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(71) Applicant: **CALIFORNIA INSTITUTE OF TECHNOLOGY** [US/US]; 1200 E. California Boulevard, Pasadena, CA 91125 (US).

(72) Inventors: **GRADINARU, Viviana**; 1200 E. California Boulevard, Pasadena, CA 91125 (US). **KUMAR, Spripriya, Ravindra**; 1200 E. California Boulevard, Pasadena, CA 91125 (US). **DEVERMAN, Benjamin**; 1200 E. California Boulevard, Pasadena, CA 91125 (US).

(74) Agent: **SCHOEN, Adam, M.** et al.; BROWN RUDNICK LLP, One Financial Center, Boston, MA 02111 (US).

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(54) **Title:** VIRUS COMPOSITIONS WITH ENHANCED SPECIFICITY IN THE BRAIN

(57) **Abstract:** Provided are compositions and kits comprising recombinant adeno-associated viruses (rAAVs) with tropisms showing increased specificity and efficiency of viral transduction in targeted cell-types, for e.g., the brain and the liver. Therapeutic and biomedical research applications of the rAAVs are also described, including without limitation methods of discovering rAAVs using a multiplexed Cre recombination-based AAV targeted evolution (M- CREATE) method, and methods of treating various diseases and conditions by rAAV-mediated transgene therapy.

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VIRUS COMPOSITIONS WITH ENHANCED SPECIFICITY IN THE BRAIN

RELATED APPLICATIONS

[0001] This Application claims the benefit of and priority to U.S. Provisional Patent Application Ser. No. 62/832,836, filed April 11, 2019, the content of which is incorporated herein in its entirety.

STATEMENT AS TO FEDERALLY SPONSORED RESEARCH

[0002] This invention was made with government support under NS087949, MH117069, and OD025535 awarded by National Institutes of Health. The government has certain rights in the invention.

SUMMARY

[0003] Recombinant adeno-associated viruses (rAAVs) are widely used as vectors for gene delivery in basic scientific research and therapeutic applications because of their ability to transduce both dividing and non-dividing cells, their long-term persistence as episomal DNA in infected cells, and their low immunogenicity. These characteristics make them appealing for applications in both basic science and in clinics, such as gene therapy. However, there is a need to significantly improve the performance of existing serotypes to specifically target distinct brain cell-types, upon systemic delivery to a subject. This need is especially acute when the AAV must across the blood brain barrier (BBB) to reach the central nervous system (CNS).

[0004] Systemic delivery of existing AAV serotypes show limited transduction of certain cell types and organs, and non-specific, overlapping tropisms in others. This leads to several complications in gene therapy applications, including but not limited to off-target effects due to transduction of unimpacted organs and cell types (in particular, the liver), and the necessity for a larger viral dosage to achieve sufficient therapeutic levels in the tissue or organ of interest.

[0005] Disclosed herein are rAAVs with engineered specificity into the capsid structure through iterative rounds of positive and negative selection, yielding variants with tropisms having an increased specificity and transduction efficiency when measured in the CNS, and in

some cases, a decreased specificity and transduction efficiency in an off-target environment, like the liver. The rAAVs described herein achieve widespread transduction to target environment (*e.g.*, target cell types or tissues) in a subject upon systemic delivery (*e.g.*, intravenous injection).

[0006] Also provided are methods of engineering the rAAVs of the present disclose using a multiplexed Cre recombination-based AAV targeted evolution (M-CREATE) method. The M-CREATE method generates enhanced transduction efficiency and/or specificity by (1) introducing variations in the capsid protein sequence, (2) *in vivo* unbiased selection and recovery of only those variants that travel to defined cell populations, (3) cross the cell membrane, (4) travel to the nucleus, and (5) unpackage and express their genetic dosage amount. Variant capsids exhibiting the most desirable tropism (*e.g.*, enhanced efficiency and specificity for a particular *in vivo* environment) are recovered and identified by deep sequencing. Strategies for unbiased selection and analysis include determining variants' enrichment score (by normalizing the target tissue library to starting virus library) and unbiased propagation between rounds of selections through a synthetic library construction (where each variant is represented equally). Also disclosed are detailed characterizations of the resultant libraries from sequencing data which provide useful insights on the selection of variants towards a target.

[0007] Disclosed herein are AAV capsid libraries generated using M-CREATE. The first library, a 7-mer peptide insertion in AAV9 (7-*mer-i* library) was built for parallel *in vivo* selections across different brain cell types – endothelial cells, neurons, and astrocytes - and yielded a large pool of AAV9 variants with enhanced ability to target as well as cross the blood-brain barrier (BBB) and broadly transduce the central nervous system (CNS). The second library, a 3-mer peptide substitution in AAV-PHP.B (3-*mer-s* library), was reinvestigated by incorporating deep sequencing to recover capsids. A pool of AAV-PHP.B variants were discovered including a variant that transduce CNS neurons with greater specificity. The rAAVs of the present disclosure can efficiently target the endothelial cells of the blood-brain barrier, variants that can broadly transduce different cell types in the central nervous system, and a variant exhibiting greater specificity towards transducing neuron.

[0008] Aspects disclosed herein provide **AAV capsids** comprising: (a) an AAV capsid protein comprising: (i) a first amino acid sequence that is at least 98% identical to amino acid 217 to amino acid 736 of SEQ ID NO: 1; and (ii) a second amino acid sequence at least 57.1%

identical to an amino acid sequence provided in **Tables 2-3** or **FIG. 33** inserted at an amino acid position 588_589 within SEQ ID NO: 1, wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a central nervous system (CNS) in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1. In some embodiments, the second amino acid sequence is at least 71.4% identical to the amino acid sequence provided in **Tables 2-3** or **FIG. 33**. In some embodiments, the second amino acid sequence is at least 86.7% identical to the amino acid sequence provided in **Tables 2-3** or **FIG. 33**. In some embodiments, the second amino acid sequence is selected from the group consisting of TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, SIERPFK, RYQGDSV, and TTLKPFS. In some embodiments, the AAV capsid protein is present in VP1, VP2, and VP3 of the AAV capsid. In some embodiments, the AAV capsid is chimeric. In some embodiments, 60 copies of the AAV capsid protein are assembled into the AAV capsid. In some embodiments, the CNS comprises a cell-type selected from the group consisting of a neuron, an oligodendrocyte, an astrocyte, and a brain vascular cell. In some embodiments, the CNS comprises a tissue that is selected from the group consisting of a brain, a thalamus, a cortex, a striatum, a ventral midbrain, and a spinal cord. In some embodiments, the AAV capsid protein further comprises an amino acid substitution A587D. In some embodiments, the AAV capsid protein further comprises an amino acid substitution Q588G. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising A589N. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising Q590P. In some embodiments, the second amino acid sequence at the amino acid position 588_589 within SEQ ID NO: 1 is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW. In some embodiments, the AAV capsid is isolated and purified. In some embodiments, the AAV capsid is formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical formulation further comprises a therapeutic agent.

[0009] Aspects disclosed herein provide **AAV capsids** comprising an AAV capsid protein comprising a seven amino acid insertion (X1-X2-X3-X4-X5-X6-X7) between amino acid 588

and amino acid 589 in an amino acid sequence of the AAV capsid protein provided in SEQ ID NO: 1, wherein X1 is an amino acid selected from the group consisting of E, D, G, R, S and T. In some embodiments, X2 is an amino acid selected from the group consisting of A, G, I, L, M, N, Q, T, and Y. In some embodiments, X3 is an amino acid selected from the group consisting of E, K, L, T, and Q. In some embodiments, X4 is an amino acid selected from the group consisting of G, I, K, L, R, T, and V. In some embodiments, X5 is an amino acid selected from the group consisting of A, D, G, P, L, Q, and V. In some embodiments, X6 is an amino acid selected from the group consisting of F, K, N, P, Q, S, and V. In some embodiments, X7 is an amino acid selected from the group consisting of I, K, L, P, and V. In some embodiments, the seven amino acid insertion is selected from the group consisting of TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, SIERPFK, RYQGDSV, and TTLKPFS. In some embodiments, the AAV capsid protein is present in VP1, VP2, and VP3 of the AAV capsid. In some embodiments, the AAV capsid is chimeric. In some embodiments, 60 copies of the AAV capsid protein are assembled into the AAV capsid. In some embodiments, the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a central nervous system (CNS) in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1. In some embodiments, the CNS comprises a cell-type selected from the group consisting of a neuron, a glial cell, a oligodendrocyte, an ependymal cell, an astrocyte, a Schwann cell, a satellite cell, and an enteric glial cell. In some embodiments, the CNS comprises a tissue that is selected from the group consisting of a brain, a thalamus, a cortex, a striatum, a ventral midbrain, and a spinal cord. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising A587D. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising Q588G. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising A589N. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising Q590P. In some embodiments, the seven amino acid insertion is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW. In some embodiments, the AAV capsid is isolated and purified. In some embodiments, the AAV capsid is formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the

liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical formulation further comprises a therapeutic agent.

[0010] Aspects provided herein provide A**AV capsids** comprising: (a) an AAV capsid protein comprising: (i) a first amino acid sequence that is at least 98% identical to amino acid 217 to amino acid 736 of SEQ ID NO: 1; and (ii) a second amino acid sequence at least 57.1% identical to an amino acid sequence provided in **Table 4** or **FIG. 35** at an amino acid position 588_589 within SEQ ID NO: 1, wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a liver in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1. In some embodiments, the second amino acid sequence is at least 71.4% identical to the amino acid sequence provided in **Table 4** or **FIG. 35**. In some embodiments, the second amino acid sequence is at least 86.7% identical to the amino acid sequence provided in **Table 4** or **FIG. 35**. In some embodiments, the second amino acid sequence is selected from the group consisting of KAYSVQV, PSGSARS, and RTANALG. In some embodiments, the AAV capsid protein is present in VP1, VP2, and VP3 of the AAV capsid. In some embodiments, the AAV capsid is chimeric. In some embodiments, 60 copies of the AAV capsid protein are assembled into the AAV capsid. In some embodiments, the AAV capsid is isolated and purified. In some embodiments, the AAV capsid is formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical formulation further comprises a therapeutic agent.

[0011] Aspects disclosed herein provide **AAV capsid proteins** comprising: (i) a first amino acid sequence that is at least 98% identical to amino acid 217 to amino acid 736 of SEQ ID NO: 1; and (ii) a second amino acid sequence at least 57.1% identical to an amino acid sequence provided in **Tables 2-3** or **FIG. 33** inserted at an amino acid position 588_589 within SEQ ID NO: 1, wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a central nervous system (CNS) in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1. In some embodiments, the second amino acid sequence is at least 71.4% identical to the amino acid sequence provided in **Tables 2-3** or **FIG. 33**. In some

embodiments, the second amino acid sequence is at least 86.7% identical to the amino acid sequence provided in **Tables 2-3** or **FIG. 33**. In some embodiments, the second amino acid sequence is selected from the group consisting of TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, SIERPFK, RYQGDSV, and TTLKPFS. In some embodiments, the AAV capsid protein is present in VP1, VP2, and VP3 of an AAV capsid. In some embodiments, the AAV capsid is chimeric. In some embodiments, 60 copies of the AAV capsid protein are assembled into the AAV capsid. In some embodiments, the CNS comprises a cell-type selected from the group consisting of a neuron, an oligodendrocyte, an astrocyte, and a brain vascular cell. In some embodiments, the CNS comprises a tissue that is selected from the group consisting of a brain, a thalamus, a cortex, a striatum, a ventral midbrain, and a spinal cord. In some embodiments, the AAV capsid protein further comprises an amino acid substitution A587D. In some embodiments, the AAV capsid protein further comprises an amino acid substitution Q588G. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising A589N. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising Q590P. In some embodiments, the second amino acid sequence at the amino acid position 588_589 within SEQ ID NO: 1 is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW. In some embodiments, the AAV capsid protein is isolated and purified. In some embodiments, the AAV capsid protein is formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical formulation further comprises a therapeutic agent.

[0012] Aspects disclosed herein provide **AAV capsids proteins** comprising a seven amino acid insertion (X1-X2-X3-X4-X5-X6-X7) between amino acid 588 and amino acid 589 in an amino acid sequence of the AAV capsid protein provided in SEQ ID NO: 1, wherein X1 is an amino acid selected from the group consisting of E, D, G, R, S and T. In some embodiments, X2 is an amino acid selected from the group consisting of A, G, I, L, M, N, Q, T, and Y. In some embodiments, X3 is an amino acid selected from the group consisting of E, K, L, T, and Q. In some embodiments, X4 is an amino acid selected from the group consisting of G, I, K, L, R, T, and V. In some embodiments, X5 is an amino acid selected from the group consisting of A, D,

G, P, L, Q, and V. In some embodiments, X6 is an amino acid selected from the group consisting of F, K, N, P, Q, S, and V. In some embodiments, X7 is an amino acid selected from the group consisting of I, K, L, P, and V. In some embodiments, the seven amino acid insertion is selected from the group consisting of TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, SIERPFK, RYQGDSV, and TTLKPFS. In some embodiments, the AAV capsid protein is present in VP1, VP2, and VP3 of a AAV capsid. In some embodiments, the AAV capsid is chimeric. In some embodiments, 60 copies of the AAV capsid protein are assembled into the AAV capsid. In some embodiments, the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a central nervous system (CNS) in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1. In some embodiments, the CNS comprises a cell-type selected from the group consisting of a neuron, a glial cell, a oligodendrocyte, an ependymal cell, an astrocyte, a Schwann cell, a satellite cell, and an enteric glial cell. In some embodiments, the CNS comprises a tissue that is selected from the group consisting of a brain, a thalamus, a cortex, a striatum, a ventral midbrain, and a spinal cord. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising A587D. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising Q588G. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising A589N. In some embodiments, the AAV capsid protein further comprises an amino acid substitution comprising Q590P. In some embodiments, the seven amino acid insertion is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW. In some embodiments, the AAV capsid protein is isolated and purified. In some embodiments, the AAV capsid protein is formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical formulation further comprises a therapeutic agent.

[0013] Aspects provided herein provide A**AV capsids proteins** comprising: (i) a first amino acid sequence that is at least 98% identical to amino acid 217 to amino acid 736 of SEQ ID NO: 1; and (ii) a second amino acid sequence at least 57.1% identical to an amino acid sequence provided in **Table 4** or **FIG. 35** at an amino acid position 588_589 within SEQ ID NO: 1,

wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a liver in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1. In some embodiments, the second amino acid sequence is at least 71.4% identical to the amino acid sequence provided in **Table 4** or **FIG. 35**. In some embodiments, the second amino acid sequence is at least 86.7% identical to the amino acid sequence provided in **Table 4** or **FIG. 35**. In some embodiments, the second amino acid sequence is selected from the group consisting of KAYSVQV, PSGSARS, and RTANALG. In some embodiments, the AAV capsid protein is present in VP1, VP2, and VP3 of an AAV capsid. In some embodiments, the AAV capsid is chimeric. In some embodiments, 60 copies of the AAV capsid protein are assembled into the AAV capsid. In some embodiments, the AAV capsid protein is isolated and purified. In some embodiments, the AAV capsid protein is formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier. In some embodiments, the pharmaceutical formulation further comprises a therapeutic agent.

[0014] Aspects disclosed herein comprise **plasmid vectors** comprising a nucleic acid sequence encoding the AAV capsids and AAV capsid proteins described herein. In some instances, the plasmid vector is bacterial. In some instances, the plasmid vector is derived from *Escherichia coli*. In some instances, the nucleic acid sequence comprises, in a 5' to 3' direction: (1) a 5' inverted terminal repeat (ITR) sequence, (2) a Replication (*Rep*) gene, (3) a Capsid (*Cap*) gene, and (4) a 3' ITR, wherein the *Cap* gene encodes the AAV capsid protein described herein. In some instances, the plasmid vector encodes a pseudotyped AAV capsid protein. In some instances, the *Cap* gene is derived from the deoxyribose nucleic acid (DNA) provided in any one of SEQ ID NOs: 6-10. In some instances, the nucleic acid sequence comprising the *Cap* gene is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of the DNA sequences provided in U.S. App. Ser. No. 16/582,635, incorporated herein by reference. In some instances, the 5' ITR and the 3' ITR are derived from an AAV2 serotype. In some instances, the 5' ITR and the 3' ITR are derived from an AAV5 serotype. In some instances, the 5' ITR and the 3' ITR are derived from an AAV9 serotype.

[0015] Aspects disclosed herein provide methods of treating a disease or condition in a subject comprising administering a therapeutically effective amount of a pharmaceutical formulation comprising the AAV capsid protein or the AAV capsid of the present disclosure. In some embodiments, the disease or the condition is a disease or a condition of a central nervous system (CNS) or a liver of the subject. In some embodiments, the disease or condition of the liver is selected from the group consisting of Alagille Syndrome, Alcohol-Related Liver Disease, Alpha-1 Antitrypsin Deficiency, Autoimmune Hepatitis, Benign Liver Tumors, Biliary Atresia, Cirrhosis, Crigler-Najjar Syndrome, Galactosemia, Gilbert Syndrome, Hemochromatosis, Hepatic Encephalopathy, Hepatitis A, Hepatitis B, Hepatitis C, Hepatorenal Syndrome, Intrahepatic Cholestasis of Pregnancy (ICP), Lysosomal Acid Lipase Deficiency (LAL-D), Liver Cysts, Liver Cancer, Newborn Jaundice, Non-Alcoholic Fatty Liver Disease, Primary Biliary Cholangitis (PBC), Primary Sclerosing Cholangitis (PSC), Reye Syndrome, Type I Glycogen Storage Disease, and Wilson Disease. In some embodiments, the disease or condition of the CNS is selected from group consisting of Absence of the Septum Pellucidum, Acid Lipase Disease, Acid Maltase Deficiency, Acquired Epileptiform Aphasia, Acute Disseminated Encephalomyelitis, Attention Deficit-Hyperactivity Disorder (ADHD), Adie's Pupil, Adie's Syndrome, Adrenoleukodystrophy, Agenesis of the Corpus Callosum, Agnosia, Aicardi Syndrome, Aicardi-Goutieres Syndrome Disorder, AIDS -Neurological Complications, Alexander Disease, Alpers' Disease, Alternating Hemiplegia, Alzheimer's Disease, Amyotrophic Lateral Sclerosis (ALS), Anencephaly, Aneurysm, Angelman Syndrome, Angiomatosis, Anoxia, Antiphospholipid Syndrome, Aphasia, Apraxia, Arachnoid Cysts, Arachnoiditis, Arnold-Chiari Malformation, Arteriovenous Malformation, Asperger Syndrome, Ataxia, Ataxia Telangiectasia, Ataxias and Cerebellar or Spinocerebellar Degeneration, Atrial Fibrillation and Stroke, Attention Deficit-Hyperactivity Disorder, Autism Spectrum Disorder, Autonomic Dysfunction, Back Pain, Barth Syndrome, Batten Disease, Becker's Myotonia, Behcet's Disease, Bell's Palsy, Benign Essential Blepharospasm, Benign Focal Amyotrophy, Benign Intracranial Hypertension, Bernhardt-Roth Syndrome, Binswanger's Disease, Blepharospasm, Bloch-Sulzberger Syndrome, Brachial Plexus Birth Injuries, Brachial Plexus Injuries, Bradbury-Eggleston Syndrome, Brain and Spinal Tumors, Brain Aneurysm, Brain Injury, Brown-Sequard Syndrome, Bulbospinal Muscular Atrophy, Cerebral Autosomal Dominant Arteriopathy with Subcortical Infarcts and

Leukoencephalopathy (CADASIL), Canavan Disease, Carpal Tunnel Syndrome, Causalgia, Cavernomas, Cavernous Angioma, Cavernous Malformation, Central Cervical Cord Syndrome, Central Cord Syndrome, Central Pain Syndrome, Central Pontine Myelinolysis, Cephalic Disorders, Ceramidase Deficiency, Cerebellar Degeneration, Cerebellar Hypoplasia, Cerebral Aneurysms, Cerebral Arteriosclerosis, Cerebral Atrophy, Cerebral Beriberi, Cerebral Cavemous Malformation, Cerebral Gigantism, Cerebral Hypoxia, Cerebral Palsy, Cerebro-Oculo-Facio-Skeletal Syndrome (COFS), Charcot-Marie-Tooth Disease, Charcot-Marie-Tooth syndrome, classical rhizomelic chondrodysplasia punctata (RCDP), Chiari Malformation, Cholesterol Ester Storage Disease, Chorea, Choreoacanthocytosis, Chronic Inflammatory Demyelinating Polyneuropathy (CIDP), Chronic Orthostatic Intolerance, Chronic Pain, Cockayne Syndrome Type II, Coffin Lowry Syndrome, Colpocephaly, Coma, Complex Regional Pain Syndrome, Congenital Facial Diplegia, Congenital Myasthenia, Congenital Myopathy, Congenital Vascular Cavernous Malformations, Corticobasal Degeneration, Cranial Arteritis, Craniosynostosis, Cree encephalitis, Creutzfeldt- Jakob Disease, Cumulative Trauma Disorders, Cushing's Syndrome, Cytomegalic Inclusion Body Disease, Cytomegalovirus Infection, Dancing Eyes-Dancing Feet Syndrome, Dandy-Walker Syndrome, Dawson Disease, Deafness, De Morsier's Syndrome, Dejerine-Klumpke Palsy, Dementia, Dementia -Multi -Infarct, Dementia - Semantic, Dementia - Subcortical, Dementia With Lewy Bodies, Dentate Cerebellar Ataxia, Dentatorubral Atrophy, Dermatomyositis, Developmental Dyspraxia, Devic's Syndrome, Diabetic Neuropathy, Diffuse Sclerosis, Dravet Syndrome, Duchenne muscular dystrophy, Dysautonomia, Dysgraphia, Dyslexia, Dysphagia, Dyspraxia, Dyssynergia Cerebellaris Myoclonica, Dyssynergia Cerebellaris Progressiva, Dystonias, Early Infantile Epileptic Encephalopathy, Empty Sella Syndrome, Encephalitis, Encephalitis Lethargica, Encephaloceles, Encephalopathy, Encephalopathy (familial infantile), Encephalotrigeminal Angiomatosis, Epilepsy, Epileptic Hemiplegia, Erb's Palsy, Erb-Duchenne and Dejerine-Klumpke Palsies, Essential Tremor, Extrapontine Myelinolysis, Fabry Disease, Fahr's Syndrome, Fainting, Familial Dysautonomia, Familial Hemangioma, Familial Idiopathic Basal Ganglia Calcification, Familial Periodic Paralyses, Familial Spastic Paralysis, Farber's Disease, Febrile Seizures, Fibromuscular Dysplasia, Fisher Syndrome, Floppy Infant Syndrome, Foot Drop, Friedreich's Ataxia, Frontotemporal Dementia, Gaucher Disease, Generalized Gangliosidoses, Gerstmann's

