783	AQVNNHD	2000	107.489	
725	GTTTCTTCGCCTAATGGTACG	784	VSSPNGT	2001	107.487	
726	GATTCTGCTCCGAGGGCTATT	785	DSAPRAI	2002	107.455	
727	TCTGCGAGTGATAGTCAGCAT	786	SASDSQH	2003	107.455	
728	TCGGCTCATCAGACGCCGACG	787	SAHQTP	2004	107.427	
729	GCGACGCTGAATAATAGTTAT	788	ATLNNSY	2005	107.411	
730	GAAGACAGTATGAGATTCTCT	789	EDSMRFS	2006	107.407	
731	GAACGAAACGGACTAATAGAA	790	ERNGLIE	2007	107.405	
732	TTAGTACTTGACTCACGGAAC	791	LVLDNRN	2008	107.382	
733	ACCGTCGAACAAATAAACTCG	792	TVEQINS	2009	107.349	
734	GGGACAGGTACCGTTGGATGG	793	GTGTVGW	2010	107.203	
735	AATCAGCAGCGTATTGATAAT	794	NQQRIDN	2011	107.185	
736	ATCCAAAACGGGTCCTGCCA	795	IQNGVLP	2012	107.184	
737	GGAGACATCTCAAGCAGAAAC	796	GDISSRN	2013	107.1386	
738	GTCCTGGCACTACCCCGGGA	797	VTGTPPG	2014	107.137	
739	ACAAGGGAATCAATGTCCATC	798	TRESMSI	2015	107.071	
740	CACACTTACTCACAAGCAGAC	799	HTYSQAD	2016	107.012	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
741	TCCAACATGGGCGTAGCCTCT	800	SNMGVAS	2017	106.985	
742	CACGACTTGAACACGGAAAA	801	HDLNHGK	2018	106.942	
743	CTGTACGGGGGAGCACACCAA	802	LYGGAHQ	2019	106.904	
744	AACGTGTACGGAGACGGAATA	803	NVYGDGI	2020	106.87	
745	TCTACTATTAATATGCGTGCG	804	STINMRA	2021	106.868	
746	AAGATGGGGAGTATTGAGGTT	805	KMGSIIEV	2022	106.864	
747	TCCGAAACGCGCGCTGGATAC	806	SETRAGY	2023	106.85	
748	AATGTGGGTAATACTCTTGGG	807	NVGNTLG	2024	106.842	
749	ATTGGTGGGACTGATACGCGG	808	IGGTDTR	2025	106.786	
750	GCCGACAAAGGATTCGGCCAC	809	ADKGFHG	2026	106.73	
751	TGGCAGGATCATAATAAGGTG	810	WQDHNKV	2027	106.719	
752	AACTACGGTTCGGACGAATC	811	NYGSGRI	2028	106.701	
753	ACTCATAAGCAGGTGGATCTT	812	THKQVDL	2029	106.695	
754	CGGCAGAATGATAAGGGTAAT	813	RQNDKGN	2030	106.658	
755	GGTAGGAATGAGAGTCCGGAG	814	GRNESPE	2031	106.658	
756	GTTTTTACTGGGCAGACGGAG	815	VFTGQTE	2032	106.632	
757	TATGTTGATCGTAAGGATAAT	816	YVDRKDN	2033	106.631	
758	AATAATACTTTGAATATTTTG	817	NNTLNIL	2034	106.63	
759	TTGAGCTACAGCATCCAACAC	818	LSYSIQH	2035	106.621	
760	GCTACCAACAGATCGCCCCTA	819	ATNRSPL	2036	106.5898	
761	GTTACACCGCAGACACAATA	820	VHTADTI	2037	106.564	
762	GGGCATTTGGTTAATATGTCT	821	GHLVNMS	2038	106.56	
763	TTAGACTACACCCCTCAAAC	822	LDYTPQN	2039	106.519	
764	TCCGCCTCTTACTCCAGGATG	823	SASYSRM	2040	106.501	
765	TCCGGAGCGGCACAAAACCCA	824	SGAAQNP	2041	106.499	
766	AGAAACACACTTGCTGACCTT	825	RNTLADL	2042	106.496	
767	GGTTCTACGGTGTCGGCGCAG	826	GSTVSAQ	2043	106.491	
768	TCTAAGGATAGTACTATGTAT	827	SKDSTMY	2044	106.48	
769	GTGGTGGTTCACACTATCCCA	828	VVVHTIP	2045	106.45	
770	CCACGTACTGTCTCATTGGAC	829	PRTVSLD	2046	106.4434	
771	ATGATGAAGAGTGAGGAGAAT	830	MMKSEEN	2047	106.425	
772	ACCACCGACCGGCCAAACGGA	831	TTDRPNG	2048	106.406	
773	CATAGTCCTCTACGACTATG	832	HSPPTTM	2049	106.376	
774	GGCCAATGGACAACAGGGACA	833	GQWTTGT	2050	106.357	
775	GACGGTATGAACGGAGTGGGT	834	DGMNGVG	2051	106.317	
776	CTTCATACTGTTGCGAATGAG	835	LHTVANE	2052	106.312	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
777	TATACGTCGCAGACGTCTACG	836	YTSQTST	2053	106.2842	
778	AACTTCTCCGAAATGTCCACA	837	NFSEMST	2054	106.27	
779	ATTAATATTCTAGTGATTG	838	INIRSDL	2055	106.266	
780	CCCTCCAACAGTGAAAGATTC	839	PSNSERF	2056	106.249	
781	TATACGAATTATGGGGATCTT	840	YTNYGDL	2057	106.241	
782	GATAAGAGTACGGCGCAGGCG	841	DKSTAQA	2058	106.238	
783	CACACCGACATGGTATCCTCT	842	HTDMVSS	2059	106.222	
784	AACAAAAGTCTGTCAATGGAC	843	NKSLSMD	2060	106.196	
785	GGGCACTACGCTACAAACACA	844	GHYATNT	2061	106.158	
786	GTCATCGTATCTACAAAATCA	845	VIVSTKS	2062	106.124	
787	ACTCATAGTCTTATGAATGAT	846	THSLMND	2063	106.116	
788	AACTACCACGGAGACAACGTT	847	NYHGDNV	2064	106.106	
789	CGTGATGATCAGCAGCTTGAT	848	RDDQQLD	2065	106.064	
790	GATGATAAGACTGGTCGGTAT	849	DDKTGRY	2066	106.055	
791	GGGTCGAGCCAACACCACGAA	850	GSSQHHE	2067	106.042	
792	CGTGTTACAGGTGTCTCAACA	851	RVTGVST	2068	106.017	
793	AGTACTGCGTCGGGCATACT	852	STASGHT	2069	106.007	
794	ACTAACAACCTCTCATACGAA	853	TNNLSYE	2070	105.998	
795	CAGCATAATAGTGCCTCGGCG	854	QHNSASA	2071	105.987	
796	CCGGCTAAGGGTTTTGGTCAT	855	PAKGFGH	2072	105.9781	
797	TGGTACGAAACAATCAGCCCG	856	WYETISP	2073	105.959	
798	ACGGATGCTACGGGGAGGCAT	857	TDATGRH	2074	105.942	
799	ATTCAGGCGAAGAATTCTGAG	858	IQAKNSE	2075	105.939	
800	AGTACTGAGACTAGGGGTGGG	859	STETRGG	2076	105.926	
801	TTCTCAACAACTCTGTAAATC	860	FSTNSVI	2077	105.918	
802	TCTAACCTTCGAAACACAATA	861	SNLRNTI	2078	105.854	
803	GGGATGATCGGGCACAACGCA	862	GMIGHNA	2079	105.832	
804	TCTGGCCAAGGATTCTCGGCA	863	SGQGFSa	2080	105.831	
805	ACCCACAACCTCTACAGGCCTT	864	THNSTGL	2081	105.802	
806	AGGATTGATAGTGCTATGGTG	865	RIDSAMV	2082	105.8	
807	GTCGCTATGGGAGGCGGTCCC	866	VAMGGGP	2083	105.795	
808	GGCTCTCACACGGCCCAGCC	867	GSHNGPA	2084	105.763	
809	CACTCCGACGCGGTGACGGT	868	HSAAGDG	2085	105.73	
810	GCACAAGGCATAACCCACGCT	869	AQGITHA	2086	105.711	
811	TCTGCGCTTTTGCGGATGGAT	870	SALLRMD	2087	105.707	
812	TGGCAAATGGGGGCCGGGAGC	871	WQMGAGS	2088	105.698	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
813	ATAGACTCGCACGCCAGCATA	872	IDSHASI	2089	105.695	
814	AGCCTAGACCACGCCCTCTA	873	SLDHAPL	2090	105.661	
815	GAAAACAACATGCAACACGGC	874	ENNMQHG	2091	105.651	
816	AAGGGTGCACAGGGTGTTCAG	875	KGAQGVQ	2092	105.646	
817	GTCGCTGTATCGAACACTCCA	876	VAVSNTF	2093	105.643	
818	GTGAGTCTTCTTATTCTCGG	877	VESSYSR	2094	105.633	
819	CATAATACGGAGTCTAAGACT	878	HNTESKT	2095	105.625	
820	AATGAGAGTACGAAGGAGAGT	879	NESTKES	2096	105.599	
821	GATGTTTATCTTAAGAGTCCG	880	DVYLKSP	2097	105.586	
822	CAGTCGGGGGCTAGGACTCTG	881	QSGARTL	2098	105.5854	
823	TCGAACAGTCAAGTACACAAC	882	SNSQVHN	2099	105.573	
824	GTAGTCTCATCGGCGGCTGG	883	VVSSGGW	2100	105.551	
825	CCATCAAGTTTCAACAGCGCC	884	PSSFNSA	2101	105.542	
826	AAGCAGACTGATAGTAGGGGT	885	KQTDSPG	2102	105.5	
827	AACACAACGCCACCTAACAC	886	NTTPPNH	2103	105.483	
828	CAAAACGGAACCTCGTCTATA	887	QNGTSSI	2104	105.483	
829	CTCATGAAAGACATGGAATCC	888	LMKDMES	2105	105.458	
830	ACTCAGACTGGTCATGTTTCT	889	TQTGHVS	2106	105.4558	
831	GAAATACACACGACCACAGGC	890	EIHITTG	2107	105.449	
832	ATACAACTACTACAAAATGC	891	IQTTTKC	2108	105.442	
833	CCCGCTGAAGGAAACAACCGT	892	PAEGNNR	2109	105.442	
834	TACATCGCCGAGGGGAACAA	893	YIAGGEQ	2110	105.415	
835	GAAGTACGCGACCAAAAAACA	894	EVRDQKT	2111	105.375	
836	TACGCCGTCGCGATAGGCACA	895	YAVAIGT	2112	105.366	
837	TCCGCTAACGAACACAACCAC	896	SANEHNN	2113	105.337	
838	GGGATGAGGGATACGCCGCCG	897	GMRDTPP	2114	105.322	
839	GCTCAGCAGATTGTTAATGGG	898	AQQIVNG	2115	105.321	
840	TCAAGTTCCCAACGGTTTTG	899	SSSQTVL	2116	105.321	
841	GTTATTCAGTCTGATAATACG	900	VIQSDNT	2117	105.32	
842	GTTCCGGCGCATTTCTCGGGGT	901	VPAHSRG	2118	105.305	
843	TCGAATACGGGTCGTTGGGT	902	SNTGSLG	2119	105.2779	
844	TGGGCCAAAGACGTCAACGTC	903	WAKDVNV	2120	105.273	
845	AATGTGTTGGGTGCTTCGAGT	904	NVLGASS	2121	105.187	
846	ACTCCGGAGGCTAGTGC GCGT	905	TPEASAR	2122	105.173	
847	AATTATAATGGGGTTAATGTG	906	NYNGVNV	2123	105.152	
848	AACACAACCGGTAGCTCGGGC	907	NTTGSSG	2124	105.145	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
849	TCCAGCGGCCAACGCTCGTC	908	SSGQPLV	2125	105.136	
850	CAGGCGGGGGTGTGGCGAGT	909	QAGGVAS	2126	105.133	
851	CCGCTTCAATCCCAATCGGGA	910	PLQSQSG	2127	105.133	
852	CAACGTACCTCGGAAGCGCCA	911	QRTSEAP	2128	105.128	
853	TTGGCTAAGACGGTTGCGATT	912	LAKTVAI	2129	105.1155	
854	ACCCACACCCTTGGGGGAACA	913	THTLGGT	2130	105.08	
855	CACGACTACAGTATGAACGCG	914	HDYSMNA	2131	105.079	
856	GGGAAACCTGCGGAAGCGCCG	915	GKPAEAP	2132	105.055	
857	AGAAACGAAAACGTAAACGCT	916	RNENVNA	2133	105.051	
858	AGTTCTCGGGAGGCGAAGTTT	917	SSREAKF	2134	105.0379	
859	TCTTCTCTGATAGTCCGCGT	918	SSSDSPR	2135	105.035	
860	ATGAATACGACTTATAATGAG	919	MNTTYNE	2136	105.031	
861	GTAAGGAGTGAATAAAACCA	920	VRSGIKP	2137	105.008	
862	CAGGAGAATCCTATGAAGATG	921	QENPMKM	2138	104.926	
863	ACTGAGCCGCTTCCGATGTCT	922	TEPLPMS	2139	104.869	
864	CGCCACGGGGACACACCGATG	923	RHGDTPM	2140	104.844	
865	GCGGTGAATACGTATAATAGT	924	AVNTYNS	2141	104.82	
866	GCGTCGACTGAGTCTCATGTG	925	ASTESHV	2142	104.816	
867	ACAAACCTAAGTCAATCGGCC	926	TNLSQSA	2143	104.791	
868	GAGCTGTCTACTCCTATGGTT	927	ELSTPMV	2144	104.783	
869	TATGCGCATCCTGTGACTCAT	928	YAHVPTH	2145	104.76	
870	CGGGGGTCTACTGGTACGCAG	929	RGSTGTQ	2146	104.749	
871	TGTGTTGGTTCGTGTGGTGTG	930	CVGSCGV	2147	104.738	
872	TCGGTTGCTAAGGATCAGACG	931	SVAKDQT	2148	104.736	
873	ACGAATCTTCTCCTAAGACG	932	TNLSPKT	2149	104.6855	
874	CTAGGTTTCACACCCCAACCG	933	LGFTPQP	2150	104.677	
875	AATATTAGTAGTATTAATCAG	934	NISSINQ	2151	104.657	
876	GTTTACGACAACGTTTCTTCT	935	VYDNVSS	2152	104.657	
877	AGTGGAACAAGACAAATAC	936	SGKQDKY	2153	104.654	
878	AGACTTACAGAAGTGGTCATA	937	RLTELVI	2154	104.651	
879	CATAAGAGTGAGAGTCATAAT	938	HKSESHN	2155	104.626	
880	GAGGCGACTCATGGTTCTTAT	939	EATHGSY	2156	104.613	
881	AACCTACTTGTGACCAACGT	940	NLLVDQR	2157	104.579	
882	AATATTAATGATACTAAGAAT	941	NINDTKN	2158	104.522	
883	CITGCGGTACGAATGTGCGG	942	LAVTNVR	2159	104.498	
884	CCGTCGACACTCGCTGAAACA	943	PSTLAET	2160	104.449	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
885	CCGAAGCCTGGGACGGGGGAG	944	PKPGTGE	2161	104.427	
886	GTGCTGTTGCAGAATTCTCAT	945	VLLQNSH	2162	104.416	
887	TACGGTAACGCGAACACCGTA	946	YGNANTV	2163	104.386	
888	ACATCTGGAGTTCTGACACGC	947	TSGVLTR	2164	104.375	
889	AAAAAACGGAAACCAACCTC	948	KITETNL	2165	104.359	
890	GTTTCGAGAGACGAAACACCT	949	VRRDETP	2166	104.359	
891	TCTAAATGTCAAACCCAGTG	950	SKMSNPV	2167	104.352	
892	TGGGAATCCCTCTCCAACGCA	951	WESLSNA	2168	104.349	
893	GCCAACGGAGGAGGATACCCC	952	ANGGGYP	2169	104.34	
894	ATGTTGGCTTCTCGGGTGCCT	953	MLASRVP	2170	104.336	
895	TGCGGCTGAAGTGCAGTAAA	954	CGLNCGK	2171	104.331	
896	ACTATTACTAGTCGTCGGTG	955	TITSPSV	2172	104.3055	
897	TGGTCGAATGCTCAGAGTCCG	956	WSNAQSP	2173	104.288	
898	ACAGAAAGCCCCAACTACTA	957	TESPKLL	2174	104.283	
899	CATTTGTTACTAGTGGTATT	958	HLVTSGI	2175	104.273	
900	CCTCCTAAGTCGGATTCTGAAT	959	PPKSDSN	2176	104.265	
901	ATTGCGGTGCATGTGCTGAGT	960	IAVHVLS	2177	104.254	
902	ACTGGTACTGCGACTTTGCCT	961	TGTATLP	2178	104.254	
903	AATACTACTCCGCCTAATCAT	962	NTTPPNH	2179	104.232	
904	TGCACCGCCACAAATGCTCA	963	CTATKCS	2180	104.23	
905	CACAGTGACATGGTCAGCGGC	964	HSDMVSG	2181	104.208	
906	CCAAACGCACACCACCTGCCC	965	PNAHHLP	2182	104.2	
907	TCTAATAATATGAATCAGCGC	966	SNNMNQA	2183	104.187	
908	AGTGATAATAATAGGCTAAT	967	SDNNRAN	2184	104.1865	
909	TTGCAGACGCCTGGGACGACG	968	LQTPGTT	2185	104.169	
910	GTGCGCGCGTTCAAGACGCC	969	VRGVQDA	2186	104.167	
911	TCTCTAGACTCGCGCTCCTCG	970	SLDSRSS	2187	104.14	
912	GTTTGTGTTACTACTTGIGCT	971	VCVTTC	2188	104.137	
913	CCGAATACTAATCATCTTGTG	972	PNTNHLV	2189	104.121	
914	CTCATGTCAGGAAAAGAAAC	973	LMSGKEN	2190	104.109	
915	ACTTCTGCTAGTGAGAATTGG	974	TSASENW	2191	104.108	
916	TTTTTGCCGACGTGGGGCAG	975	FLPQLGQ	2192	104.094	
917	CCTTTTAATCTGGGAATGTG	976	PFNPGNV	2193	104.0922	
918	GGGACACCTGGTCAAAGTATA	977	GTPGQSI	2194	104.092	
919	TATAATAATGGTGGGCATGTT	978	YNNGGHV	2195	104.085	
920	CTCGGAAACCACTACACACCC	979	LGNHYTP	2196	104.064	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
921	CAAGTCAACCAACCGAGAATA	980	QVNQPRI	2197	104.061	
922	TTAGGAAACAACCGGCCACTA	981	LGNNRPL	2198	104.06	
923	CCTCCGGAAGTGCCAGGGGC	982	PPESARG	2199	104.023	
924	AAATCTGTAGCGACGGGAGA	983	KSVGDGR	2200	104.0009	
925	TCACTTCGGACGGACGAATTC	984	SLRTDEF	2201	103.997	
926	AGTACTACTAATGTTGCGTAT	985	STTNVAY	2202	103.987	
927	AGGATGTCGGATCCTAGTGAT	986	RMSDPSD	2203	103.981	
928	AGTCTGTCTATTACTTCGGCG	987	SLSITSA	2204	103.963	
929	GAAAGTGCCACATCTCTAAAA	988	ESATSLK	2205	103.954	
930	TACACTGACGGAAGAAACACC	989	YTDGRNT	2206	103.949	
931	TCCATATCCAACCTGCGTACC	990	SISNLRT	2207	103.935	
932	CAAAACGACAAATCTGACAAC	991	QNDKSDN	2208	103.9165	
933	GGTGGAACAGGTCTTTCCAAA	992	GGTGLSK	2209	103.916	
934	AGTCAGGCTCAGATTCGTGTT	993	SQAQIRV	2210	103.915	
935	GGTTTGATGGCGCATGTGACT	994	GLMAHVT	2211	103.877	
936	CTGGTTGTTTCGAATAGTCTG	995	LVVSNSL	2212	103.865	
937	CATGATTCTGTGAATACGGCG	996	HDSVNTA	2213	103.8588	
938	ACTCTTGCGAAGGATGGGAAT	997	TLAKDGN	2214	103.842	
939	TCCGACGGATCGAACTACTA	998	SDGSKLL	2215	103.829	
940	ATAGACAAAACGTTCTCGGTC	999	IDKTFSV	2216	103.812	
941	CGGCTGGTTAACATCGACCAC	1000	RLVNIDH	2217	103.8026	
942	AAAAACTACGACAGTGACTION	1001	KNYDSDS	2218	103.794	
943	AGTACGCAGAGTACTAATCCG	1002	STQSTNP	2219	103.7868	
944	CAAAATCACTACAACCTCGGC	1003	QISLQLG	2220	103.77	
945	TCCGAACCCCTTAGAGTTGGA	1004	SEPLRVG	2221	103.749	
946	AGTCGTCTGCAGACTCAGCAG	1005	SRLQTQQ	2222	103.7406	
947	GAAGGTTACAAGGAAACCAC	1006	EGSQGNH	2223	103.739	
948	CGTTCTGACCTTACTGAAAAGT	1007	RSDLTES	2224	103.736	
949	CATACTGGTGTTTACAGCTAAT	1008	HTGVQTN	2225	103.724	
950	GAGTTGGATCATCTTTTCGCAT	1009	ELDHLSH	2226	103.714	
951	GTTACTGGTGTGATTATGCG	1010	VTGVDYA	2227	103.713	
952	GGCGGCGCACACACTCGTGTA	1011	GGAHTRV	2228	103.676	
953	GCCTACGGTATACACGAAGTG	1012	AYGIHEV	2229	103.653	
954	GCGATGCTGCGTATGGAGCAG	1013	AMLRMEQ	2230	103.652	
955	AGGCAGGCGAATCAGACGTAT	1014	RQANQTY	2231	103.652	
956	TTTTCTGGTCAGGCGTTGGCT	1015	FSGQALA	2232	103.646	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
957	GATAATGTGAATTCTCAGCCT	1016	DNVNSQP	2233	103.646	
958	GGGTTGCATGGGACGAGTAAT	1017	GLHGTSN	2234	103.633	
959	GAGAGGGAGCCTCCTAAGAAT	1018	EREPPKN	2235	103.621	
960	GTGGTGACGCTTGGGATGCTG	1019	VVTLGML	2236	103.619	
961	CATAATAATAATTTGCTGAAT	1020	HNNNLLN	2237	103.612	
962	TTGATTAATATGAGTCAGAAT	1021	LINMSQN	2238	103.6	
963	AATACTAATGCGTCGTATTCT	1022	NTNASYS	2239	103.599	
964	AGGCTTAATGCGGGTGAGCAT	1023	RLNAGEH	2240	103.594	
965	GCTGTTATTCTGAATCCTGTT	1024	AVILNPV	2241	103.576	
966	CCGAGTACTCATGGGTATGTT	1025	PSTHGYV	2242	103.571	
967	CTTAGGGCGTCTGTGTCGGAG	1026	LRASVSE	2243	103.564	
968	ATGATGACCTCTATGACGTTA	1027	MMTSMTL	2244	103.561	
969	TCGGCACACAACATAGTATAC	1028	SAHNIVY	2245	103.556	
970	CACGACAGCACAACCCGCCCA	1029	HDSTTRP	2246	103.545	
971	ATCAAAGACTCGTACCTTACT	1030	IKDSYLT	2247	103.542	
972	TATACGCCTGGGCTTACTGAG	1031	YTPGLTE	2248	103.541	
973	AAGATGGGTGTTTCTCAGAGT	1032	KMGGSQS	2249	103.477	
974	TCACGTCAAACAGCGCTAACA	1033	SRQTALT	2250	103.4599	
975	GTAGAAACCAGCAGATTGTAC	1034	VETSRLY	2251	103.45	
976	AAATCCAACAACGGGAATAC	1035	KSNNGEY	2252	103.424	
977	TCGGGTGTTTATAGTGCGCGT	1036	SGVHSAR	2253	103.3881	
978	CCTAACACGAAAAAACCCG	1037	PNNEKNP	2254	103.326	
979	ACTATTGGTGAGGGGTATCAT	1038	TIGEGYH	2255	103.325	
980	CTGCAGACTTCTGTTGCTACT	1039	LQTSVAT	2256	103.316	
981	CTATTGGGAAACGCACCCACA	1040	LLGNAPT	2257	103.308	
982	ATTCGGGGTCTCATTGAAT	1041	ISGSHLN	2258	103.297	
983	AAGTCTCTTAGTAGTGATGAT	1042	KSLSSDD	2259	103.285	
984	ACGAGGACTCAGGGGACGTCT	1043	TRTQGTS	2260	103.2635	
985	GTTAGTAGGTCITGGGAGTACT	1044	VSRSGST	2261	103.257	
986	AGCGCCGACACCCGGTCCCCC	1045	SADTRSP	2262	103.242	
987	CGTGATACTGCTAATGGGCCG	1046	RDTANGP	2263	103.2389	
988	ATGATGTCTAACAGCCTCGCG	1047	MMSNSLA	2264	103.232	
989	ACTGGGAGGATTGAGCTTAGG	1048	TGRIELR	2265	103.214	
990	GCTAATAATGCGGCTGCGTCG	1049	ANNAAAS	2266	103.209	
991	CAGTTGAATATTAATGATAAG	1050	QLNINDK	2267	103.208	
992	ATGGACGGGGCTCACACGTCA	1051	MDGAHTS	2268	103.202	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
993	ACTAGTGC GACTGATTCTGATG	1052	TSATDSM	2269	103.197	
994	GCCGCCAGCTTGTTCGCAAAGC	1053	AASLSQS	2270	103.152	
995	TCTCAGGCGGGTCTGCTTG TG	1054	SQAGLLV	2271	103.116	
996	ACGACTTATTCGGATCTGAGT	1055	TTYSDL S	2272	103.104	
997	TTCTCCTCCGGAACAACCAT A	1056	FSSGTTI	2273	103.102	
998	GTCTTCACAGAAATAGAA TCG	1057	VFTEIES	2274	103.101	
999	GCAGACCCCGCTAAAGGCAAA	1058	ADPAKGK	2275	103.083	
1000	AAAGAATCTGAATACAGAG TT	1059	KESEYRV	2276	103.07	
1001	GGGATGGTGTCTCTTAATAG G	1060	GMVSLNR	2277	103.06	
1002	ACCGTTATCGAACGCAAAGAC	1061	TVIERKD	2278	103.0575	
1003	AGGATTGATACGTTGTTGG TG	1062	RIDTLLV	2279	103.055	
1004	GGATCCACAGGCCTACCCCG	1063	GSTGLPP	2280	103.047	
1005	ATGGAGTTGACTTCTACTAG T	1064	MELTSTS	2281	103.026	
1006	CAACCAGGAGCCCCCAAACC	1065	QPGAPQT	2282	103.014	
1007	AATTCGATGGGTAATGGGGGT	1066	NSMGNGG	2283	103.009	
1008	GGTAGTACTAAGTCTGGGCAG	1067	GSTKSGQ	2284	103.0049	
1009	ACTTTTTTGCCTCAGCTTGG G	1068	TFLPQLG	2285	102.994	
1010	ATGGGAATAAACGTACTGAGC	1069	MGINVLS	2286	102.986	
1011	GTGAATCTTGGTATTTTCGGG G	1070	VNLGISG	2287	102.985	
1012	AGTGAGAATCGGGCTGGTAAT	1071	SENRA GN	2288	102.945	
1013	CACTCCAACGCGACTACGATA	1072	HSNATTI	2289	102.916	
1014	CCGGGGTCGTCCGCTTCCATC	1073	PGSSASI	2290	102.914	
1015	ATTACGTCGTTGAATGGGATG	1074	ITSLNGM	2291	102.909	
1016	TATCTGGAGGGTGCTCATCGT	1075	YLEGAHR	2292	102.896	
1017	AGGCAGGTTGAGCAGTCTGAT	1076	RQVEQSD	2293	102.889	
1018	AGCTCTCAAAGITCCGGGTCG	1077	SSQSSGS	2294	102.8836	
1019	CAGCTTACTGTTGGGAAGCCG	1078	QLTVGKP	2295	102.8762	
1020	GTTGTGCATTTCGAGTATTACT	1079	VVHSSIT	2296	102.8257	
1021	CTAGAACAAC TACGGGTCCCA	1080	LEQLRVP	2297	102.815	
1022	CAGCATTCTCCGAAGCCGTT	1081	QHSPKPV	2298	102.81	
1023	GCGGGCAGTTCGCCATCACGC	1082	AGSSPSR	2299	102.8035	
1024	GGAGTAACAATCGGTAGCAGG	1083	GVTIGSR	2300	102.7752	
1025	TACATCGCGGGAGGCGACCAA	1084	YIAGGDQ	2301	102.75	
1026	ATTAGTAGTGAGAGTTTTCT	1085	ISSERFS	2302	102.729	
1027	AGGAGTGAGGGTAATCATGCT	1086	RSEGNHA	2303	102.719	
1028	GAGAAGGGGAATAGTGGGGTT	1087	EKGNSGV	2304	102.71	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1029	TACATAGTTGACCACGCTAAC	1088	YIVDHAN	2305	102.71	
1030	CGTCGGTTGAGTACGGATCTT	1089	RRLSTD L	2306	102.702	
1031	GCGAATAGTAGGCTTGGGGCG	1090	ANSRLGA	2307	102.6979	
1032	GGTACTGCTGAGAATACGAGT	1091	GTAENTS	2308	102.696	
1033	GTGAGGGATGTTGCTAAGGAG	1092	VRDVAKE	2309	102.691	
1034	GGAGGCCTTACCAACGGTCTA	1093	GGLTNGL	2310	102.67	
1035	CCTTCGATTCCGTCGTTTTTCG	1094	PSIPSF S	2311	102.657	
1036	AACGCTCTCCTCAACGCACCT	1095	NALLNAP	2312	102.628	
1037	GACGACATGGTCAAAAAC TCA	1096	DDMVKNS	2313	102.623	
1038	ACTGCGAATACGCATGCTCTG	1097	TANTHAL	2314	102.613	
1039	GTATACGCCACCGCACTCGCA	1098	VYATALA	2315	102.611	
1040	GGTATATACCCGGCATCCACC	1099	GIYPAST	2316	102.61	
1041	GGTTTTGATGGTAAGCAGCTT	1100	GFDGKQL	2317	102.606	
1042	CACTCTATGTCGCCAAACACC	1101	HSMSANT	2318	102.605	
1043	TGGAGCATCAAAAACCAACA	1102	WSIKNQT	2319	102.586	
1044	ACCTCCACACCAAGACCTA	1103	TLHTKDL	2320	102.57	
1045	TCTTATGGTAATACTCATGAT	1104	SYGNTHD	2321	102.566	
1046	CAGTCGGGGTCTCTGGTGCCG	1105	QSGSLVP	2322	102.552	
1047	AATACTTTGCAGAATAGTCAT	1106	NTLQNSH	2323	102.5506	
1048	ACGGCTGAGTCTAGTCATCCG	1107	TAESSHP	2324	102.548	
1049	GCCTCTACAGTCTCACTCTAC	1108	ASTVSLY	2325	102.547	
1050	CTGACTGCTGTTGCGATTAGT	1109	LTAVAIS	2326	102.542	
1051	GTCTCGGACAAAGTGC GTAC	1110	VSGQSAY	2327	102.541	
1052	GGTGAAACTA ACTTCCCAACT	1111	GETNFPT	2328	102.532	
1053	AATGATAATAGGTCGATGAAT	1112	NDNRSMN	2329	102.526	
1054	CGATCAGCGCACCTAAAAAC	1113	RSGBPKN	2330	102.519	
1055	TGGGAGAGTGATAAGTTTCGT	1114	WESDKFR	2331	102.514	
1056	CAGGTTAATCATAATACTAGT	1115	QVNHNTS	2332	102.514	
1057	GGGTGGTCGAACAACGA ACTA	1116	GWSNNEL	2333	102.507	
1058	CGGGCTGTGCTTGCGACTAAT	1117	RAVLATN	2334	102.49	
1059	CATATGGGTTTGAATGAGCTT	1118	HMGLNEL	2335	102.484	
1060	GGAGAAAGCTCCTCAATAAGC	1119	GESSSIS	2336	102.477	
1061	ATACACAAATCTAGCGTCGAA	1120	IHKSSVE	2337	102.473	
1062	ATGTCCGGATCCATGATATCA	1121	MSGSMIS	2338	102.463	
1063	TTGAGTCTGGCTGGGAATAGG	1122	LSLAGNR	2339	102.448	
1064	TCTGCAACAACGAACCA CGGA	1123	SATTNHG	2340	102.441	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1065	TCTACGGAGTCTAATGCTAGT	1124	STESNAS	2341	102.43	
1066	CCGATTGCTGAGAGGCCTTCT	1125	PIAERPS	2342	102.428	
1067	TTACTTCCAAACAACCCAC	1126	LLPNNTH	2343	102.424	
1068	GGGACTCTTAAGAAGGATGCG	1127	GTLKKDA	2344	102.412	
1069	GCTCTTGAGAAATCGGAGTCTG	1128	ALENRSL	2345	102.408	
1070	ACCACCGGGAATCCACGATG	1129	TTGNSTM	2346	102.383	
1071	GTGTATGATAGTGCCTAAT	1130	VYDSAPN	2347	102.366	
1072	CTACTATCTAAAGGGGACTCC	1131	LLSKGDS	2348	102.346	
1073	TCTTACGCCATAAACCAATCA	1132	SYAINQS	2349	102.335	
1074	GGAGGAGGGGAACGTTCCACG	1133	GGGERST	2350	102.323	
1075	ATTCAGGTTAGTGGTAGTCAG	1134	IQVSGSQ	2351	102.315	
1076	TATCCTGTTTCGCTTTCGCCG	1135	YPVSLSP	2352	102.312	
1077	GAGTTGGGTAATAAGACGGCT	1136	ELGNKTA	2353	102.311	
1078	TCGGGGGTAAACTTCGGAGTA	1137	SGVNFGV	2354	102.287	
1079	GCGTGGAGTTCGCCGAGTGGG	1138	AWSSPSG	2355	102.285	
1080	GGTGTGAATTATCATACTACG	1139	GVNYHTT	2356	102.261	
1081	CTGATTGGGGAGCTTAAGATG	1140	LIGELKM	2357	102.255	
1082	TATCTGAATAGTAAGCAGCTT	1141	YLNSKQL	2358	102.212	
1083	ACTGTTGATAGCCGATTGTG	1142	TVDRPIV	2359	102.191	
1084	GTCAGCAAACCAAAGACTCG	1143	VSKTKDS	2360	102.184	
1085	CAAGCTGGGAACGCGCCAAGG	1144	QAGNAPR	2361	102.1806	
1086	CAAGACCAAACGAGCAACCGT	1145	QDQTSNR	2362	102.177	
1087	GATACTACGTATCGGAATACT	1146	DTTYRNT	2363	102.173	
1088	GGGACAACCGAAGTTAACAAA	1147	GTTEVNK	2364	102.17	
1089	GGGTTTACTAATACGAGTAAG	1148	GFTNTSK	2365	102.152	
1090	GTGCAGAAGAATGATGTGCTT	1149	VQKNDVL	2366	102.14	
1091	AGCGTCAACAACATGCGACTC	1150	SVNNMRL	2367	102.1324	
1092	TTCAGTGCCGCCTTACCGTTA	1151	FSAALPL	2368	102.13	
1093	GACGTCCCAAACAACAAAGG	1152	DVPNNKR	2369	102.126	
1094	GGTGAGACTATGCGTCATAAT	1153	GETMRHN	2370	102.119	
1095	ATTCGGACTTCTGTGATTAAT	1154	IRTSVIN	2371	102.103	
1096	CCGCGTGCTCCIGGTCATAAT	1155	PRAPGHN	2372	102.101	
1097	AGTGTTCGCGATCCTTTGTCT	1156	SVAHPLS	2373	102.101	
1098	ATGACAATAACCGTCGAACCG	1157	MTITVEP	2374	102.096	
1099	CCATTAAACGCGAACGGCTCC	1158	PLNANGS	2375	102.094	
1100	AATAGGCAGCGGGATTTTGAG	1159	NRQRDFE	2376	102.073	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1101	GATATTCATAATCCGCGTACG	1160	DIHNPRT	2377	102.073	
1102	TGGATAGCAGGAAACCACTCC	1161	WIAGNHS	2378	102.07	
1103	TCTACTCATCATGCTGATCGT	1162	STHHADR	2379	102.069	
1104	CCGGAATCCGCCGCCAAAAGC	1163	PESAASKS	2380	102.058	
1105	CACTCCGACAAAGTCTCCTCA	1164	HSDKVSS	2381	102.051	
1106	TCAAACAGCGCCGACGCGGGG	1165	SNSADAG	2382	102.047	
1107	GAGTTTCAGAGGATTCGTGAG	1166	EFQRIRE	2383	102.039	
1108	TCCGCGGGGATGACATTGGAC	1167	SAGMTLD	2384	102.016	
1109	ACTCAAACCTTCTACCTGGACC	1168	TQTSTWT	2385	102.009	
1110	ACGACACTAACGCAACCGGAC	1169	TTLTQTD	2386	102.003	
1111	GCCTCGAAAGGCTTCGGCCAC	1170	ASKGFGH	2387	101.991	
1112	CCGGCTACGATGATTAGTGAG	1171	PATMISE	2388	101.985	
1113	ACTGACTCATCTGCAGACTCC	1172	TDSSADS	2389	101.981	
1114	TCAACCAGAAAAGAACACGAC	1173	STRKEHD	2390	101.98	
1115	GGTGATATTTCTTATAGGGTT	1174	GDISYRV	2391	101.977	
1116	ATGGGGTATGTTGATAGTCTG	1175	MGYVDSL	2392	101.953	
1117	CAAACCATCACCTCACAATG	1176	QTITSQM	2393	101.941	
1118	TCGATTGGGTATTTCGCTCCG	1177	SIGYSPP	2394	101.939	
1119	TCATCCCCAGACTCGTACAGA	1178	SSPDSYR	2395	101.921	
1120	ATTAGTCCGAGTGCTTCTAAT	1179	ISPSASN	2396	101.855	
1121	TATCCGGCTGATCATCGGACT	1180	YPADHRT	2397	101.85	
1122	CACACCGGCCAAACACCATCA	1181	HTGQTPS	2398	101.837	
1123	CAGACGACTATTCTGGCTGCT	1182	QTILAA	2399	101.837	
1124	GATGGTACGAGGCAGGTTTCT	1183	DGTRQVH	2400	101.836	
1125	AGGAGTAGTCTGCGACGAAT	1184	RSSPATN	2401	101.829	
1126	GCGATGAGTCATACGTATAAG	1185	AMSHTYK	2402	101.813	
1127	ATGGCGGCTCCGCCGAGCAT	1186	MAAPPEH	2403	101.802	
1128	GGTCCTAGTACTTCGGAGGCG	1187	GPSTSEA	2404	101.794	
1129	CATAATCATGATAGGTCGTCT	1188	HNHDRSS	2405	101.7829	
1130	GTGGTCCCATCGACCAAGCA	1189	VVPSTQA	2406	101.781	
1131	ATTCCTGTGACTACTCGTAAT	1190	IPVTTRN	2407	101.722	
1132	AACCAACTCGTACGCGGGACA	1191	NQLVRGT	2408	101.717	
1133	GGGTTTGCCTTACGGGTACG	1192	GFALTGT	2409	101.696	
1134	TCTAAGGGTGGTGATATGGTG	1193	SKGGDMV	2410	101.666	
1135	GCTCGACCAGGCCAATCTATG	1194	ARPGQSM	2411	101.6287	
1136	AAAGCAGACTACGAATCCTCC	1195	KADYESS	2412	101.626	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1137	GGACCAAGTTCGCACATCGTT	1196	GPSSHIV	2413	101.616	
1138	GAAGTTGTCAAAACACGCAC	1197	EVVKTH	2414	101.61	
1139	ACTTTGGATAATAATCATTCT	1198	TLNNHS	2415	101.604	
1140	ACGATTTATAATATGGGTCCG	1199	TIYNMGP	2416	101.599	
1141	TCTACCATGAACACGATCACG	1200	STMNTIT	2417	101.597	
1142	ACGCTGGCGCGGACTACTGAG	1201	TLARTTE	2418	101.581	
1143	TTGATTTCTTCGCAGACTTCT	1202	LISSQTS	2419	101.553	
1144	CAGACTGCGTCTGGTGATACT	1203	QTASGDT	2420	101.497	
1145	GCGCATGGTGCTTTCCGGTT	1204	AHGAFPV	2421	101.495	
1146	GGGGAGACGCGGTCGACTGCT	1205	GETRSTA	2422	101.494	
1147	AACAACACGCTACTCCGCT	1206	NNYAYSA	2423	101.493	
1148	GAGGCTTATCAGACTGAGAAG	1207	EAYQTEK	2424	101.49	
1149	TCTCTAGCACACGCCGTAAGC	1208	SLAHAVS	2425	101.485	
1150	ACGTATCAGTTGAGTGGGAAT	1209	TYQLSGN	2426	101.452	
1151	ATGAGCGAAAGTTGCGGATA	1210	MSERLRI	2427	101.431	
1152	GGGTCGGGAAAGACCCAGGG	1211	GSGKDPG	2428	101.43	
1153	TACAACAGCAACGCTTCTGTA	1212	YNSNASV	2429	101.428	
1154	ACGAGGGGTGATATGGAGTTT	1213	TRGDMEF	2430	101.424	
1155	GGAATCACCGAAGCCCCGGC	1214	GITGSPG	2431	101.42	
1156	CAACACACGCCACCCCATG	1215	QHTAHPM	2432	101.416	
1157	GATACGGCGAATCGTTCGACT	1216	DTANRST	2433	101.407	
1158	TCGGCACACGACGCAAGACTA	1217	SAHDARL	2434	101.387	
1159	CTTAATCATACTCTGGGGCAT	1218	LNHTLGH	2435	101.385	
1160	GGGTTTGAGACGAGTAGTCCT	1219	GFETSSP	2436	101.369	
1161	GGTACGAGTCCGAGAGTCGG	1220	GTSAESR	2437	101.366	
1162	CATGCTAATTATGTTGAGGTG	1221	HANYVEV	2438	101.345	
1163	ACAACGAAACCGGTCGCGGAA	1222	TTKPVAE	2439	101.338	
1164	TCGACCGCGTTACTAACTCA	1223	STAVTNS	2440	101.304	
1165	CTGGGCTTGCTGGTCAGGTT	1224	LGLAGQV	2441	101.304	
1166	GTGCTTAAGGGTACGTTTCCG	1225	VLKGTFF	2442	101.298	
1167	ATGAATGAGCCTGGTAGGACG	1226	MNEPGRT	2443	101.283	
1168	ACTTCTGATCCTTTGAGGAAT	1227	TSDPLRN	2444	101.252	
1169	CGTGATACTAATACGATAAG	1228	RDTNTDK	2445	101.234	
1170	GAGTCTGATTTGCGTCAGCGG	1229	ESDLRQR	2446	101.225	
1171	TCCGGAATGGCCGGCCTTCC	1230	SGMAGLS	2447	101.211	
1172	ATAGCAACAACGCTCTGGGCGG	1231	IATTSGR	2448	101.21	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1173	ACGATTAGGAGTGAGGGTTTT	1232	TIRSEGF	2449	101.202	
1174	GGTCTGTCTATTACTATTGCG	1233	GLSITIA	2450	101.176	
1175	CCGCCTACTAATGGGCGTATG	1234	PPTNGRM	2451	101.17	
1176	CTACAAGACCGGGCAACGAAC	1235	LQDRATN	2452	101.165	
1177	CTTAAATCGACCGGTGACCAC	1236	LKSTGDH	2453	101.132	
1178	GATAATAATAATCAGGTTTAT	1237	DNNNQVY	2454	101.13	
1179	GTGCATATGGAGTCGTATGCG	1238	VHMESYA	2455	101.111	
1180	GACCAAATAGGGCAGGAACA	1239	DQIGHGT	2456	101.106	
1181	GGGACGGGGCCGCATGGTACT	1240	GTGPHGT	2457	101.0712	
1182	ATTGGGAATAATACTGGTCTT	1241	IGNNTGL	2458	101.0529	
1183	TTAAACGCAGAATACACCAAC	1242	LNAEYTN	2459	101.047	
1184	GTGACGTCGTCTGCTAGTGGT	1243	VTSSASG	2460	101.027	
1185	ACGCATGTTGCTAAGCCTGAT	1244	THVAKPD	2461	101.017	
1186	CCGATGAACAAAGACATACTG	1245	PMNKDIL	2462	100.9906	
1187	CTTAGTTTGAATATGAATGAG	1246	LSLMNE	2463	100.99	
1188	GTCGGCAACTCAAGCACTCAC	1247	VGNSSTH	2464	100.99	
1189	GGCCACGGAAGTGACTTGACC	1248	GHGSDLT	2465	100.9576	
1190	CTTACACAAAACCAACGAAC	1249	LTQNPTN	2466	100.934	
1191	CCGAGTGATCATATGCGGACT	1250	PSDHMRT	2467	100.8849	
1192	CCTGATAGTCGTTTGGCGGCT	1251	PDSRLAA	2468	100.843	
1193	TGGGGTAGTGAGGGGACGATT	1252	WGSEGTI	2469	100.84	
1194	AAACCGACAAACGACTCGTAC	1253	KPTNDSY	2470	100.821	
1195	AACCGCGGAACAGAAGTTTAC	1254	NRGTEVY	2471	100.8147	
1196	CACGTGATCACAACAAAAGAC	1255	HVITTKD	2472	100.7896	
1197	ATTGTGTCTAATCCGCCGGCG	1256	IVSNPPA	2473	100.76	
1198	ATGCGTAACGACCAACAACCTT	1257	MRNDQQL	2474	100.7503	
1199	TTTCAGCGTGATGTTGGTCAT	1258	FQRDVGH	2475	100.7392	
1200	GCCAACGACAAACCAAAACAA	1259	ANDNTKQ	2476	100.7364	
1201	TCTGTTCCGCATGCGGGGAT	1260	SVPHAGD	2477	100.7276	
1202	AATGCTACTCCGCCGAATCAT	1261	NATPPNH	2478	100.6678	
1203	TCAGAACACACATCAGTTCTA	1262	SEHTSVL	2479	100.64	
1204	GCCATGTCCCAACGGACATC	1263	AMSQTDI	2480	100.628	
1205	CCTAAGGCTCCGCTTAATAAT	1264	PKAPLNN	2481	100.627	
1206	ACCAACAACCTTACTCGCACAA	1265	TNNLLAQ	2482	100.55	
1207	CAGCGTCAGGGITCGGGGTT	1266	QRQSGSV	2483	100.5318	
1208	CGCAGTGACACCACTAACGCC	1267	RSDDTNA	2484	100.51	

TABLE 1-continued

CK8 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	Amino Acid Sequence	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1209	GAGGCTGATAAGAATGGTGTT	1268	EADKNGV	2485	100.386	
1210	ATGCTGGGGGTTTTCGCGAG	1269	MLGGFAQ	2486	100.3622	
1211	ATGACACACCTCAGCACAGAC	1270	MTHLSTD	2487	100.267	
1212	GTTTTGTCTGATAAGGCGTTT	1271	VLSDKAF	2488	100.231	
1213	ACACCTCCGGTACCATAAAA	1272	TPSGTIK	2489	100.22	
1214	ATTATTCTTATGGGTCAGAGT	1273	IILMGQS	2490	100.213	
1215	CTTTCGGGGGTGAGACTCTT	1274	LSGGETL	2491	100.154	
1216	ACCGACGGCGCCTGGGTAC	1275	TDGALGY	2492	100.129	
1217	GGGAATAAGGCTGCGCTGACG	1276	GNKAALT	2493	100.066	

TABLE 2

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100		
1	AGAGGAGACTTGACAACCCCA	2494	RGDLTTP	3737	576.12	
2	CGGGGTGATCTTAATCAGTAT	2495	RGDLNQY	3738	496.41	
3	AGGGGTGATCTTTCTACGCCT	2496	RGDLSTP	3739	475.909	
4	CGGGGTGATCAGCTTATCAT	2497	RGDQLYH	3740	460.578	
5	CGAGGAGACCATGAGCAA	2498	RGDTMSK	3741	439.771	
6	AGGGGGGATGCGACGGAGCTT	2499	RGDATEL	3742	429.74	
7	AGAGGCGACTTATCCACACCC	2500	RGDLSTP	3743	429.182	
8	CGCGGCGACATGATAAACACC	2501	RGDMINT	3744	397.62	
9	AGGGGCGACCTGAACCAATAC	2502	RGDLNQY	3745	388.417	
10	CGGGGGGATACTATGTCTAAG	2503	RGDTMSK	3746	352.268	
11	CGGGGTGATCTTACTACGCCT	2504	RGDLTTP	3747	320.042	
12	AGGGGCGACCTCAACGACAGC	2505	RGDLNDS	3748	315.615	
13	GCAAACCCCAACATACTAGAC	2506	ANPNILD	3749	302.02	
14	CGAGGCGACACAATGAACTAC	2507	RGDTMNY	3750	285.332	
15	ATGAGTAATTTGGGTATGAG	2508	MSNLGYE	3751	270.74	
16	TACACCTCTCAAACGAGCACT	2509	YTSQTST	3752	256.544	
17	CTCGGAGGAAACAGCAGGTTT	2510	LGNSRF	3753	255.425	
18	CAAAGCCAAGCGATACAATA	2511	QSQAQL	3754	254.191	
19	AACACGTACACCCGGGAAAA	2512	NTYTPGK	3755	239.565	
20	GGGGCGGAAGCGGGCCGCAA	2513	GAEAGRQ	3756	237.2829	
21	GAACACGCTACAGCAAAACAA	2514	EHATAKQ	3757	236.826	
22	GCGGCACAACCTCGTCAGTCCA	2515	AAQLVSP	3758	225.034	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
23	GATCAGACGGCTAGTATTGTT	2516	DQTASIV	3759	224.832	
24	GTTCAAACCCACATAGGAGTC	2517	VQTHIGV	3760	224.306	
25	TCTTATGGTAATACTCATGAT	2518	SYGNTHD	3761	224.26	
26	ACCTCCACGGCTTCAAACAA	2519	TSTASKQ	3762	221.617	
27	TGGTGACTCATGAGCGGATT	2520	LVTHERI	3763	219.227	
28	ATGGATAAGTCTAATAATTCT	2521	MDKSNN	3764	216.638	
29	CGTGGTGATATGTCTCGTGAG	2522	RGDMSRE	3765	214.708	
30	CGCGGTGACGTGGCAGAAATA	2523	RGDVAEI	3766	212.967	
31	GGTGGCGAAAACAGAACCCCA	2524	GGENRTP	3767	210.4	
32	GCTGGGCATCAGCAGCTTGCT	2525	AGHQQLA	3768	210.1746	
33	CGTCTTAATAGTAGTATGAAT	2526	RLNSSMN	3769	209.449	
34	TATTATGAGAAGCTTAGTGCG	2527	YYEKLSA	3770	209.263	
35	GAAGCGTCCAACACGAACGA	2528	EASNYER	3771	209.09	
36	TTCCAAACTGACACGCACCGA	2529	FQTDTHR	3772	208.95	
37	AACAGTTCCCAATGGCCCAAC	2530	NSSQWPN	3773	208.638	
38	GATGGTAAGACTACGTCTAAT	2531	DGKTTSN	3774	207.638	
39	GCTGTGCATGCGACTAGTAGT	2532	AVHATSS	3775	205.952	
40	AAAACACTCCCCGGCAGGGAA	2533	KTLPGRE	3776	205.926	
41	ATACTGAAATCCGACGCACCA	2534	ILKSDAP	3777	204.523	
42	AGTACGAATGAGGCTCCTAAG	2535	STNEAPK	3778	204.522	
43	TTTGATAGTGCGAATGGTCGG	2536	FDSANGR	3779	203.996	
44	ATGGACGCTGCGTACGGTAGT	2537	MDAAYGS	3780	203.401	
45	AACAAAGACCACAACCCTG	2538	NKDNHNL	3781	202.878	
46	GGTCAGTATAGTCAGACGCTT	2539	GQYSQTL	3782	202.553	
47	GAAGCATTCCCGCAGCGGGC	2540	EAFPRAG	3783	202.275	
48	GAACACACTCACTTAAACCCG	2541	EHTHLNP	3784	201.959	
49	ATGCAACGCGAAGACGCGAAC	2542	MQREDAN	3785	201.523	
50	CTAACCGGCTCTGACATGAAA	2543	LTGSDMK	3786	200.376	
51	CGAGTAAACAACGACGCAATA	2544	RVNNDIAI	3787	200	
52	CGTGGTGACCAAGGCACACAC	2545	RGDQGTH	3788	200	
53	ATTAATATTAGTAGTGATTTT	2546	INISSDF	3789	200	
54	AATAATGATAATGGTTTGT	2547	NNDNGFV	3790	200	
55	TTCATCGCTAACACTAACCCA	2548	FIANTNP	3791	200	
56	GGACTGCACGGCACCAACGCA	2549	GLHGTNA	3792	200	
57	AAAACCATCGACATAGCACAA	2550	KTIDIAQ	3793	200	
58	TCGAGTGATTCTCGTATTCCG	2551	SSDSRIP	3794	200	
59	TCTACATCTCCGGTTAACAGC	2552	STSPVNS	3795	200	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100		
60	GCCAGCATGCCCTCTGTAGAC	2553 ASMPDVD	3796	200		
61	GGTCATAATATGGCACAGGCG	2554 GHNMAQA	3797	200		
62	CACAACAAACCAACGGAGAC	2555 HNKPNGD	3798	197.851		
63	TACAGGATGGAACGAACCCA	2556 YRMETNP	3799	197.46		
64	CTTGGAATGTGGTTCATCCG	2557 LGNVVHP	3800	197.383		
65	GTAACGGCACACCAATTATCC	2558 VTAHQSL	3801	196.095		
66	ACTATGGTAGAAGTACTGCCA	2559 TMVEVLP	3802	195.586		
67	ATCAAAGGGTCTGGGTCGCAA	2560 IKGSGSQ	3803	195.296		
68	ACTAATGGGGGTCGCTTAAT	2561 TNGGSLN	3804	193.959		
69	CTCGGAGGAAACAGCAGGATC	2562 LGGNSRI	3805	193.21		
70	AGGGGTGATGCGGCGAATAAG	2563 RGDANK	3806	193.16		
71	GCGTTAAACGCCCAAGGGATC	2564 ALNAQGI	3807	192.986		
72	GCTGAGCATGCGACTAGTAGT	2565 AEHATSS	3808	192.59		
73	TACTTGACCACCGTACTGCC	2566 YLTTGTA	3809	191.521		
74	GCGGAGGCTCAGACGCGTGTG	2567 AEAQTRV	3810	189.899		
75	GCTGAGCAGGGGTCTCTTCG	2568 AEQGLSS	3811	188.94		
76	CTGATTGTTACTCAGCATGTG	2569 LIVTQHV	3812	188.588		
77	TCTAGTTATCAGTCTGGGCTG	2570 SSYQSGI	3813	188.4		
78	GCTACGGTTTATAATGAGTTG	2571 ATVYNEL	3814	188.18		
79	CATGATACGGTTGGGAGAGG	2572 HDTVGER	3815	187.269		
80	CGTGGGGATTTGAATGATTCT	2573 RGDNDL	3816	187.25		
81	CATGATATTAGTCTGGATCGT	2574 HDISLDR	3817	186.65		
82	ACAGAACAACTTACTCACGA	2575 TEQSYSR	3818	186.237		
83	TGGTGAGGGGCTGAGTTTGCC	2576 W*GAEFA	3819	186.1		
84	GCTGTGCATGCGACTAGTAGA	2577 AVHATSR	3820	185.9		
85	ATTGAGAGTAAGACTGTGCAG	2578 IESKTVQ	3821	185.818		
86	ACGAATGTTAGTACGCTTTTG	2579 TNVSTLL	3822	184.365		
87	CCACCAACGGCAGCAGTAGA	2580 PPNGSSR	3823	183.258		
88	CCCTCTACACACGGCTACGTA	2581 PSTHGYV	3824	183.235		
89	ACTGCGGCTAGTACTGCGAGG	2582 TAASTAR	3825	182.452		
90	TACAACGAGGCGGAGAACAA	2583 YNAGGEQ	3826	182.14		
91	ACCCACAACCAACGTGAACGTG	2584 THNQREL	3827	181.989		
92	ACCTTCACGGTCGACGGTAGA	2585 TFTVDGR	3828	181.724		
93	CACTCCAGCCCCGGTCGTCA	2586 HSSPGSS	3829	181.331		
94	AGTACGAGTGGTTATAATACT	2587 STSGYNT	3830	180.372		
95	TCTGAGAAGCTGACTGATAAG	2588 SEKLTDK	3831	180.174		
96	GGGAGGAACACAAGTAACCTTG	2589 GRNTSNL	3832	180.156		

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
97	ACCGGAACAGCGATCTCCCGA	2590	TGTAISR	3833	180.148	
98	TCTATGCAGGATCCTTCTTTG	2591	SMQDPSL	3834	179.222	
99	ACTCGGAGTGATATTGGTGTG	2592	TRSDIGV	3835	178.75	
100	ACGCAGAATCATCAGTTGTCT	2593	TQNHQLS	3836	178.39	
101	TTTGTGATAATAGGCAGCCT	2594	FVDNRQP	3837	178.388	
102	AGTTTGAATTCTTCGAGTACT	2595	SLNSSST	3838	177.704	
103	AAGGCGGTTTCGGAGATTATT	2596	KAVSEII	3839	177.335	
104	GGTACGAGTGATAATTATAGG	2597	GTSDNYR	3840	176.93	
105	ATGTCTAGCCACACCGTCCAA	2598	MSSHTVQ	3841	176.741	
106	AGTATCACCCACAGCAACACC	2599	SITHSNT	3842	176.571	
107	GTTCAGACTAGTACTGGTGCT	2600	VQTSTGA	3843	176.399	
108	CGTGGTGATATGACTCGTGCG	2601	RGDMTRA	3844	176.36	
109	ATTGGTCTGCAGAATTCTACT	2602	IGLQNST	3845	176.164	
110	AGTGCGGATCGTGATAATAAG	2603	SADRDNK	3846	173.544	
111	TACTCTCAATCCATAAAAAAC	2604	YSQSIKN	3847	172.725	
112	CGCTCGTTGGACAGCGGGATG	2605	RLDSGM	3848	172.632	
113	GCTGTGCCTCAGTCTCTGCCT	2606	AVPQSLP	3849	172.274	
114	GCGAATGATAGTATTAAGCTG	2607	ANDSIKL	3850	172.18	
115	AATGGTAATATTTATCCGTCT	2608	NGNIYPS	3851	171.981	
116	GGGCAAAACAAACGCAGTACAC	2609	GQTNVAVH	3852	171.5364	
117	CAAGGAGACCTACGTGGCTCG	2610	QGDLRGS	3853	171.042	
118	GTTAAGGCGAGTGTGGGGTT	2611	VKASAGV	3854	170.5608	
119	ATCGCGTCAACGTGGAACATG	2612	IASTWNM	3855	170.52	
120	AACCTCGGCTGAATCCTCGAGA	2613	NSAESSR	3856	170.31	
121	GTCTTCACGGGCCAAACTGAA	2614	VFTGQTE	3857	170.216	
122	TTTGGTACTTCTTATACGACT	2615	FGTSYTT	3858	169.719	
123	GCGGTTAATGAGACTAGGCTT	2616	AVNETRL	3859	168.767	
124	GGTCGGACGGATACTCCTAAT	2617	GRTDTPN	3860	168.735	
125	AACGACCGACCGCTTGCCAGC	2618	NDRPLAS	3861	168.71	
126	GCTTATCAGCTGACTCCGGCT	2619	AYQLTPA	3862	168.579	
127	ATGGGTGAGATGGGTAATATT	2620	MGEMGNI	3863	168.24	
128	GCGGACATGCAACACACCGTA	2621	ADMQHTV	3864	168.055	
129	GCGGTTGTTCTGAATAGTAAT	2622	AVVLNSN	3865	168.021	
130	TTTCGTGATGGTCAGGGTATG	2623	FRDGQGM	3866	167.193	
131	AAATCGACATCAAACATCGAA	2624	KSTSNIE	3867	166.8294	
132	ACCCAAGCCTTCTCCCTAGGC	2625	TQAFSLG	3868	166.751	
133	TGGTCGAGAACTGGAACACC	2626	WSRTGNT	3869	166.483	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
134	AGCACAAACACCGAACCTAGG	2627	STNTEPR	3870	165.304	
135	GAGAATAGTGATTTGTCTTAT	2628	ENSDLSY	3871	165.08	
136	ATAGACGAACGTTCTCTGATA	2629	IDERSSI	3872	165.02	
137	GATGTGCATTTCGAGTATTCCT	2630	DVHSSIP	3873	164.85	
138	ATAAGCGGTTCCACTACACAC	2631	ISGSTTH	3874	164.788	
139	TGGCAAACCCAAGTCACTACA	2632	WQTQVTT	3875	164.759	
140	AACATGGGTCCAATGGGCCGG	2633	NMGPMGR	3876	164.41	
141	GTTACCCAATCGTCCACGCTA	2634	VTQSSTL	3877	164.175	
142	ATTGATCGTAGTGCTAGTTTG	2635	IDRSASL	3878	164.016	
143	TCTCATAGTATTACGGGTCTT	2636	SHSITGL	3879	163.92	
144	AAAGCGGGACAAGTGTGGAA	2637	KAGQLVE	3880	163.845	
145	AGCGGTGTATCAGAAGGAAAC	2638	SGVSEGN	3881	163.413	
146	ACGCTTACATTATCTACCCCTC	2639	TLTLSTL	3882	163.242	
147	GCCCCACAACAACGAAAGT	2640	AHNKHES	3883	162.975	
148	CACAACAACAACCTGCAAAAC	2641	HNNNLQN	3884	162.633	
149	TATAATGAGTCTTCGAATGCG	2642	YNESSNA	3885	161.92	
150	CGTGAGCAGGCTGCGGAGAGG	2643	REQAAER	3886	161.523	
151	ACTCAGTATGGTACTCTGCCG	2644	TQYGTLP	3887	161.32	
152	CATCTGGGAATAGTCTGTG	2645	HPGNSSV	3888	161.2	
153	AGTTCTAGGGAGGTGAGCCG	2646	SSREVSP	3889	161.091	
154	GCAAACCTCCACAAGCCAATGG	2647	ANSTSQW	3890	160.842	
155	CGCGACATGATCAACTCATCA	2648	RDMINSS	3891	160.83	
156	GCATTGCCCGAGCGGCACGA	2649	ALPSGAR	3892	160.765	
157	CCTGGCACCAGTGGATCCCGA	2650	PGTSGSR	3893	159.7012	
158	TGGAACGGAACGCCACACAA	2651	WNGNATQ	3894	158.413	
159	GGTAAAGCAACCTTAGTCCTC	2652	GKATLVL	3895	158.386	
160	TACACCAACGGGGGCCACCTA	2653	YTNGGHL	3896	158.346	
161	TCACAATACAACGGAACGCAA	2654	SQYNGTQ	3897	157.872	
162	TATTCTAGTGAGAGTGCTTAT	2655	YSSSAY	3898	157.56	
163	GTTAAGGCGGGGTGGCTGAT	2656	VKAGVAD	3899	157.534	
164	ACGATGGGACGGTGCAGATT	2657	TMGTVQI	3900	157.384	
165	GGTGTGGCTGGTGCAGTGGTG	2658	GVAGAVV	3901	156.882	
166	TATGATAAGACTTTGAGTGTT	2659	YDKTLSV	3902	156.791	
167	CATGGGAGTGCCTATTCGCAG	2660	HGSAYSQ	3903	156.45	
168	ACGGCTAATATTATGAGTAAG	2661	TANIMSK	3904	155.935	
169	TTTTCGCGGGAGACGCTGGCG	2662	FSRETLA	3905	155.888	
170	TTGAGTGGTGCTGGTAGTCAG	2663	LSGAGSQ	3906	155.554	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
171	AGTAATGCGAATCAGATGAGT	2664	SNANQMS	3907	155.28	
172	TCGGTCCTTTTCGCCTTCGAAC	2665	SVLSPSN	3908	154.987	
173	GATAATGTGCATGGGCAGGTG	2666	DNVHGQV	3909	154.72	
174	GACGGACGAGAATACGCCCTCG	2667	DGREYAS	3910	154.33	
175	ATTTCTGAATCAGATTAAGATG	2668	ISNQIKM	3911	154.262	
176	GGTCGAGACAACCAACACGTA	2669	GRDNQHV	3912	154.136	
177	CGTAATCATGAGACTGGGGCT	2670	RNHETGA	3913	153.8093	
178	AGTGGGAGTGGTGCGAATATT	2671	SGSGANI	3914	153.55	
179	TCTATGTCTGATGGGCTTCGG	2672	SMSDGLR	3915	153.296	
180	AAGGAGAGTAGTGCTATGGAG	2673	KESSAME	3916	153.04	
181	GCTAATGCTAGTACTAGTCTG	2674	ANASTSL	3917	152.807	
182	AGTGCTTCTGGTTATTTGGTT	2675	SASGYLV	3918	152.79	
183	GATACTACTCAGAAGCCTCAT	2676	DTTQKPH	3919	152.687	
184	CTAATACGAGGTTCCATGGAA	2677	LIRGSME	3920	152.55	
185	GACCGCACCTACTCAAACACA	2678	DRTYSNT	3921	152.447	
186	GCTCTTGGGCATCAGGGGAAT	2679	ALGHQGN	3922	152.38	
187	GCTAATCATACTGTCGAGGAG	2680	ANHTSQE	3923	152.056	
188	GAGAGGGGTTTGAATACTAAT	2681	ERGLNTN	3924	151.4	
189	ACTGTTGGTGGTAATCATCAT	2682	TVGGNHH	3925	151.384	
190	CCGAGTGATAGGACTACTTAT	2683	PSDRTTY	3926	151.365	
191	TCCAGGCAAGAAACTTCTCC	2684	SRQENFS	3927	151.22	
192	AATAAGACGACGATGGAGTTT	2685	NKTTMEF	3928	151.16	
193	AAACACACAGAAAACGGGACC	2686	KHTENGT	3929	150.985	
194	GAAACCGGAGCTATGACCTCT	2687	ETGAMTS	3930	150.803	
195	GGTCATAGGGATTCTGGGTGGT	2688	GHRDSGG	3931	149.991	
196	AGAAACGCCGAAGCGGATTG	2689	RNAEGGL	3932	149.919	
197	GGGCAGCGTACGACGAATGAT	2690	GQRTTND	3933	149.903	
198	TATAATGATGCTCTTAGGCCG	2691	YNDALRP	3934	149.88	
199	GGGTATGCGACTACGGTTCAG	2692	GYATTVQ	3935	149.694	
200	ATAGGGGGAGGCATAGGAAAC	2693	IGGGIGN	3936	149.622	
201	GIGGCGGTGTCTAATACGCCT	2694	VAVSNTF	3937	148.5637	
202	CTTGCGAATGGTATGACGGCT	2695	LANGMTA	3938	148.449	
203	ATTTCTGGGTCGTCGTCTCTT	2696	ISGSSSL	3939	148.328	
204	TCTAATGTTCAITGTTTAAT	2697	SNVHVVN	3940	148.32	
205	GIGGAGACTTCGCGTCTGTAT	2698	VETSRLY	3941	148.302	
206	TCGAACGCAGACATCCTCGCC	2699	SNADILA	3942	148.08	
207	AACAACGTAAACCCGTACTCG	2700	NNVNPYS	3943	148.016	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
208	ATAAGTGTAGGTGTCCGTA	2701	ISVGVS	3944	147.84
209	TCCGCAAACAACATAGCCCC	2702	SANNIAP	3945	147.813
210	GGTGTTTACAGTACTGCGGG	2703	GVQMTAG	3946	147.527
211	CGTTACATCGCCAACCAACA	2704	RYIANQT	3947	147.305
212	ACCACCGAAAGTCTACACCTT	2705	TTESLHL	3948	146.899
213	GGCTACCAAGACAAAACACGA	2706	GYQDKTR	3949	146.705
214	GCTTCGCGGCTGCGGCTCAG	2707	ASRPAAQ	3950	146.364
215	TCTATTCAGGAGCTGTTGAGG	2708	SIQELLR	3951	146.287
216	ACTGTGCGTTTCGCCTCAGCAG	2709	TVRSPQQ	3952	145.74
217	GCGGTTCTTGGTGTAGTAAT	2710	AVLGGSN	3953	145.633
218	ATGAGTACGGTTCTTCGGGAG	2711	MSTVLRE	3954	144.928
219	ACTTATGGTATTACTCATGAT	2712	TYGITHD	3955	144.751
220	GATGCGAATGCGGGTACGAGG	2713	DANAGTR	3956	144.597
221	TTCAACGGGTACGTCATGGCA	2714	FNGYVMA	3957	144.536
222	ATTAATAATTTTAATACTCTG	2715	INNFNLT	3958	144.08
223	GTAGCCAACGAACGCTACCG	2716	VANERLP	3959	143.64
224	ACTAATTCTAATCAGGGTTCG	2717	TNSNQGS	3960	143.617
225	GCGACGCTGAATAATAGTTAT	2718	ATLNNSY	3961	143.512
226	AAAAACGCTCAATAGACCTA	2719	KNAQIDL	3962	142.66
227	CCTGCTACGCTACACCTGACA	2720	PATLHLT	3963	142.552
228	TTAGGATCGAGCACAGTATCG	2721	LGSSTVS	3964	142.325
229	AATTGGAATTCGAGGGTACG	2722	NWNSEGT	3965	142.257
230	CCAACAAACACTTAAGTATG	2723	PTNNLSM	3966	141.91
231	GCGCTTAAGCCGAATCTACG	2724	ALKPNST	3967	141.737
232	ATGGTGAATTCGGAGAATACT	2725	MVNSENT	3968	141.624
233	AGTATGGATGCTCGGTTGACG	2726	SMDARLT	3969	141.6
234	AATAATGTTGTTAGGGATGAT	2727	NNVVRDD	3970	141.597
235	ACAAGGGACCAAGGTCTACA	2728	TRDQRST	3971	141.592
236	GCTGACATCCGAACGACAAA	2729	ADIRNDK	3972	141.468
237	ATGCGGGATAAGATTAATCCG	2730	MRDKINP	3973	141.468
238	CCGACTCCTAATGAGCATATG	2731	PTPNEHM	3974	141.465
239	GGATACTCACAACTCCGAC	2732	GYSHNSD	3975	141.448
240	CTTCGGGATGGGATTGCTTCT	2733	LRDGIAS	3976	141.105
241	ATGAACCAATGGGCGGCTG	2734	MNQMGGL	3977	141.089
242	TCTTCGCCTACTAAGGTACT	2735	SSPTKGT	3978	140.803
243	TATTTGGATAATCCGTTGACG	2736	YLDNPLT	3979	140.516
244	GTCATGCAACGATCTGCACAA	2737	VMQRSAQ	3980	140.2

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100		
245	TCTCTGCAACTCACAGCGGGT	2738 SLQLTAG	3981	140.161		
246	GTGGGGTCTGGGGTTATAAT	2739 VGSGGYN	3982	140.139		
247	GATCGTCCGAATAATGTGTCG	2740 DRPNNV	3983	140.036		
248	TTGACTGAGAAGGCTTCTATT	2741 LTEKASI	3984	139.945		
249	ACCACAAAAACGACATCTATG	2742 TTKTTSM	3985	139.556		
250	CGTTTGGACCTGCAAGTCCAC	2743 RLDLQVH	3986	139.528		
251	ACTCATGTGATTGGGGCTGTG	2744 THVIGAV	3987	139.34		
252	ACCCTGACACACCTAAACCCA	2745 TLTHLNP	3988	139.142		
253	ACCTCAATATCGTCGCAAAGC	2746 TSISSQS	3989	138.884		
254	TACCACACCCACCAAGTCGCA	2747 YHTHQVA	3990	138.871		
255	ATGCAAGGGCTTAACAACATG	2748 MQGLNNM	3991	138.848		
256	GGTAGTGCGAGTAATAGTGGT	2749 GSASNSG	3992	138.841		
257	GCGAATACTACGGGGCAGGTG	2750 ANTTGQV	3993	138.7122		
258	AGCGTTGTCAACACCAACATC	2751 SVVNTNI	3994	138.699		
259	TCTAATAATCTGAATCAGGAG	2752 SNNLNQE	3995	138.543		
260	ATGAATGGGAGTGGGATGCAG	2753 MNGSGMQ	3996	138.484		
261	ATAAGTCACGACCTTAAATAC	2754 ISHDLKY	3997	138.458		
262	ACGGTTAATGCGGATGGGTCG	2755 TVNADGS	3998	138.21		
263	AATCATATTAGGAATCCTATG	2756 NHIRNPM	3999	138.143		
264	AGTACGCGGGTTACTCTGGAT	2757 STRVTL	4000	137.85		
265	GCTATGGGAGCACTCGTGCAC	2758 AMGALVH	4001	137.838		
266	GCGCAAGCCATGTCAAACAGC	2759 AQAMSNS	4002	137.76		
267	AATGCTAATGGTATGAATACT	2760 NANGMNT	4003	137.343		
268	TTGACGCTTCCTAGTGCTAAT	2761 LTLPSAN	4004	137.264		
269	TACCAAACGGGAGACAAAGAC	2762 YQTGDKD	4005	137.017		
270	AGACGGGAAGAAAACGTCAAC	2763 RREENVN	4006	136.962		
271	GGAAC TACCACGGCAGTCGCG	2764 GTTTAVA	4007	136.8811		
272	ACGGCTGGTGGGAGCGTGCG	2765 TAGGERA	4008	136.6		
273	GCCGGTAACGAACCTAGACCC	2766 AGNEPRP	4009	136.593		
274	GCAAACAACACAGCCAACAGT	2767 ANNTANS	4010	136.498		
275	CATGTGAATAGTAGGGATCTT	2768 HVNSRDL	4011	136.187		
276	ACATACCAACTTCCGGCAAC	2769 TYQLSGN	4012	136.059		
277	CGGGGTGATTCGATGGCTCGG	2770 RGDSMAR	4013	135.8517		
278	TTGAATAATTCIGCGACTGTT	2771 LNNSATV	4014	135.76		
279	CTACACGCTAACAACGAACGG	2772 LHANNER	4015	135.723		
280	ATGGGTCTACGACTGGTGTG	2773 MGSTTGV	4016	135.16		
281	GTAGTTGCAGGGCAGCAATG	2774 VVAGHAM	4017	135.1261		

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
282	GGCAACGAAAAACCATCAGGG	2775	GNEKPSG	4018	135.016	
283	CGTGGTACGGAGGGGACGCCG	2776	RGTEGTP	4019	134.8972	
284	TGGTCCCCCGGACCCGAAGCC	2777	WSPGPEA	4020	134.66	
285	ATTAATGTGAATCAGATGGCG	2778	INVNQMA	4021	134.472	
286	CGGTCCGGACGTTATGCAAAGT	2779	RSDVMQS	4022	134.362	
287	AGGGACGTAAGTACAAAAGAA	2780	RDVSTKE	4023	134.36	
288	AAAAAGTCACCCAGACTTGAA	2781	KKSPRLE	4024	134.35	
289	ACGAGCAACACAATGTCAGAC	2782	TSNTMSD	4025	134.345	
290	TCTAAAGGAAACGAACAAATG	2783	SKGNEQM	4026	134.224	
291	GGTTACGCTACGACCGTGCAA	2784	GYATTVQ	4027	134.185	
292	GGATACATGTCTAACGTCATA	2785	GYMSNVI	4028	133.922	
293	GTGACTGTTAGTCTGGATGGG	2786	VTVSLDG	4029	133.879	
294	ACGAATAATTTGCTGGCTCAG	2787	TNNLLAQ	4030	133.517	
295	GCGCAGACGACGGGTATACG	2788	AQTTGYT	4031	133.295	
296	AGTAAGTCGACTGAGATTATG	2789	SKSTEIM	4032	133.249	
297	TCTGCGATGCACACATTAGTC	2790	SAMHTLV	4033	133.226	
298	GCTGGGGTGCGTGAGTCGTTT	2791	AGVRESF	4034	133.15	
299	CAAGGCAACTCAATGGCGTCC	2792	QGNMAS	4035	132.82	
300	AAAAACCCGAGTGTCCAAGAA	2793	KNPSVQE	4036	132.519	
301	CCCATAACACGGGAATCGGGA	2794	PITRESG	4037	132.424	
302	AGCCGCTCGGCAGAAATATCG	2795	SRSAEIS	4038	131.747	
303	AACGACATCCCCACACGAGCC	2796	NDIPTRA	4039	131.424	
304	GCATACGGATCGTCCGGAAGA	2797	AYGSSGR	4040	131.375	
305	CTTCATGGGAATTTTAGTCAG	2798	LHGNFSQ	4041	131.002	
306	GCATCCAACGGGCAAGTTAAC	2799	ASNGQVN	4042	130.736	
307	CAGAAGGGGACGGTTACTCTG	2800	QKGTCTL	4043	130.375	
308	AACTCTAGTAACACTGGTTGG	2801	NSSNTGW	4044	130.26	
309	ACGTATCAGCATCAGGGTCCG	2802	TYQHQP	4045	130.231	
310	GACGGGGTCGCACACCGCTCA	2803	DGVAHRS	4046	130.216	
311	GACGGGCTCACGCTGGAACGC	2804	DGLTLER	4047	130.09	
312	AGGGGTGATCTATCTACGCT	2805	RGDLSTP	4048	130.02	
313	ATTAATGAGATTGGTAGGATG	2806	INEIGRM	4049	129.944	
314	CCCCAATGGGGAACGACCCG	2807	PQWGTDP	4050	129.94	
315	AAGCAGGTGGCGCATATTGAT	2808	KQVAHID	4051	129.831	
316	AATACTTTGCAGAATAGTCAT	2809	NTLQNSH	4052	129.563	
317	TGGAGCCAAGGGAACACAGCG	2810	WSQGNTA	4053	129.438	
318	AACGAAACGCACGTACCTAAA	2811	NETHVPK	4054	129.35	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
319	GTAACGAACGAATCCCGCGCC	2812	VTNESRA	4055	129.059	
320	CCCGAAGGCCACATGCAAGAC	2813	PEGHMQD	4056	129	
321	TTGGATTGCGACTAATTCTAGG	2814	LDSTNSR	4057	128.63	
322	CAGTCGATTGGGCATCCGGTG	2815	QSIGHPV	4058	128.17	
323	GTCCTGGTTAACGTACACAAC	2816	VLNVVHN	4059	128.078	
324	GTGCATAATCCTACTACTACG	2817	VHNPTTT	4060	127.727	
325	GGGGATAAGGCGAGTTTGCG	2818	GDKASLA	4061	127.698	
326	CTAAACGAATCCCGAGCGTCG	2819	LNESRAS	4062	127.597	
327	GGTTTTTCATATTAATGGTGAG	2820	GFHINGE	4063	127.526	
328	AGTGTTAGTTCTGTGGTGTTG	2821	SVSSVVL	4064	127.19	
329	CTTTCGACTACTTCGACGAAG	2822	LSTTSTK	4065	127.153	
330	ACTAATACGCAGAATAATCCG	2823	TNTQNNP	4066	127.089	
331	ACTAATCTGTGCTGTACGCTG	2824	TNLAVTL	4067	127.0208	
332	ATGTCCGATCGTACTTCTGAT	2825	MSDRTSD	4068	126.91	
333	TCCGCGCAATCTTTCGTAGTT	2826	SAQSFVV	4069	126.906	
334	ATGCACACAAGTAGACCCCA	2827	MHTSAPP	4070	126.861	
335	ATGTCTAGCCACACAGTCCAA	2828	MSSHTVQ	4071	126.79	
336	AGGGATACGGCTAAGGGGGTG	2829	RDTAKGV	4072	126.773	
337	GCGTTAAATCCGACAGCGCC	2830	ALKSDSA	4073	126.73	
338	CAATACGACGCCAGCCGACAA	2831	QYDASRQ	4074	126.66	
339	TTAGCCGACTCAAACAGCAAA	2832	LADSNSK	4075	126.48	
340	TTTCAGTTGGCTAGTAATCCG	2833	FQLASNP	4076	126.372	
341	AACTCTGTCTAGGGAACATC	2834	NSVVGNI	4077	126.308	
342	AGGTATGAGAGTACTAGTGCT	2835	RYESTSA	4078	126.21	
343	GCGGATCATAATCATATTGCT	2836	ADHNHIA	4079	126.21	
344	GTAGGCGACCAATCCCGCCCG	2837	VGQSRP	4080	126.106	
345	TTCAACGAAACTGCCGGGCGA	2838	FNETAGR	4081	125.693	
346	AGCAACTCGTACTTACTCAAC	2839	SNSYLLN	4082	125.52	
347	CGAGGCGACACAAAGAACTAC	2840	RGDTKNY	4083	125.09	
348	ACGACTACTACTATGGCATA	2841	TTTTMAY	4084	125.064	
349	CGACCCCGAACGAAAACAGA	2842	RPPNENR	4085	124.7157	
350	TGCGCCAACATGACCAACGGC	2843	CANMTNG	4086	124.6	
351	AATCGGTCGGATAGTTTTCG	2844	NRSDSFA	4087	124.567	
352	AATCTTTTGACITCGTCGCCT	2845	NLLTSSP	4088	124.54	
353	AACTCCAGGGAAATGGGTGTA	2846	NSREMGV	4089	124.539	
354	ATGGGGAATCAGAGTGGTGCG	2847	MGNQSGA	4090	124.506	
355	ATGCTCACAGAAACCAAAGCA	2848	MLTETKA	4091	124.3	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
356	CAAAACATCAAAAACATGACA	2849	QNIKNMT	4092	124.1
357	ATGAGTACGGTTCTTCGCGAG	2850	MSTVLRE	4093	124.05
358	GACCGTGCCCAAAACAACGAA	2851	DRAQNNE	4094	123.95
359	CATACGCAGTCGACGGGTAT	2852	HTQSTGY	4095	123.943
360	ATGAGTGTGGGAAGGTTTAT	2853	MSVGKVV	4096	123.919
361	GCCGGAACTACCAATCATCA	2854	AGNYQSS	4097	123.855
362	AGAAACGAAAACGTAAACGCT	2855	RNENVNA	4098	123.777
363	GACACCCACACACATCCAGT	2856	DTHHTSS	4099	123.766
364	ACTAGCTCCCCTGTTCTACAA	2857	TSSPVLQ	4100	123.762
365	GTGGCCGTGACGCAGAAGCT	2858	VGRDAEA	4101	123.74
366	AACATGGAAAGAGGATCGCAA	2859	NMERGSQ	4102	123.646
367	GACAGACAAACAGGCCAAAAA	2860	DRQTGQK	4103	123.6413
368	GTCTTCCGGGAAGGCATCGTG	2861	VFREGIV	4104	123.54
369	TCCGCAAACAACATAGCCACC	2862	SANNIAT	4105	123.32
370	GTATCAGAAGGACAACGAATC	2863	VSEGQRI	4106	123.005
371	CACTACGGTAACAAAGACATA	2864	HYGNKDI	4107	122.894
372	GATGTTTTGCTTAAGAATTTT	2865	DVLLKNF	4108	122.89
373	CACACGGTTCAAATACGCGAA	2866	HTVQIRE	4109	122.8082
374	ACATCAGCACTAGCACACCAA	2867	TSALAHQ	4110	122.78
375	ATCCCAACCGGCCAAACTAGC	2868	IPQTGTS	4111	122.752
376	CGCAGCGACAAAGGAACGTTG	2869	RSDKGTL	4112	122.7439
377	AATGGTCTTACGGTTCAGCGG	2870	NGLTVQR	4113	122.718
378	ACGGTTGAGGGTCTTATCCG	2871	TVEGSYP	4114	122.67
379	ACTAGCCACTTAGTACTTGCA	2872	TSHLVLA	4115	122.653
380	AATCATAGTCTGTCGGAGCAT	2873	NHSLSEH	4116	122.5
381	TTAACAGGCATGAACAGAGAC	2874	LTGMNRD	4117	122.335
382	AGTCACAACGCTGGGGTCGCC	2875	SHNAGVA	4118	122.285
383	GCGCACCAACCGCGGGCCA	2876	AHQTAGP	4119	122.22
384	AATTCTCATGATTTGAAGTAT	2877	NSHDLKY	4120	121.99
385	ACTACAATGAGTACCGGTCAA	2878	TTMSTGQ	4121	121.98
386	GGGTTGCGGCACGTGCCCGAA	2879	GFGHVPE	4122	121.974
387	ATCACCGCCGCTCACCACAA	2880	ITAASPQ	4123	121.868
388	GTTAAGGCGAGTGCTGGGGAT	2881	VKASAGD	4124	121.75
389	AGTATCACACAGCAACACC	2882	SITHSNT	4125	121.75
390	CATAATAATAATATGCTGAAT	2883	HNNMMLN	4126	121.659
391	CCCAAACTCTAACTTCGACA	2884	PKILTST	4127	121.479
392	ATAACCGCAACACCGTCGGA	2885	ITGNTVG	4128	121.385

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
393	CTCGGAAACCACTACACACCC	2886	LGNHYTP	4129	121.38	
394	TCGTTTACTAATACGAATCCT	2887	SFTNTNP	4130	121.294	
395	ACGTTGGATCGGAATCAGACT	2888	TLDRNQT	4131	121.25	
396	ATCTCTACGCAAAGACCGCAC	2889	ISTQRPH	4132	121.2071	
397	ACATTCACTACTCTGGGCAAA	2890	TFTTLGK	4133	121.179	
398	GAGAAGCCTTCTCTGTGATG	2891	EKPSLVM	4134	120.927	
399	CACATCGAAACCAACTTCG	2892	HIETNTS	4135	120.834	
400	GGTACGAAGGATATTCTGATT	2893	GTKDILI	4136	120.792	
401	GCGACTTTTAGTCATGCTGGT	2894	ATFSHAG	4137	120.788	
402	GCCAACGGCATATTCACCG	2895	ANGIFQP	4138	120.646	
403	CTTAATGTGAATACGCTTAAT	2896	LNVNTLN	4139	120.55	
404	ACTTCTGCTAGTGAGAATTGG	2897	TSASENW	4140	120.5	
405	CTTCTTCAGGGTGCCTAAG	2898	LLQGATK	4141	120.358	
406	GCTCTTGAGACTACTCGTGCT	2899	ALETTRA	4142	120.26	
407	TTAACGGGACAAAACGAATTC	2900	LTGQNEF	4143	120.24	
408	ATTTCTCATGATTTGAAGAAT	2901	ISHDLKN	4144	120.191	
409	GCACAATACAACAACGGCGTA	2902	AQYNNGV	4145	120.19	
410	ACGACGTCTGTGGAGAAGACT	2903	TTSVEKT	4146	120.106	
411	GGTACGTCGGCTATTATGCCT	2904	GTSAIMP	4147	120.093	
412	CAGCTGCAGGGGACTGAGGCG	2905	QLQGTEA	4148	120.02	
413	GCCTTAAAAATCCCAAGAACCA	2906	ALKSQEP	4149	120.007	
414	TCTAACAGCAGTGTGCGGTA	2907	SNSSVAV	4150	119.89	
415	AATCATGGTCGTGCTATTGAT	2908	NHGRAID	4151	119.776	
416	GATACGTATAATAGTAATACT	2909	DTYNSNT	4152	119.6	
417	ACATTCCACCAAGCGTCAA	2910	TFHQAVK	4153	119.54	
418	TGGCATACTGGTGTGTTTCAG	2911	WHTGVFQ	4154	119.48	
419	AGGGGTGATCTTTCTACGCCA	2912	RGDLSTP	4155	119.47	
420	ATGCTTAGTCAGGTTCTGACG	2913	MLSQVLT	4156	119.414	
421	GAAAACGAAAACGAGAAAGC	2914	ENEKRES	4157	119.391	
422	ATTTTCAGTTATGATGGTAAT	2915	ISSYDGN	4158	119.38	
423	ACTCGTGGCGACATGGAATTC	2916	TRGDMEF	4159	119.36	
424	AATGTGCAGAATGTGCCTGGG	2917	NVQNVPG	4160	119.3363	
425	TCTTTCACGAACACAAACCCA	2918	SFTNTNP	4161	119.24	
426	TCGAACGCTGGCTACCACTCG	2919	SNAGYHS	4162	119.169	
427	GACTACAAAAACAGCGGCCA	2920	DYKNSAP	4163	119.136	
428	GTCGGGAAAAACTCGTACGAA	2921	VGKNSYE	4164	119.129	
429	GCTTACGCAGGTGTACTTGGG	2922	AYAGVLG	4165	119.123	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
430	ACGACGCTCTGAGCGTGTGAAT	2923	TTSERVN	4166	119.105	
431	GACACCGGAATCAAAAACGTT	2924	DTGIKNV	4167	119.05	
432	TCGACCAGCTCTCTGGTTCCC	2925	STSSLVP	4168	119.006	
433	TGGAGCGCCGGCGAACGGGTG	2926	WSAGERV	4169	118.995	
434	AGTTCGGGGAGTTTGATTACT	2927	SSGSLIT	4170	118.945	
435	TGGATTTCTACTGAGATGAGG	2928	WISTEMR	4171	118.93	
436	TTTGCGGCTGGGGCGCATGGT	2929	FAAGAHG	4172	118.92	
437	ATAGGCGACCGCGACCAACGT	2930	IGDRDQR	4173	118.886	
438	AGTACGATTGGTAATTCTACT	2931	STIGNST	4174	118.8619	
439	GGAAGTGGCACCGTCGGTCGA	2932	GGSTVGR	4175	118.714	
440	CATGTTACGGCGGTGGTTGAT	2933	HVTAVVD	4176	118.706	
441	GATAAGCGGGGGTGGCTAAT	2934	DKAGVAN	4177	118.67	
442	CGTCTGACTGATACTATGCAT	2935	RLTDTMH	4178	118.589	
443	CTGAACACTCTAATCCACAAA	2936	LNTLIHK	4179	118.565	
444	AGTTATCAGAATCCTCCGCCT	2937	SYQNPPP	4180	118.512	
445	TTGACAGGATTAAACGCTTTC	2938	LTGLNAF	4181	118.45	
446	AGTCCTGTGCTTTCTCCTTCG	2939	SPVLSPS	4182	118.377	
447	GTTCAAACACACATAGGAGTC	2940	VQTHIGV	4183	118.36	
448	CATATGTCTTCTGTGCGACT	2941	HMSSVAT	4184	118.34	
449	GGAAAAGCCAACGACGGTTCT	2942	GKANDGS	4185	118.333	
450	AGTACTAACGACGACGCAAA	2943	STNDERK	4186	118.28	
451	CAGGGGGGAATAGTCGGTTT	2944	QGGNSRF	4187	118.236	
452	CCTAACACGAAAAAACCCG	2945	PNNEKNP	4188	118.22	
453	GTGGCTGCGACGGTGGTACT	2946	VAATGGT	4189	118.173	
454	GCGATTGTGGATAGGGGAGT	2947	AIVDRGS	4190	118.167	
455	TCCCAACACCACGCCACTG	2948	SQHHTPL	4191	118.137	
456	TTACAAAGCTCGATGAACGTA	2949	LQSSMNV	4192	118.073	
457	CGAGAAACCAACCGTCTGAA	2950	RETNPSE	4193	117.941	
458	GGGTTCGGGCACCTGCCCGAA	2951	GFGLPE	4194	117.86	
459	CGGAATGCTACTGTGACTGTT	2952	RNATVTV	4195	117.852	
460	GTTCAAACGCITCGGGCTTA	2953	VSNASGL	4196	117.707	
461	GATCGTCCGAATAATGAGTCG	2954	DRPNNES	4197	117.7	
462	CAGGTTAGTCTGGTGAAGTTG	2955	QVSLVKL	4198	117.643	
463	AGTAATATGCGTGAGGAGATT	2956	SNMREEI	4199	117.629	
464	GATATTGGGCGTTCGAATAGT	2957	DIGRSNS	4200	117.45	
465	GATCATATGAATTTGAGGTCT	2958	DHMLRS	4201	117.365	
466	ATTGAGCGTAGTAGTGATCGT	2959	IERSSDR	4202	117.358	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
467	TTGTCTCAGAAATTTAATCCT	2960	LSQNFNP	4203	117.3026	
468	TATTCTATGGGTCAGCAGCCG	2961	YSMQQP	4204	117.283	
469	TACACACAAGGATAATGAAC	2962	YTQGIMN	4205	117.22	
470	ATGCTGTCTCATGGTGCCTT	2963	MLSHGAL	4206	117.165	
471	GCTTATAATGCTCGTCTGCCT	2964	AYNARLP	4207	116.957	
472	AGACACTACTCCGACAACGCC	2965	RHYSDNA	4208	116.945	
473	GCACACACAGCCATGACCTAC	2966	AHTAMTY	4209	116.935	
474	CTAACAGGCTCTGACATGAAA	2967	LTGSDMK	4210	116.89	
475	ACCTTACACACGAAAGACTTG	2968	TLHTKDL	4211	116.879	
476	TCGGGTCAAAACGGTACATCA	2969	SGQNGTS	4212	116.851	
477	CGTGGGACGCTCCACACCAAC	2970	RGDVHTN	4213	116.829	
478	ACCGGAACGGCTACACTCCCA	2971	TGTATLP	4214	116.72	
479	CTGGGTACGCTGCTTAGTCAG	2972	LGTLISQ	4215	116.72	
480	GTCCTCTCCTCCAACCTGTAC	2973	VLSSNLY	4216	116.707	
481	AGTTTGGGGTCGGATCGTATG	2974	SLGSDRM	4217	116.61	
482	AGGGGAGATCTTTCTACGCTT	2975	RGDLSTP	4218	116.59	
483	AGGATGTCGGAGAGTTCTGAT	2976	RMSESSD	4219	116.585	
484	ATGACTGAGAAGGCTTCTATT	2977	MTEKASI	4220	116.54	
485	ACAGAACAATCTTACTAACGA	2978	TEQSY*R	4221	116.54	
486	GTTGAATCTAAATCCGAACCA	2979	VESKSEP	4222	116.536	
487	ATGAATCTTGTGAGGGATTTCG	2980	MNLVRDS	4223	116.526	
488	CAAAACCACTCTATAACAACA	2981	QNHSITT	4224	116.51	
489	ACGCTGGACAACAACCACAGC	2982	TLDNNHS	4225	116.42	
490	ACGAAGAGTTTTAATGATCTT	2983	TKSFNDL	4226	116.38	
491	GCCACAGAACTCAGGGCGC	2984	ATEHSGR	4227	116.34	
492	CAAGGGACTCTCTTGTCTCCA	2985	QGTLLSP	4228	116.293	
493	ACATTCCACCAAGGGGTCAAA	2986	TFHQGVK	4229	116.175	
494	TGTCAGCGGGCTGATTGTGCG	2987	CQRADCA	4230	116.17	
495	CGGTATGATGGTACTCTTAAT	2988	RYDGTLN	4231	115.929	
496	CAAGGCGGTACAAACAACCCC	2989	QGGTNNP	4232	115.853	
497	GGGGGTAACTACCACACCACT	2990	GGNYHTT	4233	115.838	
498	CTGGTTGTTTACAGTGCACAG	2991	LVVQSAQ	4234	115.7942	
499	TATCCTCATGAGAGTAAGAAT	2992	YPHESKN	4235	115.731	
500	GAGATTGTTAGGCATACGCAT	2993	EIVRHTH	4236	115.724	
501	GACCGGACAAACAACATGAGC	2994	DRTNNMS	4237	115.705	
502	TCCGTAACCAACGAGCGGAA	2995	SVTNGAE	4238	115.66	
503	AGCGGACAAAAAACTCAGAA	2996	SGQKNSE	4239	115.653	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100		
504	GAGCAGAAGAAGACTGATCAT	2997 EQKKT DH	4240	115.565		
505	AATATTAATGGTGGGGGAAT	2998 NINGG GN	4241	115.563		
506	AAGCTGCATACTAAGGATCTT	2999 KLHTK DL	4242	115.54		
507	AGCTTCTTGGTAGCCACCCA	3000 SFLVA HP	4243	115.4		
508	TACCAACAAAACATAGAAATC	3001 YQQNIEI	4244	115.388		
509	AGGGGTGATCTTTCTACGACT	3002 RGDLS TT	4245	115.31		
510	GCGAACCTCAACTTGACCA GT	3003 ANLNLT S	4246	115.305		
511	ACGGTGCAGCATGCGGCGACG	3004 TVQHA AT	4247	115.231		
512	ACCGTAAACCTCCTAGCGGCA	3005 TVNLL AA	4248	115.223		
513	AACCAAAGAGTTGAACAAAA	3006 NQRVE QK	4249	115.222		
514	AATACTTATACTGTGCGAAG	3007 NTYTA AK	4250	115.189		
515	ATCCAAAGAGACGTGGGCCAC	3008 IQRDV GH	4251	115.098		
516	ATCTCAGAAATGACTAGGTAC	3009 ISEMTRY	4252	115.098		
517	ATTGCTACTAATGTGATTAT	3010 IATNVIY	4253	115.089		
518	AACGGCAACCACTCCATAGAC	3011 NGNHS ID	4254	115.062		
519	ACGAGTATTGGTAGTGCTAAG	3012 TSIGSAK	4255	115.036		
520	AACGTACACTCTGTTGACAAA	3013 NVHSV DK	4256	114.987		
521	GAACCTCTCCGTTCCGAAACCA	3014 ELSV PKP	4257	114.93		
522	TTCCTCGACAAATACAAC TAC	3015 FLDK YNY	4258	114.888		
523	TACATCCC GAACA ACTCAGGA	3016 YIPNN SG	4259	114.881		
524	GGGCTAGGACAACCCCAACTC	3017 GLGQP QL	4260	114.817		
525	GAGGGGAGTCAGGGGAATCAT	3018 EGSQGNH	4261	114.66		
526	AATATTTATATGGCGAGTGGT	3019 NIYMA SG	4262	114.66		
527	AATTTGCAGACTGGTGTT CAG	3020 NLQTGVQ	4263	114.65		
528	ACCGTCGCTCCCTACAGTAGC	3021 TVAPY SS	4264	114.65		
529	TCAAAC TACTCTGACGGAATA	3022 SNYSD GI	4265	114.649		
530	GCTACTTACGTTGTCGGAACA	3023 ATYVV GT	4266	114.64		
531	TCAAGGGAAGCGGGTTCAACT	3024 SREAG ST	4267	114.622		
532	GCCGGA AAAACCCACGCCGAC	3025 AGKTH AD	4268	114.6		
533	CCGCTTTCTCTTCATAATAGT	3026 PLSLH NS	4269	114.589		
534	CTTCGAGACCTAACGGAGGA	3027 LRDLN GG	4270	114.553		
535	GATAGGACGTATTCGAATACG	3028 DRTYS NT	4271	114.548		
536	TCGGTCACCA GTGGAACACAA	3029 SVTSG TQ	4272	114.541		
537	AATATGACTTCGGCTTATCAT	3030 NMTSAYH	4273	114.52		
538	GTTATGGGTGGTCCTGGGATT	3031 VMGGP GI	4274	114.491		
539	GCTGGGACTCATACTGATAAG	3032 AGTHTDK	4275	114.444		
540	GGTACTATGAATATTGGTATT	3033 GTMNIGI	4276	114.356		