Syndrome, Gerstmann-Straussler-Scheinker Disease, Giant Axonal Neuropathy, Giant Cell Arteritis, Giant Cell Inclusion Disease, glioblastoma, Globoid Cell Leukodystrophy, Glossopharyngeal Neuralgia, Glycogen Storage Disease, Guillain-Barre Syndrome, Hallervorden-Spatz Disease, Head Injury, Headache, Hemicrania Continua, Hemifacial Spasm, Hemiplegia Alterans, Hereditary Neuropathies, Hereditary Spastic Paraplegia, Heredopathia Atactica Polyneuritiformis, Herpes Zoster, Herpes Zoster Oticus, Hirayama Syndrome, Holmes-Adie syndrome, Holoprosencephaly, HTLV-1 Associated Myelopathy, Hughes Syndrome, Huntington's Disease, Hydranencephaly, Hydrocephalus, Hydrocephalus - Normal Pressure, Hydromyelia, Hypercortisolism, Hypersomnia, Hypertonia, Hypotonia, Hypoxia, Immune-Mediated Encephalomyelitis, Inclusion Body Myositis, Incontinentia Pigmenti, Infantile Hypotonia, Infantile Neuroaxonal Dystrophy, Infantile Phytanic Acid Storage Disease, Infantile Refsum Disease, Infantile Spasms, Inflammatory Myopathies, Iniencephaly, Intestinal Lipodystrophy, Intracranial Cysts, Intracranial Hypertension, Isaacs' Syndrome, Joubert Syndrome, Kearns-Sayre Syndrome, Kennedy's Disease, Kinsbourne syndrome, Kleine-Levin Syndrome, Klippel-Feil Syndrome, Klippel-Trenaunay Syndrome (KTS), Kliiver-Bucy Syndrome, Korsakoff s Amnesic Syndrome, Krabbe Disease, Kugelberg-Welander Disease, Kuru, Lambert-Eaton Myasthenic Syndrome, Landau-Kleffner Syndrome, Lateral Femoral Cutaneous Nerve Entrapment, Lateral Medullary Syndrome, Learning Disabilities, Leigh's Disease, Lennox-Gastaut Syndrome, Lesch-Nyhan Syndrome, Leukodystrophy, Levine-Critchley Syndrome, Lewy Body Dementia, Lipid Storage Diseases, Lipoid Proteinosis, Lissencephaly, Locked-In Syndrome, Lou Gehrig's Disease, Lupus -Neurological Sequelae, Lyme Disease - Neurological Complications, Machado- Joseph Disease, Macrencephaly, Megalencephaly, Melkersson-Rosenthal Syndrome, Meningitis, Meningitis and Encephalitis, Menkes Disease, Meralgia Paresthetica, Metachromatic Leukodystrophy, Microcephaly, Migraine, Miller Fisher Syndrome, Mini Stroke, Mitochondrial Myopathy, Moebius Syndrome, Monomelic Amyotrophy, Motor Neuron Diseases, Moyamoya Disease, Mucolipidoses, Mucopolysaccharidoses, Multi-Infarct Dementia, Multifocal Motor Neuropathy, Multiple Sclerosis, Multiple System Atrophy, Multiple System Atrophy with Orthostatic Hypotension, Muscular Dystrophy, Myasthenia -Congenital, Myasthenia Gravis, Myelinoclastic Diffuse Sclerosis, Myoclonic Encephalopathy of Infants, Myoclonus, Myopathy, Myopathy- Congenital,

Myopathy -Thyrotoxic, Myotonia, Myotonia Congenita, Narcolepsy, Neuroacanthocytosis, Neurodegeneration with Brain Iron Accumulation, Neurofibromatosis, Neuroleptic Malignant Syndrome, Neurological Complications of AIDS, Neurological Complications of Lyme Disease, Neurological Consequences of Cytomegalovirus Infection, Neurological Manifestations of Pompe Disease, Neurological Sequelae Of Lupus, Neuromyelitis Optica, Neuromyotonia, Neuronal Ceroid Lipofuscinosis, Neuronal Migration Disorders, Neuropathy- Hereditary, Neurosarcoidosis, Neurosyphilis, Neurotoxicity, Nevus Cavernosus, Niemann-Pick Disease, O'Sullivan-McLeod Syndrome, Occipital Neuralgia, Ohtahara Syndrome, Olivopontocerebellar Atrophy, Opsoclonus Myoclonus, Orthostatic Hypotension, Overuse Syndrome, Pain -Chronic, Pantothenate Kinase-Associated Neurodegeneration, Paraneoplastic Syndromes, Paresthesia, Parkinson's Disease, Paroxysmal Choreoathetosis, Paroxysmal Hemicrania, Parry -Romberg, Pelizaeus-Merzbacher Disease, Pena Shokeir II Syndrome, Perineural Cysts, Periodic Paralyses, Peripheral Neuropathy, Periventricular Leukomalacia, Persistent Vegetative State, Pervasive Developmental Disorders, Phytanic Acid Storage Disease, Pick's Disease, Pinched Nerve, Piriformis Syndrome, Pituitary Tumors, Polymyositis, Pompe Disease, Porencephaly, Post-Polio Syndrome, Postherpetic Neuralgia, Postinfectious Encephalomyelitis, Postural Hypotension, Postural Orthostatic Tachycardia Syndrome, Postural Tachycardia Syndrome, Primary Dentatum Atrophy, Primary Lateral Sclerosis, Primary Progressive Aphasia, Prion Diseases, Progressive Hemifacial Atrophy, Progressive Locomotor Ataxia, Progressive Multifocal Leukoencephalopathy, Progressive Sclerosing Poliodystrophy, Progressive Supranuclear Palsy, Prosopagnosia, Pseudo-Torch syndrome, Pseudotoxoplasmosis syndrome, Pseudotumor Cerebri, Psychogenic Movement, Ramsay Hunt Syndrome I, Ramsay Hunt Syndrome II, Rasmussen's Encephalitis, Reflex Sympathetic Dystrophy Syndrome, Refsum Disease, Refsum Disease - Infantile, Repetitive Motion Disorders, Repetitive Stress Injuries, Restless Legs Syndrome, Retrovirus-Associated Myelopathy, Rett Syndrome, Reye's Syndrome, Rheumatic Encephalitis, Riley-Day Syndrome, Sacral Nerve Root Cysts, Saint Vitus Dance, Salivary Gland Disease, Sandhoff Disease, Schilder's Disease, Schizencephaly, Seitelberger Disease, Seizure Disorder, Semantic Dementia, Septo-Optic Dysplasia, Severe Myoclonic Epilepsy of Infancy (SMEI), Shaken Baby Syndrome, Shingles, Shy-Drager Syndrome, Sjogren's Syndrome, Sleep Apnea, Sleeping Sickness, Sotos Syndrome, Spasticity, Spina Bifida, Spinal Cord Infarction, Spinal

Cord Injury, Spinal Cord Tumors, Spinal Muscular Atrophy, Spinocerebellar Atrophy, Spinocerebellar Degeneration, Steele-Richardson-Olszewski Syndrome, Stiff-Person Syndrome, Striatonigral Degeneration, Stroke, Sturge-Weber Syndrome, Subacute Sclerosing Panencephalitis, Subcortical Arteriosclerotic Encephalopathy, Short-lasting, Unilateral, Neuralgiform (SUNCT) Headache, Swallowing Disorders, Sydenham Chorea, Syncope, Syphilitic Spinal Sclerosis, Syringohydromyelia, Syringomyelia, Systemic Lupus Erythematosus, Tabes Dorsalis,Tardive Dyskinesia, Tarlov Cysts, Tay-Sachs Disease, Temporal Arteritis, Tethered Spinal Cord Syndrome, Thomsen's Myotonia, Thoracic Outlet Syndrome, Thyrotoxic Myopathy, Tic Douloureux, Todd's Paralysis, Tourette Syndrome, Transient Ischemic Attack, Transmissible Spongiform Encephalopathies, Transverse Myelitis, Traumatic Brain Injury, Tremor, Trigeminal Neuralgia, Tropical Spastic Paraparesis, Troyer Syndrome, Tuberous Sclerosis, Vascular Erectile Tumor, Vasculitis Syndromes of the Central and Peripheral Nervous Systems, Von Economo's Disease, Von Hippel-Lindau Disease (VHL), Von Recklinghausen's Disease, Wallenberg's Syndrome, Werdnig-Hoffman Disease, Wernicke-Korsakoff Syndrome, West Syndrome, Whiplash, Whipple's Disease, Williams Syndrome, Wilson Disease, Wolman's Disease, and X-Linked Spinal and Bulbar Muscular Atrophy. In some embodiments, the pharmaceutical formulation comprises a therapeutic nucleic acid encoding a therapeutic gene expression product. In some instances, the therapeutic gene expression product is effective to modulate an activity or an expression of a target gene or gene expression product selected from the group consisting of Sarcoglycan Alpha (SGCA), glutamic acid decarboxylase 65 (GAD65), glutamic acid decarboxylase 67 (GAD67), CLN2, Nerve Growth Factor (NGF), Survival Of Motor Neuron 1, Telomeric (SMN1), Factor X (FIX), Retinoid Isomerohydrolase (RPE65), sarco/endoplasmic reticulum Ca2+-ATPase (SERCA2a), β-Glucocerebrosidase (GCase), Frataxin (FXN), Huntingtin (HTN), methyl-CpG binding protein 2 (MECP2), a peroxisomal biogenesis factor (PEX), progranulin (GRN), an antitubulin agent, copper-zinc superoxide dismutase (SOD1), Glucosylceramidase Beta (GBA), NPC Intracellular Cholesterol Transporter 1 (NPC1), and a NLRP3 inflammasome. In some instances, the therapeutic gene expression product comprises gene editing components. In some instances, the gene editing components are selected from the group consisting of small interfering RNA (siRNA), short hairpin RNA (shRNA), a microRNA (miRNA), artificial site-specific RNA endonuclease

(ASRE), zinc finger endonuclease (ZFN), CRISPR/Cas, and transcription factor like effector nuclease (TALEN).

[0016] Aspects disclosed herein provide **methods of manufacturing** a recombinant AAV particle from the AAV capsid of the present disclosure, the method comprising: (a) introducing into a cell a nucleic acid comprising: (i) a first nucleic acid sequence encoding a therapeutic gene expression product; (ii) a second nucleic acid sequence encoding a recombinant viral genome comprising a capsid (*Cap*) gene modified to express the AAV capsid of the present disclosure; and (iii) a third nucleic acid sequence encoding an AAV helper virus genome; and (b) assembling the recombinant AAV particle, the recombinant AAV particle comprising the AAV capsid encapsidating the first nucleic acid.

[0017] Aspects disclosed herein provide **methods of manufacturing** comprising: (a) introducing into a cell a nucleic acid comprising: (i) a first nucleic acid sequence encoding a therapeutic gene expression product enclosed by a 5' and a 3' inverted terminal repeat (ITR) sequence; (ii) a second nucleic acid sequence encoding a viral genome comprising a 5' ITR sequence, a Replication (*Rep*) gene, Capsid (*Cap*) gene, and a 3' ITR, wherein the *Cap* gene encodes the AAV capsid protein described herein; and (iii) a third nucleic acid sequence encoding a first helper virus protein selected from the group consisting of E4orf6, E2a, and VA RNA, and optionally, a second helper virus protein comprising E1a or E1b55k; (b) expressing in the cell the AAV capsid protein described herein; (c) assembling an AAV particle comprising the AAV capsid proteins disclosed herein; and (d) packaging the first nucleic acid sequence in the AAV particle. In some instances, the cell is mammalian. In some instances, the cell is immortalized. In some instances, the immortalized cell is an embryonic stem cell. In some instances, the embryonic stem cell is a human embryonic stem cell. In some instances, the human embryonic stem cell is a human embryonic kidney 293 (HEK-293) cell. In some instances, the *Cap* gene is derived from the deoxyribose nucleic acid (DNA) provided in any one of SEQ ID NOs: 6-10. In some instances, the nucleic acid sequence comprising the *Cap* gene is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identical to any one of the DNA sequences provided in U.S. App. Ser. No. 16/582,635, incorporated herein by reference. In some instances, the 5' ITR and the 3' ITR are derived from an AAV2 serotype. In some instances, the 5' ITR and the 3' ITR are derived from an AAV5 serotype. In some instances, the

5' ITR and the 3' ITR are derived from an AAV9 serotype. In some instances, the first nucleic acid sequence and the second nucleic acid sequence are in *trans*. In some instances, the first nucleic acid sequence and the second nucleic acid sequence are in *cis*. In some instances, the first nucleic acid sequence, the second nucleic acid sequence and the third nucleic acid sequence, are in *trans*.

[0018] Aspects disclosed herein provide **methods of manufacturing** a recombinant AAV particle, the method comprising: (a) providing a recombinant AAV genome comprising: (i) an AAV capsid gene, and (ii) a recognition sequence for a Cre recombinase, wherein the recognition sequence facilitates a recombinase-dependent change that is detectable, and wherein the recombinase recognition sequence comprises two Cre-recognition sites; (iii) transfecting a population of cells expressing the Cre recombinase with the recombinant AAV genome, whereby the Cre recombinase induces a recombination event to generate the recombinase-dependent change in the recombinant AAV genome, and wherein the recombinase-dependent change comprises an inversion of the sequence that is flanked by the Cre-recognition sites; (iv) detecting an increased rate of the recombinase-dependent change a target cell in the population of cells; (v) detecting a decreased rate of the recombinase-dependent change in an off-target cell in the population of cells; and (vi) identifying a recombinant AAV genome generated by the recombinase-dependent change, wherein said identified rAAV genome comprises the inversion, and wherein said identified recombinant AAV genome encodes an AAV capsid particle characterized having an increased specificity for the target cell and a decreased specificity for the off-target cell. In some embodiments, the off-target cell is a hepatocyte. In some embodiments, the target cell is a cell selected from the group consisting of a neuron, a glial cell, a oligodendrocyte, an ependymal cell, an astrocyte, a Schwann cell, a satellite cell, and an enteric glial cell.

[0019] Aspects disclosed herein provide **kits** comprising: (a) a first vector comprising the recombinant vector of the present disclosure; (b) a second vector encoding a helper virus protein; and (c) a third vector comprising a therapeutic nucleic acid encoding a therapeutic gene expression product.

[0020] Aspects disclosed herein provide **kits** comprising: (a) a first vector comprising a first nucleic acid sequence encoding a viral genome comprising in a 5' to 3' direction: (i) a 5'

inverted terminal repeat (ITR) sequence; (ii) a Replication (*Rep*) gene; (iii) a Capsid (*Cap*) gene encoding the AAV capsid proteins described herein, and (iv) a 3' ITR; and (b) optionally, a second vector comprising a second nucleic acid sequence encoding a helper virus protein comprising at least one of E4orf6, E2a, VA RNA, E1a and E1b55k. In some instances, the kit further comprises a cell. In some instances, the cell is mammalian. In some instances, the cell is immortalized. In some instances, the immortalized cell is an embryonic stem cell. In some instances, the embryonic stem cell is a human embryonic stem cell. In some instances, the human embryonic stem cell is a human embryonic kidney 293 (HEK-293) cell. In some instances, the kit further comprises an AAV vector comprising a heterologous nucleic acid encoding a therapeutic gene expression product. In some instances, the AAV vector is an episome.

INCORPORATION BY REFERENCE

[0021] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] The novel features of the invention are set forth with particularity in the appended claims. A better 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 are utilized, and the accompanying drawings of which:

[0023] **FIG. 1** shows a multiplexed selection approach to identify capsids with specific and broad tropisms. Steps 1-6 describe the workflow in Round-1 (R1) selection, steps 7-9 describe Round-2 (R2) selection using synthetic pool method, steps 1a, 2a, and 6a-b show the incorporation of deep sequencing to recover capsids after R1 and R2 selection, and steps 10-11 describe positive and/or negative selection criteria followed by variant characterization.

[0024] **FIG. 2** shows a structural model of the AAV9 capsid (PDB 3UX1) with the insertion site for the 7-mer-i library highlighted in red in the 60-meric (left), trimeric (middle), and monomeric (right) forms.

[0025] **FIG. 3** shows Empirical Cumulative Distribution Frequency (ECDF) of R1 DNA and virus libraries that were recovered by deep sequencing post Gibson assembly and virus production, respectively.

[0026] **FIG. 4** shows distributions of variants recovered from three R1 libraries from Tek-Cre, SNAP25-Cre, and GFAP-Cre brain tissue (n = 2 per Cre line), with capsid libraries sorted by decreasing order of the enrichment score. The enrichment scores of the AAV-PHP.V2 variant are mapped as well.

[0027] **FIG. 5** is a schematic of R2 synthetic pool (left) and PCR pool (right) library design.

[0028] **FIG. 6** shows an overlapping bar chart showing the percentage of library overlap between the mentioned libraries and their theoretical composition.

[0029] **FIG. 7** shows histograms of DNA and virus libraries from the two methods, where the variants in a library are binned by their read counts (in log10 scale) and the height of the histogram is proportional to their frequency.

[0030] **FIG. 8** shows distributions of R2 brain libraries from all Cre transgenic lines (n= 2 mice per Cre Line, mean is plotted) and both methods, where the libraries are sorted in decreasing order of enrichment score (log10 scale). The total number of positively enriched variants from these libraries are highlighted by dotted straight lines and AAV9's relative enrichment is mapped on the synthetic pool plot.

[0031] **FIG. 9** shows a comparison of the enrichment scores (log10 scale) of two alternate codon replicates for 8462 variants from the Tek-Cre brain library (n= 2 mice, mean is plotted). The broken line separates the high-confidence signal (>0.3) from noise. For the high-confidence signal (below), a linear least-squares regression is determined between the 2 codons and the regression line (best fit). The coefficient of determination R2 is shown.

[0032] **FIG. 10** shows heatmaps representing the magnitude (log2 fold change) of a given AA's relative enrichment or depletion at each position given statistical significance is reached (boxed if P-value ≤ 0.0001, two-sided, two-proportion z-test, p-values corrected for multiple comparisons using Bonferroni correction). R2 DNA normalized to oligopool (top, ~9000 AA

sequences), R2 virus normalized to R2 DNA (middle, n = ~9000 sequences), R2 Tek brain library with enrichment over 0.3 (high-confidence signal) from synthetic pool method normalized to R2 virus (bottom, 154 sequences) (n= 2 for brain library, one per mouse. All other libraries, n = 1).

[0033] **FIG. 11** shows heatmaps of Cre-independent relative enrichment across organs (n = 2 mice per Cre line, mean across 6 samples from 3 Cre lines is plotted) for variants enriched in the brain tissue of at least one Cre-dependent synthetic pool selection (lighter text, n = 2 mice per cell-type, mean is plotted) (left). Zoom-in of the most CNS-enriched variants (middle), and of the variants that are characterized in the current study along with spike-in library controls (right) are shown.

[0034] **FIG. 12** shows clustering analysis of variants from synthetic pool brain libraries after enrichment in Tek-Cre (left), GFAP-Cre (middle), and combined SNAP-Cre and Syn-Cre (right) selections. Size of nodes represents relative enrichment in brain. Thickness of edges (connecting lines) representing degree of relatedness. Distinct families (yellow) with the corresponding AA frequency logos (AA size represents prevalence and color encodes AA properties).

[0035] **FIG. 13** shows the 7-mer insertion peptide sequences of AAV-PHP variants between AA positions 588-589 of AAV9 capsid.

[0036] **FIG. 14** shows AAV9 (left) and AAV-PHP.V1 (right) mediated expression using ssAAV:CAG-mNeongreen genome (n = 3, 3 weeks of expression in C57BL/6J adult mice with $3x10^{11}$ vg IV dose/mouse). The images were acquired under same microscope settings as that of the sagittal sections of brain (top) with higher magnification image from cortex (bottom). αGLUT1 antibody staining was used in the image to show vasculature.

[0037] **FIG. 15** shows vascular transduction by ssAAV-PHP.V1:CAG-DIO-EYFP in Tek-Cre adult mice (left) (n = 2, 4 weeks of expression, $1x10^{12}$ vg IV dose/mouse), and by ssAAV-PHP.V1:Ple261-iCre in Ai14 reporter mice (right) (n = 2, 3 weeks of expression, $3x10^{11}$ vg IV dose/mouse). Tissues are stained with αGLUT1.

[0038] **FIG. 16** shows percentage of vasculature stained with αGLUT1 that overlaps with mNeongreen (XFP) expression in cortex. One-way ANOVA non-parametric Kruskal-Wallis test (P-value 0.0036), and follow-up multiple comparisons using uncorrected Dunn's test (P-value of

0.0070 for AAV9 vs PHP.V1) are reported. **P ≤ 0.01 is shown, P > 0.05 is not shown; data is mean ± S.E.M, n= 3 mice per AAV variant, cells quantified from 2-4 images per mouse per cell-type.

[0039] **FIG. 17** shows percentage of cells stained with each cell-type specific marker (αGLUT1, αS100 for astrocytes, αNeuN for neurons, αOlig2 for oligodendrocyte lineage cells) that overlaps with mNeongreen (XFP) expression in cortex. Kruskal-Wallis test (P-value of 0.0078), and uncorrected Dunn's test (P-value of 0.0235 for neuron vs vascular cells, and 0.0174 for neuron vs astrocyte, respectively) are reported. *P 0.05 is shown, and P > 0.05 is not shown; data is mean ± S.E.M, n= 3 mice, cells quantified from 2-4 images per mouse per cell-type.