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
541	ACAGCCGGCGCGAACGCGCC	3034	TAGGERA	4277	114.34	
542	GGTATGACTTCTAATCAGGTT	3035	GMTSNQV	4278	114.298	
543	CATTTTTCGCAGATTACTAAT	3036	HFSQITN	4279	114.278	
544	AGCAGGATAGAAAACAACAAC	3037	SRIENNN	4280	114.055	
545	GATACGGCGAGTTATAATAAT	3038	DTASYN	4281	114	
546	GTGAATCAGAGTCCTGGGGCT	3039	VNQSPGA	4282	113.85	
547	AATAATATGGGTCATGGTCAT	3040	NNMGHGH	4283	113.837	
548	TCGCGGCTATCACAAGACCCC	3041	SRLSQDP	4284	113.832	
549	TCTACGTCTCAGGCTGTGCAG	3042	STSQAVQ	4285	113.802	
550	CGATGGCAAGGACTGAGCGCG	3043	RWQGLSA	4286	113.76	
551	GCGCATATGCATTCGGAGTTG	3044	AHMHSEL	4287	113.74	
552	AATAATCTTACGAATTCGACG	3045	NNLTNST	4288	113.736	
553	CAGCCTAGTGCAGTGAGCTT	3046	QPSASEL	4289	113.731	
554	GGGACTTCCTTGGAAAACCGA	3047	GTSLENR	4290	113.709	
555	CTGTCTAATTCGATTACGCCT	3048	LSNSITP	4291	113.683	
556	ACCATAGTGTCCACTTCTTAC	3049	TIVSTSY	4292	113.628	
557	ACCCTAGGCTATCCAGACAAA	3050	TLGYDPK	4293	113.563	
558	TCAAGACACGACGTCGAAAC	3051	SRHDVRN	4294	113.559	
559	AATGGTAGTGTGGCTAATCCT	3052	NGSVANP	4295	113.48	
560	GCGATGGATGGGTATAGGTT	3053	AMDGYRV	4296	113.462	
561	TGGACGGGCGCACAACTTCT	3054	WTGAQPS	4297	113.3493	
562	AAAAACGGCGCCATAGGAACA	3055	KNGAIGT	4298	113.335	
563	GTACTTCCAAGTCGGATCGCG	3056	VLPSRIA	4299	113.3	
564	GATAATGTGAATTCTCAGCCT	3057	DNVNSQP	4300	113.207	
565	GGCGTAAACGCTAGCTACAGC	3058	GVNASYS	4301	113.174	
566	CTGTCTCAGCCATGGACCGG	3059	LSHAMDR	4302	113.127	
567	AGGGCTCATGGGGATAATCAG	3060	RAHGDNQ	4303	113.036	
568	TTGCAGACGCCCTGGGACGACG	3061	LQTPGTT	4304	113.01	
569	ACTCAGGTTGTAGTATTAT	3062	TQVVSII	4305	113.001	
570	CAGGTTCAGGGGACTCTGGGG	3063	QVQGTLG	4306	112.9928	
571	GTGGGCAACCAAACTTACCC	3064	VGNQNL	4307	112.889	
572	TATGTTGATTATAGTAAGTCG	3065	YVDYSKS	4308	112.872	
573	CTGCTTAATTCTTCGGGTGTG	3066	LLNSSGV	4309	112.857	
574	AATCAGTCGCTTACTATGGAT	3067	NQSLTMD	4310	112.793	
575	GCTGTAAGGATCTTAGTAAT	3068	AGKDLSN	4311	112.792	
576	TCTTACGTTAGCGTCCCGCC	3069	SYVSVPA	4312	112.668	
577	AATGAGGGCGTGTGCAGACT	3070	NEGRVQT	4313	112.6219	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
578	ACTTTGACGCAGACTGGGATG	3071	TLTQTGM	4314	112.588	
579	GGCTTCGCATTAACTGGCACC	3072	GFALTGT	4315	112.564	
580	CAGTCGACGCTGAATAGGCCT	3073	QSTLNRP	4316	112.5575	
581	ACAACAACACACTCCATCTCC	3074	TTTHSIS	4317	112.547	
582	AACACACACAGACAAGAATAC	3075	NTHRQEY	4318	112.522	
583	TCCCAAATAGTCAACACCACA	3076	SQIVNTT	4319	112.519	
584	CTGGTGCTTGAGATGCAGACG	3077	LVLEMQT	4320	112.492	
585	AACGACATCTCCACCCAACGG	3078	NDISTQR	4321	112.444	
586	TACACCGCCGACAAAAACAA	3079	YTADKKQ	4322	112.402	
587	TTCGGAGCAACCACCACAGCA	3080	FGATTTA	4323	112.399	
588	GTTCAAGTTTCTATGAATAAT	3081	VQISMNN	4324	112.364	
589	ATGCATGCGCAGGAGTCTCGT	3082	MHAQESR	4325	112.324	
590	CATGTGAATACTGTGATCGG	3083	HVNTADR	4326	112.313	
591	TACAGTACAGACTCCACCAA	3084	YSTDSTK	4327	112.271	
592	GGACACGACCGAACACCAAC	3085	GHDRTPN	4328	112.213	
593	ACGAGTGGTGTGCTTACGCGG	3086	TSGVLTR	4329	112.212	
594	AATATTGCTATGTCTAAGATT	3087	NIAMSKI	4330	112.204	
595	ATGGGGACTGAGTATCGTATG	3088	MGTEYRM	4331	112.185	
596	CCTTATGCGAATAGGCTTGAG	3089	PYANRLE	4332	112.174	
597	CCGCTTCAGAATAATAAGACG	3090	PLQNNKT	4333	112.172	
598	TCCTTGACGGAAAAAGCGCCG	3091	SLTEKAP	4334	112.15	
599	AATATGGTGTATACGAATGTG	3092	NMVTNV	4335	112.077	
600	ATGTTAAGTGCCACCAAGGG	3093	MLSATQG	4336	112.047	
601	AACATGACTCACTCAACCGTA	3094	NMTHSTV	4337	112.0108	
602	ATTTATACGAATAGTCATGTT	3095	IYTNSHV	4338	111.93	
603	TGGTCGCATGATCGGCCTACT	3096	WSHDRPT	4339	111.926	
604	GAAAAAGGCACACCAAGTAGC	3097	EKGTPSS	4340	111.922	
605	CATCATCTCTACTGAGTCGTTG	3098	HHSTESL	4341	111.911	
606	CCAAAAAGCACCCAAGTAATG	3099	PKSTQVM	4342	111.846	
607	AGTGATAGGACTGCTCAGCAG	3100	SDRTAQQ	4343	111.845	
608	GCTACCCTCGCACGGACCTCA	3101	ATLARTS	4344	111.8417	
609	ATTTCTCAGGTGTCTTTAAT	3102	ISQVSFN	4345	111.81	
610	CATTATGGGAATAAGGATATT	3103	HYGNKDI	4346	111.805	
611	AATGATGGGACTGATCGTAGG	3104	NDGTDRR	4347	111.574	
612	ACCAACCACATAACCGGTCCA	3105	TNHITGP	4348	111.551	
613	ACTAATTCTAATCAGAGTTCG	3106	TNSNQSS	4349	111.532	
614	GTGGCGACTCATTATAATGAG	3107	VATHYNE	4350	111.52	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
615	GACCTCGGTACGGCTAGAACC	3108	DLGTART	4351	111.516	
616	GCTCTTAGTCAGAGTGC GG GT	3109	ALSQSAG	4352	111.4957	
617	AAAACCACCCTACACCAAGCA	3110	KTTLHQA	4353	111.46	
618	ATGATAAACGCCATAACTCCA	3111	MINAITP	4354	111.432	
619	GGGTCTACGCCGGGGCGAGT	3112	GSTPGAS	4355	111.327	
620	AATGAGAAGCCGAGTCGACG	3113	NEKPQST	4356	111.309	
621	TCATTGATGGGCAGTCAGGA	3114	SLMG SAG	4357	111.287	
622	ACCGACACGCTCAGCGAAAGA	3115	TDTL SER	4358	111.25	
623	GCCTCGCAATCAGAAAAAAC	3116	ASQSEKN	4359	111.223	
624	GCTGT TAGAACCCGGCAATG	3117	AVRTPAM	4360	111.215	
625	CCTAATGCTAGTTTGGTCCG	3118	PNASF GP	4361	111.172	
626	AAAGCCCACGTTGTAGAAATA	3119	KAHVVEI	4362	111.166	
627	TATATTT CGGCGCTCCGATG	3120	YISAPPM	4363	111.15	
628	CCAATCCAAAACGAATCGTCC	3121	PIQNESS	4364	111.128	
629	GGCGTAACCAACGCTTCCAAA	3122	GVTNASK	4365	111.107	
630	GTAAACGGGGAAAAC CAGTC	3123	VNGGKPV	4366	111.096	
631	AGTGT TCTGAGTAGTTCGACT	3124	SVLSSST	4367	111.07	
632	TTAGCACAAGGCACGGACCGG	3125	LAQGTDR	4368	111.032	
633	CAGTCTGTGTCGACTGGGGCG	3126	QSVSTGA	4369	110.982	
634	TTGACGCAGGTTTATCATGAG	3127	LTQVYHE	4370	110.91	
635	AGAGAAATGAGCAGCCTATCT	3128	REMSSLS	4371	110.891	
636	ACGAGTACGATGACTGCGCGT	3129	TSTMTAR	4372	110.835	
637	ACTATTCAGCAGGTTAGTAAT	3130	TIQQVSN	4373	110.832	
638	AGGACGCAAGCAGGGGACTCA	3131	RTQAGDS	4374	110.83	
639	AATACTTATACTGCTGGGAAG	3132	NTYTAGK	4375	110.816	
640	AATGAGCAGAATACGCCGAGT	3133	NEQNTPS	4376	110.79	
641	GGATTGCCCCAACAAGAAGCG	3134	GFAQQEA	4377	110.775	
642	AGTCCGCAGCATGGTGTTATT	3135	SPQH GVI	4378	110.7	
643	GCAGTCCACGCAACATCATCA	3136	AVHATSS	4379	110.653	
644	GGAGACACCCGTGGTGACAC	3137	GDTRGAH	4380	110.63	
645	GTAAGAGAAACACACACCTC	3138	VRETHL	4381	110.627	
646	CTTTCTCAACAACGCGACTAC	3139	LSQQRDY	4382	110.6	
647	GCGACTAGGGGTGAGTCGTCT	3140	ATRGE SS	4383	110.56	
648	ACTAATGATTCTGTGGTAGT	3141	TNDSVGS	4384	110.545	
649	CTTACTAATAATTTTAAGGAT	3142	LTNNFKD	4385	110.519	
650	GTGAATGGGACTCAGATTTTT	3143	VNGTQIF	4386	110.47	
651	GGTAATACTGGGAGTCCGGGG	3144	GNTGSPG	4387	110.431	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
652	TGGACAGCTAACCAAGGCTTA	3145	WTANQGL	4388	110.43	
653	AATACTACTCCGACGAATCAT	3146	NTTPTNH	4389	110.42	
654	GAACGAGTCAACGGGATGGCA	3147	ERVNGMA	4390	110.405	
655	AAAGTCACAAACAACGCATAC	3148	KVTNNAY	4391	110.363	
656	TTATCCTCCGAATCAGCCAGG	3149	LSSESPR	4392	110.346	
657	CATACGGCGCGGTTGCTACT	3150	HTAAVAT	4393	110.27	
658	TACGACAGCCGACTCTACGCG	3151	YDSRLYA	4394	110.263	
659	ATAGAACACATGCTTAGACCC	3152	IEHMLRP	4395	110.221	
660	TACCTAGAATCCAACTACACC	3153	YLESNYT	4396	110.18	
661	GCGTACTCATCTACCGGGCAC	3154	AYSSTGH	4397	110.176	
662	ATCGACATATCGACGCAAAGC	3155	IDISTQS	4398	110.14	
663	ACAACAAACTCAGGCGCGACG	3156	TTNSGAT	4399	110.139	
664	AACGTGCTAACCACGGTTGTC	3157	NVLTTVV	4400	110.107	
665	ACAACCGGAATCGAACGTTCC	3158	TTGIERS	4401	110.106	
666	GCACGAGTGGACACCAACCAA	3159	ARVDTNQ	4402	110.09	
667	CAGAGTGTGAAGGAGCGATT	3160	QSVKEAI	4403	110.069	
668	GCGTTGCTTAGTGTGAATGAG	3161	ALLSVNE	4404	110.013	
669	GGGCGTGATAATCATCATGCG	3162	GRDNHHA	4405	109.959	
670	ATTCAGTCGCAGTCGAGTTG	3163	IQSQSQL	4406	109.941	
671	AGTGAGGGTAGTTCGCGTCTG	3164	SEGSSRS	4407	109.9403	
672	GACGTCCAAAACATACGCGAA	3165	DVQNIRE	4408	109.921	
673	AAAGGCCACGCCTACGAAGCC	3166	KGHAYEA	4409	109.897	
674	TATGTTAGGGCGCAGGATCAG	3167	YVRAQDQ	4410	109.876	
675	GTCGACGAATACCGAAGCCGC	3168	VDEYRSR	4411	109.853	
676	ACTCTCTCAGGCTACATGAGA	3169	TLSGYMR	4412	109.808	
677	CCTAGTGTCGTTTGCCCTTA	3170	PSVRLPL	4413	109.742	
678	AACATAGCAGGCGGAGAACAA	3171	NIAGGEQ	4414	109.702	
679	CTGCTCCAATCGACCTACTTG	3172	LLQSTYL	4415	109.672	
680	CAGTCGATACGACTTCGATT	3173	QSDTTSI	4416	109.605	
681	ATTAGGTCTGGGAATGCGATG	3174	IRSGNAM	4417	109.554	
682	ATGCTGTCTCAAGTCTTAACA	3175	MLSQVLT	4418	109.536	
683	ACAGAACGCCAAATCGAATTA	3176	TERQIEL	4419	109.488	
684	GGAACCCACGCCTCAGCATAC	3177	GTHASAY	4420	109.477	
685	GTTGAGTCTTCTATTCTCGG	3178	VESSYSR	4421	109.457	
686	GGTGGGAATTATCATACTAAG	3179	GGNYHTK	4422	109.445	
687	CCCACCAGTCACCAAGAACCC	3180	PTSHQEP	4423	109.418	
688	ACCATAATCGGTGTCTTACCC	3181	TIIGVLP	4424	109.381	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
689	TCTAACAGCGTTCTACCTC	3182	SNSGSTL	4425	109.379	
690	TCGATAACGACCGTAGCGAAC	3183	SITTVAN	4426	109.347	
691	GCGTCTCCGGCGCAGACCGGC	3184	ASPAQTG	4427	109.331	
692	TCGTTGCCGAGTCATAGTAAT	3185	SLPSHSN	4428	109.3106	
693	CTACACAACGCCGTCGGACCC	3186	LHNAVGP	4429	109.307	
694	CAAGCCCCGCCAACAGCACAA	3187	QAPPTAQ	4430	109.294	
695	CCTAATACTGCTAGTAATTTT	3188	PNTASNF	4431	109.249	
696	CCCTCCAACAGTGAAAGATTC	3189	PSNSERF	4432	109.227	
697	GAAGTCCACGCACAACAACCA	3190	ELHAQQP	4433	109.194	
698	GGTTCTTATTCTGATGGTAGT	3191	GSYSDGS	4434	109.162	
699	TATGGTGTGCAGGCGAATAGT	3192	YGVQANS	4435	109.152	
700	GAAGTAGGTAAAACCCAC	3193	EVGKTTH	4436	109.116	
701	ACTTCGCAGGGTAGGAGTCTT	3194	TSQGRSP	4437	109.097	
702	GTAGAACACGTAGCCACCAA	3195	VEHVAHQ	4438	109.092	
703	ATCCAAAGCAGCTACAACCGC	3196	IQSSYNR	4439	109.073	
704	ACGCTATCGGTTACCTGGGT	3197	TLSVTLG	4440	109.046	
705	CGGAATGAGCCGGTTAGTACT	3198	RNEPVST	4441	108.981	
706	GTGATTGTGGGAGTAATGAG	3199	VIVGSNE	4442	108.955	
707	GAGCTGTCTACTCTATGGTT	3200	ELSTPMV	4443	108.948	
708	GCTTACAACGACCTACGATCA	3201	AYNDLRS	4444	108.942	
709	AACGCGAACTCCGGTGAACGA	3202	NANSGER	4445	108.906	
710	TTGTCATCACAATGGACACAA	3203	LSSQWTQ	4446	108.9	
711	ATCAACGCCGCAACTACCGA	3204	INAGNYR	4447	108.883	
712	CTGAGGTCGAGTGAGGCTCCG	3205	LRSSEAP	4448	108.866	
713	ACGTCTGATACGAATGCTAGG	3206	TSDTNAR	4449	108.858	
714	CCGAATTCTCCGATGGTTCT	3207	PNSPHGS	4450	108.84	
715	ACCCAACACCTACCATCCACA	3208	TQHLPST	4451	108.803	
716	GTGCATGGGAATGCTCCGGCT	3209	VHGNAPA	4452	108.783	
717	TCTTCTCAGCGTATTCTGTT	3210	SSQRDSV	4453	108.754	
718	CCCCCTCAGTTGACCGAAAA	3211	PPSVDRK	4454	108.751	
719	GAGACTCTGCCGTATAAGAGT	3212	ETLPYKS	4455	108.728	
720	CATCTTAGTCAGGCTAATCAT	3213	HLSQANH	4456	108.727	
721	AAACCGCTAAACGGTACCAAC	3214	KPLNGTN	4457	108.683	
722	TGGCAAACCAACGGCATGCAA	3215	WQTNGMQ	4458	108.68	
723	ACCGTGAACGTCCACTCCGAC	3216	TVNVHSD	4459	108.659	
724	ACCCAATACGTCGTTGCCCT	3217	TQYVVAP	4460	108.64	
725	AACGTCGACTCCTCTAACGTG	3218	NVDSSNV	4461	108.62	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
726	AACGGATACCAACTACAAATC	3219	NGYQLQI	4462	108.573	
727	GAAGAAACACGGACCAGAATG	3220	EETRTRM	4463	108.571	
728	ACCTCTCCAGCCTCTGACCGG	3221	TSPASDR	4464	108.552	
729	CATAGTGGTGCTGGGTTCTG	3222	HSGAGVL	4465	108.539	
730	GCTGCTAATCCTAGTACGGAG	3223	AANPSTE	4466	108.527	
731	ATGTTGGTACAAAACACACC	3224	MLVQNT	4467	108.482	
732	GTGCAGCAGAATAATTAAT	3225	VQQNNIN	4468	108.473	
733	CATGATGGTTATGTTCTAAT	3226	HDGYVPN	4469	108.469	
734	AACCTCAGGTAAACACCCATC	3227	NSGNNPI	4470	108.467	
735	ACGGACAACCCGCTCTACAAA	3228	TDNPSYK	4471	108.453	
736	GGAGGCTTAAGTTTATCTCG	3229	GGLSLSS	4472	108.431	
737	AATAATGAGAATACGCGTAAT	3230	NNENTRN	4473	108.418	
738	AAGAATAATAATTCTGATTCT	3231	KNNNSDS	4474	108.367	
739	AAGGATGAGCATCTTCATTAT	3232	KDEHLHY	4475	108.358	
740	AATTTTACTATTACGGAGGCG	3233	NFTITEA	4476	108.32	
741	TTGAACCAAAACAGTGTCTCC	3234	LNQNSVS	4477	108.304	
742	AATTCTCATGTTCTAATAAT	3235	NSHVPNN	4478	108.289	
743	AATTCTACGCATATTAATTCG	3236	NSTHINS	4479	108.2563	
744	CATATGTCTAGTTATTCGTCG	3237	HMSSYSS	4480	108.253	
745	AACGTACCCAACGGACAAGGA	3238	NVPNGQG	4481	108.25	
746	AACGGTCCGACCGGATCCGCC	3239	NGPTGSA	4482	108.245	
747	AAAAGCAACGCGGATTCTGGT	3240	KSNAGFG	4483	108.23	
748	GCGGCCGCACTAGAAACAATA	3241	AAALETI	4484	108.223	
749	AACCGTCAAAGGGACTTCGAA	3242	NRQRDFE	4485	108.196	
750	GGGTCAGGGAACGAACCCGGG	3243	GSGNEPG	4486	108.192	
751	GTTAGTGTGGCTGTGCCTGCG	3244	VSVAVPA	4487	108.11	
752	CACTCTAACACACACTACGAA	3245	HSNTHYE	4488	108.11	
753	CCTGACAGAGCGAACGACAAA	3246	PDRANDK	4489	108.058	
754	CAAGTTGGGGCTCTAATGGTT	3247	QVGALMV	4490	108.037	
755	TTAACACCCCAAGGGACTAGT	3248	LTPQGTS	4491	108.028	
756	CTATACGACGGAACACGTC	3249	LYDGKHV	4492	107.972	
757	CTAACCGAATCTGTGAGAAAC	3250	LTESVRN	4493	107.93	
758	AGTACTTATGGGAATACTTAT	3251	STYGNTY	4494	107.929	
759	AATGCTATTTCTACTAATAAT	3252	NAISTNN	4495	107.907	
760	ATTGCTCATGTGTCTACTAAT	3253	IAHVSTN	4496	107.849	
761	AGTGAGGAGAGGACGCGTGCG	3254	SEERTRA	4497	107.833	
762	CGTTGGTCTGAAAACAACTCC	3255	RWSENNNS	4498	107.83	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
763	GATGGTAATAATACGACTTAT	3256	DGNNTTY	4499	107.748	
764	GTGACGACTGTTGATAGTGCT	3257	VTTVDSA	4500	107.738	
765	ACCGTAAACAAACAAGTCCG	3258	TVKQTSP	4501	107.7213	
766	TCTATCTACCTCGCTCCACT	3259	SIYLAST	4502	107.712	
767	ACGACCCGAAACGAACACTCG	3260	TTRNEHS	4503	107.707	
768	TCGTATGATATGCATACGAAT	3261	SYDMHTN	4504	107.705	
769	GTCTCTACATACCTCCTGGCA	3262	VSTYLLA	4505	107.687	
770	GGAGAACAAGCCACAACCAA	3263	GEQSHNQ	4506	107.684	
771	ACTGCCAACAACTCTCTCCG	3264	TANNHSP	4507	107.671	
772	CAATTCCACGGGACATCTGAA	3265	QFHGTSE	4508	107.652	
773	AACGTTCTGGGAGCGTCTAGC	3266	NVLGASS	4509	107.64	
774	AGGGATAGTACTATTAGTCGG	3267	RDSTISR	4510	107.635	
775	GTTATTGGGACTTCTAGGGAT	3268	VIGTSRD	4511	107.5934	
776	AATTATGAGAAGGAGTTTGTT	3269	NYEKEFV	4512	107.592	
777	ATGGACCAAAGCCACTCCCGA	3270	MDQSHSR	4513	107.563	
778	AATTCTCAGAATCCTCAGGCT	3271	NSQNPQG	4514	107.562	
779	CACACGGGCACGCAACCGA	3272	HTGTDNR	4515	107.5323	
780	TATAATACTGTTGATCAGCGG	3273	YNTVDQR	4516	107.523	
781	AAAGAAAGCCTCGAAGACGTC	3274	KESLEDV	4517	107.49	
782	ACTGCGAATAGTACGTATGTG	3275	TANSTYV	4518	107.479	
783	TATCTGAATAGTACGAGATT	3276	YLNSTQI	4519	107.436	
784	CGTGTGTAAGACCAACTCC	3277	RVEDTNS	4520	107.416	
785	AACGACGCACGCAACCGTGCA	3278	NDARNRA	4521	107.37	
786	AATACTAATAATCAGGAGCAG	3279	NTNNQEQ	4522	107.332	
787	ACCGTCGGATCGAACAGTATA	3280	TVGSNSI	4523	107.3	
788	TATGGGGAGCGTGCTAGGACG	3281	YGERART	4524	107.297	
789	CCGACCGGAGGCTCACCACCA	3282	PTGGSP	4525	107.265	
790	CTTGGGCAGGTTAATTCTACG	3283	LGQVNST	4526	107.229	
791	GTCTCGGGTCCGGTATCGGTC	3284	VSGPVS	4527	107.222	
792	GGTACTAATCATGATTTTTTCG	3285	GTNHDFS	4528	107.169	
793	AAGACGCTTGATAATAATGCT	3286	KTLDNNA	4529	107.165	
794	CACAGTGAACCTACGTCAAAAC	3287	HSELRQN	4530	107.157	
795	GAGAAGAATCTGACTAATGCT	3288	EKNLTNA	4531	107.131	
796	ACCGGACTCGGAGGCAACAGT	3289	TGLGGNS	4532	107.113	
797	AAAGACCACATCCTCAGCCTC	3290	KDHILSL	4533	107.108	
798	ATAACTACTGGCGGAGTGCTA	3291	ITTGGVL	4534	107.108	
799	CTGGCTGATTCTGAATTCTAAG	3292	LADSNK	4535	107.1	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
800	AGTATTTCTGATAAGAATCAG	3293	SISDKNQ	4536	107.08	
801	TATATTGCTGGGGGGAGCAG	3294	YIAGGEQ	4537	107.069	
802	TTGCCGATAAGGGGCGGATT	3295	LPDKGRI	4538	107.06	
803	TTGATCCAAACGCAAGGCACG	3296	LIQTQGT	4539	107.042	
804	TACTCCGAGAACTAAACAAA	3297	YSGELNK	4540	107.037	
805	TGCGCATCAGAAGTTTGCCAA	3298	CASEVCQ	4541	107.035	
806	CTTATGGCTGCTAATACTGCG	3299	LMAANTA	4542	107.032	
807	CATCAGTCTTTTGATGCTGGT	3300	HQSFDAG	4543	107.001	
808	GGGGAGACGCTGAGGTCTCAG	3301	GETLRSQ	4544	106.999	
809	CAGACTGATGGTCCTAATTTT	3302	QTDGPNF	4545	106.978	
810	ACGACGACTAATGTGAATTTT	3303	TTTNVNF	4546	106.969	
811	AACATGACCAACGAAAACGGA	3304	NMTNENG	4547	106.938	
812	GGGTATAGTCCTTCGACGCCG	3305	GYSFSTP	4548	106.892	
813	TTGCAGGTTACGGTTCATAAT	3306	LQVTVHN	4549	106.879	
814	GATCTGACGCATGTTTCATCGT	3307	DLTHVHR	4550	106.874	
815	ACGGAGCTTAGTGAGTATACT	3308	TELSEYT	4551	106.852	
816	ATGACAGTCGCCAGTACTAGC	3309	MTVASTS	4552	106.843	
817	AGCAGTCAAGCCCACGGCCCA	3310	SSQAHGP	4553	106.822	
818	ACCAGAAGCCCGAACGAAGAC	3311	TRSPNED	4554	106.81	
819	GATAATAATAAGCATGGTACT	3312	DNNKHGT	4555	106.806	
820	AGGGAGATTGTTCATAGTAAT	3313	REIVHSN	4556	106.802	
821	CGGAACTTGAACGACCTA	3314	RKLELDL	4557	106.801	
822	ATCTACGAAACCGTAACCTTG	3315	IYETVTL	4558	106.801	
823	AATAGTGGTAGTACGAGTTTT	3316	NSGSTSF	4559	106.783	
824	CCAAGTACGAACGAAAGCCGC	3317	PSTNESR	4560	106.782	
825	CAAGCCGACCTCAGGTACAAA	3318	QADLRYK	4561	106.773	
826	GATCAGCCGGGGTATGTGCGT	3319	DQPGYVR	4562	106.7387	
827	GATGTATGCTTGCTCATCCG	3320	DAMLAHP	4563	106.735	
828	ACACGTCACGACGGCAGTACG	3321	TRHDGST	4564	106.675	
829	CTGGCGAATATGAGTGCGCCG	3322	LANMSAP	4565	106.664	
830	ACTGGTCATCCGCCGCGCGC	3323	TGHPAA	4566	106.654	
831	TCGAGTATTAGTCTGCGGTAT	3324	SSISLRY	4567	106.645	
832	ATGCACGTCGACAAAACGAGT	3325	MHVDKTS	4568	106.639	
833	GGGAGTGATTCTAAGCATCCT	3326	GSDSKHP	4569	106.5782	
834	GGAGAAAGCTCCTCAATAAGC	3327	GESSSIS	4570	106.551	
835	GTCGTCCACTCACACAGTGAA	3328	VVHSHSE	4571	106.496	
836	AGTGTGCGGGCGCATGTTTTG	3329	SVRAHVL	4572	106.487	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
837	GCGGATGGGGCTAAGTCTGCT	3330	ADGAKSA	4573	106.485	
838	GGGGAAGCAGCCGAGAAGCC	3331	GEARREA	4574	106.442	
839	TTTAATGCTACGGTGGTGCAT	3332	FNATVVH	4575	106.437	
840	TGGACGGAAGGGGGCTCAGGA	3333	WTEGGSG	4576	106.423	
841	GATTCTTCTTATACGCATCCG	3334	DSSYTHP	4577	106.422	
842	TTCCCAAGTAGGGACAACGTA	3335	FPSRDNV	4578	106.39	
843	GCCATCACGCACATCGGTACA	3336	AITHIGT	4579	106.365	
844	GCTTTTAAGTCGGGTAGTATT	3337	AFKSGSI	4580	106.334	
845	ATGTCAAACGCCTCCTACATA	3338	MSNASYI	4581	106.319	
846	GCGGAGAGGAATGATAGGACG	3339	AERNDRT	4582	106.305	
847	ACATTAGAAACAACCCGACG	3340	TLETTRS	4583	106.244	
848	CGCTTACACGGCTCAGACTCG	3341	RLHGSDS	4584	106.237	
849	TATGAGGGGCATATGAATACT	3342	YEGHMNT	4585	106.2354	
850	TCTGTGACGACTAATCTGATG	3343	SVTTNLM	4586	106.217	
851	TTGCGTGATCAGACTAGTATG	3344	LRDQTSM	4587	106.167	
852	CCCGCCAGTCACAGCGCGGGA	3345	PASHSAG	4588	106.151	
853	GTGGTTGAGAATTTGAGGCAG	3346	VVENLRQ	4589	106.147	
854	CAACAATCACAAACTCTATA	3347	QQSQNSI	4590	106.115	
855	CTTGTTGATACGGATAGGAAT	3348	LVDTRN	4591	106.108	
856	AACGAAATGGGAACTACGTC	3349	NEMGNYV	4592	106.104	
857	TCCACCGACCCCGATACTCA	3350	STDPRYS	4593	106.097	
858	ACTAATGGTATTTATCAGCCT	3351	TNGIYQP	4594	106.095	
859	TGGGTAAACAGTGTGGGCAAC	3352	WVNSVGN	4595	106.084	
860	GGGGTATCTAACAACCTTAGC	3353	GVSNNSS	4596	106.079	
861	AATGTTAATGCGCAGAGTAGG	3354	NVNAQSR	4597	106.064	
862	ACGACGCCGCTTTTCTAAT	3355	TTPFSN	4598	106.044	
863	ACAGGCAGCTCCACACCAAC	3356	TGSSHTN	4599	106.0345	
864	TACGTCGACAAATCAATGACA	3357	YVDKSM	4600	106.009	
865	CTAATCAAAAACAACATGCTC	3358	LIKNNML	4601	105.9827	
866	GGGGGTACGGGGTTGTGGAAG	3359	GGTGLSK	4602	105.98	
867	GCTCTTCATAATCTGATGAAT	3360	ALHNLN	4603	105.977	
868	GTGCATGTGACTAATGTGTTG	3361	VHVTNVL	4604	105.924	
869	TCGACGACGACCCCTTCCGAA	3362	STTHPSE	4605	105.898	
870	AGCGTAGGTAGTCCAACACAC	3363	SVGSPTH	4606	105.8936	
871	ATGAGTAATGATTTGCCTGGG	3364	MSNDLPG	4607	105.877	
872	TTCTCGTCAACCGAAGCCAGA	3365	FSSTEAR	4608	105.858	
873	GCCGGTCACCAACAACTGGCC	3366	AGHQQLA	4609	105.846	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
874	GGTACCATATTACCAACCAA	3367	GTILPNQ	4610	105.829	
875	AGCGCGGTTTCTGGTAGCAGC	3368	SAVSGSS	4611	105.825	
876	GAGGTGTCTAGGGATGGTCTG	3369	EVS RDGL	4612	105.814	
877	CAATCACTCAAAGACGGCACT	3370	QSLKDGT	4613	105.804	
878	ACGCGTGAGGGTAATCATGCT	3371	TREGNHA	4614	105.8	
879	GTGGCGACCCAAAACCTTCTT	3372	VATQNLL	4615	105.795	
880	GCCGAAATGACGCACCGCCTC	3373	AEMTHRL	4616	105.771	
881	CAACGCCAGACCCGCTTAAA	3374	QRPDPLK	4617	105.764	
882	GAACACATCTCTAGCTACGGA	3375	EHISSYG	4618	105.752	
883	CAAAAAGCAACGACCAAAAC	3376	QKSNQDN	4619	105.744	
884	AATCTTGATGAGTGGGACG	3377	NLVMSGT	4620	105.742	
885	GGAGCGGGACAATCTCACGTG	3378	GAGQSHV	4621	105.721	
886	CTCAACCACACAATGCCCTC	3379	LNHTMPL	4622	105.713	
887	GTATCACAATCACACGACGTG	3380	VSQSHDV	4623	105.687	
888	GCTAATTCTGCTACTAATCAG	3381	ANSATNQ	4624	105.679	
889	GGCACAGGAGTAACCGAGAA	3382	GTG NRE	4625	105.671	
890	GCGAAGTCGTCGATTATTTTG	3383	AKSSIIL	4626	105.661	
891	GGAGGAACAGCCCTTGGGAGC	3384	GGTALGS	4627	105.613	
892	AACAAAGTAGAATCTGACCCA	3385	NKVESDP	4628	105.59	
893	AACTCGAAACAACCCGACGTC	3386	NSKQPDV	4629	105.572	
894	AGTTATGCTGATCGTCGGCTG	3387	SYADRRRL	4630	105.567	
895	AATGTGAATCCGAATGGGCCG	3388	NVNPNGP	4631	105.53	
896	GAACACAACCTCAAAACTTAC	3389	EHNSKTY	4632	105.496	
897	ACCCAAGGATCTAACACCACA	3390	TQGSNTT	4633	105.489	
898	AGCAACGTATCAGCTTACGCA	3391	SNVSAYA	4634	105.48	
899	GCGTACAGTGACAGCGCCCGC	3392	AYS DSAR	4635	105.457	
900	GGGTCGCAATACGCGAACCGC	3393	GSQYANR	4636	105.402	
901	ACAATGAGCGTAACCTTGAA	3394	TMSVTLE	4637	105.393	
902	CAGACGACTATTCTGGCTGCT	3395	QTTILAA	4638	105.386	
903	TTGCTCCAATCCATAGTGGTA	3396	LLQSIVV	4639	105.381	
904	GITCAGCTAACGCTACATTA	3397	VHANATL	4640	105.38	
905	AACAAAACAAACGCCGACTAC	3398	NKTNADY	4641	105.38	
906	AACTACGACACCGCGCCAAA	3399	NYDTGAK	4642	105.378	
907	GTCTACCACAACCGCAGGTT	3400	VYHNRDV	4643	105.358	
908	GATTCTGCTCCGAGGTCTATT	3401	DSAPRSI	4644	105.351	
909	TTGATTGCGAATCTGAGTAAT	3402	LIANLSN	4645	105.341	
910	CCGCAAGACGTCCGCCAAACA	3403	PQDVRQT	4646	105.331	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
911	ACAATGACAGCAATAGCAATG	3404	TMTAIAM	4647	105.327	
912	ACATACGCCTCTACTGAAGCG	3405	TYASTEAA	4648	105.324	
913	CCTCACGCCAACGGAGTGACA	3406	PHANGVT	4649	105.298	
914	CGGGCTGATGTTTCTTGCTCT	3407	RADVSW	4650	105.286	
915	CTGACGCACATGACCGGAACC	3408	LTHMTGT	4651	105.272	
916	GCAAACGACTCTGCCAAAACA	3409	ANDSAKT	4652	105.269	
917	GCTAATTCTGGGTTCATAAT	3410	ANSGLHN	4653	105.246	
918	AACGTGGGCACCGACAGAGAC	3411	NVGTDRD	4654	105.231	
919	GTCGGAACAACCTCGAACGGC	3412	VGTTSTNG	4655	105.226	
920	GGAGTTCTTGGGATACTGGTC	3413	GVLGILV	4656	105.184	
921	CGAATCAACGCAGCAATCGAC	3414	RINAAID	4657	105.1475	
922	CCCGACACTCGCCCATCCATA	3415	PDTRPSI	4658	105.135	
923	GGTGAATCACGTACAAACATG	3416	GESRTNM	4659	105.119	
924	ATTTTGCTTGCTCAGTCTGCT	3417	ILLAQSA	4660	105.117	
925	TATAATAGGGATAATGGTTCT	3418	YNRDNGS	4661	105.083	
926	TGGAATAGTCCGGGTGAGCG	3419	WNSPGEA	4662	105.053	
927	CTGTTGGGGGCTCATCAGCCG	3420	LLGAHQF	4663	105.052	
928	ATTGGTAAGGATAGTGTCCG	3421	IGKDSVP	4664	105.044	
929	ACGCGGGAGAGTCTGGTGGAT	3422	TRESLVD	4665	105.022	
930	GCCTCTAACCACCTACAAGCC	3423	ASNHLQA	4666	105.013	
931	AATCTTCAGACGGGTAAGGCT	3424	NLQTGKA	4667	104.976	
932	ACTGTAGGATCCTCATACGCT	3425	TVGSSYA	4668	104.9737	
933	GACACTAACGGAATAAAATCA	3426	DTNGIKS	4669	104.968	
934	AGTCTGCGGATGGAGAATAGT	3427	SLRMENS	4670	104.957	
935	ACTAAGGGTAATAATCTGGTT	3428	TKGNLNV	4671	104.92	
936	CATACGAATCAGATGCAGCCT	3429	HTNQMQP	4672	104.919	
937	AACGGCAACTACGACGGCGCG	3430	NGNYDGA	4673	104.912	
938	GAGGCGCATAATCGTGGTAAT	3431	EAHNRGN	4674	104.898	
939	GGGACGGTTAACTCAAGTGCA	3432	GTVNSSA	4675	104.861	
940	GGGCCGACGATGAATCATAAT	3433	GPTMNHN	4676	104.854	
941	GTACCAACAACAACACTTCG	3434	VPNNNTS	4677	104.834	
942	GTTTCTAACAATCTGGAAGT	3435	VSNKSGS	4678	104.818	
943	TGGGGAGTCAGTAACCTAGCA	3436	WGVNSA	4679	104.795	
944	GTCTCTAACGTCTCTACAGC	3437	VSNVLYS	4680	104.772	
945	GCCGGCCAAAACAGTGTGGGC	3438	AGQNSVG	4681	104.77	
946	GGTACGAGTCTGGAGAATAGG	3439	GTSLENR	4682	104.754	
947	CAGATGAATATTCATGATAAG	3440	QMNIHDK	4683	104.736	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
948	CCTCAACTAAGCGCACAGCG	3441	PQLSGTA	4684	104.733	
949	AGTTCGACTCCGAGGATACT	3442	SSTPQDT	4685	104.713	
950	GTGCAGGGGACACCGGCTGG	3443	VQGQTGW	4686	104.688	
951	GGTCTGACGGGTGATTGGTT	3444	GLTGDLV	4687	104.682	
952	AACCACCCCGCACCAAGCTCA	3445	NHPAPSS	4688	104.679	
953	AAAGAAAAACACCCGCGAA	3446	KEKTTRE	4689	104.665	
954	ACTACTAATCCGACAGCAG	3447	TTNPQTQ	4690	104.663	
955	GGAGGTGAACACGCAAGAAAC	3448	GGEHARN	4691	104.66	
956	ACGACCGAAGCTGTTGTAGCA	3449	TTEAVVA	4692	104.656	
957	CAAAACAGTGACCTGCCAGC	3450	QNSDLAS	4693	104.638	
958	TACTCTACAGAAGCACGAGTC	3451	YSTEARV	4694	104.609	
959	ACCGGACAAGCGGGCGGATCG	3452	TGQAGGS	4695	104.571	
960	ACTTCGTCTAATCTTTATGTG	3453	TSSNLYV	4696	104.559	
961	ACGGCTCGTGCATTGATATG	3454	TARAIDM	4697	104.551	
962	CAGGAGTCTAATAGGGGGTG	3455	QESNRGV	4698	104.547	
963	AGTATCGGATTCTCAGTAGGC	3456	SIGFSVG	4699	104.529	
964	GAGCGGAGTACGCATAATGTT	3457	ERSTHNV	4700	104.513	
965	GCAAACCACGACAACATCGTG	3458	ANHDNIV	4701	104.501	
966	TGGGCTATGAATAATGTGCCG	3459	WAMNNVP	4702	104.498	
967	TATATTGCTGCGGGTGAGCAG	3460	YIAAGEQ	4703	104.498	
968	AGTTCGAATACTTCTGGTAGT	3461	SSNTSGS	4704	104.4928	
969	ATGGGGAAGCATGAGGGTCTT	3462	MGKHEGL	4705	104.481	
970	GTGCTTACTCATCTGCCGACG	3463	VLTHLPT	4706	104.4786	
971	GAAATGGGTAACCAATACCCA	3464	EMGNQYP	4707	104.453	
972	AGTCTGCGTCCAACCTACCT	3465	SLAPTLP	4708	104.448	
973	TCGGCTAAGTTATACAAACAA	3466	SANLYKQ	4709	104.394	
974	CAAAACGACAGAAAACCGGAC	3467	QNDRKPD	4710	104.391	
975	ATTATTTTCGGGTATTACGGTG	3468	IISGITV	4711	104.365	
976	CCATCCGAAATGAGGGCCGTA	3469	PSEMRV	4712	104.361	
977	TTGGTTACGACAGCCGAAT	3470	LVTQTPN	4713	104.337	
978	ATTGCGCAGAATGAGACGTAT	3471	IAQNETY	4714	104.336	
979	CCATACTTAAGAAACATGGCG	3472	PYLRNMA	4715	104.321	
980	GGCGTGAACACAAAAATCGAA	3473	GVNTKIE	4716	104.311	
981	TACTCTTCTGAAATGAGCGAA	3474	YSSEMSE	4717	104.31	
982	TTAGAAAACCAACACCAGCA	3475	LENPTPA	4718	104.305	
983	GGTGTTATGTCTAATGCTACT	3476	GVMSNAT	4719	104.289	
984	GCCACACTGCATTAGCGGGG	3477	AHTALAG	4720	104.27	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
985	CCTGTTGTGAGGGATCGTTCT	3478 PVVRDRS	4721	104.2336	
986	TCTGCGGTATGGTGAAGTCTG	3479 SAGMVSL	4722	104.229	
987	TCGGGTGTTAATAGTGAGCGT	3480 SGVNSER	4723	104.2093	
988	AATGGGGATGTTACTAATATG	3481 NGDVTNM	4724	104.179	
989	TCTGTTGTGCCTACGGATAAG	3482 SVVPTDK	4725	104.174	
990	AGTAAGGGTGATCAGCTTAAT	3483 SKGDQLN	4726	104.166	
991	GACGGAGAATCCGATTATCA	3484 DGESRLS	4727	104.158	
992	GGTAATATGAATCATAGTATT	3485 GNMNHSI	4728	104.15	
993	AGTGGGCATGCTTCTCAGGGT	3486 SGHASQG	4729	104.148	
994	GGTTGGAGTAATAATGAGTTG	3487 GWSNNEL	4730	104.145	
995	GGTGTGCATACTCATACTGTT	3488 GVHTHTV	4731	104.139	
996	CACGTGACAGTAACGTTAAAC	3489 HVTVTLN	4732	104.124	
997	ACCCGTGGCAACGACATATCA	3490 TRGNDIS	4733	104.058	
998	AGCAAAGGCGGCGACATGGTT	3491 SKGGDMV	4734	104.043	
999	ACGCATGGTGATCATATTCAG	3492 THGDHIQ	4735	104.032	
1000	ACTACGAATTCTCATGCGATT	3493 TTNSHAI	4736	104.021	
1001	GTCAGAACAGTCCTTCAACAA	3494 VRTVLQQ	4737	104.017	
1002	ACTGTGCGTTCGCCTCAGCCG	3495 TVRSPQP	4738	104.015	
1003	AATACTTATCTGCTGGTAAG	3496 NTYTAGK	4739	104.005	
1004	ATTAGTAATCCGGAATACG	3497 ISNPENT	4740	103.998	
1005	ATCGGGTCGCCGTTGGCCAAC	3498 IGSPLAN	4741	103.928	
1006	TATACGGGTACTCTTGTGTGT	3499 YTGTLVV	4742	103.911	
1007	GGGCGGCACACATTAGCGGAC	3500 GRHTLAD	4743	103.908	
1008	ACTGATGGGCCGCTCTGGCT	3501 TDGPRLA	4744	103.881	
1009	GGGGCAGGAAACCTGGGTACC	3502 GAGNLGT	4745	103.873	
1010	CTGATGAATCGTAATGCTCCT	3503 LMNRNAP	4746	103.8648	
1011	AATGCTATGGCTTCTAGTAGG	3504 NAMASSR	4747	103.826	
1012	CAGCATCGTGCAGGATGTG	3505 QHRAQDV	4748	103.8248	
1013	AAAATAGAAAGCGGAACCAT	3506 KIESGTI	4749	103.822	
1014	ACTAATTATCTGAGGCGAAT	3507 TNYPEAN	4750	103.806	
1015	GTATACCACGGGTAGCCAGC	3508 VYHGVAS	4751	103.803	
1016	TCCAACGTCCACGTAGTAAAC	3509 SNVHVVN	4752	103.791	
1017	ACATACACCGACGGGAACCCC	3510 TYTDGNP	4753	103.788	
1018	TTTATTGCGAATACGAATCCT	3511 FIANSTP	4754	103.787	
1019	GACGCCGGGTACGGCCACGAC	3512 DAGYGHD	4755	103.785	
1020	GGTCTTAGTCGGAATGATGGT	3513 GLSRNDG	4756	103.783	
1021	ATGATGGCGCGACAACGAAA	3514 MMGATTK	4757	103.779	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1022	CCCATCAACGTACTCACGACA	3515	PINVLTT	4758	103.771	
1023	GCCGTAGACCAATCAGTTTG	3516	AVDQSRL	4759	103.765	
1024	AACGCTTCTACCTACATGGAC	3517	NASTYMD	4760	103.728	
1025	ACACAAGCAGGTCTTGCGTCA	3518	TQAGLAS	4761	103.696	
1026	GCACAATTCTGAATCAGGCCGA	3519	AQFESGR	4762	103.693	
1027	CGGAATGGTGGTACTACGGAT	3520	RNGGTTD	4763	103.669	
1028	GCTAATACGTATAATGTTTACG	3521	ANTYNVQ	4764	103.64	
1029	TCGGGTGTTTCATAGTGAGCGT	3522	SGVHSER	4765	103.636	
1030	AACACCGGCACCACGAGTGTC	3523	NTGTTSV	4766	103.635	
1031	AGTACGAGTAATAGTCATATG	3524	STNSNHM	4767	103.632	
1032	GGTGAACAACAACAACGCCCCC	3525	GEQHNAP	4768	103.629	
1033	GCTCATCATATGACGACGGAG	3526	AHHMTTE	4769	103.614	
1034	TTGATGACTGGTACTGCGTCG	3527	LMTGTAS	4770	103.575	
1035	GCTGCCGAGCCGACTCTCCA	3528	AAGADSP	4771	103.568	
1036	GTGTCTCTGAGTTCGCCTCCG	3529	VSLSSPP	4772	103.563	
1037	CGTGTGTAGCCGGTCCCAAC	3530	RVVAGPN	4773	103.534	
1038	GATAAGACTGAGATGCTGCAG	3531	DKTEMLQ	4774	103.525	
1039	GCACGAGACGACACGATACAA	3532	ARDDTIQ	4775	103.523	
1040	TTACACCTTGGGTTATCATCT	3533	LHLGLSS	4776	103.513	
1041	CTCGAAGGACAACGGGACGTC	3534	LEGQRDV	4777	103.505	
1042	GCGTCGTTGTGCGCTCCGGCG	3535	ASLSAPA	4778	103.5036	
1043	AGCAACCCCTGGGAACCACAAC	3536	SNPGNHN	4779	103.502	
1044	GGGCTGAATTCTAAGGGGACT	3537	GLNSKGT	4780	103.471	
1045	AAAAACCCCTCAGCTTCAGAA	3538	KTPSASE	4781	103.47	
1046	GTGCTGGCGTCGACTGAGAAG	3539	VLASTEK	4782	103.451	
1047	TCGGTATTGAACAAACCAACA	3540	SVLNKPT	4783	103.441	
1048	CCCGGTAACGGACAAAGTCCG	3541	PGNGQSP	4784	103.396	
1049	ATCTTGATGGGCGCTAGGACA	3542	ILMGART	4785	103.385	
1050	GCACTACCATCCCACTCCTCC	3543	ALPSHSS	4786	103.382	
1051	AGGGATCAGACTCATCCGAAT	3544	RDQTHPN	4787	103.378	
1052	TCTGGTCCGATTCTGCTGTT	3545	SGPIPAV	4788	103.376	
1053	TACGTGGACGACAACAGTCGC	3546	YVDDNSR	4789	103.35	
1054	TTGACTCGGGGGGTCGCCGCA	3547	LTRGVAA	4790	103.334	
1055	TCTGAGAAGGAGGCTCGGCTG	3548	SEKEARL	4791	103.326	
1056	TCCACAACGCCTCCCTTCAAA	3549	STTPPFK	4792	103.308	
1057	TACTCGACAACCATGCTTAAC	3550	YSTTMLN	4793	103.299	
1058	AAAAACGGTGTTATAAACGAC	3551	KNGVIND	4794	103.292	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1059	TTCGGTATAGGGCACGGAACA	3552	FGIGHGT	4795	103.278	
1060	CCTCTTCATGTTGCTTCTCCT	3553	PLHVASP	4796	103.245	
1061	TTGGGTAATGGTAGTTCTTTG	3554	LGNGSSL	4797	103.239	
1062	AGTGGCAACGCGAACATAGTA	3555	SGNANIV	4798	103.225	
1063	GGGATTAATCGTACTAGTGAG	3556	GINRTSE	4799	103.19	
1064	TCGGATAATAGGAATACTGCG	3557	SDNRNTA	4800	103.19	
1065	CGATTAGGAACCGTCACCAAC	3558	RLGTVTN	4801	103.189	
1066	GTGGAGCATGTTGCTCATCAG	3559	VEHVAHQ	4802	103.185	
1067	TATACTAAGCATCCTGTTGAG	3560	YTKHPVE	4803	103.172	
1068	TCCCGAATCACGGTGAACGCA	3561	SRITVNA	4804	103.154	
1069	ACAGTATCGTCATACGTACAA	3562	TVSSYVQ	4805	103.134	
1070	CGCGCCGAAGGGAGCTCTGGC	3563	RAEGSSG	4806	103.127	
1071	GCTGTGGGGCGGTGCGATGAT	3564	AVGRSDD	4807	103.119	
1072	CGCATAGGCGTTGGAGCACCA	3565	RIGVGAP	4808	103.113	
1073	TACTCAAACCTCGTACTTTCC	3566	YSNLVLS	4809	103.095	
1074	TCGACGAATTCTGAGGCGGTT	3567	STNSEAV	4810	103.068	
1075	GCAATGTCAACCCACATGATA	3568	AMSTHMI	4811	103.067	
1076	AGGGTTGATATTTTCGATTTT	3569	RVDISHF	4812	103.049	
1077	ATTCTTACGCCITTGGATAAG	3570	ILTPLDK	4813	103.039	
1078	GTTGCGAGTACGACGAGACT	3571	VASTTQT	4814	103.033	
1079	GACCGTAGCTCCGCGACGCTC	3572	DRSSATL	4815	103.014	
1080	GATCATAGTGAGCAGAATTCG	3573	DHSEQNS	4816	102.995	
1081	ATACGCAGCGAATTGGAAGTA	3574	IRSELEV	4817	102.969	
1082	GCGAATCTGGGTGATGTTGAG	3575	ANLGDVE	4818	102.969	
1083	GAGCTTAAGGAGAGTCAGAAG	3576	ELKESQK	4819	102.956	
1084	TCATACACAGCAGGAAGACCC	3577	SYTAGRP	4820	102.953	
1085	GGACCAGCCTACAACCAAAGC	3578	GPAYNQS	4821	102.924	
1086	CATGAGAGTCATTATGTTAGT	3579	HESHYVS	4822	102.921	
1087	AATGGTAAGCTGGGTACGACT	3580	NGKLGTT	4823	102.921	
1088	CTTCCGCTGCGTCGGCGGGT	3581	LPPASAG	4824	102.917	
1089	TTGTCGTATCAGACTGGTCAT	3582	LSYQTGH	4825	102.916	
1090	GACAGCCAAATCACAAGACTA	3583	DSQITRL	4826	102.909	
1091	AACGTATACGAAGGGCACCGC	3584	NVYEGHR	4827	102.909	
1092	TTGTTTACTGCTGGGAGTACT	3585	LFTAGST	4828	102.863	
1093	CTTGTGAATAATGATGGGACT	3586	LVNNDGT	4829	102.861	
1094	GCGATGAATGTGCGGAGTGAT	3587	AMNVRSD	4830	102.858	
1095	GCCAGCCTTGACCGCCTTCCA	3588	ASLDRLP	4831	102.857	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1096	GGCTCTCGGAACGGACCCACA	3589	GSRNGPT	4832	102.8532	
1097	ATGAGTGATGGGCATTCTGAAG	3590	MSDGHSK	4833	102.833	
1098	TCTAACCGTACGGAAATGCCA	3591	SNRTEMF	4834	102.815	
1099	AACGTGGTGAAAAACAACACA	3592	NVVKNNNT	4835	102.801	
1100	GTGGTCGACTCAACATACCCG	3593	VVDSTYP	4836	102.793	
1101	GTGGCTGGGGGACTTCGGAG	3594	VAGGTSE	4837	102.789	
1102	CGGGCAGACATGACTCCCTTA	3595	RADMTPL	4838	102.77	
1103	GGACACGAACAACTGACGCA	3596	GHEQTDA	4839	102.764	
1104	AGTGCTTTGATTAGTGTGGTT	3597	SALISVV	4840	102.756	
1105	AACTCGACAACGGCACAATCA	3598	NSTTAQS	4841	102.75	
1106	TACGGCGACCTAATACAGTC	3599	YGDLTTV	4842	102.737	
1107	GCACGCAACGACGGACAAGGA	3600	ARNDGQG	4843	102.734	
1108	CTGAACGTTAGTTCATCCAAA	3601	LNVSSEK	4844	102.693	
1109	TCTGGCGTCTCGAAAAGACGG	3602	SGVSKER	4845	102.692	
1110	AACATGGAACACACCATGGCG	3603	NMEHTMA	4846	102.687	
1111	GCTCGTCCGGCTTCGTCTGAT	3604	ARPASSD	4847	102.6705	
1112	CTTAGGGAAGAATCTGCACGT	3605	LREESAR	4848	102.639	
1113	TTGGCCAACATGTCCGCACCA	3606	LANMSAP	4849	102.61	
1114	AACCACACGGTAGAAGGACGC	3607	NHTVEGR	4850	102.598	
1115	CCTCAGCATCAGCATGAGCAT	3608	PQHQHEH	4851	102.582	
1116	AATTCTTCGGAGCTGAAGACG	3609	NSSELKT	4852	102.564	
1117	CTTGTGTCTGAGCGTTTGCCG	3610	LVAERLP	4853	102.552	
1118	AACGTTATGCACTCTTCTCTCC	3611	NVMHSSS	4854	102.525	
1119	GCGAGTGATAAGGGGGCGAAT	3612	ASDKGAN	4855	102.509	
1120	AGTCTGGATCGGAAGCCTCCG	3613	SLDRKPP	4856	102.5032	
1121	ACAGAACACGAAAAATCCACT	3614	TEHEKST	4857	102.459	
1122	CCTCATAATCAGGAGATGGGT	3615	PHNQEMG	4858	102.449	
1123	GAGTCTAAGACTGTGGTTATT	3616	ESKTVVI	4859	102.442	
1124	TCGACGGGCCAAAACCTAAAA	3617	STGQNLK	4860	102.442	
1125	GTTCTTCATGTTTCTGATGTT	3618	VLHVSDV	4861	102.441	
1126	CCTGACGACGCGTAGCCCG	3619	PDAARSP	4862	102.421	
1127	GCTCCTCGGCATGCTCATCCT	3620	APRHAHP	4863	102.414	
1128	CATGTGAATCTACGCCGGCG	3621	HVNPTPA	4864	102.401	
1129	TTGCCTAATGAGCGTCCGGGT	3622	LPNERPG	4865	102.397	
1130	GAGGCTAAGGGTTTGGTCAT	3623	EAKGFGH	4866	102.395	
1131	TCAGAAAACACCTCTGTACCC	3624	SENTSVP	4867	102.388	
1132	GGTCCCGAGAAAACCTACCGA	3625	GPGENYR	4868	102.375	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100		
1133	TTCATGAGATGAATAATGGT	3626 SHEMNNG	4869	102.366		
1134	GTAGACACCTACAGCGGTCTG	3627 VDTYSGL	4870	102.35		
1135	GGAGTCCTAGGAAACATGGTA	3628 GVLGNMV	4871	102.325		
1136	GCGCTGGATAATAGTAGTCGG	3629 ALDNSSR	4872	102.322		
1137	TTTCTGGGTTCTAGTAATCAT	3630 FLGSSNH	4873	102.321		
1138	CCTGTGGTTCATGGTGAGCCT	3631 PVVHGEP	4874	102.3142		
1139	CGCAGGGAAGGTATCCTAATG	3632 RREGILM	4875	102.305		
1140	CAGCAGGGGGCGCCTACTTCT	3633 QQGAPTS	4876	102.303		
1141	AAGGTTAGTGGTGGGAGACG	3634 KVSGET	4877	102.275		
1142	GCGAAACACGAAAGCTCGTCT	3635 AKHESSS	4878	102.272		
1143	ATTCTTATGGGTGCGCTACT	3636 ILMGART	4879	102.235		
1144	ACGCTAGGCAGCAGCAGCACC	3637 TLGSSST	4880	102.222		
1145	CTAAGATCTGAACCGACACAA	3638 LRSEPTQ	4881	102.218		
1146	CGCTCGGAACAAAAAECTCCG	3639 RSEQKTP	4882	102.207		
1147	CACGCTCCAAGCGCGCCATA	3640 HAPSGAI	4883	102.2		
1148	AGTAGTGTTACTTCGAGGGAG	3641 SSVTSRE	4884	102.197		
1149	GTGAATCCGCATCCTGCGCAG	3642 VNPHPAQ	4885	102.185		
1150	CAATACTCGATGGACACGCGC	3643 QYSMDTR	4886	102.173		
1151	ACTCTGGTGTACTAGGACG	3644 TPGVTRT	4887	102.172		
1152	CTTTATGAGGTTGGTACTCCT	3645 LYEVGTP	4888	102.165		
1153	ACGATGACGAGTGAGCTTTTCG	3646 TMTSELS	4889	102.16		
1154	TCAGGTTTCGGAATACCGTACC	3647 SGSEYRT	4890	102.153		
1155	GAAATGCAAAACAAAAACGCC	3648 EMQTKNA	4891	102.144		
1156	GGCCACGAAAACATGGGCGTG	3649 GHENMGV	4892	102.135		
1157	GGGGCGCATACGTCGGCTTCG	3650 GAHTSAS	4893	102.116		
1158	GCTGATACGCTGCTGCGTAGG	3651 ADTLLRR	4894	102.095		
1159	GACAACAGCAACAACGTCCCA	3652 DNSNNVP	4895	102.092		
1160	ATGACTGCTAAGTGGTGAA	3653 MTANLVE	4896	102.076		
1161	GAAGCGGACGACGCTTCAA	3654 EAGRTLQ	4897	102.07		
1162	AGACACGTCGTCCCCGACTCC	3655 RHVVPDS	4898	102.039		
1163	GTGAGTTCGAGCAGTATAGG	3656 VSSEQYR	4899	102.03		
1164	GGTATCGAAGCAAGTCGCGGA	3657 GIEASRG	4900	102.008		
1165	AGACAAGGCGTGAACGGAGTA	3658 RQGVNGV	4901	101.991		
1166	ACTGTGATGATGAGTACGAGG	3659 TVMMSTR	4902	101.976		
1167	TGGCAAGACCACAACAAAGTC	3660 WQDHNV	4903	101.948		
1168	GGAATCACAGGATCAACAGGA	3661 GITGSTG	4904	101.943		
1169	AATTATGCTCAGAGGGATGGT	3662 NYAQRDG	4905	101.936		

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1170	AAACAAGAAGCTCTGTCCTCA	3663 KQEALSS	4906	101.872	
1171	TCAACTTTAGACCGAAGCGAA	3664 STLDLSE	4907	101.8665	
1172	GCGATTACGAATACGCAGCAG	3665 AITNTQQ	4908	101.8615	
1173	AGGCTGGCGACTCAGAGTGCT	3666 RLATQSA	4909	101.847	
1174	TGGCAGCTTACGACGAGTCAT	3667 WQLTTS	4910	101.775	
1175	GGTGGTAGTGGTTCTAATACT	3668 GSGSNT	4911	101.759	
1176	AACCTAGTAGCGTACACGAAA	3669 NLVAYTK	4912	101.732	
1177	AAGGCTTCGCATGATACTAGT	3670 KASHDTS	4913	101.721	
1178	GCCATAACGATAATAGGCACT	3671 AITIIGT	4914	101.711	
1179	AACGCATCGTCGGACCGCTTC	3672 NASSDRF	4915	101.686	
1180	GAAACGCAACGTATCGAACTG	3673 ETQRIEL	4916	101.636	
1181	GTGATTGAGGTTAATTCGCGT	3674 VIEVNSR	4917	101.614	
1182	GATAGGGATATGGAGGGTGTT	3675 DRDMEGV	4918	101.609	
1183	ATTTTCGGAGATGACGCGGTAT	3676 ISEMTRY	4919	101.59	
1184	GAGCATGATGTGAGTACGCGT	3677 EHDVSTR	4920	101.539	
1185	CGTATGGAGGAGACTGCTTAT	3678 RMEETAY	4921	101.533	
1186	TATAGTACTGATCTTAGGATG	3679 YSTDLRM	4922	101.52	
1187	GTGCCTGAGCCTAAGAAGGCG	3680 VPEPKKA	4923	101.495	
1188	ACTTATGCGCCTAGGTCGCCT	3681 TYAPRSP	4924	101.484	
1189	GCTGCGGCTTCGCCTTTGGCT	3682 AAASPLA	4925	101.484	
1190	AGTGGGACGTATGCTAGTCGT	3683 SGTYASR	4926	101.456	
1191	ACTGAAGCATCAATCGCGCG	3684 TEASIAA	4927	101.456	
1192	CGCATCGTAGACAGTTGGGA	3685 RIVDTLG	4928	101.447	
1193	TATCTGCAGGAGAAGTTTCCT	3686 YLQEKFP	4929	101.437	
1194	GTTTCATGATCAGGGGCTGGG	3687 VHDQGAG	4930	101.436	
1195	CCCCAAGCCACTCTCAACAAC	3688 PQATLNN	4931	101.432	
1196	TGCGGAATGTCCGAATGCTCG	3689 CGMSECS	4932	101.429	
1197	GGTTCGCACAACGGCCGACA	3690 GSHNGPT	4933	101.429	
1198	TTTGGGTCTGGCCGAATCTT	3691 FSGSPNL	4934	101.413	
1199	ATGGATACGAATACGCATCGT	3692 MDTNTHR	4935	101.411	
1200	AAGAATAATCCTGAGGATGGT	3693 KNNPEDG	4936	101.41	
1201	CTGCCTACGGCTACTGGTCAG	3694 LPTATGQ	4937	101.406	
1202	ACGGCTGAGCGTACTGAGTAT	3695 TAERTEY	4938	101.383	
1203	AACTACAGGGACATCACAATG	3696 NYRDITM	4939	101.375	
1204	CCCGCGAGAAGCGACGCCCTT	3697 PARSDAL	4940	101.359	
1205	TCCGTTGTAACCTTGGGGTG	3698 SVVTLGV	4941	101.324	
1206	GTTGTTAAGGAGATTAAGCTG	3699 VVKEIKL	4942	101.324	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO:	aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1207	GACCACTCGAAACAAACTCT	3700	DHSKQNS	4943	101.293	
1208	CAGTCTAATTTGGTTATTAAT	3701	QSNLVIN	4944	101.292	
1209	ATTCCGGTTGGGGCGATGGCT	3702	IPVGAMA	4945	101.286	
1210	ACGTCGGAGATGCGTACTGCT	3703	TSEMRTA	4946	101.255	
1211	GGTAGTCAGCGTGCTATGAAT	3704	GSQRAMN	4947	101.251	
1212	CACCTGTGACAAGCAAACCAC	3705	HLSQANH	4948	101.24	
1213	GGAGGGAACCTCCACGGGGTA	3706	GGNSHGV	4949	101.219	
1214	GTGACTCGTAGTACGAAGGAG	3707	VTRSTKE	4950	101.178	
1215	ATGCTCAGAGCAAGCACCGCC	3708	MLRASTA	4951	101.171	
1216	GGCAGGCAAATACCAGAACAA	3709	GRQIPEQ	4952	101.146	
1217	TGGAATCAGAATGTGTCTCAT	3710	WNQNVSH	4953	101.125	
1218	CAGCGGGGGGAGCTTCCTGCG	3711	QRGELPA	4954	101.114	
1219	GCGAATGATAGTTTTCGTTCT	3712	ANDSLRS	4955	101.079	
1220	AACATGCCACCGGAATCGCAC	3713	NMPPESH	4956	101.037	
1221	AATTTGAGTCTTCAGAGTCTG	3714	NLSLQSL	4957	101.03	
1222	ACATCAGACGGTCTACTAAGT	3715	TSDGLLS	4958	101.028	
1223	GCGGGCCAAGCGTACCAATCC	3716	AGQAYQS	4959	101.016	
1224	CTGAGTGTGAAGGAGGAGATT	3717	LSVKEEI	4960	101.007	
1225	GATAATAGTCCTGCTAATCAT	3718	DNSPANH	4961	100.9812	
1226	ATGCACAACCTACCCTCATAC	3719	MHNLPSY	4962	100.9629	
1227	TACCAAGCCTCAAACAACAGT	3720	YQASNNS	4963	100.9594	
1228	GCGCGGGCAGAAGGGGTCTTC	3721	ARAEGVF	4964	100.9325	
1229	GGCCGAGAAGGAAACCTACCA	3722	GREGNLP	4965	100.913	
1230	CAAGCTGCAGAAAGGGACAGA	3723	QAAERDR	4966	100.8877	
1231	GTTGAGAATAATCGTATGAGT	3724	VENNRMS	4967	100.8183	
1232	AATATGTCGCATAGTACTCTG	3725	NMSHSTL	4968	100.7704	
1233	TCTTCGTTGGGICTTGCTCCG	3726	SSLGLAP	4969	100.7249	
1234	AACGTCGCTCCCTACAGTAGC	3727	NVAPYSS	4970	100.7069	
1235	AGGCCTGCGCAGCTGCCTGAG	3728	RPAQLPE	4971	100.615	
1236	ATGTCGGGTTCTGGGAACGCA	3729	MSGSGNA	4972	100.597	
1237	CACGGGGGGAACACCGGAAC	3730	HGGEHRN	4973	100.5793	
1238	GCATCCGGCGCACGCTACGTC	3731	ASGARYV	4974	100.5302	
1239	CAAAACCACGCGTCTGGTGAA	3732	QNHASGE	4975	100.499	
1240	GCACACCAAAAAGACCTACGC	3733	AHQKDLR	4976	100.4529	
1241	TTTGGGAAGGTTGGTACTGCT	3734	FGKVGTA	4977	100.433	

TABLE 2-continued

MHCK7 Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID	Nucleotide Sequence	SEQ ID NO: aa	SEQ ID NO:	Sum of muscle mRNA score_capped at 100		
1242	CTGCAGAAGTCGACTCTGGCT	3735 LQKSTLA	4978	100.3439		
1243	ATTCATAATGAGTCTTATGGT	3736 IHNESYG	4979	100.15		

TABLE 3

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO: seq.	Amino Acid	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1	AGGGGTGATCTTTCTACGCCT	4980	RGDLSTP	6647	856.3525	
2	AGAGGCGACTTATCCACACCC	4981	RGDLSTP	6648	732.672	
3	AGAGGAGACTTGACAACCCCA	4982	RGDLTTP	6649	683.373	
4	AGGGGCGACCTGAACCAATAC	4983	RGDLNQY	6650	680.6265	
5	CGGGGTGATCAGCTTTATCAT	4984	RGDQLYH	6651	624.3915	
6	AGGGGGGATGCGACGGAGCTT	4985	RGDATEL	6652	620.5	
7	CGAGGAGACCCATGAGCAAA	4986	RGDTMSK	6653	599.497	
8	CGGGGTGATCTTAATCAGTAT	4987	RGDLNQY	6654	579.731	
9	CGGGGTGATCTTACTACGCCT	4988	RGDLTTP	6655	531.1525	
10	CGCGGCGACATGATAAACACC	4989	RGDMINT	6656	528.2405	
11	CGGGGGGATACTATGTCTAAG	4990	RGDTMSK	6657	469.5075	
12	CGAGGCGACACAATGAACTAC	4991	RGDTMNY	6658	412.3247	
13	CGGGGTGACGCAACAGAATTG	4992	RGDATEL	6659	408.0865	
14	CGTTTGGACCTGCAAGTCCAC	4993	RLDLQVH	6660	397.178	
15	CGTGGTGATGTGGCGGCTAAG	4994	RGDVAAK	6661	395.174	
16	AGGGGCGACCTCAACGACAGC	4995	RGDLNDS	6662	360.4535	
17	CGTGGGGATTGTAATGATTCT	4996	RGDLNDS	6663	349.6835	
18	TCTTATGGTAATACTCATGAT	4997	SYGNTHD	6664	326.826	
19	CGTTTGGACCTGCAAGTCAAC	4998	RLDLQVN	6665	317.78	
20	AAAGCGGGACAACACTAGTGGA	4999	KAGQLVE	6666	317.023	
21	GATCAGACGGCTAGTATTGTT	5000	DQTASIV	6667	313.224	
22	TATATTGCTGCGGGTGAGCAG	5001	YIAAGEQ	6668	308.738	
23	GCGGTTGTCTGAATAGTAAT	5002	AVVLNSN	6669	307.8445	
24	TCTAAAGGAAACGAACAAATG	5003	SKGNEQM	6670	305.016	
25	GCAAACCCCAACATACTAGAC	5004	ANPNILD	6671	302.02	
26	CACAACAAACCAACGGAGAC	5005	HNKPNGD	6672	297.851	
27	GATAAGACTGAGATGCTGCAG	5006	DKTEMLQ	6673	294.655	
28	ACAGAACAACTTACTCACGA	5007	TEQSYSR	6674	290.3555	
29	ACTGTGATGATGAGTACGAGG	5008	TVMMSTR	6675	289.3945	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
30	GTCTCTACATACCTCCTGGCA	5009	VSTYLLA	6676	286.859
31	CCTAATGTACGAGTCTTAT	5010	PNVTQSY	6677	285.178
32	ATGAGTAATTTGGGTATGAG	5011	MSNLGYE	6678	284
33	ACGATGGGTGCTAATGGTACT	5012	TMGANGT	6679	278.291
34	AATGTTAATGCGCAGAGTAGG	5013	NVNAQSR	6680	275.45
35	GACCAAACTTCGAACGTAGA	5014	DQNFERR	6681	274.6045
36	AACACGTACACACGGGAAAA	5015	NTYTPGK	6682	273.83545
37	CGTGGGGATATGATTAATACG	5016	RGDMINT	6683	270.333
38	GCACAATTCGAATCAGGCCGA	5017	AQFESGR	6684	267.7345
39	ACGGCGTATCAGGCTGGTCTG	5018	TAYQAGL	6685	267.054
40	AGTGTTAGTTCTGTGGTGTG	5019	SVSSVVL	6686	266.91
41	GGGCTTTCTAAGGCGTCTGAT	5020	GLSKASD	6687	266.825
42	TGGAACGGAAACGCCACACAA	5021	WNGNATQ	6688	265.11
43	ACAGCCGCGCGCAACGCGCC	5022	TAGGERA	6689	258.785
44	TACACCTCTCAAACAGCACT	5023	YTSQTST	6690	258.1818
45	GCGAACATAGAAAACACGTCA	5024	ANIENTS	6691	257.015
46	GAACCTCTCGGTTCCGAAACCA	5025	ELSVPKP	6692	255.133
47	GATCCTGGTTCGACGGGTACG	5026	DPGRGTG	6693	254.7
48	GATCGTCCGAATAATATGACG	5027	DRPNMT	6694	254.383
49	TATAGTACTGATCTTAGGATG	5028	YSTDLRM	6695	252.146
50	CAGTCGGTTAATAGTACGAGT	5029	QSVNSTS	6696	251.508
51	GCGGCACAACCTCGTCAGTCCA	5030	AAQLVSP	6697	250.413
52	CTCGGAGGAAACAGCAGGTTC	5031	LGNSRF	6698	247.9775
53	GCGACGCTGAATAATAGTTAT	5032	ATLNNSY	6699	247.2955
54	CGCTTGGACGTTGGAAGCCCG	5033	RLDVGSP	6700	245.839
55	TATCGGGGTAGGGAGGATTGG	5034	YRGREDW	6701	244.83
56	AGGGGAGATCTTTCTACGCCT	5035	RGDLSTP	6702	243.25
57	AGTGGTCTTTCGCATGGTCAG	5036	SGLSHGQ	6703	242.486
58	GAACACGCTACAGCAAAACAA	5037	EHATAKQ	6704	241.816
59	GGGGCGGAAGCGGGCCGCCAA	5038	GAEAGRQ	6705	241.46345
60	ATAAGCGGTTCCACTACACAC	5039	ISGSTTH	6706	240.8811
61	GGCACCCTCGTCCGGGCTCC	5040	GTVVPGS	6707	240.8455
62	CATAATAATAATATGCTGAAT	5041	HNNMMLN	6708	239.0755
63	CGTCTGACTGATACTATGCAT	5042	RLTDTMH	6709	238.939
64	AACACCTACCCCTTCAACGCC	5043	NTYPFNA	6710	235.89
65	TCAACCACTACTGGCCACATG	5044	STTTGHM	6711	231.581

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
66	GTGCATAATCCTACTACTACG	5045	VHNPTTT	6712	231.5537
67	AATCTGCAGGTGAATGCGAAT	5046	NLQVNAN	6713	231.172
68	AGATACGGAGAATCCATCGAA	5047	RYGESIE	6714	230.66
69	AATACTACTCCGCCTAATCAT	5048	NTTPPNH	6715	230.225
70	AATACTTTGCAGAATAGTCAT	5049	NTLQNSH	6716	229.0666
71	AGTCTGAACAACATGGGATCG	5050	SLNNMGS	6717	228.9154
72	AGAAACGAAAACGTAAACGCT	5051	RNENVNA	6718	228.828
73	GCTGTGCATGCGACTAGTAGT	5052	AVHATSS	6719	227.882
74	ACCCAACACCTACCATCCACA	5053	TQHLPST	6720	227.0845
75	AGTGTGTGTGTCTCAGGCTAAT	5054	SVLSQAN	6721	225.4035
76	AGTAGCTCAACTGAAGGGCAA	5055	SSSTEGQ	6722	224.971
77	GGTCGGACGGATACTCCTAAT	5056	GRDTPN	6723	224.945
78	GTTCAAACCCACATAGGAGTC	5057	VQTHIGV	6724	224.616
79	ACTTCTGCTAGTGAGAATTGG	5058	TSASENW	6725	224.608
80	GGAAAAGCCAACGACGGTTCT	5059	GKANDGS	6726	224.5935
81	GTGGAGCGGAATACTGATATG	5060	VERNTDM	6727	223.9975
82	CAAAACCCACGCTCTGGTGAA	5061	QNHASGE	6728	223.871
83	TATTATGAGAAGCTTAGTGCG	5062	YYEKLSA	6729	222.1725
84	TTCATCGCTAACACTAACCCA	5063	FIANTNP	6730	221.76
85	ACCTCCACGGCTTCAAAACAA	5064	TSTASKQ	6731	221.617
86	AATAATGATAATGGTTTTGT	5065	NNDNGFV	6732	220.61
87	GCTAATTCTATTGGGGGTCCG	5066	ANSIGGP	6733	220.304
88	ACTGGCCAATTAGTAGGAACC	5067	TGQLVGT	6734	220.262
89	TACAGTCAATCGCTGTCTGAA	5068	YSQSLSE	6735	220.02
90	GTCTACAACGGCAACGTAGTA	5069	VYNGNVV	6736	219.824
91	AACTCGGCTGAATCCTCGAGA	5070	NSAESSR	6737	219.5415
92	ACGCGTAATTTGTCTGAGAGT	5071	TRNLSES	6738	218.919
93	TCTATGTCTGATGGGCTTCGG	5072	SMSDGLR	6739	218.868
94	GTAGGCGACCAATCCGCCCG	5073	VGDQSRP	6740	218.8565
95	TTTACGGTGAATCAGGATCTT	5074	FTVNQDL	6741	218.069
96	TATCATAAGTATAGTACGGAT	5075	YHKYSTD	6742	217.64
97	TATGGTGTGCAGGCGAATAGT	5076	YGVQANS	6743	217.293
98	TTGCAGACGCCTGGGACGACG	5077	LQTPGTT	6744	217.179
99	TATCAGCAGACITCTAGTACG	5078	YQQTSSST	6745	216.8135
100	CAAACGAACACCAACGACAGA	5079	QTNTNDR	6746	216.664
101	ATGGATAAGTCTAATAATTCT	5080	MDKSNNNS	6747	216.638
102	CATCTTAGTCAGGCTAATCAT	5081	HLSQANH	6748	216.575

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
103	GTTGGTGCAGTACGGCTTCG	5082	VGASTAS	6749	215.9195
104	CACAACAACAACCTGCAAAAC	5083	HNNNLQN	6750	215.084
105	AGTACTTATGGGAATACTTAT	5084	STYGNTY	6751	214.971
106	CGGGCTGATGTTTCTTGGTCT	5085	RADVSW	6752	214.499
107	CGAGGAGACAACAGCACACCG	5086	RGDNSTP	6753	214.29
108	GGTCGGGATTATGCTATAGT	5087	GRDYAMS	6754	214.166
109	CCTAACACGAAAAAACCCG	5088	PNNEKNP	6755	214.048
110	GATAATGTGAATTCTCAGCCT	5089	DNVNSQP	6756	213.6615
111	ATGGGGACTGAGTATCGTATG	5090	MGTEYRM	6757	213.606
112	AATCAGAGTATTAATAATATT	5091	NQSINNI	6758	213.36
113	GCCATAGACTCTATCAAACAA	5092	AIDSIKQ	6759	213.304
114	GTTGAGTCTTCTATTCTCGG	5093	VESSYSR	6760	212.9405
115	GGTCAGTATAGTCAGACGCTT	5094	GQYSQTL	6761	212.242
116	ACCATCCAAGACCACATAAAA	5095	TIQDHIK	6762	212.116
117	AACAGTTCCCAATGGCCCAAC	5096	NSSQWPN	6763	211.938
118	ACGGATAATGGTCTTCTTG TG	5097	TDNGLLV	6764	211.787
119	GTAAGAGAAACACACACCTC	5098	VRETHL	6765	211.44
120	CGTGGTGATATGACTCGTGCG	5099	RGDMTRA	6766	211.181
121	ACTTATGGTATTACTCATGAT	5100	TYGITHD	6767	210.641
122	ACGGCGCTGAATACGTATCCT	5101	TALNTYP	6768	210.568
123	GGTGGCGAAAACAGAACCCCA	5102	GGENRTP	6769	210.4
124	TATCTGCAGGAGAAGTTTCCT	5103	YLQEKFP	6770	210.3715
125	CTTAATCTTACTAATCATAAT	5104	LNLTNHN	6771	209.727
126	GGATTAGCTAGTCTACACCTG	5105	GLASLHL	6772	209.3585
127	GTAGAACACGTAGCCACCAA	5106	VEHVAHQ	6773	209.322
128	AGCGAACACCACGCCGAATA	5107	SEHHAGI	6774	209.188
129	GAAGCGTCCAACACGAACGA	5108	EASNYER	6775	208.926
130	CCCTCCAACAGTGAAAGATTC	5109	PSNSERF	6776	208.6635
131	TCCCCCGCAACGGGTTGCTA	5110	SPGNGLL	6777	208.4985
132	ATACTGAAATCCGACGCACCA	5111	ILKSDAP	6778	208.297
133	TTTGATAGTGCGAATGGTCGG	5112	FDSANGR	6779	208.26
134	GATGGTAAGACTACGTCTAAT	5113	DGKTTSN	6780	207.768
135	ACTAATTATCTGAGGCGAAT	5114	TNYPEAN	6781	207.706
136	CGAGGAGACCACAGCACACCG	5115	RGDHSTP	6782	207.4315
137	CAGACGACTATCTGGCTGCT	5116	QTTILAA	6783	207.223
138	GCTACTGCGCATCAGGATGGT	5117	ATAHQDG	6784	207.212

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
139	CAAGCCCTGGCCACCACAAAC	5118	QALATTN	6785	207.096	
140	TATAATGTACTCCTTCGCAG	5119	YNATPSQ	6786	206.964	
141	GAGCTGTCTACTCCTATGGTT	5120	ELSTPMV	6787	206.8655	
142	ATTAATATTAGTAGTGATTTT	5121	INISSDF	6788	206.753	
143	GTAACGGCACACCAATTATCC	5122	VTAHQLS	6789	206.7385	
144	GGAGAAAGCTCCTCAATAAGC	5123	GESSSIS	6790	206.656	
145	GAATCCCTCCCAATCTCTAAA	5124	ESLPISK	6791	206.576	
146	ACGAATGTTAGTACGCTTTTG	5125	TNVSTLL	6792	206.455	
147	TGGCAGACGAATGGTATGCAG	5126	WQTNGMQ	6793	206.4378	
148	TACAGGATGGAACGAACCCA	5127	YRMETNP	6794	206.121	
149	ATAACCGGCAACACCGTCGGA	5128	ITGNTVG	6795	205.9135	
150	CTGAACACTCTAATCCACAAA	5129	LNTLIHK	6796	205.873	
151	GGGACTTCTCTGGAAAACCGA	5130	GTSLENR	6797	205.8535	
152	TACCAACACAACCAAGCCAC	5131	YQHNQAH	6798	205.473	
153	ATTGAGAGTAAGACTGTGCAG	5132	IESKTVQ	6799	205.0365	
154	TATACGCAGGGTATTATGAAT	5133	YTQGINN	6800	204.5275	
155	AGTACGAATGAGGCTCCTAAG	5134	STNEAPK	6801	204.522	
156	TTGTCTCAGAATTTTAATCCT	5135	LSQNFNP	6802	204.3926	
157	TACTCTTCTGAAATGAGCGAA	5136	YSSEMSE	6803	204.31	
158	TCATACGGAGGATCTGGCCCC	5137	SYGSGSP	6804	204.28	
159	ATGGACGCTGCGTACGGTAGT	5138	MDAAYGS	6805	203.959	
160	CCTTTTAATCCTGGGAATGTG	5139	PFNPGNV	6806	203.2041	
161	CAAAAATCGGAAACCTACACT	5140	QKSETYT	6807	203.1248	
162	AACAAAGACCACAACCACCTG	5141	NKDHNL	6808	202.8605	
163	CTAACCGGCTCTGACATGAAA	5142	LTGSDMK	6809	202.379	
164	TCTAAGGATAGTACTATGTAT	5143	SKDSTMY	6810	202.335	
165	GAAGCATTCGCCGAGCGGGC	5144	EAFPRAG	6811	202.275	
166	GAACACACTCACTTAAACCCG	5145	EHTLNP	6812	201.959	
167	AGTTCGGACCCAAAAGGTCAA	5146	SSDPKGQ	6813	201.825	
168	AAAACCATCGACATAGCACAA	5147	KTIDIAQ	6814	201.699	
169	ACCGGTAGCTTGAATCTATG	5148	TGSLNSM	6815	201.671	
170	ATGCAACGCGAAGACGCGAAC	5149	MQREDAN	6816	201.523	
171	GCCTCTACAGTCTCACTCTAC	5150	ASTVSLY	6817	201.407	
172	GGCCGTGACGACCTCACAAAC	5151	GRDDLTN	6818	200.911	
173	TCTAATCCGGGTAATCATAAT	5152	SNPGNHN	6819	200.872	
174	GATACTTATAAGGGTAAGTGG	5153	DTYKGKW	6820	200.7787	
175	CCACCCAACGGCAGCAGTAGA	5154	PPNGSSR	6821	200.32615	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
176	GCTTCTTATAGTATTCTGAT	5155	ASYSISD	6822	200.269
177	GTGACTGTAGTCTGGATGGG	5156	VTVSLDG	6823	200.021
178	ATGGCCATAGGCCACTCCCCA	5157	MAIGHSP	6824	200
179	TTTCGGACGGTGTATACTGGT	5158	FRTVYTG	6825	200
180	AAAAAACGGCAGCCCATCGCC	5159	KKRQPIA	6826	200
181	AAAAATAAGCTCTACTATGGC	5160	KNKLYYG	6827	200
182	TCTACATCTCCGGTTAACAGC	5161	STSPVNS	6828	200
183	GGGTCTGGGATTGCGGGGACT	5162	GSGIAGT	6829	200
184	ATCGACGTACTGAACGGAAGT	5163	IDVLNGS	6830	200
185	GGTCATAATATGGCACAGGCG	5164	GHNMAQA	6831	200
186	ACGAGGAGCAACTCCGACGAA	5165	TRSNSDE	6832	200
187	GGAGCAAAAGGAACCATGGGC	5166	GAKGTMG	6833	200
188	GCTACTACTCTTACTGGTGAT	5167	ATTLTGD	6834	200
189	TTCAACACATCGTCGGAATTC	5168	FNTSSEF	6835	200
190	TATACGGCGCAGACCGGTGG	5169	YTAQTGW	6836	200
191	CGAGTAAACAACGACGCAATA	5170	RVNNDAI	6837	200
192	ACTATTACAGCTTACTGATACT	5171	TIQLTDT	6838	200
193	GCCAGCATGCCCTCTGTAGAC	5172	ASMPDVD	6839	200
194	AATCAGGTGGGTGCGTCTGCG	5173	NQVGASA	6840	200
195	GGAAACATGGTGACTCCAAAC	5174	GNMVTPN	6841	200
196	CGTGGTGACCAAGGCACACAC	5175	RGDQGTH	6842	200
197	TCGAGTGATTCTCGTATTCCG	5176	SSDSRIP	6843	200
198	GGACTGCACGGCACCAACGCA	5177	GLHGTNA	6844	200
199	TCTAGTTATCAGTCTGGGCTG	5178	SSYQSGI	6845	199.609
200	ACAGCCTACTCGCCACAGTC	5179	TAYSPTV	6846	199.236
201	CGCAGTGACACCACTAACGCC	5180	RSDTTNA	6847	198.59
202	CGTATTGTGGCTAATGAGCAG	5181	RIVANEQ	6848	197.795
203	ATCCACAACGAATCATACGTC	5182	IHNESYV	6849	197.72
204	CAGCAGAATACGCGTTTGCCG	5183	QQNTRL	6850	197.4665
205	GGTATCAACTCTCACACTTC	5184	GINSSH	6851	197.224
206	GGTATGACTTCTAATCAGGTT	5185	GMTSNQV	6852	196.916
207	AGGGAGATTGTTCATAGTAAT	5186	REIVHSN	6853	196.5775
208	GCAGAACACACGTACACGGTC	5187	AEHTYTV	6854	196.501
209	CCTGCTACGCTACACCTGACA	5188	PATLHLT	6855	196.1975
210	AAGCAGACTGATAGTAGGGGT	5189	KQTDSP	6856	196.15
211	ACTATGGTAGAAGTACTGCCA	5190	TMVEVLP	6857	195.586

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
212	ATCCCAACCGCCAACTAGC	5191	IP TGQTS	6858	195.499	
213	ATGATAAAAACCAACATGTTG	5192	MIKTNML	6859	195.198	
214	GCGGAACGACCCACTAGAGAC	5193	AERPTRD	6860	194.842	
215	CGGGATCTGGGGCAGACCGGC	5194	RDLGQTG	6861	194.34	
216	AATGAGGGGCGTGTGCAGACT	5195	NEGRVQT	6862	194.00545	
217	ACTGCGGCTAGTACTGCGAGG	5196	TAASTAR	6863	193.5855	
218	ACCCAAGGGAACAACATGGTA	5197	TQGNMNV	6864	193.362	
219	CATAGTACTTTTCCTACGACT	5198	HSTFPTT	6865	193.274	
220	CAATCTATCGGCCACCCCGTT	5199	QSIGHPV	6866	191.64595	
221	TCGGGTGTTAATAGTGAGCGT	5200	SGVNSER	6867	191.3763	
222	CCTCACGCCAACGGAGTGACA	5201	PHANGVT	6868	191.349	
223	GACCACCAACAAGCCCTAGCT	5202	DHQQALA	6869	191.305	
224	AGTCAGCAGGGTTTTACTCTG	5203	SQQGFTL	6870	191.2955	
225	ACAAACGCTGCTCTAGTACCA	5204	TNAALVP	6871	191.1973	
226	GGTGTTAGTAGTAATTCTGCG	5205	GVSSNSA	6872	190.1595	
227	CATGATACGGTTGGGAGAGG	5206	HDTVGER	6873	189.859	
228	GCGTTAAACGCCCAAGGGATC	5207	ALNAQGI	6874	189.3825	
229	CATGATAGTATGTGTTGTGCG	5208	HDSMCCA	6875	189.35	
230	TACATCGCGGCAGGGGAACAA	5209	YIAAGEQ	6876	189.046	
231	GAGAATGCTCGTGAGGGTGTG	5210	ENAREGV	6877	188.331	
232	GCTACGGTTTATAATGAGTTG	5211	ATVYNEL	6878	188.18	
233	GACACTAACGGAATAAAATCA	5212	DTNGIKS	6879	187.628	
234	AAGCCGACTGCGAATGATTGG	5213	KPTANDW	6880	187.4884	
235	TATGAGAGTACTCATGTTAAT	5214	YESTHVN	6881	187.1195	
236	TACACCAACGGGGGCCACCTA	5215	YTNGGHL	6882	187.0304	
237	GTAGACAAATCTAGCCCAGTG	5216	VDKSSPV	6883	186.9365	
238	CCAATCCAAAACGAATCGTCC	5217	PIQNESS	6884	186.748	
239	ATACACAAATCTAGCGTCGAA	5218	IHKSSVE	6885	186.654	
240	CATGATATTAGTCTGGATCGT	5219	HDISLDR	6886	186.65	
241	TGGTGAGGGGCTGAGTTTGCC	5220	W*GAEFA	6887	186.1	
242	TACTCTCAATCCATAAAAAAC	5221	YSQSIKN	6888	186.0095	
243	GCCCCAAGACAACAACCACGAC	5222	AQDNNHD	6889	185.6231	
244	GGGCAGAAGGAGACTACTGCG	5223	GQKETTA	6890	184.948	
245	AAAAGCGAAGTACCCGCCCGA	5224	KSEVPAR	6891	184.116	
246	GAACCTTAACACCGCACACGCA	5225	ELNTAHA	6892	184.059	
247	AGCACAAACGCGGGACAAAGG	5226	STNAGQR	6893	183.7145	
248	AAGGCGGTTTCGGAGATTATT	5227	KAVSEII	6894	183.539	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
249	ACCTTCACGGTCGACGGTAGA	5228	TFTVDGR	6895	183.2535	
250	AGTACGAGTGTTATAATACT	5229	STSGYNT	6896	182.703	
251	AATCATAGTCTGTCGGAGCAT	5230	NHSLSEH	6897	182.427	
252	TCTATGCAGGATCCTTCTTTG	5231	SMQDPSL	6898	182.375	
253	GAACAACAAAAACAGACAAC	5232	EQQKTDN	6899	182.331	
254	GCTGTTGTGAATGAGAATATG	5233	AVVNENM	6900	182.3	
255	GGTCCCGGAGAAAACACCGA	5234	GPGENYR	6901	182.165	
256	TACAACGCAGGCGGAGAACAA	5235	YNAGGEQ	6902	182.14	
257	GTCCTCTCCTCCAACCTGTAC	5236	VLSSNLY	6903	181.3605	
258	GGTCTTTATCAGAATCCTACG	5237	GLYQNPT	6904	181.2475	
259	AGTTCGGGGAGTTTGATTACT	5238	SSGSLIT	6905	180.8125	
260	TATAATACGGATCGGACTAAT	5239	YNTDRTN	6906	180.0485	
261	GAGAAGCCTCAGCATAATAGT	5240	EKPQHNS	6907	179.9715	
262	GCGGCTTATGAGCATGCGCCT	5241	AAEHAP	6908	178.7065	
263	GGCGGCAACTACAACAACT	5242	GGNYNTT	6909	178.62	
264	TATCTGAATAGTACGCAGATT	5243	YLNSTQI	6910	178.4905	
265	TCTAATTCTAATACTGCTGCT	5244	SNSNTAA	6911	178.119	
266	TCGGATAATAGGAATACTGCG	5245	SDNRNTA	6912	178.09355	
267	CGCTCGTTGGACAGCGGGATG	5246	RSLDSGM	6913	177.6395	
268	GTTATGGATACGCATGGGATG	5247	VMDTHGM	6914	177.54	
269	CATGTTACGGCGGTGGTTGAT	5248	HVTAVVD	6915	177.447	
270	AGTATCACCCACAGCAACACC	5249	SITHSNT	6916	177.4093	
271	GGATACGGCAGTTACAGAAC	5250	GYGSYSN	6917	177.0995	
272	CGTTGGTCTGAAAACAACTCC	5251	RWSENNS	6918	176.788	
273	ATGTCTAGCCACACCGTCCAA	5252	MSSHTVQ	6919	176.741	
274	TATGTTAGGGCGCAGGATCAG	5253	YVRAQDQ	6920	176.713	
275	TTTGAGGGTGATAAGACTTAT	5254	FEQDKTY	6921	176.655	
276	GTTAGCTCCGGCCACACGAAA	5255	VSSGHTK	6922	176.4715	
277	TCGATGAACCTGCCAACTTCA	5256	SMNLPTS	6923	176.425	
278	CTGAATCCTCAGCATGAGTTG	5257	LNPQHEL	6924	176.19	
279	CTTCCGCCTGCGTCGGCGGGT	5258	LPPASAG	6925	176.057	
280	GGAGGGAACCTCCACGGGGTA	5259	GGNSHGV	6926	175.7625	
281	GGGGGTACGGGGTTGTCGAAG	5260	GGTGLSK	6927	175.714	
282	AGTTTGAATTCTTCGAGTACT	5261	SLNSSST	6928	175.4585	
283	ATGCCTAGTGAACCAACAGGG	5262	MPSEPPG	6929	175.45	
284	GTTGTGCATTCGAGTATTACT	5263	VVHSSIT	6930	175.18685	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
285	TTGAGTCTGGCTGGGAATAGG	5264	LSLAGNR	6931	175.0985	
286	GCGGACATGCAACACACCGTA	5265	ADMQHTV	6932	175.003	
287	TTTCGTGATGGTCAGGGTATG	5266	FRDQGM	6933	174.983	
288	ACCGGAACAGCGATCTCCCGA	5267	TGTAISR	6934	174.5465	
289	ATGGGGAAGCATGAGGGTCTT	5268	MGKHEGL	6935	174.3418	
290	CCGGAATCCGCCGCCAAAAGC	5269	PESAASKS	6936	174.268	
291	ACCCAAGCCTTCTCCCTAGGC	5270	TQAFSLG	6937	174.2365	
292	ACTGATGGTATTTTTCAGCCT	5271	TDGIFQP	6938	174.014	
293	GGGAGCCCAGTGATAGTAAAC	5272	GSPVIVN	6939	173.652	
294	GGGCGTGATAATCATCATGCG	5273	GRDNHHA	6940	173.4132	
295	CCGCGTTCTATTACGGAGTTG	5274	PRSITEL	6941	173.403	
296	TGGGTAAACAGTGTGGGCAAC	5275	WVNSVGN	6942	173.244	
297	GTTTCATGGGACGTTGACTTAT	5276	VHGTLY	6943	173.1685	
298	GGTGTGTATATTGATGGTCGG	5277	GVYIDGR	6944	173.081	
299	ATGAGTAATGATTTGCCTGGG	5278	MSNDLPG	6945	172.671	
300	AATCGGTCGGATAGTTTTCGG	5279	NRSDSFA	6946	172.6595	
301	GGGCAAACAAACGCAGTACAC	5280	GQTNVAVH	6947	172.4582	
302	TACGTCGACAAATCAATGACA	5281	YVDKSMY	6948	172.1735	
303	AGTGTGATGGTGGGTACGAAT	5282	SVMVGTN	6949	171.86	
304	ATTGGTCTGCAGAATTCTACT	5283	IGLQNST	6950	171.84715	
305	AACGACCGACCGCTTGCCAGC	5284	NDRPLAS	6951	171.464	
306	CTCATGGGCAGTCCAGGCGCG	5285	LMGSPGA	6952	171.27	
307	ATTGATCGTAGTGCTAGTTTG	5286	IDRSASL	6953	171.009	
308	ATTCAGGCGAAGAATTCTGAG	5287	IQAKNSE	6954	170.983	
309	CATCAGTCTTTTGATGCTGGT	5288	HQSF DAG	6955	170.699	
310	GCGGTAAATGAGACTAGGCTT	5289	AVNETRL	6956	170.564	
311	ATCGCGTCAACGTGGAACATG	5290	IASTWNM	6957	170.52	
312	AAAGTGGACATGACCTCCAAA	5291	KVDMTSK	6958	170.4035	
313	TCTCATAGTATTACGGGTCTT	5292	SHSITGL	6959	170.333	
314	ACTATTACTAGTCCGTCGGTG	5293	TIITSPSV	6960	170.18	
315	GAACACATCTCTAGCTACGGA	5294	EHISSYG	6961	169.832	
316	TTCTCAACAACTCTGTAAATC	5295	FSTNSVI	6962	169.7245	
317	TCGATGGAGGGTCAGCAGCAT	5296	SMEGQQH	6963	169.71	
318	GTCGACAAAGCGAAGCCGTC	5297	VDKSEAV	6964	169.6265	
319	CAAGCTAACTTATCAATAATC	5298	QANLSII	6965	169.3842	
320	GTTAAGGCGAGTGCTGGGGTT	5299	VKASAGV	6966	169.1112	
321	TTTGGTACTTCTTATACGACT	5300	FGTSYTT	6967	168.915	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
322	GGGCTCACAGGATACCCAATG	5301	GLTGYPM	6968	168.8625	
323	GCTATGGGAGCACTCGTGAC	5302	AMGALVH	6969	168.807	
324	GTATACGCCACCGCACTCGCA	5303	VYATALA	6970	168.7005	
325	ACATTAACAGACGTTACCCGA	5304	TLTDVHR	6971	168.7	
326	CCATCCTCAGCGGGTAGCACA	5305	PSSAGST	6972	168.601	
327	AAAAAACGAAACACTAATA	5306	KKRKH*L	6973	168.58	
328	GCTTATCAGCTGACTCCGGCT	5307	AYQLTPA	6974	168.579	
329	CTTGCGCTGATAATATTGGG	5308	LAPDNIG	6975	168.515	
330	ACAATCGTTTCCGTTACGCC	5309	TIVSAYA	6976	168.3875	
331	GGTAATAATTTGAGTTTGTCT	5310	GNNLSLS	6977	168.1503	
332	AGCACAAACACCGAACCTAGG	5311	STNTEPR	6978	168.122	
333	TCTTTTCAGACGGATCGTGCG	5312	SFQTDRA	6979	167.793	
334	TTCTTAGAAGGAGTCGCTCAA	5313	FLEGVAQ	6980	167.647	
335	CAAGACGTAGGACGCACGAAC	5314	QDVGRTN	6981	167.4595	
336	ACGCATGGTGATCATATTGAG	5315	THGDHIQ	6982	167.197	
337	GTATCAGAAGGACAACGAATC	5316	VSEGQRI	6983	167.049	
338	AACATGGGTCCAATGGGCCGG	5317	NMGPMGR	6984	166.961	
339	CTACCCTCAACAGAAACTTTG	5318	LPSTETL	6985	166.942	
340	GGTGGTATGTCGGCGCATTCG	5319	GGMSAHS	6986	166.775	
341	GGGATGATCGGGCACAACGCA	5320	GMIGHNA	6987	166.716	
342	ATAGACGAACGTTCTCTGATA	5321	IDERSSI	6988	166.601	
343	CATGTGAATCTACGCCGGCG	5322	HVNPTPA	6989	166.586	
344	TGGTCGAGAACTGGAACACC	5323	WSRTGNT	6990	166.483	
345	ATCAAAGACTCGTACCTTACT	5324	IKDSYLT	6991	166.205	
346	TTGAACCAAAACAGTGTCTCC	5325	LNQNSVS	6992	166.174	
347	TCTGGTCCGATTCTGCTGTT	5326	SGPIPAV	6993	166.146	
348	ATGCAAGGGCTTAACAACATG	5327	MQGLNNM	6994	165.268	
349	TCAAACAGCGGAGGCAACCAC	5328	SNSGGNH	6995	165.1895	
350	ACGAGTACGATGACTGCGCGT	5329	TSTMTAR	6996	165.115	
351	GAGAATAGTGATTTGTCTTAT	5330	ENSLSY	6997	165.08	
352	CATCCTGGGAATAGTTCTGTG	5331	HPGNSSV	6998	165.062	
353	TTAACACCCCAAGGACTAGT	5332	LTPQGTS	6999	165.0315	
354	ACCGACACCCGAAAAACGAC	5333	TDTRKND	7000	164.843	
355	GGGGAGACGCTGAGGTCTCAG	5334	GETLRSQ	7001	164.72165	
356	AGCGGTGTATCAGAAGGAAAC	5335	SGVSEGN	7002	164.715	
357	ACTCAGTATGGTACTCTGCCG	5336	TQYGTLP	7003	164.526	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
358	GGGACGGTTAACTCAAGTGCA	5337	GTVNSSA	7004	164.3765	
359	GGTAAAGCAACCTTAGTCCTC	5338	GKATLVL	7005	164.3755	
360	GGTATATACCCGGCATCCACC	5339	GIYPAST	7006	164.34	
361	GGTGTTATGTCTAATGCTACT	5340	GVMSNAT	7007	164.06	
362	ACTCATGTGATTGGGGCTGTG	5341	THVIGAV	7008	163.918	
363	ACTCGGAGTGATATTGGTGTG	5342	TRSDIGV	7009	163.7255	
364	ACGCTTACATTATCTACCCCTC	5343	TLTLSTL	7010	163.5555	
365	TATAATGAGTCTTCAATGCG	5344	YNESSNA	7011	163.314	
366	TCGACGCAGGCGCAGACCGGC	5345	STQAQTG	7012	163.15	
367	CGCGACATGATCAACTCATCA	5346	RDMINSS	7013	162.984	
368	ACTAAGGGTAATAATCTGGTT	5347	TKGNNLV	7014	162.899	
369	GGTTCTACGGTGTGCGGCGAG	5348	GSTVSAQ	7015	162.631	
370	AGGGGTGATACTATGAATTAT	5349	RGDTMNY	7016	162.425	
371	CATGCGGATGTGAATGCTGGG	5350	HADVNA	7017	161.99	
372	AGCGTTGTCAACACCAACATC	5351	SVVNTNI	7018	161.9445	
373	TCTAATGTTTCATGTTGTTAAT	5352	SNVHVVN	7019	161.753	
374	TCGGTTGATAAGCGCCGGGG	5353	SVDKPPG	7020	161.487	
375	GACCGCACCTACTCAAACACA	5354	DRTYSNT	7021	161.475	
376	TACTCCGAGAACTAAACAAA	5355	YSGELNK	7022	161.125	
377	TATGATAAGACTTTGAGTGTT	5356	YDKTLSV	7023	160.90695	
378	CACACCGCCACCCTTAGCAGC	5357	HTATLSS	7024	160.8605	
379	GCTCTGGAGAGGGCTCAGTAT	5358	ALERAQY	7025	160.837	
380	GGTACGAGTGATAATTATAGG	5359	GTSNRYR	7026	160.175	
381	CATGTGAATAGTAGGGATCTT	5360	HVNSRDL	7027	160.127	
382	TCGTGAGACGTTACCAGACAA	5361	SSDVTRQ	7028	160.07	
383	GCTCATCATATGACGACGGAG	5362	AHHMTTE	7029	160.019	
384	GAGGTGTCTAGGGATGGTCTG	5363	EVS RDGL	7030	159.7445	
385	GTGGCCGTGACGCAGAAGCT	5364	VGRDAEA	7031	159.58	
386	GCACACCAAAAAGACCTACGC	5365	AHQKDLR	7032	159.3139	
387	AGTGTTCTGAGTAGTTCGACT	5366	SVLSSST	7033	159.208	
388	CTGGGTACGCTGCTTAGTCAG	5367	LGTL LSQ	7034	159.04	
389	TCACAAAAACCAATCGACGAC	5368	SQKPIDD	7035	158.663	
390	GATAATGTGCATGGGCAGGTG	5369	DNVHGQV	7036	158.321	
391	GGTTCGCACAACGGGCCGACA	5370	GSHNGPT	7037	157.748	
392	ATCTCCGGTAGTAGCAGTCTA	5371	ISGSSSL	7038	157.64	
393	GGTTTTTCATATTAATGGTGAG	5372	GFHINGE	7039	157.326	
394	ATGAGTGATGGGCATTCGAAG	5373	MSDGHSK	7040	157.296	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
395	ACTGTTGGTGGTAATCATCAT	5374	TVGGNHH	7041	156.895
396	AATGCTACTCCGCCGAATCAT	5375	NATPPNH	7042	156.8609
397	ACGGGTATGAATAGTAATAAG	5376	TGMNSNK	7043	156.85
398	ATCGAAGCCTACTCACGAGAC	5377	IEAYSRD	7044	156.774
399	CGCGACCGTCAAGACTCGGTA	5378	RDRQDSV	7045	156.7165
400	CACACGGTTCAAATACGCGAA	5379	HTVQIRE	7046	156.6241
401	ACTTTGACGCAGACTGGGATG	5380	TLTQTGM	7047	156.5735
402	ATTAATAATTTTAATACTCTG	5381	INNFNIL	7048	156.48
403	GTAGCCGCGGGACCAGAAGCG	5382	VAAGPEA	7049	156.315
404	GATGGTAAGAATAGTTATGCG	5383	DGKNSYA	7050	156.294
405	TCCAGGCAAGAAACTTCTCC	5384	SRQENFS	7051	156.182
406	TCTAACAGCAGTGTGCGGTA	5385	SNSSVAV	7052	156.048
407	GATCATAGTAAGCAGAGTTCG	5386	DHSKQSS	7053	155.89425
408	TTGAGTGGTGCTGGTAGTCAG	5387	LSGAGSQ	7054	154.9295
409	GGTTGGAGTAATAATGAGTTG	5388	GWSNNEL	7055	154.4735
410	CTAATACGAGGTTCCATGGAA	5389	LIRGSME	7056	154.426
411	AATACTTATAGTCTGGTAAG	5390	NTYTAGK	7057	154.346
412	ACTCGTGGCGACATGGAATTC	5391	TRGDMEF	7058	154.246
413	CTCATGTCAGGGAAGAAAAC	5392	LMSGKEN	7059	154.155
414	AAGGATACTAATCAGCAGATT	5393	KDTNQOI	7060	153.7595
415	CACAACGTCGGCCTAGGACAC	5394	HNVLGH	7061	153.7
416	CCTGATCAGCCTGGTCCTTCT	5395	PDQPGPS	7062	153.51
417	ATGCAAAGAGAAGCAGCCAAC	5396	MQREAN	7063	153.45
418	GGGCAGCGTACGACGAATGAT	5397	GQRTTND	7064	153.425
419	AAACACACAGAAAACGGGACC	5398	KHTENGT	7065	153.394
420	TTAGACGTGACGAGAATGAGA	5399	LDVTRMR	7066	153.086
421	ACGTTGGATCGGAATCAGACT	5400	TLDRNQT	7067	152.9552
422	ATCAACGCCGCAACTACCGA	5401	INAGNYR	7068	152.8475
423	GCCGTAGACCAATCACGTTTG	5402	AVDQSRL	7069	152.8359
424	GCTCTTGGGCATCAGGGGAAT	5403	ALGHQGN	7070	152.467
425	CTTCCGCGTCATGATCAGTAT	5404	LPRHDQY	7071	152.412
426	ATTCTGGGTCGTCGTCCTCT	5405	ISGSSSL	7072	152.2375
427	TGGAATACGAATATGGCGATT	5406	WNTNMAI	7073	151.8755
428	ATGTCGGATCGTACTTCTGAT	5407	MSDRTSD	7074	151.677
429	ACAAGGGAATCAATGTCCATC	5408	TRESMSI	7075	151.6105
430	CAGCGGGGGAGCTTCCTGCG	5409	QRGELPA	7076	151.533

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
431	TCGCTGATCCTAAGGGGCAG	5410	SSDPKGQ	7077	151.4265	
432	CCGAGTGATAGGACTACTTAT	5411	PSDRTTY	7078	151.3695	
433	TCTTCTTCTGATAGTCCGCGT	5412	SSSDSPR	7079	151.2845	
434	GTATTACACTCTGTATCAGCA	5413	VLHSVSA	7080	151.217	
435	AGTATGCAATCATACACCATG	5414	SMQSYTM	7081	151.1285	
436	TCTCTGCAACTCACAGCGGGT	5415	SLQLTAG	7082	151.106	
437	AACAACGTAAACCCGTACTCG	5416	NNVNPYS	7083	151.0935	
438	CTTGCGAATGGTATGACGGCT	5417	LANGMTA	7084	150.9825	
439	GGAATCACAGGATCAACAGGA	5418	GITGSTG	7085	150.979	
440	ATGCTTGTTTCAATACTCCT	5419	MLVQNTF	7086	150.943	
441	GATGCGAATGCGGGTACGAGG	5420	DANAGTR	7087	150.871	
442	GAAACCGGAGCTATGACCTCT	5421	ETGAMTS	7088	150.803	
443	ATACAAACTACTACAAATGC	5422	IQTTHKC	7089	150.692	
444	GCGCAGCAGAGTCTTCATGGT	5423	AQQLHGH	7090	150.673	
445	ATTGATAGTACTTGAATACG	5424	IDSTWNT	7091	150.518	
446	ACCGAATCGCAAACCATGAGG	5425	TESQTMH	7092	150.4394	
447	TTGATCCAAACGCAAGGCACG	5426	LIQTQGT	7093	150.329	
448	ATAGTAAACATAACTCAATCG	5427	IVNITQS	7094	150.305	
449	GTGGCGGTGTCTAATACGCT	5428	VAVSNTF	7095	150.03285	
450	GGTCATAGGGATTGCGGTGGT	5429	GHRDSGG	7096	149.991	
451	CGGAATGAGAATCTTAATAAT	5430	RNENLNN	7097	149.913	
452	GTCATGCACGATCTGCACAA	5431	VMQRSAQ	7098	149.77	
453	GTCTCGGGTCCGGTATCGGTC	5432	VSGPVSF	7099	149.7645	
454	GGGGATATTGAGTTCATAGT	5433	GDIQSHS	7100	149.392	
455	GTTGAGAAGCCTCTGGAGACT	5434	VEKPLET	7101	149.24	
456	GGTGTTTCAATGACTGCGGGG	5435	GVQMTAG	7102	149.14805	
457	ACCACAAAACGACATCTATG	5436	TTKTTSM	7103	149.0935	
458	CCTGGGAATCCGTCTAGTAAT	5437	PGNPSSN	7104	148.9075	
459	GCTTCGCGCCTGCGGCTCAG	5438	ASRPAAQ	7105	148.8831	
460	GTTTCATGATCAGGGGGCTGGG	5439	VHDQGAG	7106	148.829	
461	TCAGGTTCGGAATACCGTACC	5440	SGSEYRT	7107	148.812	
462	TACGTGGACGACAACAGTCGC	5441	YVDDNSR	7108	148.744	
463	ATGGCCGGTGACCAAGAACTC	5442	MAGDQEL	7109	148.7	
464	CCTTTGCACAACATACCTCCT	5443	PLHNIPP	7110	148.609	
465	AGTGGGATTGGTACTTATTCT	5444	SGIGTYS	7111	148.357	
466	TCGAACGCAGACATCCTCGCC	5445	SNADILA	7112	148.08	
467	AGTCACAACCAAGTAAACGTA	5446	SHNQVNV	7113	147.981	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
468	CAGCATTCTCCGAAGCCGGTT	5447	QHSPKPV	7114	147.97
469	TCCGCAAACAACATAGCCCCC	5448	SANNIAP	7115	147.813
470	GAAGAAACACGGACCAGAATG	5449	EETRTRM	7116	147.667
471	CTGTCTAATTCGATTACGCCT	5450	LSNSITP	7117	147.594
472	AGTGCTTTGAATAGTGTGGAT	5451	SALNSVD	7118	147.326
473	ACTAATCTTGCTGTACGCTG	5452	TNLAVTL	7119	147.1589
474	CAGTCGACGCTGAATAGGCCT	5453	QSTLNRP	7120	147.0302
475	ATAGAACACATGCTTAGACCC	5454	IEHMLRP	7121	146.9635
476	CCGACTCCTAATGAGCATATG	5455	PTPNEHM	7122	146.84
477	ATTAATGAGATTGGTAGGATG	5456	INEIGRM	7123	146.786
478	AACAACGACAACGTCTACGTG	5457	NNDNVYV	7124	146.764
479	ATAGTCCACACCCGCAAGTG	5458	IVHTPVQ	7125	146.309
480	CATAAGAGTGAGAGTCATAAT	5459	HKSESHN	7126	146.142
481	TCATCGTCAGACTCACCAGA	5460	SSSDSPR	7127	146.067
482	TACTCTACAGAAGCACGAGTC	5461	YSTEARV	7128	145.9845
483	ACCTCGGGTGACCGGTACACG	5462	TSGDRYT	7129	145.963
484	GAGAAGAATCTGACTAATGCT	5463	EKNLTNA	7130	145.88775
485	ACAAGGGACCAAGGTCTACA	5464	TRDQRST	7131	145.8855
486	GCGACTGATAAGATGACTCCT	5465	ATDKMTP	7132	145.881
487	AATAGTTATACGTGCGGAAG	5466	NSYTAGK	7133	145.87565
488	ACGCTGGATACTAAGGATCTT	5467	TLDTKDL	7134	145.82
489	GCATCCAACGGGCAAGTTAAC	5468	ASNGQVN	7135	145.7395
490	ACCTCAATATCGTCGCAAAGC	5469	TSISSQS	7136	145.707
491	GATAATAGTCTGCTAATCAT	5470	DNSPANH	7137	145.5712
492	AACTCCAGGGAAATGGGTGTA	5471	NSREMGV	7138	145.562
493	ACCAGCGCGTCTGAAACTGG	5472	TSASENW	7139	145.56
494	ACTGTAGGATCCTCATACGCT	5473	TVGSSYA	7140	145.0453
495	CAACAATCACAAACTCTATA	5474	QQSQNSI	7141	144.9825
496	CITCGGGATGGGATTGCTTCT	5475	LRDGIAS	7142	144.9725
497	GTGCAAAAACGACGGCTTGG	5476	VQKTAW	7143	144.78
498	ATGAGTACGGTTCTTCGGGAG	5477	MSTVLRE	7144	144.5125
499	AGTATGGATGCTCGGTTGACG	5478	SMDARLT	7145	144.404
500	GGCGCCCGTACAATCTTAGAC	5479	GARTILD	7146	144.3975
501	CACGAAAGCCACTACGTGTCA	5480	HESHYVS	7147	144.2755
502	CITGAGGGTCAGAATAAGACG	5481	LEGQNKI	7148	144.137
503	CGGGACTTGAGACCCGTGACG	5482	RDLRPVT	7149	143.788

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
504	CAGATTTTGAATTATAGTGTG	5483	QILNYSV	7150	143.741
505	ATAAGTGTAGGTGTGCCGTA	5484	ISVGVS	7151	143.727
506	AAGGCGGGTGAGTATAGGGAT	5485	KAGEYRD	7152	143.693
507	CTTACTACGAATGGTATGCTG	5486	LTTNGML	7153	143.66
508	ACTAGTAATTATATGCATGAG	5487	TSNYMHE	7154	143.642
509	ACCCACAACCTCTACAGGCCTT	5488	THNSTGL	7155	143.502
510	AATAATGTTGTTAGGGATGAT	5489	NNVVRDD	7156	143.142
511	AGTGGGACGTATGCTAGTCGT	5490	SGTYASR	7157	143.123
512	CTGTCTCACGCCATGGACCGG	5491	LSHAMDR	7158	142.937
513	AATTGGAATTCTGAGGGTACG	5492	NWNSEGT	7159	142.7425
514	AGTCTGCGTCCAACCTACCT	5493	SLRPTLP	7160	142.4292
515	TACCAACCGGAGACAAAGAC	5494	YQTGDKD	7161	142.104
516	CGCAGCGACAAAGAACGTTG	5495	RSDKGTL	7162	142.1004
517	TCTACCATCGGCAACAGCACG	5496	STIGNST	7163	142.0895
518	GAAAACAACATGCAACACGGC	5497	ENNMQHG	7164	142.037
519	AAGTATACGGAGTCGAATGCG	5498	KYTESNA	7165	142.0295
520	CCAACAAACAACCTTAAGTATG	5499	PTNNLSM	7166	141.91
521	TGCAAAAACAACCTCAGAATGC	5500	CKNNSEC	7167	141.874
522	ACGGTTAATGCGGATGGGTCG	5501	TVNADGS	7168	141.672
523	TTTTCTGGTCAGGCGTTGGCT	5502	FSGQALA	7169	141.6645
524	AATCATATTAGGAATCCTATG	5503	NHIRNPM	7170	141.628
525	ATGGTGAATTCGGAGAATACT	5504	MVNSENT	7171	141.624
526	ACTGATGGGCCGCTCTGGCT	5505	TDGPRLA	7172	141.5814
527	TTCAACGGGTACGTCATGGCA	5506	FNGYVMA	7173	141.042
528	AATGCGAATGGCCTGTGAGT	5507	NANGPVS	7174	141.0385
529	AGTACGAGTCAGGAGAATAGG	5508	STSQENR	7175	140.9233
530	CAAGGGACTCTCTGTCTCCA	5509	QGILLSP	7176	140.773
531	CTAATCACAGCCACCACTAAC	5510	LITATTN	7177	140.4315
532	TCTGCGCTCTCGAAAGAACGG	5511	SGVSKER	7178	140.3655
533	TCTACTTCAATAGGAGTGGTA	5512	STSIGVV	7179	140.351
534	TCTCATGTGACTGTTACGGAT	5513	SHVTITD	7180	140.31
535	TCTAATAATCTGAATCAGGAG	5514	SNNLNQE	7181	140.282
536	GCAAACCACGACAACATCGTG	5515	ANHDNIV	7182	140.0405
537	GACACGTCTCTCGGCAACAGG	5516	DTSSGSR	7183	140.01
538	GTGGTTCCTATGCCTACTACT	5517	VVPMPTT	7184	139.945
539	CTTACTAATAATTTTAAGGAT	5518	LTNNFKD	7185	139.782
540	TCTTCGCTACTAAGGGTACT	5519	SSPTKGT	7186	139.7594

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
541	GATATTCCGTCTGATAATACG	5520	DIPSDNT	7187	139.44
542	TACACGGGATTGGAATTGAGA	5521	YTGFE LR	7188	139.43
543	AACTCAGGTAACAACCCCATC	5522	NSGNNPI	7189	139.4185
544	ACGACCCGAAACGAACACTCG	5523	TTRNEHS	7190	139.3175
545	AATGTGGGTAATACTCTTGGG	5524	NVGNTLG	7191	139.128
546	TACCACACCCACCAAGTCGCA	5525	YHTHQVA	7192	138.871
547	GGTAGTGCGAGTAATAGTGGT	5526	GSASNSG	7193	138.841
548	GGGAAGAATCAGCCTACTCCG	5527	GKNQPTP	7194	138.839
549	TTCACCGCCACTTTAGGAACC	5528	FTATLGT	7195	138.809
550	ATGAACCAAATGGGCGGCCTG	5529	MNQMGG L	7196	138.794
551	AACGTGTCTACTAACGCAACG	5530	NVSLTQT	7197	138.62365
552	TCGTCTAGCAACACAAACGCT	5531	SSSNTNA	7198	138.538
553	ACTAATTCTAATCAGAGTTCTG	5532	TNSNQSS	7199	138.513
554	ATAAGTCACGACCTTAAATAC	5533	ISHDLKY	7200	138.4685
555	GATTTCGACGTATGTTTGGCT	5534	DSTYVLA	7201	138.402
556	ATGAACACCGGCTCTTCGAGT	5535	MNTGSSS	7202	138.35
557	GCCGGAACCTACCAATCATCA	5536	AGNYQSS	7203	138.2335
558	ACGATTTATAATATGGGTCGG	5537	TIYNMGP	7204	138.1385
559	GTATCAACGACAACGGACCGG	5538	VSTTTDR	7205	137.9925
560	GGGGTGACTGTTAGGGAGCTT	5539	GVTVREL	7206	137.96205
561	GATATTACTAATCAGTCGTAT	5540	DITNQSY	7207	137.802
562	AATCAGTCGCTTACTATGGAT	5541	NQSLTMD	7208	137.363
563	ACGAATTATAATATTGGTCCG	5542	TNYNIGP	7209	137.0645
564	CGTGGTACGGAGGGGACGCCG	5543	RGTEGTP	7210	137.0621
565	CCCATAACACGGGAATCGGGA	5544	PITRESG	7211	136.943
566	ACCGGACAAGCGGGCGGATCG	5545	TGQAGGS	7212	136.857
567	ATGACTAAACACGACGCGACG	5546	MTKHDAT	7213	136.624
568	CCTATACCCACGGTTCATCC	5547	PIPHGSS	7214	136.299
569	ACGACTGGGGGACGGGGATG	5548	TTGGTGM	7215	136.1295
570	CTAACCGAATCTGTGAGAAAC	5549	LTESVRN	7216	135.933
571	AGTAGTAATCTGACTTTGTCT	5550	SSNLTLS	7217	135.86
572	TTGAATAATTCTGCGACTGTT	5551	LNNSATV	7218	135.76
573	GCATACGGATCGTCCGGAAGA	5552	AYGSSGR	7219	135.5095
574	GTTTCTTATGATAATGGGTCG	5553	VSYDNGS	7220	135.48
575	CCGAGTCAGAGTAGGTCGCTT	5554	PSQSRL	7221	135.38455
576	GTCCTGGTTAACGTACACAAC	5555	VLVNVHN	7222	135.346

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
577	TTGATGACTGGTACTGCGTCG	5556	LMTGTAS	7223	135.327
578	GCTGCTGGTAATCCTACTCGT	5557	AAGNPTR	7224	135.3067
579	TCCGCGCAATCTTTCGTAGTT	5558	SAQSFFV	7225	134.721
580	CAAGACCAACGAGCAACCGT	5559	QDQTSNR	7226	134.721
581	CAGTCGATTGGGCATCCGGTG	5560	QSIGHPV	7227	134.625
582	GCTGGGGTGCGTGAGTCGTTT	5561	AGVRESF	7228	134.586
583	AATACTAATTATGCGATGCAT	5562	NTNYAMH	7229	134.493
584	GAGCGGAGTACGCATAATGTT	5563	ERSTHNV	7230	134.479
585	ATGTCCGGATCCATGATATCA	5564	MSGSMIS	7231	134.414
586	TCTGGCCAAGGATTCTCGGCA	5565	SGQGFS	7232	134.3465
587	ACATTCACACTCTGGGCAA	5566	TFCTLGK	7233	134.2015
588	GACGCAACGCTGGCACAGA	5567	DANAGTR	7234	134.063
589	AGGGATACGGCTAAGGGGTG	5568	RDTAKGV	7235	133.882
590	GTGCGGTCTGGTAATAAGCCG	5569	VRSGNKP	7236	133.87
591	CCCCAATGGGGAACGACCCG	5570	PQWGTDP	7237	133.743
592	GCCTTCCAAAACCGGCGCA	5571	AFQNTGA	7238	133.743
593	GCGACGACTCAGCTGATGACT	5572	ATTQLMT	7239	133.675
594	ACGAACGCGAGCGAAGGCTCA	5573	TNASEGS	7240	133.642
595	ATGCTCACAGAAACCAAGCA	5574	MLTETKA	7241	133.57
596	ACGAATAATTTGCTGGCTCAG	5575	TNNLLAQ	7242	133.517
597	GATGTTTTGCTTAAGAATTTT	5576	DVLLKNF	7243	133.49
598	TATACGCCCTGGCTTACTGAG	5577	YTPGLTE	7244	133.356
599	CGGCATGCTTCGGATGCTAAT	5578	RHASDAN	7245	133.22
600	AGTAAGGGTGATCAGCTTAAT	5579	SKGDQLN	7246	133.1865
601	GTGCTGGTTACTCAGAATCAT	5580	VLVTQNH	7247	133.0645
602	CGACAAGGCGACTTAAAAGAA	5581	RQGDLE	7248	132.97895
603	ATTCAGTCGAGTCGAGTTG	5582	IQSQSQL	7249	132.832
604	AAAATAGAAAGCGAACCATA	5583	KIESGTI	7250	132.825
605	ACAACTCTTAGCCAACAAAGC	5584	TTLSQQS	7251	132.567
606	TTTCAGTTGGCTAGTAATCCG	5585	FQLASNP	7252	132.4465
607	TGGATTTCTACTGAGATGAGG	5586	WISTEMR	7253	132.356
608	GCCATAACAATCACTCAAAAA	5587	AITITQK	7254	132.1895
609	GTTACTGGTGTGATTATGCG	5588	VTGVDYA	7255	131.7275
610	ATAATAGCATCTCTACCACG	5589	IIASSTI	7256	131.506
611	ATTTATACGAATAGTCATGTT	5590	IYTNSHV	7257	131.43
612	AACGACATCCCCACACGAGCC	5591	NDIPTRA	7258	131.424
613	GGCGTAACCAACGCTTCCAAA	5592	GVTNASK	7259	131.404

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
614	AGGGGTAACACTCTCGAAATG	5593	RGNTLEM	7260	131.381
615	GGTATTAATCATGTGGCGTCT	5594	GINHVAS	7261	131.36
616	TTCAACGAAACTGCCGGGCGA	5595	FNETAGR	7262	131.2915
617	GCCTCGCAATCAGAAAAAAC	5596	ASQSEKN	7263	131.243
618	GAACCTAACGAAAGGAACCTC	5597	ELNERNL	7264	131.06
619	GGAGAACAAGCCACAACCAA	5598	GEQSHNQ	7265	130.951
620	TTGACTAATGATAATAAGTTG	5599	LTNDNKL	7266	130.846
621	TCTTATGGGCAGGGTCTGGAG	5600	SYGQGLE	7267	130.8108
622	CACAGTGACATGGGCTCAAGC	5601	HSDMGSS	7268	130.758
623	GCGTTAAAAATCCGACACGCC	5602	ALKSDSA	7269	130.684
624	ACGAATCTTTCCTAAGACG	5603	TNLSPKT	7270	130.64725
625	GCTGATACGAATATTATTGTG	5604	ADTNIIV	7271	130.47
626	AGTGAGGGTAGTTCGCGGTCG	5605	SEGSSRS	7272	130.30865
627	AACTCTAGTAACACTGGTTGG	5606	NSSNTGW	7273	130.26
628	GTAACGAACGAATCCCGCGCC	5607	VTNESRA	7274	130.2145
629	GGGCGGCACACATTAGCGGAC	5608	GRHTLAD	7275	130.1035
630	GCTGTTGTGAATGTTGCGCAG	5609	AVVVAQ	7276	130.094
631	AAAAAACCACAACAGTACTA	5610	KKPQQ*L	7277	130.08
632	GGCAACGCTTCCGGAACCCA	5611	GNASGNP	7278	129.97
633	TTTGCGGCTGGGCGCATGGT	5612	FAAGAHG	7279	129.69
634	GGAGGAAACCAAAACCTTACT	5613	GGNQNL	7280	129.6198
635	CATACGCAGTCGACGGGTAT	5614	HTQSTGY	7281	129.541
636	CTATTGGGAAACGCACCCACA	5615	LLGNAPT	7282	129.534
637	GAGAAGGGGAATAGTGGGTT	5616	EKGNSGV	7283	129.5155
638	GGCACGGAACCGCGCACTGCA	5617	GTEPRTA	7284	129.37
639	ATGCATGCGCAGGAGTCTCGT	5618	MHAQESR	7285	129.14615
640	CTGATTTGACTGGTAATAAT	5619	LISTGNN	7286	129.021
641	AAGAATAATAATTCTGATTCT	5620	KNNNSDS	7287	128.767
642	GGGACATTAGCCTCAATGTCC	5621	GTLASMS	7288	128.734
643	AGGATTGATACGTTGTTGGTG	5622	RIDTLLV	7289	128.385
644	ATTTTCGGGTCTCATTTGAAT	5623	ISGSHLN	7290	128.3305
645	ACGGTTGAGGGTCTTATCCG	5624	TVEGSYP	7291	128.288
646	ACGGAGTATCTGGCTGGTCTG	5625	TEYLAGL	7292	128.224
647	TATCTGGAGGGTGCTCATCGT	5626	YLEGAHR	7293	128.166
648	TTATCCGCAACATCTACGATG	5627	LSATSTM	7294	128.1455
649	ATGCTTAGTCAGGTTCTGACG	5628	MLSQVLT	7295	128.142

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
650	GCCAGGAACGTAATGCTGGGG	5629	ARNVMLG	7296	128.128	
651	CTTCATGGGAATTTTAGTCAG	5630	LHGNFSQ	7297	128.112	
652	GGCCACGGAAGTGACTTGACC	5631	GHGSDLT	7298	128.0576	
653	GGTGTGAATTATCATACTACG	5632	GVNYHTT	7299	127.702	
654	TATCTGCAGACGGGTACTCTG	5633	YLQTGTL	7300	127.624	
655	GTAAACGGGGGAAAACAGTC	5634	VNGGKPV	7301	127.5325	
656	GAAGTAGGTAAACACCCAC	5635	EVGKTTH	7302	127.5065	
657	CGACCCCGAACGAAAACAGA	5636	RPPNENR	7303	127.49235	
658	GTGGATAAGAATCATCCTTTG	5637	VDKNHPL	7304	127.431	
659	AGTAAGTCGACTGAGATTATG	5638	SKSTEIM	7305	127.281	
660	ACCGCTCTTCTATCTAACTTA	5639	TALLSNL	7306	127.228	
661	ATGCACACAAGTAGACCCCA	5640	MHTSRPP	7307	126.861	
662	ACTCCAATAACGGGAACCT	5641	TPTNGNP	7308	126.785	
663	ACGACGTCTGTGGAGAAGACT	5642	TTSVEKT	7309	126.7725	
664	CAATACGACGCCAGCCGACAA	5643	QYDASRQ	7310	126.66	
665	TACAACGCCACGAATCATTC	5644	YNAHESF	7311	126.521	
666	GACAACCAACAAGCCCTAGCT	5645	DNQQALA	7312	126.49	
667	ACGAAGAGTTTTAATGATCTT	5646	TKSFNDL	7313	126.488	
668	TTAGCCGACTCAAACAGCAAA	5647	LADSNSK	7314	126.48	
669	CCGAGTACTCATGGGTATGTT	5648	PSTHGYV	7315	126.4775	
670	CAGGTTCAGGGGACTCTGGGG	5649	QVQGTLG	7316	126.4394	
671	CTGACTGCTGTTCGATTAGT	5650	LTAV AIS	7317	126.235	
672	AGGTATGAGAGTACTAGTGCT	5651	RYESTSA	7318	126.21	
673	GCGGATCATAATCATATTGCT	5652	ADH NHIA	7319	126.21	
674	TGGAATGCTGAGAATAGTAAG	5653	WNAENSK	7320	126.112	
675	AACTCTGTCGTAGGGAACATC	5654	NSVVGNI	7321	126.111	
676	TTCGGAGCAACCACCACAGCA	5655	FGATT TA	7322	126.048	
677	GCTTCAGGCTCTGAAATGCCT	5656	ASGSEMF	7323	125.971	
678	GACGGAACAAAAGCGGAATG	5657	DGTSKGM	7324	125.871	
679	TACACCGCCGACAAAAACAA	5658	YTADKKQ	7325	125.562	
680	CCGATTGCTGAGAGGCCTTCT	5659	PIAERPS	7326	125.558	
681	AGCAACTCGTACTTACTCAAC	5660	SNSYLLN	7327	125.52	
682	ACGAGAGAATTGACAAAAAC	5661	TRELTKN	7328	125.47	
683	CTCGGAAACCACTACACCCC	5662	LGNHYTP	7329	125.444	
684	TTGCTCCAATCCATAGTGTA	5663	LLQSIVV	7330	125.441	
685	ATGATGGCGAATAATATGCAG	5664	MMANNMQ	7331	125.38	
686	GGCGCGGACACCTCGACCCGG	5665	GADTSTR	7332	125.369	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
687	GGGTTCGGGCACGTGCCCCGAA	5666	GFGHVPE	7333	125.324
688	AACGTTATGCACTCTCTCCTCC	5667	NVMHSSS	7334	125.313
689	TCTGCGTCGAAAGTGAATAC	5668	SASKVEY	7335	125.2945
690	ATTTTCGAGTTATGATGGTAAT	5669	ISSYDGN	7336	125.273
691	AAAAAACGAAACACTAACT	5670	KTKTKLT	7337	125.26
692	GGTACCATTATTACCAACCAA	5671	GTILPNQ	7338	125.236
693	TTAAACGTCGTACCAACACAA	5672	LNVPVPTQ	7339	125.09
694	AGTAGTGTTACTTCGAGGGAG	5673	SSVTSRE	7340	124.987
695	CCCATCAACGTACTCACGACA	5674	PINVLTT	7341	124.911
696	GGGGATAAGGCGAGTTTGGCG	5675	GDKASLA	7342	124.8255
697	AGGATGTCGGAGAGTTCTGAT	5676	RMSESSD	7343	124.5625
698	AATCTTTTGACTTCGTCGCCT	5677	NLLTSSP	7344	124.54
699	TCGCGGCTATCACAAGACCCC	5678	SRLSQDP	7345	124.3495
700	TGGTCGAATGCTCAGAGTCCG	5679	WSNAQSP	7346	124.231
701	GGCAGACACCTTCAATCGGAC	5680	GRHLQSD	7347	124.19
702	ATGAGTCTCGCCTCCACCCAA	5681	MSLASTQ	7348	124.092
703	ATGAGTACGGTTCTTCGCGAG	5682	MSTVLRE	7349	124.05
704	TCTAAATCTGAAAACCTGCAA	5683	SKSENLQ	7350	124.043
705	TGGACGGAAGGGGGCTCAGGA	5684	WTEGGSG	7351	124
706	TCGACTACGGTTTGACTGCT	5685	STTVWTA	7352	123.99
707	GTTAGTTTGAGAGTCGGTTG	5686	VSLESRL	7353	123.799
708	TCTATGTATGGGCAGGCTGGG	5687	SMYQAG	7354	123.777
709	ACTAATACGCAGAATAATCCG	5688	TNTQNNP	7355	123.702
710	GTCGGTGACAGGAACCTTGTC	5689	VGDRNLV	7356	123.663
711	CTCGCCCACTACTTAAGC	5690	LAHNYLS	7357	123.6175
712	TGGACAGCTAACCAAGGCTTA	5691	WTANQGL	7358	123.566
713	GTCTTCCGGGAAGGCATCGTG	5692	VFREGIV	7359	123.54
714	CAGGTGCAGCATGAGAGGGTG	5693	QVQHERV	7360	123.5
715	CAAAATATTAACTACTCAGTC	5694	QILNYSV	7361	123.4
716	AGTACGATTGGTAATTCTACT	5695	STIGNST	7362	123.3029
717	CCTATACACCACGGTTCATCC	5696	PIHHGSS	7363	123.09
718	ATTGCTACTAATGTGATTAT	5697	IATNVIY	7364	123.055
719	CAAGGCGGTACAAACAACCCC	5698	QGGTNNP	7365	123.037
720	ACCCGTGGCAACGACATATCA	5699	TRGNDIS	7366	123.023
721	CAAACGCTCATAGTGGGGTCC	5700	QTLIVGS	7367	123.007
722	CGGGGTCTGCCTGATGTTAAT	5701	RGLPDVN	7368	122.952

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
723	CTTAATGTGAATACGCTTAAT	5702	LVNNTLN	7369	122.896
724	GGGACAAAAAGCTGGCCTGTC	5703	GTKSWPV	7370	122.8432
725	ACGCATCTTGTGAGTGATTCTG	5704	THLVSDS	7371	122.78
726	TGGACGGGCGCACACCTTCT	5705	WTGAQPS	7372	122.73955
727	TCTGCGATGCACACATTAGTC	5706	SAMHTLV	7373	122.5735
728	TCCCAACACCACACGCCACTG	5707	SQHHTPL	7374	122.4691
729	GATAATCGGATGGAGGCTACG	5708	DNRMEAT	7375	122.416
730	TGGGAGGAACCTGGGAATA	5709	LGGTLGI	7376	122.38
731	TTTCATAATGAGTCTTATGGG	5710	FHNESYG	7377	122.36
732	ATTCGGACTTCTGTGATTAAT	5711	IRTSVIN	7378	122.333
733	TATAATACTGTTGATCAGCGG	5712	YNTVDQR	7379	122.2905
734	GCGCACCAAACCGCCGGGCCA	5713	AHQTAGP	7380	122.22
735	CCTCCGGAAGTGCAGGGGC	5714	PPESARG	7381	122.2044
736	AATAATACTTTGAATATTTTG	5715	NNTLNIL	7382	122.18
737	GCTAGTTATAGTAGTATGGTG	5716	ASYSSMV	7383	122.0975
738	TCGGGTCAAAACGGTACATCA	5717	SGQNGTS	7384	122.017
739	TTGTCTAGTATGAGTACGGAT	5718	LSSMSTD	7385	121.935
740	GTCGCCTCGATGGTACACAAC	5719	VASMVHN	7386	121.8215
741	ACGCAATTGTGACAGCGCTGC	5720	TQLSDGC	7387	121.81
742	GCGATTGTGGATAGGGGAGT	5721	AIVDRGS	7388	121.757
743	AACCGTCAAAGGGACTTCGAA	5722	NRQRDFE	7389	121.734
744	GCACACCAAAAAGACATACGC	5723	AHQKDIR	7390	121.7
745	TTCACCGAACGCGCACTCCAA	5724	FTERALQ	7391	121.6915
746	ATGCTGTCTCATGGTGCCTT	5725	MLSHGAL	7392	121.682
747	TCCGTAACCAACGAGCGGAA	5726	SVTNGAE	7393	121.549
748	ATCACCCCGCGTCACCGCAA	5727	ITAASPQ	7394	121.5325
749	CAAAACACGCAACGATACTTG	5728	QNTQRYL	7395	121.5036
750	ACTGGCCAAGGATTCTCGCA	5729	TGQGFS	7396	121.45
751	AGTTTTGAGAAGAATGGTATT	5730	SFEKNGI	7397	121.45
752	CTCACGTCCCACTCTGCGGGC	5731	LTSHSAG	7398	121.378
753	TCTACAATCGGCAACAGCACG	5732	STIGNST	7399	121.27
754	GGTCTTAGTCGGAATGATGGT	5733	GLSRNDG	7400	121.2415
755	TCGACGACGACCCCTTCCGAA	5734	STTHPSE	7401	121.238
756	CCAAGTACGAACGAAAGCCGC	5735	PSTNESR	7402	121.099
757	GGTACGAAGGATATTCTGATT	5736	GTKDILI	7403	121.039
758	TCTACTATTAATATGCGTGCG	5737	STINMRA	7404	120.929
759	TATATTGCTGGGGGGAGCAG	5738	YIAGGEQ	7405	120.9

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
760	TCCAGCGGCCAACCGCTCGTC	5739	SSGQPLV	7406	120.7415
761	GACAAACAACAAACCGGACAA	5740	DKQQTGQ	7407	120.6775
762	GGGCTAGGACAACCCCAACTC	5741	GLGQPQL	7408	120.644
763	AGTCCGCAGCATGGTGTATT	5742	SPQHGI	7409	120.6145
764	TATAGGGTAGGGAGGATTGG	5743	YRGREDW	7410	120.58
765	GCGGGGGTTTGTCTCGCGG	5744	AGLLSR	7411	120.552
766	CCGATACAACAAGCCTCATTG	5745	PIQQASL	7412	120.375
767	TGGAGCGCCGCGAACGGGTG	5746	WSAGERV	7413	120.3415
768	AGGGGTGATGTTGTACGACG	5747	RGDVATT	7414	120.26
769	TTAACGGGACAAAACGAATTC	5748	LTGQNEF	7415	120.24
770	ACGACGCCGCTTTTCTAAT	5749	TTPFSN	7416	120.2205
771	ACGAGTATTGGTAGTGCTAAG	5750	TSIGSAK	7417	120.195
772	AATGTGCAGAAATGTGCCTGGG	5751	NVQNVPG	7418	120.16215
773	TATACGGGTACTCTGTGTGT	5752	YTGLVV	7419	120.047
774	GGAACCCACGCTCAGCATAAC	5753	GTHASAY	7420	119.959
775	CTGGTTGTTTCGAATAGTCTG	5754	LVVSNSL	7421	119.934
776	ACGCATCTGTGAGGATTCTG	5755	THLVRDS	7422	119.7893
777	AATCATGGTCGTGCTATTGAT	5756	NHGRAID	7423	119.776
778	CCCAAACTCTAACTTCGACA	5757	PKTLTST	7424	119.754
779	TTCGGTATAGGGCACGGAACA	5758	FGIGHGT	7425	119.734
780	GCGCTTCCGTCTCGTGAGCGG	5759	ALPSRER	7426	119.7235
781	GCGACTAGGGGTGAGTCGTCT	5760	ATRGESS	7427	119.715
782	GGGACAACCGAAGTTAACAAA	5761	GTTEVVK	7428	119.685
783	ACCCACACCCTTGGGGGAACA	5762	THTLGGT	7429	119.68
784	GAAGCAGTAACAAGTAAATGG	5763	EAVTSKW	7430	119.6575
785	CACTACGGTAACAAAGACATA	5764	HYGNKDI	7431	119.643
786	ATTTCTACGCATACGATGACG	5765	ISTHTMT	7432	119.64
787	GATACGTATAATAGTAATACT	5766	DTYNSNT	7433	119.6
788	GTTTTTACTGGGCAGACGGAG	5767	VFTGQTE	7434	119.544
789	TCGGTCACCAGTGGAACACAA	5768	SVTSGTQ	7435	119.502
790	CATACGTATTCGCAGGCTGAT	5769	HTYSQAD	7436	119.47455
791	GTAGCGGGCTTAGTCGACATA	5770	VAGLVDI	7437	119.41
792	GACTCTACCAAGCCATGCAA	5771	DSTKAMQ	7438	119.403
793	GAGGGGCATAATCGTGGTATT	5772	EGHNRGI	7439	119.354
794	GGGTTGCATGGGACGAGTAAT	5773	GLHGTSN	7440	119.343
795	CCGCTTCTCTCATAATAGT	5774	PLSLHNS	7441	119.312

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
796	GCGAGTGATAAGGGGCGAAT	5775	ASDKGAN	7442	119.249	
797	GTGCTGTTGCAGAATTCTCAT	5776	VLLQNSH	7443	119.2225	
798	CTATACGACGGAAAAACACGTC	5777	LYDGKHV	7444	119.20995	
799	ACCCAAGGATCTAACACCACA	5778	TQGSNTT	7445	119.08	
800	TTCCTCGACAAATACAACCTAC	5779	FLDKYNY	7446	119.058	
801	GACACCGGAATCAAAAACGTT	5780	DTGIKNV	7447	119.05	
802	TCCGGAGCGGCACAAAACCCA	5781	SGAAQNP	7448	119.019	
803	ACCCTCCACACCAAAGACCTA	5782	TLHTKDL	7449	118.854	
804	GCTACTTACGTTGTCGGAACA	5783	ATYVVGT	7450	118.84	
805	CTTGTTGGGACTTTGGTGTAT	5784	LVGTLVY	7451	118.809	
806	TCTAATACGACTGTGCAGCTT	5785	SNTTVQL	7452	118.76	
807	AAGGCTCAGATTAATCAGATG	5786	KAQINQM	7453	118.727	
808	CGGAATGCTACTGTGACTGTT	5787	RNATVTV	7454	118.655	
809	GCAACCAGAGTGGGCAACCAC	5788	ATRVGNH	7455	118.599	
810	AGTTATCAGAATCCTCCGCCT	5789	SYQNPPP	7456	118.512	
811	TTTGATAGTTATAATATTGTG	5790	FDSYNIV	7457	118.51	
812	GCTACTCTTTCTCCGATGCT	5791	ATLSPHA	7458	118.497	
813	TGGGAGAGTCCGACTAATGCG	5792	WESPTNA	7459	118.49	
814	ATCGAAAACGTAAACCACTTG	5793	IENVNHL	7460	118.42	
815	TATCGGGCTTCGGATGTGGCG	5794	YRASDVA	7461	118.372	
816	CATATGTCTTCTGTTGCGACT	5795	HMSSVAT	7462	118.34	
817	ATCCAAAGAGACGTGGGCCAC	5796	IQRDVGH	7463	118.2825	
818	GAGAGTGTTAGGGAGACTATT	5797	ESVRETI	7464	118.25	
819	CAGGGGGGAATAGTCGGTTT	5798	QGGNSRF	7465	118.236	
820	GAAAAAGGCACACCAAGTAGC	5799	EKGTPSS	7466	118.233	
821	CACGACAGCACAAACCGCCCA	5800	HDSTTRP	7467	118.225	
822	TTACCAACAGGCGTCTGCCCC	5801	LPTGVLP	7468	118.2065	
823	ACCCTAGGCTACCCAGACAAA	5802	TLGYPK	7469	118.1855	
824	GCTAACACCGTCACAGAACGA	5803	ANTVTER	7470	118.17415	
825	CACGACAAATCTATCCAACCA	5804	HDKSIQP	7471	118.16	
826	GGAGGAACAGCCCTTGGGAGC	5805	GGTALGS	7472	118.123	
827	GGGGTAACCTACCACACCACT	5806	GGNYHTT	7473	118.046	
828	ATCTCAGAAATGACTAGGTAC	5807	ISEMTRY	7474	118.041	
829	GTTGAATCTAAATCCGAACCA	5808	VESKSEP	7475	118.026	
830	GACCGTGCCCAAAACAACGAA	5809	DRAQNNE	7476	118.006	
831	ACGGCGCAGACCGGTGGGTT	5810	TAQTGWV	7477	117.96	
832	GGGTTCCGGCACCTGCCCGAA	5811	GFGHLPE	7478	117.86	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
833	CCTATTACGGGTTTTAGTGTT	5812	PITGFSV	7479	117.828
834	GATAGGACGTATTCGAATACG	5813	DRTYSNT	7480	117.7875
835	ATGTCAAACGCCTCCTACATA	5814	MSNASYI	7481	117.743
836	GATAATAGTAGGCCTGAGGTG	5815	DNSRPEV	7482	117.658
837	TCAAGTTCCCAAACGGTTTTG	5816	SSSQTVL	7483	117.655
838	AGTAATCTTGATGGTACTATT	5817	SNLDGTI	7484	117.643
839	AGTAATATGCGTGAGGAGATT	5818	SNMREEI	7485	117.629
840	AGACTTACAGAACTGGTCATA	5819	RLTELVI	7486	117.583
841	CAGGTTAGTCTGGTGAAGTTG	5820	QVSLVKL	7487	117.558
842	GAAATACACACGACCACAGGC	5821	EIHTTTG	7488	117.5505
843	AGCAGGATAGAAAACAACAAC	5822	SRIENNN	7489	117.5425
844	GGAACAGGCAAAGAAGTTCGA	5823	GTGKEVR	7490	117.521
845	TGGCAGGATCATAATAAGGTG	5824	WQDHNKV	7491	117.476
846	TCGACAAACTCTATAGGCGCC	5825	STNSIGA	7492	117.414
847	TCCGAATTAATGGTCAGACCC	5826	SELMVRP	7493	117.3623
848	CCGCTTCAGAATAATAAGACG	5827	PLQNNKT	7494	117.2175
849	CCTTATGCGAATAGGCTTGAG	5828	PYANRLE	7495	117.21145
850	GGGACGGTTTCGCTTATTCCT	5829	GTVSLIP	7496	117.175
851	GATGTTTATCTTAAGAGTCCG	5830	DVYLKSP	7497	117.1435
852	TTGCCGGATAAGGGCGGATT	5831	LPDKGRI	7498	117.116
853	TCGATAACGACCGTAGCGAAC	5832	SITTVAN	7499	117.112
854	CCGCTTCAATCCCAATCGGGA	5833	PLQSQSG	7500	117.1045
855	AATAATATGGGTCATGGTCAT	5834	NNMGHGH	7501	117.0365
856	AGCGGACAAAAAACTCAGAA	5835	SGQKNSE	7502	116.9665
857	ACCGAAGCGGGCCGCCCCCAA	5836	TEAGRPQ	7503	116.907
858	ACCTTACACACGAAAGACTTG	5837	TLHTKDL	7504	116.879
859	CTTCGAGACCTAAACGGAGGA	5838	LRDLNGG	7505	116.8691
860	GTTTGTGTTACTACTTGIGCT	5839	VCVTTCA	7506	116.861
861	GTCACAGCTGCTCAACCCCAA	5840	VTAAQPQ	7507	116.79
862	GCGACTTTTAGTCATGCTGGT	5841	ATFSHAG	7508	116.788
863	ACTTATGCGCCTAGGTCGCCT	5842	TYAPRSP	7509	116.75715
864	ACGTCGGAGATGCGTACTGCT	5843	TSEMRTA	7510	116.5885
865	TACTCGACAACCATGCTTAAC	5844	YSTTMLN	7511	116.584
866	TCTTTCACGAACACAAACCCA	5845	SFTNTNP	7512	116.5665
867	AGTCCTCCTAGTACGTCGGGT	5846	SPPSTSG	7513	116.551
868	GTGACGACTGTTGATAGTGCT	5847	VTTVDSA	7514	116.477

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
869	GAGGCGCATAATCGTGTATT	5848	EAHNRVI	7515	116.461	
870	ATGGAGTTGACTTCTACTAGT	5849	MELTSTS	7516	116.456	
871	CATTTGGTTACTAGTGGTATT	5850	HLVTSGI	7517	116.45	
872	CAAACCATCACCTCACAAATG	5851	QTITSQM	7518	116.431	
873	ACTGCGAATAGTACGTATGTG	5852	TANSTYV	7519	116.329	
874	CTTATCCAATTATCGGGTCAA	5853	LIQLSGQ	7520	116.317	
875	TCTTACGTTAGCGTCCCGGCC	5854	SYVSVPA	7521	116.3005	
876	GTGCATGGGAATGCTCCGGCT	5855	VHGNAPA	7522	116.2665	
877	GCCGGAAAAACCCACGCCGAC	5856	AGKTHAD	7523	116.228	
878	ACATTCCACCAAGGGTCAAA	5857	TFHQGVK	7524	116.175	
879	TTAGGAAACAACCGCCACTA	5858	LGNNRPL	7525	116.17	
880	CTGCACCTCGTCCGAGCTTC	5859	LHLVRSF	7526	116.08	
881	TCCTACAGTACTTCAACACCG	5860	SYSTSTP	7527	116.036	
882	ATATCGCAAGGCTCGAGCTC	5861	ISQGSSL	7528	116.025	
883	CTCCAACTGGCTACATCCCAC	5862	LQLATSH	7529	116.0035	
884	GTGACTCAGCGGTTTGCTGAG	5863	VTQRF AE	7530	115.952	
885	GCTATAGACTCCATCAAAATG	5864	AIDSIKM	7531	115.9415	
886	GACGCACACACTTTCAGCCGG	5865	DAHTFSR	7532	115.93	
887	CGTGGTTCAGACGAGGATTG	5866	RGSDGGL	7533	115.911	
888	TTAGCACAAAGGCACGACCGG	5867	LAQGTDR	7534	115.884	
889	AAAAACAACAATCAGACAGT	5868	KNNNSDS	7535	115.7595	
890	GAAAACGAAAACGAGAAAGC	5869	ENEKRES	7536	115.741	
891	AACGAACAATTGAAAAAGTC	5870	NEQFEKV	7537	115.705	
892	ACACAAGTAGTCGCAAGAACA	5871	TQVVART	7538	115.68045	
893	GGAGTAAACGTCACCAACAGC	5872	GVNVTNS	7539	115.64	
894	GCCGACAAAGGATTCGGCCAC	5873	ADKGF GH	7540	115.5886	
895	ACTCATAAGCAGGTGGATCTT	5874	THKQVDL	7541	115.54825	
896	TCGGCTAACTTATACAAACAA	5875	SANLYKQ	7542	115.544	
897	AAGCTGCATACTAAGGATCTT	5876	KLHTKDL	7543	115.54	
898	GTGGTGGTTCACACTATCCCA	5877	VVVHTIP	7544	115.52	
899	TCTACGTCTCAGGCTGTGCAG	5878	STSQAVQ	7545	115.496	
900	CGTAACGGCTCCGCCAAAGC	5879	RNGSAQS	7546	115.465	
901	CATTATGGGAATAAGGATATT	5880	HYGNKDI	7547	115.402	
902	AGCTTCTTGGTAGCCACCCA	5881	SFLVAHP	7548	115.4	
903	CAGCAGAATACGAGTTTGCCG	5882	QQNTSLP	7549	115.39	
904	ATGCACGTCGACAAAACGAGT	5883	MHVDKTS	7550	115.379	
905	AATAATGAGAATACGCGTAAT	5884	NNENTRN	7551	115.363	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
906	TCGATAAACACATAGGCGCA	5885	SINNIGA	7552	115.3425
907	GCTACTATATCGGACCGAGCC	5886	ATISDRA	7553	115.327
908	TACTCAAACCTCGTACTTTCC	5887	YSNLVLS	7554	115.285
909	ATGATGAATGTGAGTGGTCAT	5888	MMNVSGH	7555	115.2555
910	GGGGAGACGCGGTCGACTGCT	5889	GETRSTA	7556	115.18
911	ACGAAGGGTTATAATGATCTT	5890	TKGYNDL	7557	115.1635
912	GCGTATAATATGTCGTCTGTT	5891	AYNMSSV	7558	115.148
913	GCAGACCCCGCTAAAGGCAAA	5892	ADPAKGK	7559	115.1435
914	TATATTTGCGCGCTCCGATG	5893	YISAPPM	7560	115.1145
915	CGAAACAACCCATCGCACGAC	5894	RNNPSHD	7561	115.069
916	GGAACCTCCATAGACTACGTA	5895	GTSIDYV	7562	115.053
917	GGCACCGGGTACCCAAACCAA	5896	GTGYPNQ	7563	115.038
918	GATCATATGAATTTGAGGTCT	5897	DHMLRS	7564	114.9475
919	ATTAATTCGTATTTGCATGAG	5898	INSYLHE	7565	114.887
920	TGGCAAATGGGGCCGGGAGC	5899	WQMGAGS	7566	114.833
921	ATGGGTATCGGGTCATACAAA	5900	MGIGSYK	7567	114.827
922	CAAAACCACAACGAATAAAA	5901	QNHNELK	7568	114.749
923	GATAAGTCTAATTATAGTATT	5902	DKSNYSI	7569	114.736
924	ACAACGAAACCGGTCGCGGAA	5903	TTKPVAE	7570	114.7315
925	GTGACTGTGAGTAATAGTCTG	5904	VTVSNSL	7571	114.685
926	ACGGCGTATCTGGATGGTCTG	5905	TAYLDGL	7572	114.665
927	AATTTGCAGACTGGTGTTTCTCAG	5906	NLQTVQ	7573	114.65
928	ACCGTCGCTCCCTACAGTAGC	5907	TVAPYSS	7574	114.65
929	GTTTCAAGTTTCTATGAATAAT	5908	VQISMNN	7575	114.617
930	TACATAGCAGGTGGTGAACAA	5909	YIAGGEQ	7576	114.60015
931	TTCATGGAAGTCATGAAAAC	5910	FMEVMKN	7577	114.547
932	ACGACTGATAAGGGTATTAAT	5911	TTDKGIN	7578	114.539
933	TTGAGCTACAGCATCCAACAC	5912	LSYSIQH	7579	114.53
934	GCTTATAATGCTCTCTGCCT	5913	AYNARLP	7580	114.49305
935	AACACCGGCACACGAGTGTC	5914	NTGTTSV	7581	114.475
936	GTGCTGAGTACGGGGCTGCGG	5915	VLSTGLR	7582	114.4165
937	AACGACTCCTCGTCAATGTCC	5916	NDSSSMS	7583	114.397
938	CGCCAAGGCAGCTTGATGATA	5917	RQGSLMI	7584	114.37
939	ATCAGCACCGCATACATGTTG	5918	ISTAYML	7585	114.36
940	GGTACTATGAATATTGGTATT	5919	GTMNIGI	7586	114.356
941	CATAATAATAATTTGCTGAAT	5920	HNNNLLN	7587	114.292

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
942	CATTTTTCGCAGATTACTAAT	5921	HFSQITN	7588	114.278
943	GACCTGACCAGAGCTGCAATA	5922	DLTRAAI	7589	114.256
944	GTCGCTATGGGAGGCGGTCCC	5923	VAMGGGP	7590	114.1845
945	GCCTACGGTATCAGAGAAGTG	5924	AYGIREV	7591	114.1465
946	ACATCAGACGGTCTACTAAGT	5925	TSGLLS	7592	114.128
947	ACGATGGCTACAACTTAAGT	5926	TMATNLS	7593	114.082
948	AACAACGGCAACTCATCAAGG	5927	NNGNSSR	7594	114.047
949	ACGGAGAAGGCGAGTCCTCTG	5928	TEKASPL	7595	114.031
950	CTCAACCACACAATGCCCTC	5929	LNHTMPL	7596	114.027
951	GATACGGCGAGTTATAATAAT	5930	DTASYN	7597	114
952	AACATGACCAACGAACGGCTC	5931	NMTNERL	7598	113.9675
953	GTAGTCTCATCGGGCGGCTGG	5932	VVSSGGW	7599	113.966
954	GTGAATCAGAGTCCTGGGCT	5933	VNQSPGA	7600	113.85
955	GATCATCATCCTCAGAGTCGT	5934	DHRPQSR	7601	113.83
956	CGATGGCAAGGACTGAGCGCG	5935	RWQGLSA	7602	113.76
957	GCGGTTACGACAAGCGTGAGG	5936	AVTTSVR	7603	113.752
958	TGGGGAGTCAGTAAGTCAGCA	5937	WGVNSA	7604	113.7505
959	GCGCATATGCATTCGGAGTTG	5938	AHMHSEL	7605	113.74
960	AATAATCTTACGAATTCGACG	5939	NNLTNST	7606	113.736
961	AGTAGTGGGGTATGAAGGCG	5940	SSGGMKA	7607	113.69
962	GTTGGGTATGGGAGCATGTT	5941	VGYGEHV	7608	113.64
963	ACCATAGTGTCCTTCTTAC	5942	TIVSTSY	7609	113.628
964	CCCACCAAGTCACCAAGAACCC	5943	PTSHQEP	7610	113.62
965	TCTAACCTTCGAAACACAATA	5944	SNLRNTI	7611	113.58
966	TCAAGACACGACGTCCGAAC	5945	SRHDVRN	7612	113.559
967	CAGATGAATATTCATGATAAG	5946	QMNIHDK	7613	113.543
968	TGGGCTATGAATAATGTGCCG	5947	WAMNNVP	7614	113.531
969	GCGATGGATGGGTATAGGTT	5948	AMDGYRV	7615	113.462
970	AAAGGGGAAACCTCACCGCA	5949	KGGNLTA	7616	113.4525
971	ATTGGTAAGGATAGTGTCCG	5950	IGKDSVP	7617	113.448
972	GTGCAGTTGACGCATAATGGG	5951	VQLTHNG	7618	113.43
973	GGCCTGAACAGATCACATCG	5952	GLNQITS	7619	113.4
974	AGGGGTGATCCTTCTACGCCT	5953	RGDPSTP	7620	113.4
975	GITCCCTCCGACCCCACTGG	5954	VPSDPHW	7621	113.35
976	ACGTTAAGTTCCTCAAGTCACA	5955	TLSSQVT	7622	113.327
977	AACCAAAGAGTTGAACAAAAA	5956	NQRVEQK	7623	113.3075
978	GTAATTCAGTCGGATCGCG	5957	VLPSRIA	7624	113.3

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
979	GGGCACTACGCTACAAACACA	5958	GHYATNT	7625	113.212
980	CCTTCGATTCCGTCGTTTTTCG	5959	PSIPSFS	7626	113.207
981	ACTTATGAGTATCCGACTCGG	5960	TYEYPTR	7627	113.19
982	AAAGACCACATCCTCAGCCTC	5961	KDHILSL	7628	113.1795
983	GGCACAGGAGGTAACCGAGAA	5962	GTGGNRE	7629	113.173
984	AAGGGGGATGGTGCTTATGAG	5963	KGDGAYE	7630	113.162
985	TCTTCTTTCGGAAAAGACAAC	5964	SSFQKDN	7631	113.1603
986	ACAGTATCGTCATACGTACAA	5965	TVSSYVQ	7632	113.0595
987	AGGGCTCATGGGGATAATCAG	5966	RAHGDNQ	7633	113.036
988	TATCATGCTCATAGTAATGAG	5967	YHAHSNE	7634	113.03
989	GCAAACCTTGCCAGCGGTAC	5968	ANLPSGH	7635	113.03
990	GCGAACCTCAACTTGACCACT	5969	ANLNLT	7636	113.015
991	AGGCTTAATGCGGGTGAGCAT	5970	RLNAGEH	7637	113.0105
992	TATGTTGATTATAGTAAGTCG	5971	YVDYSKS	7638	112.9935
993	GCTAATTCTGGGTTGCATAAT	5972	ANSLHN	7639	112.9695
994	ACGAGTGGTGTGCTTACGCGG	5973	TSGVLTR	7640	112.9485
995	GGAAAACCAGCACAGAATTC	5974	GKPAQEF	7641	112.933
996	GTGGGGACGCATTTGCATTTCG	5975	VGTHLHS	7642	112.918
997	CCGATGAACAAAGACATACTG	5976	PMNKDIL	7643	112.9116
998	GACGCCCACCACTCAAGCAGC	5977	DAHSSS	7644	112.88
999	ACTAACGCCATCTCTCAAACG	5978	TNAISQT	7645	112.7997
1000	GTTTTGTCTGATAAGGCGTAT	5979	VLSDKAY	7646	112.787
1001	AACCTACTTGTGCGACCAACGT	5980	NLLVDQR	7647	112.78
1002	ACTGGTCATCCGCCGGCGCG	5981	TGHPAA	7648	112.7735
1003	ATTAGTTCGGGATTTTGTCTG	5982	ISSGILS	7649	112.7205
1004	AATACGAATTTGTTGGTTAT	5983	NTNLLGY	7650	112.72
1005	ACGCTATCGGTTACCCTGGGT	5984	TLSVTLG	7651	112.71
1006	CATACTGGTGTTCAGACTAAT	5985	HTGVQTN	7652	112.704
1007	GAGGTTAGTAATAATAATTAT	5986	EVSNNNY	7653	112.69
1008	CTGGCTAATATTTTCGCTGTAT	5987	LANISLY	7654	112.69
1009	GTGGAGCATGTTGCTCATCAG	5988	VEHVAHQ	7655	112.656
1010	GTCGACAAAGCGAAGCCGAC	5989	VDKSEAD	7656	112.6
1011	GGCTTCGCATTAACCTGGCACC	5990	GFALTGT	7657	112.564
1012	TTGTTGACGGCTCCGCATAGG	5991	LLTAPHR	7658	112.53
1013	AATGCGGGGCTCTTATGGGT	5992	NAGALMG	7659	112.518
1014	AGGACGCAAGCAGGGGACTCA	5993	RTQAGDS	7660	112.483

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1015	AACACACACAGACAAGAATAC	5994	NTHRQEY	7661	112.461	
1016	AACATAGCAGGCGGAGAACAA	5995	NIAGGEQ	7662	112.442	
1017	GAGATTAATAATCGGACTGGT	5996	EINNRTG	7663	112.43235	
1018	ACCGTTAACACAATGTACACG	5997	TVNTMYT	7664	112.4	
1019	CCTATGAATGGTATTCTGTTG	5998	PMNGILL	7665	112.388	
1020	AATCCTAGTTATGATCATCGG	5999	NPSYDHR	7666	112.363	
1021	GCTGTATTCTGAATCCTGTT	6000	AVILNPV	7667	112.36	
1022	CTGTACGGGGAGCACACCAA	6001	LYGGAHQ	7668	112.3455	
1023	CAAGTCAACCAACCGAGAATA	6002	QVNQPRI	7669	112.33	
1024	GCTGTAGAACACCGCAATG	6003	AVRTPAM	7670	112.326	
1025	AGTTTGACGCCTAATAATCTT	6004	SLTPNNL	7671	112.283	
1026	CTTGGGCAGGTTAATTCTACG	6005	LGQVNST	7672	112.205	
1027	GCTAATTCTGCTACTAATCAG	6006	ANSATNQ	7673	112.1605	
1028	TCCTTGACGGAAAAAGCGCCG	6007	SLTEKAP	7674	112.15	
1029	CAATTCACGGGACATCTGAA	6008	QFHGTSE	7675	112.125	
1030	AAAAACGGCGCCATAGGAACA	6009	KNGAIGT	7676	112.0867	
1031	GTGCTGGCGTCGACTGAGAAG	6010	VLASTEK	7677	112.058	
1032	AGTAATATGAGTGAGGCGATT	6011	SNMSEAI	7678	112.02	
1033	AACGCTAACGCCGGTGGAAC	6012	NANAGGN	7679	112.0148	
1034	CACTCTAACACACTACGAA	6013	HSNTHYE	7680	112.005	
1035	AGTGCTTTGATTAGTGTGGTT	6014	SALISVV	7681	111.993	
1036	GTGGCGACTCATTATAATGAG	6015	VATHYNE	7682	111.971	
1037	AACCAAACGTTACAAGTAGAC	6016	NQTLQVD	7683	111.97	
1038	AAAACACCCTCAGCTTCAGAA	6017	KTPSASE	7684	111.957	
1039	GGTGAATCACGTACAAACATG	6018	GESRTNM	7685	111.9393	
1040	CGGAATGAGCCGGTTAGTACT	6019	RNEPVST	7686	111.912	
1041	GCAACACACGCCATGCGCCCA	6020	ATHAMRP	7687	111.9005	
1042	TGGGAATCCCTCTCCAACGCA	6021	WESLSNA	7688	111.885	
1043	CATAGTCCTCTACGACTATG	6022	HSPPTTM	7689	111.847	
1044	TCTACCATGAACACGATCACG	6023	STMNTIT	7690	111.8162	
1045	AACATGGAACACACCATGGCG	6024	NMEHTMA	7691	111.78965	
1046	CATAATACGGAGTCTAAGACT	6025	HNTESKT	7692	111.778	
1047	CACAACTTAATGACCCAAATA	6026	HNLMTQI	7693	111.77	
1048	AACCAAAACACCTACGAACTG	6027	NQNTYEL	7694	111.756	
1049	TACGCCACTCTCGACACCATC	6028	YATLDTI	7695	111.752	
1050	GTTCAAGTTGGAGAATGCGAAT	6029	VQLENAN	7696	111.7215	
1051	GGGCTCACAGGATACACAATG	6030	GLTGYTM	7697	111.71	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1052	TTAGTACTTGACTCACGGAAC	6031	LVLDsrn	7698	111.704
1053	ATGTTGGTACAAAACACACCC	6032	MLVQNTp	7699	111.702
1054	CCTCATAATCAGGAGATGGGT	6033	PHNQEMg	7700	111.6865
1055	TCGTTGGGGGATGCGATGTTG	6034	SLGDAMl	7701	111.6776
1056	CGCGCCGAAGGAGCTCTGGC	6035	RAEGSSg	7702	111.6645
1057	AGTGAGGAGAGGACGCGTGCG	6036	SEERTRa	7703	111.616
1058	TCTAGTAAGGAGCGTACATCG	6037	SSKERTS	7704	111.57
1059	CCTGTTGTGAGGGATCGTTCT	6038	PVVRDRS	7705	111.5643
1060	AGGATGTCTGAGAGTTCGGAT	6039	RMSESSD	7706	111.51
1061	AACCAATCTATAAGCATGGAC	6040	NQsISMD	7707	111.491
1062	GTCGCTGTATCGAACACTCCA	6041	VAVSNTP	7708	111.482
1063	GGAGACATCTCAAGCAGAAAC	6042	GDISSRN	7709	111.4603
1064	GCTGCCGAGCCGACTCTCCA	6043	AAGADSP	7710	111.429
1065	TTCGGCACATCGTACACAACC	6044	FGTSYTT	7711	111.401
1066	CGTGATACTAATACGGATAAG	6045	RDNTNDK	7712	111.336
1067	GGGTCTACGCCGGGGGCGAGT	6046	GSTPGAS	7713	111.327
1068	GGTACTAATCATGATTTTTCG	6047	GTNHDFS	7714	111.302
1069	AATGAGAGTACGAAGGAGAGT	6048	NEStkes	7715	111.2845
1070	GTGCATGTGACTAATGTGTTG	6049	VHVTNVL	7716	111.2295
1071	AGTACTACTAATGTTGCGTAT	6050	STTNVAY	7717	111.2015
1072	ATTACGTCGTTGAATGGGATG	6051	ITSLNGM	7718	111.1615
1073	GAAGTACGGGGCAGCGTGCCA	6052	EVrgsVP	7719	111.1435
1074	GCACTTACCCGTATGCCTAAC	6053	ALTRMPN	7720	111.1235
1075	CTCAGTGTAGCCGACAGGCCA	6054	LSVADRP	7721	111.06
1076	GTTTCTACGGCGCAGAGGCAG	6055	VSTAQRQ	7722	111.056
1077	TTAAACGCAGAATACACCAAC	6056	LNAEYTN	7723	111.02
1078	AATGAGAAGCCGAGTCGACG	6057	NEkpQST	7724	111.009
1079	TTGAATACGCTGATTGATAAG	6058	LNTLIDK	7725	111.003
1080	GTCACACACACTGATCGAA	6059	VTHTLIE	7726	110.987
1081	GAGCAGAAGAAGACTGATCAT	6060	EQKkTDH	7727	110.936
1082	ACATCAGGCATGTACGACACG	6061	TSGMYDT	7728	110.92
1083	CCTGACGCAGCGGTAGCCCG	6062	PDAARSP	7729	110.916
1084	TTGACGCAGGTTTATCATGAG	6063	LTQVYHE	7730	110.91
1085	AGAGAAATGAGCAGCCTATCT	6064	REmSSLS	7731	110.891
1086	ATGCCTTCGAAAGGCGAAGTA	6065	MPskGEV	7732	110.816
1087	AATGAGCAGAATACGCCGAGT	6066	NEQNTPS	7733	110.79

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1088	AAAACTACGCAAGCACCACGAC	6067	KNYASTD	7734	110.7435
1089	TGTATGGATGTTGGTAAGGCG	6068	CMDVGKA	7735	110.711
1090	GCTCTTCATAATCTGATGAAT	6069	ALHNLMN	7736	110.711
1091	CCTGACAGAGCGAACGACAAA	6070	PDRANDK	7737	110.6835
1092	ATTGCTCATGTGTCTACTAAT	6071	IAHVSTN	7738	110.6805
1093	AACGGTCCGACCGGATCCGCC	6072	NGPTGSA	7739	110.6652
1094	TCTACTCATCATGTGATCGT	6073	STHHADR	7740	110.629
1095	GGTTCGCAGTATGGGCGGCAT	6074	GSQYGRH	7741	110.629
1096	ACCGGAACGGCTACACTCCCA	6075	TGTATLP	7742	110.5825
1097	AAAGCCCACGTTGTAGAAATA	6076	KAHVVEI	7743	110.5795
1098	ACTTCGCAGGGTAGGAGTCCT	6077	TSQGRSP	7744	110.511
1099	TTATCCTCCGAATCAGCCAGG	6078	LSSESPR	7745	110.5015
1100	ACCGGGGTTGAGAAACCATA	6079	TGVRETI	7746	110.4575
1101	ATGGATACTGAGCTTTATAGG	6080	MDTELYR	7747	110.4475
1102	ACACCTGAAGCGAGCGCTCGC	6081	TPEASAR	7748	110.44
1103	CACGACTTGAACACGGAAAA	6082	HDLNHGK	7749	110.428
1104	CTTACTGGTCAGAATGCGATT	6083	LTGQNAI	7750	110.416
1105	ACCGTCGGATCGAACAGTATA	6084	TVGSNSI	7751	110.411
1106	CATACTGTGGGGGCTATGCAT	6085	HTVGAMH	7752	110.41
1107	GAACGAGTCAACGGGATGGCA	6086	ERVNGMA	7753	110.405
1108	TCCGAACCCCTTAGAGTTGGA	6087	SEPLRVG	7754	110.3725
1109	GTCTCTAACGTCCTCTACAGC	6088	VSNVLYS	7755	110.346
1110	TTCTCCTCCGAACAACCATA	6089	FSSGTTI	7756	110.3
1111	ACAAACCTAAGTCAATCGGCC	6090	TNLSQSA	7757	110.24435
1112	CCTAATACTGCTAGTAATTTT	6091	PNTASNF	7758	110.2274
1113	TGCGGCCTGAACTGCGGTAAA	6092	CGLNCGK	7759	110.211
1114	CCGACCGGAGGCTCACCACCA	6093	PTGGSP	7760	110.201
1115	TACCTAGAATCCAACCTACACC	6094	YLESNYT	7761	110.18
1116	ACATTAGAAACAACCCGAGC	6095	TLETTRS	7762	110.167
1117	TCCGCTAACGAACACAACCAC	6096	SANEHNH	7763	110.137
1118	GCACGAGTGGACACCAACCAA	6097	ARVDTNQ	7764	110.09
1119	AACGTGGTGAAAAACAACACA	6098	NVVKNN	7765	110.077
1120	GGTTCTTATTCTGATGGTAGT	6099	GSYSDGS	7766	110.0355
1121	CCCGGTAACGGACAAAGTCCG	6100	PGNGQSP	7767	110.0275
1122	TCGGGGGTAAACTTCGGAGTA	6101	SGVNFGV	7768	109.998
1123	CGAATCAACGCAGCAATCGAC	6102	RINAAID	7769	109.99675
1124	CAAGCTGGGAACGCGCCAAGG	6103	QAGNAPR	7770	109.98825

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1125	CAGTCGGGGTCTCTGGTGCCG	6104	QSGSLVP	7771	109.962
1126	TTCTCAACGCAAGACATAAGC	6105	FSTQDIS	7772	109.948
1127	GTGAATCCGCATCCTGCGCAG	6106	VNPHPAQ	7773	109.948
1128	AAAGGCCACGCCTACGAAGCC	6107	KGHAYEA	7774	109.897
1129	GAAGACAGTATGAGATTCTCT	6108	EDSMRFS	7775	109.874
1130	GGTAGGAATGAGAGTCCGGAG	6109	GRNESPE	7776	109.855
1131	TCCGACGGATCGAAACTACTA	6110	SDGSKLL	7777	109.8205
1132	ACTCTCTCAGGCTACATGAGA	6111	TLSGYMR	7778	109.808
1133	GATATTCTATAATCCGCGTACG	6112	DIHNPRT	7779	109.789
1134	TGGGCCAAAGACGTCAACGTC	6113	WAKDVNV	7780	109.782
1135	GCTGTGGGGCGGTCCGATGAT	6114	AVGRSDD	7781	109.711
1136	AAAGAAAAAACCCCGCGAA	6115	KEKTTRE	7782	109.697
1137	CTGCTCCAATCGACCTACTTG	6116	LLQSTYL	7783	109.672
1138	AAGTCTAATTTGGAGGGTAAG	6117	KSNLEGK	7784	109.6285
1139	ACGAGGACGCCTTTTCTGGGG	6118	TRTPFLG	7785	109.613
1140	CAGTCGGATACGACTTCGATT	6119	QSDTTSI	7786	109.605
1141	GCGTGGTCTCAAGTCCTGACG	6120	AWSQVLT	7787	109.587
1142	ACTCAAGAACGACCACTAATC	6121	TQERPLI	7788	109.56
1143	GATGATAAGACTGGTCGGTAT	6122	DDKTGRY	7789	109.549
1144	TTTCCTTCGCATAATGGGGCG	6123	FPSHNGA	7790	109.54
1145	ATGCTGTCTCAAGTCTTAACA	6124	MLSQVLT	7791	109.536
1146	TCTGTGACGACTAATCTGATG	6125	SVTTNLM	7792	109.484
1147	GAACACAACCAAAACTTAC	6126	EHNSKTY	7793	109.4745
1148	TATGCGCATCCTGTGACTCAT	6127	YAHVPTH	7794	109.4635
1149	CCTAATCCGTCTCCGAGGCAG	6128	PNPSPRQ	7795	109.449
1150	CATATGGGTTTGAATGAGCTT	6129	HMGLNEL	7796	109.427
1151	AACAGTTTGCAAGCAAGTGCA	6130	NSLQASA	7797	109.402
1152	GACCTCGGTACGGCTAGAACC	6131	DLGTART	7798	109.388
1153	TACGACAGCCGACTCTACGCG	6132	YDSRLYA	7799	109.3853
1154	CCGAAGCCTGGGACGGGGGAG	6133	PKPGTGE	7800	109.3721
1155	AGTCTGAATGGGGTGTGGTT	6134	SLNGVLV	7801	109.3685
1156	CAGTCTAATTTGGTTATTAAT	6135	QSNLVIN	7802	109.359
1157	GCGTCTCCGGCGCAGACCGGC	6136	ASPAQTG	7803	109.331
1158	AACATGACCAACGAAAACGGA	6137	NMTNENG	7804	109.324
1159	TCACTTCGGACGGACGAATTC	6138	SLRTDEF	7805	109.31815
1160	ATATTGGACAACCACCGTTTC	6139	ILDNHRF	7806	109.2685

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1161	TTGATTAATATGAGTCAGAAT	6140	LINMSQN	7807	109.264	
1162	CCGCAAGACGTCCGCCAAACA	6141	PQDVRQT	7808	109.2625	
1163	CCCTTCGTAGCGAACGAACCA	6142	PFVANEP	7809	109.256	
1164	AATATTAATGATACTAAGAAT	6143	NINDTKN	7810	109.253	
1165	AATTTTAGTAGTGGTGATGTT	6144	NFSSGDV	7811	109.229	
1166	GAACGAAACGGACTAATAGAA	6145	ERNGLIE	7812	109.215	
1167	AATTCTCATGTTCTTAATAAT	6146	NSHVPNN	7813	109.2115	
1168	AACACAACCGTAGCTCGGGC	6147	NTTGSSG	7814	109.1925	
1169	TCAACCAGAAAAGAACACGAC	6148	STRKEHD	7815	109.1875	
1170	GCTGCTAATCCTAGTACGGAG	6149	AANPSTE	7816	109.1357	
1171	TCGGGTATGAATAGTAATAAG	6150	SGMNSNK	7817	109.129	
1172	AAGACGCTTGATAATAATGCT	6151	KTLDNNA	7818	109.09305	
1173	ACCGTAAACAAACAAGTCCG	6152	TVKQTSP	7819	109.0863	
1174	ATTTCTCAGGTGTCTTTTAAT	6153	ISQVSFN	7820	109.082	
1175	TTAGAAGTAAACCTGCAAACG	6154	LEVNLQT	7821	109.057	
1176	GAAATGCAAAACAAAACGCC	6155	EMQTKNA	7822	109.052	
1177	GCCGACAACAGAAACGACAAA	6156	ADNRNDK	7823	109.008	
1178	GCGTATGATACGCTGAATAGT	6157	AYDTLNS	7824	108.982	
1179	ACGATTCAGGATCATATTAAG	6158	TIQDHIK	7825	108.942	
1180	GACCCCACTAAAGTTGGATCC	6159	DPTKVGS	7826	108.939	
1181	TCCCTCCAACGAACCCCGAC	6160	SLQRTPD	7827	108.937	
1182	GCAAACGACTCTGCCAAAACA	6161	ANDSAKT	7828	108.9125	
1183	AAAAAAGTCGAACAAGAACCA	6162	KKVEQEP	7829	108.907	
1184	GCAAGTCGGGACCTGGGACAA	6163	ASRDLGQ	7830	108.906	
1185	TGGGAGAGTGATAAGTTTCGT	6164	WESDKFR	7831	108.876	
1186	AACCGCGAACAGAAGTTTAC	6165	NRGTEVY	7832	108.8187	
1187	AATATTAGTAGTATTAATCAG	6166	NISSINQ	7833	108.8155	
1188	GCCTCGAAAGGCTTCGGCCAC	6167	ASKGFGH	7834	108.7886	
1189	CAGTCGCAGAAATGTGACTCAG	6168	QSQNVTQ	7835	108.7825	
1190	AACGATACCAACTACAAATC	6169	NGYQLQI	7836	108.779	
1191	TGTACTAATGCGTCGGATCTT	6170	CTNASDL	7837	108.74	
1192	ACCGTCGCCTCGCCCAACACC	6171	TVASPNT	7838	108.738	
1193	AATACTGCTCCGCCGAATCAT	6172	NTAPPNH	7839	108.733	
1194	CTTTCTCAACAACGCGACTAC	6173	LSQQRDY	7840	108.69245	
1195	TGGAATCAGAAATGTGTCTCAT	6174	WNQNVSH	7841	108.6785	
1196	ACAGGTAGTTCAGACAGATTA	6175	TGSSDRL	7842	108.676	
1197	AACACAACGCCACCTAACCAC	6176	NTTPPNH	7843	108.602	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1198	GTGGTCGACTCAACATACCCG	6177	VVDSTYP	7844	108.592
1199	ACGGATGCTACGGGAGGCAT	6178	TDATGRH	7845	108.5905
1200	TTGTTTACTGCTGGGAGTACT	6179	LFTAGST	7846	108.58
1201	TTGCGTGATCAGACTAGTATG	6180	LRDQTSM	7847	108.566
1202	ATCGAAACGGACGCCACCGG	6181	IETDRHR	7848	108.531
1203	AGTGGGCCTGAGAATACGTTG	6182	SGPENTL	7849	108.526
1204	GACAACCAAAACGCCGACAGG	6183	DNQNADR	7850	108.486
1205	CATGATGGTTATGTTCTAAT	6184	HDGYVPN	7851	108.469
1206	CATATGTCTAGTTATTCGTCG	6185	HMSSYSS	7852	108.436
1207	AGTCGTCTGCAGACTCAGCAG	6186	SRLQTQQ	7853	108.4358
1208	TCATACACAGCAGGAAGACCC	6187	SYTAGRP	7854	108.417
1209	GTGCAGCAGAATAATATTAAT	6188	VQQNNIN	7855	108.376
1210	GATGCGAAGGCTCTTACGACT	6189	DAKALTT	7856	108.368
1211	AAGGATGAGCATCTTCATTAT	6190	KDEHLHY	7857	108.358
1212	CACGGTGACCGAACAGCTTTA	6191	HGDR TAL	7858	108.327
1213	AATTTTACTATTACGGAGGCG	6192	NFTITEA	7859	108.32
1214	GACACTCACATGAACAACTG	6193	DTHMNKL	7860	108.316
1215	CAACCAGGAGCCCCCAAACC	6194	QPGAPQT	7861	108.312
1216	GGGGAAGCACGCCGAGAAGCC	6195	GEARREA	7862	108.302
1217	AAGTCTCTTAGTAGTGATGAT	6196	KSLSSDD	7863	108.2375
1218	ATGAATACGACTTATAATGAG	6197	MNTTYNE	7864	108.231
1219	GCGGCCGCACTAGAAACAATA	6198	AAALETI	7865	108.223
1220	AACGTGCTCCCTACAGTAGC	6199	NVAPYSS	7866	108.21595
1221	TCTGCGGGTATGGTGAGCTG	6200	SAGMVSL	7867	108.2145
1222	TGCGACTTGTCACAATCATGC	6201	CDLSQSC	7868	108.133
1223	GTTTTGATTACGATGAGTTCG	6202	VLITMSS	7869	108.118
1224	CAAGTTGGGGCTCTAATGGTT	6203	QVGALMV	7870	108.037
1225	CAACGTACCTCGGAAGCGCCA	6204	QRTSEAP	7871	108.0315
1226	TTGGGTAATGGTAGTCTTTG	6205	LGNGSSL	7872	108.0135
1227	CCTAGTGTCGTTTGCCCTTA	6206	PSVRLPL	7873	108.007
1228	GATTCTGCTCCGAGTACTATT	6207	DSAPSTI	7874	108.003
1229	AATTATAATGGGGTTAATGTG	6208	NYNGVNV	7875	107.956
1230	TCGGCTCATCAGACGCCGACG	6209	SAHQTPPT	7876	107.932
1231	GATCATAGTAAGCAGATTTTCG	6210	DHSKQIS	7877	107.923
1232	GCCGCCAGCTTGTCGCAAAGC	6211	AASLSQS	7878	107.914
1233	CACGCCGACGTTGGCATGAGC	6212	HADV GMS	7879	107.888

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1234	CACGTGACAGTAACGTTAAAC	6213	HVTVTLN	7880	107.8865	
1235	AATTCTACGCATATTAATTCG	6214	NSTHINS	7881	107.8843	
1236	CTGGGGCTTGCTGGTCAGGTT	6215	LGLAGQV	7882	107.884	
1237	AGCAGTCAAGCCCACGGCCCA	6216	SSQAHGP	7883	107.872	
1238	GCTTTTAAGTCGGGTAGTATT	6217	AFKSGSI	7884	107.866	
1239	CACTCCCCATCCCACGACTCG	6218	HSPSHDS	7885	107.844	
1240	CCAAACGGCGAAAGTTCGCGA	6219	PNGESSR	7886	107.8303	
1241	ATTCTTACGCCTTTGGATAAG	6220	ILTPLDK	7887	107.825	
1242	TCCGCCTCTTACTCCAGGATG	6221	SASYSRM	7888	107.815	
1243	GAGGCGTTGCATGATCGGAAT	6222	EALHDRN	7889	107.793	
1244	GGTGAACAACAACGCCCC	6223	GEQHNAP	7890	107.778	
1245	GGGAATATGGTTACGCCTAAT	6224	GNMVTPN	7891	107.753	
1246	AACGCTCTCCTCAACGCACCT	6225	NALLNAP	7892	107.742	
1247	GCAAGTGACCTACAAATGACG	6226	ASDLQMT	7893	107.723	
1248	TCGTATGATATGCATACGAAT	6227	SYDMHTN	7894	107.705	
1249	AATATGTCGCATAGTACTCTG	6228	NMSHSTL	7895	107.6777	
1250	ACTGCCAACCACTCTCCG	6229	TANNHSP	7896	107.671	
1251	CAAGCCCCGCCAACAGCACAA	6230	QAPPTAQ	7897	107.668	
1252	AACTACCACGGAGACAACGTT	6231	NYHGDNV	7898	107.637	
1253	AGGGATAGTACTATTAGTCGG	6232	RDSTISR	7899	107.635	
1254	GTTTCTTCGCCTAATGGTACG	6233	VSSPNGT	7900	107.6095	
1255	TCCCCGAATCACGGTGAACGCA	6234	SRITVNA	7901	107.593	
1256	GTCGGAACAACCTCGAACGGC	6235	VGTTNSG	7902	107.575	
1257	CATACGAATCAGATGCAGCCT	6236	HTNQMQP	7903	107.5573	
1258	AAAAGCAACGCGGATTCTGGT	6237	KSNAGFG	7904	107.5065	
1259	AAAGAAAGCCTCGAAGACGTC	6238	KESLEDV	7905	107.49	
1260	GCGCAGGTTAATAATCATGAT	6239	AQVNNHD	7906	107.489	
1261	AACGCTTCTACCTACATGGAC	6240	NASTYMD	7907	107.479	
1262	ACGCTGTGATACGAATGCTAGG	6241	TSDTNAR	7908	107.4605	
1263	GAGAGTCGTATGCGTAGTATT	6242	ESRMRSI	7909	107.451	
1264	CGTGTGAAGACACCAACTCC	6243	RVEDTNS	7910	107.416	
1265	GCCTCTAACCACTACAAGCC	6244	ASNLQA	7911	107.3863	
1266	CGCTTACACGGCTCAGACTCG	6245	RLHGSDS	7912	107.358	
1267	ACCGTCGAACAAATAAACTCG	6246	TVEQINS	7913	107.349	
1268	AGGTCCGTACCATCACACAC	6247	RSVPSPH	7914	107.343	
1269	GAATACCTCGCCCTGGGACAC	6248	EYLALGH	7915	107.336	
1270	AATACTAATAATCAGGAGCAG	6249	NTNNQEQ	7916	107.332	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1271	AACTACGGTTCGGACGAATC	6250	NYGSGRI	7917	107.3205
1272	CGCCACGGGGACACCCGATG	6251	RHGDTPM	7918	107.303
1273	AACGACACCATCGGCAGACCA	6252	NDTIGRP	7919	107.2995
1274	TATGGGGAGCGTGCTAGGACG	6253	YGERART	7920	107.297
1275	GTTCTTGGGATGCAGAGGTCT	6254	VLGMQRS	7921	107.295
1276	CTTCATTTTCATGCTTCGCAG	6255	LHFHASQ	7922	107.281
1277	ACCGACACGCTCAGCGAAAGA	6256	TDTLSER	7923	107.247
1278	GGGACAGGTACCGTTGGATGG	6257	GTGTVGW	7924	107.203
1279	ACAGAAAGCCCCAAACTACTA	6258	TESPKLL	7925	107.2015
1280	ACGATTAGGAGTGAGGGTTTT	6259	TIRSEGF	7926	107.1495
1281	GCGTCTAGTTATATTAATAAT	6260	ASSYINN	7927	107.144
1282	TTACACCTTGGGTTATCATCT	6261	LHLGLSS	7928	107.1415
1283	GTCACCTGGCACTACCCCGGGA	6262	VTGTPPG	7929	107.137
1284	GTGACGTCGTCIGCTAGTGGT	6263	VTSSASG	7930	107.0606
1285	CAAAATGCACCTACACATGCAA	6264	QMHLHMQ	7931	107.057
1286	GGTACCATGAGTCTATTAATG	6265	GTMSLLM	7932	107.046
1287	TGCGCATCAGAAGTTTGCCAA	6266	CASEVCQ	7933	107.035
1288	AATCTTGTGATGAGTGGGACG	6267	NLVMST	7934	107.0225
1289	CAATCACTCAAAGACGGCACT	6268	QSLKDG	7935	106.991
1290	GCGTTGAATGGTCTGCTATT	6269	ALNGSGI	7936	106.976
1291	AGACACGTCGTCGCCGACTCC	6270	RHVVPDS	7937	106.9705
1292	CTGTATCATGATTCGCATCTT	6271	LYHDSHL	7938	106.963
1293	GGGAGTACGCCTATTACTTCT	6272	GSTPITS	7939	106.957
1294	CCCAACGACCAAATCAGCGGA	6273	PNDQISG	7940	106.936
1295	AGTGGAACAAGACAAATAC	6274	SGKQDKY	7941	106.925
1296	AGTGGCATGCITTCAGGGT	6275	SGHASQG	7942	106.8675
1297	AAGATGGGGAGTATTGAGGTT	6276	KMGSI	7943	106.864
1298	TCAACTTTAGACCGAAGCGAA	6277	STLDRSE	7944	106.8615
1299	ACGGAGCTTAGTGAGTATACT	6278	TELSEYT	7945	106.852
1300	GCCAACGGAGGAGGATACCCC	6279	ANGGGYP	7946	106.847
1301	GTAACCGAATCTAACTCTCTA	6280	VTESNSL	7947	106.83
1302	CCAGTCTACGACCGCGACGTC	6281	PVYDRDV	7948	106.812
1303	GATAATAATAAGCATGGTACT	6282	DNNKHGT	7949	106.806
1304	ATCTACGAAACCGTAACCTTG	6283	IYETVTL	7950	106.801
1305	ACTCAGACTGGTCATGTTTCT	6284	TQTGHVS	7951	106.7868
1306	CAAGCCGACCTCAGGTACAAA	6285	QADLRYK	7952	106.773