[0040] **FIG. 18** shows efficiency of vascular transduction (as described in FIG. 16) in Tek-Cre mice (n= 2, mean from 3 images per mouse per brain region).

[0041] **FIG. 19** shows efficiency of vascular transduction in Ai14 mice (n= 2, a mean from 4 images per mouse per brain region).

[0042] **FIG 20** shows transduction by AAV-PHP.B4-B6 and C1 variants, as well as B, eB, and AAV9 controls in sagittal brain and liver sections. Across each set of images (column-wise) acquired, microscope settings were matched with AAV-PHP.eB. The white box on the sagittal brain images marks the thalamus and not the precise region of the figures to the right. Vectors are packaged with ssAAV:CAG-2xNLS-EGFP genome (n = 3 per group, $1x10^{11}$ vg IV dose/ adult C57BL/6J mouse, 3 weeks of expression). Tissues are stained with cell-type specific markers: αNeuN for neurons, αS100 for astrocytes and αOlig2 for oligodendrocyte lineage cells. Liver tissues are stained with a DNA stain, DAPI.

[0043] **FIGS. 21-23** show the percentage of αNeuN+ (FIG. 21), αS100+ (FIG. 22), and αOlig2+ (FIG. 23) cells with detectable nuclear-localized EGFP in the indicated brain regions (n=3 per group, $1x10^{11}$ vg dose). A two-way ANOVA with correction for multiple comparisons using Tukey's test is reported with adjusted P-values (****P ≤ 0.0001, ***P ≤ 0.001, **P ≤ 0.01, *P ≤ 0.05, is shown, and P > 0.05 is not shown on the plot; 95% CI, data is mean ± S.E.M. The dataset comprises a mean of 2 images per region per cell-type marker per mouse).

[0044] **FIG. 24** shows the design of the 3-mer-s PHP.B library with combinations of three AA diversification between AA 587-597 of AAV-PHP.B (or corresponding AA 587-590 of

AAV9). Shared AA identity with the parent AAV-PHP.B is shown along with unique motifs for AAV-PHP.N and AAV-PHP.eB.

[0045] **FIG. 25** shows distributions of R2 brain and liver libraries (at AA level) by enrichment score (normalized to R2 virus library, with variants sorted in decreasing order of enrichment score). The enrichment of AAV-PHP.eB and AAV-PHP.N across all libraries are mapped on the plot.

[0046] **FIG. 26** shows heatmap represents the magnitude (log2 fold change) of a given AA's relative enrichment or depletion at each position across the diversified region, only if statistical significance is reached on fold change (boxed if p-value ≤ 0.0001, two-sided, two-proportion z-test, p-values corrected for multiple comparisons using Bonferroni correction). Plot includes variants that were highly enriched in brain (>0.5 mean enrichment score, where mean is drawn across Vglut2, Vgat and GFAP, n = 1 library per mouse line (sample pooled from 2 mice per line)) and underrepresented in liver (<0.0) (32 AA sequences).

[0047] **FIG. 27** shows clustering analysis of enriched variants from Vgat brain library with node size representing the degree of negative enrichment in liver and the thickness of edges (connecting lines) representing degree of relatedness between nodes. Two distinct families are highlighted in yellow and their corresponding AA frequency logos are shown below (AA size represents prevalence and color encodes AA properties).

[0048] **FIG. 28** shows the percentage of neurons, astrocytes and oligodendrocyte lineage cells with ssAAV-PHP.N:CAG-2xNLS-EGFP in the indicated brain regions (n = 3, $1x10^{11}$ vg IV dose per adult C57BL/6J mouse, 3 weeks of expression, data is mean±S.E.M, 6-8 images for cortex, thalamus and striatum, and 2 images for ventral midbrain, per mouse per cell-type marker using 20x objective covering the entire regions). A two-way ANOVA with correction for multiple comparisons using Tukey's test gave adjusted P-values reported as ****$P \leq 0.0001$, ns for $P > 0.05$, 95% CI.

[0049] **FIG. 29** shows transduction by ssAAV-PHP.N:CAG-NLS-EGFP (n = 2, $2x10^{11}$ vg IV dose per adult C57BL/6J mouse, 3 weeks of expression) with NeuN staining (magenta) across three brain areas (cortex, SNc (substantia nigra pars compacta) and thalamus).

[0050] **FIG. 30** shows clustering analysis showing the brain-enriched sequence families of all variants described herein, either identified in prior studies (PHP.B-B3, PHP.eB) or in the

current study (PHP.B4-B8, PHP.V1-2, PHP.C1-3). The thickness of edges (connecting lines) representing degree of relatedness between nodes. The AA sequences inserted between 588-589 (of AAV9 capsid) for all the variants discussed are shown below.

[0051] **FIG. 31** shows transduction of AAV9, AAV-PHP.V1 and AAV-PHP.N across three different mouse strains: C57BL/6J, BALB/cJ and FVB/NJ in sagittal brain sections (right), along with a higher magnification image of the thalamus brain region (left).

[0052] **FIG. 32** shows transduction by AAV-PHP.B, AAV-PHP.C1-C3 in C57BL/6J and BALB/cJ mice in sagittal brain sections (right), along with a higher magnification image of the thalamus brain region (left)**. In FIGS. 31 and 32, the** white box on the sagittal brain images represents the location of thalamus and not the precise area that is zoomed-in on the figure to the left. The microscope settings of acquired images were matched across all sagittal sections and across all thalamus regions. The insets in AAV-PHP.V1 are zoom-ins with enhanced brightness. The indicated capsids were used to package ssAAV:CAG-mNeongreen (*n* = 2-3 per group, $1x10^{11}$ vg IV dose per 6-8 weeks old adult mouse, 3 weeks of expression. The data reported in FIGS. 31 and 32 are from one independent trial where all viruses were freshly prepared and titered in the same assay for dosage consistency. AAV-PHP.C2 and AAV-PHP.C3 were further validated in an independent trial for BALB/cJ, n = 2 per group).

[0053] **FIG. 33** provides 7-mer and 11-mer variants that were positively enriched in the brain tissue in all cell lines.

[0054] **FIG. 34** provides 7-mer and 11-mer variants enriched in one specific library, but negatively enriched in all other brain and liver libraries.

[0055] **FIG. 35** provides 11-mer variants that were positively enriched in all cre lines in liver tissue.

[0056] **FIG. 36** is a diagram of the genetic switch used in M-CREATE. The Acceptor Vector shows the position of the forward and reverse primers between the Lox sites that are used for selective recovery of capsids from the Cre+ cells. The Rep-AAPΔCap vector shows a deletion of 480 bp in Cap gene in addition to the stop codons that are designed to prevent synthesis of VP1, VP2, and VP3 proteins. AAP protein translation is unaffected by these modifications.

[0057] **FIG. 37** is a schematic of the protocol to selectively recover rAAV genomes from the target population using the Cre-Lox flipping strategy and preparation of the sample for deep sequencing.

[0058] **FIG. 38** illustrates the library coverage for R1 DNA and virus libraries obtained from specific sequencing depths.

[0059] **FIG. 39** shows the percentage of variant overlap within the sampled DNA and virus, or across different Cre lines within tissues, or across tissues from R1 selection.

[0060] **FIG. 40** shows the distributions of AAV capsid read counts for libraries recovered by NGS from brain tissue across different Cre transgenic mice post R1 selection. The dotted line is illustrative only and roughly separates the signal from noise (see Methods for estimation of signal v.s. noise) where signal in this context represents the input for the R2 selection.

[0061] **FIG. 41** shows rAAV genome recovery from tissues using different treatments are shown with total rAAV genome recovery from 0.1 g of liver.

[0062] **FIG. 42** shows the percentage of rAAV genomes recovered per ng of total extracted DNA.

[0063] **FIG. 43** shows the CT value (cycle threshold from qPCR) of rAAV genome extracted by trizol that were treated with SmaI restriction enzyme or untreated.

[0064] **FIG. 44** shows CT value of mitochondrial DNA (internal control for smaller genome recovery, fold change = 10.79 ($2^{\Delta CT}$)) recovered from 1 ng of total DNA from liver tissue. In FIGS. 41-44, n = 4 mice; 2 from GFAP-Cre line and 2 from Tek-Cre line, each data point is drawn from the mean of three technical replicates, error bar is mean±S.E.M., Mann-Whitney test, two-tailed (exact P-value of 0.0286 (*$P \leq 0.05$), in FIGS. 41, 42, and 44, and 0.1143 (n.s., $P > 0.05$, CI 95%) in FIG. 43). The data reported FIGS. 41, 42, and 44 are from one independent trial, and FIG. 43, from three independent trials.

[0065] **FIG. 45** shows the vector yields obtained per 10 ng of capsid DNA library across R1 and R2 vector productions.

[0066] **FIG. 46** shows distributions of the DNA and virus libraries produced by the synthetic pool and PCR pool methods by the standard score of NGS read counts. The variants in virus libraries are sorted by the decreasing order of standard score and their scores from respective DNA libraries are mapped onto them.

[0067] **FIG. 47** shows correlations between the standard scores of read counts for the DNA and virus libraries (n = 1 per library) produced by the synthetic pool and PCR pool methods is determined by linear least-squares regression, and the regression line (best fit) and R2 representing the coefficient of determination.

[0068] **FIG. 48** shows distributions of capsid libraries from brain tissue of two mice used in each Cre line selection, as produced by the synthetic pool (left) and PCR pool (right) designs. The distribution of spike-in library introduced in the synthetic pool library design is shown at center.

[0069] **FIG. 49** illustrates correlations of enrichment scores of variants from the brain libraries (n = 2 per Cre line, mean is plotted) produced by synthetic pool and PCR pool methods is determined by the same method described with respect to FIG. 47.

[0070] **FIG. 50** shows correlation analysis between the enrichment score (log10) of two alternate codon replicates of variants from the GFAP-Cre (left), SNAP-Cre (center), and Syn-Cre (right) brain libraries by linear least-squares regression (n = 2 per Cre line, mean is plotted). The dotted line separates the high-confidence signal from noise. High confidence signal (below) is assessed by a linear regression line (best fit) and R2 represents the coefficient of determination.

[0071] **FIG. 51** shows the difference in enrichment score between the two codon replicates of a variant, across different brain libraries, with over 8000 variants recovered in replicates.

[0072] **FIG. 52** shows heatmaps represent the magnitude (log2 fold change) of AA bias in "output" library 1 normalized to "input" library 2 that reach statistical significance (boxed if P-value ≤ 0.0001, two-sided, two-proportion z-test, except in R1 DNA normalized to known NNK template where one-proportion z-test was performed, and P-values corrected for multiple comparisons using Bonferroni correction). R1 DNA library normalized to NNK template (top left, ~9 million sequences), R1 virus normalized to R1 DNA libraries (bottom left, ~10 million sequences), R2 GFAP library with enrichment score above 1.0 in brain normalized to R2 virus (top right, 20 sequences,) and R2 SNAP library with enrichment score above 1.2 normalized to R2 virus (bottom right, 17 sequences) are shown (n = 1 for DNA, virus, and n = 2 for brain libraries).

[0073] **FIG. 53** shows clustering analysis of positively enriched variants from Tek, GFAP, and combined neuron brain libraries (SNAP and Syn) by PCR pool design, and by synthetic pool

design with spike-in library are shown with size of nodes representing their relative enrichment in brain, and the thickness of edges (connecting lines) representing the extent of shared AA identity between nodes. A distinct family is highlighted in yellow with the corresponding AA frequency logo below (AA size reflects prevalence and color coded based on AA properties).

[0074] **FIG. 54** shows expression of AAV9 (top row) and AAV-PHP.V1 (bottom row) packaging CAG promoter driving mNeonGreen across all organs (n=3, $3x10^{11}$ vg dose per adult C57BL/6J mouse, 3 weeks of expression).

[0075] **FIG. 55** shows expression in cortical astrocytes (S100+) after IV delivery of AAV-PHP.V1 (left) and AAV-PHP.eB (right) capsids carrying the GfABC1D promoter driving expression of nuclear-localized mTurquoise2 reporter ($1x10^{12}$ vg dose per adult mouse, 4 weeks of expression). Percentage of cortical S100+ cells that overlapped with mTurquoise2 expression is quantified (n = 2, each data point is mean from 3 images per mouse).

[0076] **FIG. 56.** shows expression of single-stranded (ss) AAV9, PHP.eB in Ai14-tdTomato reporter adult mouse (n=2-3 per group, $3x10^{11}$ vg dose per adult mouse, 3 weeks of expression)

[0077] **FIG. 57** shows expression of PHP.V1 in Ai14-tdTomato reporter adult mouse (n=2-3 per group, $3x10^{11}$ vg dose per adult mouse, 3 weeks of expression)

[0078] **FIG. 58** shows expression of packaging Ple261 promoter carrying iCre transgene in Ai14-tdTomato reporter adult mouse (n=2-3 per group, $3x10^{11}$ vg dose per adult mouse, 3 weeks of expression) on the left. In the right column, FIG. 58 shows expression of self-complementary (sc) AAV-PHP.V1 carrying CB6 ubiquitous promoter driving EGFP (above) and CAG promoter driving EGFP (below). Lectin DyLight 594 staining is also shown (n=2-3, $3x10^{11}$ vg dose per adult C57BL/6J mouse, 2 weeks of expression). Experiments in FIGS. 56, 57, and the left column of FIG. 58 are reported from one independent trial from a fresh batch of viruses, and titered in the same assay for dosage consistency. Experiments in FIG. 58 were validated in two independent trials (n = 2 per group).

[0079] **FIG. 59** shows transduction of mouse brain by the AAV-PHP.V2 variant and control AAV9, carrying the CAG promoter that drives the expression of mNeonGreen ($n = 3$, $3x10^{11}$ vg IV dose per C57BL/6J adult mouse, 3 weeks of expression). The sagittal brain images (left) were acquired using the same microscope settings to that of the sagittal brain images in FIG. 14.

Higher magnification images of AAV-PHP.V2 transduced brain sections stained with αGLUT or αS100 or αOlig2 are shown.

[0080] **FIG. 60** shows Transduction of brain vasculature by AAV-PHP.V2 carrying CAG-DIO-EYFP in Tek-Cre adult mice (left, $1x10^{12}$ vg IV dose per mouse, 4 weeks of expression), and its efficiency (right) is determined by the overlap of αGLUT1 staining with EYFP expression across different brain areas (n = 2, mean of 3 images per brain region per mouse).

[0081] **FIG. 61** shows transduction of astrocytes by AAV-PHP.V2 in GFAP-Cre adult mouse ($1x10^{12}$ vg IV dose per mouse, 4 weeks of expression). Percentage of cortical $S100^+$ cells that overlapped with EYFP expression is quantified (n = 2, mean of 3 images per mouse).

[0082] **FIG. 62** shows transduction levels of liver hepatocytes quantified as the percentage of $DAPI^+$ cells that are $EGFP^+$ (n = 3, vectors packaged with CAG-2xNLS-EGFP, $1x10^{11}$ vg IV dose/adult C57BL/6J mouse, 3 weeks of expression, mean±S.E.M, 4 images per mouse per group. One-way ANOVA, non-parametric Kruskal-Wallis test gave an approximate P-value of 0.0088).

[0083] **FIG. 63** shows transduction of brain tissue by AAV-PHP.B4, B7, AAV-PHP.X1 (ARQMDLS), and AAV-PHP.X2 (TNKVGNI) packaging CAG-mNeonGreen genome (n = 3, $1x10^{11}$ vg IV dose/adult C57BL/6J mouse, 3 weeks of expression), were acquired using the same microscope settings to that of AAV9 and AAV-PHP.V1 sagittal brain images in FIG. 14.

[0084] **FIG. 64** shows transduction of the brain by AAV-PHP.B8 using the CAG-mRuby2 genome (n = 3, $3x10^{11}$ vg IV dose/ adult C57BL/6J mouse, 3 weeks of expression).

[0085] **FIG. 65** shows Transduction of AAV9 (left), AAV-PHP.X3 (QNVTKGV) (middle) and AAV-PHP.X4 (LNAIKNI) (right) vectors packaging CAG-2xNLS-EGFP (n = 2, $1x10^{11}$ vg IV dose/ adult C57BL/6J mouse, 3 weeks of expression). Data in FIGS. 62-65 is reported from one independent trial.

[0086] **FIGS. 66-67** show distributions of R1 (FIG. 66) and R2 (FIG. 67) brain libraries (at AA level, standard score (SS) of RCs sorted in decreasing order of scores). The SS for AAV-PHP.N and AAV-PHP.eB across libraries are mapped on the zoomed-in view of this plot (dotted line box).

[0087] **FIG. 68** shows a heatmap of AA distributions across the diversified region of the positively enriched variants from R2 liver library (top 100 sequences) normalized to the R2 virus (input library).

[0088] **FIG. 69** shows clustering analysis of positively enriched variants from GFAP and Vglut2 brain libraries are shown with size of nodes representing their relative negative enrichment in liver, and the thickness of edges (connecting lines) representing their relative identity between nodes.

[0089] **FIG. 70** shows expression of AAV-PHP.B (top row) and AAV-PHP.N (bottom row) packaged with ssAAV:CAG-mNeonGreen across all organs (n = 3, $3x10^{11}$ vg IV dose per adult C57BL/6J mouse, 3 weeks of expression).

[0090] **FIG. 71** shows transduction of mouse brain by the AAV-PHP.N variant, carrying the CAG promoter that drives the expression of mNeonGreen (*n* = 3, $1x10^{11}$ vg IV dose per C57BL/6J adult mouse, 3 weeks of expression). Fluorescence *in situ* hybridization chain reaction (FITC-HCR) was used to label excitatory neurons with Vglut1 and inhibitory neurons with Gad1. Few cells where EGFP expression co-localized with specific cell markers are highlighted by asterisks symbol.

[0091] **FIG. 72** shows transduction of AAV9, AAV-PHP.eB and AAV-PHP.V1 in human brain microvascular endothelial cell culture (HBMEC). The vectors were packaged with ssAAV:CAG-mNeongreen. The mean fluorescence intensity across the groups were quantified (n=3 tissue culture wells of 0.95 cm^2 surface area per group, 3 images per well per group per dose was imaged after three days of expression, doses $1x10^8$ vg and $1x10^{10}$ vg per 0.95 cm^2 surface area). A two-way ANOVA with correction for multiple comparisons using Tukey's test gave adjusted P-value of 0.0051 for AAV9 vs PHP.V1, 0.0096 for PHP.eB vs PHP.V1, 0.8222 for AAV9 vs PHP.eB for $1x10^8$ vg, and 0.0052 for AAV9 vs PHP.V1, 0.0049 for PHP.eB vs PHP.V1, 0.9996 for AAV9 vs PHP.eB for $1x10^{10}$ vg (**P $\leq$ 0.01, is shown and P > 0.05 is not shown on the plot; mean ± S.E.M., 95% CI).

[0092] **FIG. 73** shows the transduction of cortex brain region by AAV-PHP.B, AAV-PHP.C2 and AAV-PHP.C3 across two different mouse strains: C57BL/6J and BALB/cJ. The vectors were packaged with ssAAV:CAG-mNeongreen (*n* = 2-3 per group, $1x10^{11}$ vg IV dose/ adult mouse, 3 weeks of expression). All images were acquired using the same microscope

settings. The data reported in FIGS. 72 and 73 are from one independent trial where all viruses were freshly prepared and tittered in the same assay for dosage consistency, with additional validation for AAV-PHP.C2 and AAV-PHP.C3 in an independent trial for BALB/cJ.

[0093] **FIG. 74** provides details of a spike-in library of AAV9 and ~50 additional variants (and their alternative codon duplicates), identified in prior publications (includes well characterized variants like AAV-PHP.B or AAVPHP.eB as well as many variants identified using the previous methodology but uncharacterized *in vivo*) act as internal selection controls and standards for the relative performance of the new variants. Deverman, B. E. et al. Cre-dependent selection yields AAV variants for widespread gene transfer to the adult brain. Nat. Biotechnol. 34, 204–209 (2016) and Chan, K. Y. et al. Engineered AAVs for efficient noninvasive gene delivery to the central and peripheral nervous systems. Nat. Neurosci. 20, 1172–1179 (2017); the content of each of which is incorporated herein by reference. The spike-in library was generated as part of the synthetic pool library.

[0094] **FIG. 75** shows enrichment scores for the spike-in library.

DETAILED DESCRIPTION

[0095] While preferred instances of the present disclosure have been shown and described herein, it will be obvious to those skilled in the art that such instances are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the instances of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

[0096] Provided herein are modified adeno-associated (AAV) virus capsid compositions useful for integrating a transgene into a target cell or environment (*e.g.*, a cell-type or tissue) in a subject when they are administered systemically (*e.g.*, intravenous, intranasal) to the subject. The modified AAV capsid proteins of the present disclosure comprise at least one insertion or substitution of an amino acid in a corresponding parental AAV capsid protein that confers a desired tropism such as an increased or decreased specificity as compared to a reference AAV

capsid protein, or increased or decreased transgene transduction efficiency as compared to a reference AAV capsid protein.

[0097] Disclosed herein are AAV capsids engineered with desired tropisms, such as an increased specificity of viral transduction in a target *in vivo* environment, such as a tissue or cell. In some embodiments, the AAV capsids of the present disclosure are engineered to specifically target the central nervous system (CNS) of a subject. In some embodiments, the AAV capsids of the present disclosure are engineered to specifically target the liver of a subject. The AAV capsids can encapsidate a viral vector with a heterologous nucleic acid encoding, for example, a therapeutic gene expression product. Highly specific transduction of the heterologous nucleic acid in a target *in vivo* environment (*e.g.*, brain, liver) can be achieved upon systemic delivery to a subject of the AAV capsid of the present disclosure encapsidating a heterologous nucleic acid. The AAV capsids disclosed herein are advantageous for many applications, such as diagnosing and/or treating monogenetic disorders of the brain (*e.g.*, GLUT1-deficiency syndrome, mucoploysaccharidosis type IIIC), producing adoptive cellular therapies, and biomedical research applications.