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1307	TGTAAGACGAATAATGCTGGT	6286	CKTNNAG	7953	106.749	
1308	GCCGGTCACCAACAACCTGGCC	6287	AGHQQLA	7954	106.7459	
1309	GATAGGGATATGGAGGGTGTT	6288	DRDMEGV	7955	106.742	
1310	GATCAGCCGGGGTATGTGCGT	6289	DQPGYVR	7956	106.7387	
1311	GATGCTATGCTTGCTCATCCG	6290	DAMLAHP	7957	106.735	
1312	GCCCTTAACCTGTACTCCAGC	6291	ALNLYSS	7958	106.732	
1313	CTACTATCTAAAGGGGACTCC	6292	LLSKGDS	7959	106.709	
1314	TCGAGTATTAGTCTGCGGTAT	6293	SSISLRY	7960	106.645	
1315	GGGTCGAGCCAACACCACGAA	6294	GSSQHHE	7961	106.62	
1316	TCGATTGGGTATTCGCCTCCG	6295	SIGYSPP	7962	106.5773	
1317	CACTCCAACGCGACTACGATA	6296	HSNATTI	7963	106.567	
1318	TCGGCACACGACGCAAGACTA	6297	SAHDARL	7964	106.5665	
1319	GTTACACCGCAGACACAATA	6298	VHTADTI	7965	106.564	
1320	CGAGACGGCTCTACTAAAGTT	6299	RDGSTKV	7966	106.55855	
1321	TTGCAGGAGTCTCTTCCTGGT	6300	LQESLPG	7967	106.542	
1322	TTAGACTACACCCCTCAAAC	6301	LDYTPQN	7968	106.519	
1323	GGACCAAGTTCGCACATCGTT	6302	GPSSHIV	7969	106.507	
1324	AGCGCCGACACCCGGTCCCCC	6303	SADTRSP	7970	106.466	
1325	ATGATGAAGAGTGAGGAGAAT	6304	MMKSEEN	7971	106.425	
1326	GGTATGACGAGTGAGTTGACG	6305	GMTSELT	7972	106.417	
1327	GTAGACACCTACAGCGGTCTG	6306	VDTYSGL	7973	106.415	
1328	GGGATGAGGGATACGCCGCCG	6307	GMRDTPP	7974	106.385	
1329	GAGCATGATGTGAGTACGCGT	6308	EHDVSTR	7975	106.302	
1330	GAGGTGGTGAAGACTACTCAT	6309	EVVKTTH	7976	106.269	
1331	GTTTACGACAACGTTTCTTCT	6310	VYDNVSS	7977	106.268	
1332	CTCATGAAAGACATGGAATCC	6311	LMKDMES	7978	106.2609	
1333	CCTCTTCATGTTGCTTCTCCT	6312	PLHVASP	7979	106.239	
1334	GAAGTACGCGACCAAAAAACA	6313	EVRDQKT	7980	106.2075	
1335	CCAACTCCCTACTACACCGCC	6314	PTPYTA	7981	106.124	
1336	AACAACCTACGCCTACTCCGCT	6315	NNYAYSA	7982	106.1085	
1337	CITGTTGATACGGATAGGAAT	6316	LVDTRN	7983	106.108	
1338	TATCCGGCTGATCATCGGACT	6317	YPADHRT	7984	106.088	
1339	TCTGCAACAACGAACCACGGA	6318	SATTNHG	7985	106.066	
1340	CGTGATGATCAGCAGCTTGAT	6319	RDDQQLD	7986	106.064	
1341	GGAGCGGACAATCTCACGTG	6320	GAGQSHV	7987	106.0351	
1342	GATAGGACTTATCATGAGGTG	6321	DRTYHEV	7988	105.996	
1343	GATGGTAATAATACGACTTAT	6322	DGNNTTY	7989	105.99	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1344	GTGCATATGGAGTCGTATGCG	6323	VHMESYA	7990	105.983
1345	TGGTACGAAACAATCAGCCCG	6324	WYETISP	7991	105.959
1346	CTGTTGGGGGCTCATCAGCCG	6325	LLGAHQF	7992	105.9002
1347	CACGTACCTAACACTGAAGCA	6326	HVPNTEA	7993	105.893
1348	AATTCTCAGAACTCCTCAGGCT	6327	NSQNPQG	7994	105.8895
1349	CTACAAGACCGGGCAACGAAC	6328	LQDRATN	7995	105.864
1350	ATTGTGAATCAGCATTCTGGAG	6329	IVNQHSE	7996	105.832
1351	TTTGAGCAGGGTAAGGTTGAG	6330	FEQKQVE	7997	105.811
1352	GTGGCGACGGGTGTGTTTGCT	6331	VATGVFA	7998	105.808
1353	GACAAAATACAAAACGAAACA	6332	DKIQNET	7999	105.784
1354	ACGGACAACCCGCTCTACAAA	6333	TDNPSYK	8000	105.771
1355	GGCGTGAACACAAAAATCGAA	6334	GVNTKIE	8001	105.7665
1356	GGCTCTCACAACGGCCAGCC	6335	GSHNGPA	8002	105.763
1357	TCCAACATGGGCGTAGCCTCT	6336	SNMGVAS	8003	105.76
1358	AACACGGACACTAACGAAAAA	6337	NTDTNEK	8004	105.759
1359	TCTGCGCTTTTGCGGATGGAT	6338	SALLRMD	8005	105.707
1360	CCTCAACTAAGCGGCACAGCG	6339	PQLSGTA	8006	105.6914
1361	TCTATTGTTAATAATGGGGCT	6340	SIVNNGA	8007	105.684
1362	AGCCTAGACCACGCCCTCTA	6341	SLDHAPL	8008	105.661
1363	GACCACTCGAAACAAACTCT	6342	DHSKQNS	8009	105.653
1364	CACAGTGACATGGTCAGCGGC	6343	HSDMVSG	8010	105.642
1365	CAGCATCGTGCAGGATGTG	6344	QHRAQDV	8011	105.5608
1366	GGTAGTACTAAGTCTGGGCAG	6345	GSTKSGQ	8012	105.5509
1367	ACAATGAGCGTAACTCTGGAA	6346	TMSVTLE	8013	105.526
1368	TATAATAATGGTGGCATGTT	6347	YNNGGHV	8014	105.516
1369	GGTACTGCTGAGAATACGAGT	6348	GTAENTS	8015	105.494
1370	AATAGTTATGATGCGACGAGG	6349	NSYDATR	8016	105.488
1371	AGCGTCAACAACATGCGACTC	6350	SVNNMRL	8017	105.4477
1372	CTTAACCTACAATACACTCTG	6351	LNLQYTL	8018	105.443
1373	GAGGCGCAGACCGGTGGGTT	6352	EAQTGWV	8019	105.443
1374	CCCGCTGAAGGAAACAACCGT	6353	PAEGNNR	8020	105.442
1375	TCTCTGGGTGGGAATCCGCCT	6354	SLGGNPP	8021	105.4335
1376	TATAATAGGGATAATGTTCT	6355	YNRDNGS	8022	105.4285
1377	TTGACTGATCCTAAGGGGCAG	6356	LTDPKGQ	8023	105.404
1378	ACCCCAACAGGCACCAACAAA	6357	TPTGTNK	8024	105.403
1379	GTTCACGCTAACGCTACATTA	6358	VHANATL	8025	105.38

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1380	CGCGAAATAGTGCCTCAAAC	6359	REIVHSN	8026	105.376	
1381	TACGCCGTCGCGATAGGCACA	6360	YAVAIGT	8027	105.366	
1382	AACACAACACCTCCCGACCAC	6361	NTTPPDH	8028	105.348	
1383	GTTATTCTAGTCTGATAATACG	6362	VIQSDNT	8029	105.32	
1384	GTTCCGGCGCATCTCGGGGT	6363	VPAHSRG	8030	105.305	
1385	CAAAACAGTGACCTCGCCAGC	6364	QNSDLAS	8031	105.296	
1386	CGCATCGTAGACAGTTGGGA	6365	RIVDTLG	8032	105.2825	
1387	CACACTTACTCACAAGCAGAC	6366	HTYSQAD	8033	105.267	
1388	ACGGCTCCATCCGTAGGGTCT	6367	TAPSVGS	8034	105.259	
1389	AACGTGGGCACCGACAGAGAC	6368	NVGTDRD	8035	105.231	
1390	GGGATTAATCGTACTAGTGAG	6369	GINRTSE	8036	105.2145	
1391	GTAGAAACAGACAGCTTAATA	6370	VETDSLI	8037	105.195	
1392	CACTCCGACGCGGTGACGGT	6371	HSAAGDG	8038	105.195	
1393	GATGCTGGGATTAGTTCTTAT	6372	DAGISSY	8039	105.102	
1394	TGCACCGCCACAAAATGCTCA	6373	CTATKCS	8040	105.0959	
1395	CGCATAGACACTCTCCTAGTC	6374	RIDTLLV	8041	105.089	
1396	GTATCACAATCACACGACGTG	6375	VSQSHDV	8042	105.087	
1397	GCACTACCATCCCACTCCTCC	6376	ALPSHSS	8043	105.059	
1398	GGGAAACCTGCGGAAGCGCCG	6377	GKPAEAP	8044	105.055	
1399	TGGAATAGTCCGGGTGAGGCG	6378	WNSPGEA	8045	105.053	
1400	AGGCTGGAGCGTCCGGATTAT	6379	RLERPDI	8046	105.04	
1401	ACGCGGGAGAGTCTGGTGGAT	6380	TRESLVD	8047	105.022	
1402	AGACACGAAGGTCCGTACTCC	6381	RHEGPYS	8048	105.002	
1403	GTTTTGTCTGATAAGGCGTTT	6382	VLSDKAF	8049	104.981	
1404	ACTAGTGCAGCTGATTCGATG	6383	TSATDSM	8050	104.908	
1405	ACTGAGCCGCTCCGATGTCT	6384	TEPLPMS	8051	104.869	
1406	ATGCCTTACGTCGGGACAGTA	6385	MPYVGTV	8052	104.838	
1407	CGTGATTATCTCTACTGAT	6386	RDYSPTD	8053	104.836	
1408	CGGAATGGTGTACTACGGAT	6387	RNGGTTD	8054	104.7625	
1409	ATGATGGGCGCGACAACGAAA	6388	MMGATTK	8055	104.7503	
1410	GCTGCCGTGCGGAGACACC	6389	AAVGSDT	8056	104.742	
1411	CTTGTGAATAATGATGGGACT	6390	LVNNDGT	8057	104.7255	
1412	AGTTCGACTCCGACAGTACT	6391	SSTPQDT	8058	104.713	
1413	AGTCTGCGGATGGAGAATAGT	6392	SLRMENS	8059	104.7025	
1414	GTGCAGGGGACAGCCGGCTGG	6393	VQGQTGW	8060	104.688	
1415	CTAGGTTTCACACCCCAACCG	6394	LGFTQPQ	8061	104.677	
1416	TCGGTTGCTAAGGATCAGACG	6395	SVAKDQT	8062	104.675	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1417	CCGCGGCATGAGTTGAGTAAT	6396	PRHELSN	8063	104.645
1418	AAAATGGGATCGAACCCGCA	6397	KMGSNPA	8064	104.6241
1419	GAGGCGACTCATGGTTCTTAT	6398	EATHGSY	8065	104.613
1420	CCTGAGGTTGCGTGTCTGGG	6399	PEVACPG	8066	104.595
1421	GTGAATACGCGGAGGTTACG	6400	VNTREVT	8067	104.583
1422	ACGGCTCGTGCGATTGATATG	6401	TARAIDM	8068	104.551
1423	ACCGACGGCGCCCTGGGTTAC	6402	TDGALGY	8069	104.5325
1424	GGGTCGCAATACGGAACCGC	6403	GSQYANR	8070	104.524
1425	GAAATGGGTAAACCAATACCCA	6404	EMGNQYP	8071	104.453
1426	CCGTCGCACTCGCTGAAACA	6405	PSTLAET	8072	104.449
1427	CGCATAGGCGTTGGAGCACCA	6406	RIGVGAP	8073	104.4405
1428	CTGAGTGTGAAGGAGGAGATT	6407	LSVKEEI	8074	104.435
1429	TATACTACTCATGAGAGTGGG	6408	YTTHESG	8075	104.433
1430	CTTACTGCTGTCTGACTGTT	6409	LTAVLTV	8076	104.424
1431	CTGCAGACTTCTGTTGCTACT	6410	LQTSVAT	8077	104.42
1432	ACTGTGCGTTCGCCTCAGCCG	6411	TVRSPQP	8078	104.391
1433	CATCTGATGGTACTCGGCCG	6412	HPDGTRP	8079	104.375
1434	GGAGTAACAATCGGTAGCAGG	6413	GVTIGSR	8080	104.3732
1435	ACATACGCCTCTACTGAAGCG	6414	TYASTEA	8081	104.3675
1436	AGGAGTAGTCCTGCGACAAT	6415	RSSPATN	8082	104.355
1437	ATCGGGTCGCCGTTGGCCAAC	6416	IGSPLAN	8083	104.35
1438	GCGTCGACTGAGTCTCATGTG	6417	ASTESHV	8084	104.344
1439	ATTGCGCAGAATGAGACGTAT	6418	IAQNETY	8085	104.336
1440	ATGGAGTCTAAGCCGTGGCAG	6419	MESKPWQ	8086	104.307
1441	TTAGAAAACCCAACACCAGCA	6420	LENPTPA	8087	104.305
1442	CCCAACCCAGTCCAAGACAA	6421	PNPSPRQ	8088	104.258
1443	TCGACTAGTAATCCGCCTTAT	6422	STSNPPY	8089	104.242
1444	TATTTGACGGATACTCCTACT	6423	YLTDTPT	8090	104.241
1445	ATACGTGCATTGATGACGGAC	6424	IRALMTD	8091	104.237
1446	CCTATGGGTACGGATACGGTT	6425	PMGTDTV	8092	104.221
1447	ACGAGGACTCAGGGGACGTCT	6426	TRTQGTS	8093	104.19625
1448	TCTAATAATATGAATCAGGCG	6427	SNNMNQA	8094	104.187
1449	GAAGACTCTGTAAACCACATC	6428	EDSVNHI	8095	104.185
1450	TCTGTTGTGCCTACGATAAG	6429	SVVPTDK	8096	104.174
1451	GTGCGCGCGTICAAGACGCC	6430	VRGVQDA	8097	104.167
1452	CATGATGTGACTGTGCGGAAT	6431	HDVTVRN	8098	104.164

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1453	CATAATAATCATGCGGGTGAG	6432	HNNHAGE	8099	104.153
1454	GGTAATATGAATCATAGTATT	6433	GNMNHSI	8100	104.15
1455	GGTGTGCATACTCATACTGTT	6434	GVHTHTV	8101	104.139
1456	TTTTTGCCGCGAGCTGGGGCAG	6435	FLPQLGQ	8102	104.094
1457	TGGGCCAACATGTCCGCACCA	6436	LANMSAP	8103	104.093
1458	GTTTCGAGAGACGAAACACCT	6437	VRRDETP	8104	104.0585
1459	TGCCGCGACAACGTCTTAGCT	6438	CRDNVLA	8105	104.046
1460	ATGTTGGCTTCTCGGGTGCCT	6439	MLASRVP	8106	104.0205
1461	GTCAGAACAGTCCTTCAACAA	6440	VRTVLQQ	8107	104.017
1462	TCGAATCAGAAATGTGGATTGG	6441	SNQNVDW	8108	104
1463	ACTGAGGTTACGGGGGATAGT	6442	TEVTGDS	8109	103.965
1464	GAAAGTGCCACATCTCTAAAA	6443	ESATSLK	8110	103.9355
1465	AACCAACCCGCGACCAAGCTCA	6444	NHPAPSS	8111	103.9235
1466	TACGGTAACGCGAACACCGTA	6445	YGNANTV	8112	103.92115
1467	CAAAACGACAAATCTGACAAC	6446	QNDKSDN	8113	103.9165
1468	AGTCAGGCTCAGATTCTGTGTT	6447	SQAQIRV	8114	103.915
1469	TTTCAGCGTGATGTTGGTCAT	6448	FQRDVGH	8115	103.8651
1470	CTGATGAATCGTAATGCTCCT	6449	LMNRNAP	8116	103.8648
1471	GCGGGCAGTTCGCCATCACGC	6450	AGSSPSR	8117	103.8635
1472	TTATTCCACAGCCAAATGACC	6451	LFHSQMT	8118	103.849
1473	ATGATGTCTAACAGCCTCGCG	6452	MMSNSLA	8119	103.8275
1474	GTTACCACCGTCCTCCAATCA	6453	VTTVLQS	8120	103.818
1475	GGTAGTCAGCGTGCTATGAAT	6454	GSQRAMN	8121	103.8086
1476	GCATCCGGCGCACGCTACGTC	6455	ASGARYV	8122	103.7981
1477	AAAACTACGACAGTGACTCA	6456	KNYDSDS	8123	103.794
1478	GTGGGTTCTGGGGTTGGGGTT	6457	VGSGVGV	8124	103.793
1479	CGTTCTGACCTTACTGAAAGT	6458	RSDLTES	8125	103.736
1480	AGGGCGGAGTTTATTGATACG	6459	RAEFIDT	8126	103.735
1481	ACATCTGAAATGCGGACAGCC	6460	TSEMRTA	8127	103.725
1482	GAGTTGGATCATCTTTCGCAT	6461	ELDHLSH	8128	103.714
1483	ACACAAGCAGGTCTTTCGTCA	6462	TQAGLAS	8129	103.696
1484	GCGGCTCAGCATCATGATACG	6463	AAQHHTD	8130	103.693
1485	GGCGGCGCACACACTCGTGTA	6464	GGAHTRV	8131	103.676
1486	GCCTACGGTATACACGAAGTG	6465	AYGIHEV	8132	103.653
1487	GCGATGCTGCGTATGGAGCAG	6466	AMLRMEQ	8133	103.652
1488	ACGGATCGTTCGCGGCTGGGG	6467	TDRSRLG	8134	103.622
1489	GAGAGGGAGCCTCCTAAGAAT	6468	EREPPKN	8135	103.621

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1490	GTTGTTAAGGAGATTAAGCTG	6469	VVKEIKL	8136	103.6125
1491	CACACCGGCCAAACACCATCA	6470	HTGQTPS	8137	103.5945
1492	GTGTCTCTGAGTTCGCCTCCG	6471	VSLSSPP	8138	103.563
1493	GGGGCAGGAAACCTGGGTACC	6472	GAGNLGT	8139	103.5615
1494	GCACGAGACGACACGATACAA	6473	ARDDTIQ	8140	103.523
1495	GGGACTTATACTAATATGCCG	6474	GTYNMP	8141	103.522
1496	ATGCTGGGGGGTTTTGCGCAG	6475	MLGGFAQ	8142	103.5051
1497	CCATCCGAAATGAGGGCCGTA	6476	PSEMRV	8143	103.503
1498	CGTATAAGCCCAGAAAACCTCA	6477	RISPENS	8144	103.497
1499	AAGATGGGTGGTTCTCAGAGT	6478	KMGGSQS	8145	103.477
1500	GGTTTGATGGCGCATGTGACT	6479	GLMAHVT	8146	103.464
1501	TCACGTCAAACAGCGCTAACA	6480	SRQTALT	8147	103.4599
1502	AGTGATCTGAATCTTCCGCCG	6481	SDLNLPP	8148	103.455
1503	TATGTGTCTGATTATTTGCAT	6482	YVSDYLH	8149	103.393
1504	ACTAATGATAATAGTGATCGT	6483	TNDNSDR	8150	103.374
1505	TACTTAATGCACGACAGCGCA	6484	YLMHDSA	8151	103.369
1506	GGCTCTCGGAACGACCCACA	6485	GSRNGPT	8152	103.3096
1507	AAAAACGGTGTTATAAACGAC	6486	KNGVIND	8153	103.292
1508	GAGTCTGTTGCTAATCTTAAG	6487	ESVANLK	8154	103.162
1509	GCATCGGACTCGACGACACCA	6488	ASDSTTP	8155	103.149
1510	CTGAACGTTAGTTCATCCAAA	6489	LNVSSSK	8156	103.149
1511	GAGGCTAAGGGTTTTGGTCAT	6490	EAKGFGH	8157	103.1228
1512	GGTACGAGTGCAGAGAGTCGG	6491	GTSAESR	8158	103.111
1513	ATGCACAACCTACCTCATAC	6492	MHNLPST	8159	103.10145
1514	GTCTTCACAGAAATAGAATCG	6493	VFTEIES	8160	103.101
1515	ACTCAAACCTTCTACCTGGACC	6494	TQTSTWT	8161	103.094
1516	CCTATGAATAAGGATATTTTG	6495	PMNKDIL	8162	103.07
1517	AAAGAATCTGAATACAGAGTT	6496	KESEYRV	8163	103.07
1518	TCGACGAATTCTGAGCGGTT	6497	STNSEAV	8164	103.068
1519	GATACGGCGAATCGTTCGACT	6498	DTANRST	8165	103.03715
1520	CCTAAGGCTCCGCTTAATAAT	6499	PKAPLNN	8166	103.032
1521	TTAGCTACATACCCCTCCAC	6500	LATYPSH	8167	103.028
1522	GCTACGGTTCAGTCGGTTGAT	6501	ATVQSVD	8168	103.011
1523	AATTCGATGGGTAATGGGGGT	6502	NSMGNGG	8169	103.009
1524	GATCATAGTGAGCAGAATTCG	6503	DHSEQNS	8170	102.995
1525	ACTTTTTTGCCTCAGCTTGGG	6504	TFLPQLG	8171	102.994

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1526	GGGTTTACTAATACGAGTAAG	6505	GFTNTSK	8172	102.9895	
1527	ACGATGAATTATAGTCATACT	6506	TMNYSHT	8173	102.962	
1528	AGTATCGGATTCTCAGTAGGC	6507	SIGFSVG	8174	102.9565	
1529	AGTGAGAATCGGGCTGGTAAT	6508	SENRA GN	8175	102.945	
1530	AGTCTTAATCTGCATAGTGTG	6509	SLNLHSV	8176	102.93	
1531	CATGAGAGTCATTATGTTAGT	6510	HESHYVS	8177	102.921	
1532	AATGTTGTTAATGGGATGGAT	6511	NVVNGMD	8178	102.908	
1533	CACCTCCGACAAAGTCTCCTCA	6512	HSDKVSS	8179	102.8992	
1534	AAATCTGTAGGCGACGGGAGA	6513	KSVGDGR	8180	102.8979	
1535	AGGCAGGTTGAGCAGTCTGAT	6514	RQVEQSD	8181	102.889	
1536	AGGGAGCTGGTGAATACGGAT	6515	RELVNTD	8182	102.87	
1537	AACTACAGGGACATCACAATG	6516	NYRDITM	8183	102.8605	
1538	GCCAGCCTTGACCGCCTTCCA	6517	ASLDRLP	8184	102.857	
1539	AGACAACCTGCTTCTCTCCCA	6518	RQLASLP	8185	102.846	
1540	GTCAGCAAAACCAAGACTCG	6519	VSKTKDS	8186	102.832	
1541	AACGTATACGAAGGGCACCGC	6520	NVYEGHR	8187	102.815	
1542	CTAGAACAACCTACGGGTCCCA	6521	LEQLRVP	8188	102.815	
1543	ATGACCTACACATCCCCAACC	6522	MTYTSPT	8189	102.807	
1544	AACTCCCACACCGACAGAGGA	6523	NSHTDRG	8190	102.801	
1545	GTGGCTGGGGGACTTCGGAG	6524	VAGGTSE	8191	102.789	
1546	GTCGACGCACACAGGGCTAAC	6525	VDAHRAN	8192	102.77	
1547	CGGGCAGACATGACTCCCTTA	6526	RADMTPL	8193	102.77	
1548	GGACACGAACAACTGACGCA	6527	GHEQTDA	8194	102.764	
1549	TACATCGCGGGAGGCGACCAA	6528	YIAGGDQ	8195	102.75	
1550	TACGGCGACCTAATACAGTC	6529	YGD LTTV	8196	102.737	
1551	AGATTAGACCTGCAAGAACAC	6530	RLDLQEH	8197	102.719	
1552	CACCTTAACCCGGCGGCCCAA	6531	HLNPAAQ	8198	102.719	
1553	GGGGTTAACGAACAAACAAAC	6532	GVNEQTN	8199	102.703	
1554	CGTCGGTTGAGTACGGATCTT	6533	RRLSTD L	8200	102.702	
1555	GGATCCACAGGCCTACCCCG	6534	GSTGLPP	8201	102.7015	
1556	GACGACATGGTCAAAACTCA	6535	DDMVKNS	8202	102.6815	
1557	GTTATAGACCTAGTCACTCGC	6536	VIDLVTR	8203	102.673	
1558	GGAGGCCTTACCAACGGTCTA	6537	GGLTNG L	8204	102.67	
1559	CGTATGGAGGAGACTGCTTAT	6538	RMEETAY	8205	102.6535	
1560	ACCGACATCTCCGGTTACGGA	6539	TDISGYG	8206	102.642	
1561	CAGGTTAATCATAATACTAGT	6540	QVNHNTS	8207	102.637	
1562	GCGACTACTGAGGATGTTCTGT	6541	ATTEDVR	8208	102.626	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100					
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100
1563	TGGAGCATCAAAAACCAACA	6542	WSIKNQT	8209	102.586
1564	TCCCCTACCAGCAACACAATA	6543	SPTSNTI	8210	102.584
1565	ATGAAAAACTCTGGATTGCGAC	6544	MKNSGFD	8211	102.583
1566	CTTGTGCTGAGCGTTTGCCG	6545	LVAERLP	8212	102.552
1567	GGTGAAACTAACTTCCCAACT	6546	GETNFPT	8213	102.532
1568	AATGGTAAGCTGGGTACGACT	6547	NGKLGTT	8214	102.52735
1569	AACCTAGTAGCGTACACGAAA	6548	NLVAYTK	8215	102.5245
1570	TGGCAGCTTACGACGAGTCAT	6549	WQLTTS	8216	102.497
1571	AGTTTGGACCTAGGAGGCAAC	6550	SLDLGNN	8217	102.491
1572	AACGAAAGCACCAGAAATCT	6551	NESTKES	8218	102.483
1573	GGTTTGTATGGTAAGCAGCTT	6552	GFDGKQL	8219	102.462
1574	CATCTGTATATTTGCGCGGAT	6553	HLVISAD	8220	102.442
1575	TTACTTCCAAACAACCCAC	6554	LLPNNTH	8221	102.424
1576	TCCGGAATGGCCGGCCTTTCC	6555	SGMAGLS	8222	102.423
1577	ATCACCTCACTCCCGAAACC	6556	ITSLPET	8223	102.414
1578	GAGCTTAAGGAGAGTCAGAAG	6557	ELKESQK	8224	102.408
1579	AATATTGTGCAGGATTATCCG	6558	NIVQDYP	8225	102.404
1580	TCAGAAAACACCTCTGTACCC	6559	SENTSVP	8226	102.388
1581	GACCCCAACCAACCCAAAACA	6560	DPNQPKT	8227	102.376
1582	GCGGGTTTGGATGTGAATACG	6561	AGLDVNT	8228	102.372
1583	TCTCATGAGATGAATAATGGT	6562	SHEMNNG	8229	102.366
1584	TCTTACGCCATAAACCAATCA	6563	SYAINQS	8230	102.335
1585	GGTCATCTGCCTGCGGCTAAG	6564	GHLPAAK	8231	102.315
1586	GAGTTGGGTAATAAGACGGCT	6565	ELGNKTA	8232	102.311
1587	CTTGAGTCTACTCGTAAGGCT	6566	LESTRKA	8233	102.31
1588	ACTCAAGCAACTCTGAAGCA	6567	TQGNSEA	8234	102.31
1589	ATCTCTATAGACTCCGCTATG	6568	ISIDSAM	8235	102.301
1590	GAGTTTCAGAGGATTCGTGAG	6569	EFQRIRE	8236	102.259
1591	GCTAGTCTCTCCGACCAGCC	6570	ASLSAPA	8237	102.227
1592	GACAGCCAAATCACAAGACTA	6571	DSQITRL	8238	102.218
1593	GGCCACGAAAACATGGGCGTG	6572	GHENMGV	8239	102.215
1594	ATGTCGGCGGGGCATCCTACG	6573	MSAGHPT	8240	102.207
1595	CACGCTCCAAGCGCGCCATA	6574	HAPSGAI	8241	102.2
1596	ACGACTATTACTAATTCGGTT	6575	TTITNSV	8242	102.187
1597	CCTCAGCATCAGCATGAGCAT	6576	PQHQHEH	8243	102.1805
1598	CAATACTCGATGGACACGCGC	6577	QYSMDTR	8244	102.173

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice-score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID NO:	Amino Acid seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1599	CTTTATGAGGTTGGTACTCCT	6578	LYEVGTP	8245	102.165	
1600	GGTGAGACTATGCGTCATAAT	6579	GETMRHN	8246	102.119	
1601	ATGACAATAACCGTCGAACCG	6580	MTITVEP	8247	102.096	
1602	GCGCAGCATCCTGAGCGTTCG	6581	AQHPERS	8248	102.084	
1603	ACGCATGTTGCTAAGCCTGAT	6582	THVAKPD	8249	102.082	
1604	ATGACTGCTAACTTGGTGGAA	6583	MTANLVE	8250	102.076	
1605	AATAGGCAGCGGGATTTTGAG	6584	NRQRDFE	8251	102.073	
1606	TCAAACAGCGCCGACGCGGGG	6585	SNSADAG	8252	102.047	
1607	GGTGAGTATGGTGCCTCGGTT	6586	GEYGASV	8253	102.037	
1608	GACGGCATGGTCAGGTCGACA	6587	DGMVRST	8254	102.025	
1609	AATGGTCAGCTGCTGGCTAAT	6588	NGQLLAN	8255	102.023	
1610	TCCGCGGGGATGACATTGGAC	6589	SAGMTLD	8256	102.016	
1611	GATCATGTGCATCTGACTTAT	6590	DHVLHTY	8257	102.008	
1612	ACGACACTAACGCAAACGGAC	6591	TTLTQTD	8258	102.003	
1613	GTGCAGTTGGCTGATGGGCAT	6592	VQLADGH	8259	102.003	
1614	ACTGACTCATCTGCAGACTCC	6593	TDSSADS	8260	101.981	
1615	GCGATGAATGTGCGGAGTGAT	6594	AMNVRSD	8261	101.9805	
1616	GGTGATATTTCTTATAGGGTT	6595	GDISYRV	8262	101.977	
1617	ATGGGGTATGTTGATAGTCTG	6596	MGYVDSL	8263	101.953	
1618	CTTTATTTGGCGGCGGCTTCG	6597	LYLAAAS	8264	101.948	
1619	TCATCCCCAGACTCGTACAGA	6598	SSPDSYR	8265	101.921	
1620	AGTTATAATGTGGATCTGCAT	6599	SYNVDLH	8266	101.892	
1621	CAACACACCGCCACCCCATG	6600	QHTAHPM	8267	101.892	
1622	GCAGTTATGGCTACACACCCC	6601	AVMATHP	8268	101.87	
1623	ATTAGTCCGAGTGTCTTAAT	6602	ISPSASN	8269	101.855	
1624	ACTTTGGATAATAATCATTCT	6603	TLDNNHS	8270	101.833	
1625	AGTGGGTCTTATGTGGCGACG	6604	SGSYVAT	8271	101.806	
1626	ATGGCGGCTCCGCCGAGCAT	6605	MAAPPEH	8272	101.802	
1627	CAGACTGCGTCTGGTGATACT	6606	QTASGDT	8273	101.7725	
1628	GAGTCTAAGACTGTGGTTATT	6607	ESKTVVI	8274	101.7695	
1629	ACGGTATTACCACAATCAGAC	6608	TVLPQSD	8275	101.744	
1630	CCATTAAACGCGAACGGCTCC	6609	PLNANGS	8276	101.7415	
1631	CCCTGAACACAGGATTAACC	6610	PLNTGLT	8277	101.718	
1632	GCCATAACGATAATAGGCACT	6611	AITIIGT	8278	101.711	
1633	AATCCTAGTGCATTAGTTAT	6612	NPSAISY	8279	101.687	
1634	ACAGAACACGAAAAATCCACT	6613	TEHEKST	8280	101.66205	
1635	GCTGAGAGTCAGTGGCGTCG	6614	AESQLAS	8281	101.655	

TABLE 3-continued

MHCK7/CK8 Combined Results mRNA Second Round of Capsid Variant Selection in C57BL6 mice—score capped at 100						
Variant ID for Table	Nucleotide Sequence	SEQ ID	Amino Acid NO: seq.	SEQ ID NO:	Sum of muscle mRNA score_capped at 100	
1636	GTGCTTAAGGGTACGTTTCCG	6615	VLKGTFF	8282	101.652	
1637	TCGTTCCGCGAAATAACGACT	6616	SFAEITT	8283	101.651	
1638	CCGTTAAACGGCCGCGTAACC	6617	PLNGRVT	8284	101.642	
1639	TCCGAACGCCCAATCGTCA	6618	SERPQSS	8285	101.579	
1640	GCTCAGCTTCAGGATTCGGTG	6619	AQLQDSV	8286	101.568	
1641	CCCAACCGTGTAACAGCACCC	6620	PNRVTAP	8287	101.5542	
1642	GCGCTTATTGTTTCGAGTATG	6621	ALIVSSM	8288	101.54	
1643	GCGCATGGTGCTTTTCCGGTT	6622	AHGAFPV	8289	101.495	
1644	GAGGCTTATCAGACTGAGAAG	6623	EAYQTEK	8290	101.49	
1645	GCTGCGGCTTCGCCTTTGGCT	6624	AAASPLA	8291	101.484	
1646	CCCCAAGCCACTCTCAACAAC	6625	PQATLNN	8292	101.432	
1647	ACGAGGGGTGATATGGAGTTT	6626	TRGDMEF	8293	101.424	
1648	AGCAACCTAGGCGAAGCATCT	6627	SNLGEAS	8294	101.423	
1649	GGAATCACCGBAAGCCCCGGC	6628	GITGSPG	8295	101.42	
1650	GGGTTTGAGACGAGTAGTCCT	6629	GFETSSP	8296	101.369	
1651	CCCGCGAGAAGCGACGCCCTT	6630	PARSDAL	8297	101.359	
1652	CATGCTAATTATGTTGAGGTG	6631	HANYVEV	8298	101.345	
1653	GTGACTCGTAGTACGAAGGAG	6632	VTRSTKE	8299	101.32381	
1654	GATGTTGCGTTGAGGTCGAAT	6633	DVALRSN	8300	101.254	
1655	GAGTCTGATTTGCGTCAGCGG	6634	ESDLRQR	8301	101.225	
1656	CCGTTACTCGCAGCGAACCCG	6635	PLLAANP	8302	101.207	
1657	ATAAACGCCGCGCACAGGCC	6636	INAAHRP	8303	101.163	
1658	GCTCGGAGAGACGTAAACTCG	6637	ARRDVNS	8304	101.15	
1659	AGTATGGATAAGGTGGAGAAG	6638	SMDKVEK	8305	101.144	
1660	AACGTCAGCGCACGGGAAACA	6639	NVSARET	8306	101.113	
1661	CTGACGACGGCTGGTATGTGG	6640	LTTAGMW	8307	100.9605	
1662	GCGCGGGCAGAAGGGGTCTTC	6641	ARAEGVF	8308	100.9325	
1663	CCGAGTGATCATATGCGGACT	6642	PSDHMT	8309	100.8849	
1664	AGTAGGACGGTTATTTTGTG	6643	SRTVILS	8310	100.8697	
1665	CAGAGTAATGCTGCTGAGGGT	6644	QSNAPEG	8311	100.8152	
1666	TGGACCGAAACGGCCGCTCAC	6645	WTETAH	8312	100.7753	
1667	AAGGAGAATCAGCTTAGTAAG	6646	KENQLSK	8313	100.7556	

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TABLE 4

RGD Motifs from expression by a CK8 promoter			
Rank	Sequence	SEQ ID NO:	
1	RGDLSTP	13	
2	RGDLNQY	14	
3	RGDLTTP	15	
4	RGDATEL	16	
5	RGDQLYH	17	
6	RGDLSTP	18	
7	RGDVAAK	19	
8	RGDLTTP	20	
9	RGDLNQY	21	
10	RGDTMSK	22	
11	RGDVAAK	23	
12	RGDTMSK	24	
13	RGDATEL	25	

TABLE 5

RGD Motifs from expression by MHCK7 promoter			
Rank	Sequence	SEQ ID NO:	
1	RGDLTTP	26	
2	RGDLNQY	27	
3	RGDLSTP	28	
4	RGDQLYH	29	
5	RGDTMSK	30	
6	RGDATEL	31	
7	RGDLSTP	32	
8	RGDMINT	33	
9	RGDLNQY	34	
10	RGDTMSK	35	
11	RGDLTTP	36	
12	RGDLNDS	37	

TABLE 6

RGD Motifs from expression by MHCK7 and CK8 combined.			
Rank	Sequence	SEQ ID NO:	
1	RGDLSTP	38	
2	RGDLSTP	39	
3	RGDLTTP	40	
4	RGDLNQY	41	

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TABLE 6-continued

RGD Motifs from expression by MHCK7 and CK8 combined.			
Rank	Sequence	SEQ ID NO:	
5	RGDQLYH	42	
6	RGDATEL	43	
10	RGDTMSK	44	
8	RGDLNQY	45	
9	RGDLTTP	46	
15	RGDMINT	47	
11	RGDTMSK	48	
12	RGDTMNY	49	
20	RGDATEL	50	

In some embodiments, the n-mer motif is or includes an “RGD” motif. An “RGD” motif refers to n-mer motifs having the presence of the amino acids R, G, D and as the three consecutive amino acids in that order of the n-mer motif. In some embodiments, the RGD motif can have the general formula $X_m\text{RGDX}_n$, where m can be 0-4 amino acids, n can be 0-15 amino acids, and where X is any amino acid, where each amino acid present can each be independently selected from the others and can be selected from the group of any amino acid. It will be appreciated that when m=0 or n=0, that this means that there are no amino acids preceding the “RGD” in the RGD motif and/or there are no amino acids following the “RGD” in the RGD motif. In some embodiments, when m=0, RGD is the first three amino acids of the RGD motif. In some embodiments, when n=0, RGD is the last three amino acids of the RGD motif. In some embodiments, where m=0 and n=0, the RGD motif contains only the amino acids RGD. Exemplary RGD motifs are shown in e.g. Tables 1-6 and 8-9.

In some exemplary embodiments, the RGD motif is $X_1\text{RGDX}_2$ (SEQ ID NO: 9100), $X_1\text{RGDX}_2X_3$ (SEQ ID NO: 9101), $X_1\text{RGDX}_2X_3X_4$ (SEQ ID NO: 9102), $X_1\text{RGDX}_2X_3X_4X_5$ (SEQ ID NO: 9103), $X_1\text{RGDX}_2X_3X_4X_5X_6$ (SEQ ID NO: 9104), $X_1\text{RGDX}_2X_3X_4X_5X_6X_7$ (SEQ ID NO: 9105), $X_1\text{RGDX}_2X_3X_4X_5X_6X_7X_8$ (SEQ ID NO: 9106), $X_1\text{RGDX}_2X_3X_4X_5X_6X_7X_8X_9$ (SEQ ID NO: 9107), $X_1\text{RGDX}_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ (SEQ ID NO: 9108), $X_1\text{RGDX}_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}$ (SEQ ID NO: 9109), or $X_1\text{RGDX}_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}$ (SEQ ID NO: 9110).

In some exemplary embodiments, the RGD motif is $X_1X_2\text{RGDX}_3$ (SEQ ID NO: 9111), $X_1X_2\text{RGDX}_3X_4$ (SEQ ID NO: 9112), $X_1X_2\text{RGDX}_3X_4X_5$ (SEQ ID NO: 9113), $X_1X_2\text{RGDX}_3X_4X_5X_6$ (SEQ ID NO: 9114), $X_1X_2\text{RGDX}_3X_4X_5X_6X_7$ (SEQ ID NO: 9115), $X_1X_2\text{RGDX}_3X_4X_5X_6X_7X_8$ (SEQ ID NO: 9116), $X_1X_2\text{RGDX}_3X_4X_5X_6X_7X_8X_9$ (SEQ ID NO: 9117), $X_1X_2\text{RGDX}_3X_4X_5X_6X_7X_8X_9X_{10}$ (SEQ ID NO: 9118), $X_1X_2\text{RGDX}_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}$ (SEQ ID NO: 9119), or $X_1X_2\text{RGDX}_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}$ (SEQ ID NO: 9120).

In some exemplary embodiments, the RGD motif is $X_1X_2X_3\text{RGDX}_4$ (SEQ ID NO: 9121), $X_1X_2X_3\text{RGDX}_4X_5$ (SEQ ID NO: 9122), $X_1X_2X_3\text{RGDX}_4X_5X_6$ (SEQ ID NO: 9123), $X_1X_2X_3\text{RGDX}_4X_5X_6X_7$ (SEQ ID NO: 9124),

$X_1X_2X_3RGDX_4X_5X_6X_7X_8$ (SEQ ID NO: 9125), $X_1X_2X_3RGDX_4X_5X_6X_7X_8X_9$ (SEQ ID NO: 9126), $X_1X_2X_3RGDX_4X_5X_6X_7X_8X_9X_{10}$ (SEQ ID NO: 9127), ID NO: 9128), or $X_1X_2X_3RGDX_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}$ (SEQ ID NO: 9129).

In some exemplary embodiments, the RGD motif is $X_1X_2X_3X_4RGDX_5$ (SEQ ID NO: 9130), $X_1X_2X_3X_4RGDX_5X_6$ (SEQ ID NO: 9131), $X_1X_2X_3X_4RGDX_5X_6X_7$ (SEQ ID NO: 9132), $X_1X_2X_3X_4RGDX_5X_6X_7X_8$ (SEQ ID NO: 9133), $X_1X_2X_3X_4RGDX_5X_6X_7X_8X_9$ (SEQ ID NO: 9134), $X_1X_2X_3X_4RGDX_5X_6X_7X_8X_9X_{10}$ (SEQ ID NO: 9135), $X_1X_2X_3X_4RGDX_5X_6X_7X_8X_9X_{10}X_{11}$ (SEQ ID NO: 9136), or $X_1X_2X_3X_4RGDX_5X_6X_7X_8X_9X_{10}X_{11}X_{12}$ (SEQ ID NO: 9137).

In some embodiments, the RGD motif has the amino acids RGD as the first three consecutive amino acids of the n-mer motif (i.e. m=0). In some exemplary embodiments, the n-mer can have a sequence of RGD or $RGDX_n$, where n can be 1-15 amino acids and X can be any amino acid, where each amino acid present can each be independently selected from the others and can be selected from the group of any amino acid. In some embodiments, the n-mer motif can be RGD (3-mer), $RGDX_1$ (4-mer), $RGDX_1X_2$ (5-mer) (SEQ ID NO: 2), $RGDX_1X_2X_3$ (6-mer) (SEQ ID NO: 3), $RGDX_1X_2X_3X_4$ (7 mer) (SEQ ID NO: 4), $RGDX_1X_2X_3X_4X_5$ (8 mer) (SEQ ID NO: 5), $RGDX_1X_2X_3X_4X_5X_6$ (9-mer) (SEQ ID NO: 6), $RGDX_1X_2X_3X_4X_5X_6X_7$ (10-mer) (SEQ ID NO: 7), $RGDX_1X_2X_3X_4X_5X_6X_7X_8$ (11-mer) (SEQ ID NO: 8), $RGDX_1X_2X_3X_4X_5X_6X_7X_8X_9$ (12-mer) (SEQ ID NO: 9), $RGDX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}$ (13-mer) (SEQ ID NO: 10), $RGDX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}$ (14-mer) (SEQ ID NO: 11), or $RGDX_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}$ (15-mer) (SEQ ID NO: 12), where $X_1, X_2, X_3, X_4, X_5, X_6, X_7, X_8, X_9, X_{10}, X_{11}, X_{12}$ are each be independently selected from any amino acid. In some embodiments, X_1 is L, T, A, M, V, Q, or M. In some embodiments, X_2 is T, M, S, N, L, A, or I. In some embodiments, X_3 is T, E, N, O, S, Q, Y, A, or D. In some embodiments, X_4 is P, Y, K, L, H, T, or S. In some embodiments, n-mer motifs including the RGD motif is included in a muscle-specific engineered AAV capsids.

In some embodiments, the n-mer motif can be in any one of Tables 1-6. In some embodiments, the n-mer motif in any of Tables 1-6 and 8-9 can be included in a muscle specific engineered capsid.

In some embodiments, the n-mer motif can be in any one of Tables 4-6. In some embodiments, the n-mer motif in any of Tables 4-6 and 8-9 can be included in a muscle specific engineered capsid.

The muscle-specific targeting moiety can be coupled to or otherwise associated with a cargo. In some embodiments, one or more muscle-specific targeting moieties described herein is directly attached to the cargo. In some embodiments, one or more muscle-specific targeting moieties described herein is indirectly coupled to the cargo, such as via a linker molecule. In some embodiments, one or more one or more muscle-specific targeting moieties described herein is coupled to associated with a polypeptide or other particle that is coupled to, attached to, encapsulates, and/or contains a cargo.

Exemplary particles include, without limitation, viral particles (e.g. viral capsids, which is inclusive of bacteriophage capsids), polysomes, liposomes, nanoparticles, microparticles, exosomes, micelles, and the like. The term "nanoparticle" as used herein includes a nanoscale deposit of a homogenous or heterogeneous material. Nanoparticles may

be regular or irregular in shape and may be formed from a plurality of co-deposited particles that form a composite nanoscale particle. Nanoparticles may be generally spherical in shape or have a composite shape formed from a plurality of co-deposited generally spherical particles. Exemplary shapes for the nanoparticles include, but are not limited to, spherical, rod, elliptical, cylindrical, disc, and the like. In some embodiments, the nanoparticles have a substantially spherical shape.

As used herein, the term "specific" when used in relation to described an interaction between two moieties, refers to non-covalent physical association of a first and a second moiety wherein the association between the first and second moieties is at least 2 times as strong, at least 5 times as strong as, at least 10 times as strong as, at least 50 times as strong as, at least 100 times as strong as, or stronger than the association of either moiety with most or all other moieties present in the environment in which binding occurs. Binding of two or more entities may be considered specific if the equilibrium dissociation constant, K_d , is 10^{-3} M or less, 10^{-4} M or less, 10^{-5} M or less, 10^{-6} M or less, 10^{-7} M or less, 10^{-8} M or less, 10^{-9} M or less, 10^{-10} M or less, 10^{-11} M or less, or 10^{-12} M or less under the conditions employed, e.g., under physiological conditions such as those inside a cell or consistent with cell survival. In some embodiments, specific binding can be accomplished by a plurality of weaker interactions (e.g., a plurality of individual interactions, wherein each individual interaction is characterized by a K_d of greater than 10^{-3} M). In some embodiments, specific binding, which can be referred to as "molecular recognition," is a saturable binding interaction between two entities that is dependent on complementary orientation of functional groups on each entity. Examples of specific interactions include primer-polynucleotide interaction, aptamer-aptamer target interactions, antibody-antigen interactions, avidin-biotin interactions, ligand-receptor interactions, metal-chelate interactions, hybridization between complementary nucleic acids, etc.

In some embodiments, in addition to the one or more n-mer motifs the targeting moiety can include a polypeptide, a polynucleotide, a lipid, a polymer, a sugar, or a combination thereof.

Engineered Muscle Targeting Viral Capsids

In some embodiments, the muscle engineered muscle-specific targeting moiety is incorporated into a viral capsid protein, which can in turn be incorporated into an engineered viral capsid of an engineered virus particle, thus providing a muscle-specific virus particle. The muscle-specific engineered virus particle can be useful for delivering a cargo to muscle cells. In some embodiments, the targeting moiety is incorporated into a viral protein, such as a capsid protein, including but not limited to lentiviral, adenoviral, AAV, bacteriophage, retroviral proteins. In some embodiments, one or more n-mer motifs (such as an RGD or non-RGD n-mer motif) is located between two amino acids of the viral protein such that one or more of the one or more n-mer motifs are external (i.e. is presented on the surface of) to a viral capsid.

In some embodiments, the composition containing one or more of the muscle-specific targeting moieties described herein has increased muscle cell potency, muscle cell specificity, reduced immunogenicity, or any combination thereof.

Cargos include any molecule that is capable of being coupled to or associated with the muscle-specific targeting moieties described herein. Cargos include, without limitation, nucleotides, oligonucleotides, polynucleotides, amino acids, peptides, polypeptides, riboproteins, lipids, sugars,

pharmaceutically active agents (e.g. drugs, imaging and other diagnostic agents, and the like), chemical compounds, and combinations thereof. In some embodiments, the cargo is or includes, DNA, RNA, amino acids, peptide(s), polypeptide(s), antibody (ies), aptamer(s), ribozyme(s), guide sequence(s) for ribozymes that inhibit translation or transcription of essential tumor proteins and genes, hormone(s), immunomodulator(s), antipyretic(s), anxiolytic(s), antipsychotic(s), analgesic(s), antispasmodic(s), anti-inflammatory (ies), anti-histamine(s), anti-infective(s), radiation sensitizer(s), chemotherapeutic(s), radioactive compound(s), imaging agent(s), genetic modifying agent(s), and combinations thereof.

In some embodiments, the cargo is capable of treating or preventing a muscle disease or disorder. In some embodiments, the muscle disease or disorder is (a) an autoimmune disease; (b) a cancer; (c) a muscular dystrophy; (d) a neuro-muscular disease; (e) a sugar or glycogen storage disease; (f) an expanded repeat disease; (g) a dominant negative disease; (h) a cardiomyopathy; (i) a viral disease; (j) a progeroid disease; or (k) any combination thereof. In some embodiments, the expanded repeat disease is Huntington's disease, a Myotonic Dystrophy, or Facioscapulohumeral muscular dystrophy (FSHD). In some embodiments, the muscular dystrophy is Duchenne muscular dystrophy, Becker Muscular dystrophy, a Limb-Girdle muscular dystrophy, an Emery Dreifuss muscular dystrophy, a myotonic dystrophy, or FSHD. In some embodiments, the myotonic dystrophy is Type 1 or Type 2. In some embodiments, the sugar or glycogen storage disease is a MPS type III disease or Pompe disease. In some embodiments, the MPS type III disease, is MPS Type IIIA, IIIB, IIIC, or IIID. In some embodiments, the neuro-muscular disease is Charcot-Marie-Tooth disease or Friedreich's Ataxia.

In some embodiments, the cargo is a morpholino, a peptide-linked morpholino, an antisense oligonucleotide, a PMO, a therapeutic transgene, a polynucleotide encoding a therapeutic polypeptide or peptide, a PPMO, one or more peptides, one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both, a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule, a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein, or any combination thereof.

In some embodiments, the cargo is capable of inducing exon skipping in a gene.

In some embodiments, the cargo is capable of inducing exon skipping in a dystrophin gene.

In some embodiments, the cargo is a mini- or micro-dystrophin gene. In some embodiments, the mini- or micro-dystrophin gene comprises spectrin-like repeats 1, 2, 3, 16, 17, and 24, and optionally an nNOS domain.

Engineered Muscle Targeting AAV Capsids and AAVs

In some embodiments, the engineered muscle-specific targeting moiety is incorporated an adeno-associated virus (AAV) capsid. Described herein are various embodiments of engineered AAV capsids that can be engineered to confer cell-specific tropism to an engineered AAV particle. The engineered capsids can be included in an engineered virus particle and can confer cell-specific tropism, reduced immunogenicity, or both to the engineered AAV particle. The engineered AAV capsids described herein can include one or more engineered AAV capsid proteins described herein. In some embodiments, the AAV capsid protein comprises one or more n-mer motifs. In some embodiments, one or more of the n-mer motifs contains or is an RGD motif or a non-RGD n-mer motif. Such motifs are defined and described in

greater detail elsewhere herein. In some embodiments, one or more of the one or more n-mer motifs incorporated into one or more AAV capsid proteins can confer muscle specificity to an AAV virus particle having the engineered capsid with the n-mer motif(s).

The engineered AAV capsid and/or capsid proteins can be encoded by one or more engineered AAV capsid polynucleotides. In some embodiments, an engineered AAV capsid polynucleotide can include a 3' polyadenylation signal. The polyadenylation signal can be an SV40 polyadenylation signal.

The engineered AAV capsids can be variants of wild-type AAV capsids. In some embodiments, the wild-type AAV capsids can be composed of VP1, VP2, VP3 capsid proteins or a combination thereof. In other words, the engineered AAV capsids can include one or more variants of a wild-type VP1, wild-type VP2, and/or wild-type VP3 capsid proteins. In some embodiments, the serotype of the reference wild-type AAV capsid can be AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10, or any combination thereof. In some embodiments, the serotype of the wild-type AAV capsid can be AAV-9. The engineered AAV capsids can have a different tropism than that of the reference wild-type AAV capsid.

The engineered AAV capsid can contain 1-60 engineered capsid proteins. In some embodiments, the engineered AAV capsids can contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, to/or 60 engineered capsid proteins. In some embodiments, the engineered AAV capsid can contain 0-59 wild-type AAV capsid proteins. In some embodiments, the engineered AAV capsid can contain 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, to/or 59 wild-type AAV capsid proteins.

In some embodiments, the engineered AAV capsid protein has an n-mer amino acid motif, where n can be at least 3 amino acids. In some embodiments, n can be 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 amino acids. In some embodiments, the engineered AAV capsid can have a 6-mer or 7-mer amino acid motif. In some embodiments, the n-mer amino acid motif is inserted between two amino acids in the wild-type viral protein (VP) (or capsid protein). In some embodiments, the n-mer motif can be inserted between two amino acids in a variable amino acid region in an AAV capsid protein. The core of each wild-type AAV viral protein contains an eight-stranded beta-barrel motif (betaB to betaI) and an alpha-helix (alphaA) that are conserved in autonomous parvovirus capsids (see e.g. DiMattia et al. 2012. J. Virol. 86(12): 6947-6958). Structural variable regions (VRs) occur in the surface loops that connect the beta-strands, which cluster to produce local variations in the capsid surface. AAVs have 12 variable regions (also referred to as hypervariable regions) (see e.g. Weitzman and Linden. 2011. "Adeno-Associated Virus Biology." In Snyder, R. O., Moullier, P. (eds.) Totowa, NJ: Humana Press). In some embodiments, one or more n-mer motifs are inserted between two amino acids in one or more of the 12 variable regions in the wild-type AAV capsid proteins. In some embodiments, the one or more n-mer motifs are each inserted between two amino acids in VR-I, VR-II, VR-III, VR-IV, VR-V, VR-VI, VR-VII, VR-III, VR-IX, VR-X, VR-XI, VR-XII, or a combination thereof. In some embodiments, the n-mer is inserted between two amino acids in

the VR-III of a capsid protein. In some embodiments, the engineered capsid can have an n-mer inserted between any two contiguous amino acids between amino acids 262 and 269, between any two contiguous amino acids between amino acids 327 and 332, between any two contiguous amino acids between amino acids 382 and 386, between any two contiguous amino acids between amino acids 452 and 460, between any two contiguous amino acids between amino acids 488 and 505, between any two contiguous amino acids between amino acids 545 and 558, between any two contiguous amino acids between amino acids 581 and 593, between any two contiguous amino acids between amino acids 704 and 714 of an AAV9 viral protein. In some embodiments, the engineered capsid can have an n-mer inserted between amino acids 588 and 589 of an AAV9 viral protein. In some embodiments, the engineered capsid can have a 7-mer motif inserted between amino acids 588 and 589 of an AAV9 viral protein. SEQ ID NO: 1 is a reference AAV9 capsid sequence for at least referencing the insertion sites discussed above. It will be appreciated that n-mers can be inserted in analogous positions in AAV viral proteins of other serotypes. In some embodiments as previously discussed, the n-mer(s) can be inserted between any two contiguous amino acids within the AAV viral protein and in some embodiments the insertion is made in a variable region.

AAV9 capsid reference sequence

SEQ ID NO: 1

MAADGYLPDWLEDNLSEGIREWALKPGAPQPKANQQHODNARGLVLPGY
 KYLPGNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEF
 QERLKEDTSFGGNLGRAVFAQAKRLLLEPLGLVEEAAKTAPGKKRPVEQSP
 QEPDSSAGIGKSGAQPAKKRLNFGQTGDTESVPDPQPIGEPPAAPSGVGS
 LTMASGGGAPVADNNEGADGVSSSGNWHCDSSQWLGDVITTTSTRTWALP
 TYNNHLYKQISNSTSGSSNDNAYFGYSTPWGYFDNFRFHCHFSRDPWQR
 LINNNWGFPRKRLNFKLFNIQVKEVDNNGVKTIANNLITSTVQVFTDSY
 QLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLDGSAQVGRSSFYCLEYF
 PSQMLRTGNNFQFSYEFENVFPHSSYAHSQSLDRLMNPIDQYLYLSKT
 INSGSQNQQLTKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNSE
 FAWPGASSWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKGQGTGR
 DNVDADKVMITNEEEIKTTNPVATESYGVATNHQSAQAQATGWVQNQG
 ILPGMVWQDRDVLQGPWAKIPHTDGNFHPSPLMGGFGMKHPPPIILIK
 NTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSQRWNPEIQ
 YTSNYYKSNNEFAVNTEGVYSEPRPIGTRYLTRNL

In some embodiments, the n-mer motif can be any amino acid motif as shown or encoded by a nucleic acid as shown in Tables 1-3. In some embodiments, insertion of the n-mer motif in an AAV capsid can result in cell, tissue, organ, specific engineered AAV capsids. In some embodiments, the engineered capsid has a specificity (or tropism) for muscle cells. In some embodiments, the engineered capsid can have a specificity for bone tissue and/or cells, lung tissue and/or cells, liver tissues and/or cells, bladder tissue and/or cells, kidney tissue and/or cells, cardiac tissue and/or cells, skeletal muscle tissue and/or cells, smooth muscle and/or cells, neuronal tissue and/or cells, intestinal tissue and/or cells, pancreases tissue and/or cells, adrenal gland tissue and/or

cells, brain tissue and/or cells, tendon tissues or cells, skin tissues and/or cells, spleen tissue and/or cells, eye tissue and/or cells, blood cells, synovial fluid cells, immune cells (including specificity for particular types of immune cells), and combinations thereof.

In some embodiments, the AAV capsids are muscle-specific. In some embodiments, muscle-specificity of the engineered AAV capsid is conferred by a muscle specific n-mer motif incorporated in the engineered AAV capsid. While not intending to be bound by theory, it is believed that the n-mer motif confers a 3D structure to or within a domain or region of the engineered AAV capsid such that the interaction of an engineered AAV containing said engineered AAV capsid has increased or improved interactions (e.g. increased affinity) with a cell surface receptor and/or other molecule on the surface of a muscle cell. In some embodiments, the cell surface receptor is AAV receptor (AAVR). In some embodiments, the cell surface receptor is a muscle cell specific AAV receptor. In some embodiments, a muscle specific engineered AAV containing the muscle-specific capsid can have an increased transduction rate, efficiency, amount, or a combination thereof in a muscle cell as compared to other cells types and/or other AAVs that do not contain a muscle-specific engineered AAV capsid as described herein.

Methods of Generating Muscle Specific Targeting Moieties

Also provided herein are methods of generating engineered AAV capsids. The engineered AAV capsid variants can be variants of wild-type AAV capsids. FIGS. 6-8 can illustrate various embodiments of methods capable of generating engineered AAV capsids described herein. Generally, an AAV capsid library can be generated by expressing engineered capsid vectors each containing an engineered AAV capsid polynucleotide previously described in an appropriate AAV producer cell line. See e.g. FIG. 8. It will be appreciated that although FIG. 8 shows a helper-dependent method of AAV particle production, it will be appreciated that this can be done via a helper-free method as well. This can generate an AAV capsid library that can contain one more desired cell-specific engineered AAV capsid variant. As shown in FIG. 6 the AAV capsid library can be administered to various non-human animals for a first round of mRNA-based selection. As shown in FIG. 1, the transduction process by AAVs and related vectors can result in the production of an mRNA molecule that is reflective of the genome of the virus that transduced the cell. As is at least demonstrated in the Examples herein, mRNA based-selection can be more specific and effective to determine a virus particle capable of functionally transducing a cell because it is based on the functional product produced as opposed to just detecting the presence of a virus particle in the cell by measuring the presence of viral DNA.

After first-round administration, one or more engineered AAV virus particles having a desired capsid variant can then be used to form a filtered AAV capsid library. Desirable AAV virus particles can be identified by measuring the mRNA expression of the capsid variants and determining which variants are highly expressed in the desired cell type(s) as compared to non-desired cells type(s). Those that are highly expressed in the desired cell, tissue, and/or organ type are the desired AAV capsid variant particles. In some embodiments, the AAV capsid variant encoding polynucleotide is under control of a tissue-specific promoter that has selective activity in the desired cell, tissue, or organ.

The engineered AAV capsid variant particles identified from the first round can then be administered to various non-human animals. In some embodiments, the animals

used in the second round of selection and identification are not the same as those animals used for first round selection and identification. Similar to round 1, after administration the top expressing variants in the desired cell, tissue, and/or organ type(s) can be identified by measuring viral mRNA expression in the cells. The top variants identified after round two can then be optionally barcoded and optionally pooled. In some embodiments, top variants from the second round can then be administered to a non-human primate to identify the top cell-specific variant(s), particularly if the end use for the top variant is in humans. Administration at each round can be systemic.

In some embodiments, the method of generating an AAV capsid variant can include the steps of: (a) expressing a vector system described herein that contains an engineered AAV capsid polynucleotide in a cell to produce engineered AAV virus particle capsid variants; (b) harvesting the engineered AAV virus particle capsid variants produced in step (a); (c) administering engineered AAV virus particle capsid variants to one or more first subjects, wherein the engineered AAV virus particle capsid variants are produced by expressing an engineered AAV capsid variant vector or system thereof in a cell and harvesting the engineered AAV virus particle capsid variants produced by the cell; and (d) identifying one or more engineered AAV capsid variants produced at a significantly high level by one or more specific cells or specific cell types in the one or more first subjects. In this context, "significantly high" can refer to a titer that can range from between about 2×10^{11} to about 6×10^{12} vector genomes per 15 cm dish.

The method can further include the steps of: (e) administering some or all engineered AAV virus particle capsid variants identified in step (d) to one or more second subjects; and (f) identifying one or more engineered AAV virus particle capsid variants produced at a significantly high level in one or more specific cells or specific cell types in the one or more second subjects. The cell in step (a) can be a prokaryotic cell or a eukaryotic cell. In some embodiments, the administration in step (c), step (e), or both is systemic. In some embodiments, one or more first subjects, one or more second subjects, or both, are non-human mammals. In some embodiments, one or more first subjects, one or more second subjects, or both, are each independently selected from the group consisting of: a wild-type non-human mammal, a humanized non-human mammal, a disease-specific non-human mammal model, and a non-human primate.

Other methods and details of developing muscle-specific targeting moieties are described in, for example, U.S. Provisional Application Ser. Nos. 62/899,453, 62/916,207, 63/018,454, 63/055,252, and 62/916,221 and International Application No. PCT/US20/50534.

Engineered Muscle-Specific Targeting Moiety Encoding Polynucleotides, Vectors, and Vector Systems

Described herein are polynucleotides that encode the one or more muscle-specific engineered targeting moieties and vectors and/or vector systems thereof. In some embodiments, the encoding polynucleotides, vectors, and/or vector systems can be used to express and/or produce the engineered muscle-specific targeting moieties, couple the engineered muscle-specific targeting moiety to one or more other polypeptides, and/or produce particles, such as viral particles that optionally contain a cargo, that include one or more engineered muscle-specific targeting moieties described herein. The term "engineered muscle-specific targeting moiety polynucleotide" as used herein refers to a polynucleotide that encodes an engineered muscle-specific targeting moiety. As used herein, the term "encode" refers to

principle that DNA can be transcribed into RNA, which can then be translated into amino acid sequences that can form proteins. Thus, polynucleotides said to encode a subsequent polynucleotide (such as an RNA species) or proteins can also be referred to as encoding polynucleotides and refer to DNA molecules that are subsequently transcribed and/or translated as well as RNA molecules that are translated.

Also provided herein are vectors and vector systems that can contain one or more of the engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) described herein. As used in this context, engineered AAV capsid polynucleotides refers to any one or more of the polynucleotides described herein capable of encoding an engineered AAV capsid as described elsewhere herein and/or polynucleotide(s) capable of encoding one or more engineered AAV capsid proteins described elsewhere herein. Further, where the vector includes an engineered muscle-specific targeting moiety polynucleotide (including, but not limited to, an engineered AAV capsid polynucleotide) described herein, the vector can also be referred to and considered an engineered vector or system thereof although not specifically noted as such. In embodiments, the vector can contain one or more polynucleotides encoding one or more elements of an engineered viral capsid, such as an AAV capsid, described herein. The vectors and systems thereof can be useful in producing bacterial, fungal, yeast, plant cells, animal cells, and transgenic animals that can express a muscle-specific targeting moiety or composition containing a muscle-specific targeting moiety described herein. In some embodiments, the vectors and systems thereof can be useful in producing bacterial cells, fungal cells, yeast cells, plant cells, animal cells, or transgenic organisms (e.g. plants, animals) that can express the one or more components of the engineered AAV capsid described herein. Within the scope of this disclosure are vectors containing one or more of the polynucleotide sequences described herein. One or more of the polynucleotides that are part of the engineered AAV capsid and system thereof described herein can be included in a vector or vector system.

The vectors and/or vector systems can be used, for example, to express one or more of the engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) in a cell, such as a producer cell, to produce engineered viral particles containing an engineered viral capsid (e.g. an AAV containing an engineered AAV capsid) described elsewhere herein. Other uses for the vectors and vector systems described herein are also within the scope of this disclosure. In general, and throughout this specification, the term is a tool that allows or facilitates the transfer of an entity from one environment to another. In some contexts which will be appreciated by those of ordinary skill in the art, "vector" can be a term of art to refer to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. A vector can be a replicon, such as a plasmid, phage, or cosmid, into which another DNA segment may be inserted so as to bring about the replication of the inserted segment. Generally, a vector is capable of replication when associated with the proper control elements.

Vectors include, but are not limited to, nucleic acid molecules that are single-stranded, double-stranded, or partially double-stranded; nucleic acid molecules that comprise one or more free ends, no free ends (e.g. circular); nucleic acid molecules that comprise DNA, RNA, or both; and other varieties of polynucleotides known in the art. One type of vector is a "plasmid," which refers to a circular double

stranded DNA loop into which additional DNA segments can be inserted, such as by standard molecular cloning techniques. Another type of vector is a viral vector, wherein virally-derived DNA or RNA sequences are present in the vector for packaging into a virus (e.g. retroviruses, replication defective retroviruses, adenoviruses, replication defective adenoviruses, and adeno-associated viruses (AAVs)). Viral vectors also include polynucleotides carried by a virus for transfection into a host cell. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g. bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively-linked. Such vectors are referred to herein as "expression vectors." Common expression vectors of utility in recombinant DNA techniques are often in the form of plasmids.

Recombinant expression vectors can be composed of a nucleic acid (e.g. a polynucleotide) of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory elements, which can be selected on the basis of the host cells to be used for expression, that is operatively-linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" and "operatively-linked" are used interchangeably herein and further defined elsewhere herein. In the context of a vector, the term "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory element(s) in a manner that allows for expression of the nucleotide sequence (e.g., in an in vitro transcription/translation system or in a host cell when the vector is introduced into the host cell). Advantageous vectors include adeno-associated viruses, and types of such vectors can also be selected for targeting particular types of cells, such as those engineered AAV vectors containing an engineered AAV capsid polynucleotide with a desired cell-specific tropism, such as a muscle-specific tropism. These and other embodiments of the vectors and vector systems are described elsewhere herein.

In some embodiments, the vector can be a bicistronic vector. In some embodiments, a bicistronic vector can be used for expressing one or more engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) system described herein. In some embodiments, expression of an engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) described herein can be driven by the suitable constitutive or tissue specific promoter. Such embodiments can be advantageous for generating muscle-specific targeting moieties, which are described in greater detail elsewhere herein. Where the element of the engineered AAV capsid system is an RNA, its expression can be driven by a Pol III promoter, such as a U6 promoter. In some embodiments, the two are combined.

Cell-Based Vector Amplification and Expression

Vectors can be designed for expression of one or more engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) or a system including one or more engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) or product thereof described herein (e.g. nucleic

acid transcripts, proteins, enzymes, and combinations thereof) in a suitable host cell. In some embodiments, the suitable host cell is a prokaryotic cell. Suitable host cells include, but are not limited to, bacterial cells, yeast cells, insect cells, and mammalian cells. The vectors can be viral-based or non-viral based. In some embodiments, the suitable host cell is a eukaryotic cell. In some embodiments, the suitable host cell is a suitable bacterial cell. Suitable bacterial cells include, but are not limited to, bacterial cells from the bacteria of the species *Escherichia coli*. Many suitable strains of *E. coli* are known in the art for expression of vectors. These include, but are not limited to Pir1, Stb12, Stb13, Stb14, TOP10, XL1 Blue, and XL10 Gold. In some embodiments, the host cell is a suitable insect cell. Suitable insect cells include those from *Spodoptera frugiperda*. Suitable strains of *S. frugiperda* cells include, but are not limited to, Sf9 and Sf21. In some embodiments, the host cell is a suitable yeast cell. In some embodiments, the yeast cell can be from *Saccharomyces cerevisiae*. In some embodiments, the host cell is a suitable mammalian cell. Many types of mammalian cells have been developed to express vectors. Suitable mammalian cells include, but are not limited to, HEK293, Chinese Hamster Ovary Cells (CHOs), mouse myeloma cells, HeLa, U2OS, A549, HT1080, CAD, P19, NIH 3T3, L929, N2a, MCF-7, Y79, SO-Rb50, HepG G2, DIKX-X11, J558L, Baby hamster kidney cells (BHK), and chicken embryo fibroblasts (CEFs). Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990).

In some embodiments, the vector can be a yeast expression vector. Examples of vectors for expression in yeast *Saccharomyces cerevisiae* include pYepSec1 (Baldari, et al., 1987. EMBO J. 6:229-234), pMFa (Kuijan and Herskowitz, 1982. Cell 30:933-943), pJRY88 (Schultz et al., 1987. Gene 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (In Vitrogen Corp, San Diego, Calif.). As used herein, a "yeast expression vector" refers to a nucleic acid that contains one or more sequences encoding an RNA and/or polypeptide and may further contain any desired elements that control the expression of the nucleic acid(s), as well as any elements that enable the replication and maintenance of the expression vector inside the yeast cell. Many suitable yeast expression vectors and features thereof are known in the art; for example, various vectors and techniques are illustrated in Yeast Protocols, 2nd edition, Xiao, W., ed. (Humana Press, New York, 2007) and Buckholz, R. G. and Gleeson, M. A. (1991) Biotechnology (NY) 9(11): 1067-72. Yeast vectors can contain, without limitation, a centromeric (CEN) sequence, an autonomous replication sequence (ARS), a promoter, such as an RNA Polymerase III promoter, operably linked to a sequence or gene of interest, a terminator such as an RNA polymerase III terminator, an origin of replication, and a marker gene (e.g., auxotrophic, antibiotic, or other selectable markers). Examples of expression vectors for use in yeast may include plasmids, yeast artificial chromosomes, 2μ plasmids, yeast integrative plasmids, yeast replicative plasmids, shuttle vectors, and episomal plasmids.

In some embodiments, the vector is a baculovirus vector or expression vector and can be suitable for expression of polynucleotides and/or proteins in insect cells. Baculovirus vectors available for expression of proteins in cultured insect cells (e.g., SF9 cells) include the pAc series (Smith, et al., 1983. Mol. Cell. Biol. 3:2156-2165) and the pVL series (Lucklow and Summers, 1989. Virology 170:31-39). rAAV (recombinant Adeno-associated viral) vectors are preferably

produced in insect cells, e.g., *Spodoptera frugiperda* Sf9 insect cells, grown in serum-free suspension culture. Serum-free insect cells can be purchased from commercial vendors, e.g., Sigma Aldrich (EX-CELL 405).

In some embodiments, the vector is a mammalian expression vector. In some embodiments, the mammalian expression vector is capable of expressing one or more polynucleotides and/or polypeptides in a mammalian cell. Examples of mammalian expression vectors include, but are not limited to, pCDM8 (Seed, 1987. *Nature* 329:840) and pMT2PC (Kaufman, et al., 1987. *EMBO J.* 6:187-195). The mammalian expression vector can include one or more suitable regulatory elements capable of controlling expression of the one or more polynucleotides and/or proteins in the mammalian cell. For example, commonly used promoters are derived from polyoma, adenovirus 2, cytomegalovirus, simian virus 40, and others disclosed herein and known in the art. More detail on suitable regulatory elements are described elsewhere herein.

For other suitable expression vectors and vector systems for both prokaryotic and eukaryotic cells see, e.g., Chapters 16 and 17 of Sambrook, et al., *MOLECULAR CLONING: A LABORATORY MANUAL*. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In some embodiments, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert, et al., 1987. *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988. *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989. *EMBO J.* 8:729-733) and immunoglobulins (Baneiji, et al., 1983. *Cell* 33:729-740; Queen and Baltimore, 1983. *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989. *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund, et al., 1985. *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, e.g., the murine hox promoters (Kessel and Gruss, 1990. *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman, 1989. *Genes Dev.* 3:537-546). With regards to these prokaryotic and eukaryotic vectors, mention is made of U.S. Pat. No. 6,750,059, the contents of which are incorporated by reference herein in their entirety. Other embodiments can utilize viral vectors, with regards to which mention is made of U.S. patent application Ser. No. 13/092,085, the contents of which are incorporated by reference herein in their entirety. Tissue-specific regulatory elements are known in the art and in this regard, mention is made of U.S. Pat. No. 7,776,321, the contents of which are incorporated by reference herein in their entirety. In some embodiments, a regulatory element can be operably linked to or coupled to one or more engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) and/or one or more elements of a system comprising one or more engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) or product thereof so as to drive expression of the one or more elements of the engineered muscle-specific target-

ing moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides) or system thereof described herein.

Vectors may be introduced and propagated in a prokaryote or prokaryotic cell. In some embodiments, a prokaryote is used to amplify copies of a vector to be introduced into a eukaryotic cell or as an intermediate vector in the production of a vector to be introduced into a eukaryotic cell (e.g., amplifying a plasmid as part of a viral vector packaging system). In some embodiments, a prokaryote is used to amplify copies of a vector and express one or more nucleic acids, such as to provide a source of one or more proteins for delivery to a host cell or host organism.

In some embodiments, the vector can be a fusion vector or fusion expression vector. In some embodiments, fusion vectors add a number of amino acids to a protein encoded therein, such as to the amino terminus, carboxy terminus, or both of a recombinant protein. Such fusion vectors can serve one or more purposes, such as: (i) to increase expression of recombinant protein; (ii) to increase the solubility of the recombinant protein; and (iii) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. In some embodiments, expression of polynucleotides (such as non-coding polynucleotides) and proteins in prokaryotes can be carried out in *Escherichia coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polynucleotides and/or proteins. In some embodiments, the fusion expression vector can include a proteolytic cleavage site, which can be introduced at the junction of the fusion vector backbone or other fusion moiety and the recombinant polynucleotide or protein to enable separation of the recombinant polynucleotide or protein from the fusion vector backbone or other fusion moiety subsequent to purification of the fusion polynucleotide or protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Example fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988. *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann et al., (1988) *Gene* 69:301-315) and pET 11d (Studier et al., *GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY* 185, Academic Press, San Diego, Calif. (1990) 60-89).

In some embodiments, one or more vectors driving expression of one or more engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides), vector, and/or vector system thereof described herein are introduced into a host cell such that expression of one or more the engineered muscle-specific targeting moiety polynucleotides (including, but not limited to, engineered AAV capsid polynucleotides), vectors, and/or vector systems described herein direct formation of an engineered muscle-specific targeting moiety and/or compositions or engineered muscle-specific delivery systems that include one or more engineered muscle-specific targeting moieties described herein. In some embodiments, the engineered muscle-specific delivery system is a viral particle such as an engineered AAV particle that contains an engineered capsid that contains one or more engineered muscle-specific targeting moieties described elsewhere herein. For example, different elements of an engineered muscle-specific delivery system can each be operably linked to separate regulatory elements on the same

or separate vectors. RNA(s) of different elements of the engineered muscle-specific delivery system described herein that can include one or more engineered muscle-specific targeting moiety can be delivered to an animal or mammal or cell thereof to produce an animal or mammal or cell thereof that constitutively, inducibly, or conditionally expresses different elements of the engineered muscle-specific delivery system described herein or contains one or more cells that incorporates and/or expresses one or more elements of the engineered muscle-specific delivery system described herein.

In some embodiments, two or more of the elements expressed from the same or different regulatory element(s) can be combined in a single vector along with one or more additional vectors providing any components of the system not included in the first vector. Engineered muscle-specific delivery system polynucleotides (including but not limited to engineered muscle-specific targeting moiety polynucleotides) that are combined in a single vector may be arranged in any suitable orientation, such as one element located 5' with respect to ("upstream" of) or 3' with respect to ("downstream" of) a second element. The coding sequence of one element may be located on the same or opposite strand of the coding sequence of a second element, and oriented in the same or opposite direction. In some embodiments, a single promoter drives expression of a transcript encoding one or more engineered muscle-specific targeting moiety polynucleotides, embedded within one or more intron sequences (e.g., each in a different intron, two or more in at least one intron, or all in a single intron). In some embodiments, two or more engineered muscle-specific targeting moiety polynucleotides can be operably linked to and expressed from the same promoter.

Vector Features

The vectors can include additional features that can confer one or more functionalities to the vector, the polynucleotide to be delivered, a virus particle produced there from, or polypeptide expressed thereof. Such features include, but are not limited to, regulatory elements, selectable markers, molecular identifiers (e.g. molecular barcodes), stabilizing elements, and the like. It will be appreciated by those skilled in the art that the design of the expression vector and additional features included can depend on such factors as the choice of the host cell to be transformed, the level of expression desired, etc.

Regulatory Elements

In embodiments, the polynucleotides and/or vectors thereof described herein (such as the engineered muscle-specific targeting moiety polynucleotides of the present invention) can include one or more regulatory elements that can be operatively linked to the polynucleotide. The term "regulatory element" is intended to include promoters, enhancers, internal ribosomal entry sites (IRES), and other expression control elements (e.g., transcription termination signals, such as polyadenylation signals and poly-U sequences). Such regulatory elements are described, for example, in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory elements include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). A tissue-specific promoter can direct expression primarily in a desired tissue of interest, such as muscle, neuron, bone, skin, blood, specific organs (e.g., liver, pancreas), or particular cell types (e.g., lymphocytes). Regulatory elements may also

direct expression in a temporal-dependent manner, such as in a cell-cycle dependent or developmental stage-dependent manner, which may or may not also be tissue or cell-type specific. In some embodiments, a vector comprises one or more pol III promoter (e.g., 1, 2, 3, 4, 5, or more pol III promoters), one or more pol II promoters (e.g., 1, 2, 3, 4, 5, or more pol II promoters), one or more pol I promoters (e.g., 1, 2, 3, 4, 5, or more pol I promoters), or combinations thereof. Examples of pol III promoters include, but are not limited to, U6 and H1 promoters. Examples of pol II promoters include, but are not limited to, 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 α promoter. Also encompassed by the term "regulatory element" are enhancer elements, such as WPRE; CMV enhancers; the R-U5' segment in LTR of HTLV-I (Mol. Cell. Biol., Vol. 8(1), p. 466-472, 1988); SV40 enhancer; and the intron sequence between exons 2 and 3 of rabbit β -globin (Proc. Natl. Acad. Sci. USA., Vol. 78(3), p. 1527-31, 1981).

In some embodiments, the regulatory sequence can be a regulatory sequence described in U.S. Pat. No. 7,776,321, U.S. Pat. Pub. No. 2011/0027239, and PCT publication WO 2011/028929, the contents of which are incorporated by reference herein in their entirety. In some embodiments, the vector can contain a minimal promoter. In some embodiments, the minimal promoter is the Mecp2 promoter, tRNA promoter, or U6. In a further embodiment, the minimal promoter is tissue specific. In some embodiments, the length of the vector polynucleotide the minimal promoters and polynucleotide sequences is less than 4.4 Kb.

To express a polynucleotide, the vector can include one or more transcriptional and/or translational initiation regulatory sequences, e.g. promoters, that direct the transcription of the gene and/or translation of the encoded protein in a cell. In some embodiments a constitutive promoter may be employed. Suitable constitutive promoters for mammalian cells are generally known in the art and include, but are not limited to SV40, CAG, CMV, EF-1 α , β -actin, RSV, and PGK. Suitable constitutive promoters for bacterial cells, yeast cells, and fungal cells are generally known in the art, such as a T-7 promoter for bacterial expression and an alcohol dehydrogenase promoter for expression in yeast.

In some embodiments, the regulatory element can be a regulated promoter. "Regulated promoter" refers to promoters that direct gene expression not constitutively, but in a temporally- and/or spatially-regulated manner, and includes tissue-specific, tissue-preferred and inducible promoters. In some embodiments, the regulated promoter is a tissue specific promoter as previously discussed elsewhere herein. Regulated promoters include conditional promoters and inducible promoters. In some embodiments, conditional promoters can be employed to direct expression of a polynucleotide in a specific cell type, under certain environmental conditions, and/or during a specific state of development. Suitable tissue specific promoters can include, but are not limited to, liver specific promoters (e.g. APOA2, SERPIN A1 (hAAT), CYP3A4, and MIR122), pancreatic cell promoters (e.g. INS, IRS2, Pdx1, Alx3, Ppy), cardiac specific promoters (e.g. Myh6 (alpha MHC), MYL2 (MLC-2v), TNI3 (cTnl), NPPA (ANF), Slc8a1 (Ncx1)), central nervous system cell promoters (SYN1, GFAP, INA, NES, MOBP, MBP, TH, FOXA2 (HNF3 beta)), skin cell specific promoters (e.g. FLG, K14, TGM3), immune cell specific promot-

ers, (e.g. ITGAM, CD43 promoter, CD14 promoter, CD45 promoter, CD68 promoter), urogenital cell specific promoters (e.g. Pbsn, Upk2, Sbp, Fer114), endothelial cell specific promoters (e.g. ENG), pluripotent and embryonic germ layer cell specific promoters (e.g. Oct4, NANOG, Synthetic Oct4, T brachyury, NES, SOX17, FOXA2, MIR122), and muscle cell specific promoter (e.g. Desmin). Other tissue and/or cell specific promoters are discussed elsewhere herein and can be generally known in the art and are within the scope of this disclosure.

Inducible/conditional promoters can be positively inducible/conditional promoters (e.g. a promoter that activates transcription of the polynucleotide upon appropriate interaction with an activated activator, or an inducer (compound, environmental condition, or other stimulus) or a negative/conditional inducible promoter (e.g. a promoter that is repressed (e.g. bound by a repressor) until the repressor condition of the promoter is removed (e.g. inducer binds a repressor bound to the promoter stimulating release of the promoter by the repressor or removal of a chemical repressor from the promoter environment). The inducer can be a compound, environmental condition, or other stimulus. Thus, inducible/conditional promoters can be responsive to any suitable stimuli such as chemical, biological, or other molecular agents, temperature, light, and/or pH. Suitable inducible/conditional promoters include, but are not limited to, Tet-On, Tet-Off, Lac promoter, pBad, AlcA, LexA, Hsp70 promoter, Hsp90 promoter, pDawn, XVE/OlexA, GVG, and pOp/LhGR.

Where expression in a plant cell is desired, the components of the engineered AAV capsid system described herein are typically placed under control of a plant promoter, i.e. a promoter operable in plant cells. The use of different types of promoters is envisaged. In some embodiments, inclusion of a engineered AAV capsid system vector in a plant can be for AAV vector production purposes.

A constitutive plant promoter is a promoter that is able to express the open reading frame (ORF) that it controls in all or nearly all of the plant tissues during all or nearly all developmental stages of the plant (referred to as "constitutive expression"). One non-limiting example of a constitutive promoter is the cauliflower mosaic virus 35S promoter. Different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions. In particular embodiments, one or more of the engineered AAV capsid system components are expressed under the control of a constitutive promoter, such as the cauliflower mosaic virus 35S promoter issue-preferred promoters can be utilized to target enhanced expression in certain cell types within a particular plant tissue, for instance vascular cells in leaves or roots or in specific cells of the seed. Examples of particular promoters for use in the engineered AAV capsid system are found in Kawamata et al., (1997) Plant Cell Physiol 38:792-803; Yamamoto et al., (1997) Plant J 12:255-65; Hire et al, (1992) Plant Mol Biol 20:207-18, Kuster et al, (1995) Plant Mol Biol 29:759-72, and Capana et al., (1994) Plant Mol Biol 25:681-91.

Examples of promoters that are inducible and that can allow for spatiotemporal control of gene editing or gene expression may use a form of energy. The form of energy may include but is not limited to sound energy, electromagnetic radiation, chemical energy and/or thermal energy. Examples of inducible systems include tetracycline inducible promoters (Tet-On or Tet-Off), small molecule two-hybrid transcription activations systems (FKBP, ABA, etc.), or light inducible systems (Phytochrome, LOV domains, or

cryptochrome), such as a Light Inducible Transcriptional Effector (LITE) that direct changes in transcriptional activity in a sequence-specific manner. The components of a light inducible system may include one or more elements of the engineered muscle-specific delivery system described herein, a light-responsive cytochrome heterodimer (e.g. from *Arabidopsis thaliana*), and a transcriptional activation/repression domain. In some embodiments, the vector can include one or more of the inducible DNA binding proteins provided in PCT publication WO 2014/018423 and US Publications, 2015/0291966, 2017/0166903, 2019/0203212, which describe e.g. embodiments of inducible DNA binding proteins and methods of use and can be adapted for use with the present invention.

In some embodiments, transient or inducible expression can be achieved by including, for example, chemical-regulated promoters, i.e. whereby the application of an exogenous chemical induces gene expression. Modulation of gene expression can also be obtained by including a chemical-repressible promoter, where application of the chemical represses gene expression. Chemical-inducible promoters include, but are not limited to, the maize In2-2 promoter, activated by benzene sulfonamide herbicide safeners (De Veylder et al., (1997) Plant Cell Physiol 38:568-77), the maize GST promoter (GST-11-27, WO93/01294), activated by hydrophobic electrophilic compounds used as pre-emergent herbicides, and the tobacco PR-1 a promoter (Ono et al., (2004) Biosci Biotechnol Biochem 68:803-7) activated by salicylic acid. Promoters which are regulated by antibiotics, such as tetracycline-inducible and tetracycline-repressible promoters (Gatz et al., (1991) Mol Gen Genet 227: 229-37; U.S. Pat. Nos. 5,814,618 and 5,789,156) can also be used herein.

In some embodiments, the vector or system thereof can include one or more elements capable of translocating and/or expressing an engineered muscle-specific targeting moiety polynucleotide to/in a specific cell component or organelle. Such organelles can include, but are not limited to, nucleus, ribosome, endoplasmic reticulum, golgi apparatus, chloroplast, mitochondria, vacuole, lysosome, cytoskeleton, plasma membrane, cell wall, peroxisome, centrioles, etc.

Selectable Markers and Tags

One or more of the engineered muscle-specific targeting moiety polynucleotides can be operably linked, fused to, or otherwise modified to include a polynucleotide that encodes or is a selectable marker or tag, which can be a polynucleotide or polypeptide. In some embodiments, the polynucleotide encoding a polypeptide selectable marker is incorporated in the engineered muscle-specific delivery system polynucleotide such that the selectable marker polynucleotide, when translated, is inserted between two amino acids between the N- and C-terminus of the engineered muscle-specific targeting moiety polypeptide (including but not limited to an engineered AAV capsid polypeptide) or at the N- and/or C-terminus of the engineered muscle-specific targeting moiety polypeptide (including but not limited to an engineered AAV capsid polypeptide). In some embodiments, the selectable marker or tag is a polynucleotide barcode or unique molecular identifier (UMI).

The term "barcode" as used herein refers to a short sequence of nucleotides (for example, DNA or RNA) that is used as an identifier for an associated molecule, such as a target molecule and/or target nucleic acid, or as an identifier of the source of an associated molecule, such as a cell-of-origin. A barcode may also refer to any unique, non-naturally occurring, nucleic acid sequence that may be used

to identify the originating source of a nucleic acid fragment. Although it is not necessary to understand the mechanism of an invention, it is believed that the barcode sequence provides a high-quality individual read of a barcode associated with a single cell, a viral vector, labeling ligand (e.g., an aptamer), protein, shRNA, sgRNA or cDNA such that multiple species can be sequenced together.

Barcoding may be performed based on any of the compositions or methods disclosed in patent publication WO 2014047561 A1, compositions and methods for labeling of agents, incorporated herein in its entirety. In certain embodiments barcoding uses an error correcting scheme (T. K. Moon, Error Correction Coding: Mathematical Methods and Algorithms (Wiley, New York, ed. 1, 2005)). Not being bound by a theory, amplified sequences from single cells can be sequenced together and resolved based on the barcode associated with each cell.

In preferred embodiments, sequencing is performed using unique molecular identifiers (UMI). The term "unique molecular identifiers" (UMI) as used herein refers to a sequencing linker or a subtype of nucleic acid barcode used in a method that uses molecular tags to detect and quantify unique amplified products. A UMI is used to distinguish effects through a single clone from multiple clones. The term "clone" as used herein may refer to a single mRNA or target nucleic acid to be sequenced. The UMI may also be used to determine the number of transcripts that gave rise to an amplified product, or in the case of target barcodes as described herein, the number of binding events. In preferred embodiments, the amplification is by PCR or multiple displacement amplification (MDA).

It will be appreciated that the polynucleotide encoding such selectable markers or tags can be incorporated into a polynucleotide encoding one or more components of the engineered muscle-specific delivery system described herein in an appropriate manner to allow expression of the selectable marker or tag. Such techniques and methods are described elsewhere herein and will be instantly appreciated by one of ordinary skill in the art in view of this disclosure. Many such selectable markers and tags are generally known in the art and are intended to be within the scope of this disclosure.

Suitable selectable markers and tags include, but are not limited to, affinity tags, such as chitin binding protein (CBP), maltose binding protein (MBP), glutathione-S-transferase (GST), poly (His) tag; solubilization tags such as thioredoxin (TRX) and poly (NANP), MBP, and GST; chromatography tags such as those consisting of polyanionic amino acids, such as FLAG-tag; epitope tags such as V5-tag, Myc-tag, HA-tag and NE-tag; protein tags that can allow specific enzymatic modification (such as biotinylation by biotin ligase) or chemical modification (such as reaction with FLASH-EDT2 for fluorescence imaging), DNA and/or RNA segments that contain restriction enzyme or other enzyme cleavage sites; DNA segments that encode products that provide resistance against otherwise toxic compounds including antibiotics, such as spectinomycin, ampicillin, kanamycin, tetracycline, Basta, neomycin phosphotransferase II (NEO), hygromycin phosphotransferase (HPT)) and the like; DNA and/or RNA segments that encode products that are otherwise lacking in the recipient cell (e.g., tRNA genes, auxotrophic markers); DNA and/or RNA segments that encode products which can be readily identified (e.g., phenotypic markers such as β -galactosidase, GUS; fluorescent proteins such as green fluorescent protein (GFP), cyan (CFP), yellow (YFP), red (RFP), luciferase, and cell surface proteins); polynucleotides that can generate one or more

new primer sites for PCR (e.g., the juxtaposition of two DNA sequences not previously juxtaposed), DNA sequences not acted upon or acted upon by a restriction endonuclease or other DNA modifying enzyme, chemical, etc.; epitope tags (e.g. GFP, FLAG- and His-tags), and, DNA sequences that make a molecular barcode or unique molecular identifier (UMI), DNA sequences required for a specific modification (e.g., methylation) that allows its identification. Other suitable markers will be appreciated by those of skill in the art.

Selectable markers and tags can be operably linked to one or more components of the engineered AAV capsid system described herein via suitable linker, such as a glycine or glycine serine linkers as short as GS or GG up to (GGGGG)₃ (SEQ ID NO: 51) or (GGGGS)₃ (SEQ ID NO: 56). Other suitable linkers are described elsewhere herein.

The vector or vector system can include one or more polynucleotides encoding one or more engineered muscle-specific targeting moiety (ies) described elsewhere herein. In some embodiments, the targeting moiety encoding polynucleotides can be included in the vector or vector system, such as a viral vector system, such that they are expressed within and/or on the virus particle(s) produced such that the virus particles can be targeted to specific cells, tissues, organs, etc. In some embodiments, one or more engineered muscle-specific targeting moiety encoding polynucleotides are included in the vector or vector system such that the engineered muscle-specific targeting moiety polynucleotide(s) and/or products expressed therefrom include the targeting moiety and can be targeted to specific cells, tissues, organs, etc., such as muscle cells, muscle tissue, or muscle containing organs (e.g. heart). In some embodiments, such as non-viral carriers, the targeting moiety can be attached to the carrier (e.g. polymer, lipid, inorganic molecule etc.) and can be capable of targeting the carrier and any attached or associated engineered muscle-specific targeting moiety polynucleotide(s) to specific cells, tissues, organs, etc., such as muscle cells, muscle tissue, or muscle containing organs (e.g. heart).

Cell-Free Vector and Polynucleotide Expression

In some embodiments, the polynucleotide encoding one or more features of the engineered muscle-specific delivery system containing one or more engineered muscle-specific targeting moieties described herein is expressed from a vector or suitable polynucleotide in a cell-free in vitro system. In other words, the polynucleotide can be transcribed and optionally translated in vitro. In vitro transcription/translation systems and appropriate vectors are generally known in the art and commercially available. Generally, in vitro transcription and in vitro translation systems replicate the processes of RNA and protein synthesis, respectively, outside of the cellular environment. Vectors and suitable polynucleotides for in vitro transcription can include T7, SP6, T3, promoter regulatory sequences that can be recognized and acted upon by an appropriate polymerase to transcribe the polynucleotide or vector.

In vitro translation can be stand-alone (e.g. translation of a purified polyribonucleotide) or linked/coupled to transcription. In some embodiments, the cell-free (or in vitro) translation system can include extracts from rabbit reticulocytes, wheat germ, and/or *E. coli*. The extracts can include various macromolecular components that are needed for translation of exogenous RNA (e.g. 70S or 80S ribosomes, tRNAs, aminoacyl-tRNA, synthetases, initiation, elongation factors, termination factors, etc.). Other components can be included or added during the translation reaction, including but not limited to, amino acids, energy sources (ATP, GTP),

energy regenerating systems (creatine phosphate and creatine phosphokinase (eukaryotic systems)) (phosphoenol pyruvate and pyruvate kinase for bacterial systems), and other co-factors (Mg²⁺, K⁺, etc.). As previously mentioned, in vitro translation can be based on RNA or DNA starting material. Some translation systems can utilize an RNA template as starting material (e.g. reticulocyte lysates and wheat germ extracts). Some translation systems can utilize a DNA template as a starting material (e.g. *E. coli*-based systems). In these systems, transcription and translation are coupled and DNA is first transcribed into RNA, which is subsequently translated. Suitable standard and coupled cell-free translation systems are generally known in the art and are commercially available.

Codon Optimization of Vector Polynucleotides

As described elsewhere herein, the polynucleotide encoding one or more embodiments of the engineered muscle-specific delivery system described herein is codon optimized. In some embodiments, one or more polynucleotides contained in a vector ("vector polynucleotides") described herein that are in addition to an optionally codon optimized polynucleotide encoding embodiments of the engineered muscle-specific delivery system described herein described herein can be codon optimized. In general, codon optimization refers to a process of modifying a nucleic acid sequence for enhanced expression in the host cells of interest by replacing at least one codon (e.g., about or more than about 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more codons) of the native sequence with codons that are more frequently or most frequently used in the genes of that host cell while maintaining the native amino acid sequence. Various species exhibit particular bias for certain codons of a particular amino acid. Codon bias (differences in codon usage between organisms) often correlates with the efficiency of translation of messenger RNA (mRNA), which is in turn believed to be dependent on, among other things, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at www.kazusa.or.jp/codon/ and these tables can be adapted in a number of ways. See Nakamura, Y., et al. "Codon usage tabulated from the international DNA sequence databases: status for the year 2000" Nucl. Acids Res. 28:292(2000). Computer algorithms for codon optimizing a particular sequence for expression in a particular host cell are also available, such as Gene Forge (Aptagen; Jacobus, PA), are also available. In some embodiments, one or more codons (e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 50, or more, or all codons) in a sequence encoding a DNA/RNA-targeting Cas protein corresponds to the most frequently used codon for a particular amino acid. As to codon usage in yeast, reference is made to the online Yeast Genome database available at www.yeastgenome.org/community/codon_usage.shtml, or *Codon selection in yeast*, Bennetzen and Hall, J Biol Chem. 1982 Mar. 25; 257(6): 3026-31. As to codon usage in plants including algae, reference is made to *Codon usage in higher plants, green algae, and cyanobacteria*, Campbell and Gowri, Plant Physiol. 1990 January; 92(1): 1-11.; as well as *Codon usage in plant genes*, Murray et al, Nucleic Acids Res. 1989 Jan. 25; 17(2): 477-98; or *Selection on the codon bias of chlo-*

roplast and cyanelle genes in different plant and algal lineages, Morton B R, J Mol Evol. 1998 April; 46(4): 449-59.

The vector polynucleotide can be codon optimized for expression in a specific cell-type, tissue type, organ type, and/or subject type. In some embodiments, a codon optimized sequence is a sequence optimized for expression in a eukaryote, e.g., humans (i.e. being optimized for expression in a human or human cell), or for another eukaryote, such as another animal (e.g. a mammal or avian) as is described elsewhere herein. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein. In some embodiments, the polynucleotide is codon optimized for a specific cell type. Such cell types can include, but are not limited to, epithelial cells (including skin cells, cells lining the gastrointestinal tract, cells lining other hollow organs), nerve cells (nerves, brain cells, spinal column cells, nerve support cells (e.g. astrocytes, glial cells, Schwann cells etc.), muscle cells (e.g. cardiac muscle, smooth muscle cells, and skeletal muscle cells), connective tissue cells (fat and other soft tissue padding cells, bone cells, tendon cells, cartilage cells), blood cells, stem cells and other progenitor cells, immune system cells, germ cells, and combinations thereof. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein. In some embodiments, the polynucleotide is codon optimized for a specific tissue type. Such tissue types can include, but are not limited to, muscle tissue, connective tissue, connective tissue, nervous tissue, and epithelial tissue. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein. In some embodiments, the polynucleotide is codon optimized for a specific organ. Such organs include, but are not limited to, muscles, skin, intestines, liver, spleen, brain, lungs, stomach, heart, kidneys, gallbladder, pancreas, bladder, thyroid, bone, blood vessels, blood, and combinations thereof. Such codon optimized sequences are within the ambit of the ordinary skilled artisan in view of the description herein.

In some embodiments, a vector polynucleotide is codon optimized for expression in particular cells, such as prokaryotic or eukaryotic cells. The eukaryotic cells may be those of or derived from a particular organism, such as a plant or a mammal, including but not limited to human, or non-human eukaryote or animal or mammal as discussed herein, e.g., mouse, rat, rabbit, dog, livestock, or non-human mammal or primate.