[0098] The AAV capsids comprise AAV capsid proteins (*e.g.*, VP1, VP2, and VP3), each with an insertion or a substitution of at least one amino acid at an amino acid in the 588 loop of a parental AAV capsid protein structure (AAV9 VP1 numbering). The 588 loop contains the site of heparan sulfate binding of AAV2 and amenable to peptide display. The only known receptors for AAV9 is N-linked terminal galactose and AAV receptor (AAVR), but many indications point toward there being others. Modifications to AAV9 588 loop are shown herein to confer an increased specificity and transgene transduction in target *in vivo* environments as compared to a reference AAV in rodent models. In some cases, the parental AAV capsid protein has an AAV serotype 9 (alias AAV9).

[0099] The most common method of AAV-mediated transgene delivery is by direct injection to the target *in vivo* environment, which is disadvantageous for many reasons, including risk of injury or death, pain, and higher cost, as compared to less invasive methods. For example, intracranial injection can cause hemorrhaging of the brain. Previous AAV-mediated delivery by intravenous administration avoids a need for a direct injection, but suffers from reduced specificity for the target *in vivo* environment (*e.g.*, tissue or cell) resulting in off-target

transduction events and necessitating a larger viral load to achieve sufficient therapeutic levels in the target *in vivo* environment. This is especially evident when the AAV must cross the blood brain barrier (BBB).

[0100] Methods are disclosed comprising systemically administering an AAV capsid of the present disclosure encapsidating a viral vector comprising a transgene (*e.g.*, therapeutic nucleic acid) with an increased specificity, as compared to a reference AAV capsid protein. The AAV capsids of the present disclosure are capable of crossing the BBB, and transducing a transgene in a particular target cell-type (*e.g.*, neuron, endothelial cell) in a subject. Accordingly, the AAV capsid proteins of the present disclosure are suitable for transgene therapy to treat human disease, particularly disease that effects the target *in vivo* environment.

[0101] The transgenes contained in a recombinant AAV (rAAV) vector and encapsidated by the AAV capsid proteins of the present disclosure are also provided herein. The transgenes disclosed herein are delivered to a subject for a variety of purposes, such as to treat a disease or condition in the subject. The transgene can be gene editing components that modulate the activity or expression of a target gene or gene expression product. Alternatively, the transgene is a gene encoding a therapeutic gene expression product that is effective to modulate the activity or expression of itself, or another target gene or gene expression product.

[0102] Provided herein, are methods of identifying the 7-mer or 3-mer peptide insertions comprising multiplexed Cre recombination-based AAV targeted evolution (M-CREATE). The M-CREATE method of the present disclosure supports (1) the calculation of a true enrichment score for each variant by using deep sequencing to correct for biases in viral production prior to selection, (2) reduced propagation of bias in successive rounds of selection through the creation of a post-round 1 synthetic pool library with equal variant representation, (3) the reduction of false positives by including two codon replicates of each selected variant in the pool, and (4) both positive and negative selection criteria by comparing deep sequencing of recovered capsid libraries among multiple targets (cells types or organs). These features allow informed, confident choices on variants worthy of validation and characterization *in vivo*.

[0103] Disclosed herein are methods of producing the AAV capsids comprising the AAV capsid proteins and viral vector encoding a therapeutic nucleic acid. The AAV capsid proteins are produced by introducing into a cell (*e.g.*, immortalized stem cell) a first vector encoding the

transgene (*e.g.*, containing the therapeutic nucleic acid), a second vector encoding the AAV genome with a AAV capsid protein, and a third vector encoding helper virus proteins, required for assembly of the AAV capsid structure and packaging of the transgene in the AAV capsid. The assembled AAV capsid can be isolated and purified from the cell using suitable methods known in the art.

[0104] The recombinant AAV vectors comprising a nucleic acid sequence encoding the AAV capsid proteins of the present disclosure as also provided herein. For example, the viral vectors of the present disclosure comprise a nucleic acid sequence comprising the AAV viral Cap (Capsid) encoding VP1, VP2, and VP3, at least one of which is modified to produce the AAV capsid proteins of the present disclosure. The recombinant AAV vector provided can be derived from an AAV serotype (*e.g.*, AAV9).

I. COMPOSITIONS

[0105] Recombinant adeno-associated virus (rAAV) mediated gene delivery leverages the AAV mechanism of viral transduction for nuclear expression of an episomal heterologous nucleic acid (*e.g.,* a transgene, therapeutic nucleic acid). Upon delivery to a host *in vivo* environment, a rAAV will (1) bind or attach to cellular surface receptors on the target cell, (2) endocytose, (3) traffic to the nucleus, (4) uncoat the virus to release the encapsidated heterologous nucleic acid , (5) convert of the heterologous nucleic acid from single-stranded to double-stranded DNA as a template for transcription in the nucleus, and (6) transcribe of the episomal heterologous nucleic acid in the nucleus of the host cell ("transduction"). rAAVs engineered to have an increased specificity (binding to cellular surface receptors on the target cell) and transduction efficiency (transcription of the episomal heterologous nucleic acid in the host cell) are desirable for gene therapy applications.

[0106] A rAAV comprises an AAV capsid that can be engineered to encapsidate a heterologous nucleic acid (*e.g.,* therapeutic nucleic acid, gene editing machinery). The AAV capsid is made up of three AAV capsid protein monomers, VP1, VP2, and VP3. Sixty copies of these three VP proteins interact in a 1:1:10 ratio to form the viral capsid (**FIG. 2**). VP1 covers the whole of VP2 protein in addition to a ~137 amino acid N-terminal region (VP1u), VP2 covers the whole of VP3 in addition to ~65 amino acid N-terminal region (VP1/2 common

region). The three capsid proteins share a conserved amino acid sequence of VP3, which in some cases is the region beginning at amino acid position 138 (*e.g.*, AA139-736).

[0107] The AAV VP3 structure contains highly conserved regions that are common to all serotypes, a core eight-stranded β-barrel motif (βB-βI) and a small α-helix (αA). The loop regions inserted between the β-strands consist of the distinctive HI loop between β-strands H and I, the DE loop between β-strands D and E, and nine variable regions (VRs), which form the top of the loops. These VRs, such as the AA588 loop, are found on the capsid surface and can be associated with specific functional roles in the AAV life cycle including receptor binding, transduction and antigenic specificity.

[0108] Disclosed herein are AAV capsids comprising AAV capsid proteins with a substitution at the 588 loop that confer a desired tropism characterized by a higher specificity for transduction in specific cell-types, including for *e.g.*, brain cell types (*e.g.,* brain endothelial cells, neurons, astrocytes) and liver cell types. In particular, the AAV capsid proteins disclosed herein enable rAAV-mediated transduction of a heterologous nucleic acid (*e.g.*, transgene) in the brain or the liver of a subject. The AAV capsids of the present disclosure, or the AAV capsid proteins, may be formulated as a pharmaceutical composition. In addition, the AAV capsids or the AAV capsid proteins can be isolated and purified to be used for a variety of applications.

A. ADENO-ASSOCIATED VIRUS (AAV) CAPSID PROTEINS

[0109] Disclosed herein are recombinant AAV (rAAV) capsids comprise AAV capsid proteins that are engineered with a modified capsid protein (*e.g.,* VP1, VP2, VP3). In some embodiments, the rAAV capsid proteins of the present disclosure are generated using the methods disclosed herein (*e.g.,* M-CREATE). In some embodiments, the AAV capsid proteins are used in the methods of delivering a therapeutic nucleic acid (*e.g.,* a transgene) to a subject. In some instances, the rAAV capsid proteins have desired AAV tropisms rendering them particularly suitable for certain therapeutic applications, *e.g.*, the treatment of a disease or disorder in a subject such as those disclosed herein.

[0110] The rAAV capsid proteins are engineered for optimized entry into and through the blood brain barrier (BBB) of a subject upon systemic administration of the rAAV to the subject, such as those provided in **Tables 2-3, and FIG. 33**. Prior methods of AAV-mediated delivery of

a therapeutic transgene to the brain required intracranial injection. Intracranial injection is an invasive procedure that causes a subject discomfort, and in some cases, pain. For example, intracranial injection can cause hemorrhaging of the brain. Additionally, intracranial delivery has limited spread and is highly heterogeneous. The rAAV capsid proteins provided in **Tables 2-4**, and **FIG. 33** are engineered to have tropisms that eliminate the need for intracranial injection, while also achieving widespread and efficient transduction of an encapsidated transgene. In particular, the tropisms comprise at least one of an increased specificity and efficiency (*e.g.*, of viral transduction) in the central nervous system (CNS) of a subject, as compared to a reference AAV.

[0111] The engineered AAV capsid proteins described herein have, in some cases, an insertion of an amino acid that is heterologous to the parental AAV capsid protein at the amino acid position in the 588 loop. In some embodiments, the amino acid is not endogenous to the parental AAV capsid protein at the amino acid position of the insertion. The amino acid may be a naturally occurring amino acid in the same or equivalent amino acid position as the insertion of the substitution in a different AAV capsid protein.

[0112] Aspects provided herein provide amino acid insertions comprising seven amino acid polymer (7-mer) inserted at AA588_589, and may additionally include a substitution of one or two amino acids at amino acid positions flanking the 7-mer sequence (*e.g.*, AA587-588 and/or AA589-590) to produce an eleven amino acid polymer (11-mer) at the 588 loop of a parental AAV capsid protein. The 7-mers described herein were advantageously generated using polymerase chain reaction (PCR) with degenerate primers, where each of the seven amino acids is encoded by a deoxyribose nucleic acid (DNA) sequence N-N-K. "N" is any of the four DNA nucleotides and K is guanine (G) or thymine (T). This method of generating random 7-mer amino acid sequences enables 1.28 billion possible combinations at the protein level. Since the 7-mers developed are random, some amino acids in the 7-mer may be naturally occurring in the AAC capsid protein at that amino acid position, while other amino acids may differ.

[0113] Recombinant AAVs (rAAVs) were generated, each with a unique 7-mer or 11-mer at the 588 loop and each encapsidating a reporter gene that, when administered systemically in multiple transgenic animals, enabled the selective amplification and recovery of sequences that effectively transduced the reporter gene in a target *in vivo* environment of the transgenic animal.

7-mers and 11-mers that were found to be positively enriched in the target *in vivo* environment (e.g, central nervous system, liver) are provided herein. "Enrichment" is the prevalence of a given 7-mer or an 11-mer in the tissue of the *in vivo* environment compared to its prevalence in the viral library that was administered to the transgenic animal. An enrichment score above 0 indicates a positive enrichment. An enrichment score below 0 indicates a negative enrichment. A subset of the rAAVs with desired enrichment profiles were tested individually *in vivo* to determine exact systemic expression (*e.g.*, specificity and transduction efficiency). rAAVs from this subset exhibiting a desired tropism comprising increased specificity of viral transduction, and in some cases, transduction efficiency are considered to be uniquely suited for targeted rAAV-mediated transgene delivery useful for a wide variety of purposes (*e.g.*, therapeutic, diagnostic, scientific discovery).

[0114] The rAAV particles with the 7-mers or 11-mers described herein have an increased transduction efficiency in a target *in vivo* environment (*e.g.*, tissue or cell type). In some instances, the increased transduction efficiency comprises a 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, 16-fold, 17-fold, 18-fold, 19-fold, 20-fold, 21-fold, 22-fold, 23-fold, 24-fold, 25-fold, 26-fold, 27-fold, 28-fold, 29-fold, 30-fold, 31-fold, 32-fold, 33-fold, 34-fold, 35-fold, 36-fold, 37-fold, 38-fold, 39-fold, 40-fold, 41-fold, 42-fold, 43-fold, 44-fold, 45-fold, 46-fold, 47-fold, 48-fold, 49-fold, 50-fold, 75-fold, or 100-fold increase, or more, relative to a reference AAV. In some instances, the increased transduction efficiency is at least 30-fold. In some instances, the increased transduction efficiency is at least 40-fold. In some instances, the increased transduction efficiency is at least 50-fold. In some instances, the increased transduction efficiency is at least 60-fold. In some instances, the increased transduction efficiency is at least 80-fold. In some instances, the increased transduction efficiency is at least 90-fold. In some instances, the increased transduction efficiency is at least 100-fold.

[0115] The rAAV particles with the 7-mers or 11-mers described herein have an increased specificity in a target *in vivo* environment (*e.g.*, tissue or cell type), as compared to a reference AAV. Detecting whether a rAAV possesses more or less specificity for a target *in vivo* environment than a reference AAV, includes measuring a level of gene expression product (*e.g.*, RNA or protein) expressed from the heterologous nucleic acid encapsidated by the rAAV in a

tissue sample obtained from the target *in vivo* environment in a subject; and comparing the measured level to a control level (such as, for *e.g.*, the gene expression product expressed from a heterologous nucleic acid encapsidated by a reference AAV (*e.g.*, AAV9)). Suitable methods for measuring expression of a gene expression product luciferase reporter assay and quantitative polymerase chain reaction (qPCR).

[0116] The increased specificity is correlated with an increased enrichment in the target *in vivo* environment, which in some cases is represented with an enrichment score provided herein in **FIGS. 33-35**. As a non-limiting example, AAV-PHP.V2 (TTLKPFL), which is shown herein to be positively enriched in the brain (enrichment score of ~2.51) also exhibited an increase in reporter gene expression (*e.g.*, measured by fluorescence reporter assay) in the brain (~60% of cortical brain vasculature cells and ~60% cortical astrocytes transduced with the reporter gene) as compared to a reference AAV9 (~0%). Without being bound by a particular theory, the inventors of the present disclosure would expect to see this correlation for all rAAVs disclosed herein, and further, would expect that a more significant the enrichment score (whether negative or positive) would correlate with a more significant specificity to the *in vivo* environment(s) as indicated by a measured level of the gene expression product in the *in vivo* environment(s).

[0117] Transduction efficiency, as disclosed herein, may be measured by at least one of (1) a number of cells in a target *in vivo* or off-target *in vivo* environment expressing the heterologous nucleic acid encapsidated by the modified AAV capsid proteins disclosed herein, and (2) a quantity of expression of the heterologous nucleic acid in a single cell. Specificity for a target *in vivo* environment may be inferred when a presence, or an increase in a level, of rAAV-mediated transduction in a target *in vivo* environment is observed, as compared to a reference AAV. A lack of, or reduced, specificity to an off-target *in vivo* environment may be inferred when an absence, or a decrease in a level, of rAAV-mediated transduction in the off-target *in vivo* environment is observed, as compared to a reference AAV.

[0118] The reference AAV may have a serotype selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or variant thereof. For example, the reference AAV can have a serotype selected from the group consisting of AAV-PHP.B, AAV-PHP.eB, and AAV-PHP.S.

[0119] The rAAV capsid proteins of the present disclosure comprise an insertion of an amino acid in an amino acid sequence of an AAV capsid protein. The AAV capsid, from which an engineered AAV capsid protein of the present disclosure is produced, is referred to as a "parental" AAV capsid. In some cases, the parental AAV has a serotype selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, and AAV12. The complete genome of AAV-1 is provided in GenBank Accession No. NC_002077; the complete genome of AAV-2 is provided in GenBank Accession No. NC_001401 and Srivastava et al., J. Virol., 45: 555-564 (1983); the complete genome of AAV-3 is provided in GenBank Accession No. NC_1829; the complete genome of AAV-4 is provided in GenBank Accession No. NC_001829; the AAV-5 genome is provided in GenBank Accession No. AF085716; the complete genome of AAV-6 is provided in GenBank Accession No. NC_00 1862; at least portions of AAV-7 and AAV-8 genomes are provided in GenBank Accession Nos. AX753246 and AX753249, respectively; the AAV -9 genome is provided in Gao et al., J. Virol., 78: 6381-6388 (2004); the AAV-10 genome is provided in Mol. Ther., 13(1): 67-76 (2006); the AAV-11 genome is provided in Virology, 330(2): 375-383 (2004); portions of the AAV-12 genome are provided in Genbank Accession No. DQ813647; portions of the AAV-13 genome are provided in Genbank Accession No. EU285562.

[0120] In some cases, the parental AAV is derived from an AAV with a serotype selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, and AAV12. The AAV capsid protein that is "derived" from another may be a variant AAV capsid protein. A variant may include, for example, a heterologous amino acid in an amino acid sequence of the AAV capsid protein. The heterologous amino acid may be non-naturally occurring in the AAV capsid protein. The heterologous amino acid may be naturally occurring in a different AAV capsid protein. In some instances, the parental AAV capsid is described in U.S. Pat. App. Ser. Nos. 62/736,904; 16/582,635; 62/832,812; and 62/832,826; the content of each of which is incorporated herein. For example, the parental AAV capsid may be modified at the 455 loop of the AAV capsid protein (*e.g.,* substitutions of 7-mer at AA452-458, AAV9 VP1 numbering).

[0121] In some instances, the parental AAV is AAV9. In some instances, the amino acid sequence of the AAV9 capsid protein comprises SEQ ID NO: 1. The amino acid sequence of

AAV9 VP1 capsid protein (>tr|Q6JC40|Q6JC40_9VIRU Capsid protein VP1 OS=Adeno-associated virus 9 OX=235455 GN=cap PE=1 SV=1) is provided in SEQ ID NO: 1 (MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPG NGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGG NLGRAVFQAKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAKKRL NFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWH CDSQWLGDRVITTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFN RFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTSTVQVFT DSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDGSQAVGRSSFYCLEYFPSQML RTGNNFQFSYEFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSKTINGSGQNQQTLKFSV AGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALNGRNSLMNPGP AMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADKVMITNEEEIKTTNPVATESYGQVA TNHQS**AQAQ**AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHPSPLMGGF GMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKENSKRWNPE IQYTSNYYKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL). In some instances, the parental AAV capsid protein sequence is 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% homologous to SEQ ID NO: 1.

[0122] Disclosed herein are insertions of an amino acid (or amino acid sequence) in an amino acid sequence of an AAV capsid protein at an amino acid position between amino acid 588 and amino acid 589. As used herein, "AA588_589" indicates that the insertion of the amino acid (or amino acid sequence) is immediately after an amino acid (AA) at position 588 and immediately before an AA at position 589 within an amino acid sequence of a parental AAV VP capsid protein (VP1 numbering). Amino acids 587-591 include a motif comprising "**AQAQA**" as set forth in SEQ ID NO: 1. Exemplary AAV capsid protein sequences are provided in **Table 1**. For example, QAVRTSL is inserted at AA588_589 in an AAV9 capsid amino acid sequence, and is provided SEQ ID NO: 3. In another example, TLAVPFK is inserted at AA588_589 in an AAV9 capsid amino acid sequence, and is provided in SEQ ID NO: 2. It is envisioned that the 7-mer insertions disclosed herein (**FIGS. 33-35**, **Tables 2-4**) may be inserted at AA588_589 in an amino acid sequence of a parental AAV9 capsid protein, a variant thereof, or equivalent amino acid position a parental AAV of a different serotype (*e.g.,* AAV1, AAV2, AAV3, and the like).

[0123] The 11-mers described herein may, in some cases, comprise a 7-mer insertion at AA588_589, and substitutions of one or more amino acids at amino acid positions AA587-590. In some cases, the amino acids 587-590 are substituted with an amino acid that is not endogenous to the parental AAV capsid protein at that position. In some cases, AA587 is substituted with D (*e.g.,* A587D). In some cases, AA587 is substituted with an A (*e.g.,* Q587A). In some cases, AA587 is substituted with an S (*e.g.,* Q587S). In some cases, AA587 is substituted with a G (*e.g.,* Q587G). In some cases, AA588 is substituted with a G (*e.g.,* Q588G). In some cases, AA589 is substituted with an N (*e.g.,* A589N). In some cases, AA590 is substituted with a P (*e.g.,* A590). In a non-limiting example SEQ ID NO: 4 (PHP-AAV.eB) comprises an insertion at AA588_AA589 of TLAVPFK, and substitutions A587D and Q588G. In another non-limiting example, SEQ ID NO: 5 (PHP-AAV.N) comprises an insertion at AA588_AA589 of TTLKPFS, and substitutions A587D, Q588G, A589N, and Q590P. It is envisioned that any 7-mer insertion disclosed herein in addition to a substitution with any amino acid at amino acid positions 587-590 may comprise an 11-mer.

[0124] **TABLE 1. Exemplary AAV Capsid Protein Sequences**

SEQ ID NO:	Identifier	Sequence
2	AAV-PHP.B	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKK RLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQP AKKRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGA PVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIAN NLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGY LTLNDGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPF HSSYAHSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSV AGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGAS SWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTG RDNVDADKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**TLA** **VPFK**AQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHT DGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLN SFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNV EFAVNTEGVYSEPRPIGTRYLTRNL

3	AAV-PHP.S	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKK RLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQP AKKRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGA PVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIAN NLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGY LTLNDGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPF HSSYAHSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSV AGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGAS SWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTG RDNVDADKVMITNEEEIKTTNPVATESYGQVATNHQSAQ**QAV** **RTSL**AQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHT DGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLN SFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNV EFAVNTEGVYSEPRPIGTRYLTRNL
4	AAV-PHP.eB	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKK RLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQP AKKRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGA PVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIAN NLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGY LTLNDGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPF HSSYAHSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSV AGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGAS SWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTG RDNVDADKVMITNEEEIKTTNPVATESYGQVATNHQS**DGTLA** **VPFKAQ**AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHT DGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLN SFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNV EFAVNTEGVYSEPRPIGTRYLTRNL
5	AAV-PHP.N	MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDN ARGLVLPGYKYLGPGNGLDKGEPVNAADAAALEHDKAYDQQ LKAGDNPYLKYNHADAEFQERLKEDTSFGGNLGRAVFQAKK RLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQP AKKRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGA PVADNNEGADGVGSSSGNWHCDSQWLGDRVITTSTRTWALPT YNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFNRFHCHFS PRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIAN NLTSTVQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGY

		LTLNDGSQAVGRSSFYCLEYFPSQMLRTGNNFQFSYEFENVPF HSSYAHSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSV AGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGAS SWALNGRNSLMNPGPAMASHKEGEDRFFPLSGSLIFGKQGTG RDNVDADKVMITNEEEIKTTNPVATESYGQVATNHQS**AQTLA** **VPFSNP**AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHT DGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLN SFITQYSTGQVSVEIEWELQKENSKRWNPEIQYTSNYYKSNNV EFAVNTEGVYSEPRPIGTRYLTRNL

[0125] The rAAV capsid proteins described herein may be isolated and purified. The AAV may be isolated and purified by methods standard in the art such as by column chromatography or cesium chloride gradients. Methods for purifying AAV from helper virus are known in the art and may include methods disclosed in, for example, Clark et al., Hum. Gene Ther., 10(6): 1031-1039 (1999); Schenpp and Clark, Methods Mol. Med., 69: 427-443 (2002); U.S. Patent No. 6,566,118 and WO 98/09657.