Non-Viral Vectors

In some embodiments, the vector is a non-viral vector or carrier. In some embodiments, non-viral vectors can have the advantage(s) of reduced toxicity and/or immunogenicity and/or increased biosafety as compared to viral vectors. The terms of art "Non-viral vectors and carriers" and as used herein in this context refers to molecules and/or compositions that are not based on one or more component of a virus or virus genome (excluding any nucleotide to be delivered and/or expressed by the non-viral vector) that can be capable of attaching to, incorporating, coupling, and/or otherwise interacting with an engineered muscle-specific targeting moiety polynucleotide of the present invention and can be capable of ferrying the polynucleotide to a cell and/or expressing the polynucleotide. It will be appreciated that this does not exclude the inclusion of a virus-based polynucleotide that is to be delivered. For example, if a gRNA to be delivered is directed against a virus component and it is inserted or otherwise coupled to an otherwise non-viral vector or carrier, this would not make said vector a "viral

vector". Non-viral vectors and carriers include naked polynucleotides, chemical-based carriers, polynucleotide (non-viral) based vectors, and particle-based carriers. It will be appreciated that the term "vector" as used in the context of non-viral vectors and carriers refers to polynucleotide vectors and "carriers" used in this context refers to a non-nucleic acid or polynucleotide molecule or composition that be attached to or otherwise interact with a polynucleotide to be delivered, such as an engineered muscle-specific targeting moiety polynucleotide of the present invention.

Naked Polynucleotides

In some embodiments, one or more engineered muscle specific targeting moiety polynucleotides described elsewhere herein can be included in a naked polynucleotide. The term of art "naked polynucleotide" as used herein refers to polynucleotides that are not associated with another molecule (e.g. proteins, lipids, and/or other molecules) that can often help protect it from environmental factors and/or degradation. As used herein, associated with includes, but is not limited to, linked to, adhered to, adsorbed to, enclosed in, enclosed in or within, mixed with, and the like. Naked polynucleotides that include one or more of the engineered muscle specific targeting moiety polynucleotides described herein can be delivered directly to a host cell and optionally expressed therein. The naked polynucleotides can have any suitable two- and three-dimensional configurations. By way of non-limiting examples, naked polynucleotides can be single-stranded molecules, double stranded molecules, circular molecules (e.g. plasmids and artificial chromosomes), molecules that contain portions that are single stranded and portions that are double stranded (e.g. ribozymes), and the like. In some embodiments, the naked polynucleotide contains only the engineered muscle specific targeting moiety polynucleotide(s) of the present invention. In some embodiments, the naked polynucleotide can contain other nucleic acids and/or polynucleotides in addition to the engineered muscle specific targeting moiety polynucleotide(s) of the present invention. The naked polynucleotides can include one or more elements of a transposon system. Transposons and system thereof are described in greater detail elsewhere herein.

Non-Viral Polynucleotide Vectors

In some embodiments, one or more of the engineered muscle specific targeting moiety polynucleotides can be included in a non-viral polynucleotide vector. Suitable non-viral polynucleotide vectors include, but are not limited to, transposon vectors and vector systems, plasmids, bacterial artificial chromosomes, yeast artificial chromosomes, AR (antibiotic resistance)-free plasmids and miniplasmids, circular covalently closed vectors (e.g. minicircles, minivectors, miniknots), linear covalently closed vectors ("dumbbell shaped"), MIDGE (minimalistic immunologically defined gene expression) vectors, MiLV (micro-linear vector) vectors, Ministrings, mini-intronic plasmids, PSK systems (post-segregationally killing systems), ORT (operator repressor titration) plasmids, and the like. See e.g. Hardee et al. 2017. *Genes*. 8(2): 65.

In some embodiments, the non-viral polynucleotide vector can have a conditional origin of replication. In some embodiments, the non-viral polynucleotide vector can be an ORT plasmid. In some embodiments, the non-viral polynucleotide vector can have a minimalistic immunologically defined gene expression. In some embodiments, the non-viral polynucleotide vector can have one or more post-segregationally killing system genes. In some embodiments, the non-viral polynucleotide vector is AR-free. In some embodiments, the non-viral polynucleotide vector is a mini-

vector. In some embodiments, the non-viral polynucleotide vector includes a nuclear localization signal. In some embodiments, the non-viral polynucleotide vector can include one or more CpG motifs. In some embodiments, the non-viral polynucleotide vectors can include one or more scaffold/matrix attachment regions (S/MARs). See e.g. Mirkovitch et al. 1984. *Cell*. 39:223-232, Wong et al. 2015. *Adv. Genet.* 89:113-152, whose techniques and vectors can be adapted for use in the present invention. S/MARs are AT-rich sequences that play a role in the spatial organization of chromosomes through DNA loop base attachment to the nuclear matrix. S/MARs are often found close to regulatory elements such as promoters, enhancers, and origins of DNA replication. Inclusion of one or S/MARs can facilitate a once-per-cell-cycle replication to maintain the non-viral polynucleotide vector as an episome in daughter cells. In embodiments, the S/MAR sequence is located downstream of an actively transcribed polynucleotide (e.g. one or more engineered muscle specific targeting moiety polynucleotides of the present invention) included in the non-viral polynucleotide vector. In some embodiments, the S/MAR can be a S/MAR from the beta-interferon gene cluster. See e.g. Verghese et al. 2014. *Nucleic Acid Res.* 42: e53; Xu et al. 2016. *Sci. China Life Sci.* 59:1024-1033; Jin et al. 2016. *8:702-711*; Koirala et al. 2014. *Adv. Exp. Med. Biol.* 801: 703-709; and Nehlsen et al. 2006. *Gene Ther. Mol. Biol.* 10:233-244, whose techniques and vectors can be adapted for use in the present invention.

In some embodiments, the non-viral vector is a transposon vector or system thereof. As used herein, "transposon" (also referred to as transposable element) refers to a polynucleotide sequence that is capable of moving from location in a genome to another. There are several classes of transposons. Transposons include retrotransposons and DNA transposons. Retrotransposons require the transcription of the polynucleotide that is moved (or transposed) in order to transpose the polynucleotide to a new genome or polynucleotide. DNA transposons are those that do not require reverse transcription of the polynucleotide that is moved (or transposed) in order to transpose the polynucleotide to a new genome or polynucleotide. In some embodiments, the non-viral polynucleotide vector can be a retrotransposon vector. In some embodiments, the retrotransposon vector includes long terminal repeats. In some embodiments, the retrotransposon vector does not include long terminal repeats. In some embodiments, the non-viral polynucleotide vector can be a DNA transposon vector. DNA transposon vectors can include a polynucleotide sequence encoding a transposase. In some embodiments, the transposon vector is configured as a non-autonomous transposon vector, meaning that the transposition does not occur spontaneously on its own. In some of these embodiments, the transposon vector lacks one or more polynucleotide sequences encoding proteins required for transposition. In some embodiments, the non-autonomous transposon vectors lack one or more Ac elements.

In some embodiments, a non-viral polynucleotide transposon vector system can include a first polynucleotide vector that contains the engineered muscle specific targeting moiety polynucleotide(s) of the present invention flanked on the 5' and 3' ends by transposon terminal inverted repeats (TIRs) and a second polynucleotide vector that includes a polynucleotide capable of encoding a transposase coupled to a promoter to drive expression of the transposase. When both are expressed in the same cell the transposase can be expressed from the second vector and can transpose the material between the TIRs on the first vector (e.g. the

engineered muscle specific targeting moiety polynucleotide(s) of the present invention) and integrate it into one or more positions in the host cell's genome. In some embodiments, the transposon vector or system thereof can be configured as a gene trap. In some embodiments, the TIRs can be configured to flank a strong splice acceptor site followed by a reporter and/or other gene (e.g. one or more of the engineered muscle specific targeting moiety polynucleotide(s) of the present invention) and a strong poly A tail. When transposition occurs while using this vector or system thereof, the transposon can insert into an intron of a gene and the inserted reporter or other gene can provoke a mis-splicing process and as a result it inactivates the trapped gene.

Any suitable transposon system can be used. Suitable transposon and systems thereof can include, Sleeping Beauty transposon system (Tcl/mariner superfamily) (see e.g. Ivics et al. 1997. *Cell*. 91(4): 501-510), piggyBac (piggyBac superfamily) (see e.g. Li et al. 2013 110(25): E2279-E2287 and Yusa et al. 2011. *PNAS*. 108(4): 1531-1536), Tol2 (superfamily hAT), Frog Prince (Tcl/mariner superfamily) (see e.g. Miskey et al. 2003 *Nucleic Acid Res.* 31(23): 6873-6881) and variants thereof.

Viral Vectors

In some embodiments, the vector is a viral vector. The term of art "viral vector" and as used herein in this context refers to polynucleotide based vectors that contain one or more elements from or based upon one or more elements of a virus that can be capable of expressing and packaging a polynucleotide, such as an engineered muscle specific targeting moiety polynucleotide of the present invention, into a virus particle and producing said virus particle when used alone or with one or more other viral vectors (such as in a viral vector system). Viral vectors and systems thereof can be used for producing viral particles for delivery of and/or expression of one or more components of the engineered muscle-specific system described herein. The viral vector can be part of a viral vector system involving multiple vectors. In some embodiments, systems incorporating multiple viral vectors can increase the safety of these systems. Suitable viral vectors can include adenoviral-based vectors, adeno associated vectors, helper-dependent adenoviral (HdAd) vectors, hybrid adenoviral vectors, and the like. Other embodiments of viral vectors and viral particles produce therefrom are described elsewhere herein. In some embodiments, the viral vectors are configured to produce replication incompetent viral particles for improved safety of these systems.

Adenoviral Vectors, Helper-Dependent Adenoviral Vectors, and Hybrid Adenoviral Vectors

In some embodiments, the vector can be an adenoviral vector. Accordingly, the present invention is applicable to a virus within the family Adenoviridae, such as Atadenovirus, e.g., Ovine atadenovirus D, Aviadenovirus, e.g., Fowl aviadenovirus A, Ichtadenovirus, e.g., Sturgeon ichtadenovirus A, Mastadenovirus (which includes adenoviruses such as all human adenoviruses), e.g., Human mastadenovirus C, and Siadenovirus, e.g., Frog siadenovirus A. Thus, a virus of within the family Adenoviridae is contemplated as within the invention with discussion herein as to adenovirus applicable to other family members. In some embodiments, the adenoviral vector can include elements such that the virus particle produced using the vector or system thereof can be serotype 2, 5, or 9. In some embodiments, the polynucleotide to be delivered via the adenoviral particle can be up to about 8 kb. Thus, in some embodiments, an adenoviral vector can include a DNA polynucleotide to be delivered

that can range in size from about 0.001 kb to about 8 kb. Adenoviral vectors have been used successfully in several contexts (see e.g. Teramoto et al. 2000. *Lancet*. 355:1911-1912; Lai et al. 2002. *DNA Cell. Biol.* 21:895-913; Flotte et al., 1996. *Hum. Gene. Ther.* 7:1145-1159; and Kay et al. 2000. *Nat. Genet.* 24:257-261. The engineered muscle specific targeting moiety (ies) can be included in an adenoviral vector to produce adenoviral particles containing said engineered AAV capsids containing the engineered muscle specific targeting moiety(ies).

In some embodiments, the vector can be a helper-dependent adenoviral vector or system thereof. These are also referred to in the field as "gutless" or "guttled" vectors and are a modified generation of adenoviral vectors (see e.g. Thrasher et al. 2006. *Nature*. 443: E5-7). In embodiments of the helper-dependent adenoviral vector system, one vector (the helper) can contain all the viral genes required for replication but contains a conditional gene defect in the packaging domain. The second vector of the system can contain only the ends of the viral genome, one or more engineered AAV capsid polynucleotides, and the native packaging recognition signal, which can allow selective packaged release from the cells (see e.g. Cideciyan et al. 2009. *N Engl J Med.* 361:725-727). Helper-dependent Adenoviral vector systems have been successful for gene delivery in several contexts (see e.g. Simonelli et al. 2010. *J Am Soc Gene Ther.* 18:643-650; Cideciyan et al. 2009. *N Engl J Med.* 361:725-727; Crane et al. 2012. *Gene Ther.* 19(4): 443-452; Alba et al. 2005. *Gene Ther.* 12:18-S27; Croyle et al. 2005. *Gene Ther.* 12:579-587; Amalfitano et al. 1998. *J. Virol.* 72:926-933; and Morral et al. 1999. *PNAS*. 96:12816-12821). The techniques and vectors described in these publications can be adapted for inclusion of the engineered AAV capsid polynucleotides described herein. In some embodiments, the viral particle containing an engineered muscle specific targeting moiety or encoding polynucleotide is produced from a helper-dependent adenoviral vector or system thereof can be up to about 38 kb. Thus, in some embodiments, an adenoviral vector can range in size from about 0.001 kb to about 37 kb (see e.g. Rosewell et al. 2011. *J. Genet. Syndr. Gene Ther. Suppl.* 5:001).

In some embodiments, the vector is a hybrid-adenoviral vector or system thereof. Hybrid adenoviral vectors are composed of the high transduction efficiency of a gene-deleted adenoviral vector and the long-term genome-integrating potential of adeno-associated, retroviruses, lentivirus, and transposon based-gene transfer. In some embodiments, such hybrid vector systems can result in stable transduction and limited integration site. See e.g. Balague et al. 2000. *Blood*. 95:820-828; Morral et al. 1998. *Hum. Gene Ther.* 9:2709-2716; Kubo and Mitani. 2003. *J. Virol.* 77(5): 2964-2971; Zhang et al. 2013. *PLoS One*. 8(10): e76771; and Cooney et al. 2015. *Mol. Ther.* 23(4): 667-674), whose techniques and vectors described therein can be modified and adapted for use in the engineered AAV muscle-specific delivery system of the present invention. In some embodiments, a hybrid-adenoviral vector can include one or more features of a retrovirus and/or an adeno-associated virus. In some embodiments, the hybrid-adenoviral vector can include one or more features of a spuma retrovirus or foamy virus (FV). See e.g. Ehrhardt et al. 2007. *Mol. Ther.* 15:146-156 and Liu et al. 2007. *Mol. Ther.* 15:1834-1841, whose techniques and vectors described therein can be modified and adapted for use in the engineered AAV capsid system of the present invention. Advantages of using one or more features from the FVs in the hybrid-adenoviral vector or system thereof can include the ability of the viral particles

produced therefrom to infect a broad range of cells, a large packaging capacity as compared to other retroviruses, and the ability to persist in quiescent (non-dividing) cells. See also e.g. Ehrhardt et al. 2007. *Mol. Ther.* 15:146-156 and Shuji et al. 2011. *Mol. Ther.* 19:76-82, whose techniques and vectors described therein can be modified and adapted for use in the engineered AAV capsid system of the present invention.

Adeno Associated Vectors

In an embodiment, the engineered vector or system thereof can be an adeno-associated vector (AAV). See, e.g., West et al., *Virology* 160:38-47(1987); U.S. Pat. No. 4,797,368; WO 93/24641; Kotin, *Human Gene Therapy* 5:793-801(1994); and Muzyczka, *J. Clin. Invest.* 94:1351(1994). Although similar to adenoviral vectors in some of their features, AAVs have some deficiency in their replication and/or pathogenicity and thus can be safer than adenoviral vectors. In some embodiments the AAV can integrate into a specific site on chromosome 19 of a human cell with no observable side effects. In some embodiments, the capacity of the AAV vector, system thereof, and/or AAV particles can be up to about 4.7 kb. The AAV vector or system thereof can include one or more engineered capsid polynucleotides described herein.

The AAV vector or system thereof can include one or more regulatory molecules. In some embodiments the regulatory molecules can be promoters, enhancers, repressors and the like, which are described in greater detail elsewhere herein. In some embodiments, the AAV vector or system thereof can include one or more polynucleotides that can encode one or more regulatory proteins. In some embodiments, the one or more regulatory proteins can be selected from Rep78, Rep68, Rep52, Rep40, variants thereof, and combinations thereof. In some embodiments, the promoter can be a tissue specific promoter as previously discussed. In some embodiments, the tissue specific promoter can drive expression of an engineered capsid AAV capsid polynucleotide described herein. This can be advantageous such as for determining muscle-specific targeting moieties as previously described and as set forth in 62/899,453, 62/916,207, 63/018,454, 63/055,252, and 62/916,221 and International Application No. PCT/US20/50534.

The AAV vector or system thereof can include one or more polynucleotides that can encode one or more capsid proteins, such as the engineered AAV capsid proteins described elsewhere herein. The engineered capsid proteins can be capable of assembling into a protein shell (an engineered capsid) of the AAV virus particle. The engineered capsid can have a cell-, tissue-, and/or organ-specific tropism. In some embodiments, the AAV capsid protein can include one or more engineered muscle-specific targeting moieties described elsewhere herein. In some embodiments, one or more muscle-specific targeting moieties included in the AAV capsid includes an RGD motif as described in greater detail elsewhere herein.

In some embodiments, the AAV vector or system thereof can include one or more adenovirus helper factors or polynucleotides that can encode one or more adenovirus helper factors. Such adenovirus helper factors can include, but are not limited, E1A, E1B, E2A, E4ORF6, and VA RNAs. In some embodiments, a producing host cell line expresses one or more of the adenovirus helper factors.

The AAV vector or system thereof can be configured to produce AAV particles having a specific serotype. In some embodiments, the serotype can be AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV rh.74, AAV rh.10, or any combination thereof. In some embodi-

ments, the AAV can be AAV1, AAV-2, AAV-5, AAV-9 or any combination thereof. One can select the AAV of the AAV with regard to the cells to be targeted; e.g., one can select AAV serotypes 1, 2, 5, 9 or a hybrid capsid AAV-1, AAV-2, AAV-5, AAV-9 or any combination thereof for targeting brain and/or neuronal cells; and one can select AAV-4 for targeting cardiac tissue; and one can select AAV-8 for delivery to the liver. Thus, in some embodiments, an AAV vector or system thereof capable of producing AAV particles capable of targeting the brain and/or neuronal cells can be configured to generate AAV particles having serotypes 1, 2, 5 or a hybrid capsid AAV-1, AAV-2, AAV-5 or any combination thereof. In some embodiments, an AAV vector or system thereof capable of producing AAV particles capable of targeting cardiac tissue can be configured to generate an AAV particle having an AAV-4 serotype. In some embodiments, an AAV vector or system thereof capable of producing AAV particles capable of targeting the liver can be configured to generate an AAV having an AAV-8 serotype. See also Srivastava. 2017. *Curr. Opin. Virol.* 21:75-80.

It will be appreciated that while the different serotypes can provide some level of cell, tissue, and/or organ specificity, each serotype still is multi-tropic and thus can result in tissue-toxicity if using that serotype to target a tissue that the serotype is less efficient in transducing. Thus, in addition to achieving some tissue targeting capacity via selecting an AAV of a particular serotype, it will be appreciated that the tropism of the AAV serotype can be modified by an engineered AAV capsid described herein. As described elsewhere herein, variants of wild-type AAV of any serotype can be generated via a method described herein and determined to have a particular cell-specific tropism, which can be the same or different as that of the reference wild-type AAV serotype. In some embodiments, the cell, tissue, and/or specificity of the wild-type serotype can be enhanced (e.g. made more selective or specific for a particular cell type that the serotype is already biased towards). For example, wild-type AAV-9 is biased towards muscle and brain in humans (see e.g. Srivastava. 2017. *Curr. Opin. Virol.* 21:75-80.) By including an engineered AAV capsid and/or capsid protein variant of wild-type AAV-9 as described herein, the bias for e.g. brain can be reduced or eliminated and/or the muscle specificity increased such that the brain specificity appears reduced in comparison, thus enhancing the specificity for the muscle as compared to the wild-type AAV-9. As previously mentioned, inclusion of an engineered capsid and/or capsid protein variant of a wild-type AAV serotype can have a different tropism than the wild-type reference AAV serotype. For example, an engineered AAV capsid and/or capsid protein variant of AAV-9 can have specificity for a tissue other than muscle or brain in humans.

In some embodiments, the AAV vector is a hybrid AAV vector or system thereof. Hybrid AAVs are AAVs that include genomes with elements from one serotype that are packaged into a capsid derived from at least one different serotype. For example, if it is the rAAV2/5 that is to be produced, and if the production method is based on the helper-free, transient transfection method discussed above, the 1st plasmid and the 3rd plasmid (the adeno helper plasmid) will be the same as discussed for rAAV2 production. However, the 2nd plasmid, the pRepCap will be different. In this plasmid, called pRep2/Cap5, the Rep gene is still derived from AAV2, while the Cap gene is derived from AAV5. The production scheme is the same as the above-mentioned approach for AAV2 production. The resulting rAAV is called rAAV2/5, in which the genome is based on recombinant AAV2, while the capsid is based on AAV5. It

is assumed the cell or tissue-tropism displayed by this AAV2/5 hybrid virus should be the same as that of AAV5. It will be appreciated that wild-type hybrid AAV particles suffer the same specificity issues as with the non-hybrid wild-type serotypes previously discussed.

Advantages achieved by the wild-type based hybrid AAV systems can be combined with the increased and customizable cell-specificity that can be achieved with the engineered AAV capsids can be combined by generating a hybrid AAV that can include an engineered AAV capsid described elsewhere herein. It will be appreciated that hybrid AAVs can contain an engineered AAV capsid containing a genome with elements from a different serotype than the reference wild-type serotype that the engineered AAV capsid is a variant of. For example, a hybrid AAV can be produced that includes an engineered AAV capsid that is a variant of an AAV-9 serotype that is used to package a genome that contains components (e.g. rep elements) from an AAV-2 serotype. As with wild-type based hybrid AAVs previously discussed, the tropism of the resulting AAV particle will be that of the engineered AAV capsid.

A tabulation of certain wild-type AAV serotypes as to these cells can be found in Grimm, D. et al, J. Virol. 82:5887-5911(2008) reproduced below as Table 7. Further tropism details can be found in Srivastava. 2017. Curr. Opin. Virol. 21:75-80 as previously discussed.

TABLE 7

Cell Line	AAV-1	AAV-2	AAV-3	AAV-4	AAV-5	AAV-6	AAV-8	AAV-9
Huh-7	13	100	2.5	0.0	0.1	10	0.7	0.0
HEK293	25	100	2.5	0.1	0.1	5	0.7	0.1
HeLa	3	100	2.0	0.1	6.7	1	0.2	0.1
HepG2	3	100	16.7	0.3	1.7	5	0.3	ND
Hep1A	20	100	0.2	1.0	0.1	1	0.2	0.0
911	17	100	11	0.2	0.1	17	0.1	ND
CHO	100	100	14	1.4	333	50	10	1.0
COS	33	100	33	3.3	5.0	14	2.0	0.5
MeWo	10	100	20	0.3	6.7	10	1.0	0.2
NIH3T3	10	100	2.9	2.9	0.3	10	0.3	ND
A549	14	100	20	ND	0.5	10	0.5	0.1
HT1180	20	100	10	0.1	0.3	33	0.5	0.1
Monocytes	1111	100	ND	ND	125	1429	ND	ND
Immature DC	2500	100	ND	ND	222	2857	ND	ND
Mature DC	2222	100	ND	ND	333	3333	ND	ND

In some embodiments, the AAV vector or system thereof is AAV rh.74 or AAV rh.10.

In some embodiments, the AAV vector or system thereof is configured as a “gutless” vector, similar to that described in connection with a retroviral vector. In some embodiments, the “gutless” AAV vector or system thereof can have the cis-acting viral DNA elements involved in genome amplification and packaging in linkage with the heterologous sequences of interest (e.g. the engineered AAV capsid polynucleotide(s)).

Retroviral and Lentiviral Vectors

In some embodiments, the engineered muscle-specific delivery system or component thereof is or is incorporated into a retroviral or lentiviral vector. Retroviral vectors can be composed of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the therapeutic gene into the target cell to provide permanent transgene expression. Suitable retroviral vectors for the CRISPR-Cas systems can include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV),

Simian immunodeficiency virus (SIV), human immunodeficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., J. Virol. 66:2731-2739(1992); Johann et al., J. Virol. 66:1635-1640(1992); Sommerfelt et al., Virol. 176:58-59(1990); Wilson et al., J. Virol. 63:2374-2378 (1989); Miller et al., J. Virol. 65:2220-2224(1991); PCT/US94/05700). Selection of a retroviral gene transfer system may therefore depend on the target tissue.

The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. Lentiviral vectors are retroviral vectors that are able to transduce or infect non-dividing cells and are described in greater detail elsewhere herein. A retrovirus can also be engineered to allow for conditional expression of the inserted transgene, such that only certain cell types are infected by the lentivirus. In some embodiments where the end product is a muscle-specific viral particle, the tropism is defined at least in part by the presence of a muscle-specific targeting moiety described herein, such as incorporated within a capsid protein and/or capsid of the retrovirus or lentivirus particles.

Lentiviruses are complex retroviruses that have the ability to infect and express their genes in both mitotic and post-mitotic cells. Advantages of using a lentiviral approach can include the ability to transduce or infect non-dividing cells and their ability to typically produce high viral titers, which

can increase efficiency or efficacy of production and delivery. Suitable lentiviral vectors include, but are not limited to, human immunodeficiency virus (HIV)-based lentiviral vectors, feline immunodeficiency virus (FIV)-based lentiviral vectors, simian immunodeficiency virus (SIV)-based lentiviral vectors, Moloney Murine Leukaemia Virus (Mo-MLV), Visna-maedi virus (VMV)-based lentiviral vector, caprine arthritis-encephalitis virus (CAEV)-based lentiviral vector, bovine immune deficiency virus (BIV)-based lentiviral vector, and Equine infectious anemia (EIAV)-based lentiviral vector. In some embodiments, an HIV-based lentiviral vector system can be used. In some embodiments, a FIV-based lentiviral vector system can be used.

In some embodiments, the lentiviral vector is an EIAV-based lentiviral vector or vector system. EIAV vectors have been used to mediate expression, packaging, and/or delivery in other contexts, such as for ocular gene therapy (see, e.g., Balagaan, J Gene Med 2006; 8:275-285). In another embodiment, RetinoStat®, (see, e.g., Binley et al., HUMAN GENE THERAPY 23:980-991 (September 2012)), which describes RetinoStat®, an equine infectious anemia virus-based lentiviral gene therapy vector that expresses angio-

static proteins endostatin and angiostatin that is delivered via a subretinal injection for the treatment of the wet form of age-related macular degeneration. Any of these vectors described in these publications can be modified for the elements of the engineered muscle-specific delivery system described herein.

In some embodiments, the lentiviral vector or vector system thereof can be a first-generation lentiviral vector or vector system thereof. First-generation lentiviral vectors can contain a large portion of the lentivirus genome, including the gag and pol genes, other additional viral proteins (e.g. VSV-G) and other accessory genes (e.g. vif, vpr, vpu, nef, and combinations thereof), regulatory genes (e.g. tat and/or rev) as well as the gene of interest between the LTRs. First generation lentiviral vectors can result in the production of virus particles that can be capable of replication in vivo, which may not be appropriate for some instances or applications.

In some embodiments, the lentiviral vector or vector system thereof can be a second-generation lentiviral vector or vector system thereof. Second-generation lentiviral vectors do not contain one or more accessory virulence factors and do not contain all components necessary for virus particle production on the same lentiviral vector. This can result in the production of a replication-incompetent virus particle and thus increase the safety of these systems over first-generation lentiviral vectors. In some embodiments, the second-generation vector lacks one or more accessory virulence factors (e.g. vif, vpr, vpu, nef, and combinations thereof). Unlike the first-generation lentiviral vectors, no single second generation lentiviral vector includes all features necessary to express and package a polynucleotide into a virus particle. In some embodiments, the envelope and packaging components are split between two different vectors with the gag, pol, rev, and tat genes being contained on one vector and the envelope protein (e.g. VSV-G) are contained on a second vector. The gene of interest, its promoter, and LTRs can be included on a third vector that can be used in conjunction with the other two vectors (packaging and envelope vectors) to generate a replication-incompetent virus particle.

In some embodiments, the lentiviral vector or vector system thereof can be a third-generation lentiviral vector or vector system thereof. Third-generation lentiviral vectors and vector systems thereof have increased safety over first- and second-generation lentiviral vectors and systems thereof because, for example, the various components of the viral genome are split between two or more different vectors but used together in vitro to make virus particles, they can lack the tat gene (when a constitutively active promoter is included up-stream of the LTRs), and they can include one or more deletions in the 3'LTR to create self-inactivating (SIN) vectors having disrupted promoter/enhancer activity of the LTR. In some embodiments, a third-generation lentiviral vector system can include (i) a vector plasmid that contains the polynucleotide of interest and upstream promoter that are flanked by the 5' and 3' LTRs, which can optionally include one or more deletions present in one or both of the LTRs to render the vector self-inactivating; (ii) a "packaging vector(s)" that can contain one or more genes involved in packaging a polynucleotide into a virus particle that is produced by the system (e.g. gag, pol, and rev) and upstream regulatory sequences (e.g. promoter(s)) to drive expression of the features present on the packaging vector, and (iii) an "envelope vector" that contains one or more envelope protein genes and upstream promoters. In certain embodiments, the third-generation lentiviral vector system

can include at least two packaging vectors, with the gag-pol being present on a different vector than the rev gene.

In some embodiments, self-inactivating lentiviral vectors with an siRNA targeting a common exon shared by HIV tat/rev, a nucleolar-localizing TAR decoy, and an anti-CCR5-specific hammerhead ribozyme (see, e.g., DiGiusto et al. (2010) *Sci Transl Med* 2: 36ra43) can be used/and or adapted to the CRISPR-Cas system of the present invention.

In some embodiments, the pseudotype and infectivity or tropism of a lentivirus particle can be tuned by altering the type of envelope protein(s) included in the lentiviral vector or system thereof. As used herein, an "envelope protein" or "outer protein" means a protein exposed at the surface of a viral particle that is not a capsid protein. For example, envelope or outer proteins typically comprise proteins embedded in the envelope of the virus. In some embodiments, a lentiviral vector or vector system thereof can include a VSV-G envelope protein. VSV-G mediates viral attachment to an LDL receptor (LDLR) or an LDLR family member present on a host cell, which triggers endocytosis of the viral particle by the host cell. Because LDLR is expressed by a wide variety of cells, viral particles expressing the VSV-G envelope protein can infect or transduce a wide variety of cell types. Other suitable envelope proteins can be incorporated based on the host cell that a user desires to be infected by a virus particle produced from a lentiviral vector or system thereof described herein and can include, but are not limited to, feline endogenous virus envelope protein (RD114) (see e.g. Hanawa et al. *Molec. Ther.* 2002 5(3) 242-251), modified Sindbis virus envelope proteins (see e.g. Morizono et al. 2010. *J. Virol.* 84(14) 6923-6934; Morizono et al. 2001. *J. Virol.* 75:8016-8020; Morizono et al. 2009. *J. Gene Med.* 11:549-558; Morizono et al. 2006 *Virology* 355:71-81; Morizono et al. *J. Gene Med.* 11:655-663, Morizono et al. 2005 *Nat. Med.* 11:346-352), baboon retroviral envelope protein (see e.g. Girard-Gagnepain et al. 2014. *Blood.* 124:1221-1231); Tupaia paramyxovirus glycoproteins (see e.g. Enkirch T. et al., 2013. *Gene Ther.* 20:16-23); measles virus glycoproteins (see e.g. Funke et al. 2008. *Molec. Ther.* 16(8): 1427-1436), rabies virus envelope proteins, MLV envelope proteins, Ebola envelope proteins, baculovirus envelope proteins, filovirus envelope proteins, hepatitis E1 and E2 envelope proteins, gp41 and gp120 of HIV, hemagglutinin, neuraminidase, M2 proteins of influenza virus, and combinations thereof.

In some embodiments, the tropism of the resulting lentiviral particle can be tuned by incorporating cell targeting peptides into a lentiviral vector such that the cell targeting peptides are expressed on the surface of the resulting lentiviral particle. In some embodiments, a lentiviral vector can contain an envelope protein that is fused to a cell targeting protein (see e.g. Buchholz et al. 2015. *Trends Biotechnol.* 33:777-790; Bender et al. 2016. *PLOS Pathog.* 12(e1005461); and Friedrich et al. 2013. *Mol. Ther.* 2013. 21:849-859).

In some embodiments, a split-intein-mediated approach to target lentiviral particles to a specific cell type can be used (see e.g. Chamoun-Emaneulli et al. 2015. *Biotechnol. Bioeng.* 112:2611-2617, Ramirez et al. 2013. *Protein. Eng. Des. Sel.* 26:215-233. In these embodiments, a lentiviral vector can contain one half of a splicing-deficient variant of the naturally split intein from *Nostoc punctiforme* fused to a cell targeting peptide and the same or different lentiviral vector can contain the other half of the split intein fused to an envelope protein, such as a binding-deficient, fusion-competent virus envelope protein. This can result in production of a virus particle from the lentiviral vector or vector system

that includes a split intein that can function as a molecular Velcro linker to link the cell-binding protein to the pseudotyped lentivirus particle. This approach can be advantageous for use where surface-incompatibilities can restrict the use of, e.g., cell targeting peptides.

In some embodiments, a covalent-bond-forming protein-peptide pair can be incorporated into one or more of the lentiviral vectors described herein to conjugate a cell targeting peptide to the virus particle (see e.g. Kasaraneni et al. 2018. *Sci. Reports* (8) No. 10990). In some embodiments, a lentiviral vector can include an N-terminal PDZ domain of InaD protein (PDZ1) and its pentapeptide ligand (TEFCA) from NorpA, which can conjugate the cell targeting peptide to the virus particle via a covalent bond (e.g. a disulfide bond). In some embodiments, the PDZ1 protein can be fused to an envelope protein, which can optionally be binding deficient and/or fusion competent virus envelope protein and included in a lentiviral vector. In some embodiments, the TEFCA can be fused to a cell targeting peptide and the TEFCA-CPT fusion construct can be incorporated into the same or a different lentiviral vector as the PDZ1-envelope protein construct. During virus production, specific interaction between the PDZ1 and TEFCA facilitates producing virus particles covalently functionalized with the cell targeting peptide and thus capable of targeting a specific cell-type based upon a specific interaction between the cell targeting peptide and cells expressing its binding partner. This approach can be advantageous for use where surface-incompatibilities can restrict the use of, e.g., cell targeting peptides.

Lentiviral vectors have been disclosed as in the treatment for Parkinson's Disease, see, e.g., US Patent Publication No. 20120295960 and U.S. Pat. Nos. 7,303,910 and 7,351,585. Lentiviral vectors have also been disclosed for the treatment of ocular diseases, see e.g., US Patent Publication Nos. 20060281180, 20090007284, US20110117189; US20090017543; US20070054961, US20100317109. Lentiviral vectors have also been disclosed for delivery to the brain, see, e.g., US Patent Publication Nos. US20110293571; US20110293571, US20040013648, US20070025970, US20090111106 and U.S. Pat. No. 7,259, 015. Any of these systems or a variant thereof can be used to deliver an engineered muscle-specific polynucleotide to a cell and/or incorporate a muscle-specific targeting moiety described herein for muscle-specific delivery to a cell.

In some embodiments, a lentiviral vector system can include one or more transfer plasmids. Transfer plasmids can be generated from various other vector backbones and can include one or more features that can work with other retroviral and/or lentiviral vectors in the system that can, for example, improve safety of the vector and/or vector system, increase virial titers, and/or increase or otherwise enhance expression of the desired insert to be expressed and/or packaged into the viral particle. Suitable features that can be included in a transfer plasmid can include, but are not limited to, 5'LTR, 3'LTR, SIN/LTR, origin of replication (Ori), selectable marker genes (e.g. antibiotic resistance genes), Psi (4), RRE (rev response element), cPPT (central polypurine tract), promoters, WPRE (woodchuck hepatitis post-transcriptional regulatory element), SV40 polyadenylation signal, pUC origin, SV40 origin, F1 origin, and combinations thereof.

In another embodiment, Cocal vesiculovirus envelope pseudotyped retroviral or lentiviral vector particles are contemplated (see, e.g., US Patent Publication No. 20120164118 assigned to the Fred Hutchinson Cancer Research Center). Cocal virus is in the Vesiculovirus genus

and is a causative agent of vesicular stomatitis in mammals. Cocal virus was originally isolated from mites in Trinidad (Jonkers et al., *Am. J. Vet. Res.* 25:236-242(1964)), and infections have been identified in Trinidad, Brazil, and Argentina from insects, cattle, and horses. Many of the vesiculoviruses that infect mammals have been isolated from naturally infected arthropods, suggesting that they are vector-borne. Antibodies to vesiculoviruses are common among people living in rural areas where the viruses are endemic and laboratory-acquired; infections in humans usually result in influenza-like symptoms. The Cocal virus envelope glycoprotein shares 71.5% identity at the amino acid level with VSV-G Indiana, and phylogenetic comparison of the envelope gene of vesiculoviruses shows that Cocal virus is serologically distinct from, but most closely related to, VSV-G Indiana strains among the vesiculoviruses. Jonkers et al., *Am. J. Vet. Res.* 25:236-242(1964) and Travassos da Rosa et al., *Am. J. Tropical Med. & Hygiene* 33:999-1006(1984). The Cocal vesiculovirus envelope pseudotyped retroviral vector particles may include for example, lentiviral, alpharetroviral, betaretroviral, gammaretroviral, deltaretroviral, and epsilon-retroviral vector particles that may comprise retroviral Gag, Pol, and/or one or more accessory protein(s) and a Cocal vesiculovirus envelope protein. In certain embodiments of these embodiments, the Gag, Pol, and accessory proteins are lentiviral and/or gammaretroviral. In some embodiments, a retroviral vector can contain encoding polypeptides for one or more Cocal vesiculovirus envelope proteins such that the resulting viral or pseudoviral particles are Cocal vesiculovirus envelope pseudotyped.

Herpes Simplex Viral Vectors

In some embodiments, the vector can be a Herpes Simplex Viral (HSV)-based vector or system thereof. HSV systems can include the disabled infections single copy (DISC) viruses, which are composed of a glycoprotein H defective mutant HSV genome. When the defective HSV is propagated in complementing cells, virus particles can be generated that are capable of infecting subsequent cells permanently replicating their own genome but are not capable of producing more infectious particles. See e.g. 2009. Trobridge. *Exp. Opin. Biol. Ther.* 9:1427-1436, whose techniques and vectors described therein can be modified and adapted for use in the CRISPR-Cas system of the present invention. In some embodiments where an HSV vector or system thereof is utilized, the host cell can be a complementing cell. In some embodiments, HSV vector or system thereof can be capable of producing virus particles capable of delivering a polynucleotide cargo of up to 150 kb. Thus, in some embodiment the engineered muscle-specific targeting moiety polynucleotide(s) included in the HSV-based viral vector or system thereof can sum from about 0.001 to about 150 kb. HSV-based vectors and systems thereof have been successfully used in several contexts including various models of neurologic disorders. See e.g. Cockrell et al. 2007. *Mol. Biotechnol.* 36:184-204; Kafri T. 2004. *Mol. Biol.* 246:367-390; Balaggan and Ali. 2012. *Gene Ther.* 19:145-153; Wong et al. 2006. *Hum. Gen. Ther.* 2002. 17:1-9; Azzouz et al. *J. Neurosci.* 22L10302-10312; and Betchen and Kaplitt. 2003. *Curr. Opin. Neurol.* 16:487-493. Any of these systems or a variant thereof can be used to deliver an engineered muscle-specific polynucleotide to a cell and/or incorporate a muscle-specific targeting moiety described herein for muscle-specific delivery to a cell.

Poxvirus Vectors

In some embodiments, the vector can be a poxvirus vector or system thereof. In some embodiments, the poxvirus

vector can result in cytoplasmic expression of one or more cargos that can be packaged by such virus of the present invention. In some embodiments, the capacity of a poxvirus vector or system thereof can be about 25 kb or more. In some embodiments, a poxvirus vector or system thereof can include one or more engineered muscle-specific targeting moiety polynucleotides and/or muscle-specific targeting moieties, engineered capsid proteins, and/or capsids described herein.

Viral Vectors for Delivery to Plants

The systems and compositions may be delivered to plant cells using viral vehicles. Plant cells can be engineered to express compositions (such as proteins) that can contain muscle-specific targeting moiety (ies) that can be subsequently harvested and used as appropriate, such as a therapy for humans or non-human animals. In particular embodiments, the compositions and systems may be introduced in the plant cells using a plant viral vector (e.g., as described in Scholthof et al. 1996, *Annu Rev Phytopathol.* 1996; 34:299-323). Such viral vector may be a vector from a DNA virus, e.g., geminivirus (e.g., cabbage leaf curl virus, bean yellow dwarf virus, wheat dwarf virus, tomato leaf curl virus, maize streak virus, tobacco leaf curl virus, or tomato golden mosaic virus) or nanovirus (e.g., Faba bean necrotic yellow virus). The viral vector may be a vector from an RNA virus, e.g., tobnavirus (e.g., tobacco rattle virus, tobacco mosaic virus), potexvirus (e.g., potato virus X), or hordei-virus (e.g., barley stripe mosaic virus). The replicating genomes of plant viruses may be non-integrative vectors.

Vector Construction

The vectors described herein can be constructed using any suitable process or technique. In some embodiments, one or more suitable recombination and/or cloning methods or techniques can be used to the vector(s) described herein. Suitable recombination and/or cloning techniques and/or methods can include, but not limited to, those described in U.S. Application publication No. US 2004-0171156 A1. Other suitable methods and techniques are described elsewhere herein.

Construction of recombinant AAV vectors are described in a number of publications, including U.S. Pat. No. 5,173, 414; Tratschin et al., *Mol. Cell. Biol.* 5:3251-3260 (1985); Tratschin, et al., *Mol. Cell. Biol.* 4:2072-2081(1984); Hermonat & Muzyczka, *PNAS* 81:6466-6470(1984); and Samulski et al., *J. Virol.* 63:03822-3828(1989). Any of the techniques and/or methods can be used and/or adapted for constructing an AAV or other vector described herein. AAV vectors are discussed elsewhere herein.

In some embodiments, the vector can have one or more insertion sites, such as a restriction endonuclease recognition sequence (also referred to as a "cloning site"). In some embodiments, one or more insertion sites (e.g., about or more than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more insertion sites) are located upstream and/or downstream of one or more sequence elements of one or more vectors.

Delivery vehicles, vectors, particles, nanoparticles, formulations and components thereof for expression of one or more elements of an engineered AAV capsid system described herein are as used in the foregoing documents, such as WO 2014/093622 (PCT/US2013/074667) and are discussed in greater detail herein.

Virus Particle Production from Viral Vectors

AAV Particle Production

There are two main strategies for producing AAV particles from AAV vectors and systems thereof, such as those described herein, which depend on how the adenovirus helper factors are provided (helper v. helper free). In some

embodiments, a method of producing AAV particles from AAV vectors and systems thereof can include adenovirus infection into cell lines that stably harbor AAV replication and capsid encoding polynucleotides along with AAV vector containing the polynucleotide to be packaged and delivered by the resulting AAV particle (e.g. the engineered AAV capsid polynucleotide(s)). In some embodiments, a method of producing AAV particles from AAV vectors and systems thereof can be a "helper free" method, which includes co-transfection of an appropriate producing cell line with three vectors (e.g. plasmid vectors): (1) an AAV vector that contains a polynucleotide of interest (e.g. the engineered AAV capsid polynucleotide(s)) between 2 ITRs; (2) a vector that carries the AAV Rep-Cap encoding polynucleotides; and (helper polynucleotides. One of skill in the art will appreciate various methods and variations thereof that are both helper and -helper free and as well as the different advantages of each system.

The engineered AAV vectors and systems thereof described herein can be produced by any of these methods.

Retroviral Production

In some embodiments, one or more viral vectors and/or system thereof can be delivered to a suitable cell line for production of virus particles containing the polynucleotide or other payload to be delivered to a host cell. Suitable host cells for virus production from viral vectors and systems thereof described herein are known in the art and are commercially available. For example, suitable host cells include HEK 293 cells and its variants (HEK 293T and HEK 293TN cells). In some embodiments, the suitable host cell for virus production from viral vectors and systems thereof described herein can stably express one or more genes involved in packaging (e.g. pol, gag, and/or VSV-G) and/or other supporting genes.

In some embodiments, after delivery of one or more viral vectors to the suitable host cells for or virus production from viral vectors and systems thereof, the cells are incubated for an appropriate length of time to allow for viral gene expression from the vectors, packaging of the polynucleotide or other cargo to be delivered (e.g. an CRISPR-Cas system polynucleotide), and virus particle assembly, and secretion of mature virus particles into the culture media. Various other methods and techniques are generally known to those of ordinary skill in the art.

Mature virus particles can be collected from the culture media by a suitable method. In some embodiments, this can involve centrifugation to concentrate the virus. The titer of the composition containing the collected virus particles can be obtained using a suitable method. Such methods can include transducing a suitable cell line (e.g. NIH 3T3 cells) and determining transduction efficiency, infectivity in that cell line by a suitable method. Suitable methods include PCR-based methods, flow cytometry, and antibiotic selection-based methods. Various other methods and techniques are generally known to those of ordinary skill in the art. The concentration of virus particle can be adjusted as needed. In some embodiments, the resulting composition containing virus particles can contain 1×10^1 - 1×10^{20} particles/mL.

Lentiviruses may be prepared from any lentiviral vector or vector system described herein. In one example embodiment, after cloning pCasES10 (which contains a lentiviral transfer plasmid backbone), HEK293FT at low passage (p=5) can be seeded in a T-75 flask to 50% confluence the day before transfection in DMEM with 10% fetal bovine serum and without antibiotics. After 20 hours, the media can be changed to OptiMEM (serum-free) media and transfection of the lentiviral vectors can done 4 hours later. Cells can

be transfected with 10 µg of lentiviral transfer plasmid (pCasES10) and the appropriate packaging plasmids (e.g., 5 µg of pMD2.G (VSV-g pseudotype), and 7.5 µg of psPAX2 (gag/pol/rev/tat)). Transfection can be carried out in 4 mL OptiMEM with a cationic lipid delivery agent (50 µL Lipofectamine 2000 and 100 µL Plus reagent). After 6 hours, the media can be changed to antibiotic-free DMEM with 10% fetal bovine serum. These methods can use serum during cell culture, but serum-free methods are preferred.

Following transfection and allowing the producing cells (also referred to as packaging cells) to package and produce virus particles with packaged cargo, the lentiviral particles can be purified. In an exemplary embodiment, virus-containing supernatants can be harvested after 48 hours. Collected virus-containing supernatants can first be cleared of debris and filtered through a 0.45 µm low protein binding (PVDF) filter. They can then be spun in an ultracentrifuge for 2 hours at 24,000 rpm. The resulting virus-containing pellets can be resuspended in 50 µL of DMEM overnight at 4 degrees C. They can be then aliquoted and used immediately or immediately frozen at -80 degrees C. for storage.

Vector and Virus Particle Delivery

A vector (including non-viral carriers) described herein can be introduced into host cells to thereby produce transcripts, proteins, or peptides, including fusion proteins or peptides encoded by nucleic acids as described herein (e.g., engineered AAV capsid system transcripts, proteins, enzymes, mutant forms thereof, fusion proteins thereof, etc.), and virus particles (such as from viral vectors and systems thereof).

One or more engineered AAV capsid polynucleotides can be delivered using adeno associated virus (AAV), adenovirus or other plasmid or viral vector types as previously described, in particular, using formulations and doses from, for example, U.S. Pat. No. 8,454,972 (formulations, doses for adenovirus), U.S. Pat. No. 8,404,658 (formulations, doses for AAV) and U.S. Pat. No. 5,846,946 (formulations, doses for DNA plasmids) and from clinical trials and publications regarding the clinical trials involving lentivirus, AAV and adenovirus. For examples, for AAV, the route of administration, formulation and dose can be as in U.S. Pat. No. 8,454,972 and as in clinical trials involving AAV. For Adenovirus, the route of administration, formulation and dose can be as in U.S. Pat. No. 8,404,658 and as in clinical trials involving adenovirus.

For plasmid delivery, the route of administration, formulation and dose can be as in U.S. Pat. No. 5,846,946 and as in clinical studies involving plasmids. In some embodiments, doses can be based on or extrapolated to an average 70 kg individual (e.g. a male adult human), and can be adjusted for patients, subjects, mammals of different weight and species. Frequency of administration is within the ambit of the medical or veterinary practitioner (e.g., physician, veterinarian), depending on usual factors including the age, sex, general health, other conditions of the patient or subject and the particular condition or symptoms being addressed. The viral vectors can be injected into or otherwise delivered to the tissue or cell of interest.

In terms of in vivo delivery, AAV is advantageous over other viral vectors for a couple of reasons such as low toxicity (this may be due to the purification method not requiring ultra-centrifugation of cell particles that can activate the immune response) and a low probability of causing insertional mutagenesis because it doesn't integrate into the host genome.

The vector(s) and virus particles described herein can be delivered in to a host cell in vitro, in vivo, and/or ex vivo.

Delivery can occur by any suitable method including, but not limited to, physical methods, chemical methods, and biological methods. Physical delivery methods are those methods that employ physical force to counteract the membrane barrier of the cells to facilitate intracellular delivery of the vector. Suitable physical methods include, but are not limited to, needles (e.g. injections), ballistic polynucleotides (e.g. particle bombardment, micro projectile gene transfer, and gene gun), electroporation, sonoporation, photoporation, magnetofection, hydroporation, and mechanical massage. Chemical methods are those methods that employ a chemical to elicit a change in the cells membrane permeability or other characteristic(s) to facilitate entry of the vector into the cell. For example, the environmental pH can be altered which can elicit a change in the permeability of the cell membrane. Biological methods are those that rely and capitalize on the host cell's biological processes or biological characteristics to facilitate transport of the vector (with or without a carrier) into a cell. For example, the vector and/or its carrier can stimulate an endocytosis or similar process in the cell to facilitate uptake of the vector into the cell.

Delivery of engineered AAV capsid system components (e.g. polynucleotides encoding engineered AAV capsid and/or capsid proteins) to cells via particles. The term "particle" as used herein, refers to any suitable sized particles for delivery of the engineered AAV capsid system components described herein. Suitable sizes include macro-, micro-, and nano-sized particles. In some embodiments, any of the engineered AAV capsid system components (e.g. polypeptides, polynucleotides, vectors and combinations thereof described herein) can be attached to, coupled to, integrated with, otherwise associated with one or more particles or component thereof as described herein. The particles described herein can then be administered to a cell or organism by an appropriate route and/or technique. In some embodiments, particle delivery can be selected and be advantageous for delivery of the polynucleotide or vector components. It will be appreciated that in embodiments, particle delivery can also be advantageous for other engineered capsid system molecules and formulations described elsewhere herein.

Engineered Virus Particles

Also described herein are engineered virus particles (also referred to herein as "engineered viral particles") that can contain an engineered muscle-specific capsid (e.g. a capsid containing one or more engineered capsid polypeptides having one or more engineered muscle-specific targeting moieties as described in detail elsewhere herein). Also described herein are virus particles containing, as cargo, one or more engineered muscle-specific targeting moiety polynucleotides described elsewhere herein.

It will be appreciated that the engineered viral particles can be lentiviral-based, retroviral-based, poxvirus-based, herpesvirus-based, adenovirus-based particles, helper adenovirus-based particles, AAV-based particles, or hybrid adenovirus-based particles that contain at least one engineered capsid protein as previously described. An engineered viral capsid is one that contains one or more engineered capsid proteins that contain one or more muscle-specific targeting moieties as are described elsewhere herein. In some embodiments, the engineered viral capsid is an engineered AAV capsids.

In some embodiments, the engineered AAV particles can include 1-60 engineered AAV capsid proteins described herein. In some embodiments, the engineered AAV particles can contain 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16,

17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, or 60 engineered capsid proteins. In some embodiments, the engineered AAV particles can contain 0-59 wild-type AAV capsid proteins. In some embodiments, the engineered AAV particles can contain 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, or 59 wild-type AAV capsid proteins. The engineered AAV particles can thus include one or more n-mer motifs as is previously described. In some embodiments, the n-mer is an RGD motif.

The engineered virus particles can each include one or more cargo polynucleotides. Cargo polynucleotides are discussed in greater detail elsewhere herein. Methods of making the engineered AAV particles from viral and non-viral vectors are described elsewhere herein. Formulations containing the engineered virus particles are described elsewhere herein.

Engineered Non-Vector Delivery Vehicles

In some embodiments, the muscle-specific targeting moiety is incorporated in a non-vector delivery vehicle. In some embodiments, the muscle specific targeting moiety is operably coupled or otherwise attached to the non-vector delivery vehicle. As used herein, "attached" can refer to covalent or non-covalent interaction between two or more molecules. Non-covalent interactions can include ionic bonds, electrostatic interactions, van der Waals forces, dipole-dipole interactions, dipole-induced-dipole interactions, London dispersion forces, hydrogen bonding, halogen bonding, electromagnetic interactions, x-x interactions, cation-x interactions, anion-x interactions, polar x-interactions, and hydrophobic effects. In some embodiments, the muscle-specific targeting moiety is incorporated into a composition (such as a protein or polynucleotide) that is operably coupled to or is otherwise attached to the non-vector delivery vehicle. In some embodiments, the engineered muscle-specific targeting moiety is operatively coupled or otherwise attached such that the muscle specific targeting moiety is on a surface of the non-vector delivery vehicle. The delivery vehicles may comprise non-viral vehicles. In general, methods and vehicles capable of delivering nucleic acids and/or proteins may be used for delivering the systems compositions herein. Examples of non-viral vehicles include lipid nanoparticles, cell-penetrating peptides (CPPs), DNA nanoclews, metal nanoparticles, streptolysin O, multifunctional envelope-type nanodevices (MENDs), lipid-coated mesoporous silica particles, and other inorganic nanoparticles. Lipid Particles

The delivery vehicles may comprise lipid particles, e.g., lipid nanoparticles (LNPs) and liposomes. Lipofection is described in e.g., U.S. Pat. Nos. 5,049,386, 4,946,787; and 4,897,355 and lipofection reagents are sold commercially (e.g., Transfectam™ and Lipofectin™). Cationic and neutral lipids that are suitable for efficient receptor-recognition lipofection of polynucleotides include those of Felgner, International Patent Publication Nos. WO 91/17424 and WO 91/16024. The preparation of lipid: nucleic acid complexes, including targeted liposomes such as immunolipid complexes, is well known to one of skill in the art (see, e.g., Crystal, Science 270:404-410(1995); Blaese et al., Cancer Gene Ther. 2:291-297 (1995); Behr et al., Bioconjugate Chem. 5:382-389(1994); Remy et al., Bioconjugate Chem. 5:647-654(1994); Gao et al., Gene Therapy 2:710-722 (1995); Ahmad et al., Cancer Res. 52:4817-4820(1992);

U.S. Pat. Nos. 4,186,183, 4,217,344, 4,235,871, 4,261,975, 4,485,054, 4,501,728, 4,774,085, 4,837,028, and 4,946,787).

Lipid Nanoparticles (LNPs)

LNPs may encapsulate nucleic acids within cationic lipid particles (e.g., liposomes) and may be delivered to cells with relative ease. In some examples, lipid nanoparticles do not contain any viral components, which helps minimize safety and immunogenicity concerns. Lipid particles may be used for in vitro, ex vivo, and in vivo deliveries. Lipid particles may be used for various scales of cell populations.

In some embodiments, LNPs may be used for delivering DNA molecules (e.g., those comprising coding sequences of Cas and/or gRNA) and/or RNA molecules (e.g., mRNA of Cas, gRNAs). In certain cases, LNPs may be used for delivering RNP complexes of Cas/gRNA.

Components in LNPs may comprise cationic lipids 1,2-dilinoyleyl-3-dimethylammonium-propane (DLinDAP), 1,2-dilinoyleloxy-3-N,N-dimethylaminopropane (DLinDMA), 1,2-dilinoyleloxyketo-N,N-dimethyl-3-aminopropane (DLinK-DMA), 1,2-dilinoylel-4-(2-dimethylaminoethyl)-[1,3]-dioxolane (DLinKC2-DMA), (3-oxo-[2"-(methoxypolyethyleneglycol 2000) succinoyl]-1,2-dimyristoyl-sn-glycol (PEG-S-DMG), R-3-[(ro-methoxy-poly (ethylene glycol) 2000) carbamoyl]-1,2-dimyristyloxypropyl-3-amine (PEG-C-DMG, and any combination thereof. Preparation of LNPs and encapsulation may be adapted from Rosin et al, Molecular Therapy, vol. 19, no. 12, pages 1286-2220, December 2011).

In some embodiments, an LNP delivery vehicle can be used to deliver a virus particle containing a CRISPR-Cas system and/or component(s) thereof. In some embodiments, the virus particle(s) can be adsorbed to the lipid particle, such as through electrostatic interactions, and/or can be attached to the liposomes via a linker.

In some embodiments, the LNP contains a nucleic acid, wherein the charge ratio of nucleic acid backbone phosphates to cationic lipid nitrogen atoms is about 1:1.5-7 or about 1:4.

In some embodiments, the LNP also includes a shielding compound, which is removable from the lipid composition under in vivo conditions. In some embodiments, the shielding compound is a biologically inert compound. In some embodiments, the shielding compound does not carry any charge on its surface or on the molecule as such. In some embodiments, the shielding compounds are polyethylene glycols (PEGs), hydroxyethylglucose (HEG) based polymers, polyhydroxyethyl starch (polyHES) and polypropylene. In some embodiments, the PEG, HEG, polyHES, and a polypropylene weight between about 500 to 10,000 Da or between about 2000 to 5000 Da. In some embodiments, the shielding compound is PEG2000 or PEG5000.

In some embodiments, the LNP can include one or more helper lipids. In some embodiments, the helper lipid can be a phosphor lipid or a steroid. In some embodiments, the helper lipid is between about 20 mol % to 80 mol % of the total lipid content of the composition. In some embodiments, the helper lipid component is between about 35 mol % to 65 mol % of the total lipid content of the LNP. In some embodiments, the LNP includes lipids at 50 mol % and the helper lipid at 50 mol % of the total lipid content of the LNP.

Other non-limiting, exemplary LNP delivery vehicles are described in U.S. Patent Publication Nos. US20160174546, US 20140301951, US 20150105538, US 20150250725, Wang et al., J. Control Release, 2017 Jan. 31. pii: S0168-3659(17) 30038-X. doi: 10.1016/j.jconrel.2017.01.037. [Epub ahead of print]; Altinoğlu et al., Biomater Sci., 4(12):

1773-80, Nov. 15, 2016; Wang et al., PNAS, 113(11): 2868-73 Mar. 15, 2016; Wang et al., PLoS One, 10(11): e0141860. doi: 10.1371/journal.pone.0141860. eCollection 2015, Nov. 3, 2015; Takeda et al., Neural Regen Res. 10(5): 689-90, May 2015; Wang et al., Adv. Healthc Mater., 3(9): 1398-403, September 2014; and Wang et al., Agnew Chem Int Ed Engl., 53(11): 2893-8, Mar. 10, 2014; James E. Dahlman and Carmen Barnes et al. Nature Nanotechnology (2014) published online 11 May 2014, doi: 10.1038/nnano.2014.84; Coelho et al., N Engl J Med 2013; 369:819-29; Aleku et al., Cancer Res., 68(23): 9788-98 (Dec. 1, 2008), Strumberg et al., Int. J. Clin. Pharmacol. Ther., 50(1): 76-8 (January 2012), Schultheis et al., *J. Clin. Oncol.*, 32(36): 4141-48 (Dec. 20, 2014), and Fehring et al., Mol. Ther., 22(4): 811-20 (Apr. 22, 2014); Novobrantseva, Molecular Therapy-Nucleic Acids (2012) 1, e4; doi: 10.1038/mtna.2011.3; WO2012135025; US20140348900; US20140328759; US 20140308304; WO 2005/105152; WO 2006/069782; WO 2007/121947; US 2015/082080; US 20120251618; U.S. Pat. Nos. 7,982,027; 7,799,565; 8,058,069; 8,283,333; 7,901,708; 7,745,651; 7,803,397; 8,101,741; 8,188,263; 7,915,399; 8,236,943 and 7,838,658 and European Pat. Nos 1766035; 1519714; 1781593 and 1664316.

Liposomes

In some embodiments, a lipid particle may be liposome. Liposomes are spherical vesicle structures composed of a uni- or multilamellar lipid bilayer surrounding internal aqueous compartments and a relatively impermeable outer lipophilic phospholipid bilayer. In some embodiments, liposomes are biocompatible, nontoxic, can deliver both hydrophilic and lipophilic drug molecules, protect their cargo from degradation by plasma enzymes, and transport their load across biological membranes and the blood brain barrier (BBB).

Liposomes can be made from several different types of lipids, e.g., phospholipids. A liposome may comprise natural phospholipids and lipids such as 1,2-distearoyl-sn-glycero-3-phosphatidyl choline (DSPC), sphingomyelin, egg phosphatidylcholines, monosialoganglioside, or any combination thereof.

Several other additives may be added to liposomes in order to modify their structure and properties. For instance, liposomes may further comprise cholesterol, sphingomyelin, and/or 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (DOPE), e.g., to increase stability and/or to prevent the leakage of the liposomal inner cargo.

In some embodiments, a liposome delivery vehicle can be used to deliver a virus particle containing a CRISPR-Cas system and/or component(s) thereof. In some embodiments, the virus particle(s) can be adsorbed to the liposome, such as through electrostatic interactions, and/or can be attached to the liposomes via a linker.

In some embodiments, the liposome can be a Trojan Horse liposome (also known in the art as Molecular Trojan Horses), see e.g. cshprotocols.cshlp.org/content/2010/4/pdb.prot5407.long, the teachings of which can be applied and/or adapted to generated and/or deliver the CRISPR-Cas systems described herein.

Other non-limiting, exemplary liposomes can be those as set forth in Wang et al., ACS Synthetic Biology, 1, 403-07 (2012); Wang et al., PNAS, 113(11) 2868-2873(2016); Spuch and Navarro, Journal of Drug Delivery, vol. 2011, Article ID 469679, 12 pages, 2011. doi: 10.1155/2011/469679; WO 2008/042973; U.S. Pat. No. 8,071,082; WO 2014/186366; 20160257951; US20160129120; US20160244761; 20120251618; WO2013/093648; Lipo-

fectin (a combination of DOTMA and DOPE), Lipofectase, LIPOFECTAMINE® (e.g., LIPOFECTAMINE® 2000, LIPOFECTAMINE® 3000, LIPOFECTAMINE® RNAiMAX, LIPOFECTAMINE® LTX), SAINT-RED (Synvolux Therapeutics, Groningen Netherlands), DOPE, Cytofectin (Gilead Sciences, Foster City, Calif.), and Eufectins (JBL, San Luis Obispo, Calif.). Stable Nucleic-Acid-Lipid Particles (SNALPs)

In some embodiments, the lipid particles may be stable nucleic acid lipid particles (SNALPs). SNALPs may comprise an ionizable lipid (DLinDMA) (e.g., cationic at low pH), a neutral helper lipid, cholesterol, a diffusible polyethylene glycol (PEG)-lipid, or any combination thereof. In some examples, SNALPs may comprise synthetic cholesterol, dipalmitoylphosphatidylcholine, 3-N-[(w-methoxy polyethylene glycol) 2000] carbamoyl]-1,2-dimyristoyloxypropylamine, and cationic 1,2-dilinoleyloxy-3-N,N-dimethylaminopropane. In some examples, SNALPs may comprise synthetic cholesterol, 1,2-distearoyl-sn-glycero-3-phosphocholine, PEG-CDMA, and 1,2-dilinoleyloxy-3-(N,N-dimethyl)aminopropane (DLinDMAo).

Other non-limiting, exemplary SNALPs that can be used to deliver the CRISPR-Cas systems described herein can be any such SNALPs as described in Morrissey et al., Nature Biotechnology, Vol. 23, No. 8, August 2005, Zimmerman et al., Nature Letters, Vol. 441, 4 May 2006; Geisbert et al., Lancet 2010; 375:1896-905; Judge, J. Clin. Invest. 119:661-673 (2009); and Semple et al., Nature Biotechnology, Volume 28 Number 2 February 2010, pp. 172-177.

Other Lipids

The lipid particles may also comprise one or more other types of lipids, e.g., cationic lipids, such as amino lipid 2,2-dilinoley-1-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), DLin-KC2-DMA4, C12-200 and colipids distearoylphosphatidyl choline, cholesterol, and PEG-DMG.

In some embodiments, the delivery vehicle can be or include a lipidoid, such as any of those set forth in, for example, US 20110293703.

In some embodiments, the delivery vehicle can be or include an amino lipid, such as any of those set forth in, for example, Jayaraman, Angew. Chem. Int. Ed. 2012, 51, 8529-8533.

In some embodiments, the delivery vehicle can be or include a lipid envelope, such as any of those set forth in, for example, Korman et al., 2011. Nat. Biotech. 29:154-157.

Lipoplexes/Polyplexes

In some embodiments, the delivery vehicles comprise lipoplexes and/or polyplexes. Lipoplexes may bind to negatively charged cell membrane and induce endocytosis into the cells. Examples of lipoplexes may be complexes comprising lipid(s) and non-lipid components. Examples of lipoplexes and polyplexes include FuGENE-6 reagent, a non-liposomal solution containing lipids and other components, zwitterionic amino lipids (ZALs), Ca2p (e.g., forming DNA/Ca2+ microcomplexes), polyethenimine (PEI) (e.g., branched PEI), and poly (L-lysine) (PLL).

Sugar-Based Particles

In some embodiments, the delivery vehicle can be a sugar-based particle. In some embodiments, the sugar-based particles can be or include GalNAc, such as any of those described in WO2014118272; US20020150626; Nair, J K et al., 2014, Journal of the American Chemical Society 136 (49), 16958-16961; Østergaard et al., Bioconjugate Chem., 2015, 26(8), pp 1451-1455.

Cell Penetrating Peptides

In some embodiments, the delivery vehicles comprise cell penetrating peptides (CPPs). CPPs are short peptides that facilitate cellular uptake of various molecular cargo (e.g., from nanosized particles to small chemical molecules and large fragments of DNA).

CPPs may be of different sizes, amino acid sequences, and charges. In some examples, CPPs can translocate the plasma membrane and facilitate the delivery of various molecular cargoes to the cytoplasm or an organelle. CPPs may be introduced into cells via different mechanisms, e.g., direct penetration in the membrane, endocytosis-mediated entry, and translocation through the formation of a transitory structure.

CPPs may have an amino acid composition that either contains a high relative abundance of positively charged amino acids such as lysine or arginine or has sequences that contain an alternating pattern of polar/charged amino acids and non-polar, hydrophobic amino acids. These two types of structures are referred to as polycationic or amphipathic, respectively. A third class of CPPs are the hydrophobic peptides, containing only apolar residues, with low net charge or have hydrophobic amino acid groups that are crucial for cellular uptake. Another type of CPPs is the trans-activating transcriptional activator (Tat) from Human Immunodeficiency Virus 1 (HIV-1). Examples of CPPs include to Penetratin, Tat (48-60), Transportan, and (R-Ahx-R4) (Ahx refers to aminohexanoyl), Kaposi fibroblast growth factor (FGF) signal peptide sequence, integrin β 3 signal peptide sequence, polyarginine peptide Args sequence, Guanine rich-molecular transporters, and sweet arrow peptide. Examples of CPPs and related applications also include those described in U.S. Pat. No. 8,372,951.

CPPs can be used for in vitro and ex vivo work quite readily, and extensive optimization for each cargo and cell type is usually required. In some examples, CPPs may be covalently attached to the Cas protein directly, which is then complexed with the gRNA and delivered to cells. In some examples, separate delivery of CPP-Cas and CPP-gRNA to multiple cells may be performed. CPP may also be used to delivery RNPs.

CPPs may be used to deliver the compositions and systems to plants. In some examples, CPPs may be used to deliver the components to plant protoplasts, which are then regenerated to plant cells and further to plants.

DNA Nanoclews

In some embodiments, the delivery vehicles comprise DNA nanoclews. A DNA nanoclew refers to a sphere-like structure of DNA (e.g., with a shape of a ball of yarn). The nanoclew may be synthesized by rolling circle amplification with palindromic sequences that aide in the self-assembly of the structure. The sphere may then be loaded with a payload. An example of DNA nanoclew is described in Sun W et al, J Am Chem Soc. 2014 Oct. 22; 136(42): 14722-5; and Sun W et al, Angew Chem Int Ed Engl. 2015 Oct. 5; 54(41): 12029-33. DNA nanoclew may have a palindromic sequences to be partially complementary to the gRNA within the Cas: gRNA ribonucleoprotein complex. A DNA nanoclew may be coated, e.g., coated with PEI to induce endosomal escape.

Metal Nanoparticles

In some embodiments, the delivery vehicles comprise gold nanoparticles (also referred to AuNPs or colloidal gold). Gold nanoparticles may form complex with cargos, e.g., Cas: gRNA RNP. Gold nanoparticles may be coated, e.g., coated in a silicate and an endosomal disruptive polymer, PAsp (DET). Examples of gold nanoparticles include

AuraSense Therapeutics' Spherical Nucleic Acid (SNATM) constructs, and those described in Mout R, et al. (2017). ACS Nano 11:2452-8; Lee K, et al. (2017). Nat Biomed Eng 1:889-901. Other metal nanoparticles can also be complexed with cargo(s). Such metal particles include, tungsten, palladium, rhodium, platinum, and iridium particles. Other non-limiting, exemplary metal nanoparticles are described in US20100129793.

iTOP

In some embodiments, the delivery vehicles comprise iTOP. iTOP refers to a combination of small molecules drives the highly efficient intracellular delivery of native proteins, independent of any transduction peptide. iTOP may be used for induced transduction by osmocytosis and propanebetaine, using NaCl-mediated hyperosmolality together with a transduction compound (propanebetaine) to trigger macropinocytotic uptake into cells of extracellular macromolecules. Examples of iTOP methods and reagents include those described in D'Astolfo D S, Pagliero R J, Pras A, et al. (2015). Cell 161:674-690.

Polymer-Based Particles

In some embodiments, the delivery vehicles may comprise polymer-based particles (e.g., nanoparticles). In some embodiments, the polymer-based particles may mimic a viral mechanism of membrane fusion. The polymer-based particles may be a synthetic copy of Influenza virus machinery and form transfection complexes with various types of nucleic acids ((siRNA, miRNA, plasmid DNA or shRNA, mRNA) that cells take up via the endocytosis pathway, a process that involves the formation of an acidic compartment. The low pH in late endosomes acts as a chemical switch that renders the particle surface hydrophobic and facilitates membrane crossing. Once in the cytosol, the particle releases its payload for cellular action. This Active Endosome Escape technology is safe and maximizes transfection efficiency as it is using a natural uptake pathway. In some embodiments, the polymer-based particles may comprise alkylated and carboxyalkylated branched polyethylenimine. In some examples, the polymer-based particles are VIROMER, e.g., VIROMER RNAi, VIROMER RED, VIROMER mRNA, VIROMER CRISPR. Example methods of delivering the systems and compositions herein include those described in Bawage S S et al., Synthetic mRNA expressed Cas13a mitigates RNA virus infections, www.biorxiv.org/content/10.1101/370460v1.full doi: doi.org/10.1101/370460, Viromer® RED, a powerful tool for transfection of keratinocytes. doi: 10.13140/RG.2.2.16993.61281, Viromer® Transfection—Factbook 2018: technology, product overview, users' data., doi: 10.13140/RG.2.2.23912.16642. Other exemplary and non-limiting polymeric particles are described in US20170079916, US 20160367686, US 20110212179, US 20130302401, U.S. Pat. Nos. 6,007,845, 5,855,913, 5,985,309, 5,543,158, WO2012135025, US 20130252281, US 20130245107, US 20130244279; US20050019923, 20080267903.

Streptolysin O (SLO)

The delivery vehicles may be streptolysin O (SLO). SLO is a toxin produced by Group A streptococci that works by creating pores in mammalian cell membranes. SLO may act in a reversible manner, which allows for the delivery of proteins (e.g., up to 100 kDa) to the cytosol of cells without compromising overall viability. Examples of SLO include those described in Sierig G, et al. (2003). Infect Immun 71:446-55; Walev I, et al. (2001). Proc Natl Acad Sci USA 98:3185-90; Teng K W, et al. (2017). Elife 6: e25460. Multifunctional Envelope-Type Nanodevice (MEND)

The delivery vehicles may comprise multifunctional envelope-type nanodevice (MENDs). MENDs may comprise condensed plasmid DNA, a PLL core, and a lipid film shell. A MEND may further comprise cell-penetrating peptide (e.g., stearyl octaarginine). The cell penetrating peptide may be in the lipid shell. The lipid envelope may be modified with one or more functional components, e.g., one or more of: polyethylene glycol (e.g., to increase vascular circulation time), ligands for targeting of specific tissues/cells, additional cell-penetrating peptides (e.g., for greater cellular delivery), lipids to enhance endosomal escape, and nuclear delivery tags. In some examples, the MEND may be a tetra-lamellar MEND (T-MEND), which may target the cellular nucleus and mitochondria. In certain examples, a MEND may be a PEG-peptide-DOPE-conjugated MEND (PPD-MEND), which may target bladder cancer cells. Examples of MENDs include those described in Kogure K, et al. (2004). *J Control Release* 98:317-23; Nakamura T, et al. (2012). *Acc Chem Res* 45:1113-21.

Cargo Polynucleotides

The engineered muscle-specific delivery system polynucleotides, viral capsid polynucleotides, other AAV polynucleotide(s), and/or vector polynucleotides, virus particles, and/or non-vector delivery vehicles can contain one or more cargo polynucleotides. In some embodiments, the one or more cargo polynucleotides are operably linked to the engineered muscle-specific delivery system polynucleotides(s) and is, in some embodiments, be part of the engineered viral genome of an engineered viral system of the present invention. The cargo polynucleotides can be packaged into an engineered virus particle, which can be delivered to, e.g., a cell. In some embodiments, the cargo polynucleotide can be capable of modifying a polynucleotide (e.g. gene or transcript) of a cell to which it is delivered. In some embodiments, the cargo is a polynucleotide that encodes a replacement polypeptide to correct for a defective polypeptide. As used herein, "gene" can refer to a hereditary unit corresponding to a sequence of DNA that occupies a specific location on a chromosome and that contains the genetic instruction for a characteristic(s) or trait(s) in an organism. The term gene can refer to translated and/or untranslated regions of a genome. "Gene" can refer to the specific sequence of DNA that is transcribed into an RNA transcript that can be translated into a polypeptide or be a catalytic RNA molecule, including but not limited to, tRNA, siRNA, piRNA, miRNA, long-non-coding RNA and shRNA. Polynucleotide, gene, transcript, etc. modification includes all genetic engineering techniques including, but not limited to, gene editing as well as conventional recombinational gene modification techniques (e.g. whole or partial gene insertion, deletion, and mutagenesis (e.g. insertional and deletional mutagenesis) techniques.

In some embodiments, the cargo molecule is a polynucleotide that is or can encode a vaccine. In some embodiments, the vaccine can stimulate an immune response against a cancer. In some embodiments, the vaccine can stimulate an immune response against colorectal or pancreatic cancer. In some embodiments, the vaccine can create an unstable environment for hCG-producing cells, such as hCG producing cancer cells.

In some embodiments the cargo is a polynucleotide that itself or a product thereof can be effective to treat a muscle disease or a symptom thereof.

Gene Modification Cargo Polynucleotides

In some embodiments, the cargo molecule can be a polynucleotide or polypeptide that can alone or when delivered as part of a system, whether or not delivered with other

components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered. Such systems include, but are not limited to, CRISPR-Cas systems. Other gene modification systems, e.g. TALENs, Zinc Finger nucleases, Cre-Lox, morpholinos, etc. are other non-limiting examples of gene modification systems whose one or more components can be delivered by the engineered AAV particles described herein.

In some embodiments, the cargo molecule is a gene editing system or component thereof. In some embodiments, the cargo molecule is a CRISPR-Cas system molecule or a component thereof. In some embodiments, the cargo molecule is a polynucleotide that encodes one or more components of a gene modification system (such as a CRISPR-Cas system). In some embodiments, the cargo molecule is a gRNA.

In some embodiments, the cargo molecule can be a polynucleotide or polypeptide that can alone or when delivered as part of a system, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that it treats or prevents a disease, a disorder, or a symptom thereof of a muscle or skeletal disorder, a neurologic disease or disorder, and/or viruses (such as single stranded RNA viruses). In some embodiments, the cargo molecule, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that it treats or prevents, a progeroid disease (e.g. progeroid laminopathy) a glycogen storage disease an immune disorder (such as an autoimmune disease), a cancer, Duchenne muscular dystrophy (DMD), 6 Limb-girdle muscular dystrophy diseases (LGMD), Charcot-Marie-Tooth (CMT), MPS IIIA, Pompe disease, or other CNS-related diseases such as Huntington's and other expanded repeat diseases.

In some embodiments, the cargo molecule, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that can modify the GAA gene, such as any of those described in US Pat. App. Pub. 20190284555, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

In some embodiments, the cargo molecule includes an oligonucleotide coupled to a MHCK7, CK8, or other muscle specific promoter.

In some embodiments, the cargo molecule is a micro-dystrophin oligonucleotide that contains only selected regions of the dystrophin gene optimized for protein functionality. In some embodiments, the selected regions include spectrin-like repeats 1, 2, 3, and 24. See e.g. Harper S Q, Hauser M A, DelloRusso C, et al. Modular flexibility of dystrophin: implications for gene therapy of Duchenne muscular dystrophy. *Nat Med.* 2002; 8(3): 253-261. In some embodiments, the micro-dystrophin oligonucleotide is that is delivered by the rAAV agent known as AAVrh74.MHCK7 microdystrophin gene or SRP-9001, which is subject to the clinical trials NCT03375164 and NCT03769116. This microdystrophin gene construct includes NT-H1-R1-R2-R3-H2-R24-H4-CR-CT. In some embodiments, the microdystrophin gene includes ABD-H1-R1-R2-R3-H2-R24-H4-CR-CT. In some embodiments, the microdystrophin gene includes H stands for hinge region. England S B, et al. *Nature.* 1990; 343(6254): 180-182; Wells D J, et al. *Hum Mol Genet.* 1995; 4(8): 1245-1250, Salva M Z, et al. *Mol Ther.* 2007; 15(2): 320-329; Mendell J R, et al. *Neurosci*

Lett. 2012; 527(2): 90-99; Rodino-Klapac L R, et al. Hum Mol Genet. 2013; 22(24): 4929-4937; Velazquez V M, et al. Mol Ther Methods Clin Dev. 2017; 4:159-168; Harper S Q, et al. Nat Med. 2002; 8(3): 253-261; Nelson D M, et al. Hum Mol Genet. 2018; 27(12): 2090-2100. In some embodiments, the selected regions at least include spectrin-like repeats 2 and 3. In some embodiments, the micro-dystrophin gene contains a nNOS domain. In some embodiments, the nNOS domain is composed of spectrin-like repeats 16 and/or 17. In some embodiments, the micro-dystrophin gene includes spectrin-like repeats 16 and 17. In some embodiments, the nNOS domain is composed of spectrin-like repeats R1, R16, R17, R23, and R24. In some embodiments, the micro-dystrophin gene is coupled to a muscle specific promoter. In some embodiments, the micro-dystrophin oligonucleotide is coupled to a MHCK7, CK8, SNP18, SP0033, SP0051, SP0173, tmCK, or another muscle specific promoter.

In some embodiments, the cargo microdystrophin includes an ABD (actin binding domain), one or more hinge regions (e.g. H1, H2, H3, H4.), and one or more spectrin-like repeats (e.g. R1, R1' R2, R3, R16, R17, R20, R21, R22, R23, R24, R24' and optionally a dystroglycan binding domain (DBD). In some embodiments, the microdystrophin is composed of ABD-H1-R1-R16-R17-R23-R24-H4-DBD. In some embodiments, the microdystrophin is composed of ABD-H1-R1-R2-R3-H2-R24-H4-CR. In some embodiments, the microdystrophin gene includes ABD-H1-R1-R2-R3-H2-R24-H4-CR-CT. In some embodiments, the microdystrophin gene includes ABD-H1-R1'-R24'-H4-CR-CT.

In some embodiments, the cargo molecule is a polynucleotide that can encode a microdystrophin gene, where the microdystrophin gene contains spectrin-like repeats, R1, R16, R17, R23 and R24. In some embodiments, the microdystrophin gene contains hinge region (H) 4 and/or H1. In some embodiments, the microdystrophin gene contains the N-terminal actin binding domain. In some embodiments, the microdystrophin gene contains the C-terminal dystroglycan binding domain of the human full-length dystrophin protein. The micro-dystrophin gene can contain an nNOS domain. In some embodiments, the nNOS domain is composed of spectrin-like repeats 16 and/or 17. In some embodiments, the micro-dystrophin gene includes spectrin-like repeats 16 and 17. The microdystrophin gene can be as described in WO2019118806A1 and WO2016/115543, which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention. In some embodiments, the cargo polynucleotide can encode a 5-repeat microdystrophin protein that contains, from N- to C-terminus, the N-terminal actin binding domain, Hinge region 1 (H1), spectrin-like repeats R1, R16, R17, R23, and R24, Hinge region 4 (H4), and the C-terminal dystroglycan binding domain of the human full-length dystrophin protein. The protein sequence of this 5-repeat microdystrophin and the related dystrophin minigene are described in WO2016/115543. In some embodiments, the cargo polynucleotide can correspond to a microdystrophin gene that is part of the agent known as SGT001 as currently in clinical trial having the identifier number NCT03368742.

In some embodiments, the cargo molecule is a minidys gene or vector. In some embodiments, the minidys gene or vector can be composed of ABD-H1-R1-R2-R3-R16-R17-H3-R20-R21; ABD-H1-R1-R2-R3-R16-R17-H3-R20-R21-R22-R23-R24-H4-CR; or H3-R20-R21-R22-R23-R24-H4-CR-CT.

In some embodiments, the cargo molecule is an SCGB cDNA. In some embodiments, the SGCB cDNA is coupled

to a MHCK7, CK8 promoter, SNP18 promoter, SP0033 promoter, SP0051, SP0173 promoter, tmCK promoter or another muscle specific promoter. In some embodiments, the cargo molecule is a beta-sarcoglycan cDNA, an alpha-sarcoglycan cDNA, a dysferlin cDNA, a gamma-sarcoglycan cDNA, a Calpin-3 cDNA, a SGSH cDNA (e.g., LYS-SAF302), a neurotrophin 3 cDNA, an anoctamin-5 cDNA, or any combination thereof.

In some embodiments, the cargo molecule, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that treat, prevent, and/or modify a gene or gene product associated with an expanded repeat disease, such as Huntington's disease, such as those described in U.S. Pat. App. Pub. 20190100755, U.S. patent Ser. No. 10/066,228, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

In some embodiments, the cargo molecule is an antisense oligomer or RNA molecule, such as those described in U.S. Pat. App. Pub. US20160251398, US20150267202, US20190015440, US20140287983, US20180216111, WO/2017/062835, US20190177723, US20170051278, US20180271893, WO/2016/14965, U.S. patent Ser. No. 10/076,536, WO/2018/00580, WO/2018/11866, WO/2019/059973, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

In some embodiments, the cargo molecule, whether or not delivered with other components of the system, operate to modify the genome, epigenome, and/or transcriptome of a cell to which it is delivered, is such that it treats or prevents a single stranded RNA virus, such as influenza, West Nile Virus, SARS, Hepatitis C, dengue fever, Ebola, Marburg, and/or Calicivirus. In some embodiments the cargo molecule can be an antisense antiviral compound, such as any of those described in U.S. Pat. No. 8,703,735B2, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

Additional, exemplary genetic and gene associated diseases and genes capable of being modified by a cargo molecule described herein are listed elsewhere herein, see e.g. Tables A-B.

In some embodiments, the cargo molecule can add or modify a GALGT2 gene.

Instead of acting to resupply missing dystrophin, GALGT2 gene therapy fortifies the structural integrity of muscle in ways that compensate for the absence of dystrophin, by increasing expression of proteins not mutated or lost in the disease. GALGT2 offers the potential to treat DMD irrespective of specific dystrophin mutation, as well as having utility in other muscular dystrophies.

In some embodiments, the cargo molecule is a morpholino, such as in US20180161359, US 20190054113 the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention. In some embodiments, the morpholino is a morpholino oligomer (PMO) or a peptide linked morpholino PPMO. PMO based platforms can be used to treat genetic diseases by altering mRNA transcription. PMOs are synthetic chemical structures modeled after the natural framework of RNA. While PMOs have the same nucleic acid bases found in RNA, they are bound to six-sided morpholine rings instead of five-sided ribose rings. In addition, the morpholine rings are connected to each other by phosphorodiamidate linkages instead of the phosphodi-

ester linkages found in RNA. PMOs and PPMOs can be used for exon skipping and translation suppression.

In some embodiments, the cargo molecule can be a peptide-oligomer, conjugate as described in e.g. WO2017106304A1, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

In some embodiments, the morpholino is the morpholino found in Eteplirsen, which can be effective to target Exon 51 of the dystrophin mRNA. In some embodiments, the cargo molecule can generate exon skipping in the context of DMD, such as those described in e.g. US20140315977A1, US2018010581, the contents of which are incorporated by reference as if expressed in their entirety herein and can be adapted for use with the present invention.

Exon Skipping

In some embodiments, the nucleotide sequences may encode nucleic acids capable of inducing exon skipping. Such encoded nucleic acids may be antisense oligonucleotides or antisense nucleotide systems. As used herein, the term “exon skipping” refers to the modification of pre-mRNA splicing by the targeting of splice donor and/or acceptor sites within a pre-mRNA with one or more complementary antisense oligonucleotide(s) (AONs). By blocking access of a spliceosome to one or more splice donor or acceptor site, an AON may prevent a splicing reaction thereby causing the deletion of one or more exons from a fully-processed mRNA. Exon skipping may be achieved in the nucleus during the maturation process of pre-mRNAs. In some examples, exon skipping may include the masking of key sequences involved in the splicing of targeted exons by using antisense oligonucleotides (AON) that are complementary to splice donor sequences within a pre-mRNA.

In some embodiments, the nucleotide sequences encode antisense oligonucleotides or antisense nucleotide systems capable of inducing exon skipping in dystrophin mRNA. For example, a non-sense or frameshift mutation within exon x of a dystrophin gene yields a carboxy-terminally truncated, non-functional dystrophin protein. The expression of that mature mRNA transcript may yield a functional dystrophin protein that is deleted in the amino acids encoded by exon x but that includes dystrophin amino acids both N-terminal and C-terminal to those deleted amino acids.

The nucleotide sequences may encode antisense oligonucleotides or antisense nucleotide systems capable of inducing exon skipping at exon 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, or any combination thereof. In some embodiments, nucleotide sequences may encode antisense oligonucleotides or antisense nucleotide systems capable of inducing exon skipping at exon 43, 44, 50, 51, 52, 55, or any combination thereof.

CRISPR-Cas System Cargo Molecules

In general, a CRISPR-Cas or CRISPR system as used in herein and in documents, such as WO 2014/093622 (PCT/US2013/074667), refers collectively to transcripts and other elements involved in the expression of or directing the activity of CRISPR-associated (“Cas”) genes, including sequences encoding a Cas gene, a tracr (trans-activating CRISPR) sequence (e.g. tracrRNA or an active partial tracrRNA), a tracr-mate sequence (encompassing a “direct repeat” and a tracrRNA-processed partial direct repeat in the context of an endogenous CRISPR system), a guide sequence (also referred to as a “spacer” in the context of an

endogenous CRISPR system), or “RNA(s)” as that term is herein used (e.g., RNA(s) to guide Cas, such as Cas9, e.g. CRISPR RNA and transactivating (tracr) RNA or a single guide RNA (sgRNA) (chimeric RNA)) or other sequences and transcripts from a CRISPR locus. In general, a CRISPR system is characterized by elements that promote the formation of a CRISPR complex at the site of a target sequence (also referred to as a protospacer in the context of an endogenous CRISPR system). See, e.g., Shmakov et al. (2015) “Discovery and Functional Characterization of Diverse Class 2 CRISPR-Cas Systems”, *Molecular Cell*, DOI: dx.doi.org/10.1016/j.molcel.2015.10.008.

Class 1 Systems

The methods, systems, and tools provided herein may be designed for use with Class 1 CRISPR proteins. In certain example embodiments, the Class 1 system may be Type I, Type III or Type IV Cas proteins as described in Makarova et al. “Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants” *Nature Reviews Microbiology*, 18:67-81 (February 2020), incorporated in its entirety herein by reference, and particularly as described in FIG. 1, p. 326. The Class 1 systems typically use a multi-protein effector complex, which can, in some embodiments, include ancillary proteins, such as one or more proteins in a complex referred to as a CRISPR-associated complex for antiviral defense (Cascade), one or more adaptation proteins (e.g. Cas1, Cas2, RNA nuclease), and/or one or more accessory proteins (e.g. Cas 4, DNA nuclease), CRISPR associated Rossman fold (CARF) domain containing proteins, and/or RNA transcriptase. Although Class 1 systems have limited sequence similarity, Class 1 system proteins can be identified by their similar architectures, including one or more Repeat Associated Mysterious Protein (RAMP) family subunits, e.g. Cas 5, Cas6, Cas7. RAMP proteins are characterized by having one or more RNA recognition motif domains. Large subunits (for example cas8 or cas10) and small subunits (for example, cas11) are also typical of Class 1 systems. See, e.g., FIGS. 1 and 2. Koonin E V, Makarova K S. 2019 Origins and evolution of CRISPR-Cas systems. *Phil. Trans. R. Soc. B* 374:20180087, DOI: 10.1098/rstb.2018.0087. In one aspect, Class 1 systems are characterized by the signature protein Cas3. The Cascade in particular Class1 proteins can comprise a dedicated complex of multiple Cas proteins that binds pre-crRNA and recruits an additional Cas protein, for example Cas6 or Cas5, which is the nuclease directly responsible for processing pre-crRNA. In one aspect, the Type I CRISPR protein comprises an effector complex comprises one or more Cas5 subunits and two or more Cas7 subunits. Class 1 subtypes include Type I-A, I-B, I-C, I-U, I-D, I-E, and I-F, Type IV-A and IV-B, and Type III-A, III-D, III-C, and III-B. Class 1 systems also include CRISPR-Cas variants, including Type I-A, I-B, I-E, I-F and I-U variants, which can include variants carried by transposons and plasmids, including versions of subtype I-F encoded by a large family of Tn7-like transposon and smaller groups of Tn7-like transposons that encode similarly degraded subtype I-B systems. Peters et al., *PNAS* 114 (35) (2017); DOI: 10.1073/pnas.1709035114; see also, Makarova et al, the CRISPR Journal, v. 1, n5, FIG. 5.

Class 2 Systems

The compositions, systems, and methods described in greater detail elsewhere herein can be designed and adapted for use with Class 2 CRISPR-Cas systems. Thus, in some embodiments, the CRISPR-Cas system is a Class 2 CRISPR-Cas system. Class 2 systems are distinguished from Class 1 systems in that they have a single, large,

multi-domain effector protein. In certain example embodiments, the Class 2 system can be a Type II, Type V, or Type VI system, which are described in Makarova et al. "Evolutionary classification of CRISPR-Cas systems: a burst of class 2 and derived variants" *Nature Reviews Microbiology*, 18:67-81 (February 2020), incorporated herein by reference. Each type of Class 2 system is further divided into subtypes. See Markova et al. 2020, particularly at Figure. 2. Class 2, Type II systems can be divided into 4 subtypes: II-A, II-B, II-C1, and II-C2. Class 2, Type V systems can be divided into 17 subtypes: V-A, V-B1, V-B2, V-C, V-D, V-E, V-F1, V-F1 (V-U3), V-F2, V-F3, V-G, V-H, V-I, V-K (V-U5), V-U1, V-U2, and V-U4. Class 2, Type IV systems can be divided into 5 subtypes: VI-A, VI-B1, VI-B2, VI-C, and VI-D.

The distinguishing feature of these types is that their effector complexes consist of a single, large, multi-domain protein. Type V systems differ from Type II effectors (e.g., Cas9), which contain two nuclear domains that are each responsible for the cleavage of one strand of the target DNA, with the HNH nuclease inserted inside the RuvC-like nuclease domain sequence. The Type V systems (e.g., Cas12) only contain a RuvC-like nuclease domain that cleaves both strands. Type VI (Cas13) are unrelated to the effectors of Type II and V systems and contain two HEPN domains and target RNA. Cas13 proteins also display collateral activity that is triggered by target recognition. Some Type V systems have also been found to possess this collateral activity with two single-stranded DNA in *in vitro* contexts.

In some embodiments, the Class 2 system is a Type II system. In some embodiments, the Type II CRISPR-Cas system is a II-A CRISPR-Cas system. In some embodiments, the Type II CRISPR-Cas system is a II-B CRISPR-Cas system. In some embodiments, the Type II CRISPR-Cas system is a II-C1 CRISPR-Cas system. In some embodiments, the Type II CRISPR-Cas system is a II-C2 CRISPR-Cas system. In some embodiments, the Type II system is a Cas9 system. In some embodiments, the Type II system includes a Cas9.

In some embodiments, the Class 2 system is a Type V system. In some embodiments, the Type V CRISPR-Cas system is a V-A CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-B1 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-B2 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-C CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-D CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-E CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-F1 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-F1 (V-U3) CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-F2 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-F3 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-G CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-H CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-I CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-K (V-U5) CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-U1 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-U2 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas system is a V-U4 CRISPR-Cas system. In some embodiments, the Type V CRISPR-Cas

system includes a Cas12a (Cpf1), Cas12b (C2c1), Cas12c (C2c3), Cas12d (CasY), Cas12e (CasX), Cas14, and/or CasΦ.

In some embodiments, the Class 2 system is a Type VI system. In some embodiments, the Type VI CRISPR-Cas system is a VI-A CRISPR-Cas system. In some embodiments, the Type VI CRISPR-Cas system is a VI-B1 CRISPR-Cas system. In some embodiments, the Type VI CRISPR-Cas system is a VI-B2 CRISPR-Cas system. In some embodiments, the Type VI CRISPR-Cas system is a VI-C CRISPR-Cas system. In some embodiments, the Type VI CRISPR-Cas system is a VI-D CRISPR-Cas system. In some embodiments, the Type VI CRISPR-Cas system includes a Cas13a (C2c2), Cas13b (Group 29/30), Cas13c, and/or Cas13d.

Cas Molecules

In some embodiments, the cargo molecule can be or include a Cas polypeptide and/or a polynucleotide that can encode a Cas polypeptide or a fragment thereof. Any Cas molecule can be a cargo molecule. In some embodiments, the cargo molecule is Class I CRISPR-Cas system Cas polypeptide. In some embodiments, the cargo molecule is a Class II CRISPR-Cas system Cas polypeptide. In some embodiments, the Cas polypeptide is a Type I Cas polypeptides. In some embodiments, the Cas polypeptide is a Type II Cas polypeptides. In some embodiments, the Cas polypeptides is a Type III Cas polypeptide. In some embodiments, the Cas polypeptides is a Type IV Cas polypeptide. In some embodiments, the Cas polypeptides is a Type V Cas polypeptide. In some embodiments, the Cas polypeptides is a Type VI Cas polypeptide. In some embodiments, the Cas polypeptides is a Type VII Cas polypeptide. Non-limiting examples of Cas proteins include Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas10, Cas 12, Cas 12a, Cas 13a, Cas 13b, Cas 13c, Cas 13d, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, homologues thereof, or modified versions thereof. Other suitable Cas proteins or encoding polynucleotides that can be included as cargo are described elsewhere herein such as with discussion related to CRISPR-Cas systems.

Specialized Cas-Based Systems

In some embodiments, the system is a Cas-based system that is capable of performing a specialized function or activity. For example, the Cas protein may be fused, operably coupled to, or otherwise associated with one or more functional domains. In certain example embodiments, the Cas protein may be a catalytically dead Cas protein ("dCas") and/or have nickase activity. A nickase is a Cas protein that cuts only one strand of a double stranded target. In such embodiments, the dCas or nickase provide a sequence specific targeting functionality that delivers the functional domain to or proximate a target sequence. Example functional domains that may be fused to, operably coupled to, or otherwise associated with a Cas protein can be or include, but are not limited to a nuclear localization signal (NLS) domain, a nuclear export signal (NES) domain, a translational activation domain, a transcriptional activation domain (e.g. VP64, p65, MyoD1, HSF1, RTA, and SET7/9), a translation initiation domain, a transcriptional repression domain (e.g., a KRAB domain, NuE domain, NcoR domain, and a SID domain such as a SID4X domain), a nuclease domain (e.g., FokI), a histone modification domain (e.g., a histone acetyltransferase), a light inducible/controllable

domain, a chemically inducible/controllable domain, a transposase domain, a homologous recombination machinery domain, a recombinase domain, an integrase domain, and combinations thereof. Methods for generating catalytically dead Cas9 or a nickase Cas9 (International Patent Publication No. WO 2014/204725, Ran et al. Cell. 2013 Sep. 12; 154(6): 1380-1389), Cas12 (Liu et al. Nature Communications, 8, 2095 (2017), and Cas13 (International Patent Publication Nos. WO 2019/005884 and WO2019/060746) are known in the art and incorporated herein by reference.

In some embodiments, the functional domains can have one or more of the following activities: methylase activity, demethylase activity, translation activation activity, translation initiation activity, translation repression activity, transcription activation activity, transcription repression activity, transcription release factor activity, histone modification activity, nuclease activity, single-strand RNA cleavage activity, double-strand RNA cleavage activity, single-strand DNA cleavage activity, double-strand DNA cleavage activity, molecular switch activity, chemical inducibility, light inducibility, and nucleic acid binding activity. In some embodiments, the one or more functional domains may comprise epitope tags or reporters. Non-limiting examples of epitope tags include histidine (His) tags, V5 tags, FLAG tags, influenza hemagglutinin (HA) tags, Myc tags, VSV-G tags, and thioredoxin (Trx) tags. Examples of reporters include, but are not limited to, glutathione-S-transferase (GST), horseradish peroxidase (HRP), chloramphenicol acetyltransferase (CAT) beta-galactosidase, beta-glucuronidase, luciferase, green fluorescent protein (GFP), HcRed, DsRed, cyan fluorescent protein (CFP), yellow fluorescent protein (YFP), and auto-fluorescent proteins including blue fluorescent protein (BFP).

The one or more functional domain(s) may be positioned at, near, and/or in proximity to a terminus of the effector protein (e.g., a Cas protein). In embodiments having two or more functional domains, each of the two can be positioned at or near or in proximity to a terminus of the effector protein (e.g., a Cas protein). In some embodiments, such as those where the functional domain is operably coupled to the effector protein, the one or more functional domains can be tethered or linked via a suitable linker (including, but not limited to, GlySer linkers) to the effector protein (e.g., a Cas protein). When there is more than one functional domain, the functional domains can be same or different. In some embodiments, all the functional domains are the same. In some embodiments, all of the functional domains are different from each other. In some embodiments, at least two of the functional domains are different from each other. In some embodiments, at least two of the functional domains are the same as each other.

Other suitable functional domains can be found, for example, in International Patent Publication No. WO 2019/018423.

Split CRISPR-Cas Systems

In some embodiments, the CRISPR-Cas system is a split CRISPR-Cas system. See e.g., Zetche et al., 2015. Nat. Biotechnol. 33(2): 139-142 and International Patent Publication WO 2019/018423, the compositions and techniques of which can be used in and/or adapted for use with the present invention. Split CRISPR-Cas proteins are set forth herein and in documents incorporated herein by reference in further detail herein. In certain embodiments, each part of a split CRISPR protein are attached to a member of a specific binding pair, and when bound with each other, the members of the specific binding pair maintain the parts of the CRISPR protein in proximity. In certain embodiments, each part of a

split CRISPR protein is associated with an inducible binding pair. An inducible binding pair is one which is capable of being switched “on” or “off” by a protein or small molecule that binds to both members of the inducible binding pair. In some embodiments, CRISPR proteins may preferably split between domains, leaving domains intact. In particular embodiments, said Cas split domains (e.g., RuvC and HNH domains in the case of Cas9) can be simultaneously or sequentially introduced into the cell such that said split Cas domain(s) process the target nucleic acid sequence in the algae cell. The reduced size of the split Cas compared to the wild type Cas allows other methods of delivery of the systems to the cells, such as the use of cell penetrating peptides as described herein.

DNA and RNA Base Editing

In some embodiments, a polynucleotide of the present invention described elsewhere herein can be modified using a base editing system. In some embodiments, a Cas protein is connected or fused to a nucleotide deaminase. Thus, in some embodiments the Cas-based system can be a base editing system. As used herein, “base editing” refers generally to the process of polynucleotide modification via a CRISPR-Cas-based or Cas-based system that does not include excising nucleotides to make the modification. Base editing can convert base pairs at precise locations without generating excess undesired editing byproducts that can be made using traditional CRISPR-Cas systems.

In certain example embodiments, the nucleotide deaminase may be a DNA base editor used in combination with a DNA binding Cas protein such as, but not limited to, Class 2 Type II and Type V systems. Two classes of DNA base editors are generally known: cytosine base editors (CBEs) and adenine base editors (ABEs). CBEs convert a C-G base pair into a T-A base pair (Komor et al. 2016. Nature. 533:420-424; Nishida et al. 2016. Science. 353; and Li et al. Nat. Biotech. 36:324-327) and ABEs convert an A-T base pair to a G-C base pair. Collectively, CBEs and ABEs can mediate all four possible transition mutations (C to T, A to G, T to C, and G to A). Rees and Liu. 2018. Nat. Rev. Genet. 19(12): 770-788, particularly at FIGS. 1b, 2a-2c, 3a-3f, and Table 1. In some embodiments, the base editing system includes a CBE and/or an ABE. In some embodiments, a polynucleotide of the present invention described elsewhere herein can be modified using a base editing system. Rees and Liu. 2018. Nat. Rev. Genet. 19(12): 770-788. Base editors also generally do not need a DNA donor template and/or rely on homology-directed repair. Komor et al. 2016. Nature. 533:420-424; Nishida et al. 2016. Science. 353; and Gaudeli et al. 2017. Nature. 551:464-471. Upon binding to a target locus in the DNA, base pairing between the guide RNA of the system and the target DNA strand leads to displacement of a small segment of ssDNA in an “R-loop”. Nishimasu et al. Cell. 156:935-949. DNA bases within the ssDNA bubble are modified by the enzyme component, such as a deaminase. In some systems, the catalytically disabled Cas protein can be a variant or modified Cas can have nickase functionality and can generate a nick in the non-edited DNA strand to induce cells to repair the non-edited strand using the edited strand as a template. Komor et al. 2016. Nature. 533:420-424; Nishida et al. 2016. Science. 353; and Gaudeli et al. 2017. Nature. 551:464-471.

Other Example Type V base editing systems are described in International Patent Publication Nos. WO 2018/213708, WO 2018/213726, and International Patent Applications No. PCT/US2018/067207, PCT/US2018/067225, and PCT/US2018/067307, each of which is incorporated herein by reference.

In certain example embodiments, the base editing system may be an RNA base editing system. As with DNA base editors, a nucleotide deaminase capable of converting nucleotide bases may be fused to a Cas protein. However, in these embodiments, the Cas protein will need to be capable of binding RNA. Example RNA binding Cas proteins include, but are not limited to, RNA-binding Cas9s such as *Francisella novicida* Cas9 (“FnCas9”), and Class 2 Type VI Cas systems. The nucleotide deaminase may be a cytidine deaminase or an adenosine deaminase, or an adenosine deaminase engineered to have cytidine deaminase activity. In certain example embodiments, the RNA base editor may be used to delete or introduce a post-translation modification site in the expressed mRNA. In contrast to DNA base editors, whose edits are permanent in the modified cell, RNA base editors can provide edits where finer, temporal control may be needed, for example in modulating a particular immune response. Example Type VI RNA-base editing systems are described in Cox et al. 2017. Science 358:1019-1027, International Patent Publication Nos. WO 2019/005884, WO 2019/005886, and WO 2019/071048, and International Patent Application Nos. PCT/US20018/05179 and PCT/US2018/067207, which are incorporated herein by reference. An example FnCas9 system that may be adapted for RNA base editing purposes is described in International Patent Publication No. WO 2016/106236, which is incorporated herein by reference.

An example method for delivery of base-editing systems, including use of a split-intein approach to divide CBE and ABE into reconstitutable halves, is described in Levy et al. Nature Biomedical Engineering doi.org/10.1038/s41441-019-0505-5(2019), which is incorporated herein by reference.

Prime Editors

In some embodiments, a polynucleotide of the present invention described elsewhere herein can be modified using a prime editing system. See e.g. Anzalone et al. 2019. Nature. 576:149-157. Like base editing systems, prime editing systems can be capable of targeted modification of a polynucleotide without generating double stranded breaks and does not require donor templates. Further prime editing systems can be capable of all 12 possible combination swaps. Prime editing can operate via a “search-and-replace” methodology and can mediate targeted insertions, deletions, all 12 possible base-to-base conversion and combinations thereof. Generally, a prime editing system, as exemplified by PE1, PE2, and PE3 (Id.), can include a reverse transcriptase fused or otherwise coupled or associated with an RNA-programmable nickase and a prime-editing extended guide RNA (pegRNA) to facility direct copying of genetic information from the extension on the pegRNA into the target polynucleotide. Embodiments that can be used with the present invention include these and variants thereof. Prime editing can have the advantage of lower off-target activity than traditional CRISPR-Cas systems along with few byproducts and greater or similar efficiency as compared to traditional CRISPR-Cas systems.

In some embodiments, the prime editing guide molecule can specify both the target polynucleotide information (e.g., sequence) and contain a new polynucleotide cargo that replaces target polynucleotides. To initiate transfer from the guide molecule to the target polynucleotide, the PE system can nick the target polynucleotide at a target site to expose a 3'hydroxyl group, which can prime reverse transcription of an edit-encoding extension region of the guide molecule (e.g. a prime editing guide molecule or peg guide molecule) directly into the target site in the target polynucleotide. See

e.g. Anzalone et al. 2019. Nature. 576:149-157, particularly at FIGS. 1b, 1c, related discussion, and Supplementary discussion.

In some embodiments, a prime editing system can be composed of a Cas polypeptide having nickase activity, a reverse transcriptase, and a guide molecule. The Cas polypeptide can lack nuclease activity. The guide molecule can include a target binding sequence as well as a primer binding sequence and a template containing the edited polynucleotide sequence. The guide molecule, Cas polypeptide, and/or reverse transcriptase can be coupled together or otherwise associate with each other to form an effector complex and edit a target sequence. In some embodiments, the Cas polypeptide is a Class 2, Type V Cas polypeptide. In some embodiments, the Cas polypeptide is a Cas9 polypeptide (e.g. is a Cas9 nickase). In some embodiments, the Cas polypeptide is fused to the reverse transcriptase. In some embodiments, the Cas polypeptide is linked to the reverse transcriptase.

In some embodiments, the prime editing system can be a PE1 system or variant thereof, a PE2 system or variant thereof, or a PE3 (e.g. PE3, PE3b) system. See e.g., Anzalone et al. 2019. Nature. 576:149-157, particularly at pgs. 2-3, FIGS. 2a, 3a-3f, 4a-4b, Extended data FIGS. 3a-3b, and 4.

The peg guide molecule can be about 10 to about 200 or more nucleotides in length, such as 10 to/or 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, or 200 or more nucleotides in length. Optimization of the peg guide molecule can be accomplished as described in Anzalone et al. 2019. Nature. 576:149-157, particularly at pg. 3, FIG. 2a-2b, and Extended Data FIGS. 5a-c.

CRISPR Associated Transposase (CAST) Systems

In some embodiments, a polynucleotide of the present invention described elsewhere herein can be modified using a CRISPR Associated Transposase (“CAST”) system. CAST system can include a Cas protein that is catalytically inactive, or engineered to be catalytically active, and further comprises a transposase (or subunits thereof) that catalyze RNA-guided DNA transposition. Such systems are able to insert DNA sequences at a target site in a DNA molecule without relying on host cell repair machinery. CAST systems can be Class1 or Class 2 CAST systems. An example Class 1 system is described in Klompe et al. Nature, doi: 10.1038/s41586-019-1323, which is incorporated herein by reference. An example Class 2 system is described in Strecker et al. Science. 10/1126/science. aax9181 (2019), and PCT/US2019/066835 which are incorporated herein by reference.

Guide Sequences

In some embodiments, the cargo is or includes one or more guide molecules for a CRISPR-Cas system. The terms guide molecule, guide sequence and guide polynucleotide refer to polynucleotides capable of guiding Cas to a target

genomic locus and are used interchangeably as in foregoing cited documents such as International Patent Publication No. WO 2014/093622 (PCT/US2013/074667). In general, a guide sequence is any polynucleotide sequence having sufficient complementarity with a target polynucleotide sequence to hybridize with the target sequence and direct sequence-specific binding of a CRISPR complex to the target sequence. The guide molecule can be a polynucleotide.

The ability of a guide sequence (within a nucleic acid-targeting guide RNA) to direct sequence-specific binding of a nucleic acid-targeting complex to a target nucleic acid sequence may be assessed by any suitable assay. For example, the components of a nucleic acid-targeting CRISPR system sufficient to form a nucleic acid-targeting complex, including the guide sequence to be tested, may be provided to a host cell having the corresponding target nucleic acid sequence, such as by transfection with vectors encoding the components of the nucleic acid-targeting complex, followed by an assessment of preferential targeting (e.g., cleavage) within the target nucleic acid sequence, such as by Surveyor assay (Qui et al. 2004. *BioTechniques*. 36(4) 702-707). Similarly, cleavage of a target nucleic acid sequence may be evaluated in a test tube by providing the target nucleic acid sequence, components of a nucleic acid-targeting complex, including the guide sequence to be tested and a control guide sequence different from the test guide sequence, and comparing binding or rate of cleavage at the target sequence between the test and control guide sequence reactions. Other assays are possible and will occur to those skilled in the art.

In some embodiments, the guide molecule is an RNA. The guide molecule(s) (also referred to interchangeably herein as guide polynucleotide and guide sequence) that are included in the CRISPR-Cas or Cas based system can be any polynucleotide sequence having sufficient complementarity with a target nucleic acid sequence to hybridize with the target nucleic acid sequence and direct sequence-specific binding of a nucleic acid-targeting complex to the target nucleic acid sequence. In some embodiments, the degree of complementarity, when optimally aligned using a suitable alignment algorithm, can be about or more than about 50%, 60%, 75%, 80%, 85%, 90%, 95%, 97.5%, 99%, or more. Optimal alignment may be determined with the use of any suitable algorithm for aligning sequences, non-limiting examples of which include the Smith-Waterman algorithm, the Needleman-Wunsch algorithm, algorithms based on the Burrows-Wheeler Transform (e.g., the Burrows Wheeler Aligner), Clustal W, Clustal X, BLAT, Novoalign (Novocraft Technologies; available at www.novocraft.com), ELAND (Illumina, San Diego, CA), SOAP (available at soap.genomics.org.cn), and Maq (available at maq.sourceforge.net).

A guide sequence, and hence a nucleic acid-targeting guide, may be selected to target any target nucleic acid sequence. The target sequence may be DNA. The target sequence may be any RNA sequence. In some embodiments, the target sequence may be a sequence within an RNA molecule selected from the group consisting of messenger RNA (mRNA), pre-mRNA, ribosomal RNA (rRNA), transfer RNA (tRNA), micro-RNA (miRNA), small interfering RNA (siRNA), small nuclear RNA (snRNA), small nucleolar RNA (snoRNA), double stranded RNA (dsRNA), non-coding RNA (ncRNA), long non-coding RNA (lncRNA), and small cytoplasmic RNA (scRNA). In some preferred embodiments, the target sequence may be a sequence within an RNA molecule selected from the group consisting of mRNA, pre-mRNA, and rRNA. In some preferred embodi-

ments, the target sequence may be a sequence within an RNA molecule selected from the group consisting of ncRNA, and lncRNA. In some more preferred embodiments, the target sequence may be a sequence within an mRNA molecule or a pre-mRNA molecule.

In some embodiments, a nucleic acid-targeting guide is selected to reduce the degree secondary structure within the nucleic acid-targeting guide. In some embodiments, about or less than about 75%, 50%, 40%, 30%, 25%, 20%, 15%, 10%, 5%, 1%, or fewer of the nucleotides of the nucleic acid-targeting guide participate in self-complementary base pairing when optimally folded. Optimal folding may be determined by any suitable polynucleotide folding algorithm. Some programs are based on calculating the minimal Gibbs free energy. An example of one such algorithm is mFold, as described by Zuker and Stiegler (*Nucleic Acids Res.* 9(1981), 133-148). Another example folding algorithm is the online webserver RNAfold, developed at Institute for Theoretical Chemistry at the University of Vienna, using the centroid structure prediction algorithm (see e.g., A. R. Gruber et al., 2008, *Cell* 106(1): 23-24; and PA Carr and GM Church, 2009, *Nature Biotechnology* 27(12): 1151-62).

In certain embodiments, a guide RNA or crRNA may comprise, consist essentially of, or consist of a direct repeat (DR) sequence and a guide sequence or spacer sequence. In certain embodiments, the guide RNA or crRNA may comprise, consist essentially of, or consist of a direct repeat sequence fused or linked to a guide sequence or spacer sequence. In certain embodiments, the direct repeat sequence may be located upstream (i.e., 5') from the guide sequence or spacer sequence. In other embodiments, the direct repeat sequence may be located downstream (i.e., 3') from the guide sequence or spacer sequence.

In certain embodiments, the crRNA comprises a stem loop, preferably a single stem loop. In certain embodiments, the direct repeat sequence forms a stem loop, preferably a single stem loop.

In certain embodiments, the spacer length of the guide RNA is from 15 to 35 nt. In certain embodiments, the spacer length of the guide RNA is at least 15 nucleotides. In certain embodiments, the spacer length is from 15 to 17 nt, e.g., 15, 16, or 17 nt, from 17 to 20 nt, e.g., 17, 18, 19, or 20 nt, from 20 to 24 nt, e.g., 20, 21, 22, 23, or 24 nt, from 23 to 25 nt, e.g., 23, 24, or 25 nt, from 24 to 27 nt, e.g., 24, 25, 26, or 27 nt, from 27 to 30 nt, e.g., 27, 28, 29, or 30 nt, from 30 to 35 nt, e.g., 30, 31, 32, 33, 34, or 35 nt, or 35 nt or longer.

The "tracrRNA" sequence or analogous terms includes any polynucleotide sequence that has sufficient complementarity with a crRNA sequence to hybridize. In some embodiments, the degree of complementarity between the tracrRNA sequence and crRNA sequence along the length of the shorter of the two when optimally aligned is about or more than about 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97.5%, 99%, or higher. In some embodiments, the tracr sequence is about or more than about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 25, 30, 40, 50, or more nucleotides in length. In some embodiments, the tracr sequence and crRNA sequence are contained within a single transcript, such that hybridization between the two produces a transcript having a secondary structure, such as a hairpin.

In general, degree of complementarity is with reference to the optimal alignment of the sca sequence and tracr sequence, along the length of the shorter of the two sequences. Optimal alignment may be determined by any suitable alignment algorithm and may further account for secondary structures, such as self-complementarity within either the sca sequence or tracr sequence. In some embodi-

ments, the degree of complementarity between the tracr sequence and sca sequence along the length of the shorter of the two when optimally aligned is about or more than about 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97.5%, 99%, or higher.

In some embodiments, the degree of complementarity between a guide sequence and its corresponding target sequence can be about or more than about 50%, 60%, 75%, 80%, 85%, 90%, 95%, 97.5%, 99%, or 100%; a guide or RNA or sgRNA can be about or more than about 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, 75, or more nucleotides in length; or guide or RNA or sgRNA can be less than about 75, 50, 45, 40, 35, 30, 25, 20, 15, 12, or fewer nucleotides in length; and tracr RNA can be 30 or 50 nucleotides in length. In some embodiments, the degree of complementarity between a guide sequence and its corresponding target sequence is greater than 94.5% or 95% or 95.5% or 96% or 96.5% or 97% or 97.5% or 98% or 98.5% or 99% or 99.5% or 99.9%, or 100%. Off target is less than 100% or 99.9% or 99.5% or 99% or 99% or 98.5% or 98% or 97.5% or 97% or 96.5% or 96% or 95.5% or 95% or 94.5% or 94% or 93% or 92% or 91% or 90% or 89% or 88% or 87% or 86% or 85% or 84% or 83% or 82% or 81% or 80% complementarity between the sequence and the guide, with it being advantageous that off target is 100% or 99.9% or 99.5% or 99% or 99% or 98.5% or 98% or 97.5% or 97% or 96.5% or 96% or 95.5% or 95% or 94.5% complementarity between the sequence and the guide.

In some embodiments according to the invention, the guide RNA (capable of guiding Cas to a target locus) may comprise (1) a guide sequence capable of hybridizing to a genomic target locus in the eukaryotic cell; (2) a tracr sequence; and (3) a tracr mate sequence. All (1) to (3) may reside in a single RNA, i.e., an sgRNA (arranged in a 5' to 3' orientation), or the tracr RNA may be a different RNA than the RNA containing the guide and tracr sequence. The tracr hybridizes to the tracr mate sequence and directs the CRISPR/Cas complex to the target sequence. Where the tracr RNA is on a different RNA than the RNA containing the guide and tracr sequence, the length of each RNA may be optimized to be shortened from their respective native lengths, and each may be independently chemically modified to protect from degradation by cellular RNase or otherwise increase stability.

Many modifications to guide sequences are known in the art and are further contemplated within the context of this invention. Various modifications may be used to increase the specificity of binding to the target sequence and/or increase the activity of the Cas protein and/or reduce off-target effects. Example guide sequence modifications are described in International Patent Application No. PCT US2019/045582, specifically paragraphs [0178]-[0333], which is incorporated herein by reference.

Target Sequences, PAMs, and PES's

Target Sequences

In the context of formation of a CRISPR complex, "target sequence" refers to a sequence to which a guide sequence is designed to have complementarity, where hybridization between a target sequence and a guide sequence promotes the formation of a CRISPR complex. A target sequence may comprise RNA polynucleotides. The term "target RNA" refers to an RNA polynucleotide being or comprising the target sequence. In other words, the target polynucleotide can be a polynucleotide or a part of a polynucleotide to which a part of the guide sequence is designed to have complementarity with and to which the effector function

mediated by the complex comprising the CRISPR effector protein and a guide molecule is to be directed. In some embodiments, a target sequence is located in the nucleus or cytoplasm of a cell.

The guide sequence can specifically bind a target sequence in a target polynucleotide. The target polynucleotide may be DNA. The target polynucleotide may be RNA. The target polynucleotide can have one or more (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, etc. or more) target sequences. The target polynucleotide can be on a vector. The target polynucleotide can be genomic DNA. The target polynucleotide can be episomal. Other forms of the target polynucleotide are described elsewhere herein.

The target sequence may be DNA. The target sequence may be any RNA sequence. In some embodiments, the target sequence may be a sequence within an RNA molecule selected from the group consisting of messenger RNA (mRNA), pre-mRNA, ribosomal RNA (rRNA), transfer RNA (tRNA), micro-RNA (miRNA), small interfering RNA (siRNA), small nuclear RNA (snRNA), small nucleolar RNA (snoRNA), double stranded RNA (dsRNA), non-coding RNA (ncRNA), long non-coding RNA (lncRNA), and small cytoplasmic RNA (scRNA). In some preferred embodiments, the target sequence (also referred to herein as a target polynucleotide) may be a sequence within an RNA molecule selected from the group consisting of mRNA, pre-mRNA, and rRNA. In some preferred embodiments, the target sequence may be a sequence within an RNA molecule selected from the group consisting of ncRNA, and lncRNA. In some more preferred embodiments, the target sequence may be a sequence within an mRNA molecule or a pre-mRNA molecule.

PAM and PFS Elements

PAM elements are sequences that can be recognized and bound by Cas proteins. Cas proteins/effector complexes can then unwind the dsDNA at a position adjacent to the PAM element. It will be appreciated that Cas proteins and systems that include them that target RNA do not require PAM sequences (Marraffini et al. 2010. *Nature*. 463:568-571). Instead, many rely on PFSs, which are discussed elsewhere herein. In certain embodiments, the target sequence should be associated with a PAM (protospacer adjacent motif) or PFS (protospacer flanking sequence or site), that is, a short sequence recognized by the CRISPR complex. Depending on the nature of the CRISPR-Cas protein, the target sequence should be selected, such that its complementary sequence in the DNA duplex (also referred to herein as the non-target sequence) is upstream or downstream of the PAM. In the embodiments, the complementary sequence of the target sequence is downstream or 3' of the PAM or upstream or 5' of the PAM. The precise sequence and length requirements for the PAM differ depending on the Cas protein used, but PAMs are typically 2-5 base pair sequences adjacent the protospacer (that is, the target sequence). Examples of the natural PAM sequences for different Cas proteins are provided herein below and the skilled person will be able to identify further PAM sequences for use with a given Cas protein.

The ability to recognize different PAM sequences depends on the Cas polypeptide(s) included in the system. See e.g., Gleditsch et al. 2019. *RNA Biology*. 16(4): 504-517. Table 10 (from Gleditsch et al. 2019) below shows several Cas polypeptides and the PAM sequence they recognize.

TABLE 10

Example PAM Sequences	
Cas Protein	PAM Sequence
SpCas9	NGG/NRG
SaCas9	NGRRT or NGRRN
NmeCas9	NNNGATT
CjCas9	NNNNRYAC
StCas9	NNAGAAW
Cas12a (Cpf1) (including LbCpf1 and AsCpf1)	TTTV
Cas12b (C2c1)	TTT, TTA, and TTC
Cas12c (C2c3)	TA
Cas12d (CasY)	TA
Cas12e (CasX)	5'-TTCN-3'

In a preferred embodiment, the CRISPR effector protein may recognize a 3' PAM. In certain embodiments, the CRISPR effector protein may recognize a 3' PAM which is 5'H, wherein His A, C or U.

Further, engineering of the PAM Interacting (PI) domain on the Cas protein may allow programming of PAM specificity, improve target site recognition fidelity, and increase the versatility of the CRISPR-Cas protein, for example as described for Cas9 in Kleinstiver B P et al. Engineered CRISPR-Cas9 nucleases with altered PAM specificities. *Nature*. 2015 Jul. 23; 523(7561): 481-5. doi: 10.1038/nature14592. As further detailed herein, the skilled person will understand that Cas13 proteins may be modified analogously. Gao et al, "Engineered Cpf1 Enzymes with Altered PAM Specificities," bioRxiv 091611; doi: dx.doi.org/10.1101/091611 (Dec. 4, 2016). Doench et al. created a pool of sgRNAs, tiling across all possible target sites of a panel of six endogenous mouse and three endogenous human genes and quantitatively assessed their ability to produce null alleles of their target gene by antibody staining and flow cytometry. The authors showed that optimization of the PAM improved activity and also provided an on-line tool for designing sgRNAs.

PAM sequences can be identified in a polynucleotide using an appropriate design tool, which are commercially available as well as online. Such freely available tools include, but are not limited to, CRISPRFinder and CRISPR-Target. Mojica et al. 2009. *Microbiol.* 155 (Pt. 3): 733-740; Atschul et al. 1990. *J. Mol. Biol.* 215:403-410; Biswass et al. 2013 *RNA Biol.* 10:817-827; and Grissa et al. 2007. *Nucleic Acid Res.* 35: W52-57. Experimental approaches to PAM identification can include, but are not limited to, plasmid depletion assays (Jiang et al. 2013. *Nat. Biotechnol.* 31:233-239; Esvelt et al. 2013. *Nat. Methods.* 10:1116-1121; Kleinstiver et al. 2015. *Nature.* 523:481-485), screened by a high-throughput in vivo model called PAM-SCNAR (Patnayak et al. 2013. *Nat. Biotechnol.* 31:839-843 and Leenay et al. 2016. *Mol. Cell.* 16:253), and negative screening (Zetsche et al. 2015. *Cell.* 163:759-771).

As previously mentioned, CRISPR-Cas systems that target RNA do not typically rely on PAM sequences. Instead such systems typically recognize protospacer flanking sites (PFSs) instead of PAMs. Thus, Type VI CRISPR-Cas systems typically recognize protospacer flanking sites (PFSs)

instead of PAMs. PFSs represents an analogue to PAMs for RNA targets. Type VI CRISPR-Cas systems employ a Cas13. Some Cas13 proteins analyzed to date, such as Cas13a (C2c2) identified from *Leptotrichia shahii* (LSHCas13a) have a specific discrimination against G at the 3' end of the target RNA. The presence of a C at the corresponding crRNA repeat site can indicate that nucleotide pairing at this position is rejected. However, some Cas13 proteins (e.g., LwCas13a and PspCas13b) do not seem to have a PFS preference. See e.g., Gleditsch et al. 2019. *RNA Biology.* 16(4): 504-517.

Some Type VI proteins, such as subtype B, have 5'-recognition of D (G, T, A) and a 3'-motif requirement of NAN or NNA. One example is the Cas13b protein identified in *Bergeyella zoohelcum* (BzCas13b). See e.g., Gleditsch et al. 2019. *RNA Biology.* 16(4): 504-517.

Overall Type VI CRISPR-Cas systems appear to have less restrictive rules for substrate (e.g., target sequence) recognition than those that target DNA (e.g., Type V and type II).

Sequences Related to Nucleus Targeting and Transportation

In some embodiments, one or more components (e.g., the Cas protein and/or deaminase) in the composition for engineering cells may comprise one or more sequences related to nucleus targeting and transportation. Such sequence may facilitate the one or more components in the composition for targeting a sequence within a cell. In order to improve targeting of the CRISPR-Cas protein and/or the nucleotide deaminase protein or catalytic domain thereof used in the methods of the present disclosure to the nucleus, it may be advantageous to provide one or both of these components with one or more nuclear localization sequences (NLSs).

In some embodiments, the NLSs used in the context of the present disclosure are heterologous to the proteins. Non-limiting examples of NLSs include an NLS sequence derived from: the NLS of the SV40 virus large T-antigen, having the amino acid sequence PKKKRKV (SEQ ID NO: 52) or PKKKRKVEAS (SEQ ID NO: 53); the NLS from nucleoplasmin (e.g., the nucleoplasmin bipartite NLS with the sequence KRPAATKKAGQAKKKK (SEQ ID NO: 54); the c-myc NLS having the amino acid sequence PAAKRVKLD (SEQ ID NO: 55) or QRRLNELKRSP (SEQ ID NO: 57); the hRNP A1 M9 NLS having the sequence NQSSNFGPMKGGNFGGRSSGPGYGGGGQYFAK-PRNQGGY (SEQ ID NO: 58); the sequence RMRIZFKNKGKDTAELRRRRVEVSVELRKAKKD-EQILKRRNV (SEQ ID NO: 59) of the IBB domain from importin- α ; the sequences VSRKRPRP (SEQ ID NO: 9088) and PPKKARED (SEQ ID NO: 9089) of the myoma T protein; the sequence PQPKKKPL (SEQ ID NO: 9090) of human p53; the sequence SALIKKKKKMAP (SEQ ID NO: 9091) of mouse c-abl IV; the sequences DRLRR (SEQ ID NO: 9092) and PKQKKRK (SEQ ID NO: 9093) of the influenza virus NS1; the sequence RKLKKIKKL (SEQ ID NO: 9094) of the Hepatitis virus delta antigen; the sequence REKKKFLKRR (SEQ ID NO: 9095) of the mouse Mx1 protein; the sequence KRKGDEVGVDEVAKKKSKK (SEQ ID NO: 9096) of the human poly (ADP-ribose) polymerase; and the sequence RKCLQAGMNLARKTKK (SEQ ID NO: 9097) of the steroid hormone receptors (human) glucocorticoid. In general, the one or more NLSs are of sufficient strength to drive accumulation of the DNA-targeting Cas protein in a detectable amount in the nucleus of a eukaryotic cell. In general, strength of nuclear localization activity may derive from the number of NLSs in the CRISPR-Cas protein, the particular NLS(s) used, or a combination of these factors. Detection of accumulation in the nucleus may be performed by any suitable technique. For

example, a detectable marker may be fused to the nucleic acid-targeting protein, such that location within a cell may be visualized, such as in combination with a means for detecting the location of the nucleus (e.g., a stain specific for the nucleus such as DAPI). Cell nuclei may also be isolated from cells, the contents of which may then be analyzed by any suitable process for detecting protein, such as immunohistochemistry, Western blot, or enzyme activity assay. Accumulation in the nucleus may also be determined indirectly, such as by an assay for the effect of nucleic acid-targeting complex formation (e.g., assay for deaminase activity) at the target sequence, or assay for altered gene expression activity affected by DNA-targeting complex formation and/or DNA-targeting), as compared to a control not exposed to the CRISPR-Cas protein and deaminase protein, or exposed to a CRISPR-Cas and/or deaminase protein lacking the one or more NLSs.

The CRISPR-Cas and/or nucleotide deaminase proteins may be provided with 1 or more, such as with, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more heterologous NLSs. In some embodiments, the proteins comprises about or more than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near the amino-terminus, about or more than about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more NLSs at or near the carboxy-terminus, or a combination of these (e.g., zero or at least one or more NLS at the amino-terminus and zero or at one or more NLS at the carboxy terminus). When more than one NLS is present, each may be selected independently of the others, such that a single NLS may be present in more than one copy and/or in combination with one or more other NLSs present in one or more copies. In some embodiments, an NLS is considered near the N- or C-terminus when the nearest amino acid of the NLS is within about 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more amino acids along the polypeptide chain from the N- or C-terminus. In preferred embodiments of the CRISPR-Cas proteins, an NLS attached to the C-terminal of the protein.

In certain embodiments, the CRISPR-Cas protein and the deaminase protein are delivered to the cell or expressed within the cell as separate proteins. In these embodiments, each of the CRISPR-Cas and deaminase protein can be provided with one or more NLSs as described herein. In certain embodiments, the CRISPR-Cas and deaminase proteins are delivered to the cell or expressed with the cell as a fusion protein. In these embodiments one or both of the CRISPR-Cas and deaminase protein is provided with one or more NLSs. Where the nucleotide deaminase is fused to an adaptor protein (such as MS2) as described above, the one or more NLS can be provided on the adaptor protein, provided that this does not interfere with aptamer binding. In particular embodiments, the one or more NLS sequences may also function as linker sequences between the nucleotide deaminase and the CRISPR-Cas protein.

In certain embodiments, guides of the disclosure comprise specific binding sites (e.g. aptamers) for adapter proteins, which may be linked to or fused to a nucleotide deaminase or catalytic domain thereof. When such a guide forms a CRISPR complex (e.g., CRISPR-Cas protein binding to guide and target), the adapter proteins bind and the nucleotide deaminase or catalytic domain thereof associated with the adapter protein is positioned in a spatial orientation which is advantageous for the attributed function to be effective.

The skilled person will understand that modifications to the guide which allow for binding of the adapter+nucleotide deaminase, but not proper positioning of the adapter+nucleotide deaminase (e.g. due to steric hindrance within the

three-dimensional structure of the CRISPR complex) are modifications which are not intended. The one or more modified guide may be modified at the tetra loop, the stem loop 1, stem loop 2, or stem loop 3, as described herein, preferably at either the tetra loop or stem loop 2, and in some cases at both the tetra loop and stem loop 2.

In some embodiments, a component (e.g., the dead Cas protein, the nucleotide deaminase protein or catalytic domain thereof, or a combination thereof) in the systems may comprise one or more nuclear export signals (NES), one or more nuclear localization signals (NLS), or any combinations thereof. In some cases, the NES may be an HIV Rev NES. In certain cases, the NES may be MAPK NES. When the component is a protein, the NES or NLS may be at the C terminus of component. Alternatively, or additionally, the NES or NLS may be at the N terminus of component. In some examples, the Cas protein and optionally said nucleotide deaminase protein or catalytic domain thereof comprise one or more heterologous nuclear export signal(s) (NES(s)) or nuclear localization signal(s) (NLS(s)), preferably an HIV Rev NES or MAPK NES, preferably C-terminal.

Templates

In some embodiments, the composition for engineering cells comprise a template, e.g., a recombination template. A template may be a component of another vector as described herein, contained in a separate vector, or provided as a separate polynucleotide. In some embodiments, a recombination template is designed to serve as a template in homologous recombination, such as within or near a target sequence nicked or cleaved by a nucleic acid-targeting effector protein as a part of a nucleic acid-targeting complex.

In an embodiment, the template nucleic acid alters the sequence of the target position. In an embodiment, the template nucleic acid results in the incorporation of a modified, or non-naturally occurring base into the target nucleic acid.

The template sequence may undergo a breakage mediated or catalyzed recombination with the target sequence. In an embodiment, the template nucleic acid may include sequence that corresponds to a site on the target sequence that is cleaved by a Cas protein mediated cleavage event. In an embodiment, the template nucleic acid may include a sequence that corresponds to both, a first site on the target sequence that is cleaved in a first Cas protein mediated event, and a second site on the target sequence that is cleaved in a second Cas protein mediated event.

In certain embodiments, the template nucleic acid can include a sequence which results in an alteration in the coding sequence of a translated sequence, e.g., one which results in the substitution of one amino acid for another in a protein product, e.g., transforming a mutant allele into a wild type allele, transforming a wild type allele into a mutant allele, and/or introducing a stop codon, insertion of an amino acid residue, deletion of an amino acid residue, or a nonsense mutation. In certain embodiments, the template nucleic acid can include a sequence which results in an alteration in a non-coding sequence, e.g., an alteration in an exon or in a 5' or 3' non-translated or non-transcribed region. Such alterations include an alteration in a control element, e.g., a promoter, enhancer, and an alteration in a cis-acting or trans-acting control element.

A template nucleic acid having homology with a target position in a target gene may be used to alter the structure of a target sequence. The template sequence may be used to alter an unwanted structure, e.g., an unwanted or mutant nucleotide. The template nucleic acid may include a

sequence which, when integrated, results in decreasing the activity of a positive control element; increasing the activity of a positive control element; decreasing the activity of a negative control element; increasing the activity of a negative control element; decreasing the expression of a gene; increasing the expression of a gene; increasing resistance to a disorder or disease; increasing resistance to viral entry; correcting a mutation or altering an unwanted amino acid residue conferring, increasing, abolishing or decreasing a biological property of a gene product, e.g., increasing the enzymatic activity of an enzyme, or increasing the ability of a gene product to interact with another molecule.

The template nucleic acid may include a sequence which results in a change in sequence of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or more nucleotides of the target sequence.

A template polynucleotide may be of any suitable length, such as about or more than about 10, 15, 20, 25, 50, 75, 100, 150, 200, 500, 1000, or more nucleotides in length. In an embodiment, the template nucleic acid may be 20+/-10, 30+/-10, 40+/-10, 50+/-10, 60+/-10, 70+/-10, 80+/-10, 90+/-10, 100+/-10, 110+/-10, 120+/-10, 130+/-10, 140+/-10, 150+/-10, 160+/-10, 170+/-10, 180+/-10, 190+/-10, 200+/-10, 210+/-10, or 220+/-10 nucleotides in length. In an embodiment, the template nucleic acid may be 30+/-20, 40+/-20, 50+/-20, 60+/-20, 70+/-20, 80+/-20, 90+/-20, 100+/-20, 110+/-20, 120+/-20, 130+/-20, 140+/-20, 150+/-20, 160+/-20, 170+/-20, 180+/-20, 190+/-20, 200+/-20, 210+/-20, or 220+/-20 nucleotides in length. In an embodiment, the template nucleic acid is 10 to 1,000, 20 to 900, 30 to 800, 40 to 700, 50 to 600, 50 to 500, 50 to 400, 50 to 300, 50 to 200, or 50 to 100 nucleotides in length.

In some embodiments, the template polynucleotide is complementary to a portion of a polynucleotide comprising the target sequence. When optimally aligned, a template polynucleotide might overlap with one or more nucleotides of a target sequences (e.g. about or more than about 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100 or more nucleotides). In some embodiments, when a template sequence and a polynucleotide comprising a target sequence are optimally aligned, the nearest nucleotide of the template polynucleotide is within about 1, 5, 10, 15, 20, 25, 50, 75, 100, 200, 300, 400, 500, 1000, 5000, 10000, or more nucleotides from the target sequence.

The exogenous polynucleotide template comprises a sequence to be integrated (e.g., a mutated gene). The sequence for integration may be a sequence endogenous or exogenous to the cell. Examples of a sequence to be integrated include polynucleotides encoding a protein or a non-coding RNA (e.g., a microRNA). Thus, the sequence for integration may be operably linked to an appropriate control sequence or sequences. Alternatively, the sequence to be integrated may provide a regulatory function.

An upstream or downstream sequence may comprise from about 20 bp to about 2500 bp, for example, about 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, or 2500 bp. In some methods, the exemplary upstream or downstream sequence have about 200 bp to about 2000 bp, about 600 bp to about 1000 bp, or more particularly about 700 bp to about 1000.

An upstream or downstream sequence may comprise from about 20 bp to about 2500 bp, for example, about 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, or 2500 bp. In some methods, the exemplary upstream or downstream sequence have about

200 bp to about 2000 bp, about 600 bp to about 1000 bp, or more particularly about 700 bp to about 1000.

In certain embodiments, one or both homology arms may be shortened to avoid including certain sequence repeat elements. For example, a 5' homology arm may be shortened to avoid a sequence repeat element. In other embodiments, a 3' homology arm may be shortened to avoid a sequence repeat element. In some embodiments, both the 5' and the 3' homology arms may be shortened to avoid including certain sequence repeat elements.

In some methods, the exogenous polynucleotide template may further comprise a marker. Such a marker may make it easy to screen for targeted integrations. Examples of suitable markers include restriction sites, fluorescent proteins, or selectable markers. The exogenous polynucleotide template of the disclosure can be constructed using recombinant techniques (see, for example, Sambrook et al., 2001 and Ausubel et al., 1996).

In certain embodiments, a template nucleic acid for correcting a mutation may be designed for use as a single-stranded oligonucleotide. When using a single-stranded oligonucleotide, 5' and 3' homology arms may range up to about 200 base pairs (bp) in length, e.g., at least 25, 50, 75, 100, 125, 150, 175, or 200 bp in length.

Suzuki et al. describe in vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration (2016, Nature 540:144-149), which is incorporated by reference herein and can be adapted for use with the present invention.

TALE Nucleases

In some embodiments, a TALE nuclease or TALE nuclease system can be used to modify a polynucleotide. In some embodiments, the methods provided herein use isolated, non-naturally occurring, recombinant or engineered DNA binding proteins that comprise TALE monomers or TALE monomers or half monomers as a part of their organizational structure that enable the targeting of nucleic acid sequences with improved efficiency and expanded specificity.

Naturally occurring TALEs or "wild type TALEs" are nucleic acid binding proteins secreted by numerous species of proteobacteria. TALE polypeptides contain a nucleic acid binding domain composed of tandem repeats of highly conserved monomer polypeptides that are predominantly 33, 34 or 35 amino acids in length and that differ from each other mainly in amino acid positions 12 and 13. In advantageous embodiments the nucleic acid is DNA. As used herein, the term "polypeptide monomers", "TALE monomers" or "monomers" will be used to refer to the highly conserved repetitive polypeptide sequences within the TALE nucleic acid binding domain and the term "repeat variable di-residues" or "RVD" will be used to refer to the highly variable amino acids at positions 12 and 13 of the polypeptide monomers. As provided throughout the disclosure, the amino acid residues of the RVD are depicted using the IUPAC single letter code for amino acids. A general representation of a TALE monomer which is comprised within the DNA binding domain is $X_{1-11}-(X_{12}X_{13})-X_{14-33}$ or $_{34}$ or $_{35}$, where the subscript indicates the amino acid position and X represents any amino acid. $X_{12}X_{13}$ indicate the RVDs. In some polypeptide monomers, the variable amino acid at position 13 is missing or absent and in such monomers, the RVD consists of a single amino acid. In such cases the RVD may be alternatively represented as X^* , where X represents X_{12} and (*) indicates that X_{13} is absent. The DNA binding domain comprises several repeats of TALE monomers and this may be represented as $(X_{1-11}-(X_{12}X_{13})-X_{14-33})_{34}$

or $35)_z$, where in an advantageous embodiment, z is at least 5 to 40. In a further advantageous embodiment, z is at least 10 to 26.

The TALE monomers can have a nucleotide binding affinity that is determined by the identity of the amino acids in its RVD. For example, polypeptide monomers with an RVD of NI can preferentially bind to adenine (A), monomers with an RVD of NG can preferentially bind to thymine (T), monomers with an RVD of HD can preferentially bind to cytosine (C) and monomers with an RVD of NN can preferentially bind to both adenine (A) and guanine (G). In some embodiments, monomers with an RVD of IG can preferentially bind to T. Thus, the number and order of the polypeptide monomer repeats in the nucleic acid binding domain of a TALE determines its nucleic acid target specificity. In some embodiments, monomers with an RVD of NS can recognize all four base pairs and can bind to A, T, G or C. The structure and function of TALEs is further described in, for example, Moscou et al., *Science* 326:1501 (2009); Boch et al., *Science* 326:1509-1512 (2009); and Zhang et al., *Nature Biotechnology* 29:149-153 (2011).

The polypeptides used in methods of the invention can be isolated, non-naturally occurring, recombinant or engineered nucleic acid-binding proteins that have nucleic acid or DNA binding regions containing polypeptide monomer repeats that are designed to target specific nucleic acid sequences.

As described herein, polypeptide monomers having an RVD of HN or NH preferentially bind to guanine and thereby allow the generation of TALE polypeptides with high binding specificity for guanine containing target nucleic acid sequences. In some embodiments, polypeptide monomers having RVDs RN, NN, NK, SN, NH, KN, HN, NQ, HH, RG, KH, RH and SS can preferentially bind to guanine. In some embodiments, polypeptide monomers having RVDs RN, NK, NQ, HH, KH, RH, SS and SN can preferentially bind to guanine and can thus allow the generation of TALE polypeptides with high binding specificity for guanine containing target nucleic acid sequences. In some embodiments, polypeptide monomers having RVDs HH, KH, NH, NK, NQ, RH, RN and SS can preferentially bind to guanine and thereby allow the generation of TALE polypeptides with high binding specificity for guanine containing target nucleic acid sequences. In some embodiments, the RVDs that have high binding specificity for guanine are RN, NH RH and KH. Furthermore, polypeptide monomers having an RVD of NV can preferentially bind to adenine and guanine. In some embodiments, monomers having RVDs of H*, HA, KA, N*, NA, NC, NS, RA, and S* bind to adenine, guanine, cytosine and thymine with comparable affinity.

The predetermined N-terminal to C-terminal order of the one or more polypeptide monomers of the nucleic acid or DNA binding domain determines the corresponding predetermined target nucleic acid sequence to which the polypeptides of the invention will bind. As used herein the monomers and at least one or more half monomers are "specifically ordered to target" the genomic locus or gene of interest. In plant genomes, the natural TALE-binding sites always begin with a thymine (T), which may be specified by a cryptic signal within the non-repetitive N-terminus of the TALE polypeptide; in some cases, this region may be referred to as repeat 0. In animal genomes, TALE binding sites do not necessarily have to begin with a thymine (T) and polypeptides of the invention may target DNA sequences that begin with T, A, G or C. The tandem repeat of TALE monomers always ends with a half-length repeat or a stretch of sequence that may share identity with only the first 20

amino acids of a repetitive full-length TALE monomer and this half repeat may be referred to as a half-monomer. Therefore, it follows that the length of the nucleic acid or DNA being targeted is equal to the number of full monomers plus two.

As described in Zhang et al., *Nature Biotechnology* 29:149-153 (2011), TALE polypeptide binding efficiency may be increased by including amino acid sequences from the "capping regions" that are directly N-terminal or C-terminal of the DNA binding region of naturally occurring TALEs into the engineered TALEs at positions N-terminal or C-terminal of the engineered TALE DNA binding region. Thus, in certain embodiments, the TALE polypeptides described herein further comprise an N-terminal capping region and/or a C-terminal capping region.

An exemplary amino acid sequence of a N-terminal capping region is:

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(SEQ ID NO: 9098)
5  M D P I R S R T P S P A R E L L S G P Q P D G V Q
10 P T A D R G V S P P A G G P L D G L P A R R T M S
15 R T R L P S P P A P S P A F S A D S F S D L L R Q
20 F D P S L F N T S L F D S L P P F G A H H T E A A
25 T G E W D E V Q S G L R A A D A P P P T M R V A V
30 T A A R P P R A K P A P R R R A A Q P S D A S P A
35 A Q V D L R T L G Y S Q Q Q O E K I K P K V R S T
40 V A Q H H E A L V G H G F T H A H I V A L S Q H P
45 A A L G T V A V K Y Q D M I A A L P E A T H E A I
50 V G V G K Q W S G A R A L E A L L T V A G E L R G
55 P P L Q L D T G Q L L K I A K R G G V T A V E A V
60 H A W R N A L T G A P L N
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An exemplary amino acid sequence of a C-terminal capping region is:

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(SEQ ID NO: 9099)
45 R P A L E S I V A Q L S R P D P A L A A L T N D H
50 L V A L A C L G G R P A L D A V K K G L P H A P A
55 L I K R T N R R I P E R T S H R V A D H A Q V V R
60 V L G F F Q C H S H P A Q A F D D A M T Q F G M S
65 R H G L L Q L F R R V G V T E L E A R S G T L P P
70 A S Q R W D R I L Q A S G M K R A K P S P T S T Q
75 T P D Q A S L H A F A D S L E R D L D A P S P M H
80 E G D Q T R A S
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As used herein the predetermined "N-terminus" to "C terminus" orientation of the N-terminal capping region, the DNA binding domain comprising the repeat TALE monomers and the C-terminal capping region provide structural basis for the organization of different domains in the d-TALEs or polypeptides of the invention.

The entire N-terminal and/or C-terminal capping regions are not necessary to enhance the binding activity of the DNA binding region. Therefore, in certain embodiments, fragments of the N-terminal and/or C-terminal capping regions are included in the TALE polypeptides described herein.

In certain embodiments, the TALE polypeptides described herein contain a N-terminal capping region fragment that included at least 10, 20, 30, 40, 50, 54, 60, 70, 80, 87, 90, 94, 100, 102, 110, 117, 120, 130, 140, 147, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260 or 270 amino acids of an N-terminal capping region. In certain embodiments, the N-terminal capping region fragment amino acids are of the C-terminus (the DNA-binding region proximal end) of an N-terminal capping region. As described in Zhang et al., *Nature Biotechnology* 29:149-153 (2011), N-terminal capping region fragments that include the C-terminal 240 amino acids enhance binding activity equal to the full length capping region, while fragments that include the C-terminal 147 amino acids retain greater than 80% of the efficacy of the full length capping region, and fragments that include the C-terminal 117 amino acids retain greater than 50% of the activity of the full-length capping region.

In some embodiments, the TALE polypeptides described herein contain a C-terminal capping region fragment that included at least 6, 10, 20, 30, 37, 40, 50, 60, 68, 70, 80, 90, 100, 110, 120, 127, 130, 140, 150, 155, 160, 170, 180 amino acids of a C-terminal capping region. In certain embodiments, the C-terminal capping region fragment amino acids are of the N-terminus (the DNA-binding region proximal end) of a C-terminal capping region. As described in Zhang et al., *Nature Biotechnology* 29:149-153(2011), C-terminal capping region fragments that include the C-terminal 68 amino acids enhance binding activity equal to the full-length capping region, while fragments that include the C-terminal 20 amino acids retain greater than 50% of the efficacy of the full-length capping region.

In certain embodiments, the capping regions of the TALE polypeptides described herein do not need to have identical sequences to the capping region sequences provided herein. Thus, in some embodiments, the capping region of the TALE polypeptides described herein have sequences that are at least 50%, 60%, 70%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical or share identity to the capping region amino acid sequences provided herein. Sequence identity is related to sequence homology. Homology comparisons may be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These commercially available computer programs may calculate percent (%) homology between two or more sequences and may also calculate the sequence identity shared by two or more amino acid or nucleic acid sequences. In some preferred embodiments, the capping region of the TALE polypeptides described herein have sequences that are at least 95% identical or share identity to the capping region amino acid sequences provided herein.

Sequence homologies can be generated by any of a number of computer programs known in the art, which include but are not limited to BLAST or FASTA. Suitable computer programs for carrying out alignments like the GCG Wisconsin Bestfit package may also be used. Once the software has produced an optimal alignment, it is possible to calculate % homology, preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

In some embodiments described herein, the TALE polypeptides of the invention include a nucleic acid binding domain linked to the one or more effector domains. The terms "effector domain" or "regulatory and functional domain" refer to a polypeptide sequence that has an activity other than binding to the nucleic acid sequence recognized

by the nucleic acid binding domain. By combining a nucleic acid binding domain with one or more effector domains, the polypeptides of the invention may be used to target the one or more functions or activities mediated by the effector domain to a particular target DNA sequence to which the nucleic acid binding domain specifically binds.

In some embodiments of the TALE polypeptides described herein, the activity mediated by the effector domain is a biological activity. For example, in some embodiments the effector domain is a transcriptional inhibitor (i.e., a repressor domain), such as an mSin interaction domain (SID). SID4X domain or a Krüppel-associated box (KRAB) or fragments of the KRAB domain. In some embodiments, the effector domain is an enhancer of transcription (i.e., an activation domain), such as the VP16, VP64 or p65 activation domain. In some embodiments, the nucleic acid binding is linked, for example, with an effector domain that includes but is not limited to a transposase, integrase, recombinase, resolvase, invertase, protease, DNA methyltransferase, DNA demethylase, histone acetylase, histone deacetylase, nuclease, transcriptional repressor, transcriptional activator, transcription factor recruiting, protein nuclear-localization signal or cellular uptake signal.

In some embodiments, the effector domain is a protein domain which exhibits activities which include but are not limited to transposase activity, integrase activity, recombinase activity, resolvase activity, invertase activity, protease activity, DNA methyltransferase activity, DNA demethylase activity, histone acetylase activity, histone deacetylase activity, nuclease activity, nuclear-localization signaling activity, transcriptional repressor activity, transcriptional activator activity, transcription factor recruiting activity, or cellular uptake signaling activity. Other preferred embodiments of the invention may include any combination of the activities described herein.

Meganucleases

In some embodiments, a meganuclease or system thereof can be used to modify a polynucleotide. Meganucleases, which are endodeoxyribonucleases characterized by a large recognition site (double-stranded DNA sequences of 12 to 40 base pairs). Exemplary methods for using meganucleases can be found in U.S. Pat. Nos. 8,163,514, 8,133,697, 8,021, 867, 8,119,361, 8,119,381, 8,124,369, and 8,129,134, which are specifically incorporated herein by reference.

RNAi

In certain embodiments, the genetic modifying agent is RNAi (e.g., shRNA). As used herein, "gene silencing" or "gene silenced" in reference to an activity of an RNAi molecule, for example a siRNA or miRNA refers to a decrease in the mRNA level in a cell for a target gene by at least about 5%, about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, about 99%, about 100% of the mRNA level found in the cell without the presence of the miRNA or RNA interference molecule. In one preferred embodiment, the mRNA levels are decreased by at least about 70%, about 80%, about 90%, about 95%, about 99%, about 100%.

As used herein, the term "RNAi" refers to any type of interfering RNA, including but not limited to, siRNAi, shRNAi, endogenous microRNA and artificial microRNA. For instance, it includes sequences previously identified as siRNA, regardless of the mechanism of down-stream processing of the RNA (i.e. although siRNAs are believed to have a specific method of in vivo processing resulting in the cleavage of mRNA, such sequences can be incorporated into the vectors in the context of the flanking sequences described herein). The term "RNAi" can include both gene

silencing RNAi molecules, and also RNAi effector molecules which activate the expression of a gene.

As used herein, a "siRNA" refers to a nucleic acid that forms a double stranded RNA, which double stranded RNA has the ability to reduce or inhibit expression of a gene or target gene when the siRNA is present or expressed in the same cell as the target gene. The double stranded RNA siRNA can be formed by the complementary strands. In one embodiment, a siRNA refers to a nucleic acid that can form a double stranded siRNA. The sequence of the siRNA can correspond to the full-length target gene, or a subsequence thereof. Typically, the siRNA is at least about 15-50 nucleotides in length (e.g., each complementary sequence of the double stranded siRNA is about 15-50 nucleotides in length, and the double stranded siRNA is about 15-50 base pairs in length, preferably about 19-30 base nucleotides, preferably about 20-25 nucleotides in length, e.g., 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length).

As used herein "shRNA" or "small hairpin RNA" (also called stem loop) is a type of siRNA. In one embodiment, these shRNAs are composed of a short, e.g. about 19 to about 25 nucleotide, antisense strand, followed by a nucleotide loop of about 5 to about 9 nucleotides, and the analogous sense strand. Alternatively, the sense strand can precede the nucleotide loop structure and the antisense strand can follow.

The terms "microRNA" or "miRNA" are used interchangeably herein are endogenous RNAs, some of which are known to regulate the expression of protein-coding genes at the posttranscriptional level. Endogenous microRNAs are small RNAs naturally present in the genome that are capable of modulating the productive utilization of mRNA. The term artificial microRNA includes any type of RNA sequence, other than endogenous microRNA, which is capable of modulating the productive utilization of mRNA. MicroRNA sequences have been described in publications such as Lim, et al., *Genes & Development*, 17, p. 991-1008 (2003), Lim et al *Science* 299, 1540 (2003), Lee and Ambros *Science*, 294, 862 (2001), Lau et al., *Science* 294, 858-861 (2001), Lagos-Quintana et al, *Current Biology*, 12, 735-739 (2002), Lagos Quintana et al, *Science* 294, 853-857 (2001), and Lagos-Quintana et al, *RNA*, 9, 175-179 (2003), which are incorporated herein by reference. Multiple microRNAs can also be incorporated into a precursor molecule. Furthermore, miRNA-like stem-loops can be expressed in cells as a vehicle to deliver artificial miRNAs and short interfering RNAs (siRNAs) for the purpose of modulating the expression of endogenous genes through the miRNA and/or RNAi pathways.

As used herein, "double stranded RNA" or "dsRNA" refers to RNA molecules that are comprised of two strands. Double-stranded molecules include those comprised of a single RNA molecule that doubles back on itself to form a two-stranded structure. For example, the stem loop structure of the progenitor molecules from which the single-stranded miRNA is derived, called the pre-miRNA (Bartel et al. 2004. *Cell* 116:281-297), comprises a dsRNA molecule.

Engineered Cells and Organisms

Described herein are engineered cells that can include one or more of the engineered muscle-specific targeting moiety polynucleotides, polypeptides, vectors, and/or vector systems. In some embodiments, one or more of the engineered muscle-specific targeting moiety polynucleotides can be expressed in the engineered cells. In some embodiments, the engineered cells can be capable of producing engineered muscle-specific viral capsid proteins and/or engineered muscle-specific viral particles that are described elsewhere

herein. Also described herein are modified or engineered organisms that can include one or more engineered cells described herein. The engineered cells can be engineered to express a cargo molecule (e.g. a cargo polynucleotide) dependently or independently of an engineered muscle-specific viral capsid polynucleotide as described elsewhere herein.

A wide variety of animals, plants, algae, fungi, yeast, etc. and animal, plant, algae, fungus, yeast cell or tissue systems may be engineered to express one or more nucleic acid constructs of the engineered muscle-specific delivery system described herein using various transformation methods mentioned elsewhere herein. This can produce organisms that can produce engineered muscle-specific targeting moiety or composition thereof, such as for production purposes, engineered muscle-specific viral capsid design and/or generation, and/or model organisms. In some embodiments, the polynucleotide(s) encoding one or more components of the engineered viral capsid system described herein can be stably or transiently incorporated into one or more cells of a plant, animal, algae, fungus, and/or yeast or tissue system. In some embodiments, one or more of engineered viral capsid system polynucleotides are genomically incorporated into one or more cells of a plant, animal, algae, fungus, and/or yeast or tissue system. Further embodiments of the modified organisms and systems are described elsewhere herein. In some embodiments, one or more components of the engineered viral capsid system described herein are expressed in one or more cells of the plant, animal, algae, fungus, yeast, or tissue systems.

Engineered Cells

Described herein are various embodiments of engineered cells that can include one or more of the engineered muscle-specific targeting moiety, composition thereof, and/or delivery system thereof polynucleotides, polypeptides, vectors, and/or vector systems described elsewhere herein. In some embodiments, the cells can express one or more of the engineered muscle-specific targeting moiety polynucleotides and can produce one or more engineered muscle-specific viral particles, which are described in greater detail herein. Such cells are also referred to herein as "producer cells". It will be appreciated that these engineered cells are different from "modified cells" described elsewhere herein in that the modified cells are not necessarily producer cells (i.e. they do not make engineered muscle-specific delivery particles (i.e. particles that can deliver a cargo to a cell in a muscle-specific manner guided by a muscle-specific targeting moiety described herein) unless they include one or more of the engineered viral capsid polynucleotides, engineered viral capsid vectors or other vectors described herein that render the cells capable of producing an engineered virus particle or are modified to produce compositions (such as proteins) that include one or more engineered muscle-specific targeting moieties.

Modified cells can be recipient cells of a cargo delivered by a delivery vehicle (e.g. viral, vector, or non-vector delivery vehicle) that includes one or more engineered muscle-specific targeting moieties, and can, in some embodiments, be modified by the delivery vehicle and/or a cargo polynucleotide delivered to the recipient cell. Modified cells are discussed in greater detail elsewhere herein. The term modification can be used in connection with modification of a cell that is not dependent on being a recipient cell. For example, isolated cells can be modified prior to receiving an engineered delivery vehicle described herein.

In an embodiment, the invention provides a non-human eukaryotic organism; for example, a multicellular eukaryotic organism, including a eukaryotic host cell containing one or more components of an engineered muscle-specific delivery system described herein according to any of the described embodiments. In other embodiments, the invention provides a eukaryotic organism; preferably a multicellular eukaryotic organism, comprising a eukaryotic host cell containing one or more components of an engineered delivery system described herein according to any of the described embodiments. In some embodiments, the organism is a host of AAV.

In particular embodiments, the plants, algae, fungi, yeast, etc., cells or parts obtained are transgenic plants, comprising an exogenous DNA sequence incorporated into the genome of all or part of the cells.

The engineered cell can be a prokaryotic cell. The prokaryotic cell can be bacterial cell. The prokaryotic cell can be an archaea cell. The bacterial cell can be any suitable bacterial cell. Suitable bacterial cells can be from the genus *Escherichia*, *Bacillus*, *Lactobacillus*, *Rhodococcus*, *Rhodobacter*, *Synechococcus*, *Synechocystis*, *Pseudomonas*, *Pseudoalteromonas*, *Stenotrophomonas*, and *Streptomyces*. Suitable bacterial cells include, but are not limited to *Escherichia coli* cells, *Caulobacter crescentus* cells, *Rhodobacter sphaeroides* cells, *Pseudoalteromonas haloplanktis* cells. Suitable strains of bacterial include, but are not limited to BL21(DE3), DL21(DE3)-pLysS, BL21 Star-pLysS, BL21-SI, BL21-AI, Tuner, Tuner pLysS, Origami, Origami B pLysS, Rosetta, Rosetta pLysS, Rosetta-gami-pLysS, BL21 CodonPlus, AD494, BL21trxB, HMS174, NovaBlue (DE3), BLR, C41(DE3), C43(DE3), Lemo21(DE3), Shuffle T7, ArcticExpress and Arctic Express (DE3).

The engineered cell can be a eukaryotic cell. The eukaryotic cells may be those of or derived from a particular organism, such as a plant or a mammal, including but not limited to human, or non-human eukaryote or animal or mammal as herein discussed, e.g., mouse, rat, rabbit, dog, livestock, or non-human mammal or primate. In some embodiments the engineered cell can be a cell line. Examples of cell lines include, but are not limited to, C8161, CCRF-CEM, MOLT, mIMCD-3, NHDF, HeLa-S3, Huh1, Huh4, Huh7, HUVEC, HASMC, HEK293, HEK293T, MiaPaCell, Panc1, PC-3, TF1, CTLL-2, CIR, Rat6, CV1, RPTE, A10, T24, J82, A375, ARH-77, Calu1, SW480, SW620, SKOV3, SK-UT, CaCo2, P388D1, SEM-K2, WEHI-231, HB56, TIB55, Jurkat, J45.01, LRMB, Bcl-1, BC-3, IC21, DLD2, Raw264.7, NRK, NRK-52E, MRC5, MEF, Hep G2, HeLa B, HeLa T4, COS, COS-1, COS-6, COS-M6A, BS-C-1 monkey kidney epithelial, BALB/3T3 mouse embryo fibroblast, 3T3 Swiss, 3T3-L1, 132-d5 human fetal fibroblasts; 10.1 mouse fibroblasts, 293-T, 3T3, 721, 9L, A2780, A2780ADR, A2780cis, A172, A20, A253, A431, A-549, ALC, B16, B35, BCP-1 cells, BEAS-2B, bEnd.3, BHK-21, BR 293, BxPC3, C3H-10T1/2, C6/36, Cal-27, CHO, CHO-7, CHO-IR, CHO-K1, CHO-K2, CHO-T, CHO Dhfr -/-, COR-L23, COR-L23/CPR, COR-L23/5010, COR-L23/R23, COS-7, COV-434, CML T1, CMT, CT26, D17, DH82, DU145, DuCaP, EL4, EM2, EM3, EMT6/AR1, EMT6/AR10.0, FM3, H1299, H69, HB54, HB55, HCA2, HEK-293, HeLa, Hepalcl7, HL-60, HMEC, HT-29, Jurkat, JY cells, K562 cells, Ku812, KCL22, KG1, KYO1, LNCap, Ma-Mel 1-48, MC-38, MCF-7, MCF-10A, MDA-MB-231, MDA-MB-468, MDA-MB-435, MDCK II, MDCK II, MOR/0.2R, MONO-MAC 6, MTD-1A, MyEnd, NCI-H69/CPR, NCI-H69/LX10, NCI-H69/LX20, NCI-H69/LX4, NIH-3T3, NALM-1, NW-145, OPCN/OPCT cell lines, Peer, PNT-1A/PNT 2, RenCa, RIN-5F, RMA/RMAS, Saos-2

cells, Sf-9, SkBr3, T2, T-47D, T84, THP1 cell line, U373, U87, U937, VCaP, Vero cells, WM39, WT-49, X₆₃, YAC-1, YAR, and transgenic varieties thereof. Cell lines are available from a variety of sources known to those with skill in the art (see, e.g., the American Type Culture Collection (ATCC) (Manassas, Va.)).

In some embodiments, the engineered or modified cell is a muscle cell (e.g. cardiac muscle, skeletal muscle, and/or smooth muscle), bone cell, blood cell, immune cell (including but not limited to B cells, macrophages, T-cells, CAR-T cells, and the like), kidney cells, bladder cells, lung cells, heart cells, liver cells, brain cells, neurons, skin cells, stomach cells, neuronal support cells, intestinal cells, epithelial cells, endothelial cells, stem or other progenitor cells, adrenal gland cells, cartilage cells, and combinations thereof.

In some embodiments, the engineered cell can be a fungus cell. As used herein, a "fungal cell" refers to any type of eukaryotic cell within the kingdom of fungi. Phyla within the kingdom of fungi include Ascomycota, Basidiomycota, Blastocladiomycota, Chytridiomycota, Glomeromycota, Microsporidia, and Neocallimastigomycota. Fungal cells may include yeasts, molds, and filamentous fungi. In some embodiments, the fungal cell is a yeast cell.

As used herein, the term "yeast cell" refers to any fungal cell within the phyla Ascomycota and Basidiomycota. Yeast cells may include budding yeast cells, fission yeast cells, and mold cells. Without being limited to these organisms, many types of yeast used in laboratory and industrial settings are part of the phylum Ascomycota. In some embodiments, the yeast cell is an *S. cerevisiae*, *Kluyveromyces marxianus*, or *Issatchenkia orientalis* cell. Other yeast cells may include without limitation *Candida* spp. (e.g., *Candida albicans*), *Yarrowia* spp. (e.g., *Yarrowia lipolytica*), *Pichia* spp. (e.g., *Pichia pastoris*), *Kluyveromyces* spp. (e.g., *Kluyveromyces lactis* and *Kluyveromyces marxianus*), *Neurospora* spp. (e.g., *Neurospora crassa*), *Fusarium* spp. (e.g., *Fusarium oxysporum*), and *Issatchenkia* spp. (e.g., *Issatchenkia orientalis*, a.k.a. *Pichia kudriavzevii* and *Candida acidothermophilum*). In some embodiments, the fungal cell is a filamentous fungal cell. As used herein, the term "filamentous fungal cell" refers to any type of fungal cell that grows in filaments, i.e., hyphae or mycelia. Examples of filamentous fungal cells may include without limitation *Aspergillus* spp. (e.g., *Aspergillus niger*), *Trichoderma* spp. (e.g., *Trichoderma reesei*), *Rhizopus* spp. (e.g., *Rhizopus oryzae*), and *Mortierella* spp. (e.g., *Mortierella isabellina*).

In some embodiments, the fungal cell is an industrial strain. As used herein, "industrial strain" refers to any strain of fungal cell used in or isolated from an industrial process, e.g., production of a product on a commercial or industrial scale. Industrial strain may refer to a fungal species that is typically used in an industrial process, or it may refer to an isolate of a fungal species that may be also used for non-industrial purposes (e.g., laboratory research). Examples of industrial processes may include fermentation (e.g., in production of food or beverage products), distillation, biofuel production, production of a compound, and production of a polypeptide. Examples of industrial strains can include, without limitation, JAY270 and ATCC4124.

In some embodiments, the fungal cell is a polyploid cell. As used herein, a "polyploid" cell may refer to any cell whose genome is present in more than one copy. A polyploid cell may refer to a type of cell that is naturally found in a polyploid state, or it may refer to a cell that has been induced to exist in a polyploid state (e.g., through specific regulation, alteration, inactivation, activation, or modification of meio-

sis, cytokinesis, or DNA replication). A polyploid cell may refer to a cell whose entire genome is polyploid, or it may refer to a cell that is polyploid in a particular genomic locus of interest.

In some embodiments, the fungal cell is a diploid cell. As used herein, a “diploid” cell may refer to any cell whose genome is present in two copies. A diploid cell may refer to a type of cell that is naturally found in a diploid state, or it may refer to a cell that has been induced to exist in a diploid state (e.g., through specific regulation, alteration, inactivation, activation, or modification of meiosis, cytokinesis, or DNA replication). For example, the *S. cerevisiae* strain S228C may be maintained in a haploid or diploid state. A diploid cell may refer to a cell whose entire genome is diploid, or it may refer to a cell that is diploid in a particular genomic locus of interest. In some embodiments, the fungal cell is a haploid cell. As used herein, a “haploid” cell may refer to any cell whose genome is present in one copy. A haploid cell may refer to a type of cell that is naturally found in a haploid state, or it may refer to a cell that has been induced to exist in a haploid state (e.g., through specific regulation, alteration, inactivation, activation, or modification of meiosis, cytokinesis, or DNA replication). For example, the *S. cerevisiae* strain S228C may be maintained in a haploid or diploid state. A haploid cell may refer to a cell whose entire genome is haploid, or it may refer to a cell that is haploid in a particular genomic locus of interest.

In some embodiments, the engineered cell is a cell obtained from a subject. In some embodiments, the subject is a healthy or non-diseased subject. In some embodiments, the subject is a subject with a desired physiological and/or biological characteristic such that when an engineered AAV capsid particle is produced it can package one or more cargo polynucleotides that can be related to the desired physiological and/or biological characteristic and/or capable of modifying the desired physiological and/or biological characteristic. Thus, the cargo polynucleotides of the produced engineered AAV capsid particle can be capable of transferring the desired characteristic to a recipient cell. In some embodiments, the cargo polynucleotides are capable of modifying a polynucleotide of the engineered cell such that the engineered cell has a desired physiological and/or biological characteristic.

In some embodiments, a cell transfected with one or more vectors described herein is used to establish a new cell line comprising one or more vector-derived sequences.

The engineered cells can be used to produce engineered AAV capsid polynucleotides, vectors, and/or particles. In some embodiments, the engineered AAV capsid polynucleotides, vectors, and/or particles are produced, harvested, and/or delivered to a subject in need thereof. In some embodiments, the engineered cells are delivered to a subject. Other uses for the engineered cells are described elsewhere herein. In some embodiments, the engineered cells can be included in formulations and/or kits described elsewhere herein.

The engineered cells can be stored short-term or long-term for use at a later time. Suitable storage methods are generally known in the art. Further, methods of restoring the stored cells for use (such as thawing, reconstitution, and otherwise stimulating metabolism in the engineered cell after storage) at a later time are also generally known in the art.

Formulations

The compositions, polynucleotides, polypeptides, particles, cells, vector systems and combinations thereof described herein can be contained in a formulation, such as

a pharmaceutical formulation. In some embodiments, the formulations can be used to generate polypeptides and other particles that include one or more muscle-specific targeting moieties described herein. In some embodiments, the formulations can be delivered to a subject in need thereof. In some embodiments, the engineered muscle-specific targeting moieties, compositions thereof, delivery systems thereof, engineered cells, engineered viral particles, and/or combinations thereof described herein can be included in a formulation that can be delivered to a subject or a cell. In some embodiments, the formulation is a pharmaceutical formulation. One or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be provided to a subject in need thereof or a cell alone or as an active ingredient, such as in a pharmaceutical formulation. As such, also described herein are pharmaceutical formulations containing an amount of one or more of the polypeptides, polynucleotides, vectors, cells, or combinations thereof described herein. In some embodiments, the pharmaceutical formulation can contain an effective amount of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein. The pharmaceutical formulations described herein can be administered to a subject in need thereof or a cell.

In some embodiments, the amount of the one or more of the polypeptides, polynucleotides, vectors, cells, virus particles, nanoparticles, other delivery particles, and combinations thereof described herein contained in the pharmaceutical formulation can range from about 1 pg/kg to about 10 mg/kg based upon the bodyweight of the subject in need thereof or average bodyweight of the specific patient population to which the pharmaceutical formulation can be administered. The amount of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein in the pharmaceutical formulation can range from about 1 µg to about 10 g or from about 10 nL to about 10 mL. In embodiments where the pharmaceutical formulation contains one or more cells, the amount can range from about 1 cell to 1×10^2 , 1×10^3 , 1×10^4 , 1×10^5 , 1×10^6 , 1×10^7 , 1×10^8 , 1×10^9 , 1×10^{10} or more cells. In embodiments where the pharmaceutical formulation contains one or more cells, the amount can range from about 1 cell to 1×10^2 , 1×10^3 , 1×10^4 , 1×10^5 , 1×10^6 , 1×10^7 , 1×10^8 , 1×10^9 , 1×10^{10} or more cells per nL, µL, mL, or L.

In embodiments, where engineered AAV capsid particles are included in the formulation, the formulation can contain 1 to 1×10^1 , 1×10^2 , 1×10^3 , 1×10^4 , 1×10^5 , 1×10^6 , 1×10^7 , 1×10^8 , 1×10^9 , 1×10^{10} , 1×10^{11} , 1×10^{12} , 1×10^{13} , 1×10^{14} , 1×10^{15} , 1×10^{16} , 1×10^{17} , 1×10^{18} , 1×10^{19} , or 1×10^{20} transducing units (TU)/mL of the engineered AAV capsid particles. In some embodiments, the formulation can be 0.1 to 100 mL in volume and can contain 1 to 1×10^1 , 1×10^2 , 1×10^3 , 1×10^4 , 1×10^5 , 1×10^6 , 1×10^7 , 1×10^8 , 1×10^9 , 1×10^{10} , 1×10^{11} , 1×10^{12} , 1×10^{13} , 1×10^{14} , 1×10^{15} , 1×10^{16} , 1×10^{17} , 1×10^{18} , 1×10^{19} , or 1×10^{20} transducing units (TU)/mL of the engineered viral particles.

Pharmaceutically Acceptable Carriers and Auxiliary Ingredients and Agents

In embodiments, the pharmaceutical formulation containing an amount of one or more of the polypeptides, polynucleotides, vectors, cells, virus particles, nanoparticles, other delivery particles, and combinations thereof described herein can further include a pharmaceutically acceptable carrier. Suitable pharmaceutically acceptable carriers include, but are not limited to, water, salt solutions, alcohols, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or

starch, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxy methylcellulose, and polyvinyl pyrrolidone, which do not deleteriously react with the active composition.

The pharmaceutical formulations can be sterilized, and if desired, mixed with auxiliary agents, such as lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances, and the like which do not deleteriously react with the active composition.

In addition to an amount of one or more of the polypeptides, polynucleotides, vectors, cells, viral particles, nanoparticles, other delivery particles, and combinations thereof described herein, the pharmaceutical formulation can also include an effective amount of an auxiliary active agent, including but not limited to, polynucleotides, amino acids, peptides, polypeptides, antibodies, aptamers, ribozymes, hormones, immunomodulators, antipyretics, anxiolytics, antipsychotics, analgesics, antispasmodics, anti-inflammatories, anti-histamines, anti-infectives, chemotherapeutics, and combinations thereof.

Suitable hormones include, but are not limited to, amino acid derived hormones (e.g. melatonin and thyroxine), small peptide hormones and protein hormones (e.g. thyrotropin-releasing hormone, vasopressin, insulin, growth hormone, luteinizing hormone, follicle-stimulating hormone, and thyroid-stimulating hormone), eicosanoids (e.g. arachidonic acid, lipoxins, and prostaglandins), and steroid hormones (e.g. estradiol, testosterone, tetrahydro testosterone Cortisol). Suitable immunomodulators include, but are not limited to, prednisone, azathioprine, 6-MP, cyclosporine, tacrolimus, methotrexate, interleukins (e.g. IL-2, IL-7, and IL-12), cytokines (e.g. interferons (e.g. IFN- α , IFN- β , IFN- γ , IFN-K, IFN- ω , and IFN- γ), granulocyte colony-stimulating factor, and imiquimod), chemokines (e.g. CCL3, CCL26 and CXCL7), cytosine phosphate-guanosine, oligodeoxynucleotides, glucans, antibodies, and aptamers).

Suitable antipyretics include, but are not limited to, non-steroidal anti-inflammants (e.g. ibuprofen, naproxen, ketoprofen, and nimesulide), aspirin and related salicylates (e.g. choline salicylate, magnesium salicylate, and sodium salicylate), paracetamol/acetaminophen, metamizole, nabumetone, phenazone, and quinine.

Suitable anxiolytics include, but are not limited to, benzodiazepines (e.g. alprazolam, bromazepam, chlorthalidopexide, clonazepam, clorazepate, diazepam, flurazepam, lorazepam, oxazepam, temazepam, triazolam, and tofisopam), serotonergic antidepressants (e.g. selective serotonin reuptake inhibitors, tricyclic antidepressants, and monoamine oxidase inhibitors), mebicar, afobazole, selank, bromantane, emoxypine, azapirone, barbiturates, hydroxyzine, pregabalin, validol, and beta blockers.

Suitable antipsychotics include, but are not limited to, benperidol, bromperidol, droperidol, haloperidol, moperone, pipaperone, timiperone, fluspirilene, penfluridol, pimozide, acepromazine, chlorpromazine, cyamemazine, dixyrazine, fluphenazine, levomepromazine, mesoridazine, perazine, pericyazine, perphenazine, pipotiazine, prochlorperazine, promazine, promethazine, prothipendyl, thioproperazine, thioridazine, trifluoperazine, triflupromazine, chlorprothixene, clopenthixol, flupenthixol, tiotixene, zuclopenthixol, clozapine, loxapine, prothipendyl, caripramine, clocapramine, molindone, mosapramine, sulpiride, veralipride, amisulpride, amoxapine, aripiprazole, asenapine, clozapine, blonanserin, iloperidone, lurasidone, melperone, nemonapride, olanzapine, paliperidone, perospirone, quetiapine, remoxipride, risperidone, sertindole, trimipramine, ziprasidone,

zotepine, alstonie, bifeprunox, bitopertin, brexpiprazole, cannabidiol, cariprazine, pimavanserin, pomaglumetad methionil, vabicaserin, xanomeline, and zicronapine.

Suitable analgesics include, but are not limited to, paracetamol/acetaminophen, nonsteroidal anti-inflammants (e.g. ibuprofen, naproxen, ketoprofen, and nimesulide), COX-2 inhibitors (e.g. rofecoxib, celecoxib, and etoricoxib), opioids (e.g. morphine, codeine, oxycodone, hydrocodone, dihydromorphine, pethidine, buprenorphine), tramadol, norepinephrine, flupirtine, nefopam, orphenadrine, pregabalin, gabapentin, cyclobenzaprine, scopolamine, methadone, ketobemidone, piritramide, and aspirin and related salicylates (e.g. choline salicylate, magnesium salicylate, and sodium salicylate).

Suitable antispasmodics include, but are not limited to, mebeverine, papaverine, cyclobenzaprine, carisoprodol, orphenadrine, tizanidine, metaxalone, methocarbamol, chlorzoxazone, baclofen, dantrolene, baclofen, tizanidine, and dantrolene. Suitable anti-inflammatories include, but are not limited to, prednisone, non-steroidal anti-inflammants (e.g. ibuprofen, naproxen, ketoprofen, and nimesulide), COX-2 inhibitors (e.g. rofecoxib, celecoxib, and etoricoxib), and immune selective anti-inflammatory derivatives (e.g. submandibular gland peptide-T and its derivatives).

Suitable anti-histamines include, but are not limited to, H1-receptor antagonists (e.g. acrivastine, azelastine, bilastine, brompheniramine, buclizine, bromodiphenhydramine, carbinoxamine, cetirizine, chlorpromazine, cyclizine, chlorpheniramine, clemastine, cyproheptadine, desloratadine, dexbrompheniramine, dexchlorpheniramine, dimenhydrinate, dimetindene, diphenhydramine, doxylamine, ebastine, embramine, fexofenadine, hydroxyzine, levocetirizine, loratadine, meclozine, mirtazapine, olopatadine, orphenadrine, phenindamine, pheniramine, phenyltoloxamine, promethazine, pyrilamine, quetiapine, rupatadine, tripeleminamine, and triprolidine), H2-receptor antagonists (e.g. cimetidine, famotidine, lafutidine, nizatidine, ranitidine, and roxatidine), tritoqualine, catechin, cromoglicate, nedocromil, and p2-adrenergic agonists.

Suitable anti-infectives include, but are not limited to, amebicides (e.g. nitazoxanide, paromomycin, metronidazole, tinidazole, chloroquine, miltefosine, amphotericin b, and iodoquinol), aminoglycosides (e.g. paromomycin, tobramycin, gentamicin, amikacin, kanamycin, and neomycin), anthelmintics (e.g. pyrantel, mebendazole, ivermectin, praziquantel, albendazole, thiabendazole, oxamniquine), antifungals (e.g. azole antifungals (e.g. itraconazole, fluconazole, parconazole, ketoconazole, clotrimazole, miconazole, and voriconazole), echinocandins (e.g. caspofungin, anidulafungin, and micafungin), griseofulvin, terbinafine, flucytosine, and polyenes (e.g. nystatin, and amphotericin b), antimalarial agents (e.g. pyrimethamine/sulfadoxine, artemether/lumefantrine, atovaquone/proguanil, quinine, hydroxychloroquine, mefloquine, chloroquine, doxycycline, pyrimethamine, and halofantrine), antituberculosis agents (e.g. aminosaliclates (e.g. aminosaliclic acid), isoniazid/rifampin, isoniazid/pyrazinamide/rifampin, bedaquiline, isoniazid, ethambutol, rifampin, rifabutin, rifapentine, capreomycin, and cycloserine), antivirals (e.g. amantadine, rimantadine, abacavir/lamivudine, emtricitabine/tenofovir, cobicistat/elvitegravir/emtricitabine/tenofovir, efavirenz/emtricitabine/tenofovir, abacavir/lamivudine/zidovudine, lamivudine/zidovudine, emtricitabine/tenofovir, emtricitabine/lopinavir/ritonavir/tenofovir, interferon alfa-2v/ribavirin, peginterferon alfa-2b, maraviroc, raltegravir, dolutegravir, enfuvirtide, foscarnet, fomivirsen, oseltamivir, zanamivir, nevirapine, efavirenz, etravirine, rilpivirine, dela-

viridine, nevirapine, entecavir, lamivudine, adefovir, sofosbuvir, didanosine, tenofovir, abacavir, zidovudine, stavudine, emtricitabine, zalcitabine, telbivudine, simeprevir, boceprevir, telaprevir, lopinavir/ritonavir, boceprevir, darunavir, ritonavir, tipranavir, atazanavir, nelfinavir, amprenavir, indinavir, saquinavir, ribavirin, valacyclovir, acyclovir, famciclovir, ganciclovir, and valganciclovir), carbapenems (e.g. doripenem, meropenem, ertapenem, and cilastatin/imipenem), cephalosporins (e.g. cefadroxil, cephadrine, cefazolin, cephalexin, cefepime, cefazoline, loracarbef, cefotetan, cefuroxime, cefprozil, loracarbef, cefoxitin, cefaclor, ceftibuten, ceftriaxone, cefotaxime, cefpodoxime, cefdinir, cefixime, cefditoren, ceftizoxime, and ceftazidime), glycopeptide antibiotics (e.g. vancomycin, dalbavancin, oritavancin, and telavancin), glycyclines (e.g. tigecycline), leprostatics (e.g. clofazimine and thalidomide), lincomycin and derivatives thereof (e.g. clindamycin and lincomycin), macrolides and derivatives thereof (e.g. telithromycin, fidaxomicin, erythromycin, azithromycin, clarithromycin, dirithromycin, and troleandomycin), linezolid, sulfamethoxazole/trimethoprim, rifaximin, chloramphenicol, Fosfomycin, metronidazole, aztreonam, bacitracin, penicillin (amoxicillin, ampicillin, piperacillin, bacampicillin, carbenicillin, ticarcillin, amoxicillin/clavulanate, ampicillin/sulbactam, piperacillin/tazobactam, clavulanate/ticarcillin, penicillin, procaine penicillin, oxacillin, dicloxacillin, and nafcillin), quinolones (e.g. lomefloxacin, norfloxacin, ofloxacin, gatifloxacin, moxifloxacin, ciprofloxacin, levofloxacin, gemifloxacin, moxifloxacin, cinoxacin, nalidixic acid, enoxacin, grepafloxacin, gatifloxacin, trovafloxacin, and sparfloxacin), sulfonamides (e.g. sulfamethoxazole/trimethoprim, sulfasalazine, and sulfisoxazole), tetracyclines (e.g. doxycycline, demeclocycline, minocycline, doxycycline/salicylic acid, doxycycline/omega-3 polyunsaturated fatty acids, and tetracycline), and urinary anti-infectives (e.g. nitrofurantoin, methenamine, Fosfomycin, cinoxacin, nalidixic acid, trimethoprim, and methylene blue).

Suitable chemotherapeutics include, but are not limited to, paclitaxel, brentuximab vedotin, doxorubicin, 5-FU (fluorouracil), everolimus, pemetrexed, melphalan, pamidronate, anastrozole, exemestane, nelarabine, ofatumumab, bevacizumab, belinostat, tositumomab, carmustine, bleomycin, bosutinib, busulfan, alemtuzumab, irinotecan, vandetanib, bicalutamide, lomustine, daunorubicin, clofarabine, cabozantinib, dactinomycin, ramucicromab, cytarabine, Cytosan, cyclophosphamide, decitabine, dexamethasone, docetaxel, hydroxyurea, dacarbazine, leuprolide, epirubicin, oxaliplatin, asparaginase, estramustine, cetuximab, vismodegib, asparaginase *Erwinia chrysanthemi*, amifostine, etoposide, flutamide, toremifene, fulvestrant, letrozole, degarelix, pralatrexate, methotrexate, floxuridine, obinutuzumab, gemcitabine, afatinib, imatinib mesylate, carmustine, eribulin, trastuzumab, altretamine, topotecan, ponatinib, idarubicin, ifosfamide, ibrutinib, axitinib, interferon alfa-2a, gefitinib, romidepsin, ixabepilone, ruxolitinib, cabazitaxel, ado-trastuzumab emtansine, carfilzomib, chlorambucil, sargramostim, cladribine, mitotane, vincristine, procabazine, megestrol, trametinib, mesna, strontium-89 chloride, mechlorethamine, mitomycin, busulfan, gemtuzumab ozogamicin, vinorelbine, filgrastim, pegfilgrastim, sorafenib, nilutamide, pentostatin, tamoxifen, mitoxantrone, pegaspargase, denileukin diftitox, alitreteonin, carboplatin, pertuzumab, cisplatin, pomalidomide, prednisone, aldesleukin, mercaptopurine, zoledronic acid, lenalidomide, rituximab, octreotide, dasatinib, regorafenib, histrelin, sunitinib, siltuximab, omacetaxine, thioguanine (tioguanine), dabrafenib,

erlotinib, bexarotene, temozolomide, thiotepa, thalidomide, BCG, temsirolimus, bendamustine hydrochloride, triptorelin, arsenic trioxide, lapatinib, valrubicin, panitumumab, vinblastine, bortezomib, tretinoin, azacitidine, pazopanib, teniposide, leucovorin, crizotinib, capecitabine, enzalutamide, ipilimumab, goserelin, vorinostat, idelalisib, ceritinib, abiraterone, epothilone, tafluposide, azathioprine, doxifluridine, vindesine, and all-trans retinoic acid.

In embodiments where there is an auxiliary active agent contained in the pharmaceutical formulation in addition to the one or more of the polypeptides, polynucleotides, vectors, cells, virus particles, nanoparticles, other delivery particles, and combinations thereof described herein, amount, such as an effective amount, of the auxiliary active agent will vary depending on the auxiliary active agent. In some embodiments, the amount of the auxiliary active agent ranges from 0.001 micrograms to about 1 milligram. In other embodiments, the amount of the auxiliary active agent ranges from about 0.01 IU to about 1000 IU. In further embodiments, the amount of the auxiliary active agent ranges from 0.001 mL to about 1 mL. In yet other embodiments, the amount of the auxiliary active agent ranges from about 1% w/w to about 50% w/w of the total pharmaceutical formulation. In additional embodiments, the amount of the auxiliary active agent ranges from about 1% v/v to about 50% v/v of the total pharmaceutical formulation. In still other embodiments, the amount of the auxiliary active agent ranges from about 1% w/v to about 50% w/v of the total pharmaceutical formulation.

30 Dosage Forms

In some embodiments, the pharmaceutical formulations described herein may be in a dosage form. The dosage forms can be adapted for administration by any appropriate route. Appropriate routes include, but are not limited to, oral (including buccal or sublingual), rectal, epidural, intracranial, intraocular, inhaled, intranasal, topical (including buccal, sublingual, or transdermal), vaginal, intraurethral, parenteral, intracranial, subcutaneous, intramuscular, intravenous, intraperitoneal, intradermal, intraosseous, intracardiac, intraarticular, intracavernous, intrathecal, intravitreal, intracerebral, gingival, subgingival, intracerebroventricular, and intradermal. Such formulations may be prepared by any method known in the art.

Dosage forms adapted for oral administration can be discrete dosage units such as capsules, pellets or tablets, powders or granules, solutions, or suspensions in aqueous or non-aqueous liquids; edible foams or whips, or in oil-in-water liquid emulsions or water-in-oil liquid emulsions. In some embodiments, the pharmaceutical formulations adapted for oral administration also include one or more agents which flavor, preserve, color, or help disperse the pharmaceutical formulation. Dosage forms prepared for oral administration can also be in the form of a liquid solution that can be delivered as foam, spray, or liquid solution. In some embodiments, the oral dosage form can contain about 1 ng to 1000 g of a pharmaceutical formulation containing a therapeutically effective amount or an appropriate fraction thereof of the targeted effector fusion protein and/or complex thereof or composition containing the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein. The oral dosage form can be administered to a subject in need thereof.

Where appropriate, the dosage forms described herein can be microencapsulated.

The dosage form can also be prepared to prolong or sustain the release of any ingredient. In some embodiments, the one or more of the polypeptides, polynucleotides, vec-

tors, cells, and combinations thereof described herein can be the ingredient whose release is delayed. In other embodiments, the release of an optionally included auxiliary ingredient is delayed. Suitable methods for delaying the release of an ingredient include, but are not limited to, coating or embedding the ingredients in material in polymers, wax, gels, and the like. Delayed release dosage formulations can be prepared as described in standard references such as "Pharmaceutical dosage form tablets," eds. Liberman et al. (New York, Marcel Dekker, Inc., 1989), "Remington—The science and practice of pharmacy", 20th ed., Lippincott Williams & Wilkins, Baltimore, MD, 2000, and "Pharmaceutical dosage forms and drug delivery systems", 6th Edition, Ansel et al., (Media, PA: Williams and Wilkins, 1995). These references provide information on excipients, materials, equipment, and processes for preparing tablets and capsules and delayed release dosage forms of tablets and pellets, capsules, and granules. The delayed release can be anywhere from about an hour to about 3 months or more.

Examples of suitable coating materials include, but are not limited to, cellulose polymers such as cellulose acetate phthalate, hydroxypropyl cellulose, hydroxypropyl methylcellulose, hydroxypropyl methylcellulose phthalate, and hydroxypropyl methylcellulose acetate succinate; polyvinyl acetate phthalate, acrylic acid polymers and copolymers, and methacrylic resins that are commercially available under the trade name EUDRAGIT® (Roth Pharma, Weiterstadt, Germany), zein, shellac, and polysaccharides.

Coatings may be formed with a different ratio of water-soluble polymer, water insoluble polymers, and/or pH dependent polymers, with or without water insoluble/water soluble non-polymeric excipient, to produce the desired release profile. The coating is either performed on the dosage form (matrix or simple) which includes, but is not limited to, tablets (compressed with or without coated beads), capsules (with or without coated beads), beads, particle compositions, "ingredient as is" formulated as, but not limited to, suspension form or as a sprinkle dosage form.

Dosage forms adapted for topical administration can be formulated as ointments, creams, suspensions, lotions, powders, solutions, pastes, gels, sprays, aerosols, or oils. In some embodiments for treatments of the eye or other external tissues, for example the mouth or the skin, the pharmaceutical formulations are applied as a topical ointment or cream. When formulated in an ointment, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be formulated with a paraffinic or water-miscible ointment base. In some embodiments, the active ingredient can be formulated in a cream with an oil-in-water cream base or a water-in-oil base. Dosage forms adapted for topical administration in the mouth include lozenges, pastilles, and mouth washes.

Dosage forms adapted for nasal or inhalation administration include aerosols, solutions, suspension drops, gels, or dry powders. In some embodiments, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein is contained in a dosage form adapted for inhalation is in a particle-size-reduced form that is obtained or obtainable by micronization. In some embodiments, the particle size of the size reduced (e.g. micronized) compound or salt or solvate thereof, is defined by a D50 value of about 0.5 to about 10 microns as measured by an appropriate method known in the art. Dosage forms adapted for administration by inhalation also include particle dusts or mists. Suitable dosage forms wherein the carrier or excipient is a liquid for administration as a nasal spray or drops include aqueous or oil solutions/suspensions of an active

ingredient (e.g. the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein and/or auxiliary active agent), which may be generated by various types of metered dose pressurized aerosols, nebulizers, or insufflators.

In some embodiments, the dosage forms can be aerosol formulations suitable for administration by inhalation. In some of these embodiments, the aerosol formulation can contain a solution or fine suspension of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein and a pharmaceutically acceptable aqueous or non-aqueous solvent. Aerosol formulations can be presented in single or multi-dose quantities in sterile form in a sealed container. For some of these embodiments, the sealed container is a single dose or multi-dose nasal or an aerosol dispenser fitted with a metering valve (e.g. metered dose inhaler), which is intended for disposal once the contents of the container have been exhausted.

Where the aerosol dosage form is contained in an aerosol dispenser, the dispenser contains a suitable propellant under pressure, such as compressed air, carbon dioxide, or an organic propellant, including but not limited to a hydrofluorocarbon. The aerosol formulation dosage forms in other embodiments are contained in a pump-atomizer. The pressurized aerosol formulation can also contain a solution or a suspension of one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein. In further embodiments, the aerosol formulation can also contain co-solvents and/or modifiers incorporated to improve, for example, the stability and/or taste and/or fine particle mass characteristics (amount and/or profile) of the formulation. Administration of the aerosol formulation can be once daily or several times daily, for example 2, 3, 4, or 8 times daily, in which 1, 2, or 3 doses are delivered each time.

For some dosage forms suitable and/or adapted for inhaled administration, the pharmaceutical formulation is a dry powder inhalable formulation. In addition to the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein, an auxiliary active ingredient, and/or pharmaceutically acceptable salt thereof, such a dosage form can contain a powder base such as lactose, glucose, trehalose, mannitol, and/or starch. In some of these embodiments, the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein is in a particle-size reduced form. In further embodiments, a performance modifier, such as L-leucine or another amino acid, cellobiose octaacetate, and/or metals salts of stearic acid, such as magnesium or calcium stearate.

In some embodiments, the aerosol dosage forms can be arranged so that each metered dose of aerosol contains a predetermined amount of an active ingredient, such as the one or more of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein.

Dosage forms adapted for vaginal administration can be presented as pessaries, tampons, creams, gels, pastes, foams, or spray formulations. Dosage forms adapted for rectal administration include suppositories or enemas.

Dosage forms adapted for parenteral administration and/or adapted for any type of injection (e.g. intravenous, intraperitoneal, subcutaneous, intramuscular, intradermal, intraosseous, epidural, intracardiac, intraarticular, intracavernous, gingival, subgingival, intrathecal, intravitreal, intracerebral, and intracerebroventricular) can include aqueous and/or non-aqueous sterile injection solutions, which

can contain anti-oxidants, buffers, bacteriostatic, solutes that render the composition isotonic with the blood of the subject, and aqueous and non-aqueous sterile suspensions, which can include suspending agents and thickening agents. The dosage forms adapted for parenteral administration can be presented in a single-unit dose or multi-unit dose containers, including but not limited to sealed ampoules or vials. The doses can be lyophilized and resuspended in a sterile carrier to reconstitute the dose prior to administration. Extemporaneous injection solutions and suspensions can be prepared in some embodiments, from sterile powders, granules, and tablets.

Dosage forms adapted for ocular administration can include aqueous and/or nonaqueous sterile solutions that can optionally be adapted for injection, and which can optionally contain anti-oxidants, buffers, bacteriostats, solutes that render the composition isotonic with the eye or fluid contained therein or around the eye of the subject, and aqueous and nonaqueous sterile suspensions, which can include suspending agents and thickening agents.

For some embodiments, the dosage form contains a predetermined amount of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein per unit dose. In some embodiments, the predetermined amount of the such unit doses may therefore be administered once or more than once a day. Such pharmaceutical formulations may be prepared by any of the methods well known in the art.

Kits

Also described herein are kits that contain one or more of the one or more of the compositions, polypeptides, polynucleotides, vectors, cells, viral particles, other delivery vehicles, or other components described herein and combinations thereof and pharmaceutical formulations described herein. In embodiments, one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof described herein can be presented as a combination kit. As used herein, the terms "combination kit" or "kit of parts" refers to the compounds, or formulations and additional components that are used to package, screen, test, sell, market, deliver, and/or administer the combination of elements or a single element, such as the active ingredient, contained therein. Such additional components include but are not limited to, packaging, syringes, blister packages, bottles, and the like. The combination kit can contain one or more of the components (e.g. one or more of the one or more of the polypeptides, polynucleotides, vectors, cells, and combinations thereof) or formulation thereof can be provided in a single formulation (e.g. a liquid, lyophilized powder, etc.), or in separate formulations. The separate components or formulations can be contained in a single package or in separate packages within the kit. The kit can also include instructions in a tangible medium of expression that can contain information and/or directions regarding the content of the components and/or formulations contained therein, safety information regarding the content of the components(s) and/or formulation(s) contained therein, information regarding the amounts, dosages, indications for use, screening methods, component design recommendations and/or information, recommended treatment regimen(s) for the components(s) and/or formulations contained therein. As used herein, "tangible medium of expression" refers to a medium that is physically tangible or accessible and is not a mere abstract thought or an unrecorded spoken word. "Tangible medium of expression" includes, but is not limited to, words on a cellulosic or plastic material, or data stored in a suitable computer read-

able memory form. The data can be stored on a unit device, such as a flash memory drive or CD-ROM or on a server that can be accessed by a user via, e.g. a web interface.

In one embodiment, the invention provides a kit comprising one or more of the components described herein. In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system includes a regulatory element operably linked to one or more engineered polynucleotides, such as those containing a muscle-specific targeting moiety and/or composition thereof, as described elsewhere herein and, optionally, a cargo molecule, which can optionally be operably linked to a regulatory element. The one or more engineered delivery system polynucleotides can be included on the same or different vectors as the cargo molecule in embodiments containing a cargo molecule within the kit.