[0126] The rAAV capsid protein can be conjugated to a nanoparticle, a second molecule, or a viral capsid protein. In some cases, the nanoparticle or viral capsid protein would encapsidate the therapeutic nucleic acid described herein. In some instances, the second molecule is a therapeutic agent, e.g., a small molecule, antibody, antigen-binding fragment, peptide, or protein, such as those described herein. In some instances, the second molecule is a detectable moiety. For example, the modified AAV capsid protein conjugated to a detectable moiety may be used for *in vitro*, *ex vivo*, or *in vivo* biomedical research applications, the detectable moiety used to visualize the modified capsid protein. The modified AAV capsid protein conjugated to a detectable moiety may also be used for diagnostic purposes.

[0127] ***AAV Capsid Proteins Targeting the Central Nervous System***

[0128] Disclosed herein are AAV capsid proteins with a substitution or an insertion of at least one amino acid at an amino acid position described above in a parental AAV capsid protein that confers an increased specificity for a central nervous system (CNS) or peripheral nervous system (PNS) in a subject, even when delivered systemically. One of the many advantages of the AAV capsid proteins described herein is their ability to target the CNS and penetrate the blood brain barrier (BBB).

[0129] The *in vivo* environment can be a cell. The cell can be a cell-type selected from the group consisting of a central nervous system (CNS) cell and a peripheral nervous system (PNS)

cell. Non-limiting examples of CNS cells include a neuron and a glial cell. Glial cells can be selected from the group consisting of an oligodendrocyte, an ependymal cell, and an astrocyte. Non-limiting examples of a PNS cell includes a neuron or a glial cell. The glial cell can be selected from the group consisting of a Schwann cell, a satellite cell, and an enteric glial cell.

[0130] The *in vivo* environment can be a tissue. The tissue can be the brain, or the spinal cord. The tissue can be a region of an organ, example, the cerebrum, the cerebellum, the brainstem, the cortex, the striatum, the thalamus, the lateral ventricles, the putamen, the hypothalamus, the medulla, the pons, the hippocampus, the amygdala, the motor cortex, or a combination thereof.

[0131] Disclosed herein are AAV capsid proteins with at least one amino acid insertion or substitution in a parental AAV capsid protein. The insertion or substitution can be of at least one, two, three, four, five, six, seven, eight, nine, ten, or eleven amino acids, or more. In some instances, the amino acids are contiguous. In some instances, the amino acids are not contiguous.

[0132] In some instances, the insertion is of at least one amino acid is provided in any one of the sequences provided in any one of **Tables 2-3**, or **FIG 6**. In some instances, the insertion is of at least two amino acids provided in any one of the sequences provided in any one of **Tables 2-3**, or **FIG 6**. In some instances, the insertion is of at least three amino acids provided in any one of the sequences provided in any one of **Tables 2-3**, or **FIG 6**. In some instances, the insertion is of at least four amino acids provided in any one of the sequences provided in any one of **Tables 2-3**, or **FIG 6**. In some instances, the insertion is of at least five amino acids provided in any one of **Tables 2-3**, or **FIG 6**. In some instances, the insertion is of at least six amino acids provided in any one of **Tables 2-3**, or **FIG 6**. In some instances, the insertion is of at least seven amino acids provided in any one of **Tables 2-3**, or **FIG 6**.

[0133] Disclosed herein are AAV capsid proteins with an insertion of at least one amino acid X1, wherein X1 is selected from the group consisting of A, E, D, G, R, S and T. In some instances, the insertion further comprises two amino acids, wherein X2 is selected from the group consisting of A, G, I, L, M, N, Q, R, T, and Y. In some instances, the insertion further comprises three amino acids, wherein X3 is selected from the group consisting of E, K, L, T, and Q. In some instances, the insertion further comprises at least four amino acids, wherein X1 is selected from the group consisting of A, E, D, G, R, S and T, X2 is selected from the group

consisting of A, G, I, L, M, N, Q, R, T, and Y, X3 is selected from the group consisting of E, K, L, T, and Q, and X4 is selected from the group consisting of G, I, K, L, M, R, T, and V. In some instances, the insertion further comprises five amino acids wherein X5 is selected from the group consisting of A, D, G, P, L, Q, and V. In some instances, the insertion further comprises at least six amino acids, wherein X6 is selected from the group consisting of F, K, L, N, P, Q, S, and V. In some instances, the insertion further comprises at least seven amino acids, wherein X7 is selected from the group consisting of I, K, L, P, S, and V.

[0134] In some embodiments, X1, X2, X3, X4, X5, X6, and X7 are contiguous (X1-X2-X3-X4-X5-X6-X7). In some embodiments, any two of X1, X2, X3, X4, X5, X6, and X7 are contiguous. In some embodiments, any three of X1, X2, X3, X4, X5, X6, and X7 are contiguous. In some embodiments, any four of X1, X2, X3, X4, X5, X6, and X7 are contiguous. In some embodiments, any five of X1, X2, X3, X4, X5, X6, and X7 are contiguous. In some embodiments, any six of X1, X2, X3, X4, X5, X6, and X7 are contiguous. In some embodiments, any seven of X1, X2, X3, X4, X5, X6, and X7 are contiguous. In some embodiments, X1, X2, X3, X4, X5, X6, and X7 are not contiguous. In some embodiments, the insertion is not TLAVPFK.

[0135] The 7-mers disclosed herein, in some cases share a common motif. A 7-mer (X1-X2-X3-X4-X5-X6-X7) may in some cases advantageously have a T in position X1, an L in position X2, a P in positive X5, an F in position X6, and a K or L in position X7. In some embodiments, the 7-mer comprises T-L-X3-X4-P-F-K, wherein X3 and X4 are any amino acid. In some embodiments, the 7-mer comprises T-L-X3-X4-P-F-L, wherein X3 and X4 are any amino acid. In some cases, X3 is not an A. In some cases, X3 is A, S, Q, or E or L. In some cases, X4 is not a V. In some cases, X4 is R, K, V, or a Q.

[0136] In some cases, the 7-mer may be X1-L-A-V-P-F-K, wherein X1 is any amino acid other than T, S, or N; X1-X2-A-V-P-F-K, wherein X1 is any amino acid other than T, S, or N, and X2 is any amino acid other than L or V; or X1-X2-X3-V-P-F-K, wherein X1 is any amino acid other than T, S, or N, X2 is any amino acid other than L or V, and X3 is any amino acid other than A, S, Q, P, or T; or X1-X2-X3-X4-P-F-K, wherein X1 is any amino acid other than T, S, or N, X2 is any amino acid other than L or V, X3 is any amino acid other than A, S, Q, P, or T, and X4 is any amino acid other than V, T, Q, N, L, or M. In some instances, the 7-mer is T-L-

A-X4-P-F-K, wherein X is any amino acid other than V. In some instances, the 7-mer is T-L-A-X4-P-F-K, wherein X is any amino acid other than, T, Q, N, L, or M.

[0137] In some cases, the 7-mer (X1-X2-X3-X4-X5-X6-X7) comprises TALKPFL. In some instances, the 7-mer comprises TTLKPFL. In some instances, the 7-mer comprises TLQIPFK. In some instances, the 7-mer comprises TMQKPFI. In some instances, the 7-mer comprises SIERPFK. In some instances, the 7-mer comprises RYQGDSV.

[0138] In some instances, the AAV capsid protein comprises an insertion of at least or about three, four, five, six, or seven amino acids of an amino acid sequence T-X2-L-K-P-F-L at an amino acid position 588_589 in a parental AAV9 capsid protein (SEQ ID NO: 1), wherein X2 is A or T. In some cases, the AAV capsid protein has an increased specificity for viral transduction in brain vascular cells (GLUT1+), as compared to a reference AAV (*e.g.*, AAV9). In some cases, the AAV capsid protein has increased specificity for viral tranduction in astrocytes, as compared to a reference AAV (*e.g.*, AAV9).

[0139] In some instances, the AAV capsid protein comprises an insertion of at least or about three, four, five, six, or seven amino acids of an amino acid sequence T-X2-Q-X4-P-F-X7 at an amino acid position 588_589 in a parental AAV9 capsid protein (SEQ ID NO: 1), wherein X2 is L or M; X4 is I, K, or L; X7 is K or I. In some cases, the AAV capsid protein has increased specificity for viral transduction in neurons and astrocytes, as compared to a reference AAV (*e.g.*, AAV9). In some instances, the amino acid sequence is TLQIPFK. In some instances, the amino acid sequence is TMQKPFI. In some instances, the amino acid sequence is TLQLPFK.

[0140] In some instances, the AAV capsid protein comprises an insertion of at least or about three, four, five, six, or seven amino acids of an amino acid sequence S-I-E-R-P-F-K at an amino acid position 588_589 in a parental AAV9 capsid protein (SEQ ID NO: 1). In some cases, the AAV capsid protein has increased specificity for viral transduction in neurons and astrocytes, as compared to a reference AAV (*e.g.*, AAV9).

[0141] In some instances, the AAV capsid protein comprises an insertion of at least or about three, four, five, six, or seven amino acids of an amino acid sequence R-Y-Q-G-D-S-V at an amino acid position 588_589 in a parental AAV9 capsid protein (SEQ ID NO: 1). In some cases, the AAV capsid protein has increased specificity for viral transduction in astrocytes, as compared to a reference AAV (*e.g.*, AAV9).

[0142] TABLE 2: List of 7-mer targeting peptides that can target the CNS with greater efficiency and specificity

SEQ ID NO	Sequence (7mer Amino acid)	SEQ ID NO	7 mer Amino acid	Brain-mean-enrich (log10)
10	ACGTTGCAGATTCCTTTTAAG	435	TLQIPFK	2.730563
11	ACCGCCCTCAAACCCTTCCTC	436	TALKPFL	2.536397
12	ACCACCCTCAAACCCTTCCTC	437	TTLKPFL	2.513839
13	AGCATCGAAAGACCCTTCAAA	438	SIERPFK	2.357132
14	ACCCAAAACAGACCCTTCCTC	439	TQNRPFL	2.22812
15	ACCATGCAAAAACCCTTCATC	440	TMQKPFI	2.165359
16	ACTAGTACGCGGCCGTTTTTG	441	TSTRPFL	2.14357
17	GGCACCTTCGTCCCCCCCACC	442	GTFVPPT	2.110151
18	TGGTCGACTAATGCGGGTTAT	443	WSTNAGY	1.979177
19	ACCCTCGAAAGACCCTTCACC	444	TLERPFT	1.892846
20	ACTGCTGCTAAGCCGTTTCTG	445	TAAKPFL	1.863541
21	ATTAGGATTGGTTATTCGCAG	446	IRIGYSQ	1.835644
22	GAGCGTGTGGGTTTTGCTCAG	447	ERVGFAQ	1.73803
23	GCCGACCTCCTCAACTACAGA	448	ADLLNYR	1.599571
24	CTCGTCGCCGGCTTCAGCCAA	449	LVAGFSQ	1.591793
25	TCGTCTCTGAAGCCTTTTCTG	450	SSLKPFL	1.574365
26	ACGCATTCTAGGCCGTTTATT	451	THSRPFI	1.566468
27	CCTTTTCCTGGTTATTCTGCG	452	PFPGYSA	1.555967
28	ATTATTGTTGGGTATAGTCAG	453	IIVGYSQ	1.515858
29	AGGTATCAGGGTGATTCTGTT	454	RYQGDSV	1.486197
30	AGGTATGCTGGGGATTCTATT	455	RYAGDSI	1.456352
31	AAGACGATTGGGGAGCATTGG	456	KTIGEHW	1.44094
32	TGGATGACGCATGGTTCTGCG	457	WMTHGSA	1.432726
33	GCTGCTTCGAGGCCGTTTCTT	458	AASRPFL	1.3791
34	ACTACTTCTAGGCCGTTTCTT	459	TTSRPFL	1.353519
35	GCTCGTGTGGGTTTGGCTCAG	460	ARVGLAQ	1.345499
36	GGGACTAGTCCGAATCTTGCG	461	GTSPNLA	1.306429
37	GTGCGTACGGGGTATAGTTCT	462	VRTGYSS	1.302979
38	ATTCGGGTGGGGTATAGTTCT	463	IRVGYSS	1.286795
39	ACTACTTTGCGTCCGTTTATT	464	TTLRPFI	1.284391
40	GGTATTACGTCTCTGTTTAAG	465	GITSLFK	1.251837

41	ACCACCCAAACCCCCTTCAGA	466	TTQTPFR	1.192121
42	ACTGTGTCGAGGCCGTTTTTG	467	TVSRPFL	1.171604
43	TATGGGACGAATCCGTTTCGT	468	YGTNPFR	1.13664
44	CCCACCATGGTCGACAGCAGC	469	PTMVDSS	1.099202
45	AATAAGGCTAGTTCTCAGAAT	470	NKASSQN	1.084711
46	ACTTTTCGTAGTTCGAATGAT	471	TFRSSND	1.032118
47	CTGCCGGATCGTTATCCTAAT	472	LPDRYPN	1.019382
48	CAGAATGTTACGAAGGGTGTT	473	QNVTKGV	1.000865
49	GCTCAGTCTCCGATTCTTCGG	474	AQSPILR	0.979922
50	GTGGCTACTGGTTATTCTTCG	475	VATGYSS	0.978116
51	TTGAATTCGAATCGGCCTAAT	476	LNSNRPN	0.9672
52	ACGATTCGTAATAATACGATT	477	TIRNNTI	0.959641
53	GATCTTAGTCGTATTTTTAAG	478	DLSRIFK	0.950386
54	CTCAGCAACAGCGCCAGCCAA	479	LSNSASQ	0.941212
55	CTCGAAAACATGGTCATGAGC	480	LENMVMS	0.937552
56	TTGACTCAGCAGACGGATGTT	481	LTQQTDV	0.936974
57	GCCGGCCTCGCCCACGCCACC	482	AGLAHAT	0.936046
58	AATGCTCATACTGCGCTGGAT	483	NAHTALD	0.933184
59	TGGCCGATTCTTCGGGCTGAT	484	WPILRAD	0.931545
60	GCGCTGGCTGGTCTGTCTCTG	485	ALAGLSL	0.930454
61	CGTATTGATATGCCTTTTAAG	486	RIDMPFK	0.920205
62	ACGATGTCGTTGAGTAGTAGT	487	TMSLSSS	0.919718
63	CAAAACGTCGCCAAAAACCTC	488	QNVAKNL	0.916602
64	TTCGACAACCCCAACAACGTC	489	FDNPNNV	0.915503
65	GTCCTCATGAGAGAAAGCCTC	490	VLMRESL	0.914386
66	CACCACGACACCGGCAGCGCC	491	HHDTGSA	0.912951
67	GATGCGCCGAATAGTGTGGAT	492	DAPNSVD	0.901999
68	ACTGCGAGTAGGGATGCTAAG	493	TASRDAK	0.889552
69	ACTAATTATACGAAGCAGATT	494	TNYTKQI	0.889024
70	CCTCATAATGCTTCTGTGTTG	495	PHNASVL	0.864707
71	ACCAACAACACCAGAAACATC	496	TNNTRNI	0.862873
72	ATGGTTCCTAATCATTCTGGT	497	MVPNHSG	0.859604
73	CCGGTGCCGCAGTCTGAGCAT	498	PVPQSEH	0.852761
74	CTCTACCACGGCGGCAGCACC	499	LYHGGST	0.851158
75	ATGATTCATACTAGGGAGACG	500	MIHTRET	0.850116
76	ACTAATAATACGAAGCCTCTT	501	TNNTKPL	0.849557
77	CTCAACACCACCAGAAACACC	502	LNTTRNT	0.839304

78	GCTTTGCATAATTCTCAGAAT	503	ALHNSQN	0.827469
79	GTGAATAGTACGAGGAATGTT	504	VNSTRNV	0.826565
80	GGTGTTGGGGTTGTTACGAAG	505	GVGVVTK	0.820556
81	GTTTTGTCGAAGCAGTTGGCT	506	VLSKQLA	0.816495
82	TCTAAGTCTCTGCAGCCGTTG	507	SKSLQPL	0.815502
83	TCGAATTCTACGCGGTTGGTT	508	SNSTRLV	0.815119
84	CTCAACCAAACCAAACAAATC	509	LNQTKQI	0.811665
85	AACAACAGCGTCAGACAACTC	510	NNSVRQL	0.806765
86	ATGTCGGGGTATTCGCATACT	511	MSGYSHT	0.804194
87	GTCAAAGTCCCCATCATCACC	512	VKVPIIT	0.799412
88	GGGAATAATACTCGGGCGGTG	513	GNNTRAV	0.797634
89	CAGAATCAGATTAAGAATATT	514	QNQIKNI	0.797303
90	ACCAACATGACCAAACCCCTC	515	TNMTKPL	0.791064
91	AACAACAGCACCAGACTCAGC	516	NNSTRLS	0.790429
92	AGCATGCTCACCAGCATCGTC	517	SMLTSIV	0.790252
93	CTCAACGCCACCGCCAGCAGA	518	LNATASR	0.785269
94	AATACTGGGGTGCAGGTTAGG	519	NTGVQVR	0.785026
95	ACCAACACCGTCAGACCCATC	520	TNTVRPI	0.780569
96	CAGTCTACGCCGGGGGCTACT	521	QSTPGAT	0.779842
97	GGTCATTCTGAGAATTCTCGT	522	GHSENSR	0.778724
98	CTCCCCACCCAAACCCTCAGA	523	LPTQTLR	0.773756
99	AAGAATGCTCCGATGCCTGAT	524	KNAPMPD	0.772397
100	AGCAACAGCACCAAACCCACC	525	SNSTKPT	0.768053
101	CCTATTATTACTATGCCTGCT	526	PIITMPA	0.767318
102	CCCCTCAAAGGCATCGGCAGC	527	PLKGIGS	0.767253
103	GTCCTCAGCGTCAACCACCTC	528	VLSVNHL	0.765014
104	AGTGTGGCTGCTGTGCATATG	529	SVAAVHM	0.764013
105	AGCAACAGCATCAGACTCGTC	530	SNSIRLV	0.763114
106	CATAATGATACTCGTCCTCTT	531	HNDTRPL	0.759962
107	CCTCCGGTGAGGTCTACGGCT	532	PPVRSTA	0.755777
108	ATGAACACCGTCAGAAACCTC	533	MNTVRNL	0.754463
109	TTGACGGATGGTCATCGGATT	534	LTDGHRI	0.754429
110	ACGAATGCGGTGAAGCTGACT	535	TNAVKLT	0.752766
111	CGTGTGGATGCGGTTTTGAGT	536	RVDAVLS	0.750458
112	ACCAACGCCGTCAAAAGCACC	537	TNAVKST	0.749271
113	ATGCTCAACACCACCGCCAGA	538	MLNTTAR	0.747921
114	GGCAACAACACCAGACCCACC	539	GNNTRPT	0.747523

115	CAGTCTGGGGGTAGTGCGTTG	540	QSGGSAL	0.744332
116	GTGATTGCTTTGTCTACTATG	541	VIALSTM	0.743901
117	CTGAATACGATTCGGAATGTG	542	LNTIRNV	0.743811
118	AGCAACGCCACCAGAAGCGTC	543	SNATRSV	0.740235
119	GGCAACGGCACCAAATTCATC	544	GNGTKFI	0.736944
120	AGCAACACCATCAGACCCGTC	545	SNTIRPV	0.736197
121	AGCAACAGCACCAGAGCCATC	546	SNSTRAI	0.734716
122	TTTCATTTGACTGATAGGGGT	547	FHLTDRG	0.733831
123	CCGATTAGGTCGGATACTGTG	548	PIRSDTV	0.731286
124	GCCAACCAAATCCACAACACC	549	ANQIHNT	0.730071
125	TCGAATACGGTTCGGAATACT	550	SNTVRNT	0.727807
126	ACCAGCCTCGGCTACAGCAGC	551	TSLGYSS	0.727167
127	ATCAGCGGCGTCCAAACCAGA	552	ISGVQTR	0.724309
128	TCGAATGCTGTTAGGCAGACT	553	SNAVRQT	0.72361
129	TCTCTTTCTGAGCTTAGGATT	554	SLSELRI	0.723061
130	AGTACTGAGAAGAGGGATGAG	555	STEKRDE	0.721349
131	AACCTCGTCGGCACCCTCATC	556	NLVGTLI	0.72103
132	GGCAACAACATCAGACTCACC	557	GNNIRLT	0.719643
133	GCCGTCCCCACCGGCCTCAGA	558	AVPTGLR	0.717951
134	GGTGATAATAGTCTGACTAGG	559	GDNSLTR	0.717624
135	CACGCCGACAACAGACTCAAA	560	HADNRLK	0.714815
136	AGCAACGCCACCAGAAACTTC	561	SNATRNF	0.714052
137	GGGAATACGACTAGGGGGCTG	562	GNTTRGL	0.713945
138	CTCAACCTCACCGCCACCAAC	563	LNLTATN	0.71358
139	AGCGGCGTCAGCACCACCGAC	564	SGVSTTD	0.711249
140	TATGCTAAGACGTTGGCTATG	565	YAKTLAM	0.710703
141	ATGAACCACACCAAACCCACC	566	MNHTKPT	0.710702
142	GCTAATGCTACGAGGAATTCT	567	ANATRNS	0.707423
143	CAAAACCAAACCAAAATCACC	568	QNQTKIT	0.707235
144	TCTAATGCTATTAAGGCTACG	569	SNAIKAT	0.70699
145	TATCCTGATAATTATGGTAAG	570	YPDNYGK	0.706343
146	GGCAACACCACCATCAGAAGC	571	GNTTIRS	0.705947
147	CTGGGTCTTACGGGTGCGGTT	572	LGLTGAV	0.705628
148	GCGAATAGTACGCGTATTCTG	573	ANSTRIL	0.704068
149	GATAATGCGATTCGTGCGCAG	574	DNAIRAQ	0.703945
150	ACGAATTATACTAAGCTTATG	575	TNYTKLM	0.702916
151	CATAATAGTCCTAGTAGTTAT	576	HNSPSSY	0.70154

152	GAGAATATGGTTCGGTCTGTG	577	ENMVRSV	0.700139
153	ACCAACAACATCAAAAGCTAC	578	TNNIKSY	0.698201
154	ACTAATTCGACGAGGCCTGTG	579	TNSTRPV	0.696679
155	CATACGGCTCCGCCTCATCCT	580	HTAPPHP	0.695156
156	GCCCTCAGCCAAAACACCAGC	581	ALSQNTS	0.692869
157	CCGAATGTGACTAAGAATGCT	582	PNVTKNA	0.692038
158	CTTGATACGCTGACGGGTTAT	583	LDTLTGY	0.690142
159	CCTAATAGTGTGCGTTCTGTT	584	PNSVRSV	0.689082
160	ACCAGCAGCCACCTCCCCCAC	585	TSSHLPH	0.688469
161	GTTCTTCATGGTGGTAATGAT	586	VLHGGND	0.687991
162	AGCAACTACGTCAAAAGCGCC	587	SNYVKSA	0.687276
163	GACAACAACAGCACCAGATGG	588	DNNSTRW	0.687057
164	ACTGTGATGAAGGGTTTTACT	589	TVMKGFT	0.687036
165	AGCCACACCCTCAGCACCCTC	590	SHTLSTL	0.686592
166	CCTGGTCCTCAGCAGGCGAAG	591	PGPQQAK	0.685365
167	ACTTTTGGGACGTCTAAGTTG	592	TFGTSKL	0.684153
168	AGCAACGCCGTCACCAACAGA	593	SNAVTNR	0.683838
169	TTGTCTATGTCGACGGTGCCT	594	LSMSTVP	0.682136
170	AGGCGTTATGATGGTAGGGAG	595	RRYDGRE	0.681722
171	ACCAACAGCACCAAAAACATC	596	TNSTKNI	0.678439
172	ATTAATGCTCAGTGGTCTGCG	597	INAQWSA	0.672085
173	GCCCAAACCAGCAACGACCCC	598	AQTSNDP	0.669325
174	ACGAATGAGACTAGGATGGTG	599	TNETRMV	0.669307
175	GCCAACGCCACCAGAGGCGTC	600	ANATRGV	0.667153
176	GCGGATGTGAATGCTTCGGGT	601	ADVNASG	0.666574
177	CTTAGTGAGCGGAATTATGTG	602	LSERNYV	0.665675
178	AGTGGTGAGCTTGCGCGGGCG	603	SGELARA	0.663381
179	GGGAATACTGCTAAGAATATT	604	GNTAKNI	0.662988
180	GACAACGCCGTCAGACCCCTC	605	DNAVRPL	0.662435
181	ATGATGCTCAGCGGCCTCAAC	606	MMLSGLN	0.660837
182	CCCAACACCATCAGAAACGTC	607	PNTIRNV	0.660528
183	GAGAATTTGACGCGTGGGGTG	608	ENLTRGV	0.659884
184	TTTAGTGCTCGGAGTACGGGG	609	FSARSTG	0.659095
185	GAAAACGCCACCAGAACCTAC	610	ENATRTY	0.657305
186	GGCAACAGCACCAGAATGAAC	611	GNSTRMN	0.656999
187	GGGAATTCTACTAAGTCTCCT	612	GNSTKSP	0.656908
188	ATGCAAACCACCCTCCACCTC	613	MQTTLHL	0.656525

189	AACCCCACCCTCATCACCCTC	614	NPTLITL	0.655924
190	CTTATTTCTGGTCATGCGCAG	615	LISGHAQ	0.655121
191	TTCAACCAAGTCAGAAGCCTC	616	FNQVRSL	0.65493
192	ATGAACATCCTCAGAGAAGTC	617	MNILREV	0.654097
193	AGTGCTATGATGCGTGGTGTT	618	SAMMRGV	0.653566
194	CCCATGCTCAGCAGCCCCAGC	619	PMLSSPS	0.652269
195	CAGAATAATACGCTTAGGTCG	620	QNNTLRS	0.651653
196	AGGCATTCGGATCCGGTGGAG	621	RHSDPVE	0.65144
197	GTGAATACGACGTTTTCTACG	622	VNTTFST	0.65142
198	ATCAACAGCACCAGAGGCATC	623	INSTRGI	0.650374
199	ACCAACGCCGTCAGAGACCTC	624	TNAVRDL	0.649865
200	TCTAATAGTACTAGGCTGTCG	625	SNSTRLS	0.649567
201	ACGTCTATTGCTGGGTCGTTT	626	TSIAGSF	0.647793
202	CTCGGCAGCACCTACCCCAGA	627	LGSTYPR	0.644533
203	GCCAACGTCACCACCCAAAGA	628	ANVTTQR	0.643299
204	AGCAACAGCGTCAGACTCAGC	629	SNSVRLS	0.641635
205	GCTACGAATGAGCCTGATCGG	630	ATNEPDR	0.641008
206	AGAATGAACCCCGAACAAAGC	631	RMNPEQS	0.640866
207	TCGGTTAGTGGTTCGGCTAAT	632	SVSGSAN	0.640362
208	CCGAGTAATAGTACTACGCGT	633	PSNSTTR	0.639664
209	CTTTTTCATGGTACGCATGAG	634	LFHGTHE	0.639176
210	CCCCAACTCGGCAGCACCAAA	635	PQLGSTK	0.638022
211	CCCATCAGCGCCAACAGACTC	636	PISANRL	0.637814
212	AATTCGGGTAATCTTTCTATG	637	NSGNLSM	0.637206
213	AAGGTTGAGGCTATTGGGATG	638	KVEAIGM	0.63585
214	AAGACTTTGCTTAATAGTGTT	639	KTLLNSV	0.635567
215	AATGCTATGGATCTTAAGGTG	640	NAMDLKV	0.633592
216	ATGATGGGTAATGGGTCTTCG	641	MMGNGSS	0.632846
217	AGCAACAGCACCAAAGCCCTC	642	SNSTKAL	0.630646
218	TCTAATAGTACGCGGGGTACG	643	SNSTRGT	0.630359
219	AGCCTCAGCAGCCTCCACGTC	644	SLSSLHV	0.629137
220	ACCCTCAGCGGCGCCCTCACC	645	TLSGALT	0.628275
221	CCGAATACGGTGAGGAATAAT	646	PNTVRNN	0.627943
222	AATAATAATGTGAAGATGACT	647	NNNVKMT	0.627302
223	TCTGTTGCTAAGCCTTTTATG	648	SVAKPFM	0.627075
224	ACGCAGACGACTCGGCTTTCG	649	TQTTRLS	0.625657
225	AATAATGCGACTCGGGGTGGG	650	NNATRGG	0.622765

226	ACCAACACCACCGCCAGAATC	651	TNTTARI	0.621665
227	GAGAATAGTATTCGGACTATT	652	ENSIRTI	0.619021
228	ATTAGGGAGACTTCTGGGAAG	653	IRETSGK	0.618732
229	AGCATCTACTACCACACCGAA	654	SIYYHTE	0.618441
230	GTCCTCGACAACAGCGGCCAA	655	VLDNSGQ	0.618183
231	AGCCACAACATGACCATCAGA	656	SHNMTIR	0.614114
232	ACCATCCCCAGCGCCGGCAAA	657	TIPSAGK	0.612816
233	CCTAGGCATACTTTGAGTCAG	658	PRHTLSQ	0.60799
234	TCGCTTAATGTGCAGGATGTG	659	SLNVQDV	0.607203
235	TATCAGTCTCTGGCTAATCCG	660	YQSLANP	0.607005
236	ATTCTGAATATGTCTACGGAT	661	ILNMSTD	0.606834
237	GTCCTCCACCTCGGCCACAGC	662	VLHLGHS	0.605932
238	GGTGTTACTCAGACTCCGCGT	663	GVTQTPR	0.6059
239	ACCAACGACACCAGAAGAATC	664	TNDTRRI	0.604587
240	CAAACCGACCACACCAGCAGA	665	QTDHTSR	0.604031
241	AAGAATGAGATTAAGAATGTG	666	KNEIKNV	0.603838
242	TGGACTGGTAATGAGAGGCTT	667	WTGNERL	0.603412
243	GGTAAGAGTGATGCTATGCGG	668	GKSDAMR	0.603322
244	GGGAATGCGACTCGTACTTAT	669	GNATRTY	0.602016
245	GCCAGCAACCTCGGCCTCCCC	670	ASNLGLP	0.600647
246	AGCAGCCTCAGCGGCAGCCCC	671	SSLSGSP	0.599424
247	GCCGCCGTCAACCAAGGCGTC	672	AAVNQGV	0.599283
248	GACCAAAACCAACCCAGAGAA	673	DQNQPRE	0.59872
249	CTCACCCAAGACAAACAAGCC	674	LTQDKQA	0.59843
250	TTCGGCAGCAACGAACACAAC	675	FGSNEHN	0.59773
251	CTGAATCAGCCGAATGTGCGG	676	LNQPNVR	0.59703
252	ATGAATACTACGCGTAATCTG	677	MNTTRNL	0.596819
253	ACTAATTCTACTAGGACGAGT	678	TNSTRTS	0.596817
254	TTTGAGCTTTCGCATGTGCCT	679	FELSHVP	0.595373
255	GAAGGCCTCGGCAACGCCGCC	680	EGLGNAA	0.59339
256	CTCACCGTCACCCTCAACCAC	681	LTVTLNH	0.593104
257	TTTGGGAATGCGATTCAGTCT	682	FGNAIQS	0.593063
258	CCGGGTGGGGGTTTGACTCCG	683	PGGGLTP	0.591748
259	CCCAACATGACCAGAAGCCTC	684	PNMTRSL	0.591633
260	AGTCAGCTGCATAGGTTGCAG	685	SQLHRLQ	0.588997
261	AATGATCCTGTGCTGACTGTG	686	NDPVLTV	0.587622
262	GAAAACAGCGTCAGAACCACC	687	ENSVRTT	0.586872

263	GATCGTGTGACTAATCCGAAG	688	DRVTNPK	0.585898
264	CTCAACACCGGCCAAATGAGA	689	LNTGQMR	0.584482
265	ATTAGTCCTTCTCAGGTGAAG	690	ISPSQVK	0.583565
266	TACAGCGCCGACAAAACCACC	691	YSADKTT	0.583168
267	ATTGATAGTGCGGGGATGGCG	692	IDSAGMA	0.582726
268	AGCAACAACATCAAACTCAAC	693	SNNIKLN	0.582501
269	CTTGAGACGCAGCCTAGGACT	694	LETQPRT	0.582054
270	AATTTGCATAGTAATGTGCTG	695	NLHSNVL	0.581653
271	ATGGTCAAAGACACCCAACTC	696	MVKDTQL	0.581409
272	CTCATGCACCTCACCAACCCC	697	LMHLTNP	0.579725
273	GTCGCCAGCCCCGACAAAAGA	698	VASPDKR	0.579259
274	GTCGTCGCCGTCCTCACCAGC	699	VVAVLTS	0.578391
275	AACATCATGGTCAACGTCCCC	700	NIMVNVP	0.578008
276	CCGTATAGTGGGCAGCGGACT	701	PYSGQRT	0.577882
277	CCTCTGCTTAAGACGAATACT	702	PLLKTNT	0.575523
278	GGGAATACTACGGTGCGTGGG	703	GNTTVRG	0.574402
279	ACCAACAAAGTCAGAGACGAC	704	TNKVRDD	0.573889
280	CCCAGCACCGCCCTCCTCGTC	705	PSTALLV	0.573034
281	ATCCAAAGCATCACCCTCAAA	706	IQSITLK	0.572783
282	CCCCTCCACGCCAACATGAGC	707	PLHANMS	0.570881
283	ACCGCCCACGCCGAAGCCAGA	708	TAHAEAR	0.570572
284	ACGAATACGGATTCGTATCGT	709	TNTDSYR	0.569365
285	ACCCACGTCAGCCTCGACAGA	710	THVSLDR	0.569228
286	TTTAGTACGAAGGATCATGTT	711	FSTKDHV	0.568654
287	GACAACACCCAAACCGCCCCC	712	DNTQTAP	0.568553
288	AGCAACAGAATCATCAGCGGC	713	SNRIISG	0.568551
289	ACTAATTCTGTTAGGAATAAT	714	TNSVRNN	0.568237
290	AGCAACGAAGTCAGAAACATG	715	SNEVRNM	0.567847
291	GAACTCTACAAACCCAGCAGA	716	ELYKPSR	0.567258
292	TGGATTACGGGGGGTGCGAGT	717	WITGGAS	0.567159
293	AACAACAGCGTCAGACCCACC	718	NNSVRPT	0.566945
294	CACACCGCCGTCCTCAGAACC	719	HTAVLRT	0.565911
295	AATACTTTGTCTCTTGCTCCT	720	NTLSLAP	0.564955
296	CCCAACGCCAGCGTCAACAGC	721	PNASVNS	0.564885
297	GTTACTGGTGGGAATACTTAT	722	VTGGNTY	0.564099
298	GTCAACGAAAACCTCATCGAA	723	VNENLIE	0.563902
299	GTTTTGACGACTCATTCGAAT	724	VLTTHSN	0.563552

300	CACACCCAACTCCCCCTCACC	725	HTQLPLT	0.562802
301	CGGCAGTCTCTTGAGGCGTTG	726	RQSLEAL	0.562715
302	CCCGACGTCACCGAAGGCAGA	727	PDVTEGR	0.560929
303	CCGACTAATATTATGCTTGAT	728	PTNIMLD	0.560313
304	CCCAACATGAGCGCCATGATC	729	PNMSAMI	0.559451
305	ATTATGAATGGTCAGGCTCTG	730	IMNGQAL	0.558677
306	AATAATAATTCGACGCGTTTT	731	NNNSTRF	0.558656
307	GCCAACGTCACCAGAAGCACC	732	ANVTRST	0.558653
308	CAGAATCTTGGTCTTAATGTG	733	QNLGLNV	0.558202
309	CAAGCCCAAATGAGCAGCGCC	734	QAQMSSA	0.557238
310	CTCACCATGGCCACCAACGTC	735	LTMATNV	0.556779
311	GATCGTGATTCTGTGCAGAAT	736	DRDSVQN	0.55654
312	GTCAACCCCACCAACAACCTC	737	VNPTNNL	0.555076
313	CCGTCTTTTACGACTATGAGT	738	PSFTTMS	0.554811
314	AGGGAGACGCCTATTCCTAAG	739	RETPIPK	0.553803
315	AGCCTCAACTTCACCACCGCC	740	SLNFTTA	0.553055
316	GGTATGAGTGGGGTTGCTCAG	741	GMSGVAQ	0.552736
317	AAGGTTGATGCGGCTCAGAGT	742	KVDAAQS	0.552569
318	CATATTACGACTAATGTGTCT	743	HITTNVS	0.552479
319	GAGCGGGAGTCGGCTCGTCTT	744	ERESARL	0.551876
320	GATAATAGGACTCAGAGGACG	745	DNRTQRT	0.551636
321	TCTGCGCCTAATGTGACTATT	746	SAPNVTI	0.551278
322	GAAAACGGCACCAGAAACACC	747	ENGTRNT	0.55012
323	GGCACCGCCGTCTTCACCGCC	748	GTAVFTA	0.549912
324	GCCAACAACATGAGCCAAACC	749	ANNMSQT	0.549519
325	GGTAATCATACTTATAATCTG	750	GNHTYNL	0.549264
326	CTGAGTCCTTCGAATTCTAAT	751	LSPSNSN	0.549019
327	ATGGGCGCCGACCACAGAACC	752	MGADHRT	0.548749
328	AGTAATTCGACGCGTGGTTCT	753	SNSTRGS	0.548705
329	AATACTTCTGGTGTGCCTAAG	754	NTSGVPK	0.548579
330	ATCAACACCGCCGTCGTCAGC	755	INTAVVS	0.54846
331	ATGGGGGTTCAGGCTTATGTG	756	MGVQAYV	0.54845
332	GGGAATTTTGTTAAGCCGAAT	757	GNFVKPN	0.547942
333	GTGAATTCGGTGAGGATGATT	758	VNSVRMI	0.547171
334	CACGACAGCGCCAACAGCAGA	759	HDSANSR	0.54671
335	CTCGGCGTCAGAGACGACAGC	760	LGVRDDS	0.545708
336	AGCAACGCCGTCAGAGCCAAC	761	SNAVRAN	0.545674

337	CCCGTCCTCGCCGCCACCATG	762	PVLAATM	0.545458
338	AATAAGCCTGTGTCTGGTAAT	763	NKPVSGN	0.544076
339	GTCGGCCTCGCCAGCCACACC	764	VGLASHT	0.541637
340	GGCAGCAACACCAACATGAAA	765	GSNTNMK	0.540634
341	GTTGCTACTACTGTGCATAAT	766	VATTVHN	0.540191
342	AACACCCTCGACAGCAGAGTC	767	NTLDSRV	0.539923
343	AGGGAGGCTAATTTGCAGGCG	768	REANLQA	0.539717
344	GTCGACGCCCTCAGCCACATG	769	VDALSHM	0.539694
345	CTTCGTCTTGCTGGTCTTGCT	770	LRLAGLA	0.539525
346	ATTACGGTGACTAATTATTCG	771	ITVTNYS	0.539447
347	TGGGACAGCGGCAGCGGCGAA	772	WDSGSGE	0.539198
348	TTCGCCAGCGAAACCGTCGCC	773	FASETVA	0.537906
349	CAGAATGTTACGGGGACGAGG	774	QNVTGTR	0.537867
350	CTTAATGGGTTGAATGTGTCT	775	LNGLNVS	0.537505
351	AATATGCTTAAGCAGAGTGAG	776	NMLKQSE	0.537354
352	TTTAATGAGGTTCCGAAGGCG	777	FNEVPKA	0.537144
353	CTCGGCGACATCACCGGCTTC	778	LGDITGF	0.537047
354	ATTTCGGCTTCTCATTCTCGT	779	ISASHSR	0.536983
355	AGTCAGACGCAGATTGCTCTT	780	SQTQIAL	0.53684
356	AATATGGCTACTCAGATGAAG	781	NMATQMK	0.536747
357	GTCAACCACAACATCAGACTC	782	VNHNIRL	0.53652
358	AACGCCCTCCAAGTCCCCGTC	783	NALQVPV	0.536474
359	AATTCGACGGGTATTGATACG	784	NSTGIDT	0.53526
360	GTTGTTGCTGGGCATCTTAAT	785	VVAGHLN	0.534827
361	CGGAATGATGCGATTCTGAAT	786	RNDAILN	0.53456
362	AATCGGGTTGATTCGCGGGCT	787	NRVDSRA	0.53408
363	TCGACGCATTCTACTTATGTG	788	STHSTYV	0.533753
364	AGTGGGCATGGGACTCTGCGG	789	SGHGTLR	0.532267
365	CCCAACAGCACCACCCTCAGC	790	PNSTTLS	0.531723
366	GACACCAAACCCACCAACACC	791	DTKPTNT	0.531589
367	AACAGAGACACCATCAACAAC	792	NRDTINN	0.531212
368	CCCAGAACCCTCAGCGACGGC	793	PRTLSDG	0.530962
369	ACCAAAGACGTCACCACCAGC	794	TKDVTTS	0.53023
370	CTGGGTAATCCTACGCCTTCT	795	LGNPTPS	0.529624
371	TATCAGGCGATGTATAGGGAT	796	YQAMYRD	0.528592
372	AGCGGCGTCCAAGAATTCGAC	797	SGVQEFD	0.528493
373	TCTAATCATCTGTCGACGGTT	798	SNHLSTV	0.528046