In some embodiments, the kit comprises a vector system and instructions for using the kit. In some embodiments, the vector system comprises (a) a first regulatory element operably linked to a direct repeat sequence and one or more insertion sites for inserting one or more guide sequences up- or downstream (whichever applicable) of the direct repeat sequence, wherein when expressed, the guide sequence directs sequence-specific binding of a Cas9 CRISPR complex to a target sequence in a eukaryotic cell, wherein the Cas9 CRISPR complex comprises a Cas9 enzyme complexed with the guide sequence that is hybridized to the target sequence; and/or (b) a second regulatory element operably linked to an enzyme-coding sequence encoding said Cas9 enzyme comprising a nuclear localization sequence. Where applicable, a tracr sequence may also be provided. In some embodiments, the kit comprises components (a) and (b) located on the same or different vectors of the system. In some embodiments, component (a) further comprises two or more guide sequences operably linked to the first regulatory element, wherein when expressed, each of the two or more guide sequences direct sequence specific binding of a CRISPR complex to a different target sequence in a eukaryotic cell. In some embodiments, the Cas9 enzyme comprises one or more nuclear localization sequences of sufficient strength to drive accumulation of said CRISPR enzyme in a detectable amount in the nucleus of a eukaryotic cell. In some embodiments, the CRISPR enzyme is a type V or VI CRISPR system enzyme. In some embodiments, the CRISPR enzyme is a Cas9 enzyme. In some embodiments, the Cas9 enzyme is derived from *Francisella tularensis* 1, *Francisella tularensis* subsp. *novicida*, *Prevotella albensis*, *Lachnospiraceae* bacterium MC2017 1, *Butyrivibrio proteoclasticus*, *Peregrinibacteria* bacterium GW2011_GWA2_33_10, *Parcubacteria* bacterium GW2011_GWC2_44_17, *Smithella* sp. SCADC, *Acidaminococcus* sp. BV3L6, *Lachnospiraceae* bacterium MA2020, *Candidatus Methanoplasma termitum*, *Eubacterium eligens*, *Moraxella bovoculi* 237, *Leptospira inadai*, *Lachnospiraceae* bacterium ND2006, *Porphyromonas crevioricanis* 3, *Prevotella disiens*, or *Porphyromonas macacae* Cas9 (e.g., modified to have or be associated with at least one DD), and may include further alteration or mutation of the Cas9, and can be a chimeric Cas9. In some embodiments, the DD-CRISPR enzyme is codon-optimized for expression in a eukaryotic cell. In some embodiments, the DD-CRISPR enzyme directs cleavage of one or two strands at the location of the target sequence. In some embodiments, the DD-CRISPR enzyme lacks or substantially DNA strand cleavage activity (e.g., no more than 5% nuclease activity as compared with a wild type enzyme or enzyme not having the mutation or alteration that decreases nuclease activity). In some embodiments, the

first regulatory element is a polymerase III promoter. In some embodiments, the second regulatory element is a polymerase II promoter. In some embodiments, the guide sequence is at least 16, 17, 18, 19, 20, 25 nucleotides, or between 16-30, or between 16-25, or between 16-20 nucleotides in length.

Methods of Use

General Discussion

The compositions including one or more of the muscle-specific targeting moieties, engineered muscle-specific delivery system, engineered viral capsids and particles, polynucleotides, polypeptides, vector(s), engineered cells of the present invention can be used generally to package and/or deliver one or more cargos to a recipient cell. In some embodiments, delivery is done in cell-specific manner based upon the specificity of the targeting moiety, such as in a muscle specific manner. In some embodiments, this is conferred by the tropism of the engineered viral capsid, which can be influenced at least in part by the inclusion of one or more RGD and/or n-mer motifs described elsewhere herein. In some embodiments, the tropism is muscle specific. In some embodiments, compositions including one or more of the muscle-specific targeting moieties, engineered viral capsids and viral particles, can be administered to a subject or a cell, tissue, and/or organ and facilitate the transfer and/or integration of the cargo to the recipient cell. In other embodiments, engineered cells capable of producing compositions, such as polypeptides and other particles (e.g. engineered AAV capsids and viral particles), containing one or more of the muscle-specific targeting moieties can be generated from the polynucleotides, vectors, and vector systems etc., described herein. This includes without limitation, the engineered AAV capsid system molecules (e.g. polynucleotides, vectors, and vector systems, etc.). In some embodiments, the polynucleotides, vectors, and vector systems etc., described herein capable of generating the compositions, such as polypeptides and other particles (e.g. engineered AAV capsids and viral particles), containing one or more of the muscle-specific targeting moieties can be delivered to a cell or tissue, in vivo, ex vivo, or in vitro. In some embodiments, when delivered to a subject, the composition can transform a subject's cell in vivo or ex vivo to produce an engineered cell that can be capable of making a composition described herein that contains one or more of the muscle-specific targeting moieties described herein, including but not limited to the engineered AAV capsid particles, which can be released from the engineered cell and deliver cargo molecule(s) to a recipient cell in vivo or produce personalized engineered compositions (e.g. AAV capsid particles) for reintroduction into the subject from which the recipient cell was obtained.

In some embodiments, an engineered cell can be delivered to a subject, where it can release produced compositions of the present invention (including but not limited to engineered AAV capsid particles) such that they can then deliver a cargo (e.g. a cargo polynucleotide(s)) to a recipient cell. These general processes can be used in a variety of ways to treat and/or prevent disease or a symptom thereof in a subject, generate model cells, generate modified organisms, provide cell selection and screening assays, in bioproduction, and in other various applications.

In some embodiments, the compositions, such as polypeptides and other particles (e.g. engineered AAV capsids and viral particles), containing one or more of the muscle-specific targeting moieties) can be delivered to a subject or

a cell, tissue, and/or organ. In this way they can be used to deliver any cargo they may contain or are associated with to a muscle cell.

In some embodiments, the engineered AAV capsid polynucleotides, vectors, and systems thereof can be used to generate engineered AAV capsid variant libraries that can be mined for variants with a desired cell-specificity. The description provided herein as supported by the various Examples can demonstrate that one having a desired cell-specificity in mind could utilize the present invention as described herein to obtain a capsid with the desired cell-specificity.

The subject invention may be used as part of a research program wherein there is transmission of results or data. A computer system (or digital device) may be used to receive, transmit, display and/or store results, analyze the data and/or results, and/or produce a report of the results and/or data and/or analysis. A computer system may be understood as a logical apparatus that can read instructions from media (e.g. software) and/or network port (e.g. from the internet), which can optionally be connected to a server having fixed media. A computer system may comprise one or more of a CPU, disk drives, input devices such as keyboard and/or mouse, and a display (e.g. a monitor). Data communication, such as transmission of instructions or reports, can be achieved through a communication medium to a server at a local or a remote location. The communication medium can include any means of transmitting and/or receiving data. For example, the communication medium can be a network connection, a wireless connection, or an internet connection. Such a connection can provide for communication over the World Wide Web. It is envisioned that data relating to the present invention can be transmitted over such networks or connections (or any other suitable means for transmitting information, including but not limited to mailing a physical report, such as a print-out) for reception and/or for review by a receiver. The receiver can be but is not limited to an individual, or electronic system (e.g. one or more computers, and/or one or more servers). In some embodiments, the computer system comprises one or more processors. Processors may be associated with one or more controllers, calculation units, and/or other units of a computer system, or implanted in firmware as desired. If implemented in software, the routines may be stored in any computer readable memory such as in RAM, ROM, flash memory, a magnetic disk, a laser disk, or other suitable storage medium. Likewise, this software may be delivered to a computing device via any known delivery method including, for example, over a communication channel such as a telephone line, the internet, a wireless connection, etc., or via a transportable medium, such as a computer readable disk, flash drive, etc. The various steps may be implemented as various blocks, operations, tools, modules and techniques which, in turn, may be implemented in hardware, firmware, software, or any combination of hardware, firmware, and/or software. When implemented in hardware, some or all of the blocks, operations, techniques, etc. may be implemented in, for example, a custom integrated circuit (IC), an application specific integrated circuit (ASIC), a field programmable logic array (FPGA), a programmable logic array (PLA), etc. A client-server, relational database architecture can be used in embodiments of the invention. A client-server architecture is a network architecture in which each computer or process on the network is either a client or a server. Server computers are typically powerful computers dedicated to managing disk drives (file servers), printers (print servers), or network traffic (network servers). Client computers include PCs

(personal computers) or workstations on which users run applications, as well as example output devices as disclosed herein. Client computers rely on server computers for resources, such as files, devices, and even processing power. In some embodiments of the invention, the server computer handles all of the database functionality. The client computer can have software that handles all the front-end data management and can also receive data input from users. A machine readable medium comprising computer-executable code may take many forms, including but not limited to, a tangible storage medium, a carrier wave medium or physical transmission medium. Non-volatile storage media include, for example, optical or magnetic disks, such as any of the storage devices in any computer(s) or the like, such as may be used to implement the databases, etc. shown in the drawings. Volatile storage media include dynamic memory, such as main memory of such a computer platform. Tangible transmission media include coaxial cables; copper wire and fiber optics, including the wires that comprise a bus within a computer system. Carrier-wave transmission media may take the form of electric or electromagnetic signals, or acoustic or light waves such as those generated during radio frequency (RF) and infrared (IR) data communications. Common forms of computer-readable media therefore include for example: a floppy disk, a flexible disk, hard disk, magnetic tape, any other magnetic medium, a CD-ROM, DVD or DVD-ROM, any other optical medium, punch cards paper tape, any other physical storage medium with patterns of holes, a RAM, a ROM, a PROM and EPROM, a FLASH-EPROM, any other memory chip or cartridge, a carrier wave transporting data or instructions, cables or links transporting such a carrier wave, or any other medium from which a computer may read programming code and/or data. Many of these forms of computer readable media may be involved in carrying one or more sequences of one or more instructions to a processor for execution. Accordingly, the invention comprehends performing any method herein-discussed and storing and/or transmitting data and/or results therefrom and/or analysis thereof, as well as products from performing any method herein-discussed, including intermediates.

Therapeutics

In some embodiments, the compositions containing one or more of the muscle-specific targeting moieties described herein, including, but not limited to the engineered AAV capsids, engineered viral particles, engineered cells, and/or formulations thereof described herein can be delivered to a subject in need thereof as a therapy for one or more diseases. In some embodiments, the disease to be treated is a genetic- or epigenetic-based disease. In some embodiments, the disease to be treated is not a genetic- or epigenetic-based disease. In some embodiments, one the compositions containing one or more of the muscle-specific targeting moieties described herein, including, but not limited to, the engineered viral capsids, viral particles, engineered cells, and/or formulations thereof described herein can be delivered to a subject in need thereof as a treatment or prevention (or as a part of a treatment or prevention) of a disease. It will be appreciated that the specific disease to be treated and/or prevented by delivery of a composition, formulation, cell and the like of the present invention, can be dependent on the cargo coupled to, attached to, contained in, or otherwise associated with the composition, formulation, cell and the like of the present invention.

Genetic diseases that can be treated are discussed in greater detail elsewhere herein (see e.g. discussion on Genomodification based-therapies below). Other diseases include but are not limited to any of the following: cancer, Acube-

tivacter infections, actinomycosis, African sleeping sickness, AIDS/HIV, amoebiasis, Anaplasmosis, Angiostrongyliasis, Anisakiasis, Anthrax, Arcanobacterium haemolyticum infection, Argentine hemorrhagic fever, Ascariasis, Aspergillosis, Astrovirus infection, Babesiosis, Bacterial meningitis, Bacterial pneumonia, Bacterial vaginosis, Bacteroides infection, balantidiasis, Bartonellosis, Baylisascaris infection, BK virus infection, Black Piedra, Blastocystis, Blastomycosis, Bolivian hemorrhagic fever, Botulism, Brazilian hemorrhagic fever, brucellosis, Bubonic plague, Burkholderia infection, buruli ulcer, calicivirus infection, campylobacteriosis, Candidiasis, Capillariasis, Carrion's disease, Cat-scratch disease, cellulitis, Chagas Disease, Chancroid, Chickenpox, Chikungunya, *Chlamydia*, *Chlamydia pneumoniae*, Cholera, Chromoblastomycosis, Chytridiomycosis, Clonorchiasis, *Clostridium difficile* colitis, Coccidioidomycosis, Colorado tick fever, rhinovirus/coronavirus infection (common cold), Creutzfeldt-Jakob disease, Crimean-congo hemorrhagic fever, Cryptococcosis, Cryptosporidiosis, Cutaneous larva migrans (CLM), cyclosporiasis, cysticercosis, cytomegalovirus infection, Dengue fever, Desmodermatitis, Dientamoebiasis, Diphtheria, Diphyllorhynchiasis, Dracunculiasis, Ebola, Echinococcosis, Ehrlichiosis, Enterobiasis, *Enterococcus* infection, Enterovirus infection, Epidemic typhus, Erythema Infectiosum, Exanthem subitum, Fascioliasis, Fasciolopsiasis, fatal familial insomnia, filariasis, *Clostridium perfringens* infection, *Fusobacterium* infection, Gas gangrene (clostridial myonecrosis), Geotrichosis, Gerstmann-Straussler-Scheinker syndrome, Giardiasis, Glanders, Gnathostomiasis, Gonorrhea, Granuloma inguinale, Group A streptococcal infection, Group B streptococcal infection, *Haemophilus influenzae* infection, Hand, foot, and mouth disease, hanta virus pulmonary syndrome, heartland virus disease, *Helicobacter pylori* infection, hemorrhagic fever with renal syndrome, Hendra virus infection, Hepatitis (all groups A, B, C, D, E), herpes simplex, histoplasmosis, hookworm infection, human bocavirus infection, human ewingii ehrlichiosis, Human granulocytic anaplasmosis, human metapneumovirus infection, human monocytic ehrlichiosis, human papilloma virus, Hymenolepiasis, Epstein-Barr infection, mononucleosis, influenza, isosporiasis, Kawasaki disease, Kingella kingae infection, Kuru, Lassa fever, Legionellosis (Legionnaire's disease and Potomac Fever), Leishmaniasis, Leprosy, Leptospirosis, Listeriosis, Lyme disease, lymphatic filariasis, lymphocytic choriomeningitis, Malaria, Marburg hemorrhagic fever, measles, Middle East respiratory syndrome, Melioidosis, meningitis, Meningococcal disease, Metagonimiasis, Microsporidiosis, Molluscum contagiosum, Monkeypox, Mumps, Murine typhus, *Mycoplasma pneumoniae*, *Mycoplasma genitalium* infection, Mycetoma, Myiasis, Conjunctivitis, Nipah virus infection, Norovirus, Variant Creutzfeldt-Jakob disease, Nocardiosis, Onchocerciasis, Opisthorchiasis, Paracoccidioidomycosis, Paragonimiasis, Pasteurellosis, Pediculosis capitis, Pediculosis corporis, Pediculosis pubis, pelvic inflammatory disease, pertussis, plague, pneumococcal infection, pneumocystis pneumonia, pneumonia, poliomyelitis, prevotella infection, primary amoebic meningoencephalitis, progressive multifocal leukoencephalopathy, Psittacosis, Q fever, rabies, relapsing fever, respiratory syncytial virus infection, rhinovirus infection, rickettsial infection, Rickettsialpox, Rift Valley Fever, Rocky Mountain Spotted Fever, Rotavirus infection, Rubella, *Salmonellosis*, SARS, Scabies, Scarlet fever, Schistosomiasis, Sepsis, Shigellosis, Shingles, Smallpox, Sporotrichosis, Staphylococcal infection (including MRSA), strongyloidiasis, subacute

sclerosing panencephalitis, Syphilis, Taeniasis, tetanus, *Trichophyton* species infection, Toxocariasis, Toxoplasmosis, Trachoma, Trichinosis, Trichuriasis, Tuberculosis, Tularemia, Typhoid Fever, Typhus Fever, *Ureaplasma urealyticum* infection, Valley fever, Venezuelan equine encephalitis, Venezuelan hemorrhagic fever, *Vibrio* species infection, Viral pneumonia, West Nile Fever, White Piedra, *Yersinia pseudotuberculosis*, Yersiniosis, Yellow fever, Zeaspora, Zika fever, Zygomycosis and combinations thereof.

Other diseases and disorders that can be treated using embodiments of the present invention include, but are not limited to, endocrine diseases (e.g. Type I and Type II diabetes, gestational diabetes, hypoglycemia, Glucagonoma, Goiter, Hyperthyroidism, hypothyroidism, thyroiditis, thyroid cancer, thyroid hormone resistance, parathyroid gland disorders, Osteoporosis, osteitis deformans, rickets, osteomalacia, hypopituitarism, pituitary tumors, etc.), skin conditions of infectious or non-infectious origin, eye diseases of infectious or non-infectious origin, gastrointestinal disorders of infectious or non-infectious origin, cardiovascular diseases of infectious or non-infectious origin, brain and neuron diseases of infectious or non-infectious origin, nervous system diseases of infectious or non-infectious origin, muscle diseases of infectious or non-infectious origin, bone diseases of infectious or non-infectious origin, reproductive system diseases of infectious or non-infectious origin, renal system diseases of infectious or non-infectious origin, blood diseases of infectious or non-infectious origin, lymphatic system diseases of infectious or non-infectious origin, immune system diseases of infectious or non-infectious origin, mental-illness of infectious or non-infectious origin and the like.

In some embodiments, the disease to be treated is a muscle or muscle related disease or disorder, such as a genetic muscle disease or disorder.

Other diseases and disorders will be appreciated by those of skill in the art.

Adoptive Cell Therapies

Generally speaking, adoptive cell transfer involves the transfer of cells (autologous, allogeneic, and/or xenogeneic) to a subject. The cells may or may not be modified and/or otherwise manipulated prior to delivery to the subject.

In some embodiments, an engineered cell as described herein can be included in an adoptive cell transfer therapy. In some embodiments, an engineered cell as described herein can be delivered to a subject in need thereof. In some embodiments, the cell can be isolated from a subject, manipulated in vitro such that it contains and/or is capable of generating a composition of the present invention containing a muscle-specific targeting moiety described elsewhere herein (including but not limited to an engineered viral particle) described herein to produce an engineered cell and delivered back to the subject in an autologous manner or to a different subject in an allogeneic or xenogeneic manner. The cell isolated, manipulated, and/or delivered can be a eukaryotic cell. The cell isolated, manipulated, and/or delivered can be a stem cell. The cell isolated, manipulated, and/or delivered can be a differentiated cell. The cell isolated, manipulated, and/or delivered can be an immune cell, a blood cell, an endocrine cell, a renal cell, an exocrine cell, a nervous system cell, a vascular cell, a muscle cell, a urinary system cell, a bone cell, a soft tissue cell, a cardiac cell, a neuron, or an integumentary system cell. Other specific cell types will instantly be appreciated by one of ordinary skill in the art.

In some embodiments, the isolated cell can be manipulated such that it becomes an engineered cell as described

elsewhere herein (e.g. contain and/or express one or more engineered delivery system molecules or vectors described elsewhere herein). Methods of making such engineered cells are described in greater detail elsewhere herein.

The administration of the cells or population of cells according to the present invention may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The cells or population of cells may be administered to a patient subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous or intralymphatic injection, or intraperitoneally. In one embodiment, the cell compositions of the present invention are preferably administered by intravenous injection.

The administration of the cells or population of cells can be or involve the administration of 10^4 - 10^9 cells per kg body weight including all integer values of cell numbers within those ranges. In some embodiments, 10^5 to 10^6 cells/kg are delivered. Dosing in adoptive cell therapies may for example involve administration of from 10^6 to 10^9 cells/kg, with or without a course of lymphodepletion, for example with cyclophosphamide. The cells or population of cells can be administered in one or more doses. In another embodiment, the effective amount of cells are administered as a single dose. In another embodiment, the effective amount of cells are administered as more than one dose over a period time. Timing of administration is within the judgment of managing physician and depends on the clinical condition of the patient. The cells or population of cells may be obtained from any source, such as a blood bank or a donor. While individual needs vary, determination of optimal ranges of effective amounts of a given cell type for a particular disease or conditions are within the skill of one in the art. An effective amount means an amount which provides a therapeutic or prophylactic benefit. The dosage administered will be dependent upon the age, health and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment and the nature of the effect desired.

In another embodiment, the effective amount of cells or composition comprising those cells are administered parenterally. The administration can be an intravenous administration. The administration can be directly done by injection within a tissue. In some embodiments, the tissue can be a tumor.

To guard against possible adverse reactions, engineered cells can be equipped with a transgenic safety switch, in the form of a transgene that renders the cells vulnerable to exposure to a specific signal. For example, the herpes simplex viral thymidine kinase (TK) gene may be used in this way, for example by introduction into the engineered cell similar to that discussed in Greco, et al., improving the safety of cell therapy with the TK-suicide gene. Front. Pharmacol. 2015; 6:95. In such cells, administration of a nucleoside prodrug such as ganciclovir or acyclovir causes cell death. Alternative safety switch constructs include inducible caspase 9, for example triggered by administration of a small-molecule dimerizer that brings together two nonfunctional icasp9 molecules to form the active enzyme. A wide variety of alternative approaches to implementing cellular proliferation controls have been described (see U.S. Patent Publication No. 20130071414; PCT Patent Publication WO2011146862; PCT Patent Publication WO2014011987; PCT Patent Publication WO2013040371; Zhou et al. BLOOD, 2014, 123/25:3895-3905; Di Stasi et al., The New England Journal of Medicine 2011; 365:1673-

1683; Sadelain M, *The New England Journal of Medicine* 2011; 365:1735-173; Ramos et al., *Stem Cells* 28(6): 1107-15(2010)).

Methods of modifying isolated cells to obtain the engineered cells with the desired properties are described elsewhere herein. In some embodiments, the methods can include genome modification, including, but not limited to, genome editing using a CRISPR-Cas system to modify the cell. This can be in addition to introduction of an e.g., engineered AAV capsid system molecule describe elsewhere herein.

Allogeneic cells are rapidly rejected by the host immune system. It has been demonstrated that, allogeneic leukocytes present in non-irradiated blood products will persist for no more than 5 to 6 days (Boni, Muranski et al. 2008 *Blood* 1; 112(12): 4746-54). Thus, to prevent rejection of allogeneic cells, the host's immune system usually has to be suppressed to some extent. However, in the case of adoptive cell transfer the use of immunosuppressive drugs also have a detrimental effect on the introduced therapeutic cells, such as engineered cells described herein. Therefore, to effectively use an adoptive immunotherapy approach in these conditions, the introduced cells would need to be resistant to the immunosuppressive treatment. Thus, in a particular embodiment, the present invention further comprises a step of modifying the engineered cells to make them resistant to an immunosuppressive agent, preferably by inactivating at least one gene encoding a target for an immunosuppressive agent. An immunosuppressive agent is an agent that suppresses immune function by one of several mechanisms of action. An immunosuppressive agent can be, but is not limited to a calcineurin inhibitor, a target of rapamycin, an interleukin-2 receptor α -chain blocker, an inhibitor of inosine monophosphate dehydrogenase, an inhibitor of dihydrofolic acid reductase, a corticosteroid or an immunosuppressive anti-metabolite. The present invention allows conferring immunosuppressive resistance to engineered cells for adoptive cell therapy by inactivating the target of the immunosuppressive agent in engineered cells. As non-limiting examples, targets for an immunosuppressive agent can be a receptor for an immunosuppressive agent such as: CD52, glucocorticoid receptor (GR), a FKBP family gene member and a cyclophilin family gene member.

Immune checkpoints are inhibitory pathways that slow down or stop immune reactions and prevent excessive tissue damage from uncontrolled activity of immune cells. In certain embodiments, the immune checkpoint targeted is the programmed death-1 (PD-1 or CD279) gene (PDCD1). In other embodiments, the immune checkpoint targeted is cytotoxic T-lymphocyte-associated antigen (CTLA-4). In additional embodiments, the immune checkpoint targeted is another member of the CD28 and CTLA4 Ig superfamily such as BTLA, LAG3, ICOS, PDL1 or KIR. In further additional embodiments, the immune checkpoint targeted is a member of the TNFR superfamily such as CD40, OX40, CD137, GITR, CD27 or TIM-3.

Additional immune checkpoints include Src homology 2 domain-containing protein tyrosine phosphatase 1 (SHP-1) (Watson H A, et al., *SHP-1: the next checkpoint target for cancer immunotherapy?* *Biochem Soc Trans.* 2016 Apr. 15; 44(2): 356-62). SHP-1 is a widely expressed inhibitory protein tyrosine phosphatase (PTP). In T-cells, it is a negative regulator of antigen-dependent activation and proliferation. It is a cytosolic protein, and therefore not amenable to antibody-mediated therapies, but its role in activation and proliferation makes it an attractive target for genetic manipulation in adoptive transfer strategies, such as chimeric

antigen receptor (CAR) T cells. Immune checkpoints may also include T cell immunoreceptor with Ig and ITIM domains (TIGIT/Vstm3/WUCAM/VSIG9) and VISTA (Le Mercier I, et al., (2015) *Beyond CTLA-4 and PD-1, the generation Z of negative checkpoint regulators.* *Front. Immunol.* 6:418).

International Patent Publication No. WO2014172606 relates to the use of MTI and/or MT1 inhibitors to increase proliferation and/or activity of exhausted CD8+ T-cells and to decrease CD8+ T-cell exhaustion (e.g., decrease functionally exhausted or unresponsive CD8+ immune cells). In certain embodiments, metallothioneins are targeted by gene editing in adoptively transferred T cells.

In certain embodiments, targets of gene editing may be at least one targeted locus involved in the expression of an immune checkpoint protein. Such targets may include, but are not limited to CTLA4, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCDI, ICOS (CD278), PDL1, KIR, LAG3, HAVCR2, BTLA, CD160, TIGIT, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244(2B4), TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, TGFBRII, TGFRBRI, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAGI, SITI, FOXP3, PRDMI, BATF, VISTA, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, MTI, MT2, CD40, OX40, CD137, GITR, CD27, SHP-1 or TIM-3. In some embodiments, the gene locus involved in the expression of PD-1 or CTLA-4 genes is targeted. In some embodiments, combinations of genes are targeted, such as but not limited to PD-1 and TIGIT.

In some embodiments, at least two genes are edited. Pairs of genes may include, but are not limited to PD1 and TCR α , PD1 and TCR β , CTLA-4 and TCR α , CTLA-4 and TCR β , LAG3 and TCR α , LAG3 and TCR β , Tim3 and TCR α , Tim3 and TCR β , BTLA and TCR α , BTLA and TCR β , BY55 and TCR α , BY55 and TCR β , TIGIT and TCR α , TIGIT and TCR β , B7H5 and TCR α , B7H5 and TCR β , LAIR1 and TCR α , LAIR1 and TCR β , SIGLEC10 and TCR α , SIGLEC10 and TCR β , 2B4 and TCR α , 2B4 and TCR β .

Whether prior to or after genetic or other modification of the engineered cells (such as engineered T cells (e.g. the isolated cell is a T cell), the engineered cells can be activated and expanded generally using methods as described, for example, in U.S. Pat. Nos. 6,352,694; 6,534,055; 6,905,680; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and 7,572,631. The engineered cells can be expanded in vitro or in vivo.

In some embodiments, the method comprises editing the engineered cells ex vivo by a suitable gene modification method described elsewhere herein (e.g. gene editing via a CRISPR-Cas system) to eliminate potential alloreactive TCRs or other receptors to allow allogeneic adoptive transfer. In some embodiments, T cells are edited ex vivo by a CRISPR-Cas system or other suitable genome modification technique to knock-out or knock-down an endogenous gene encoding a TCR (e.g., an $\alpha\beta$ TCR) or other relevant receptor to avoid graft-versus-host-disease (GVHD). In some embodiments, where the engineered cells are T cells, the engineered cells are edited ex vivo by CRISPR or other appropriate gene modification method to mutate the TRAC locus. In some embodiments, T cells are edited ex vivo via a CRISPR-Cas system using one or more guide sequences targeting the first exon of TRAC. See Liu et al., *Cell Research* 27:154-157 (2017). In some embodiments, the first exon of TRAC is modified using another appropriate gene

modification method. In some embodiments, the method comprises use of CRISPR or other appropriate method to knock-in an exogenous gene encoding a CAR or a TCR into the TRAC locus, while simultaneously knocking-out the endogenous TCR (e.g., with a donor sequence encoding a self-cleaving P2A peptide following the CAR cDNA). See Eyquem et al., Nature 543:113-117(2017). In some embodiments, the exogenous gene comprises a promoter-less CAR-encoding or TCR-encoding sequence which is inserted operably downstream of an endogenous TCR promoter.

In some embodiments, the method comprises editing the engineered cell, e.g. engineered T cells, ex vivo via a CRISPR-Cas system to knock-out or knock-down an endogenous gene encoding an HLA-I protein to minimize immunogenicity of the edited cells, e.g. engineered T cells. In some embodiments, engineered T cells can be edited ex vivo via a CRISPR-Cas system to mutate the beta-2 microglobulin (B2M) locus. In some embodiments, engineered cell, e.g. engineered T cells, are edited ex vivo via a CRISPR-Cas system using one or more guide sequences targeting the first exon of B2M. The first exon of B2M can also be modified using another appropriate modification method. See Liu et al., Cell Research 27:154-157 (2017). The first exon of B2M can also be modified using another appropriate modification method, which will be appreciated by those of ordinary skill in the art. In some embodiments, the method comprises use a CRISPR-Cas system to knock-in an exogenous gene encoding a CAR or a TCR into the B2M locus, while simultaneously knocking-out the endogenous B2M (e.g., with a donor sequence encoding a self-cleaving P2A peptide following the CAR cDNA). See Eyquem et al., Nature 543:113-117 (2017). This can also be accomplished using another appropriate modification method, which will be appreciated by those of ordinary skill in the art. In some

embodiments, the exogenous gene comprises a promoter-less CAR-encoding or TCR-encoding sequence which is inserted operably downstream of an endogenous B2M promoter.

In some embodiments, the method comprises editing the engineered cell, e.g. engineered T cells, ex vivo via a CRISPR-Cas system to knock-out or knock-down an endogenous gene encoding an antigen targeted by an exogenous CAR or TCR. This can also be accomplished using another appropriate modification method, which will be appreciated by those of ordinary skill in the art. In some embodiments, the engineered cells, such as engineered T cells, are edited ex vivo via a CRISPR-Cas system to knock-out or knock-down the expression of a tumor antigen selected from human telomerase reverse transcriptase (hTERT), survivin, mouse double minute 2 homolog (MDM2), cytochrome P450 1B 1 (CYP1B), HER2/neu, Wilms' tumor gene 1 (WT1), livin, alphafetoprotein (AFP), carcinoembryonic antigen (CEA), mucin 16 (MUC16), MUC1, prostate-specific membrane antigen (PSMA), p53 or cyclin (DI) (see WO2016/011210). This can also be accomplished using another appropriate modification method, which will be appreciated by those of ordinary skill in the art. In some embodiments, the engineered cells, such as engineered T cells are edited ex vivo via a CRISPR-Cas system to knock-out or knock-down the expression of an antigen selected from B cell maturation antigen (BCMA), transmembrane activator and CAML Interactor (TACI), or B-cell activating factor receptor (BAFF-R), CD38, CD138, CS-1, CD33, CD26, CD30, CD53, CD92, CD100, CD148, CD150, CD200, CD261, CD262, or CD362 (see WO2017/011804). This can also be accomplished using another

appropriate modification method, which will be appreciated by those of ordinary skill in the art.

Gene Drives

The present invention also contemplates use of the compositions containing a muscle-specific targeting moiety described elsewhere herein, formulations thereof, cells thereof, vector systems, and the like to generate a gene drive via delivery of one or more cargo polynucleotides or production of a composition containing a muscle-specific targeting moiety described elsewhere herein (including but not limited to engineered AAV capsid particles) with one or more cargo polynucleotides capable of producing a gene drive. In some embodiments, the gene drive can be a Cas-mediated RNA-guided gene drive e.g. Cas-to provide RNA-guided gene drives, for example in systems analogous to gene drives described in International Patent Publication WO 2015/105928. Systems of this kind may for example provide methods for altering eukaryotic germline cells, by introducing into the germline cell a nucleic acid sequence encoding an RNA-guided DNA nuclease and one or more guide RNAs. The guide RNAs may be designed to be complementary to one or more target locations on genomic DNA of the germline cell. The nucleic acid sequence encoding the RNA guided DNA nuclease and the nucleic acid sequence encoding the guide RNAs may be provided on constructs between flanking sequences, with promoters arranged such that the germline cell may express the RNA guided DNA nuclease and the guide RNAs, together with any desired cargo-encoding sequences that are also situated between the flanking sequences. The flanking sequences will typically include a sequence which is identical to a corresponding sequence on a selected target chromosome, so that the flanking sequences work with the components encoded by the construct to facilitate insertion of the foreign nucleic acid construct sequences into genomic DNA at a target cut site by mechanisms such as homologous recombination, to render the germline cell homozygous for the foreign nucleic acid sequence. In this way, gene-drive systems are capable of introgressing desired cargo genes throughout a breeding population (Gantz et al., 2015, Highly efficient Cas9-mediated gene drive for population modification of the malaria vector mosquito *Anopheles stephensi*, PNAS 2015, published ahead of print Nov. 23, 2015, doi: 10.1073/pnas.1521077112; Esvelt et al., 2014, Concerning RNA-guided gene drives for the alteration of wild populations eLife 2014; 3: e03401). In select embodiments, target sequences may be selected which have few potential off-target sites in a genome. Targeting multiple sites within a target locus, using multiple guide RNAs, may increase the cutting frequency and hinder the evolution of drive resistant alleles. Truncated guide RNAs may reduce off-target cutting. Paired nickases may be used instead of a single nuclease, to further increase specificity. Gene drive constructs (such as gene drive engineered delivery system constructs) may include cargo sequences encoding transcriptional regulators, for example to activate homologous recombination genes and/or repress non-homologous end-joining. Target sites may be chosen within an essential gene, so that non-homologous end-joining events may cause lethality rather than creating a drive-resistant allele. The gene drive constructs can be engineered to function in a range of hosts at a range of temperatures (Cho et al. 2013, Rapid and Tunable Control of Protein Stability in *Caenorhabditis elegans* Using a Small Molecule, PLOS ONE 8(8): e72393. doi: 10.1371/journal.pone.0072393).

Transplantation and Xenotransplantation

The compositions containing a muscle-specific targeting moiety described elsewhere herein, formulations thereof, cells thereof, vector systems, and the like, can be used to deliver cargo polynucleotides and/or otherwise be involved in modifying tissues for transplantation between two different persons (transplantation) or between species (xenotransplantation). Such techniques for generation of transgenic animals is described elsewhere herein. Interspecies transplantation techniques are generally known in the art. For example, RNA-guided DNA nucleases can be delivered using via engineered viral particles or other delivery vehicles, polynucleotides, vectors, and/or engineered cells of the present invention described herein and can be used to knockout, knockdown or disrupt selected genes in an organ for transplant (e.g. ex vivo (e.g. after harvest but before transplantation) or in vivo (in donor or recipient)), animal, such as a transgenic pig (such as the human heme oxygenase-1 transgenic pig line), for example by disrupting expression of genes that encode epitopes recognized by the human immune system, i.e. xenoantigen genes. Candidate porcine genes for disruption may for example include a (1,3)-galactosyltransferase and cytidine monophosphate-N-acetylneuraminic acid hydroxylase genes (see International Patent Publication WO 2014/066505). In addition, genes encoding endogenous retroviruses may be disrupted, for example the genes encoding all porcine endogenous retroviruses (see Yang et al., 2015, Genome-wide inactivation of porcine endogenous retroviruses (PERVs), *Science* 27 Nov. 2015: Vol. 350 no. 6264 pp. 1101-1104). In addition, RNA-guided DNA nucleases may be used to target a site for integration of additional genes in xenotransplant donor animals, such as a human CD55 gene to improve protection against hyperacute rejection.

Where it is interspecies transplantation (such as human to human) the composition compositions containing a muscle-specific targeting moiety described elsewhere herein, or composition containing a muscle-specific targeting moiety (e.g. an engineered AAV capsid system molecule, vectors, engineered cells, and/or engineered delivery particles described herein), can be used to deliver cargo polynucleotides and/or otherwise be involved to modify the tissue to be transplanted. In some embodiments, the modification can include modifying one or more HLA antigens or other tissue type determinants, such that the immunogenic profile is more similar or identical to the recipient's immunogenic profile than to the donor's so as to reduce the occurrence of rejection by the recipient. Relevant tissue type determinants are known in the art (such as those used to determine organ matching) and techniques to determine the immunogenic profile (which is made up of the expression signature of the tissue type determinants) are generally known in the art.

In some embodiments, the donor (such as before harvest) or recipient (after transplantation) can receive one or more of the compositions containing a muscle-specific targeting moiety described elsewhere herein, formulations thereof, cells thereof, vector systems, engineered muscle-specific delivery system molecules, vectors, engineered cells, and/or engineered delivery particles described herein that are capable of modifying the immunogenic profile of the transplanted cells, tissue, and/or organ. In some embodiments, the transplanted cells, tissue, and/or organ can be harvested from the donor and the compositions containing a muscle-specific targeting moiety described elsewhere herein, formulations thereof, cells thereof, vector systems, engineered muscle-specific delivery system molecules, vectors, engineered cells, and/or engineered delivery particles described

herein capable of modifying the harvested cells, tissue, and/or organ to be, for example, less immunogenic or be modified to have some specific characteristic when transplanted in the recipient can be delivered to the harvested cells, tissue, and/or organ ex vivo. After delivery the cells, tissue, and/or organs can be transplanted into the donor. Gene Modification and Treatment of Diseases with Genetic or Epigenetic Aspects

The engineered muscle-specific delivery system molecules, vectors, engineered cells, and/or engineered delivery particles described herein containing a muscle-specific targeting moiety can be used to modify genes or other polynucleotides and/or treat diseases with genetic and/or epigenetic aspects. As described elsewhere herein the cargo molecule can be a polynucleotide that can be delivered to a cell and, in some embodiments, be integrated into the genome of the cell. In some embodiments, the cargo molecule(s) can be one or more CRISPR-Cas system components. In some embodiments, the CRISPR-Cas components, when delivered by a composition or formulation thereof of the present invention, such as an engineered muscle-specific viral particle or other engineered delivery vehicle described herein, can be optionally expressed in the recipient cell and act to modify the genome of the recipient cell in a sequence specific manner. In some embodiments, the cargo molecules that can be packaged and delivered by the engineered viral particles or other engineered delivery vehicles and/or compositions described herein can facilitate/mediate genome modification via a method that is not dependent on CRISPR-Cas. Such non-CRISPR-Cas genome modification systems will instantly be appreciated by those of ordinary skill in the art and are also, at least in part, described elsewhere herein. In some embodiments, modification is at a specific target sequence. In other embodiments, modification is at locations that appear to be random throughout the genome.

Examples of disease-associated genes and polynucleotides and disease specific information is available from McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University (Baltimore, Md.) and National Center for Biotechnology Information, National Library of Medicine (Bethesda, Md.), available on the World Wide Web. Any of these can be appropriate to be treated by one or more of the methods described herein. In some embodiments, the disease is a muscle disease or disorder, neuro-muscular disease or disorder, or a cardiomyopathy. In some embodiments, the disease or disorder selected from any one or more of the following:

- (a) an auto immune disease;
- (b) a cancer;
- (c) a muscular dystrophy;
- (d) a neuro-muscular disease;
- (e) a sugar or glycogen storage disease;
- (f) an expanded repeat disease;
- (g) a dominant negative disease;
- (h) a cardiomyopathy;
- (i) a viral disease;
- (j) a progeroid disease; or
- (k) any combination thereof.

In some embodiments, the expanded repeat disease is Huntington's disease, a Myotonic Dystrophy, or Facioscapulohumeral muscular dystrophy (FSHD). In some embodiments, the muscular dystrophy is Duchene muscular dystrophy, Becker Muscular dystrophy, a Limb-Girdle muscular dystrophy, an Emery Dreifuss muscular dystrophy, a myotonic dystrophy, or FSHD. In some embodiments, the

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myotonic dystrophy is Type 1 or Type 2. In some embodiments, the LGMD is subtype 2A, 2B, 2C, 2D, 2E, or 2L. In some embodiments, the cardiomyopathy is dilated cardiomyopathy, hypertrophic cardiomyopathy, DMD-associated cardiomyopathy, or Dannon disease. In some embodiments, the sugar or glycogen storage disease is a MPS type III disease or Pompe disease. In some embodiments, the MPS type III disease, is MPS Type IIIA, IIIB, IIIC, or IIID. In some embodiments, the neuro-muscular disease is Charcot-Marie-Tooth disease or Friedreich's Ataxia.

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More specifically, mutations in these genes and pathways can result in production of improper proteins or proteins in improper amounts which affect function. Further examples of genes, diseases and proteins are hereby incorporated by reference from U.S. Provisional application 61/736,527 filed Dec. 12, 2012. Such genes, proteins and pathways may be the target polynucleotide of a CRISPR complex of the present invention. Examples of disease-associated and/or cell function-associated genes and polynucleotides are listed in Tables A and B.

TABLE A

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Achondroplasia	Bone and Muscle		fibroblast growth factor receptor 3 (FGFR3)
Achromatopsia	eye		CNGA3, CNGB3, GNAT2, PDE6C, PDE6H, ACHM2, ACHM3, NFKappaB, AATF, p85alpha, FAS, Apoptosis cascade elements (e.g. FASR, Caspase 2, 3, 4, 6, 7, 8, 9, 10, AKT, TNF alpha, IGF1, IGF1R, RIPK1), p53
Acute Renal Injury	kidney		Aber; CCL2; CC2; CP (ceruloplasmin); Timp3; cathepsinD; VLDLR, CCR2
Age Related Macular Degeneration	eye		KIR3DL1, NKAT3, NKB1, AMB11, KIR3DS1, IFNG, CXCL12, SDF1
AIDS	Immune System		TYR, OCA2, TYRP1, and SLC45A2, SLC24A5 and C10orf11
Albinism (including oculocutaneous albinism (types 1-7) and ocular albinism)	Skin, hair, eyes,		
Alkaptonuria	Metabolism of amino acids	Tissues/organs where homogentisic acid accumulates, particularly cartilage (joints), heart valves, kidneys	HGD
alpha-1 antitrypsin deficiency (AATD or A1AD)	Lung	Liver, skin, vascular system, kidneys, GI	SERPINA1, those set forth in WO2017165862, Piz allele
ALS	CNS		SOD1; ALS2; ALS3; ALS5; ALS7; STEX; FUS; TARDBP; VEGF (VEGF-a; VEGF-b; VEGF-c); DPP6; NEFH, PTGS1, SLC1A2, TNFRSF10B, PRPH, HSP90AA1, CRIA2, IFNG, AMPA2 S100B, FGF2, AOX1, CS, TXN, RAPHJ1, MAP3K5, NBEAL1, GPX1, ICA1L, RAC1, MAPT, ITPR2, ALS2CR4, GLS, ALS2CR8, CNTFR, ALS2CR11, FOLH1, FAM117B, P4HB, CNTF, SQSTM1, STRADB, NAIP, NLR, YWHAQ, SLC33A1, TRAK2, SCA1, NIF3L1, NIF3, PARD3B, COX8A, CDK15, HECW1, HECT, C2, WW 15, NOS1, MET, SOD2, HSPB1, NEFL, CTSB, ANG, HSPA8, RNase A, VAPB, VAMP, SNCA, alpha HGF, CAT, ACTB, NEFM, TH, BCL2, FAS, CASP3, CLU, SMN1, G6PD, BAX, HSF1, RNF19A, JUN, ALS2CR12, HSPA5, MAPK14, APEX1, TXNRD1, NOS2, TIMP1, CASP9, XIAP, GLG1, EPO, VEGFA, ELN, GDNF, NFE2L2, SLC6A3, HSPA4, APOE, PSMB8, DCTN2, TIMP3, KIFAP3, SLC1A1, SMN2, CCNC, STUB1, ALS2, PRDX6, SYP, CABIN1, CASP1, GART, CDK5, ATXN3, RTN4, C1QB, VEGFC, HTT, PARK7, XDH,

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Alzheimer's Disease	Brain		GFAP, MAP2, CYCS, FCGR3B, CCS, UBL5, MMP9m SLC18A3, TRPM7, HSPB2, AKT1, DEERL1, CCL2, NGRN, GSR, TPPP3, APAF1, BTBD10, GLUD1, CXCR4, S:C1A3, FLT1, PON1, AR, LIF, ERBB3, :GA:S1, CD44, TP53, TLR3, GRIA1, GAPDH, AMPA, GRIK1, DES, CHAT, FLT4, CHMP2B, BAG1, CHRNA4, GSS, BAK1, KDR, GSTP1, OGG1, IL6 E1; CHIP; UCH; UBB; Tau; LRP; PICALM; CLU; PS1; SORL1; CR1; VLDLR; UBA1; UBA3; CHIP28; AQP1; UCHL1; UCHL3; APP, AAA, CVAP, AD1, APOE, AD2, DCP1, ACE1, MPO, PACIP1, PAXIP1L, PTIP, A2M, BLMH, BMH, PSEN1, AD3, ALAS2, ABCA1, BIN1, BDNF, BTNL8, C1ORF49, CDH4, CHRN2B, CKLFSF2, CLEC4E, CR1L, CSF3R, CST3, CYP2C, DAPK1, ESR1, FCAR, FCGR3B, FFA2, FGA, GAB2, GALP, GAPDHS, GMPB, HP, HTR7, IDE, IF127, IFI6, IFIT2, IL1RN, IL- 1RA, IL8RA, IL8RB, JAG1, KCNJ15, LRP6, MAPT, MARK4, MPHOSPH1, MTHFR, NBN, NCSTN, NIACR2, NMNAT3, NTM, ORM1, P2RY13, PBEF1, PCK1, PICALM, PLAUI, PLXNC1, PRNP, PSEN1, PSEN2, PTPRA, RALGPS2, RGS2, SELENBP1, SLC25A37, SORL1, Mitoferrin-1, TF, TFAM, TNF, TNFRSF10C, UBE1C APOA1, APP, AAA, CVAP, AD1, GSN, FGA, LYZ, TTR, PALB TTR, PALB
Amyloidosis			
Amyloid neuropathy			
Anemia	Blood		CDAN1, CDA1, RPS19, DBA, PKLR, PK1, NT5C3, UMPH1, PSN1, RHAG, RH50A, NRAMP2, SPTB, ALAS2, ANH1, ASB, ABCB7, ABC7, ASAT UBE3A
Angelman Syndrome	Nervous system, brain		
Attention Deficit Hyperactivity Disorder (ADHD)	Brain		PTCHD1
Autoimmune lymphoproliferative syndrome	Immune system		TNFRSF6, APT1, FAS, CD95, ALPS1A
Autism, Autism spectrum disorders (ASDs), including Asperger's and a general diagnostic category called Pervasive Developmental Disorders (PDDs)	Brain		PTCHD1; Mecp2; BZRAP1; MDGA2; Sema5A; Neurexin 1; GLO1, RTT, PPMX, MRX16, RX79, NLGN3, NLGN4, KIAA1260, AUTSX2, FMR1, FMR2; FXR1; FXR2; MGLUR5, ATP10C, CDH10, GRM6, MGLUR6, CDH9, CNTN4, NLGN2, CNTNAP2, SEMA5A, DHCR7, NLGN4X, NLGN4Y, DPP6, NLGN5, EN2, NRCAM, MDGA2, NRXN1, FMR2, AFF2, FOXP2, OR4M2, OXTR, FXR1, FXR2, PAH, GABRA1, PTEN, GABRA5, PTPRZ1, GABRB3, GABRG1, HIRIP3, SEZ6L2, HOXA1, SHANK3, IL6, SHBZRAP1, LAMB1, SLC6A4, SERT, MAPK3, TAS2R1, MAZ, TSC1, MDGA2, TSC2, MECP2, UBE3A, WNT2, see also 20110023145

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
autosomal dominant polycystic kidney disease (ADPKD)- (includes diseases such as von Hippel-Lindau disease and tuberosus sclerosis complex disease)	kidney	liver	PKD1, PKD2
Autosomal Recessive Polycystic Kidney Disease (ARPKD)	kidney	liver	PKDH1
Ataxia-Telangiectasia (a.k.a Louis Bar syndrome)	Nervous system, immune system	various	ATM
B-Cell Non-Hodgkin Lymphoma			BCL7A, BCL7
Bardet-Biedl syndrome	Eye, musculoskeletal system, kidney, reproductive organs	Liver, ear, gastrointestinal system, brain	ARL6, BBS1, BBS2, BBS4, BBS5, BBS7, BBS9, BBS10, BBS12, CEP290, INPP5E, LZTFL1, MKKS, MKS1, SDCCAG8, TRIM32, TTC8
Bare Lymphocyte Syndrome	blood		TAPBP, TPSN, TAP2, ABCB3, PSF2, RING11, MHC2TA, C2TA, RFX5, RFXAP, RFX5
Barter's Syndrome (types I, II, III, IVA and B, and V)	kidney		SLC12A1 (type I), KCNJ1 (type II), CLCNKB (type III), BSND (type IV A), or both the CLCNKA CLCNKB genes (type IV B), CASR (type V). DMD, BMD, MYF6
Becker muscular dystrophy	Muscle		VMD2
Best Disease (Vitelliform)	eye		
Macular Dystrophy type 2)			
Bleeding Disorders	blood		TBXA2R, P2RX1, P2X1
Blue Cone Monochromacy	eye		OPN1LW, OPN1MW, and LCR
Breast Cancer	Breast tissue		BRCA1, BRCA2, COX-2
Bruton's Disease (aka X-linked Agammaglobulinemia)	Immune system, specifically B cells		BTX
Cancers (e.g., lymphoma, chronic lymphocytic leukemia (CLL), B cell acute lymphocytic leukemia (B-ALL), acute lymphoblastic leukemia, acute myeloid leukemia, non-Hodgkin's lymphoma (NHL), diffuse large cell lymphoma (DLCL), multiple myeloma, renal cell carcinoma (RCC), neuroblastoma, colorectal cancer, breast cancer, ovarian cancer, melanoma, sarcoma, prostate cancer, lung cancer, esophageal cancer, hepatocellular carcinoma, pancreatic cancer, astrocytoma, mesothelioma, head and neck cancer, and medulloblastoma)	Various		FAS, BID, CTLA4, PDCD1, CBLB, PTPN6, TRAC, TRBC, those described in WO2015048577
Cardiovascular Diseases	heart	Vascular system	IL1B, XDH, TP53, PTGS, MB, IL4, ANGPT1, ABCG8, CTSK, PTGIR, KCNJ11, INS, CRP, PDGFRB, CCNA2, PDGFB, KCNJ5, KCNN3, CAPN10, ADRA2B, ABCG5, PRDX2, CPAN5, PARP14, MEX3C, ACE, RNF, IL6, TNF, STN, SERPINE1, ALB, ADIPOQ, APOB, APOE, LEP, MTHFR, APOA1, EDN1, NPPB, NOS3, PPARG, PLAT, PTGS2, CETP, AGTR1, HMGCR, IGF1, SELE, REN, PPARA, PON1, KNG1, CCL2, LPL, VWF, F2, ICAM1, TGFB, NPPA, IL10, EPO, SOD1, VCAM1, IFNG, LPA, MPO, ESR1, MAPK, HP, F3, CST3, COG2, MMP9, SERPINC1, F8, HMOX1, APOC3, IL8, PROL1, CBS, NOS2, TLR4, SELP, ABCA1, AGT, LDLR, GPT, VEGFA, NR3C2, IL18, NOS1, NR3C1, FGB, HGF, IL1A, AKT1, LIPC, HSPD1, MAPK14, SPP1, ITGB3, CAT, UTS2, THBD, F10, CP,

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
			TNFRSF11B, EGFR, MMP2, PLG, NPY, RHOD, MAPK8, MYC, FN1, CMA1, PLA1, GNB3, ADRB2, SOD2, F5, VDR, ALOX5, HLA- DRB1, PARP1, CD40LG, PON2, AGER, IRS1, PTGS1, ECE1, F7, IRMN, EPHX2, IGFBP1, MAPK10, FAS, ABCB1, JUN, IGFBP3, CD14, PDE5A, AGTR2, CD40, LCAT, CCR5, MMP1, TIMP1, ADM, DYT10, STAT3, MMP3, ELN, USF1, CFH, HSPA4, MMP12, MME, F2R, SELL, CTSB, ANXA5, ADRB1, CYBA, FGA, GGT1, LIPG, HIF1A, CXCR4, PROC, SCARB1, CD79A, PLTP, ADD1, FGG, SAA1, KCNH2, DPP4, NPR1, VTN, KIAA0101, FOS, TLR2, PPIG, IL1R1, AR, CYP1A1, SERPINA1, MTR, RBP4, APOA4, CDKN2A, FGF2, EDNRB, ITGA2, VLA-2, CABIN1, SHBG, HMGB1, HSP90B2P, CYP3A4, GJA1, CAV1, ESR2, LTA, GDF15, BDNF, CYP2D6, NGF, SP1, TGIF1, SRC, EGF, PIK3CG, HLA-A, KCNQ1, CNR1, FBN1, CHKA, BEST1, CTNNA1, IL2, CD36, PRKAB1, TPO, ALDH7A1, CX3CR1, TH, F9, CH1, TF, HFE, IL17A, PTEN, GSTM1, DMD, GATA4, F13A1, TTR, FABP4, PON3, APOC1, INSR, TNFRSF1B, HTR2A, CSF3, CYP2C9, TXN, CYP11B2, PTH, CSF2, KDR, PLA2G2A, THBS1, GCG, RHOA, ALDH2, TCF7L2, NFE2L2, NOTCH1, UGT1A1, IFNA1, PPARG, SIRT1, GNHR1, PAPA, ARR3, NPPC, AHSP, PTK2, IL13, MTOR, ITGB2, GSTT1, IL6ST, CPB2, CYP1A2, HNF4A, SLC64A, PLA2G6, TNFSF11, SLC8A1, F2RL1, AKR1A1, ALDH9A1, BGLAP, MTPP, MTRR, SULT1A3, RAGE, C4B, P2RY12, RNLS, CREB1, POMC, RAC1, LMNA, CD59, SCM5A, CYP1B1, MIF, MMP13, TIMP2, CYP19A1, CUP21A2, PTPN22, MYH14, MBL2, SELPLG, AOC3, CTSL1, PCNA, IGF2, ITGB1, CAST, CXCL12, IGHE, KCNE1, TFRC, COL1A1, COL1A2, IL2RB, PLA2G10, ANGPT2, PROCR, NOX4, HAMP, PTPN11, SLCA1, IL2RA, CCL5, IRF1, CF:AR, CA:CA, EIF4E, GSTP1, JAK2, CYP3A5, HSPG2, CCL3, MYD88, VIP, SOAT1, ADRBK1, NR4A2, MMP8, NPR2, GCH1, EPRS, PPARGC1A, F12, PECAM1, CCL4, CERPINA34, CASR, FABP2, TTF2, PROS1, CTF1, SGC8, YME1L1, CAMP, ZC3H12A, AKR1B1, MMP7, AHR, CSF1, HDAC9, CTGF, KCNMA1, UGT1A, PRKCA, COMT, S100B, EGR1, PRL, IL15, DRD4, CAMK2G, SLC22A2, CCL11, PGF, THPO, GP6, TACR1, NTS, HNF1A, SST, KCDN1, LOC646627, TBXA1, CUP2J2, TBXA2R, ADH1C, ALOX12, AHSG, BHMT, GJA4, SLC25A4, ACLY, ALOX5AP, NUMA1, CYP27B1, CYSLTR2, SOD3, LTC4S, UCN, GHRL, APOC2, CLEC4A,

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Cataract	eye		KBTBD10, TNC, TYMS, SHC1, LRP1, SOCS3, ADH1B, KLK3, HSD11B1, VKORC1, SERPINB2, TNS1, RNF19A, EPOR, ITGAM, PITX2, MAPK7, FCGR3A, LEEPR, ENG, GPX1, GOT2, HRH1, NR112, CRH, HTR1A, VDAC1, HPSE, SFTPD, TAP2, RMF123, PTK2Bm NTRK2, IL6R, ACHE, GLP1R, GHR, GSR, NQO1, NR5A1, GJB2, SLC9A1, MAOA, PCSK9, FCGR2A, SERPINF1, EDN3, UCP2, TFAP2A, C4BPA, SERPINF2, TYMP, ALPP, CXCR2, SLC3A3, ABCG2, ADA, JAK3, HSPA1A, FASN, FGF1, F11, ATP7A, CR1, GFPA, ROCK1, MECP2, MYLK, BCHE, LIPE, ADORA1, WRN, CXCR3, CD81, SMAD7, LAMC2, MAP3K5, CHGA, IAPP, RHO, ENPP1, PTHLH, NRG1, VEGFC, ENPEP, CEBPB, NAGLU, F2RL3, CX3CL1, BDKRB1, ADAMTS13, ELANE, ENPP2, CISH, GAST, MYOC, ATP1A2, NF1, GJB1, MEF2A, VCL, BMPR2, TUBB, CDC42, KRT18, HSF1, MYB, PRKAA2, ROCK2, TFP1, PRKG1, BMP2, CTNND1, CTH, CTSS, VAV2, NPY2R, IGFBP2, CD28, GSTA1, PPIA, APOH, S100A8, IL11, ALOX15, FBLN1, NR1H3, SCD, GIP, CHGB, PRKCB, SRD5A1, HSD11B2, CALCRL, GALNT2, ANGPTL4, KCNN4, PIK3C2A, HBEGF, CYP7A1, HLA-DRB5, BNIP3, GCKR, S100A12, PADI4, HSPA14, CXCR1, H19, KRTAP19-3, IDDM2, RAC2, YRY1, CLOCK, NGFR, DBH, CHRNA4, CACNA1C, PRKAG2, CHAT, PTGDS, NR1H2, TEK, VEGFB, MEF2C, MAPKAPK2, TNFRSF11A, HSPA9, CYSLTR1, MATIA, OPRL1, IMPA1, CLCN2, DLD, PSMA6, PSMB8, CHI3L1, ALDH1B1, PARP2, STAR, LBP, ABCC6, RGS2, EFN2, GJB6, APOA2, AMPD1, DYSF, FDFT1, EMD2, CCR6, GJB3, IL1RL1, ENTPD1, BBS4, CELSR2, F11R, RAPGEF3, HYAL1, ZNF259, ATOX1, ATF6, KHK, SAT1, GGH, TIMP4, SLC4A4, PDE2A, PDE3B, FADS1, FADS2, TMSB4X, TXNIP, LIMS1, RHOB, LY96, FOXO1, PNPLA2, TRH, GJC1, SLC17A5, FTO, GJD2, PRSC1, CASP12, GPBAR1, PXX, IL33, TRIB1, PBX4, NUPR1, 15-SEP, CILP2, TERC, GGT2, MTCO1, UOX, AVP
			CRYAA, CRYA1, CRYBB2, CRYB2, PITX3, BFSP2, CP49, CP47, CRYAA, CRYA1, PAX6, AN2, MGDA, CRYBA1, CRYB1, CRYGC, CRYG3, CCL, LIM2, MP19, CRYGD, CRYG4, BFSP2, CP49, CP47, HSF4, CTM, HSF4, CTM, MIP, AQP0, CRYAB, CRYA2, CTPP2, CRYBB1, CRYGD, CRYG4, CRYBB2, CRYB2, CRYGC, CRYG3, CCL, CRYAA, CRYA1, GJA8, CX50, CAE1, GJA3, CX46, CZP3, CAE3, CCM1, CAM, KRIT1

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
CDKL-5 Deficiencies or Mediated Diseases	Brain, CNS		CDKL5
Charcot-Marie-Tooth (CMT) disease (Types 1, 2, 3, 4,)	Nervous system	Muscles (dystrophy)	PMP22 (CMT1A and E), MPZ (CMT1B), LITAF (CMT1C), EGR2 (CMT1D), NEFL (CMT1F), GJB1 (CMT1X), MFN2 (CMT2A), KIF1B (CMT2A2B), RAB7A (CMT2B), TRPV4 (CMT2C), GARS (CMT2D), NEFL (CMT2E), GAPD1 (CMT2K), HSPB8 (CMT2L), DYNC1H1, CMT20), LRSAM1 (CMT2P), IGHMBP2 (CMT2S), MORC2 (CMT2Z), GDAP1 (CMT4A), MTMR2 or SBF2/MTMR13 (CMT4B), SH3TC2 (CMT4C), NDRG1 (CMT4D), PRX (CMT4F), FIG4 (CMT4J), NT-3
Chédiak-Higashi Syndrome	Immune system	Skin, hair, eyes, neurons	LYST
Choroideremia			CHM, REP1,
Chorioretinal atrophy	eye		PRDM13, RGR, TEAD1
Chronic Granulomatous Disease	Immune system		CYBA, CYBB, NCF1, NCF2, NCF4
Chronic Mucocutaneous Candidiasis	Immune system		AIRE, CARD9, CLEC7A IL12B, IL12B1, IL1F, IL17RA, IL17RC, RORC, STAT1, STAT3, TRAF3IP2
Cirrhosis	liver		KRT18, KRT8, CIRH1A, NAIC, TEX292, KIAA1988
Colon cancer (Familial adenomatous polyposis (FAP) and hereditary nonpolyposis colon cancer (HNPCC))	Gastrointestinal		FAP: APC HNPCC: MSH2, MLH1, PMS2, SH6, PMS1
Combined Immunodeficiency	Immune System		IL2RG, SCIDX1, SCIDX, IMD4); HIV-1 (CCL5, SCYA5, D17S136E, TCP228
Cone(-rod) dystrophy	eye		AIPL1, CRX, GUA1A, GUCY2D, PITPM3, PROM1, PRPH2, RIMS1, SEMA4A, ABCA4, ADAM9, ATF6, C21ORF2, C8ORF37, CACNA2D4, CDHR1, CERKL, CNGA3, CNGB3, CNNM4, CNAT2, IFT81, KCNV2, PDE6C, PDE6H, POC1B, RAX2, RDH5, RPGRIP1, TTLL5, RetCG1, GUCY2E
Congenital Stationary Night Blindness	eye		CABP4, CACNA1F, CACNA2D4, GNAT1, CPR179, GRK1, GRM6, LRIT3, NYX, PDE6B, RDH5, RHO, RLBP1, RPE65, SAG, SLC24A1, TRPM1, ALDOB
Congenital Fructose Intolerance	Metabolism		AGL
Cori's Disease (Glycogen Storage Disease Type III)	Various-wherever glycogen accumulates, particularly liver, heart, skeletal muscle		
Corneal clouding and dystrophy	eye		APOA1, TGFBI, CSD2, CDGG1, CSD, BIGH3, CDG2, TACSTD2, TROP2, M1S1, VSX1, RINX, PPCD, PPD, KTCN, COL8A2, FECD, PPCD2, PIP5K3, CFD
Cornea plana congenital			KERA, CNA2
Cri du chat Syndrome, also known as 5p syndrome and cat cry syndrome			Deletions involving only band 5p15.2 to the entire short arm of chromosome 5, e.g. CTNND2, TERT,
Cystic Fibrosis (CF)	Lungs and respiratory system	Pancreas, liver, digestive system, reproductive system, exocrine, glands,	CTFR, ABCC7, CF, MRP7, SCN1A, those described in WO2015157070

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Diabetic nephropathy	kidney		Gremlin, 12/15- lipoxigenase, TIM44,
Dent Disease (Types 1 and 2)	Kidney		Type 1: CLCN5, Type 2: ORCL
Dentatorubro-Pallidolusian Atrophy (DRPLA) (aka Haw River and Naito-Oyanagi Disease)	CNS, brain, muscle		Atrophin-1 and Atn1
Down Syndrome	various		Chromosome 21 trisomy
Drug Addiction	Brain		Prkce; Drd2; Drd4; ABAT; GRIA2; Grm5; Grin1; Htr1b; Grin2a; Drd3; Pdyn; Gria1
Duane syndrome (Types 1, 2, and 3, including subgroups A, B and C). Other names for this condition include: Duane's Retraction Syndrome (or DR syndrome), Eye Retraction Syndrome, Retraction Syndrome, Congenital retraction syndrome and Stilling-Turk-Duane Syndrome	eye		CHN1, indels on chromosomes 4 and 8
Duchenne muscular dystrophy (DMD)	muscle	Cardiovascular, respiratory	DMD, BMD, dystrophin gene, intron flanking exon 51 of DMD gene, exon 51 mutations in DMD gene, see also WO2013163628 and US Pat. Pub. 20130145487
Edward's Syndrome (Trisomy 18)			Complete or partial trisomy of chromosome 18
Ehlers-Danlos Syndrome (Types I-VI)	Various depending on type: including musculoskeletal, eye, vasculature, immune, and skin		COL5A1, COL5A2, COL1A1, COL3A1, TNXB, PLOD1, COL1A2, FKBP14 and ADAMTS2
Emery-Dreifuss muscular dystrophy	muscle		LMNA, LMN1, EMD2, FPLD, CMD1A, HGPS, LGMD1B, LMNA, LMN1, EMD2, FPLD, CMD1A
Enhanced S-Cone Syndrome	eye		NR2E3, NRL
Fabry's Disease	Various - including skin, eyes, and gastrointestinal system, kidney, heart, brain, nervous system		GLA
Facioscapulohumeral muscular dystrophy	muscles		FSHMD1A, FSHD1A, FRG1,
Factor H and Factor H-like 1	blood		HF1, CFH, HUS
Factor V Leiden thrombophilia and Factor V deficiency	blood		Factor V (F5)
Factor V and Factor VII deficiency	blood		MCFD2
Factor VII deficiency	blood		F7
Factor X deficiency	blood		F10
Factor XI deficiency	blood		F11
Factor XII deficiency	blood		F12, HAF
Factor XIIIa deficiency	blood		F13A1, F13A
Factor XIIIb deficiency	blood		F13B
Familial Hypercholesterolemia	Cardiovascular system		APOB, LDLR, PCSK9
Familial Mediterranean Fever (FMF) also called recurrent polyserositis or familial paroxysmal polyserositis	Various-organs/tissues with serous or synovial membranes, skin, joints	Heart, kidney, brain/CNS, reproductive organs	MEFV

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Fanconi Anemia	Various - blood (anemia), immune system, cognitive, kidneys, eyes, musculoskeletal		FANCA, FACA, FA1, FA, FAA, FAAP95, FAAP90, FLJ34064, FANCC, FANCG, RAD51, BRCA1, BRCA2, BRIP1, BACH1, FANCI, FANCB, FANCD1, FANCD2, FANCD, FAD, FANCE, FACE, FANCF, FANCI, ERCC4, FANCL, FANCM, PALB2, RAD51C, SLX4, UBE2T, FANCB, XRCC9, PHF9, KIAA1596
Fanconi Syndrome Types I (Childhood onset) and II (Adult Onset)	kidneys		FRTS1, GATM
Fragile X syndrome and related disorders	brain		FMR1, FMR2; FXR1; FXR2; mGLUR5
Fragile XE Mental Retardation (aka Martin Bell syndrome)	Brain, nervous system		FMR1
Friedreich Ataxia (FRDA)	Brain, nervous system	heart	FXN/X25
Fuchs endothelial corneal dystrophy	Eye		TCF4; COL8A2
Galactosemia	Carbohydrate metabolism disorder	Various-where galactose accumulates - liver, brain, eyes	GALT, GALK1, and GALE
Gastrointestinal Epithelial Cancer, GI cancer			CISH
Gaucher Disease (Types 1, 2, and 3, as well as other unusual forms that may not fit into these types)	Fat metabolism disorder	Various-liver, spleen, blood, CNS, skeletal system	GBA
Griselli syndrome			
Glaucoma	eye		MYOC, TIGR, GLC1A, JOAG, GPOA, OPTN, GLC1E, FIP2, HYPL, NRP, CYP1B1, GLC3A, OPA1, NTG, NPG, CYP1B1, GLC3A, those described in WO2015153780
Glomerulo sclerosis	kidney		CC chemokine ligand 2
Glycogen Storage Diseases	Metabolism		SLC2A2, GLUT2, G6PC, G6PT, G6PT1, GAA, LAMP2, LAMPB, AGL, GDE, GBE1, GYS2, PYGL, PFKM, see also Cori's Disease, Pompe's Disease, McArdle's disease, Hers Disease, and Von Gierke's disease
Types I-VI -See also Cori's Disease, Pompe's Disease, McArdle's disease, Hers Disease, and Von Gierke's disease			
RBC Glycolytic enzyme deficiency	blood		any mutations in a gene for an enzyme in the glycolysis pathway including mutations in genes for hexokinases I and II, glucokinase, phosphoglucose isomerase, phosphofructokinase, aldolase Bm triosephosphate isomerase, glyceraldehyde-3-phosphate dehydrogenase, phosphoglycerokinase, phosphoglycerate mutase, enolase I, pyruvate kinase
Hartnup's disease	Malabsorption disease	Various- brain, gastrointestinal, skin,	SLC6A19
Hearing Loss	ear		NOX3, Hes5, BDNF,
Hemochromatosis (HH)	Iron absorption regulation disease	Various- wherever iron accumulates, liver, heart, pancreas, joints, pituitary gland	HFE and H63D
Hemophagocytic lymphohistiocytosis disorders	blood		PRF1, HPLH2, UNC13D, MUNC13-4, HPLH3, HLH3, FHL3
Hemorrhagic disorders	blood		PI, ATT, F5
Hers disease (Glycogen storage disease Type VI)	liver	muscle	PYGL

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Hereditary angioedema (HAE)			kalikrein B1
Hereditary Hemorrhagic Telangiectasia (Osler-Weber-Rendu Syndrome)	Skin and mucous membranes		ACVRL1, ENG and SMAD4
Hereditary Spherocytosis	blood		NK1, EPB42, SLC4A1, SPTA1, and SPTB
Hereditary Persistence of Fetal Hemoglobin	blood		HBG1, HBG2, BCL11A, promoter region of HBG 1 and/or 2 (in the CCAAT box)
Hemophilia (hemophilia A (Classic) a B (aka Christmas disease) and C)	blood		A: FVIII, F8C, HEMA B: FVIX, HEMB, FIX C: F9, F11
Hepatic adenoma	liver		TCF1, HNF1A, MODY3
Hepatic failure, early onset, and neurologic disorder	liver		SCOD1, SCO1
Hepatic lipase deficiency	liver		LIPC
Hepatoblastoma, cancer and carcinomas	liver		CTNNB1, PDGFRL, PDGRL, PRLTS, AXIN1, AXIN, CTNNB1, TP53, P53, LFS1, IGF2R, MPRI, MET, CASP8, MCH5
Hermansky-Pudlak syndrome	Skin, eyes, blood, lung, kidneys, intestine		HPS1, HPS3, HPS4, HPS5, HPS6, HPS7, DTNBP1, BLOC1, BLOC1S2, BLOC3
HIV susceptibility or infection	Immune system		IL10, CSIF, CMKBR2, CCR2, CMKBR5, CCCR5 (CCR5), those in WO2015148670A1
Holoprosencephaly (HPE) (Alobar, Semilobar, and Lobar)	brain		ACVRL1, ENG, SMAD4
Homocystinuria	Metabolic disease	Various-connective tissue, muscles, CNS, cardiovascular system	CBS, MTHFR, MTR, MTRR, and MMADHC
HPV			HPV16 and HPV18 E6/E7
HSV1, HSV2, and related keratitis	eye		HSV-1 genes (immediate early and late HSV-1 genes (UL1, 1.5, 5, 6, 8, 9, 12, 15, 16, 18, 19, 22, 23, 26, 26.5, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 42, 48, 49.5, 50, 52, 54, S6, RL2, RS1, those described in WO2015153789, WO2015153791
Hunter's Syndrome (aka Mucopolysaccharidosis type II)	Lysosomal storage disease	Various- liver, spleen, eye, joint, heart, brain, skeletal	IDS
Huntington's disease (HD) and HD-like disorders	Brain, nervous system		HD, HTT, IT15, PRNP, PRIP, JPH3, JP3, HDL2, TBP, SCA17, PRKCE; IGF1; EP300; RCOR1; PRKCZ; HDAC4; and TGM2, and those described in WO2013130824, WO2015089354
Hurler's Syndrome (aka mucopolysaccharidosis type I H, MPS IH)	Lysosomal storage disease	Various- liver, spleen, eye, joint, heart, brain, skeletal	IDUA, α -L-iduronidase
Hurler-Scheie syndrome (aka mucopolysaccharidosis type I H-S, MPS I H-S)	Lysosomal storage disease	Various- liver, spleen, eye, joint, heart, brain, skeletal	IDUA, α -L-iduronidase
hyaluronidase deficiency (aka MPS IX)	Soft and connective tissues		HYAL1
Hyper IgM syndrome	Immune system		CD40L
Hyper-tension caused renal damage	kidney		Mineral corticoid receptor
Immunodeficiencies	Immune System		CD3E, CD3G, AICDA, AID, HIGM2, TNFRSF5, CD40, UNG, DGU, HIGM4, TNFSF5, CD40LG, HIGM1, IGM, FOXP3, IPEX, AIID, XPID, PIDX, TNFRSF14B, TAC1

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Inborn errors of metabolism: including urea cycle disorders, organic acidemias, fatty acid oxidation defects, amino acidopathies, carbohydrate disorders, mitochondrial disorders	Metabolism diseases, liver	Various organs and cells	See also: Carbohydrate metabolism disorders (e.g. galactosemia), Amino acid Metabolism disorders (e.g. phenylketonuria), Fatty acid metabolism (e.g. MCAD deficiency), Urea Cycle disorders (e.g. Citrullinemia), Organic acidemias (e.g. Maple Syrup Urine disease), Mitochondrial disorders (e.g. MELAS), peroxisomal disorders (e.g. Zellweger syndrome)
Inflammation	Various		IL-10; IL-1 (IL-1a; IL-1b); IL-13; IL-17 (IL-17a (CTLA8); IL-17b; IL-17c; IL-17d; IL-17f); IL-23; Cx3cr1; ptpn22; TNFa; NOD2/CARD15 for IBD; IL-6; IL-12 (IL-12a; IL-12b); CTLA4; Cx3cl1
Inflammatory Bowel Diseases (e.g. Ulcerative Colitis and Chron's Disease)	Gastrointestinal	Joints, skin	NOD2, IRGM, LRRK2, ATG5, ATG16L1, IRGM, GATM, ECM1, CDH1, LAMB1, HNF4A, GNA12, IL10, CARD9/15, CCR6, IL2RA, MST1, TNFSF15, REL, STAT3, IL23R, IL12B, FUT2
Interstitial renal fibrosis	kidney		TGF- β type II receptor
Job's Syndrome (aka Hyper IgE Syndrome)	Immune System		STAT3, DOCK8
Juvenile Retinoschisis	eye		RS1, XLR51
Kabuki Syndrome 1			MLL4, KMT2D
Kennedy Disease (aka Spinobulbar Muscular Atrophy)	Muscles, brain, nervous system		SBMA/SMAX1/AR
Klinefelter syndrome	Various-particularly those involved in development of male characteristics		Extra X chromosome in males
Lafora Disease	Brain, CNS		EMP2A and EMP2B
Leber Congenital Amaurosis	eye		CRB1, RP12, CORD2, CRD, CRX, IMPDH1, OTX2, APL1, CABP4, CCT2, CEP290, CLUAP1, CRB1, CRX, DTHD1, GDF6, GUCY2D, IFT140, IQCB1, KCNJ13, LCA5, LRAT, NMNAT1, PRPH2, RD3, RDH12, RPE65, RP20, RPGRIP1, SPATA7, TULP1, LCA1, LCA4, GUC2D, CORD6, LCA3,
Lesch-Nyhan Syndrome	Metabolism disease	Various - joints, cognitive, brain, nervous system	HPRT1
Leukocyte deficiencies and disorders	blood		ITGB2, CD18, LCAMB, LAD, EIF2B1, EIF2BA, EIF2B2, EIF2B3, EIF2B5, LVWM, CACH, CLE, EIF2B4
Leukemia	Blood		TAL1, TCL5, SCL, TAL2, FLT3, NBS1, NBS, ZNFN1A1, IK1, LYF1, HOXD4, HOX4B, BCR, CML, PHL, ALL, ARNT, KRAS2, RASK2, GMPS, AF10, ARHGEF12, LARG, KIAA0382, CALM, CLTH, CEBPA, CEBP, CHIC2, BTL, FLT3, KIT, PBT, LPP, NPM1, NUP214, D9S46E, CAN, CAIN, RUNX1, CBFA2, AML1, WHSC1L1, NSD3, FLT3, AF1Q, NPM1, NUMA1, ZNF145, PLZF, PML, MYL, STAT5B, AF10, CALM, CLTH, ARL11, ARLTS1, P2RX7, P2X7, BCR, CML, PHL, ALL, GRAF, NF1, VRNF, WSS,

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Limb-girdle muscular dystrophy diseases	muscle		NFNS, PTPN11, PTP2C, SHP2, NS1, BCL2, CCND1, PRAD1, BCL1, TCRA, GATA1, GF1, ERYF1, NFE1, ABL1, NQO1, DIA4, NMOR1, NUP214, D9S46E, CAN, CAIN
Lowe syndrome	brain, eyes, kidneys		LGMD
Lupus glomerulo- nephritis	kidney		OCRL
Machado-Joseph's Disease (also known as Spinocerebellar ataxia Type 3)	Brain, CNS, muscle		MAPK1
Macular degeneration	eye		ATX3
Macular Dystrophy	eye		ABC4, CBC1, CHM1, APOE, C1QTNF5, C2, C3, CCL2, CCR2, CD36, CFB, CFH, CFHR1, CFHR3, CNGB3, CP, CRP, CST3, CTSD, CX3CR1, ELOVL4, ERCC6, FBLN5, FBLN6, FSCN2, HMCN1, HIRAI, IL6, IL8, PLEKHA1, PROM1, PRPH2, RPGR, SERPING1, TCOF1, TIMP3, TLR3
Malattia Leventinese	eye		BEST1, C1QTNF5, CTNNA1, EFEMP1, ELOVL4, FSCN2, GUCA1B, HMCN1, IMPG1, OTX2, PRDM13, PROM1, PRPH2, RP1L1, TIMP3, ABCA4, CFH, DRAM2, IMG1, MFSB8, ADMD, STGD2, STGD3, RDS, RP7, PRPH, AVMD, AOFMD, VMD2
Maple Syrup Urine Disease	Metabolism disease		EFEMP1, FBLN3
Marfan syndrome	Connective tissue	Musculoskeletal	BCKDHA, BCKDHB, and DBT
Maroteaux-Lamy Syndrome (aka MPS VI)	Musculoskeletal system, nervous system	Liver, spleen	FBN1
McArdle's Disease (Glycogen Storage Disease Type V)	Glycogen storage disease	muscle	ARSB
Medullary cystic kidney disease	kidney		PYGM
Metachromatic leukodystrophy	Lysosomal storage disease	Nervous system	UMOD, HNFJ, FJHN, MCKD2, ADMCKD2
Methylmalonic acidemia (MMA)	Metabolism disease		ARSA
Morquio Syndrome (aka MPS IV A and B)	Connective tissue, skin, bone, eyes	heart	MMAA, MMAB, MUT, MMACHC, MMADHC, LMBRD1
Mucopolysaccharidosis diseases (Types I H/S, I H, II, III A B and C, I S, IVA and B, IX, VII, and VI)	Lysosomal storage disease - affects various organs/tissues		GALNS
Muscular Atrophy	muscle		See also Hurler/Scheie syndrome, Hurler disease, Sanfillipo syndrome, Scheie syndrome, Morquio syndrome, hyaluronidase deficiency, Sly syndrome, and Maroteaux-Lamy syndrome
Muscular dystrophy	muscle		VAPB, VAPC, ALS8, SMN1, SMA1, SMA2, SMA3, SMA4, BSCL2, SPG17, GARS, SMAD1, CMT2D, HEXB, IGHMBP2, SMUBP2, CATF1, SMARD1
			FKRP, MDC1C, LGMD2I, LAMA2, LAMM, LARGE, KIAA0609, MDC1D, FCMD, TTID, MYOT, CAPN3, CANP3, DYSE, LGMD2B, SGCG, LGMD2C, DMDA1, SCG3, SGCA, ADL, DAG2, LGMD2D, DMDA2, SGCB, LGMD2E, SGCD, SGD, LGMD2F, CMD1L, TCAP, LGMD2G, CMD1N, TRIM32, HT2A, LGMD2H, FKRP, MDC1C, LGMD2I, TTN, CMD1G, TMD, LGMD2J, POMT1, CAV3, LGMD1C, SEPN1, SELN, RSMD1, PLEC1, PLTN, EBS1

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Myotonic dystrophy (Type 1 and Type 2) Neoplasia	Muscles	Eyes, heart, endocrine	CNBP (Type 2) and DMPK (Type 1) PTEN; ATM; ATR; EGFR; ERBB2; ERBB3; ERBB4; Notch1; Notch2; Notch3; Notch4; AKT; AKT2; AKT3; HIF; HIF1a; HIF3a; Met; HRG; Bcl2; PPAR alpha; PPAR gamma; WT1 (Wilms Tumor); FGF Receptor Family members (5 members: 1, 2, 3, 4, 5); CDKN2a; APC; RB (retinoblastoma); MEN1; VHL; BRCA1; BRCA2; AR (Androgen Receptor); TSG101; IGF; IGF Receptor; Igf1 (4 variants); Igf2 (3 variants); Igf 1 Receptor; Igf 2 Receptor; Bax; Bcl2; caspases family (9 members: 1, 2, 3, 4, 6, 7, 8, 9, 12); Kras; Apc NF1, NF2
Neurofibromatosis (NF) (NF1, formerly Recklinghausen's NF, and NF2) Niemann-Pick Lipidosis (Types A, B, and C)	brain, spinal cord, nerves, and skin Lysosomal Storage Disease	Various- where sphingomyelin accumulates, particularly spleen, liver, blood, CNS	Types A and B: SMPD1; Type C: NPC1 or NPC2
Noonan Syndrome	Various - musculoskeletal, heart, eyes, reproductive organs, blood eye		PTPN11, SOS1, RAF1 and KRAS
Norrie Disease or X-linked Familial Exudative Vitreoretinopathy			NDP
North Carolina Macular Dystrophy	eye		MCDR1
Osteogenesis imperfecta (OI) (Types I, II, III, IV, V, VI, VII) Osteopetrosis	bones, musculoskeletal bones		COL1A1, COL1A2, CRTAP, P3H LRP5, BMND1, LRP7, LR3, OPPG, VBCH2, CLCN7, CLC7, OPTA2, OSTM1, GL, TCIRG1, TIRC7, OC116, OPTB1
Patau's Syndrome (Trisomy 13) Parkinson's disease (PD)	Brain, heart, skeletal system Brain, nervous system		Additional copy of chromosome 13 SNCA (PARK1), UCHL1 (PARK 5), and LRRK2 (PARK8), (PARK3), PARK2, PARK4, PARK7 (PARK7), PINK1 (PARK6); x-Synuclein, DJ-1, Parkin, NR4A2, NURR1, NOT, TINUR, SNCAIP, TBP, SCA17, NCAP, PRKN, PDJ, DBH, NDUFV2 RDS/peripherin PAH, PKU1, QDPR, DHPR, PTS
Pattern Dystrophy of the RPE Phenylketonuria (PKU)	eye Metabolism disorder	Various due to build-up of phenylalanine, phenyl ketones in tissues and CNS	
Polycystic kidney and hepatic disease	Kidney, liver		FCYT, PKHD1, ARPKD, PKD1, PKD2, PKD4, PKDTS, PRKCSH, G19P1, PCLD, SEC63 GAA
Pompe's Disease	Glycogen storage disease	Various - heart, liver, spleen	
Porphyria (actually refers to a group of different diseases all having a specific heme production process abnormality) posterior polymorphous corneal dystrophy	Various- wherever heme precursors accumulate eyes		ALAD, ALAS2, CPOX, FECH, HMBS, PPOX, UROD, or UROS TCF4; COL8A2

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Primary Hyperoxaluria (e.g. type 1)	Various - eyes, heart, kidneys, skeletal system		LDHA (lactate dehydrogenase A) and hydroxyacid oxidase 1 (HAO1)
Primary Open Angle Glaucoma (POAG)	eyes		MYOC
Primary sclerosing cholangitis	Liver, gallbladder		TCF4; COL8A2
Progeria (also called Hutchinson-Gilford progeria syndrome)	All		LMNA
Prader-Willi Syndrome	Musculoskeletal system, brain, reproductive and endocrine system		Deletion of region of short arm of chromosome 15, including UBE3A
Prostate Cancer	prostate		HOXB13, MSMB, GPRC6A, TP53
Pyruvate Dehydrogenase Deficiency	Brain, nervous system		PDHA1
Kidney/Renal carcinoma	kidney		RLIP76, VEGF
Rett Syndrome	Brain		MECP2, RTT, PPMX, MRX16, MRX79, CDKL5, STK9, MECP2, RTT, PPMX, MRX16, MRX79, x-Synuclein, DJ-1
Retinitis pigmentosa (RP)	eye		ADIPOR1, ABCA4, AGBL5, ARHGEF18, ARL2BP, ARL3, ARL6, BEST1, BBS1, BBS2, C2ORF71, C8ORF37, CA4, CERKL, CLRN1, CNGA1, CMGB1, CRB1, CRX, CYP4V2, DHDDS, DHX38, EMC1, EYS, FAM161A, FSCN2, GPR125, GUCA1B, HK1, HPRPF3, HGSNAT, IDH3B, IMPDH1, IMPG2, IFT140, IFT172, KLHL7, KIAA1549, KIZ, LRAT, MAK, MERTK, MVK, NEK2, NUROD1, NR2E3, NRL, OFD1, PDE6A, PDE6B, PDE6G, POMGNT1, PRCD, PROM1, PRPF3, PRPF4, PRPF6, PRPF8, PRPF31, PRPH2, RPB3, RDH12, REEP6, RP39, RGR, RHO, RLBP1, ROM1, RP1, RP1L1, RPY, RP2, RP9, RPE65, RPGR, SAMD11, SAG, SEMA4A, SLC7A14, SNRNP200, SPP2, SPATA7, TRNT1, TOPORS, TTC8, TULP1, USH2A, ZFN408, ZNF513, see also 20120204282
Scheie syndrome (also known as mucopolysaccharidosis type I S(MPS I-S))	Various- liver, spleen, eye, joint, heart, brain, skeletal		IDUA, α -L-iduronidase
Schizophrenia	Brain		Neuregulin1 (Nrg1); Erb4 (receptor for Neuregulin); Complexin1 (Cplx1); Tph1 Tryptophan hydroxylase; Tph2 Tryptophan hydroxylase 2; Neurexin 1; GSK3; GSK3a; GSK3b; 5-HTT (Slc6a4); COMT; DRD (Drd1a); SLC6A3; DAOA; DTNBP1; Dao (Dao1); TCF4; COL8A2
Secretase Related Disorders	Various		APH-1 (alpha and beta); PSEN1; NCSTN; PEN-2; Nos1, Parp1, Nat1, Nat2, CTSB, APP, APH1B, PSEN2, PSENEN, BACE1, ITM2B, CTSD, NOTCH1, TNF, INS, DYT10, ADAM17, APOE, ACE, STN, TP53, IL6, NGFR, IL1B, ACHE, CTNNA1, IGF1, IFNG, NRG1, CASP3, MAPK1, CDH1, APBB1, HMGCR, CREB1, PTGS2, HES1, CAT, TGFB1, ENO2, ERBB4, TRAPPC10, MAOB, NGF, MMP12, JAG1, CD40LG, PPARG, FGF2, LRP1, NOTCH4, MAPK8, PREP, NOTCH3, PRNP, CTSG, EGF,

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
			REN, CD44, SELP, GHR, ADCYAP1, INSR, GFAP, MMP3, MAPK10, SP1, MYC, CTSE, PPARA, JUN, TIMP1, IL5, IL1A, MMP9, HTR4, HSPG2, KRAS, CYCS, SMG1, IL1R1, PROK1, MAPK3, NTRK1, IL13, MME, TKT, CXCR2, CHRM1, ATXN1, PAWR, NOTCH2, M6PR, CYP46A1, CSNK1D, MAPK14, PRG2, PRKCA, L1 CAM, CD40, NR1H2, JAG2, CTNND1, CMA1, SORT1, DLK1, THEM4, JUP, CD46, CCL11, CAV3, RNASE3, HSPA8, CASP9, CYP3A4, CCR3, TFAP2A, SCP2, CDK4, JOF1A, TCF7L2, B3GALT1, MDM2, RELA, CASP7, IDE, FANP4, CASK, ADCYAP1R1, ATF4, PDGFA, C21ORF33, SCG5, RMF123, NKFB1, ERBB2, CAV1, MMP7, TGFA, RXRA, STX1A, PSMC4, P2RY2, TNFRSF21, DLG1, NUMBL, SPN, PLSCR1, UBQLN2, UBQLN1, PCSK7, SPON1, SILV, QPCT, HESS, GCC1
Selective IgA Deficiency	Immune system		Type 1: MSH5; Type 2: TNFRSF13B
Severe Combined Immunodeficiency (SCID) and SCID- γ I, and ADA-SCID	Immune system		JAK3, JAK1, DCLRE1C, ARTEMIS, SCID1A, RAG1, RAG2, ADA, PTPRC, CD45, LCA, IL7R, CD3D, T3D, IL2RG, SCID1, SCID2, IMD4, those identified in US Pat. App. Pub. 20110225664, 20110091441, 20100229252, 20090271881 and 20090222937;
Sickle cell disease	blood		HBB, BCL11A, BCL11Ae, cis-regulatory elements of the B-globin locus, HBG 1/2 promoter, HBG distal CCAAT box region between -92 and -130 of the HBG Transcription Start Site, those described in WO2015148863, WO 2013/126794, US Pat. Pub. 20110182867
Sly Syndrome (aka MPS VII)			GUSB
Spinocerebellar Ataxias (SCA types 1, 2, 3, 6, 7, 8, 12 and 17)			ATXN1, ATXN2, ATX3
Sorsby Fundus Dystrophy	eye		TIMP3
Stargardt disease	eye		ABCR, ELOVL4, ABCA4, PROM1
Tay-Sachs Disease	Lysosomal Storage disease	Various - CNS, brain, eye	HEX-A
Thalassemia (Alpha, Beta, Delta)	blood		HBA1, HBA2 (Alpha), HBB (Beta), HBB and HBD (delta), LCRB, BCL11A, BCL11Ae, cis-regulatory elements of the B-globin locus, HBG 1/2 promoter, those described in WO2015148860, US Pat. Pub. 20110182867, 2015/148860
Thymic Aplasia (DiGeorge Syndrome; 22q11.2 deletion syndrome)	Immune system, thymus		deletion of 30 to 40 genes in the middle of chromosome 22 at a location known as 22q11.2, including TBX1, DGCR8
Transthyretin amyloidosis (ATTR)	liver		TTR (transthyretin)
trimethylaminuria	Metabolism disease		FMO3
Trinucleotide Repeat Disorders (generally)	Various		HTT; SBMA/SMAX1/AR; FXN/X25 ATX3; ATXN1; ATXN2; DMPK; Atrophin-1 and Atn1 (DRPLA Dx); CBP (Creb-BP - global instability); VLDLR; Atxn7; Atxn10; FEN1, TNRC6A, PABPN1, JPH3, MED15, ATXN1, ATXN3, TBP, CACNA1A, ATXN80S, PPP2R2B, ATXN7, TNRC6B, TNRC6C, CELF3,

TABLE A-continued

Exemplary Genetic and Other Diseases and Associated Genes			
Disease Name	Primary Tissues or System Affected	Additional Tissues/ Systems Affected	Genes
Turner's Syndrome (XO)	Various - reproductive organs, and sex characteristics, vasculature		MAB21L1, MSH2, TMEM185A, SIX5, CNPY3, RAXE, GNB2, RPL14, ATXN8, ISR, TTR, EP400, GIGYF2, OGG1, STC1, CNDP1, C10ORF2, MAML3, DKC1, PAXIP1, CASK, MAPT, SPI, POLG, AFF2, THBS1, TP53, ESR1, CGGBP1, ABT1, KLK3, PRNP, JUN, KCNN3, BAX, FRAXA, KBTBD10, MBNL1, RAD51, NCOA3, ERDA1, TSC1, COMP, GGLC, RRAD, MSH3, DRD2, CD44, CTCF, CCND1, CLSPN, MEF2A, PTPRU, GAPDH, TRIM22, WT1, AHR, GPX1, TPMT, NDP, ARX, TYR, EGR1, UNG, NUMBL, FABP2, EN2, CRYGC, SRP14, CRYGB, PDCD1, HOXA1, ATXN2L, PMS2, GLA, CBL, FTH1, IL12RB2, OTX2, HOXA5, POLG2, DLX2, AHRR, MANF, RMEM158, see also 20110016540
Tuberous Sclerosis	CNS, heart, kidneys		Monosomy X
Usher syndrome (Types I, II, and III)	Ears, eyes		TSC1, TSC2
Velocardiofacial syndrome (aka 22q11.2 deletion syndrome, DiGeorge syndrome, conotruncal anomaly face syndrome (CTAF), autosomal dominant Opitz G/BB syndrome or Cayler cardiofacial syndrome)	Various - skeletal, heart, kidney, immune system, brain		ABHD12, CDH23, CIB2, CLRN1, DFNB31, GPR98, HARS, MYO7A, PCDH15, USH1C, USH1G, USH2A, USH11A, those described in WO2015134812A1
Von Gierke's Disease (Glycogen Storage Disease type I)	Glycogen Storage disease	Various - liver, kidney	Many genes are deleted, COM, TBX1, and other are associated with symptoms
Von Hippel-Lindau Syndrome	Various - cell growth regulation disorder	CNS, Kidney, Eye, visceral organs	G6PC and SLC37A4
Von Willebrand Disease (Types I, II and III)	blood		VHL
Wilson Disease	Various - Copper Storage Disease	Liver, brains, eyes, other tissues where copper builds up	VWF
Wiskott-Aldrich Syndrome	Immune System		ATP7B
Xeroderma Pigmentosum	Skin	Nervous system	WAS
XXX Syndrome	Endocrine, brain		POLH
			X chromosome trisomy

TABLE B

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
PI3K/AKT Signaling	PRKCE; ITGAM; ITGA5; IRAK1; PRKAA2; EIF2AK2; PTEN; EIF4E; PRKCZ; GRK6; MAPK1; TSC1; PLK1; AKT2; IKBKB; PIK3CA; CDK8; CDKN1B; NFKB2; BCL2; PIK3CB; PPP2R1A; MAPK8; BCL2L1; MAPK3; TSC2; ITGA1; KRAS; EIF4EBP1; RELA; PRKCD; NOS3; PRKAA1; MAPK9; CDK2; PPP2CA; PIM1; ITGB7; YWHAZ; ILK; TP53; RAF1; IKBKG; RELB; DYRK1A; CDKN1A; ITGB1; MAP2K2; JAK1; AKT1; JAK2; PIK3R1;

TABLE B-continued

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
ERK/MAPK Signaling	CHUK; PDPK1; PPP2R5C; CTNNB1; MAP2K1; NFKB1; PAK3; ITGB3; CCND1; GSK3A; FRAP1; SFN; ITGA2; TTK; CSNK1A1; BRAF; GSK3B; AKT3; FOXO1; SGK; HSP90AA1; RPS6KB1
Glucocorticoid Receptor Signaling	PRKCE; ITGAM; ITGA5; HSPB1; IRAK1; PRKAA2; EIF2AK2; RAC1; RAP1A; TLN1; EIF4E; ELK1; GRK6; MAPK1; RAC2; PLK1; AKT2; PIK3CA; CDK8; CREB1; PRKCI; PTK2; FOS; RPS6KAA4; PIK3CB; PPP2R1A; PIK3C3; MAPK8; MAPK3; ITGA1; ETS1; KRAS; MYCN; EIF4EBP1; PPARG; PRKCD; PRKAA1; MAPK9; SRC; CDK2; PPP2CA; PIM1; PIK3C2A; ITGB7; YWHAZ; PPP1CC; KSR1; PXN; RAF1; FYN; DYRK1A; ITGB1; MAP2K2; PAK4; PIK3R1; STAT3; PPP2R5C; MAP2K1; PAK3; ITGB3; ESR1; ITGA2; MYC; TTK; CSNK1A1; CRKL; BRAF; ATF4; PRKCA; SRF; STAT1; SGK
Axonal Guidance Signaling	RAC1; TAF4B; EP300; SMAD2; TRAF6; PCAF; ELK1; MAPK1; SMAD3; AKT2; IKBKB; NCOR2; UBE2I; PIK3CA; CREB1; FOS; HSPA5; NFKB2; BCL2; MAP3K14; STAT5B; PIK3CB; PIK3C3; MAPK8; BCL2L1; MAPK3; TSC22D3; MAPK10; NR1P1; KRAS; MAPK13; RELA; STAT5A; MAPK9; NOS2A; PBX1; NR3C1; PIK3C2A; CDKN1C; TRAF2; SERPINE1; NCOA3; MAPK14; TNF; RAF1; IKBKG; MAP3K7; CREBBP; CDKN1A; MAP2K2; JAK1; IL8; NCOA2; AKT1; JAK2; PIK3R1; CHUK; STAT3; MAP2K1; NFKB1; TGFB1; ESR1; SMAD4; CEBPB; JUN; AR; AKT3; CCL2; MMP1; STAT1; IL6; HSP90AA1
Ephrin Receptor Signaling	PRKCE; ITGAM; ROCK1; ITGA5; CXCR4; ADAM12; IGF1; RAC1; RAP1A; EIF4E; PRKCZ; NRP1; NTRK2; ARHGEF7; SMO; ROCK2; MAPK1; PGF; RAC2; PTPN11; GNAS; AKT2; PIK3CA; ERBB2; PRKCI; PTK2; CFL1; GNAQ; PIK3CB; CXCL12; PIK3C3; WNT11; PRKD1; GNB2L1; ABL1; MAPK3; ITGA1; KRAS; RHOA; PRKCD; PIK3C2A; ITGB7; GLI2; PXN; VASP; RAF1; FYN; ITGB1; MAP2K2; PAK4; ADAM17; AKT1; PIK3R1; GLI1; WNT5A; ADAM10; MAP2K1; PAK3; ITGB3; CDC42; VEGFA; ITGA2; EPHA8; CRKL; RND1; GSK3B; AKT3; PRKCA
Actin Cytoskeleton Signaling	PRKCE; ITGAM; ROCK1; ITGA5; CXCR4; IRAK1; PRKAA2; EIF2AK2; RAC1; RAP1A; GRK6; ROCK2; MAPK1; PGF; RAC2; PTPN11; GNAS; PLK1; AKT2; DOK1; CDK8; CREB1; PTK2; CFL1; GNAQ; MAP3K14; CXCL12; MAPK8; GNB2L1; ABL1; MAPK3; ITGA1; KRAS; RHOA; PRKCD; PRKAA1; MAPK9; SRC; CDK2; PIM1; ITGB7; PXN; RAF1; FYN; DYRK1A; ITGB1; MAP2K2; PAK4; AKT1; JAK2; STAT3; ADAM10; MAP2K1; PAK3; ITGB3; CDC42; VEGFA; ITGA2; EPHA8; TTK; CSNK1A1; CRKL; BRAF; PTPN13; ATF4; AKT3; SGK
Huntington's Disease Signaling	ACTN4; PRKCE; ITGAM; ROCK1; ITGA5; IRAK1; PRKAA2; EIF2AK2; RAC1; INS; ARHGEF7; GRK6; ROCK2; MAPK1; RAC2; PLK1; AKT2; PIK3CA; CDK8; PTK2; CFL1; PIK3CB; MYH9; DIAPH1; PIK3C3; MAPK8; F2R; MAPK3; SLC9A1; ITGA1; KRAS; RHOA; PRKCD; PRKAA1; MAPK9; CDK2; PIM1; PIK3C2A; ITGB7; PPP1CC; PXN; VIL2; RAF1; GSN; DYRK1A; ITGB1; MAP2K2; PAK4; PIP5K1A; PIK3R1; MAP2K1; PAK3; ITGB3; CDC42; APC; ITGA2; TTK; CSNK1A1; CRKL; BRAF; VAV3; SGK
Apoptosis Signaling	PRKCE; IGF1; EP300; RCOR1; PRKCZ; HDAC4; TGM2; MAPK1; CAPNS1; AKT2; EGFR; NCOR2; SPI1; CAPN2; PIK3CA; HDAC5; CREB1; PRKCI; HSPA5; REST; GNAQ; PIK3CB; PIK3C3; MAPK8; IGF1R; PRKD1; GNB2L1; BCL2L1; CAPN1; MAPK3; CASP8; HDAC2; HDAC7A; PRKCD; HDAC11; MAPK9; HDAC9; PIK3C2A; HDAC3; TP53; CASP9; CREBBP; AKT1; PIK3R1; PDPK1; CASP1; APAF1; FRAP1; CASP2; JUN; BAX; ATF4; AKT3; PRKCA; CLTC; SGK; HDAC6; CASP3
	PRKCE; ROCK1; BID; IRAK1; PRKAA2; EIF2AK2; BAK1; BIRC4; GRK6; MAPK1; CAPNS1; PLK1; AKT2; IKBKB; CAPN2; CDK8; FAS; NFKB2; BCL2; MAP3K14; MAPK8; BCL2L1; CAPN1; MAPK3; CASP8; KRAS; RELA; PRKCD; PRKAA1; MAPK9; CDK2; PIM1; TP53; TNF; RAF1; IKBKG; RELB; CASP9; DYRK1A; MAP2K2;