374	CACGACGAAAGAGCCAACATG	799	HDERANM	0.526932
375	ACGAATAGTACTCGGTCGCCT	800	TNSTRSP	0.526707
376	CCGACGGATAAGTCTTATCCG	801	PTDKSYP	0.525687
377	ATGACCGAACAAAGAACCGCC	802	MTEQRTA	0.524729
378	ACCAACGCCACCCACAGCAAA	803	TNATHSK	0.523113
379	AATCGGGGTACTTTTAGTGCG	804	NRGTFSA	0.522986
380	AACACCACCAAATTCAACACC	805	NTTKFNT	0.522899
381	GGGATTCCGCCTTTGACTAAG	806	GIPPLTK	0.522659
382	ACCGCCAACAGCACCCAAAGA	807	TANSTQR	0.522626
383	ACTCAGGGTCCGGGTCCGAAG	808	TQGPGPK	0.522239
384	ATGAATACTACGCGGAATTAT	809	MNTTRNY	0.522193
385	CTCAGAGAAGGCACCTTCATG	810	LREGTFM	0.521554
386	AACATCAGCAGCACCGACAGA	811	NISSTDR	0.521154
387	TCGGTTAGTCGGCCGTTTCAG	812	SVSRPFQ	0.520365
388	CCTATGTCTGCTAATGGGAAG	813	PMSANGK	0.518792
389	GAAGTCAGAGGCAACACCTTC	814	EVRGNTF	0.518514
390	TCGCAGAAGGGTCTGTCTGTG	815	SQKGLSV	0.518477
391	ATTGCTGAGAATCTGAGTGCT	816	IAENLSA	0.517935
392	TTCAGCAACATGAACCTCAAA	817	FSNMNLK	0.517734
393	CCTCGTGAGCGGACTTATACT	818	PRERTYT	0.516835
394	TGGTCGCATAATCCGGATTCT	819	WSHNPDS	0.516248
395	GGTCTTCAGACTCTGATTACG	820	GLQTLIT	0.516123
396	AGCAACAGAACCAAAGACATC	821	SNRTKDI	0.515515
397	GTGACTGAGACGATTCTTAAG	822	VTETILK	0.515459
398	TATGTTACGCGTAGTGGTCTG	823	YVTRSGL	0.515319
399	ATGAACGCCAACATCCTCGTC	824	MNANILV	0.514679
400	ACTACGAATCGGGTGGGTACG	825	TTNRVGT	0.51427
401	GTCCTCAAAAGCCACCTCCAA	826	VLKSHLQ	0.51406
402	AGCGACGGCCTCAGAACCCAA	827	SDGLRTQ	0.514048
403	CTCAACAGCGTCAAACCCAAC	828	LNSVKPN	0.513525
404	AGCCAAGCCATCGCCCCCAAA	829	SQAIAPK	0.51343
405	TCTAATAATGTTCGTGCTCCG	830	SNNVRAP	0.513257
406	ATCAGCCACCTCAGCGAAAGC	831	ISHLSES	0.511503
407	CTCCTCCCCGGCATGAGATTC	832	LLPGMRF	0.5114
408	CTTCTTGCGTCGGCTACGAAG	833	LLASATK	0.510718
409	AACCACAACGGCATGGTCAGC	834	NHNGMVS	0.510709
410	CACAGCGGCGAACTCAACAAC	835	HSGELNN	0.510488

411	CTTTCTGCGCCTAAGGATACT	836	LSAPKDT	0.509967
412	ATTGGGACTCATGTGGGGACG	837	IGTHVGT	0.509748
413	GCCGTCGCCCTCGCCAGCGCC	838	AVALASA	0.509614
414	ATTACTCTTCAGTCTAATGCT	839	ITLQSNA	0.509556
415	GTCGACCACAGCCTCACCAGC	840	VDHSLTS	0.509193
416	GGCAACGAAGCCACCAGCCTC	841	GNEATSL	0.508729
417	CCCGTCAGCAGCACCACCCTC	842	PVSSTTL	0.507682
418	CCCTACCAAACCAGCAGCGCC	843	PYQTSSA	0.507351
419	ACCAGCGTCGTCAGCGCCTTC	844	TSVVSAF	0.507058
420	AACGGCGTCCCCGACAACAAC	845	NGVPDNN	0.50693
421	AGCACCCAAACCATCGGCTTC	846	STQTIGF	0.505905
422	ATTCGGAGTTCTGATCTTGCG	847	IRSSDLA	0.505273
423	AACACCCAAAGCGCCAAATAC	848	NTQSAKY	0.504002
424	AGTCTTGAGTCGTCTAGGCAG	849	SLESSRQ	0.503575
425	CTCAACCTCGCCAGCGGCAGA	850	LNLASGR	0.503463
426	ATGCAGGAGCGTCGGGAGTAT	851	MQERREY	0.503055
427	TGGCTCCTCAAAGACGGCTAC	852	WLLKDGY	0.502893
428	GGCAGATACCAAACCACCAGC	853	GRYQTTS	0.502776
429	AATACGACGAAGTTTCCGTTT	854	NTTKFPF	0.502408
430	ATGAGCAACGGCATCAGCAGA	855	MSNGISR	0.501897
431	CCGATTCGGGATCCGGAGAAG	856	PIRDPEK	0.501479
432	AGTACGCTGAGTCCGCATGTT	857	STLSPHV	0.501315
433	TTCATGCCCATCAGCAGCGCC	858	FMPISSA	0.50124
434	AGAAGCGACACCCAAAGCAGC	859	RSDTQSS	0.500462

[0143] TABLE 3: 11-mer targeting peptides that can target the CNS

SEQ ID NO	**11-mer DNA Sequence**	**SEQ ID NO**	**11-mer Amino Acid Sequence**	**Mean enrichment score (log 10 scale)**
860	GCCCAAACCACCCTCAAACCCTTCAGCAACCCC	864	AQTTLKPFSNP	1.101507461
861	GACGGCACCACCCTCAAACCCTTCAGCAACCCC	865	DGTTLKPFSNP	0.172425316
862	GACGGCACCGCCCTCAAACCCTTCCTCGCCCAA	866	DGTALKPFLAQ	0.647416071
863	GATGGGACGACTCTTAAGCCGTTTCTGGCACAG	867	DGTTLKPFLAQ	sequence predicted based on PHP.eB

				sequence

[0144] ***AAV Capsid Proteins Targeting the Liver***

[0145] Disclosed herein are AAV capsid proteins with a substitution or an insertion of at least one amino acid at an amino acid position described above in a parental AAV capsid protein that confers an increased specificity for the liver. In some instances, the insertion comprises at least one amino acid provided in any one of the sequences provided in **Table 4** and/or **FIG. 35**. In some instances, the insertion comprises at least two amino acids provided in any one of the sequences provided in **Table 4** and/or **FIG. 35**. In some instances, the insertion comprises at least three amino acids provided in any one of the sequences provided in **Table 4** and/or **FIG. 35**. In some instances, the insertion comprises at least four amino acids provided in any one of the sequences provided in **Table 4** and/or **FIG. 35**. In some instances, the insertion comprises at least five amino acids provided in **Table 4** and/or **FIG. 35**. In some instances, the insertion comprises at least six amino acids provided in **Table 4** and/or **FIG. 35**. In some instances, the insertion comprises at least seven amino acids provided in **Table 4** and/or **FIG. 35**. In some instances, the amino acids are contiguous. In some instances, the amino acids are not contiguous. In some instances, the insertion is at an amino acid position 588_589 in a parental AAV capsid protein. In some instances, the parental capsid protein is AAV9 capsid protein, provided in SEQ ID NO: 1.

[0146] **TABLE 4. List of 7-mer targeting peptides that target the liver**

SEQ ID NO	DNA sequence for 7 mer amino acid	SEQ ID NO	7 mer amino acid	liver-mean-enrich (log10)
868	GCCGAATACAACACCGGCGTC	950	AEYNTGV	0.585999
869	GCTAATGCGATGGGTGATCAT	951	ANAMGDH	0.611245
870	GAAAGCATCCAACAACTCAGC	952	ESIQQLS	0.525712
871	TTTAAGGTTAGTATTCAGCAG	953	FKVSIQQ	0.591275
872	TTTCTTCTTACTTCGGATCCG	954	FLLTSDP	0.515975
873	TTTCAGCAGGATACTTATCTG	955	FQQDTYL	0.548808
874	TTTTCTGGTAGTGCTAGGGTT	956	FSGSARV	0.509852
875	TTCAGCGTCACCAGACAAGCC	957	FSVTRQA	0.718621
876	GGGGCTGCTGGTAAGAGTTTG	958	GAAGKSL	0.571307
877	GGTCATATTTCGGCGCTTGCG	959	GHISALA	0.552655
878	GGGCTGAAGGTGTCTGGGTCT	960	GLKVSGS	0.777335
879	GGTCTTCAGTCGCCGAGGTCT	961	GLQSPRS	0.572095
880	GGGAGGACGGTGCAGGATAGG	962	GRTVQDR	0.528631
881	GGCACCAAAACCCACAGCCTC	963	GTKTHSL	0.518459

882	GGCACCACCAGAAGCCCCACC	964	GTTRSPT	0.560705
883	CACCCCAGCCTCAGACAAAGC	965	HPSLRQS	0.508478
884	CATTCTGCGAAGACTATTGCG	966	HSAKTIA	0.579949
885	CACAGCGGCCCCACCAGCAGC	967	HSGPTSS	0.505295
886	ATCAACAAAGACAACAACCAA	968	INKDNNQ	0.531458
887	ATCAACACCGCCAGCTACAAA	969	INTASYK	0.542125
888	AAAGCCATCAGCACCGCCAAC	970	KAISTAN	0.616958
889	AAAGCCAACAGCCAAATCACC	971	KANSQIT	0.519425
890	AAAGCCTACAGCGTCCAAGTC	972	KAYSVQV	1.15776
891	AAACTCAGCACCCTCCACCAA	973	KLSTLHQ	0.568791
892	AAGCGGGCGCCTGCTGATTCT	974	KRAPADS	0.611303
893	AAAACCAACAACACCGTCCTC	975	KTNNTVL	0.504377
894	AAAACCCAACTCGGCCAAATG	976	KTQLGQM	0.519843
895	CTTGGTTCTGCGCTTACGAGG	977	LGSALTR	0.563314
896	CTCATCAGCACCACCCACAGA	978	LISTTHR	0.502083
897	CTTAAGGTTGCGTCTGGTTTG	979	LKVASGL	0.540598
898	CTTCTTGCGACTGGGCTTAAG	980	LLATGLK	0.545453
899	CTTCCGGGTGGTGCGAGGTTG	981	LPGGARL	0.564086
900	CTTAGGGGTTCTGCTCAGGTG	982	LRGSAQV	0.648123
901	TTGTCTGCTCAGCTTCCGCGG	983	LSAQLPR	0.503052
902	CTTTCTACTGCGTTGACTGTG	984	LSTALTV	0.591029
903	CTCACCAGAGTCGGCACCGTC	985	LTRVGTV	0.520831
904	ATGGCCAACACCAGAAGCGCC	986	MANTRSA	0.525721
905	ATGATCAGAGGCACCAGCAGC	987	MIRGTSS	0.512891
906	ATGCTCAGCGGCCAAGCCAGA	988	MLSGQAR	0.668364
907	ATGAGAGGCCAAGGCGTCCAC	989	MRGQGVH	0.567657
908	AACAACAACCAAAAAGTCTAC	990	NNNQKVY	0.610002
909	AACAACAGCGGCCACATCAGC	991	NNSGHIS	0.518228
910	AACACCCTCATCAACGTCAGC	992	NTLINVS	0.607212
911	AATACTTCTGGTGTGCCTAAG	993	NTSGVPK	0.684638
912	AATGTGCCGACTTCGCCGCGG	994	NVPTSPR	0.520245
913	CCCGCCAGAATCCCCGGCAGC	995	PARIPGS	0.50309
914	CCCCTCAGAAACATCAGCGCC	996	PLRNISA	0.50497
915	CCGTTGAGTGGGGGTGTTCGT	997	PLSGGVR	0.598554
916	CCCAACAGAGCCGCCAACAAC	998	PNRAANN	0.508143
917	CCGCGTCATGCGACTCAGTCG	999	PRHATQS	0.711312
918	CCGCGGCCGGTGTCGAATGGG	1000	PRPVSNG	0.7305
919	CCTTCTGGTTCTGCGCGGAGT	1001	PSGSARS	0.82811
920	CCCAGCCACGCCAGAGCCAGC	1002	PSHARAS	0.520336
921	CCCGTCGGCACCAGAACCAGC	1003	PVGTRTS	0.560759
922	AGAGACACCGTCAGCAGATAC	1004	RDTVSRY	0.535765
923	AGAATCAGCACCCTCGGCCTC	1005	RISTLGL	0.595844
924	AGGCTTGATAGGACTGGTTTG	1006	RLDRTGL	0.588542
925	AGACTCACCAACAGCAACCAA	1007	RLTNSNQ	0.516161
926	CGTCAGCATCAGCTTCCTATG	1008	RQHQLPM	0.505918
927	AGAACCGCCAACGCCCTCGGC	1009	RTANALG	0.802247

928	CGGACGGATGTGCGGACGAAT	1010	RTDVRTN	0.682169
929	CGGACTACGGCTAATTCGCTT	1011	RTTANSL	0.509233
930	AGCGGCGGCACCAGAGAAGGC	1012	SGGTREG	0.501512
931	AGCATCAGAGCCCCCGTCAGC	1013	SIRAPVS	0.572426
932	TCGATTTCTCCTCCTCGTACG	1014	SISPPRT	0.550578
933	TCGAAGGTTACGCCTCCTCTG	1015	SKVTPPL	0.687491
934	AGCAGCAGACTCAGCGTCGGC	1016	SSRLSVG	0.637971
935	AGCACCAGAAACGTCGTCGGC	1017	STRNVVG	0.532567
936	TCGGTTCCTCCGAATAGGAAT	1018	SVPPNRN	0.508166
937	ACGGCTGCGCATGTTAGTTAT	1019	TAAHVSY	0.520336
938	ACCAGAAGCGAAGTCATGAAA	1020	TRSEVMK	0.683884
939	GTGGCGGGTCTGACTGTTCAG	1021	VAGLTVQ	0.581695
940	GTTGGTTCTAGTAATACGTAT	1022	VGSSNTY	0.502229
941	GTTAAGACTGATCGGGTTCTG	1023	VKTDRVL	0.51183
942	GTCAACAGCCACGAAAGAGCC	1024	VNSHERA	0.573043
943	GTCCAAGTCGCCATGAGAGCC	1025	VQVAMRA	0.520831
944	GTCAGCATCAGCGTCATGGGC	1026	VSISVMG	0.510987
945	GTGACGGGGGTTCGGATTGGG	1027	VTGVRIG	0.75699
946	TGGTCTGATCCTAGTGATCTG	1028	WSDPSDL	0.59828
947	TACCTCACCAGCGGCGGCTAC	1029	YLTSGGY	0.538789
948	TACCCCCACATGACCCACGAC	1030	YPHMTHD	0.655794
949	TATGTTAATAGTGCTCCGAAG	1031	YVNSAPK	0.551681

[0147] The AAV capsids and AAV capsid proteins disclosed herein, in some embodiments, are isolated. In some instances, the AAV capsids and AAV capsid proteins disclosed herein are isolated and purified. In addition, the AAV capsids and AAV capsid proteins disclosed herein, either isolated and purified, or not, may be formulated into a pharmaceutical formulation, which in some cases, further comprises a pharmaceutically acceptable carrier.

B. Heterologous Nucleic Acids

[0148] Disclosed herein are therapeutic nucleic acids useful for the treatment or prevention of a disease or condition, or symptom of the disease or condition, disclosed herein. In some embodiments, the therapeutic nucleic acids encode a therapeutic gene expression product. Non-limiting examples of gene expression products include proteins, polypeptides, peptides, enzymes, antibodies, antigen binding fragments, nucleic acid (RNA, DNA, antisense oligonucleotide, siRNA, and the like), and gene editing components, for use in the treatment, prophylaxis, and/or amelioration of the disease or disorder, or symptoms of the disease or disorder. In some

instances, the therapeutic nucleic acids are placed in an organism, cell, tissue or organ of a subject by way of a rAAV, such as those disclosed herein.

[0149] Disclosed herein are rAAVs, each comprising a viral vector (*e.g.*, a single stranded DNA molecule (ssDNA)). In some instances, the viral vector comprises two inverted terminal repeat (ITR) sequences that are about 145 bases each, flanking a transgene. In some embodiments, the transgene comprises a therapeutic nucleic acid, and in some cases, a promoter in cis with the therapeutic nucleic acid in an open reading frame (ORF). The promoter is capable of initiating transcription of therapeutic nucleic acid in the nucleus of the target cell. The ITR sequences can be from any AAV serotype. Non-limiting examples of AAV serotypes include AV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, and AAV12. In some cases, an ITR is from AAV2. In some cases, an ITR is from AAV9.

[0150] Disclosed herein are transgenes that can comprise any number of nucleotides. In some cases, a transgene can comprise less than about 100 nucleotides. In some cases, a transgene can comprise at least about 100 nucleotides. In some cases, a transgene can comprise at least about 200 nucleotides. In some cases, a transgene can comprise at least about 300 nucleotides. In some cases, a transgene can comprise at least about 400 nucleotides. In some cases, a transgene can comprise at least about 500 nucleotides. In some cases, a transgene can comprise at least about 1000 nucleotides. In some cases, a transgene can comprise at least about 5000 nucleotides. In some cases, a transgene can comprise at least about 10,000 nucleotides. In some cases, a transgene can comprise at least about 20,000 nucleotides. In some cases, a transgene can comprise at least about 30,000 nucleotides. In some cases, a transgene can comprise at least about 40,000 nucleotides. In some cases, a transgene can comprise at least about 50,000 nucleotides. In some cases, a transgene can comprise between about 500 and about 5000 nucleotides. In some cases, a transgene can comprise between about 5000 and about 10,000 nucleotides. In any of the cases disclosed herein, the transgene can comprise DNA, RNA, or a hybrid of DNA and RNA. In some cases, the transgene can be single stranded. In some cases, the transgene can be double stranded.

[0151] Disclosed herein are transgenes useful for modulating the expression or activity of a target gene or gene expression product thereof. In some instances, the transgene is encapsidated by an rAAV capsid protein of an rAAV particle described herein. In some instances, the rAAV

particle is delivered to a subject to treat a disease or condition disclosed herein in the subject. In some instances, the delivery is systemic (*e.g.*, intravenous, intranasal).

[0152] The transgenes disclosed herein are useful for expressing an endogenous gene at a level similar to that of a healthy or normal individual. This is particularly useful in the treatment of a disease or condition related to the underexpression, or lack of expression, of a gene expression product. In some embodiments, the transgenes disclosed herein are useful for overexpressing an endogenous gene, such that an expression level of the endogenous gene is above the expression level of a healthy or normal individual. Additionally, transgenes can be used to express exogenous genes (*e.g.*, active agent such as an antibody, peptide, nucleic acid, or gene editing components). In some embodiments, the therapeutic gene expression product is capable of altering, enhancing, increasing, or inducing the activity of one or more endogenous biological processes in the cell. In some embodiments, the transgenes disclosed herein are useful for reducing expressing an endogenous gene, example, a dominant negative gene. In some embodiments, the therapeutic gene expression product is capable of altering, inhibiting, reducing, preventing, eliminating, or impairing the activity of one or more endogenous biological processes in the cell. In some aspects, the increase of gene expression refers to an increase by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%. In one aspect, the protein product of the targeted gene may be increased by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%. In some aspects, the decrease of gene expression refers to an increase by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%. In one aspect, the protein product of the targeted gene may be decreased by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%.

[0153] When endogenous sequences (endogenous or part of a transgene) are expressed with a transgene, the endogenous sequences can be full-length sequences (wild-type or mutant) or partial sequences. The endogenous sequences can be functional. Non-limiting examples of the function of these full length or partial sequences include increasing the serum half-life of the polypeptide expressed by a transgene (*e.g.*, therapeutic gene) and/or acting as a carrier.

[0154] A transgene can be inserted into an endogenous gene such that all, some or none of the endogenous gene is expressed. For example, a transgene as described herein can be inserted into an endogenous locus such that some (N-terminal and/or C-terminal to a transgene) or none

of the endogenous sequences are expressed, for example as a fusion with a transgene. In other cases, a transgene (*e.g.*, with or without additional coding sequences of the endogenous gene) is integrated into any endogenous locus, for example a safe-harbor locus. For example, a Frataxin (FXN) transgene can be inserted into an endogenous FXN gene. A transgene can be inserted into any gene, *e.g.*, the genes as described herein.

[0155] At least one advantage of the present disclosure is that virtually any therapeutic nucleic acid may be used to express any therapeutic gene expression product. In some instances, the therapeutic gene expression product is a therapeutic protein or a peptide (*e.g.*, antibody, antigen-binding fragment, peptide, or protein). In one embodiment the protein encoded by the therapeutic nucleic acid is between 50-5000 amino acids in length. In some embodiments the protein encoded is between 50-2000 amino acids in length. In some embodiments the protein encoded is between 50-1000 amino acids in length. In some embodiments the protein encoded is between 50-1500 amino acids in length. In some embodiments the protein encoded is between 50-800 amino acids in length. In some embodiments the protein encoded is between 50-600 amino acids in length. In some embodiments the protein encoded is between 50-400 amino acids in length. In some embodiments the protein encoded is between 50-200 amino acids in length. In some embodiments the protein encoded is between 50-100 amino acids in length. In some embodiments the peptide encoded is between 4-50 amino acids in length. In some embodiments, the protein encoded is a tetrapeptide, a pentapeptide, a hexapeptide, a heptapeptide, an octapeptide, a nonapeptide, or a decapeptide. In some embodiments, the protein encoded comprises a peptide of 2-30 amino acids, such as for example 5-30, 10-30, 2-25, 5-25, 10-25, or 10-20 amino acids. In some embodiments, the protein encoded comprises a peptide of at least 11, 12, 13, 14, 15, 17, 20, 25 or 30 amino acids, or a peptide that is no longer than 50 amino acids, *e.g.* no longer than 35, 30, 25, 20, 17, 15, 14, 13, 12, 11 or 10 amino acids.

[0156] Non-limiting examples of therapeutic protein or peptides include an adrenergic agonist, an anti-apoptosis factor, an apoptosis inhibitor, a cytokine receptor, a cytokine, a cytotoxin, an erythropoietic agent, a glutamic acid decarboxylase, a glycoprotein, a growth factor, a growth factor receptor, a hormone, a hormone receptor, an interferon, an interleukin, an interleukin receptor, a kinase, a kinase inhibitor, a nerve growth factor, a netrin, a neuroactive peptide, a neuroactive peptide receptor, a neurogenic factor, a neurogenic factor receptor, a

neuropilin, a neurotrophic factor, a neurotrophin, a neurotrophin receptor, an N-methyl-D-aspartate antagonist, a plexin, a protease, a protease inhibitor, a protein decarboxylase, a protein kinase, a protein kinsase inhibitor, a proteolytic protein, a proteolytic protein inhibitor, a semaphoring, a semaphorin receptor, a serotonin transport protein, a serotonin uptake inhibitor, a serotonin receptor, a serpin, a serpin receptor, and a tumor suppressor. In certain embodiments, the therapeutic protein or peptide is selected from the group consisting of brain-derived neurotrophic factor (BDNF), ciliary neurotrophic factor (CNTF), macrophage colony-stimulating factor (CSF), epidermal growth factor (EGF), fibroblast growth factor (FGF), gonadotropin, interferon-gamma (IFN), insulin-like growth factor 1 (IFG-1), nerve growth factor (NGF), platelet-derived growth factor (PDGF), pigment epithelium-derived factor (PEDF), transforming growth factor (TGF), transforming growth factor-beta (TGF-B), tumor necrosis factor (TNF), vascular endothelial growth factor (VEGF), prolactin, somatotropin, X-linked inhibitor of apoptosis protein 1 (XIAP1), interleukin 1 (IL-1), IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-10, viral IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, and IL-18.