TABLE B-continued

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
B Cell Receptor Signaling	CHUK; APAF1; MAP2K1; NFKB1; PAK3; LMNA; CASP2; BIRC2; TTK; CSNK1A1; BRAF; BAX; PRKCA; SGK; CASP3; BIRC3; PARP1 RAC1; PTEN; LYN; ELK1; MAPK1; RAC2; PTPN11; AKT2; IKKBK; PIK3CA; CREB1; SYK; NFKB2; CAMK2A; MAP3K14; PIK3CB; PIK3C3; MAPK8; BCL2L1; ABL1; MAPK3; ETS1; KRAS; MAPK13; RELA; PTPN6; MAPK9; EGR1; PIK3C2A; BTK; MAPK14; RAF1; IKKBK; RELB; MAP3K7; MAP2K2; AKT1; PIK3R1; CHUK; MAP2K1; NFKB1; CDC42; GSK3A; FRAP1; BCL6; BCL10; JUN; GSK3B; ATF4; AKT3; VAV3; RPS6KB1
Leukocyte Extravasation Signaling	ACTN4; CD44; PRKCE; ITGAM; ROCK1; CXCR4; CYBA; RAC1; RAP1A; PRKCZ; ROCK2; RAC2; PTPN11; MMP14; PIK3CA; PRKCI; PTK2; PIK3CB; CXCL12; PIK3C3; MAPK8; PRKD1; ABL1; MAPK10; CYBB; MAPK13; RHOA; PRKCD; MAPK9; SRC; PIK3C2A; BTK; MAPK14; NOX1; PXN; VIL2; VASP; ITGB1; MAP2K2; CTNND1; PIK3R1; CTNNB1; CLDN1; CDC42; F11R; ITK; CRKL; VAV3; CTTN; PRKCA; MMP1; MMP9
Integrin Signaling	ACTN4; ITGAM; ROCK1; ITGA5; RAC1; PTEN; RAP1A; TLN1; ARHGEF7; MAPK1; RAC2; CAPNS1; AKT2; CAPN2; PIK3CA; PTK2; PIK3CB; PIK3C3; MAPK8; CAV1; CAPN1; ABL1; MAPK3; ITGA1; KRAS; RHOA; SRC; PIK3C2A; ITGB7; PPP1CC; ILK; PXN; VASP; RAF1; FYN; ITGB1; MAP2K2; PAK4; AKT1; PIK3R1; TNK2; MAP2K1; PAK3; ITGB3; CDC42; RND3; ITGA2; CRKL; BRAF; GSK3B; AKT3
Acute Phase Response Signaling	IRAK1; SOD2; MYD88; TRAF6; ELK1; MAPK1; PTPN11; AKT2; IKKBK; PIK3CA; FOS; NFKB2; MAP3K14; PIK3CB; MAPK8; RIPK1; MAPK3; IL6ST; KRAS; MAPK13; IL6R; RELA; SOCS1; MAPK9; FTL; NR3C1; TRAF2; SERPINE1; MAPK14; TNF; RAF1; PDK1; IKKBK; RELB; MAP3K7; MAP2K2; AKT1; JAK2; PIK3R1; CHUK; STAT3; MAP2K1; NFKB1; FRAP1; CEBPB; JUN; AKT3; IL1R1; IL6
PTEN Signaling	ITGAM; ITGA5; RAC1; PTEN; PRKCZ; BCL2L11; MAPK1; RAC2; AKT2; EGFR; IKKBK; CBL; PIK3CA; CDKN1B; PTK2; NFKB2; BCL2; PIK3CB; BCL2L1; MAPK3; ITGA1; KRAS; ITGB7; ILK; PDGFRB; INSR; RAF1; IKKBK; CASP9; CDKN1A; ITGB1; MAP2K2; AKT1; PIK3R1; CHUK; PDGFRA; PDPK1; MAP2K1; NFKB1; ITGB3; CDC42; CCND1; GSK3A; ITGA2; GSK3B; AKT3; FOXO1; CASP3; RPS6KB1
p53 Signaling Aryl Hydrocarbon Receptor Signaling	PTEN; EP300; BBC3; PCAF; FASN; BRCA1; GADD45A; BIRC5; AKT2; PIK3CA; CHEK1; TP53INP1; BCL2; PIK3CB; PIK3C3; MAPK8; THBS1; ATR; BCL2L1; E2F1; PMAIP1; CHEK2; TNFRSF10B; TP73; RB1; HDAC9; CDK2; PIK3C2A; MAPK14; TP53; LRDD; CDKN1A; HIPK2; AKT1; PIK3R1; RRM2B; APAF1; CTNNB1; SIRT1; CCND1; PRKDC; ATM; SFN; CDKN2A; JUN; SNAI2; GSK3B; BAX; AKT3 HSPB1; EP300; FASN; TGM2; RXRA; MAPK1; NQO1; NCOR2; SP1; ARNT; CDKN1B; FOS; CHEK1; SMARCA4; NFKB2; MAPK8; ALDH1A1; ATR; E2F1; MAPK3; NRIP1; CHEK2; RELA; TP73; GSTP1; RB1; SRC; CDK2; AHR; NFE2L2; NCOA3; TP53; TNF; CDKN1A; NCOA2; APAF1; NFKB1; CCND1; ATM; ESR1; CDKN2A; MYC; JUN; ESR2; BAX; IL6; CYP1B1; HSP90AA1
Xenobiotic Metabolism Signaling	PRKCE; EP300; PRKCZ; RXRA; MAPK1; NQO1; NCOR2; PIK3CA; ARNT; PRKCI; NFKB2; CAMK2A; PIK3CB; PPP2R1A; PIK3C3; MAPK8; PRKD1; ALDH1A1; MAPK3; NRIP1; KRAS; MAPK13; PRKCD; GSTP1; MAPK9; NOS2A; ABCB1; AHR; PPP2CA; FTL; NFE2L2; PIK3C2A; PPARGC1A; MAPK14; TNF; RAF1; CREBBP; MAP2K2; PIK3R1; PPP2R5C; MAP2K1; NFKB1; KEAP1; PRKCA; EIF2AK3; IL6; CYP1B1; HSP90AA1
SAPK/JNK Signaling	PRKCE; IRAK1; PRKAA2; EIF2AK2; RAC1; ELK1; GRK6; MAPK1; GADD45A; RAC2; PLK1; AKT2; PIK3CA; FADD; CDK8; PIK3CB; PIK3C3; MAPK8; RIPK1; GNB2L1; IRS1; MAPK3; MAPK10; DAXX; KRAS; PRKCD; PRKAA1; MAPK9; CDK2; PIM1; PIK3C2A; TRAF2; TP53; LCK; MAP3K7; DYRK1A; MAP2K2; PIK3R1; MAP2K1; PAK3; CDC42; JUN; TTK; CSNK1A1; CRKL; BRAF; SGK

TABLE B-continued

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
PPAr/RXR Signaling	PRKAA2; EP300; INS; SMAD2; TRAF6; PPARA; FASN; RXRA; MAPK1; SMAD3; GNAS; IKBKB; NCOR2; ABCA1; GNAQ; NFKB2; MAP3K14; STAT5B; MAPK8; IRS1; MAPK3; KRAS; RELA; PRKAA1; PPARGC1A; NCOA3; MAPK14; INSR; RAF1; IKBKG; RELB; MAP3K7; CREBBP; MAP2K2; JAK2; CHUK; MAP2K1; NFKB1; TGFB1; SMAD4; JUN; IL1R1; PRKCA; IL6; HSP90AA1; ADIPOQ
NF-KB Signaling	IRAK1; EIF2AK2; EP300; INS; MYD88; PRKCZ; TRAF6; TBK1; AKT2; EGFR; IKBKB; PIK3CA; BTRC; NFKB2; MAP3K14; PIK3CB; PIK3C3; MAPK8; RIPK1; HDAC2; KRAS; RELA; PIK3C2A; TRAF2; TLR4; PDGFRB; TNF; INSR; LCK; IKBKG; RELB; MAP3K7; CREBBP; AKT1; PIK3R1; CHUK; PDGFRA; NFKB1; TLR2; BCL10; GSK3B; AKT3; TNFAIP3; IL1R1
Neuregulin Signaling Wnt & Beta catenin Signaling	ERBB4; PRKCE; ITGAM; ITGA5; PTEN; PRKCZ; ELK1; MAPK1; PTPN11; AKT2; EGFR; ERBB2; PRKCI; CDKN1B; STAT5B; PRKD1; MAPK3; ITGA1; KRAS; PRKCD; STAT5A; SRC; ITGB7; RAF1; ITGB1; MAP2K2; ADAM17; AKT1; PIK3R1; PDPK1; MAP2K1; ITGB3; EREG; FRAP1; PSEN1; ITGA2; MYC; NRG1; CRKL; AKT3; PRKCA; HSP90AA1; RPS6KB1 CD44; EP300; LRP6; DVL3; CSNK1E; GJA1; SMO; AKT2; PIN1; CDH1; BTRC; GNAQ; MARK2; PPP2R1A; WNT11; SRC; DKK1; PPP2CA; SOX6; SFRP2; ILK; LEF1; SOX9; TP53; MAP3K7; CREBBP; TCF7L2; AKT1; PPP2R5C; WNT5A; LRP5; CTNNB1; TGFB1; CCND1; GSK3A; DVL1; APC; CDKN2A; MYC; CSNK1A1; GSK3B; AKT3; SOX2
Insulin Receptor Signaling	PTEN; INS; EIF4E; PTPN1; PRKCZ; MAPK1; TSC1; PTPN11; AKT2; CBL; PIK3CA; PRKCI; PIK3CB; PIK3C3; MAPK8; IRS1; MAPK3; TSC2; KRAS; EIF4EBP1; SLC2A4; PIK3C2A; PPP1CC; INSR; RAF1; FYN; MAP2K2; JAK1; AKT1; JAK2; PIK3R1; PDPK1; MAP2K1; GSK3A; FRAP1; CRKL; GSK3B; AKT3; FOXO1; SGK; RPS6KB1
IL-6 Signaling	HSPB1; TRAF6; MAPKAPK2; ELK1; MAPK1; PTPN11; IKBKB; FOS; NFKB2; MAP3K14; MAPK8; MAPK3; MAPK10; IL6ST; KRAS; MAPK13; IL6R; RELA; SOCS1; MAPK9; ABCB1; TRAF2; MAPK14; TNF; RAF1; IKBKG; RELB; MAP3K7; MAP2K2; IL8; JAK2; CHUK; STAT3; MAP2K1; NFKB1; CEBPB; JUN; IL1R1; SRF; IL6
Hepatic Cholestasis	PRKCE; IRAK1; INS; MYD88; PRKCZ; TRAF6; PPARA; RXRA; IKBKB; PRKCI; NFKB2; MAP3K14; MAPK8; PRKD1; MAPK10; RELA; PRKCD; MAPK9; ABCB1; TRAF2; TLR4; TNF; INSR; IKBKG; RELB; MAP3K7; IL8; CHUK; NR1H2; TJP2; NFKB1; ESR1; SREBF1; FGFR4; JUN; IL1R1; PRKCA; IL6
IGF-1 Signaling	IGF1; PRKCZ; ELK1; MAPK1; PTPN11; NEDD4; AKT2; PIK3CA; PRKCI; PTK2; FOS; PIK3CB; PIK3C3; MAPK8; IGF1R; IRS1; MAPK3; IGFBP7; KRAS; PIK3C2A; YWHAZ; PXN; RAF1; CASP9; MAP2K2; AKT1; PIK3R1; PDPK1; MAP2K1; IGFBP2; SFN; JUN; CYR61; AKT3; FOXO1; SRF; CTGF; RPS6KB1
NRF2-mediated Oxidative Stress Response	PRKCE; EP300; SOD2; PRKCZ; MAPK1; SQSTM1; NQO1; PIK3CA; PRKCI; FOS; PIK3CB; PIK3C3; MAPK8; PRKD1; MAPK3; KRAS; PRKCD; GSTP1; MAPK9; FTL; NFE2L2; PIK3C2A; MAPK14; RAF1; MAP3K7; CREBBP; MAP2K2; AKT1; PIK3R1; MAP2K1; PPIB; JUN; KEAP1; GSK3B; ATF4; PRKCA; EIF2AK3; HSP90AA1
Hepatic Fibrosis/Hepatic Stellate Cell Activation	EDN1; IGF1; KDR; FLT1; SMAD2; FGFR1; MET; PGF; SMAD3; EGFR; FAS; CSF1; NFKB2; BCL2; MYH9; IGF1R; IL6R; RELA; TLR4; PDGFRB; TNF; RELB; IL8; PDGFRA; NFKB1; TGFB1; SMAD4; VEGFA; BAX; IL1R1; CCL2; HGF; MMP1; STAT1; IL6; CTGF; MMP9
PPAR Signaling	EP300; INS; TRAF6; PPARA; RXRA; MAPK1; IKBKB; NCOR2; FOS; NFKB2; MAP3K14; STAT5B; MAPK3; NRIP1; KRAS; PPARG; RELA; STAT5A; TRAF2; PPARGC1A; PDGFRB; TNF; INSR; RAF1; IKBKG; RELB; MAP3K7; CREBBP; MAP2K2; CHUK; PDGFRA; MAP2K1; NFKB1; JUN; IL1R1; HSP90AA1

TABLE B-continued

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
Fc Epsilon RI Signaling	PRKCE; RAC1; PRKCZ; LYN; MAPK1; RAC2; PTPN11; AKT2; PIK3CA; SYK; PRKCI; PIK3CB; PIK3C3; MAPK8; PRKD1; MAPK3; MAPK10; KRAS; MAPK13; PRKCD; MAPK9; PIK3C2A; BTK; MAPK14; TNF; RAF1; FYN; MAP2K2; AKT1; PIK3R1; PDPK1; MAP2K1; AKT3; VAV3; PRKCA
G-Protein Coupled Receptor Signaling	PRKCE; RAPIA; RGS16; MAPK1; GNAS; AKT2; IKKBK; PIK3CA; CREB1; GNAQ; NFKB2; CAMK2A; PIK3CB; PIK3C3; MAPK3; KRAS; RELA; SRC; PIK3C2A; RAF1; IKKBK; RELB; FYN; MAP2K2; AKT1; PIK3R1; CHUK; PDPK1; STAT3; MAP2K1; NFKB1; BRAF; ATF4; AKT3; PRKCA
Inositol Phosphate Metabolism	PRKCE; IRAK1; PRKAA2; EIF2AK2; PTEN; GRK6; MAPK1; PLK1; AKT2; PIK3CA; CDK8; PIK3CB; PIK3C3; MAPK8; MAPK3; PRKCD; PRKAA1; MAPK9; CDK2; PIM1; PIK3C2A; DYRK1A; MAP2K2; PIP5K1A; PIK3R1; MAP2K1; PAK3; ATM; TTK; CSNK1A1; BRAF; SGK
PDGF Signaling	EIF2AK2; ELK1; ABL2; MAPK1; PIK3CA; FOS; PIK3CB; PIK3C3; MAPK8; CAV1; ABL1; MAPK3; KRAS; SRC; PIK3C2A; PDGFRB; RAF1; MAP2K2; JAK1; JAK2; PIK3R1; PDGFRA; STAT3; SPHK1; MAP2K1; MYC; JUN; CRKL; PRKCA; SRF; STAT1; SPHK2
VEGF Signaling	ACTN4; ROCK1; KDR; FLT1; ROCK2; MAPK1; PGF; AKT2; PIK3CA; ARNT; PTK2; BCL2; PIK3CB; PIK3C3; BCL2L1; MAPK3; KRAS; HIF1A; NOS3; PIK3C2A; PXN; RAF1; MAP2K2; ELAVL1; AKT1; PIK3R1; MAP2K1; SFN; VEGFA; AKT3; FOXO1; PRKCA
Natural Killer Cell Signaling	PRKCE; RAC1; PRKCZ; MAPK1; RAC2; PTPN11; KIR2DL3; AKT2; PIK3CA; SYK; PRKCI; PIK3CB; PIK3C3; PRKD1; MAPK3; KRAS; PRKCD; PTPN6; PIK3C2A; LCK; RAF1; FYN; MAP2K2; PAK4; AKT1; PIK3R1; MAP2K1; PAK3; AKT3; VAV3; PRKCA
Cell Cycle: G1/S Checkpoint Regulation	HDAC4; SMAD3; SUV39H1; HDAC5; CDKN1B; BTRC; ATR; ABL1; E2F1; HDAC2; HDAC7A; RB1; HDAC11; HDAC9; CDK2; E2F2; HDAC3; TP53; CDKN1A; CCND1; E2F4; ATM; RBL2; SMAD4; CDKN2A; MYC; NRG1; GSK3B; RBL1; HDAC6
T Cell Receptor Signaling	RAC1; ELK1; MAPK1; IKKBK; CBL; PIK3CA; FOS; NFKB2; PIK3CB; PIK3C3; MAPK8; MAPK3; KRAS; RELA; PIK3C2A; BTK; LCK; RAF1; IKKBK; RELB; FYN; MAP2K2; PIK3R1; CHUK; MAP2K1; NFKB1; ITK; BCL10; JUN; VAV3
Death Receptor Signaling	CRADD; HSPB1; BID; BIRC4; TBK1; IKKBK; FADD; FAS; NFKB2; BCL2; MAP3K14; MAPK8; RIPK1; CASP8; DAXX; TNFRSF10B; RELA; TRAF2; TNF; IKKBK; RELB; CASP9; CHUK; APAF1; NFKB1; CASP2; BIRC2; CASP3; BIRC3
FGF Signaling	RAC1; FGFR1; MET; MAPKAPK2; MAPK1; PTPN11; AKT2; PIK3CA; CREB1; PIK3CB; PIK3C3; MAPK8; MAPK3; MAPK13; PTPN6; PIK3C2A; MAPK14; RAF1; AKT1; PIK3R1; STAT3; MAP2K1; FGFR4; CRKL; ATF4; AKT3; PRKCA; HGF
GM-CSF Signaling	LYN; ELK1; MAPK1; PTPN11; AKT2; PIK3CA; CAMK2A; STAT5B; PIK3CB; PIK3C3; GNB2L1; BCL2L1; MAPK3; ETS1; KRAS; RUNX1; PIM1; PIK3C2A; RAF1; MAP2K2; AKT1; JAK2; PIK3R1; STAT3; MAP2K1; CCND1; AKT3; STAT1
Amyotrophic Lateral Sclerosis Signaling	BID; IGF1; RAC1; BIRC4; PGF; CAPNS1; CAPN2; PIK3CA; BCL2; PIK3CB; PIK3C3; BCL2L1; CAPN1; PIK3C2A; TP53; CASP9; PIK3R1; RAB5A; CASP1; APAF1; VEGFA; BIRC2; BAX; AKT3; CASP3; BIRC3
JAK/Stat Signaling	PTPN1; MAPK1; PTPN11; AKT2; PIK3CA; STAT5B; PIK3CB; PIK3C3; MAPK3; KRAS; SOCS1; STAT5A; PTPN6; PIK3C2A; RAF1; CDKN1A; MAP2K2; JAK1; AKT1; JAK2; PIK3R1; STAT3; MAP2K1; FRAP1; AKT3; STAT1
Nicotinate and Nicotinamide Metabolism	PRKCE; IRAK1; PRKAA2; EIF2AK2; GRK6; MAPK1; PLK1; AKT2; CDK8; MAPK8; MAPK3; PRKCD; PRKAA1; PBEF1; MAPK9; CDK2; PIM1; DYRK1A; MAP2K2; MAP2K1; PAK3; NT5E; TTK; CSNK1A1; BRAF; SGK
Chemokine Signaling	CXCR4; ROCK2; MAPK1; PTK2; FOS; CFL1; GNAQ; CAMK2A; CXCL12; MAPK8; MAPK3; KRAS; MAPK13; RHOA; CCR3; SRC; PPP1CC; MAPK14; NOX1; RAF1; MAP2K2; MAP2K1; JUN; CCL2; PRKCA

TABLE B-continued

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
IL-2 Signaling	ELK1; MAPK1; PTPN11; AKT2; PIK3CA; SYK; FOS; STAT5B; PIK3CB; PIK3C3; MAPK8; MAPK3; KRAS; SOCS1; STAT5A; PIK3C2A; LCK; RAF1; MAP2K2; JAK1; AKT1; PIK3R1; MAP2K1; JUN; AKT3
Synaptic Long Term Depression	PRKCE; IGF1; PRKCZ; PRDX6; LYN; MAPK1; GNAS; PRKCI; GNAQ; PPP2R1A; IGF1R; PRKD1; MAPK3; KRAS; GRN; PRKCD; NOS3; NOS2A; PPP2CA; YWHAZ; RAF1; MAP2K2; PPP2R5C; MAP2K1; PRKCA
Estrogen Receptor Signaling	TAF4B; EP300; CARM1; PCAF; MAPK1; NCOR2; SMARCA4; MAPK3; NRIP1; KRAS; SRC; NR3C1; HDAC3; PPARGC1A; RBM9; NCOA3; RAF1; CREBBP; MAP2K2; NCOA2; MAP2K1; PRKDC; ESR1; ESR2
Protein Ubiquitination Pathway	TRAF6; SMURF1; BIRC4; BRCA1; UCHL1; NEDD4; CBL; UBE2I; BTRC; HSPA5; USP7; USP10; FBXW7; USP9X; STUB1; USP22; B2M; BIRC2; PARK2; USP8; USP1; VHL; HSP90AA1; BIRC3
IL-10 Signaling	TRAF6; CCR1; ELK1; IKBKB; SP1; FOS; NFKB2; MAP3K14; MAPK8; MAPK13; RELA; MAPK14; TNF; IKBKG; RELB; MAP3K7; JAK1; CHUK; STAT3; NFKB1; JUN; IL1R1; IL6
VDR/RXR Activation	PRKCE; EP300; PRKCZ; RXRA; GADD45A; HES1; NCOR2; SP1; PRKCI; CDKN1B; PRKD1; PRKCD; RUNX2; KLF4; YY1; NCOA3; CDKN1A; NCOA2; SPP1; LRP5; CEBPB; FOXO1; PRKCA
TGF-beta Signaling	EP300; SMAD2; SMURF1; MAPK1; SMAD3; SMAD1; FOS; MAPK8; MAPK3; KRAS; MAPK9; RUNX2; SERPINE1; RAF1; MAP3K7; CREBBP; MAP2K2; MAP2K1; TGFBF1; SMAD4; JUN; SMAD5
Toll-like Receptor Signaling	IRAK1; EIF2AK2; MYD88; TRAF6; PPARA; ELK1; IKBKB; FOS; NFKB2; MAP3K14; MAPK8; MAPK13; RELA; TLR4; MAPK14; IKBKG; RELB; MAP3K7; CHUK; NFKB1; TLR2; JUN
p38 MAPK Signaling	HSPB1; IRAK1; TRAF6; MAPKAPK2; ELK1; FADD; FAS; CREB1; DDIT3; RPS6KA4; DAXX; MAPK13; TRAF2; MAPK14; TNF; MAP3K7; TGFBF1; MYC; ATF4; IL1R1; SRF; STAT1
Neurotrophin/TRK Signaling	NTRK2; MAPK1; PTPN11; PIK3CA; CREB1; FOS; PIK3CB; PIK3C3; MAPK8; MAPK3; KRAS; PIK3C2A; RAF1; MAP2K2; AKT1; PIK3R1; PDPK1; MAP2K1; CDC42; JUN; ATF4
FXR/RXR Activation	INS; PPARA; FASN; RXRA; AKT2; SDC1; MAPK8; APOB; MAPK10; PPARG; MTPP; MAPK9; PPARGC1A; TNF; CREBBP; AKT1; SREBF1; FGFR4; AKT3; FOXO1
Synaptic Long Term Potentiation	PRKCE; RAP1A; EP300; PRKCZ; MAPK1; CREB1; PRKCI; GNAQ; CAMK2A; PRKD1; MAPK3; KRAS; PRKCD; PPP1CC; RAF1; CREBBP; MAP2K2; MAP2K1; ATF4; PRKCA
Calcium Signaling	RAP1A; EP300; HDAC4; MAPK1; HDAC5; CREB1; CAMK2A; MYH9; MAPK3; HDAC2; HDAC7A; HDAC11; HDAC9; HDAC3; CREBBP; CALR; CAMKK2; ATF4; HDAC6
EGF Signaling	ELK1; MAPK1; EGFR; PIK3CA; FOS; PIK3CB; PIK3C3; MAPK8; MAPK3; PIK3C2A; RAF1; JAK1; PIK3R1; STAT3; MAP2K1; JUN; PRKCA; SRF; STAT1
Hypoxia Signaling in the Cardiovascular System	EDN1; PTEN; EP300; NQO1; UBE2I; CREB1; ARNT; HIF1A; SLC2A4; NOS3; TP53; LDHA; AKT1; ATM; VEGFA; JUN; ATF4; VHL; HSP90AA1
LPS/IL-1 Mediated Inhibition of RXR Function	IRAK1; MYD88; TRAF6; PPARA; RXRA; ABCA1; MAPK8; ALDH1A1; GSTP1; MAPK9; ABCB1; TRAF2; TLR4; TNF; MAP3K7; NR1H2; SREBF1; JUN; IL1R1
LXR/RXR Activation	FASN; RXRA; NCOR2; ABCA1; NFKB2; IRF3; RELA; NOS2A; TLR4; TNF; RELB; LDLR; NR1H2; NFKB1; SREBF1; IL1R1; CCL2; IL6; MMP9
Amyloid Processing	PRKCE; CSNK1E; MAPK1; CAPNS1; AKT2; CAPN2; CAPN1; MAPK3; MAPK13; MAPT; MAPK14; AKT1; PSEN1; CSNK1A1; GSK3B; AKT3; APP
IL-4 Signaling	AKT2; PIK3CA; PIK3CB; PIK3C3; IRS1; KRAS; SOCS1; PTPN6; NR3C1; PIK3C2A; JAK1; AKT1; JAK2; PIK3R1; FRAP1; AKT3; RPS6KB1
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	EP300; PCAF; BRCA1; GADD45A; PLK1; BTRC; CHEK1; ATR; CHEK2; YWHAZ; TP53; CDKN1A; PRKDC; ATM; SFN; CDKN2A
Nitric Oxide Signaling in the Cardiovascular System	KDR; FLT1; PGF; AKT2; PIK3CA; PIK3CB; PIK3C3; CAV1; PRKCD; NOS3; PIK3C2A; AKT1; PIK3R1; VEGFA; AKT3; HSP90AA1

TABLE B-continued

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
Purine Metabolism	NME2; SMARCA4; MYH9; RRM2; ADAR; EIF2AK4; PKM2; ENTPD1; RAD51; RRM2B; TJP2; RAD51C; NT5E; POLD1; NME1
cAMP-mediated Signaling	RAP1A; MAPK1; GNAS; CREB1; CAMK2A; MAPK3; SRC; RAF1; MAP2K2; STAT3; MAP2K1; BRAF; ATF4
Mitochondrial Dysfunction	SOD2; MAPK8; CASP8; MAPK10; MAPK9; CASP9; PARK7; PSEN1; PARK2; APP; CASP3
Notch Signaling	HES1; JAG1; NUMB; NOTCH4; ADAM17; NOTCH2; PSEN1; NOTCH3; NOTCH1; DLL4
Endoplasmic Reticulum Stress Pathway	HSPA5; MAPK8; XBP1; TRAF2; ATF6; CASP9; ATF4; EIF2AK3; CASP3
Pyrimidine Metabolism	NME2; AICDA; RRM2; EIF2AK4; ENTPD1; RRM2B; NT5E; POLD1; NME1
Parkinson's Signaling	UCHL1; MAPK8; MAPK13; MAPK14; CASP9; PARK7; PARK2; CASP3
Cardiac & Beta Adrenergic Signaling	GNAS; GNAQ; PPP2R1A; GNB2L1; PPP2CA; PPP1CC; PPP2R5C
Glycolysis/Gluconeogenesis	HK2; GCK; GPI; ALDH1A1; PKM2; LDHA; HK1
Interferon Signaling	IRF1; SOCS1; JAK1; JAK2; IFITM1; STAT1; IFIT3
Sonic Hedgehog Signaling	ARRB2; SMO; GLI2; DYRK1A; GLI1; GSK3B; DYRK1B
Glycerophospholipid Metabolism	PLD1; GRN; GPAM; YWHAZ; SPHK1; SPHK2
Phospholipid Degradation	PRDX6; PLD1; GRN; YWHAZ; SPHK1; SPHK2
Tryptophan Metabolism	SIAH2; PRMT5; NEDD4; ALDH1A1; CYP1B1; SIAH1
Lysine Degradation	SUV39H1; EHMT2; NSD1; SETD7; PPP2R5C
Nucleotide Excision Repair Pathway	ERCC5; ERCC4; XPA; XPC; ERCC1
Starch and Sucrose Metabolism	UCHL1; HK2; GCK; GPI; HK1
Aminosugars Metabolism	NQO1; HK2; GCK; HK1
Arachidonic Acid Metabolism	PRDX6; GRN; YWHAZ; CYP1B1
Circadian Rhythm Signaling	CSNK1E; CREB1; ATF4; NR1D1
Coagulation System	BDKRB1; F2R; SERPINE1; F3
Dopamine Receptor Signaling	PPP2R1A; PPP2CA; PPP1CC; PPP2R5C
Glutathione Metabolism	IDH2; GSTP1; ANPEP; IDH1
Glycerolipid Metabolism	ALDH1A1; GPAM; SPHK1; SPHK2
Linoleic Acid Metabolism	PRDX6; GRN; YWHAZ; CYP1B1
Methionine Metabolism	DNMT1; DNMT3B; AHCY; DNMT3A
Pyruvate Metabolism	GLO1; ALDH1A1; PKM2; LDHA
Arginine and Proline Metabolism	ALDH1A1; NOS3; NOS2A
Eicosanoid Signaling	PRDX6; GRN; YWHAZ
Fructose and Mannose Metabolism	HK2; GCK; HK1
Galactose Metabolism	HK2; GCK; HK1
Stilbene, Coumarine and Lignin Biosynthesis	PRDX6; PRDX1; TYR
Antigen Presentation Pathway	CALR; B2M
Biosynthesis of Steroids	NQO1; DHCR7
Butanoate Metabolism	ALDH1A1; NLGN1
Citrate Cycle	IDH2; IDH1
Fatty Acid Metabolism	ALDH1A1; CYP1B1
Glycerophospholipid Metabolism	PRDX6; CHKA
Histidine Metabolism	PRMT5; ALDH1A1
Inositol Metabolism	ERO1L; APEX1
Metabolism of Xenobiotics by Cytochrome p450	GSTP1; CYP1B1
Methane Metabolism	PRDX6; PRDX1
Phenylalanine Metabolism	PRDX6; PRDX1
Propanoate Metabolism	ALDH1A1; LDHA
Selenoamino Acid Metabolism	PRMT5; AHCY
Sphingolipid Metabolism	SPHK1; SPHK2
Aminophosphonate Metabolism	PRMT5
Androgen and Estrogen Metabolism	PRMT5
Ascorbate and Aldarate Metabolism	ALDH1A1
Bile Acid Biosynthesis	ALDH1A1
Cysteine Metabolism	LDHA
Fatty Acid Biosynthesis	FASN

Exemplary Genes controlling Cellular Functions	
CELLULAR FUNCTION	GENES
Glutamate Receptor Signaling	GNB2L1
NRF2-mediated Oxidative Stress Response	PRDX1
Pentose Phosphate Pathway	GPI
Pentose and Glucuronate Interconversions	UCHL1
Retinol Metabolism	ALDH1A1
Riboflavin Metabolism	TYR
Tyrosine Metabolism	PRMT5, TYR
Ubiquinone Biosynthesis	PRMT5
Valine, Leucine and Isoleucine Degradation	ALDH1A1
Glycine, Serine and Threonine Metabolism	CHKA
Lysine Degradation	ALDH1A1
Pain/Taste	TRPM5; TRPA1
Pain	TRPM7; TRPC5; TRPC6; TRPC1; Cnr1; cnr2; Grk2; Trpa1; Pomc; Cgrp; Crf; Pka; Era; Nr2b; TRPM5; Prkaca; Prkacb; Prkar1a; Prkar2a
Mitochondrial Function	AIF; CytC; SMAC (Diablo); Aifm-1; Aifm-2
Developmental Neurology	BMP-4; Chordin (Chrd); Noggin (Nog); WNT (Wnt2; Wnt2b; Wnt3a; Wnt4; Wnt5a; Wnt6; Wnt7b; Wnt8b; Wnt9a; Wnt9b; Wnt10a; Wnt10b; Wnt16); beta-catenin; Dkk-1; Frizzled related proteins; Otx-2; Gbx2; FGF-8; Reelin; Dab1; unc-86 (Pou4f1 or Brn3a); Numb; Reln

Thus, also described herein are methods of inducing one or more mutations in a eukaryotic or prokaryotic cell (in vitro, i.e. in an isolated eukaryotic cell) as herein discussed comprising delivering to cell a vector as described herein. The mutation(s) can include the introduction, deletion, or substitution of one or more nucleotides at a target sequence of cell(s). In some embodiments, the mutations can include the introduction, deletion, or substitution of 1-75 nucleotides at each target sequence of said cell(s). The mutations can include the introduction, deletion, or substitution of 1, 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, or 75 nucleotides at each target sequence. The mutations can include the introduction, deletion, or substitution of 5, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, or 75 nucleotides at each target sequence of said cell(s). The mutations include the introduction, deletion, or substitution of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, or 75 nucleotides at each target sequence of said cell(s). The mutations can include the introduction, deletion, or substitution of 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 35, 40, 45, 50, or 75 nucleotides at each target sequence of said cell(s). The mutations can include the introduction, deletion, or substitution of 40, 45, 50, 75, 100, 200, 300, 400 or 500 nucleotides at each target sequence of said cell(s). The mutations can include the introduction, deletion, or substitution of 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, 2800, 2900, 3000, 3100, 3200, 3300, 3400, 3500, 3600, 3700, 3800, 3900, 4000, 4100, 4200, 4300, 4400, 4500, 4600, 4700, 4800, 4900, 5000, 5100, 5200, 5300, 5400, 5500, 5600, 5700, 5800, 5900, 6000, 6100, 6200, 6300, 6400, 6500, 6600, 6700, 6800, 6900, 7000, 7100, 7200, 7300, 7400, 7500, 7600, 7700, 7800, 7900, 8000, 8100, 8200, 8300, 8400, 8500, 8600, 8700, 8800, 8900, 9000, 9100, 9200, 9300, 9400, 9500, 9600, 9700, 9800, or 9900 to 10000 nucleotides at each target sequence of said cell(s).

In some embodiments, the modifications can include the introduction, deletion, or substitution of nucleotides at each target sequence of said cell(s) via nucleic acid components (e.g. guide(s) RNA(s) or sgRNA(s)), such as those mediated by a CRISPR-Cas system.

In some embodiments, the modifications can include the introduction, deletion, or substitution of nucleotides at a target or random sequence of said cell(s) via a non CRISPR-Cas system or technique. Such techniques are discussed elsewhere herein, such as where engineered cells and methods of generating the engineered cells and organisms are discussed.

For minimization of toxicity and off-target effect when using a CRISPR-Cas system, it may be important to control the concentration of Cas mRNA and guide RNA delivered. Optimal concentrations of Cas mRNA and guide RNA can be determined by testing different concentrations in a cellular or non-human eukaryote animal model and using deep sequencing to analyze the extent of modification at potential off-target genomic loci. Alternatively, to minimize the level of toxicity and off-target effect, Cas nickase mRNA (for example *S. pyogenes* Cas9-like with the D10A mutation) can be delivered with a pair of guide RNAs targeting a site of interest. Guide sequences and strategies to minimize toxicity and off-target effects can be as in WO 2014/093622 (PCT/US2013/074667); or, via mutation as herein.

Typically, in the context of an endogenous CRISPR system, formation of a CRISPR complex (comprising a guide sequence hybridized to a target sequence and complexed with one or more Cas proteins) results in cleavage of one or both strands in or near (e.g. within 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 20, 50, or more base pairs from) the target sequence. Without wishing to be bound by theory, a tracr sequence, which may comprise or consist of all or a portion of a wild-type tracr sequence (e.g. about or more than about 20, 26, 32, 45, 48, 54, 63, 67, 85, or more nucleotides of a wild-type tracr sequence), may also form part of a CRISPR complex, such as by hybridization along at least a portion of

the tracr sequence to all or a portion of a tracr mate sequence that is operably linked to a guide sequence.

In one embodiment, the invention provides a method of modifying a target polynucleotide in a eukaryotic cell. In some embodiments, the method includes delivering an engineered cell described herein and/or an engineered AAV capsid particle described herein having a CRISPR-Cas molecule as a cargo molecule to a subject and/or cell. The CRISPR-Cas system molecule(s) delivered can complex to bind to the target polynucleotide, e.g., to effect cleavage of said target polynucleotide, thereby modifying the target polynucleotide, wherein the CRISPR complex comprises a CRISPR enzyme complexed with a guide sequence hybridized to a target sequence within said target polynucleotide, wherein said guide sequence can be linked to a tracr mate sequence which in turn hybridizes to a tracr sequence. In some embodiments, said cleavage comprises cleaving one or two strands at the location of the target sequence by said CRISPR enzyme. In some embodiments, said cleavage results in decreased transcription of a target gene. In some embodiments, the method further comprises repairing said cleaved target polynucleotide by homologous recombination with an exogenous template polynucleotide, wherein said repair results in a mutation comprising an insertion, deletion, or substitution of one or more nucleotides of said target polynucleotide. In some embodiments, said mutation results in one or more amino acid changes in a protein expressed from a gene comprising the target sequence. In some embodiments, the method further comprises delivering one or more vectors to said eukaryotic cell, wherein one or more vectors comprise the CRISPR enzyme and one or more vectors drive expression of one or more of: the guide sequence linked to the tracr mate sequence, and the tracr sequence. In some embodiments, said CRISPR enzyme drive expression of one or more of: the guide sequence linked to the tracr mate sequence, and the tracr sequence. In some embodiments such CRISPR enzyme are delivered to the eukaryotic cell in a subject. In some embodiments, said modifying takes place in said eukaryotic cell in a cell culture. In some embodiments, the method further comprises isolating said eukaryotic cell from a subject prior to said modifying. In some embodiments, the method further comprises returning said eukaryotic cell and/or cells derived therefrom to said subject. In some embodiments, the isolated cells can be returned to the subject after delivery of one or more engineered viral particles or other engineered delivery vehicles to the isolated cell. In some embodiments, the isolated cells can be returned to the subject after delivering one or more molecules of the engineered delivery system described herein to the isolated cell, thus making the isolated cells engineered cells as previously described.

Screening and Cell Selection

The engineered muscle-specific delivery system vectors, engineered cells, engineered viral particles, and/or engineered muscle-specific delivery systems described herein can be used in a screening assay and/or cell selection assay. The engineered delivery system vectors, engineered cells, and/or engineered viral particles, and/or other engineered delivery system of the present invention can be delivered to a subject and/or cell. In some embodiments, the cell is a eukaryotic cell. The cell can be in vitro, ex vivo, in situ, or in vivo. The engineered delivery system molecules, delivery vehicles, vectors, engineered cells, and/or engineered viral particles described herein can introduce an exogenous molecule or compound to subject or cell to which they are delivered. The presence of an exogenous molecule or compound can be detected which can allow for identification of

a cell and/or attribute thereof. In some embodiments, the delivered molecules or particles can impart a gene or other nucleotide modification (e.g. mutations, gene or polynucleotide insertion and/or deletion, etc.). In some embodiments the nucleotide modification can be detected in a cell by sequencing. In some embodiments, the nucleotide modification can result in a physiological and/or biological modification to the cell that results in a detectable phenotypic change in the cell, which can allow for detection, identification, and/or selection of the cell. In some embodiments, the phenotypic change can be cell death, such as embodiments where binding of a CRISPR complex to a target polynucleotide results in cell death. Embodiments of the invention allow for selection of specific cells without requiring a selection marker or a two-step process that may include a counter-selection system. The cell(s) may be prokaryotic or eukaryotic cells.

In one embodiment the invention provides for a method of selecting one or more cell(s) by introducing one or more mutations in a gene in the one or more cell(s), the method comprising: introducing one or more vectors, which can include one or more engineered delivery system molecules or vectors described elsewhere herein, into the cell(s), wherein the one or more vectors can include a CRISPR enzyme and/or drive expression of one or more of: a guide sequence linked to a tracr mate sequence, a tracr sequence, and an editing template; or other polynucleotide to be inserted into the cell and/or genome thereof; wherein, for example that which is being expressed is within and expressed in vivo by the CRISPR enzyme and/or the editing template, when included, comprises the one or more mutations that abolish CRISPR enzyme cleavage; allowing homologous recombination of the editing template with the target polynucleotide in the cell(s) to be selected; allowing a CRISPR complex to bind to a target polynucleotide to effect cleavage of the target polynucleotide within said gene, wherein the CRISPR complex comprises the CRISPR enzyme complexed with (1) the guide sequence that is hybridized to the target sequence within the target polynucleotide, and (2) the tracr mate sequence that is hybridized to the tracr sequence, wherein binding of the CRISPR complex to the target polynucleotide induces cell death, thereby allowing one or more cell(s) in which one or more mutations have been introduced to be selected. In a preferred embodiment, the CRISPR enzyme is a Cas protein. In another embodiment of the invention the cell to be selected may be a eukaryotic cell.

The screening methods involving the engineered AAV capsid system molecules, vectors, engineered cells, and/or engineered AAV capsid particles, including but not limited to those that deliver one more CRISPR-Cas system molecules to cell, can be used in detection methods such as fluorescence in situ hybridization (FISH). In some embodiments, one or more components of an engineered CRISPR-Cas system that includes a catalytically inactive Cas protein, can be delivered by an engineered delivery system molecule (such as an engineered virus particle or other engineered delivery vehicle), engineered cell, or other composition including an engineered muscle-specific targeting moiety described elsewhere herein to a cell and used in a FISH method. The CRISPR-Cas system can include an inactivated Cas protein (dCas) (e.g. a dCas9), which lacks the ability to produce DNA double-strand breaks may be fused with a marker, such as fluorescent protein, such as the enhanced green fluorescent protein (eGFP) and co-expressed with small guide RNAs to target pericentric, centric and telomeric repeats in vivo. The dCas system can be used to

visualize both repetitive sequences and individual genes in the human genome. Such new applications of labelled dCas, dCas CRISPR-Cas systems, engineered AAV delivery system molecules, engineered cells, and/or engineered delivery particles (viral or non-viral) can be used in imaging cells and studying the functional nuclear architecture, especially in cases with a small nucleus volume or complex 3-D structures. (Chen B, Gilbert L A, Cimini B A, Schnitzbauer J, Zhang W, Li G W, Park J, Blackburn E H, Weissman J S, Qi L S, Huang B. 2013. Dynamic imaging of genomic loci in living human cells by an optimized CRISPR/Cas system. *Cell* 155(7): 1479-91. doi: 10.1016/j.cell.2013.12.001., the teachings of which can be applied and/or adapted to the CRISPR systems described herein. A similar approach involving a polynucleotide fused to a marker (e.g. a fluorescent marker) can be delivered to a cell via an engineered AAV capsid system molecule, vector, engineered cell, and/or engineered AAV capsid particle described herein and integrated into the genome of the cell and/or otherwise interact with a region of the genome of a cell for FISH analysis.

Similar approaches for studying other cell organelles and other cell structures can be accomplished by delivering to the cell (e.g. via an engineered delivery AAV capsid molecule, engineered cell, and/or engineered AAV capsid particle described herein) one or more molecules fused to a marker (such as a fluorescent marker), wherein the molecules fused to the marker are capable of targeting one or more cell structures. By analyzing the presence of the markers, one can identify and/or image specific cell structures.

In some embodiments, the engineered muscle-specific delivery system molecules can be used in a screening assay inside or outside of a cell. In some embodiments, the screening assay can include delivering a CRISPR-Cas cargo molecule(s) via an engineered muscle-specific delivery particle of the present invention.

Use of the present system in screening is also provided by the present invention, e.g., gain of function screens. Cells which are artificially forced to overexpress a gene are able to down regulate the gene over time (re-establishing equilibrium) e.g. by negative feedback loops. By the time the screen starts the unregulated gene might be reduced again. Other screening assays are discussed elsewhere herein.

In an embodiment, the invention provides a cell from or of an in vitro method of delivery, wherein the method comprises contacting the delivery system with a cell, optionally a eukaryotic cell, whereby there is delivery into the cell of constituents of the delivery system, and optionally obtaining data or results from the contacting, and transmitting the data or results.

In an embodiment, the invention provides a cell from or of an in vitro method of delivery, wherein the method comprises contacting the delivery system with a cell, optionally a eukaryotic cell, whereby there is delivery into the cell of constituents of the delivery system, and optionally obtaining data or results from the contacting, and transmitting the data or results; and wherein the cell product is altered compared to the cell not contacted with the delivery system, for example altered from that which would have been wild type of the cell but for the contacting. In an embodiment, the cell product is non-human or animal. In some embodiments, the cell product is human.

In some embodiments, a host cell is transiently or non-transiently transfected with one or more vectors described herein. In some embodiments, a cell is transfected as it

naturally occurs in a subject optionally to be reintroduced therein. In some embodiments, a cell that is transfected is taken from a subject. In some embodiments, the cell obtained from or is derived from cells taken from a subject, such as a cell line. Delivery mechanisms and techniques of the engineered muscle-specific delivery system and particles thereof that are described elsewhere herein.

In some embodiments it is envisaged to introduce the engineered muscle-specific delivery system molecule(s) directly to the host cell. For instance, the engineered muscle-specific delivery system molecule(s) can be delivered together with one or more cargo molecules that are packaged into an engineered muscle-specific viral particle or contained in or coupled to a non-viral engineered muscle-specific delivery particle.

In some embodiments, the invention provides a method of expressing an engineered delivery molecule and cargo molecule to be packaged in an engineered viral particle (such as an engineered muscle-specific AAV particle) in a cell that can include the step of introducing the vector according any of the vector delivery systems disclosed herein.

The invention is further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1—mRNA Based Detection Methods are More Stringent for Selection of AAV Variants

FIG. 1 demonstrates the adeno-associated virus (AAV) transduction mechanism, which results in production of mRNA. As is demonstrated in FIG. 1, functional transduction of a cell by an AAV particle can result in the production of an mRNA strand. Non-functional transduction would not produce such a product despite the viral genome being detectable using a DNA-based assay. Thus, mRNA-based detection assays to detect transduction by e.g. an AAV can be more stringent and provide feedback as to the functionality of a virus particle that is able to functionally transduce a cell. FIG. 2 shows a graph that can demonstrate that mRNA-based selection of AAV variants can be more stringent than DNA-based selection. The virus library was expressed under the control of a CMV promoter.

Example 2—mRNA Based Detection Methods can be Used to Detect AAV Capsid Variants from a Capsid Variant Library

FIGS. 3A-3B show graphs that can demonstrate a correlation between the virus library and vector genome DNA (FIG. 3A) and mRNA (FIG. 3B) in the liver. FIGS. 4A-4F show graphs that can demonstrate capsid variants expressed at the mRNA level identified in different tissues.

Example 3—Capsid mRNA Expression can be Driven by Tissue Specific Promoters

FIGS. 5A-5C show graphs that can demonstrate capsid mRNA expression in different tissues under the control of cell-type specific promoters (as noted on x-axis). CMV was included as an exemplary constitutive promoter. CK8 is a muscle-specific promoter. MHCK7 is a muscle-specific promoter. hSyn is a neuron specific promoter.

Example 4—Capsid Variant Library Generation, Variant Screening, and Variant Identification

Generally, an AAV capsid library can be generated by expressing engineered capsid vectors each containing an

engineered AAV capsid polynucleotide previously described in an appropriate AAV producer cell line. See e.g. FIG. 8. This can generate an AAV capsid library that can contain one more desired cell-specific engineered AAV capsid variant. FIG. 7 shows a schematic demonstrating embodiments of generating an AAV capsid variant library, particularly insertion of a random n-mer (n=3-15 amino acids) into a wild-type AAV, e.g. AAV9. In this example, random 7-mers were inserted between aa588-589 of variable region VIII of AAV9 viral protein and used to form the viral genome containing vectors with one variant per vector. As shown in FIG. 8, the capsid variant vector library was used to generate AAV particles where each capsid variant encapsulated its coding sequence as the vector genome. FIG. 9 shows vector maps of representative AAV capsid plasmid library vectors (see e.g. FIG. 8) that can be used in an AAV vector system to generate an AAV capsid variant library. The library can be generated with the capsid variant polynucleotide under the control of a tissue specific promoter or constitutive promoter. The library was also made with capsid variant polynucleotide that included a polyadenylation signal.

As shown in FIG. 6 the AAV capsid library can be administered to various non-human animals for a first round of mRNA-based selection. As shown in FIG. 1, the transduction process by AAVs and related vectors can result in the production of an mRNA molecule that is reflective of the genome of the virus that transduced the cell. As is at least demonstrated in the Examples herein, mRNA based-selection can be more specific and effective to determine a virus particle capable of functionally transducing a cell because it is based on the functional product produced as opposed to just detecting the presence of a virus particle in the cell by measuring the presence of viral DNA.

After first-round administration, one or more engineered AAV virus particles having a desired capsid variant can then be used to form a filtered AAV capsid library. Desirable AAV virus particles can be identified by measuring the mRNA expression of the capsid variants and determining which variants are highly expressed in the desired cell type(s) as compared to non-desired cells type(s). Those that are highly expressed in the desired cell, tissue, and/or organ type are the desired AAV capsid variant particles. In some embodiments, the AAV capsid variant encoding polynucleotide is under control of a tissue-specific promoter that has selective activity in the desired cell, tissue, or organ.

The engineered AAV capsid variant particles identified from the first round can then be administered to various non-human animals. In some embodiments, the animals used in the second round of selection and identification are not the same as those animals used for first round selection and identification. Similar to round 1, after administration the top expressing variants in the desired cell, tissue, and/or organ type(s) can be identified by measuring viral mRNA expression in the cells. The top variants identified after round two can then be optionally barcoded and optionally pooled. In some embodiments, top variants from the second round can then be administered to a non-human primate to identify the top cell-specific variant(s), particularly if the end use for the top variant is in humans. Administration at each round can be systemic.

FIG. 10 shows a graph that can demonstrate the viral titer (calculated as AAV9 vector genome/15 cm dish) produced by libraries generated using different promoters. As demonstrated in FIG. 10, virus titer was not affected significantly by the use of different promoters.

FIGS. 11A-11F show graphs that can demonstrate the results obtained after the first round of selection in C57BL/6

mice using a capsid library expressed under the control of the MHCK7 muscle-specific promoter.

FIGS. 12A-12D show graphs that can demonstrate the results obtained after the second round of selection in C57BL/6 mice.

FIGS. 13A-13B shows graphs that can demonstrate a correlation between the abundance of variants encoded by synonymous codons. This graph can demonstrate that there is little to no codon bias in both the virus library and the functional virus particles.

FIG. 14 shows a graph that can demonstrate a correlation between the abundance of the same variants expressed under the control of two different muscle specific promoters (MHCK7 and CK8). This graph can demonstrate that there is little effect of which tissue-specific promoter is used to generate the capsid variant library, at least for muscle cells.

Example 5—Muscle-Tropic rAAV Capsids

FIG. 15 shows a graph that can demonstrate muscle-tropic capsid variants that produce rAAV with similar titers to wild-type AAV9 capsid.

FIG. 16 shows images that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 17 shows a panel of images that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 18 shows a panel of images that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 19 shows a schematic of selection of potent capsid variants for muscle-directed gene delivery across species.

FIGS. 20A-20C show tables that can demonstrate selection in different strains of mice identifies the same variants as the top muscle-tropic hits.

Example 6—Comparison of MyoAAV and AAV9 and AAV8

As previously discussed, FIG. 17 can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 21 shows images that can demonstrate a comparison of mouse muscle transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 22 shows graphs that can demonstrate a comparison of mouse tissue transduction between rAAV9-GFP and rMyoAAV-GFP.

FIG. 23 shows graphs that can demonstrate a comparison of vector genome biodistribution between rAAV9-GFP and rMyoAAV-GFP.

FIGS. 24A-24B show images that can demonstrate faster kinetics of in vivo gene expression in muscle by MyoAAV as compared to AAV9 and AAV8.

FIG. 25 can demonstrate a mechanism of correction of a DMD mutation in model mdx mice by MyoAAV-CRISPR or AAV9-CRISPR.

FIGS. 26A-26C can demonstrate correction of a DMD mutation in model mdx mice with MyoAAV-CRISPR as compared to AAV9-CRISPR.

FIG. 27 can demonstrate that MyoAAV uses integrin heterodimers as the receptor to enter cells.

FIG. 28 shows graphs that can demonstrate that myoAAV can transduce both mouse and human primary myotubes more effectively than AAV9.

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FIGS. 29A-29B can demonstrate that integrin alpha V small molecule inhibitors suppress transduction of human and mouse primary myotubes by MyoAAV.

Example 7-Top n-Mer Motifs in Non-Human Primates

Muscle specific AAV capsids were developed using a muscle specific promoter and the resulting capsid libraries were screened in non-human primates as described elsewhere herein and/or in U.S. Provisional Application Ser. Nos. 62/899,453, 62/916,207, 63/018,454, 63/055,252, and 62/916,221 and International Application No. PCT/US20/50534. Tables 8 and 9 show the top hits of muscle specific n-mer motifs and their encoding sequence in rank order within each table.

TABLE 8

N-Mer Motif	SEQ ID NO:	Encoding Sequence	score	SEQ ID NO:
RGDYHAI	8314	AGGGGCGACTACCAAGCCATC	4178	8503
RGDYASL	8315	CGGGGCGACTACGCAAGCCTG	3851	8504
RGDYVGL	8316	CGGGGTGATTATGTGGGCTG	3686	8505
RGDLRPT	8317	CGTGGGATCTTAGGCCGACG	3610	8506
RGDHVSL	8318	CGTGGGATCATGTGTCTTTG	3050	8507
DVRSLHG	8319	GACGTTAGATCCCTTCACGGC	2985	8508
RGDYHAI	8320	CGTGGTGATTATCATGCTATT	2944	8509
RGDYGGL	8321	CGTGGTGATTATGGTGGCTG	2816	8510
RGDHGVL	8322	CGGGGTGATCATGGGGTTCTT	2692	8511
RGDYREL	8323	AGAGGAGACTACCGGAACTC	2690	8512
VSRGDVP	8324	GTTAGTCGGGTGATGTGCCT	2675	8513
RGDYVGL	8325	CGCGGGGACTACGTAGGTTTA	2666	8514
RGDYSGL	8326	CGGGGTGATTATTCGGGGTTG	2642	8515
RGDLTVT	8327	AGGGGGGACCTGACAGTCACG	2604	8516
RGDHASW	8328	CGTGGTGATCATGCTTCTTGG	2603	8517
RGDLVGY	8329	AGGGGGGATCTTGTGGGGTAT	2543	8518
RGDGAAM	8330	CGTGGGATGGTGCGGCGATG	2439	8519
VSAARSL	8331	GTGAGTGCGGCGCTTCTCTG	2437	8520
LTAQYVT	8332	TTGACTGCTCAGTATGTGACG	2430	8521
RGDHGVL	8333	CGCGGAGACCACGGTGTATTA	2429	8522
VGNRFSP	8334	GTTGGGAATAGGTTTTCGCCG	2410	8523
TGVHTRV	8335	ACGGGTGTTTCATACGAGGGTG	2405	8524
VRTGDAS	8336	GTGCGTACTGGTGATGCGTCG	2401	8525
MVVRGGV	8337	ATGGTGGTGCCTGGGGGTGTT	2393	8526
RGDRESH	8338	CGCGGAGACCAGAAAGCCAC	2370	8527
RGDYSGL	8339	CGTGGCGACTACTCTGTGCTA	2306	8528
RGDLSSV	8340	CGGGGTGATCTTTCGAGTGTT	2292	8529
LLGQRAA	8341	CTGCTTGCTCAGAGGGCTGCT	2269	8530

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TABLE 8-continued

N-Mer Motif	SEQ ID NO:	Encoding Sequence	score	SEQ ID NO:
GKGTVPS	8342	GGGAAGGGGACTGTGCCGAGT	2262	8531
SSIGVKI	8343	TCGTCGATTGGTGTGAAGATT	2256	8532
ANKGLGT	8344	GCAAACAAAGCCCTGGGCACG	2246	8533
RGDHASW	8345	CGGGGGGATCATGCTTCTTGG	2245	8534
RGDRLVI	8346	AGAGGAGACAGGCTGTGCATC	2219	8535
GQGHRRG	8347	GGACAAGGCCACCGGGGAGAC	2215	8536
ERTRAGE	8348	GAGAGGACTCGGGCGGGTGAG	2209	8537
RGDLSGT	8349	AGGGGCGACCTGTCTGGCACC	2203	8538
RGDYREM	8350	CGGGGGGATTATCGTGAGATG	2201	8539
RGDLAHN	8351	AGGGGTGATCTTGCGCATAAT	2183	8540
GFSGRTV	8352	GGGTTTAGTGGGAGGACGGTG	2183	8541
VMRAGAT	8353	GTTATGCGAGCAGGTGCGACG	2173	8542
EGGIYRV	8354	GAAGGAGGAATCTACCGTGTT	2168	8543
RGDYREL	8355	CGTGGTGATTATCGTGAGTTG	2168	8544
QSVSIKS	8356	CAGAGTGTGTCTATTAAGTCT	2167	8545
RGDLVHV	8357	CGAGGAGACTTGGTCCACGTC	2161	8546
YRGDIRV	8358	TACCGTGGTGACATACGGGTG	2156	8547
RGDASTW	8359	CGTGGGACGCCAGTACCTGG	2148	8548
RGDYGGI	8360	CGTGGGGATTATGGTGGTATT	2146	8549
VGTRGDT	8361	GTGGGTACGCGGGGGATACG	2146	8550
RGDLTTV	8362	CGGGGGGATCTGACGACTGTT	2133	8551
RGDMRPV	8363	CGTGGTGATATGCGTCCGGTT	2126	8552
AAGRLTT	8364	GCTGCTGGTAGGCCTACGACG	2125	8553
NAGRSTL	8365	AACGCAGGGCGCTCTACCTTA	2108	8554
ERDRISG	8366	GAGCGGGATCGGATTTCCGGT	2091	8555
RGDLTTT	8367	CGGGGTGACCTGACAACCACG	2082	8556
TTGLRLA	8368	ACGACTGGGCTTCGTCTGGCT	2082	8557
RGDHSGW	8369	CGTGGTGATCATAGTGGTTGG	2080	8558
SGGTYLA	8370	AGCGGGGGAACGTACCTTGCC	2078	8559
AVVRGGP	8371	GCTGTTGTGCGGGGTGGTCCT	2064	8560
IVRGLSD	8372	ATTGTGAGGGGTCTGAGTGAT	2054	8561
RGDTMRL	8373	CGCGGAGACACGATGAGACTG	2054	8562
TRVPVSG	8374	ACGCGAGTACCGGTGAGCGGG	2052	8563
RTYDSNV	8375	CGAACGTACGACTCAAACGTA	2052	8564
RGDRMGV	8376	CGGGGTGATCGTAITGGGTGTG	2043	8565
QLNAYSG	8377	CAGTTGAATGCGTATAGTGGG	2042	8566
SLGITSG	8378	TCATTGGGTATAACCTCGGGC	2040	8567
TAAVRTY	8379	ACGGCTGCGGTGCGTACGTAT	2031	8568

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TABLE 8-continued

N-Mer Motif	SEQ ID NO: Encoding Sequence	score	SEQ ID NO:
RGDLTTT	8380 CGTGGGGATCTTACTACGACT	2031	8569
RGDYATF	8381 CGGGGTGATTATGCTACTTTT	2028	8570
RGDIVGL	8382 AGGGGTGACATAGTGGGCCTC	2027	8571
GSRGDLs	8383 GGTAAGTCGTGGCGACTTATCG	2027	8572
RGDVTHI	8384 AGAGGAGACGTTACGCACATC	2024	8573
IGGTRVQ	8385 ATTGGTGGGACTCGGGTGCAG	2023	8574
ENHTHRA	8386 GAGAATCATACTCATAGGGCT	2023	8575
RGDLTYA	8387 CGTGGTGATCTGACGTATGCT	2022	8576
LLHESRV	8388 TTGTGTCATGAGTCGCGGGT	2021	8577
RGDVSGI	8389 CGTGGTGATGTTAGTGGGATT	2018	8578
LNSAMRT	8390 CTGAATTCTGCGATGCGTACT	2015	8579
RGDYATL	8391 AGGGGGGACTACGCCACACTG	2010	8580
SANVVRG	8392 TCTGCGAATGTTGTGAGGGGG	2010	8581
VAGQRSV	8393 GTTGCTGGGCAGCGTTCTGTT	2008	8582
RGDREHF	8394 CGTGGTGATAGGGAGCATTTT	2007	8583
RGDYVTI	8395 CGCGGAGACTACGTTACAATA	1999	8584
RLVSTAP	8396 CGTCTTGTTCGACTGCTCCG	1998	8585
HQSFHGA	8397 CACCAATCATCCACGCGCA	1996	8586
VRGDSRF	8398 GTAAGGGGCGACAGCAGATTC	1991	8587
RGDFGGV	8399 AGGGGTGACTTCGGAGGTGTC	1990	8588
LVRTTVS	8400 CTTGTGCAAGTACAGTGTC	1989	8589
RGDYVSV	8401 CGTGGGATTATGTGTCTGTG	1989	8590
RGDYASL	8402 AGGGGTGATTATGCGTCTCTT	1983	8591
IVRDGRL	8403 ATCGTCCGAGACGGAAGACTT	1978	8592
LTHGMIG	8404 CTGACGCATGGTATGATTGGT	1973	8593
RGDVRVI	8405 CGAGGCGACGTTCCGGGCATA	1964	8594
KAQPSSS	8406 AAGGCTCAGCCGTCTTCGTCT	1964	8595
GMRGASV	8407 GGGATGAGGGGTGCTTCGGTG	1961	8596
AAGRVGT	8408 GCTGCGGTTAGGTTGGGACG	1955	8597
QMGRVQV	8409 CAGATGGGTGCGGTTACGGTG	1954	8598
LMSRGDT	8410 TTGATGTCGCGGGTGATACT	1953	8599
VHSRGDM	8411 GTCCACTCTCGCGGAGACATG	1952	8600
RGDLVTV	8412 CGGGGGATCTGTTACGGTT	1952	8601
RNYGDHS	8413 AGAAACTACGGCGACCACTCG	1951	8602
RGDYSQI	8414 AGAGGCGACTACAGCCAAATA	1950	8603
RGDLANS	8415 AGGGGTGATTGGCTAATTCT	1945	8604
RSSHLDV	8416 CGTTCAGTCACCTTGACGTT	1940	8605
RSQTVGL	8417 CGCTCCGGGACCGTTGGACTG	1939	8606

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TABLE 8-continued

N-Mer Motif	SEQ ID NO: Encoding Sequence	score	SEQ ID NO:
IGARGDT	8418 ATAGGAGCGAGGGGGACACG	1938	8607
SNAPVPT	8419 TCGAATGCGGTTCTCTGGTACT	1935	8608
LDARGHL	8420 TTGGATGCTAGGGGGCATCTG	1930	8609
TSVSVKY	8421 ACTTCTGTGTCGGTGAAGTAT	1928	8610
TRVMGAT	8422 ACGCGGGTGATGGGGGCGACT	1920	8611
RGGTGVN	8423 CGAGGCGGGACTGGAGTAAAC	1919	8612
VASRTSV	8424 GTGGCTAGTCGTACGTCTGTT	1918	8613
RGDRLQI	8425 CGTGGTGATCGGCTTCAGATT	1917	8614
RGDYERL	8426 CGCGGTGACTACGAACGACTA	1916	8615
LAALKALV	8427 CTTGCGGCTAAGGCTCTGGTT	1915	8616
LGTTTSAS	8428 CTGGGGACGACTTCTGCGTCG	1914	8617
RGDHGTI	8429 CGTGGGGATCATGGGACGATT	1914	8618
GLRVVQA	8430 GGACTCCGAGTAGTCCAAGCC	1913	8619
RQTVGMG	8431 CGTCAGACTGTGGGGATGGGT	1909	8620
RGDLLTN	8432 AGGGGGATCTGTTGACGAAT	1905	8621
YGHGMVG	8433 TACGGACACGGCATGGTCGGG	1904	8622
VVAALRG	8434 GTTGTTGCTGCTCTTCGGGGT	1904	8623
QLSRSGT	8435 CAGTTGTCGAGGAGTGATACG	1902	8624
GLSRTGV	8436 GGTCTTTCGAGGACGGGGGTG	1902	8625
MGGRLT	8437 ATGGGTGGTGGTCTCTTACT	1896	8626
RGDLVMV	8438 AGAGGCGACTTAGTGATGGTG	1896	8627
RGDVVGL	8439 AGGGGTGACGTCGTAGGCCTG	1888	8628
VTKVGV	8440 GTGACGAAGGTTGGGGTGCTG	1887	8629
RTSYPEA	8441 CGCACCTCATACCTGAAGCC	1887	8630
ESRATMS	8442 GAATCGCGGGCAACGATGTCT	1885	8631
SRVGVGA	8443 AGTCGGGTGGGTGTTGGTGCG	1883	8632
RGDYVTM	8444 CGAGGCGACTACGTGACTATG	1880	8633
RAQGPQA	8445 AGGGCTCAGGGTCCTCAGGCG	1878	8634
VTSHAMA	8446 GTCACATCCCACGCCATGGCC	1877	8635
RGDLGGV	8447 CGAGGGGACTTAGCGCGCTC	1873	8636
SIRGELG	8448 AGTATTCTGGTGAGCTGGGT	1867	8637
RGDGSAL	8449 CGTGGTGATGGGAGTGCTCTT	1863	8638
SRSGIAI	8450 TCTAGGAGTGGTATTGCGATT	1860	8639
QAGTLGY	8451 CAGGCGGGGACGCTTGGGTAT	1860	8640
RGDLTTA	8452 AGGGGTGATCTTACGACTGCG	1859	8641
LGHRGDV	8453 CTTGGTCATCGGGTGATGTT	1859	8642
RGDLTIT	8454 AGAGGCGACCTGACCATCACA	1856	8643
RGDLRVP	8455 CGTGGGGATCTTCGGGTGCCT	1856	8644

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TABLE 8-continued

N-Mer Motif	SEQ ID NO: Encoding Sequence	score	SEQ ID NO:
NSDHRIL	8456 AACTCGGACCACCGCATACTC	1852	8645
RGDYHSF	8457 CGTGAGACTACCACTCATTC	1851	8646
GTGRYVS	8458 GGGACAGGTCGATACGTGAGC	1851	8647
PLLRSGT	8459 CCGTTGTTGAGGAGTGGGACG	1849	8648
RGDVVSW	8460 CGTGAGACGTCGTAAGTTGG	1849	8649
VMRVGHA	8461 GTGATGCGTGTGGGGCATGCT	1848	8650
RGDLVSV	8462 AGGGGGGATCTGGTGTCTGTT	1847	8651
RGDLTGV	8463 CGGGGTGATTTGACGGGGGTG	1845	8652
VSSTKMA	8464 GTGTCGTCTACGAAGATGGCT	1844	8653
RGDHTQW	8465 CGCGGAGACCACACGCAATGG	1843	8654
VVRGVTD	8466 GTAGTTAGAGGTGTGACCGAC	1842	8655
VQVAVQR	8467 GTTCAGGTTGCGGTGCAGAGG	1838	8656
RTVTAVE	8468 CGTACTGTGACGGCGGTGGAG	1838	8657
RTQLGMA	8469 CGAACTCAATTAGGAATGGCG	1835	8658
GGSVRGS	8470 GGGGGTTCGGTGAGGGGTTTCG	1835	8659
RGDHSSL	8471 AGGGGGGATCATTCTAGTCTG	1834	8660
LAGTSGA	8472 CTTGCTGGGACTAGTGGGGCG	1831	8661
LRTGTLS	8473 CTTAGGACTGGGACTTTGAGT	1830	8662
WKAQVQA	8474 TGAAAGCCCAAGTTCAAGCT	1827	8663
NSTALRG	8475 AATTCTACGGCTCTTCGTGGG	1825	8664
DGGRMAY	8476 GACGGTGGGCGAATGGCTTAC	1825	8665
TRTPSPA	8477 ACAAGAACACCTTCTCCCGCT	1824	8666
STVARGD	8478 TCAACGGTCGCAAGGGGGGAC	1823	8667
RAGTAMS	8479 AGGGCTGGCACGGCCATGAGT	1822	8668
RGDRESH	8480 AGGGGGGATCGTGAGAGTCAT	1820	8669
LSRSGEL	8481 CTGAGTCGGAGTGGTGAGCTG	1819	8670
TAGRVQV	8482 ACTGCTGGGCGTGTTCAAGTG	1813	8671
VTTRGDV	8483 GTGACGACTCGTGGTGATGTG	1809	8672
VMRAGTS	8484 GTTATGCGTGCAGGGGACTAGT	1809	8673
LSRSGDL	8485 TTGTCTCGGAGTGGTGATCTT	1808	8674
GYGHDRS	8486 GGTATGGTCATGATCGGAGT	1807	8675
HAYKTSP	8487 CATGCTTATAAGACGTCTCCT	1804	8676
SPGKSGG	8488 AGTCCGGTAAGTCTGGGGGT	1802	8677
SAGKTVV	8489 TCGCGGGGAAGACGGTTGTT	1799	8678
VRGQQND	8490 GTGAGGGGGCAGCAGAATGAT	1799	8679
AVTRGGF	8491 GCTGTGACTAGGGGTGGTTTT	1796	8680
RGDLYTP	8492 AGGGGTGATCTTTATACGCCG	1796	8681
RAGTAIT	8493 CGTGGGGTACTGCTATTACT	1796	8682

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TABLE 8-continued

N-Mer Motif	SEQ ID NO: Encoding Sequence	score	SEQ ID NO:
SLVRAAA	8494 TCGTTGGTTCGTGCTGCTGCT	1795	8683
VVRGDVG	8495 GTCGTCCGAGGCGACGTCGGC	1793	8684
RGDLSGT	8496 CGTGGTGATCTTTCGGGTACG	1792	8685
RYGATGT	8497 AGGTATGGTGCTACGGGGACT	1787	8686
PGLRGVA	8498 CCTGGTCTGAGGGGGTTGCG	1782	8687
IPMRGQM	8499 ATTCCGATGAGGGGTCAGATG	1781	8688
SAGRSQG	8500 AGTGCTGGTCGTAGTCAGGGG	1779	8689
VRGVGTA	8501 GTTCGGGGGTTGGTACGGCT	1778	8690
RGDYVSV	8502 CGGGGAGACTACGTCAGTGTC	1777	8691

TABLE 9

N-mer Rank motif	SEQ ID NO: Encoding sequence	SEQ ID NO:
1 RGDYVGL	8692 CGGGGTGATTATGTGGGGCTG	8890
2 RGDYSSV	8693 CGGGGTGATTATTCGAGTGTT	8891
3 RGDYSGL	8694 CGGGGTGATTATTCGGGGTTG	8892
4 RGDHERL	8695 CGTGGTGATCATGAGCGTTTG	8893
5 RGDLTVT	8696 AGGGGGGACCTGACAGTCACG	8894
6 RGDYHAI	8697 AGGGGCGACTACCACGCCATC	8895
7 RGDYREL	8698 AGAGGAGACTACCGGGAATC	8896
8 RGDHGV L	8699 CGGGGTGATCATGGGGTTCTT	8897
9 RGDHASW	8700 CGTGGTGATCATGCTTCTTGG	8898
10 RGDYSGL	8701 CGTGGCGACTACTCTGGTCTA	8899
11 RGDAMHL	8702 CGTGGGGATGCGATGCATCTG	8900
12 RGDHVSL	8703 CGTGGGGATCATGTGTCTTTG	8901
13 RGDHGQL	8704 CGGGGGGATCATGGGCAGTTG	8902
14 RGDYGGL	8705 CGTGGTGATTATGGTGGGCTG	8903
15 RGDYVTM	8706 CGAGGCGACTACGTGACTATG	8904
16 RGDHSTW	8707 CGCGGGGACCACTCTACCTGG	8905
17 RGDLSGT	8708 AGGGGCGACCTGTCTGGCACC	8906
18 RGDYREM	8709 CGGGGGGATTATCGTGAGATG	8907
19 RGDTERL	8710 AGAGGGGACACCGAAAGATTG	8908
20 RGDHSTW	8711 CGGGGTGATCATAGTACTTGG	8909
21 RGDLSGT	8712 CGTGGTGATCTTTCGGGTACG	8910
22 RGDHASW	8713 CGGGGGGATCATGCTTCTTGG	8911
23 RGDLSV	8714 CGGGGTGATCTTTCGAGTGTT	8912
24 RGDTVVL	8715 CGAGGAGACACGGTGGTCCTA	8913
25 RGDAAGL	8716 CGTGGGGACGCGGCTGGGTTG	8914

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TABLE 9-continued

N-mer Rank motif	SEQ ID NO:	Encoding sequence	SEQ ID NO:
26 RGDGATL	8717	CGGGGTGATGGTGC GACTCTG	8915
27 RGDYASL	8718	AGGGGTGATTATGCGTCTCTT	8916
28 MTARNPM	8719	ATGACTGCTCGGAATCCGATG	8917
29 YVVGSR	8720	TATGTGGTGGGAGTAGGAGT	8918
30 YAVGSR	8721	TATGCGGTGGGAGTAGGAGT	8919
31 RGDYVGL	8722	CGCGGGGACTACGTAGGTTTA	8920
32 RGDLT	8723	CGGGGTGACCTGACAACCACG	8921
33 RGDYERL	8724	CGCGGTGACTACGAACGACTA	8922
34 RGDYREL	8725	CGTGGTGATTATCGTGAGTTG	8923
35 RGDHGV	8726	CGCGGAGACCACGGTGATTA	8924
36 RGDYHAI	8727	CGTGGTGATTATCATGCTATT	8925
37 RGDHTQW	8728	CGCGGAGACCACACGCAATGG	8926
38 RGDLLGT	8729	CGGGGTGATTGTTGGGGACT	8927
39 RGDLTGV	8730	CGGGGTGATTGACGGGGTG	8928
40 RGDSTL	8731	CGTGGCGACTCCTACACCTTG	8929
41 RGDYGT	8732	CGCGGAGACTACGAACGGTC	8930
42 RGDVVG	8733	AGGGGTGACGTCGTAGGCCTG	8931
43 RGDTERL	8734	CGGGGTGATACTGAGCGTCTG	8932
44 RGDHSSL	8735	CGCGGCGACCCTCCTCAT	8933
45 RGDHGQL	8736	AGGGGCGACCACGGTCAACTT	8934
46 RGDVTGM	8737	CGTGGCGACGTAACGGAATG	8935
47 RGDYGG	8738	CGCGGCGACTACGGGGCTTA	8936
48 RGDYAGH	8739	CGTGGGGATTATGCGGGCAT	8937
49 RGDIVGL	8740	AGGGGTGACATAGTGGGCCTC	8938
50 RGDLVGY	8741	AGGGGGGATCTTGTGGGTAT	8939
51 RGDGAHL	8742	CGTGGTGATGGTGCTCATCTG	8940
52 RGDQVV	8743	CGTGGTGATCAGGTTGTGGTT	8941
53 RGDIMG	8744	CGTGGGATACGATGGGTATG	8942
54 RGDLLGT	8745	CGTGGGGATTGTTGGGGACT	8943
55 RGDLSGN	8746	CGTGGGGATCTTCTGGTAAT	8944
56 FNVSTRT	8747	TTCAACGTAAGTACGAGAACA	8945
57 RGDRTVI	8748	CGTGGTGATCGTACTGTGATT	8946
58 RGDVSGI	8749	CGTGGTGATGTTAGTGGGATT	8947
59 RGDYASL	8750	CGGGGCGACTACGCAAGCCTG	8948
60 RGDQALI	8751	CGTGGTGATCAGGCGCTTATT	8949
61 RGDRLSW	8752	CGTGGTGATCGTGATTCGTGG	8950
62 RGDREGL	8753	CGTGGTGATCGTGAGGTCTT	8951
63 RGDYVSV	8754	CGGGGAGACTACGTCAGTGTC	8952

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TABLE 9-continued

N-mer Rank motif	SEQ ID NO:	Encoding sequence	SEQ ID NO:
5 64 RGDIMRL	8755	CGCGGAGACACGATGAGACTG	8953
65 RGDYAHT	8756	AGGGGTGACTACGCTCACACG	8954
66 RGDTEKL	8757	CGGGGTGATACGGAGAAGTTG	8955
10 67 RGDQWQV	8758	AGGGGGGATCAGTGGCAGGTG	8956
68 RGDILNV	8759	CGGGGTGATATTCTGAATGTG	8957
69 RGDREQV	8760	CGTGGTGATCGTGAGCAGGTT	8958
15 70 RGDNIQM	8761	CGAGGCGACAACGCGAAATG	8959
71 RGDYGGM	8762	AGGGGGGATTATGGTGGGATG	8960
72 RGDLDGR	8763	CGTGGTGATCTGGATGGGCGG	8961
73 RGDHERL	8764	AGAGGGGACCACGAACGGCTT	8962
74 RGD LGV	8765	AGGGGTGATCTGGGTGTGGTG	8963
75 RGDRESH	8766	CGCGGAGACCAGAAAGCCAC	8964
76 RGDAAIM	8767	CGGGGGGATGCTGCGACGATG	8965
77 RGD LGV	8768	CGTGGTGATTGGGTGGGGTG	8966
78 RGDAGQL	8769	CGGGGTGATGCGGGGCGAGCTT	8967
79 RGD RGEI	8770	CGGGGGGATCGTGGTGAGATT	8968
80 RGDVVS	8771	CGTGGAGACGTCGTAAGTTGG	8969
81 MTARSPM	8772	ATGACTGCTCGGAGTCCGATG	8970
82 TIRDGRL	8773	ACGATCCGTGACGGCAGGTTG	8971
83 RGDIVGL	8774	CGTGGGGATATTGTMGTCTG	8972
84 RGDYQAV	8775	CGCGGTGACTACCAAGCAGTG	8973
85 RGDGAHM	8776	CGTGGTGATGGGGCGCATATG	8974
40 86 RGDAAI	8777	CGGGGTGATGCTGCTTCGATT	8975
87 RGDNSQW	8778	CGTGGGGATAATCTCTAGTGG	8976
88 RGDHSL	8779	AGAGGCGACCACTCGGGCCTC	8977
45 89 RGD MGT	8780	CGAGGCGACATGGGAGGCACC	8978
90 RGDLTGV	8781	AGGGGAGACCTCACAGGTGTA	8979
91 RGDVSGY	8782	CGGGGTGATGTGTCTGGTTAT	8980
50 92 RGDLT	8783	CGTGGGGATCTTACTACGACT	8981
93 RGDYGT	8784	AGGGGTGATTATGGGACTGTT	8982
94 RGDIMG	8785	CGCGGTGACCATGGGCATG	8983
55 95 RGDYSSV	8786	CGTGGGGATTATCTGCTGTG	8984
96 RGDYGGM	8787	CGGGGTGACTACGGCGGTATG	8985
97 RGDYVSV	8788	CGTGGGGATTATGTGTCTGTG	8986
98 RGDVTGL	8789	CGTGGAGACGTGACCGGACTG	8987
99 RGDLLTN	8790	CGAGGTGACCTTCTCACAAAC	8988
100 RGDHSGW	8791	CGTGGTGATCATAGTGGTTGG	8989
101 VSRGDVP	8792	GTTAGTCGGGGTGATGTGCCT	8990
65 102 RGDVSGM	8793	CGTGGTGATGTGAGTGGGATG	8991

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TABLE 9-continued

N-mer Rank motif	SEQ ID NO:	Encoding sequence	SEQ ID NO:
103 RGDVRGM	8794	CGGGGAGACCGCGTGGGCATG	8992
104 RGDGGVL	8795	CGTGGGGATGGTGGTGTGCTT	8993
105 RGDYVTI	8796	AGGGGTGATTATGTGACGATT	8994
106 RGDIAGV	8797	CGGGGTGATATTGCTGGTGTT	8995
107 RGDREQV	8798	CGCGGAGACAGAGAACAAGTG	8996
108 RGDLDNK	8799	CGTGGGGATTGGATAATAAG	8997
109 RGDLTSTV	8800	CGTGGTGATCTGACGTCTGTT	8998
110 FNVSVRN	8801	TTCAACGTAAGTGTTCGCAAC	8999
111 RGDLVHT	8802	CGTGGTGATCTGGTTCATACT	9000
112 RGDHGVI	8803	AGGGGTGACCACGGTGTGATA	9001
113 RGDAREM	8804	CGTGGTGATGCTCGTGAGATG	9002
114 RGDQASY	8805	CGTGGTGATCAGGCGTCTTAT	9003
115 RGDHSSL	8806	AGGGGGGATCATTCTAGTCTG	9004
116 RGDVRVI	8807	CGAGGCGACGTTCCGGTCATA	9005
117 TVGRGDT	8808	ACGGTTGGTCGTGGTGATACG	9006
118 RGDHGS	8809	CGAGGCGACCACGGTTCAC	9007
119 RGD FERT	8810	CGAGGGGACTTCGAACGAACC	9008
120 RGDHSG	8811	CGTGGTGATCATAGTGGGCTT	9009
121 RGD MSTV	8812	AGAGGCGACATGTCTACGGTG	9010
122 RGDYATL	8813	CGGGGTGATTATGCTACGCTT	9011
123 LPGVGHA	8814	CTGCCTGGTGTGGGTCATGCT	9012
124 RGDALHL	8815	AGGGGCGACGCGCTCCACCTT	9013
125 SGGTYLA	8816	AGCGGGGAACGTACCTTGCC	9014
126 RGDVVHL	8817	AGGGGTGATGTTGTGCATCTG	9015
127 RGDQVQL	8818	CGGGGTGATCAGGTGCAGCTG	9016
128 SSIGVKI	8819	TCGTCGATTGGTGTGAAGATT	9017
129 RGDHMS	8820	CGCGGCGACCACATGTCTCTA	9018
130 RGD MSTV	8821	AGGGGGGATATGAGTACTGTT	9019
131 VMRAGAT	8822	GTATGCGAGCAGGTGCGACG	9020
132 RGDVVGL	8823	CGGGGGGATGTTGTTGGGCTT	9021
133 RGD TVVL	8824	CGTGGTGATACTGTTGTGTG	9022
134 GTKVGVL	8825	GGGACGAAGTTGGTGTGCTG	9023
135 TGVHTRV	8826	ACAGGAGTGCACCCGGGTT	9024
136 RGDAGVL	8827	CGTGGTGATGCTGGGTTCTT	9025
137 RGD LSTT	8828	CGTGGTGATCTTTCGACTACT	9026
138 RGDRLQI	8829	CGTGGTGATCGGCTTCAGATT	9027
139 RGD AVTL	8830	CGTGGGGATGCGGTGACTTTG	9028
140 RGD MVSV	8831	CGGGGGGATATGGTTAGTGTG	9029

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TABLE 9-continued

N-mer Rank motif	SEQ ID NO:	Encoding sequence	SEQ ID NO:
141 RGDREN	8832	CGTGGGGATAGGGAGAATCTT	9030
142 RGDGAAM	8833	CGTGGGGATGGTGC	9031
143 RGD LTRT	8834	CGGGGGGATCTTACTAGGACG	9032
144 RGDYGGI	8835	CGTGGGGATTATGGTGGTATT	9033
145 RGDMEPR	8836	CGGGGTGATATGGAGCCTCGT	9034
146 RGD TAVQ	8837	CGTGGGGATACGCGGTTT	9035
147 AVTRGGV	8838	GCTGTGACTAGGGGTGGTGT	9036
148 VSAARSL	8839	GTGAGTGC	9037
149 GRLPQQT	8840	GGTCGGCTTCTCAGCAGACT	9038
150 RGD LVGY	8841	CGAGGCGACTTGGTTGGTTAC	9039
151 RGD LVTV	8842	CGGGGGGATCTGGTTACGGTT	9040
152 RGDYVVH	8843	CGCGGGGACTACGTCGTTT	9041
153 RGD AARL	8844	CGCGGCGACGTCGACGACTA	9042
154 RGDYTG	8845	AGGGGTGACTACACAGGCGTC	9043
155 RGD LGGT	8846	AGGGGTGATCTTGGGGGTACG	9044
156 RGD TVYL	8847	CGGGGTGATACGGTGATCTG	9045
157 RGD LMGS	8848	CGGGGGGATCTTATGGGGAGT	9046
158 LGRGDVS	8849	TTGGGTCGGGGTGATGTGTCG	9047
159 TAGRVQV	8850	ACTGCTGGGCGTGTTCAGGTG	9048
160 VVVRGGV	8851	GTGGTGGTGCGTGGTGGGGTT	9049
161 RGD HTNI	8852	AGAGGGGACCACACTAACATC	9050
162 RGD LVGI	8853	AGGGGCGACTTAGTAGGAATC	9051
163 RGD LSPV	8854	AGAGGAGACTTGTCCCGGTG	9052
164 RGD LSGV	8855	CGGGGTGATTGTGCGGGGTT	9053
165 YGIAARS	8856	TACGGCATCGCAGCAAGATCT	9054
166 RGDREGL	8857	CGGGGGGACCAGAAAGGGCTA	9055
167 RGD LHST	8858	CGTGGTGATTGTGATTCGACG	9056
168 RGD ATGW	8859	CGGGGTGATGCGACGGGTTGG	9057
169 RGD QSHV	8860	CGAGGCGACCAAGCCACGTA	9058
170 DKRVGTP	8861	GATAAGAGGGTTGGGACTCCT	9059
171 RGD LVVT	8862	AGAGGCGACCTGGTCGTA	9060
172 RGD FGGV	8863	AGGGGTGACTTCGGAGGTGTC	9061
173 RGD LSNT	8864	CGTGGAGACCTCAGCAACACA	9062
174 HRGQAVD	8865	CATCGGGGTGAGCGGTGAT	9063
175 SMVRS	8866	AGTATGGTTCGTTCCGGGACG	9064
176 TSVSVKY	8867	ACTTCTGTGTCGGTGAAGTAT	9065
177 RGDYSQI	8868	AGAGGCGACTACAGCCAAATA	9066
178 RGD ISGV	8869	CGGGGTGATATTCGGGGGTT	9067
179 RGD VAGV	8870	CGGGGTGATGTGGCGGGGTT	9068

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TABLE 9-continued

N-mer Rank motif	SEQ ID NO:	Encoding sequence	SEQ ID NO:
180 RGDQVTI	8871	AGGGGTGATCAGGTTACTATT	9069
181 RGDRLVI	8872	AGAGGAGACAGGCTGGTCATC	9070
182 PLLRSGT	8873	CCGTTGTTGAGGAGTGGGACG	9071
183 RGDFGSV	8874	CGGGGTGATTTTGGTAGTGTG	9072
184 RGDVAYV	8875	CGGGGTGATGTTGCTTATGTG	9073
185 ARMGTGV	8876	GTCGTATGGGTACGGGTGTG	9074
186 VMRVGHA	8877	GTGATGCGTGTGGGCATGCT	9075
187 ARVQSSP	8878	GTCGTGTTTCAGAGTTCGCCT	9076
188 RGDGGIL	8879	CGGGGTGATGGGGGATTCTT	9077
189 RSDLGAL	8880	AGGTCTGATCTTGGGGCTTTG	9078
190 SYSRSAV	8881	TCGTATTTCGCGAGTGCAGTT	9079
191 RGDVLLV	8882	AGGGGGATGTTCTTCTGGTG	9080
192 TGVHTRV	8883	ACGGGTGTTTCATACGAGGGTG	9081
193 TVGNLRG	8884	ACTGTGGGAATTTGCGTGGT	9082
194 TVVGQGY	8885	ACTGTCGTCGGACAAGGTTAC	9083
195 RGDGGAL	8886	CGTGGTGATGGTGGTCTCTG	9084
196 NSYHAGA	8887	AACAGCTACCACGCTGGGGCC	9085

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TABLE 9-continued

N-mer Rank motif	SEQ ID NO:	Encoding sequence	SEQ ID NO:
197 RGDLTVT	8888	CGGGGTGATTGACTGTGACT	9086
198 RGDVHGF	8889	CGGGGAGACGTCCACGGCTTC	9087

Muscle specific AAV capsids were developed using expression from two different muscle specific promoters and the resulting capsid libraries for each promoter were screened in non-human primates as described elsewhere herein and/or in U.S. Provisional Application Ser. Nos. 62/899,453, 62/916,207, 63/018,454, 63/055,252, and 62/916,221 and International Application No. PCT/US20/50534.

Various modifications and variations of the described methods, pharmaceutical compositions, and kits of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific embodiments, it will be understood that it is capable of further modifications and that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention that are obvious to those skilled in the art are intended to be within the scope of the invention. This application is intended to cover any variations, uses, or adaptations of the invention following, in general, the principles of the invention and including such departures from the present disclosure come within known customary practice within the art to which the invention pertains and may be applied to the essential features herein before set forth.

SEQUENCE LISTING

The patent contains a lengthy sequence listing. A copy of the sequence listing is available in electronic form from the USPTO web site (<https://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US12410447B2>). An electronic copy of the sequence listing will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. A composition comprising a targeting moiety effective to target a muscle cell, wherein the targeting moiety comprises an n-mer motif comprising $X_m\text{RGDYX}_1\text{X}_2\text{L}$,

wherein X is selected from any amino acid, and wherein m is 0-4.

2. The composition of claim 1, wherein X_1 is S and X_2 is G.

3. The composition of claim 2, wherein m is 3.

4. The composition of claim 3, wherein the first three amino acids of the n-mer motif are ESR, NNG, NT, SNN, SSN, or TDK.

5. The composition of claim 1, wherein X_1 is R and X_2 is E.

6. The composition of claim 5, wherein m is 3.

7. The composition of claim 6, wherein the first three amino acids of the n-mer motif are AAA, ATT, NNN, NNS, NSN, SNG, TAG, TAT, TNT, or TTI.

8. The composition of claim 1, wherein the targeting moiety is an engineered adeno associated virus (AAV) capsid polypeptide.

9. The composition of claim 8, wherein the n-mer motif is inserted into a surface variable region of the engineered AAV capsid polypeptide.

10. The composition of claim 9, wherein the surface variable region is selected from VR-IV, VR-V, or VR-VIII.

11. The composition of claim 8, wherein the n-mer motif is inserted between any two amino acids between amino acids 262-269, 327-332, 382-386, 452-460, 488-505, 527-539, 545-558, 581-593, 704-714, or any combination thereof, in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide; or is inserted between amino acids 588 and 589, in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide.

12. The composition of claim 1, further comprising a cargo.

13. The composition of claim 12, wherein the cargo is (a) capable of treating or preventing a muscle disease or disorder;

(b) a morpholino; a peptide-linked morpholino; an antisense oligonucleotide; a PMO, a therapeutic transgene; a polynucleotide encoding a therapeutic polypeptide or peptide; a PPMO; one or more peptides or polypeptides; one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both; a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule; a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein; or any combination thereof; or (c) both (a) and (b).

14. The composition of claim 13, wherein the muscle disease or disorder is an auto immune disease; a cancer; a muscular dystrophy; a neuro-muscular disease; a sugar or glycogen storage disease; an expanded repeat disease; a dominant negative disease; a cardiomyopathy; a viral disease; a progeroid disease; or any combination thereof.

15. An engineered particle comprising composition of claim 1.

16. The engineered particle of claim 15, wherein the wherein the targeting moiety is an engineered adeno associated virus (AAV) capsid polypeptide.

17. The engineered particle of claim 16, wherein the n-mer motif is inserted into a surface variable region of the engineered AAV capsid polypeptide.

18. The engineered particle of claim 17, wherein the surface variable region is selected from VR-IV, VR-V, or VR-VIII.

19. The engineered particle of claim 16, wherein the n-mer motif is inserted between any two amino acids between amino acids 262-269, 327-332, 382-386, 452-460, 488-505, 527-539, 545-558, 581-593, 704-714, or any combination thereof, in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide; or is inserted between amino acids 588 and 589, in an AAV9 capsid polypeptide or in an analogous position in an AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV rh.74, or AAV rh.10 capsid polypeptide.

20. The engineered particle of claim 15, wherein the engineered particle is an adeno associated virus (AAV) capsid.

21. The engineered particle of claim 15, further comprising a cargo.

22. The engineered particle of claim 21, wherein the cargo is

(a) capable of treating or preventing a muscle disease or disorder;

(b) a morpholino; a peptide-linked morpholino; an antisense oligonucleotide; a PMO, a therapeutic transgene; a polynucleotide encoding a therapeutic polypeptide or peptide; a PPMO; one or more peptides or polypeptides; one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both; a ribonucleoprotein, wherein the ribonucleoprotein com-

prises a CRISPR-Cas system molecule; a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein; or any combination thereof; or

(c) both (a) and (b).

23. The engineered particle of claim 22, wherein the muscle disease or disorder is an auto immune disease; a cancer; a muscular dystrophy; a neuro-muscular disease; a sugar or glycogen storage disease; an expanded repeat disease; a dominant negative disease; a cardiomyopathy; a viral disease; a progeroid disease; or any combination thereof.

24. A vector system comprising:

a polynucleotide encoding the composition of claim 1.

25. The vector system of claim 24, further comprising a cargo polynucleotide.

26. The vector system of claim 25, wherein the cargo polynucleotide

(a) is capable of treating or preventing a muscle disease or disorder;

(b) is or encodes a morpholino; a peptide-linked morpholino; an antisense oligonucleotide; a PMO, a therapeutic transgene; a polynucleotide encoding a therapeutic polypeptide or peptide; a PPMO; one or more peptides or polypeptides; one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both; a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule; a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein; or any combination thereof; or

(c) both (a) and (b).

27. A method of treating or preventing a muscle disease or disorder in a subject in need thereof, comprising:

administering a composition of claim 1 or an engineered particle comprising the composition to a subject in need thereof.

28. The method of claim 27, wherein the composition or the engineered particle comprises a cargo.

29. The method of claim 28, wherein the cargo is

(a) capable of treating or preventing the muscle disease or disorder;

(b) a morpholino; a peptide-linked morpholino; an antisense oligonucleotide; a PMO, a therapeutic transgene; a polynucleotide encoding a therapeutic polypeptide or peptide; a PPMO; one or more peptides or polypeptides; one or more polynucleotides encoding a CRISPR-Cas protein, a guide RNA, or both; a ribonucleoprotein, wherein the ribonucleoprotein comprises a CRISPR-Cas system molecule; a therapeutic transgene RNA, or other gene modifying or therapeutic RNA and/or protein; or any combination thereof; or

(c) both (a) and (b).

30. The method of claim 27, wherein the muscle disease or disorder is an auto immune disease; a cancer; a muscular dystrophy; a neuro-muscular disease; a sugar or glycogen storage disease; an expanded repeat disease; a dominant negative disease; a cardiomyopathy; a viral disease; a progeroid disease; or any combination thereof.