[0157] A therapeutic gene expression product can comprise gene editing components. Non-limiting examples of gene editing components include those required for CRISPR/Cas, artificial site-specific RNA endonuclease (ASRE), zinc finger endonuclease (ZFN), and transcription factor like effector nuclease (TALEN). In a non-limiting example, a subject having Huntington's disease is identified. The subject is then systemically administered a first amount of a rAAV encapsidating a viral vector encoding ZFN engineered to represses the transcription of the Huntingtin (HTT) gene. In some instances, the route of administration is intravenous. The rAAV will include a modified AAV capsid protein that includes an amino acid sequence provided in any one of **Tables 2-3**, or **FIG. 33**, so as to allow proper targeting of the ZFN to the nervous system, while retargeting off-target organs, such as the liver. If needed, the subject is administered a second or third dose of the rAAV, until a therapeutically effective amount of the ZFN is expressed in the subject's nervous system. In another non-limiting example, a subject with cystic fibrosis is identified. The subject is then systemically administered a first amount of a rAAV encapsidating a viral vector encoding ZFN engineered to represses the transcription of the cystic fibrosis transmembrane conductance regulator (CFTR) gene. In some instances, the route of administration is intranasal (*e.g.*, intranasal spray). The rAAV will include a modified AAV

capsid protein that includes an amino acid sequence provided in **FIG. 33** or **Tables 2-3**, so as to allow proper targeting of the ZFN to the lung. If needed, the subject is administered a second or third dose of the rAAV, until a therapeutically effective amount of the ZFN is expressed in the subject's lung.

[0158] A therapeutic nucleic acid can comprise a non-protein coding gene *e.g.*, sequences encoding antisense RNAs, RNAi, shRNAs and micro RNAs (miRNAs), miRNA sponges or decoys, recombinase delivery for conditional gene deletion, conditional (recombinase-dependent) expression, includes those required for the gene editing components described herein. The non-protein coding gene may also encode a tRNA, rRNA, tmRNA, piRNA, double stranded RNA, snRNA, snoRNA, and/or long non-coding RNA (IncRNA). In some cases, the non-protein coding gene can modulate the expression or the activity of a target gene or gene expression product. For example, the RNAs described herein may be used to inhibit gene expression in a target cell, for example, a cell in the central nervous system (CNS) or peripheral organ (*e.g.*, lung). In some cases, inhibition of gene expression refers to an inhibition by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%. In some cases, the protein product of the targeted gene may be inhibited by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% and 100%. The gene can be either a wild type gene or a gene with at least one mutation. The targeted protein may be either a wild type protein or a protein with at least one mutation.

[0159] A therapeutic nucleic acid can modulate the expression or activity of a gene or gene expression product expressed from the gene that is implicated in disease or disorder of the brain. For example, the therapeutic nucleic acid, in some cases is a gene or a modified version of the gene described herein. In another example, the therapeutic nucleic acid comprises an effector gene expression product such as a gene editing component specific to target a gene therein. Non-limited examples of genes include Sarcoglycan Alpha (SGCA), glutamic acid decarboxylase 65 (GAD65), glutamic acid decarboxylase 67 (GAD67), CLN2 gene, Nerve Growth Factor (NGF), glial cell derived neurotrophic factor(GDNF), Neurturin, Survival Of Motor Neuron 1, Telomeric (SMN1), β-Glucocerebrosidase (GCase), Frataxin (FXN), Huntingtin (HTN), methyl-CpG binding protein 2 (MECP2), peroxisomal biogenesis factor (PEX), progranulin (GRN), an antitubulin agent, copper-zinc superoxide dismutase (SOD1), Glucosylceramidase Beta (GBA),

NPC Intracellular Cholesterol Transporter 1 (NPC1), and NPS3. In some embodiments, the peroxisomal biogenesis factor (PEX) is selected from the group consisting of PEX1, PEX2, PEX3, PEX4, PEX5, PEX6, PEX7, PEX10, PEX11β, PEX12, PEX13, PEX14, PEX16, PEX19, and PEX26. In some instances, the gene or gene expression product is inhibited. In some instances, the gene or gene expression product is enhanced.

[0160] A therapeutic nucleic acid modulates expression or activity of a gene or gene expression product expressed from the gene that is implicated in disease or disorder of a particular organ (*e.g.*, lung, heart, liver, muscle, eye). Non-limited examples of genes include Cystic Fibrosis Transmembrane Conductance Regulator (CFTR), Factor X (FIX), RPE65, Retinoid Isomerohydrolase (RPE65), Sarcoglycan Alpha (SGCA), and sarco/endoplasmic reticulum Ca2+-ATPase (SERCA2a). In some embodiments, the therapeutic gene expression product is of human, murine, avian, porcine, bovine, ovine, feline, canine, equine, epine, caprine, lupine or primate origin. In some instances, the gene or gene expression product is inhibited. In some instances, the gene or gene expression product is enhanced.

C. AAV Vectors

[0161] Disclosed herein are adeno-associated virus (AAV) vectors comprising genetic information. AAV vectors described herein are useful for the assembly of a rAAV and viral packaging of a heterologous nucleic acid. In addition, an AAV vector may encode a transgene comprising the heterologous nucleic acid. In some instances, the AAV vector is from an AAV serotypes selected from the group consisting of AV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, and AAV12. In some instances, the AAV vector is selected from a modified AAV serotype selected from the group consisting of AAV-PHP.B, AAV-PHP.eB, and AAV-PHP.S.

[0162] An AAV vector can comprise a transgene, which in some cases encodes a heterologous gene expression product (*e.g.*, therapeutic gene expression product, recombinant capsid protein, and the like). The transgene is in cis with two inverted terminal repeats (ITRs) flanking the transgene. The transgene may comprise a therapeutic nucleic acid encoding a therapeutic gene expression product. Due to the limited packaging capacity of the rAAV (~2.5kB), in some cases, a longer transgene may be split between two AAV vectors, the first

with 3' splice donor and the second with a 5' splice acceptor. Upon co-infection of a cell, concatemers form, which are spliced together to express a full-length transgene.

[0163] A transgene is generally inserted so that its expression is driven by the endogenous promoter at the integration site, namely the promoter that drives expression of the endogenous gene into which a transgene is inserted. In some instances, a transgene comprises a promoter and/or enhancer, for example a constitutive promoter or an inducible or tissue/cell specific promoter. As a non-limiting example, the promoter may be CMV promoter, a CMV-β-Actin-intron-β-Globin hybrid promoter (CAG), CBA promoter, FRDA or FXN promoter, UBC promoter, GUSB promoter, NSE promoter, Synapsin promoter, MeCP2 promoter, GFAP promoter, H1 promoter, U6 promoter, NFL promoter, NFH promoter, SCN8A promoter, or PGK promoter. As a non-limiting example, promoters can be tissue-specific expression elements include, but are not limited to, human elongation factor 1α-subunit (EF1α), immediate-early cytomegalovirus (CMV), chicken β-actin (CBA) and its derivative CAG, the β glucuronidase (GUSB), and ubiquitin C (UBC). The transgene may include a tissue-specific expression elements for neurons such as, but not limited to, neuron-specific enolase (NSE), platelet-derived growth factor (PDGF), platelet-derived growth factor B-chain (PDGF-β), the synapsin (Syn), the methyl-CpG binding protein 2 (MeCP2), Ca2+/calmodulin-dependent protein kinase II (CaMKII), metabotropic glutamate receptor 2 (mGluR2), NFL, NFH, np32, PPE, Enk and EAAT2 promoters. The transgene may comprise a tissue-specific expression element for astrocytes such as, but not limited to, the glial fibrillary acidic protein (GFAP) and EAAT2 promoters. The transgene may comprise tissue-specific expression elements for oligodendrocytes such as, but not limited to, the myelin basic protein (MBP) promoter.

[0164] In some embodiments, the promoter is less than 1 kb. The promoter may have a length of 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800 or more than 800. The promoter may have a length between 200-300, 200-400, 200-500, 200-600, 200-700, 200-800, 300-400, 300-500, 300-600, 300-700, 300-800, 400-500, 400-600, 400-700, 400-800, 500-600, 500-700, 500-800, 600-700, 600-800 or 700-800. The promoter may provide expression of the therapeutic gene expression product for a

period of time in targeted tissues such as, but not limited to, the central nervous system and peripheral organs (*e.g.*, lung). Expression of the therapeutic gene expression product may be for a period of 1 hour, 2, hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 2 weeks, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 3 weeks, 22 days, 23 days, 24 days, 25 days, 26 days, 27 days, 28 days, 29 days, 30 days, 31 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 13 months, 14 months, 15 months, 16 months, 17 months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, 11 years, 12 years, 13 years, 14 years, 15 years, 16 years, 17 years, 18 years, 19 years, 20 years, 21 years, 22 years, 23 years, 24 years, 25 years, 26 years, 27 years, 28 years, 29 years, 30 years, 31 years, 32 years, 33 years, 34 years, 35 years, 36 years, 37 years, 38 years, 39 years, 40 years, 41 years, 42 years, 43 years, 44 years, 45 years, 46 years, 47 years, 48 years, 49 years, 50 years, 55 years, 60 years, 65 years, or more than 65 years. Expression of the payload may be for 1-5 hours, 1-12 hours, 1-2 days, 1-5 days, 1-2 weeks, 1-3 weeks, 1-4 weeks, 1-2 months, 1-4 months, 1-6 months, 2-6 months, 3-6 months, 3-9 months, 4-8 months, 6-12 months, 1-2 years, 1-5 years, 2-5 years, 3-6 years, 3-8 years, 4-8 years or 5-10 years or 10-15 years, or 15-20 years, or 20-25 years, or 25-30 years, or 30-35 years, or 35-40 years, or 40-45 years, or 45-50 years, or 50-55 years, or 55-60 years, or 60-65 years.

[0165] An AAV vector can comprise a genome of a helper virus. Helper virus proteins are required for the assembly of a recombinant AAV (rAAV), and packaging of a transgene containing a heterologous nucleic acid into the rAAV. The helper virus genes are adenovirus genes E4, E2a and VA, that when expressed in the cell, assist with AAV replication. In some embodiments, an AAV vector comprises E2. In some embodiments, an AAV vector comprises E4. In some embodiments, an AAV vector comprises VA. In some instances, the AAV vector comprises one of helper virus proteins, or any combination.

[0166] An AAV vector can comprise a viral genome comprising a nucleic acid encoding the recombinant AAV (rAAV) capsid protein described herein. The viral genome can comprise a

Replication (Rep) gene encoding a Rep protein, and Capsid (Cap) gene encoding an AAP protein in the first open reading frame (ORF1) or a Cap protein in the second open reading frame (ORF2). The Rep protein is selected from the group consisting of Rep78, Rep68, Rep52, and Rep40. In some instances, the Cap gene is modified encoding a modified AAV capsid protein described herein. A wild-type Cap gene encodes three proteins, VP1, VP2, and VP3. In some cases, VP1 is modified. In some cases, VP2 is modified. In some cases, VP3 is modified. In some cases, all three VP1-VP3 are modified. The AAV vector can comprise nucleic acids encoding wild-type Rep78, Rep68, Rep52, Rep40 and AAP proteins.

[0167] Disclosed herein are AAV vectors comprising any one of SEQ ID NOS: 10-434, 860-863, 868-949, 1068-5661, 14841-14880, and 14961-15053 which are the DNA sequences encoding modified portions of AAV capsid proteins of the present disclosure. In some instances, the AAV vector comprises a nucleic acid sequences provided in any one of SEQ ID NOS: 10-434 and 868-949, encoding 7-mer modified AAV capsid protein portions. The AAV vector of the present disclosure can comprise the VP1 Cap gene comprises any one of SEQ ID NOS: 6-9 provided in Table 5. An AAV vector can comprise 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% of any one of SEQ ID NOS: 6-9.

[0168] In some instances, the AAV9 VP1 gene provided in SEQ ID NO: 6, which is provided in Table 5, is modified to include any one of SEQ ID NOS: 10-434, 860-863, 868-949, 1068-5661, 14841-14880, and 14961-15053. In some instances, the AAV-PHP.eB VP1 (SEQ ID NO: 9), which is also provided in Table 5 is modified to include any one of SEQ ID NOS: 10-434, 860-863, 868-949, 1068-5661, 14841-14880, and 14961-15053. The AAV vector described herein may be used to produce a variant AAV capsid by the methods described herein.

[0169] **TABLE 5. VP1 Capsid Protein Nucleic Acid Sequences**

SEQ ID NO:	Identifier	Sequence
6	AAV9 >AY530579 .1 Adeno-associated virus 9 isolate hu.14 capsid	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAA CCTTAGTGAAGGAATTCGCGAGTGGTGGGCTTTGAAACCTG GAGCCCCTCAACCCAAGGCAAATCAACAACATCAAGACAA CGCTCGAGGTCTTGTGCTTCCGGGTTACAAATACCTTGGACC CGGCAACGGACTCGACAAGGGGGAGCCGGTCAACGCAGCA GACGCGGCGGCCCTCGAGCACGACAAGGCCTACGACCAGC

	protein VP1 (cap) gene, complete cds	AGCTCAAGGCCGGAGACAACCCGTACCTCAAGTACAACCAC GCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTC TTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAA AGAGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCT AAGACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCAGTCTCC TCAGGAACCGGACTCCTCCGCGGGTATTGGCAAATCGGGTG CACAGCCCGCTAAAAAGAGACTCAATTTCGGTCAGACTGGC GACACAGAGTCAGTCCCAGACCCTCAACCAATCGGAGAACC TCCCGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTTC AGGTGGTGGCGCACCAGTGGCAGACAATAACGAAGGTGCC GATGGAGTGGGTAGTTCCTCGGGAAATTGGCATTGCGATTC CCAATGGCTGGGGGACAGAGTCATCACCACCAGCACCCGAA CCTGGGCCCTGCCCACCTACAACAATCACCTCTACAAGCAA ATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGC CTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGACTTCAA CAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCGAC TCATCAACAACAACTGGGGATTCCGGCCTAAGCGACTCAAC TTCAAGCTCTTCAACATTCAGGTCAAAGAGGTTACGGACAA CAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGG TCCAGGTCTTCACGGACTCAGACTATCAGCTCCCGTACGTGC TCGGGTCGGCTCACGAGGGCTGCCTCCCGCCGTTCCCAGCG GACGTTTTCATGATTCCTCAGTACGGGTATCTGACGCTTAAT GATGGAAGCCAGGCCGTGGGTCGTTCGTCCTTTTACTGCCT GGAATATTTCCCGTCGCAAATGCTAAGAACGGGTAACAACT TCCAGTTCAGCTACGAGTTTGAGAACGTACCTTTCCATAGCA GCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATCCA CTCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAC GGTTCTGGACAGAATCAACAAACGCTAAAATTCAGTGTGGC CGGACCCAGCAACATGGCTGTCCAGGGAAGAAACTACATAC CTGGACCCAGCTACCGACAACAACGTGTCTCAACCACTGTG ACTCAAAACAACAACAGCGAATTTGCTTGGCCTGGAGCTTC TTCTTGGGCTCTCAATGGACGTAATAGCTTGATGAATCCTGG ACCTGCTATGGCCAGCCACAAAGAAGGAGAGGACCGTTTCT TTCCTTTGTCTGGATCTTTAATTTTTGGCAAACAAGGAACTG GAAGAGACAACGTGGATGCGGACAAAGTCATGATAACCAA CGAAGAAGAAATTAAAACTACTAACCCGGTAGCAACGGAG TCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAGC ACAGGCGCAGACCGGCTGGGTTCAAAACCAAGGAATACTTC CGGGTATGGTTTGGCAGGACAGAGATGTGTACCTGCAAGGA CCCATTTGGGCCAAAATTCCTCACACGGACGGCAACTTTCA CCCTTCTCCGCTGATGGGAGGGTTTGGAATGAAGCACCCGC CTCCTCAGATCCTCATCAAAAACACACCTGTACCTGCGGAT CCTCCAACGGCCTTCAACAAGGACAAGCTGAACTCTTTCAT CACCCAGTATTCTACTGGCCAAGTCAGCGTGGAGATCGAGT GGGAGCTGCAGAAGGAAAACAGCAAGCGCTGGAACCCGGA

		GATCCAGTACACTTCCAACTATTACAAGTCTAATAATGTTGA ATTTGCTGTTAATACTGAAGGTGTATATAGTGAACCCCGCCC CATTGGCACCAGATACCTGACTCGTAATCTGTAA
7	AAV-PHP.B	ATGGCTGCCG ATGGTTATCT TCCAGATTGG CTCGAGGACA ACCTTAGTGAAGGAATTCGC GAGTGGTGGG CTTTGAAACC TGGAGCCCCT CAACCCAAGGCAAATCAACA ACATCAAGAC AACGCTCGAG GTCTTGTGCT TCCGGGTTACAAATACCTTG GACCCGGCAA CGGACTCGAC AAGGGGGAGC GGTCAACGC AGCAGACGCG GCGGCCCTCG AGCACGACAA GCCTACGAC CAGCAGCTCAAGGCCGGAGA CAACCCGTAC CTCAAGTACA ACCACGCCGA CGCCGAGTTCCAGGAGCGGC TCAAAGAAGA TACGTCTTTT GGGGGCAACC TCGGGCGAGCAGTCTTCCAG GCCAAAAAGA GGCTTCTTGA ACCTCTTGGT CTGGTTGAGG AAGCGGCTAA GACGGCTCCT GGAAAGAAGA GGCCTGTAGA GCAGTCTCCTCAGGAACCGG ACTCCTCCGC GGGTATTGGC AAATCGGGTG CACAGCCCGCTAAAAAGAGA CTCAATTTCG GTCAGACTGG CGACACAGAG TCAGTCCCAGACCCTCAACC AATCGGAGAA CCTCCCGCAG CCCCCTCAGG TGTGGGATCT CTTACAATGG CTTCAGGTGG TGGCGCACCA GTGGCAGACA ATAACGAAGGTGCCGATGGA GTGGGTAGTT CCTCGGGAAA TTGGCATTGC GATTCCCAATGGCTGGGGGA CAGAGTCATC ACCACCAGCA CCCGAACCTG GGCCCTGCCCACCTACAACA ATCACCTCTA CAAGCAAATC TCCAACAGCA CATCTGGAGG ATCTTCAAAT GACAACGCCT ACTTCGGCTA CAGCACCCCC TGGGGGTATTTTGACTTCAA CAGATTCCAC TGCCACTTCT CACCACGTGA CTGGCAGCGACTCATCAACA ACAACTGGGG ATTCCGGCCT AAGCGACTCA ACTTCAAGCTCTTCAACATT CAGGTCAAAG AGGTTACGGA CAACAATGGA GTCAAGACCA TCGCCAATAA CCTTACCAGC ACGGTCCAGG TCTTCACGGA CTCAGACTATCAGCTCCCGT ACGTGCTCGG GTCGGCTCAC GAGGGCTGCC TCCCGCCGTTCCCAGCGGAC GTTTTCATGA TTCCTCAGTA CGGGTATCTG ACGCTTAATGATGGAAGCCA GGCCGTGGGT CGTTCGTCCT TTTACTGCCT GGAATATTTC CCGTCGCAAA TGCTAAGAAC GGGTAACAAC TTCCAGTTCA GCTACGAGTTTGAGAACGTA CCTTTCCATA GCAGCTACGC TCACAGCCAA AGCCTGGACCGACTAATGAA TCCACTCATC GACCAATACT TGTACTATCT CTCTAGAACT ATTAACGGTT CTGGACAGAA TCAACAAACG CTAAAATTCA GTGTGGCCGG

		ACCCAGCAAC ATGGCTGTCC AGGGAAGAAA CTACATACCT GGACCCAGCTACCGACAACA ACGTGTCTCA ACCACTGTGA CTCAAAACAA CAACAGCGAATTTGCTTGGC CTGGAGCTTC TTCTTGGGCT CTCAATGGAC GTAATAGCTT GATGAATCCT GGACCTGCTA TGGCCAGCCA CAAAGAAGGA GAGGACCGTTTCTTTCCTTT GTCTGGATCT TTAATTTTTG GCAAACAAGG TACCGGCAGAGACAACGTGG ATGCGGACAA AGTCATGATA ACCAACGAAG AAGAAATTAAAACTACTAAC CCGGTAGCAA CGGAGTCCTA TGGACAAGTG GCCACAAACCACCAGAGTGC CCAAACTTTG GCGGTGCCTT TTAAGGCACA GGCGCAGACCGGTTGGGTTC AAAACCAAGG AATACTTCCG GGTATGGTTT GGCAGGACAGAGATGTGTAC CTGCAAGGAC CCATTTGGGC CAAAATTCCT CACACGGACG GCAACTTTCA CCCTTCTCCG CTGATGGGAG GGTTTGGAAT GAAGCACCCGCCTCCTCAGA TCCTCATCAA AAACACACCT GTACCTGCGG ATCCTCCAACGGCCTTCAAC AAGGACAAGC TGAACTCTTT CATCACCCAG TATTCTACTGGCCAAGTCAG CGTGGAGATC GAGTGGGAGC TGCAGAAGGA AAACAGCAAG CGCTGGAACC CGGAGATCCA GTACACTTCC AACTATTACA AGTCTAATAATGTTGAATTT GCTGTTAATA CTGAAGGTGT ATATAGTGAA CCCCGCCCCATTGGCACCAG ATACCTGACT CGTAATCTGT AA
8	AAV- PHP.S	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAA CCTTAGTGAAGGAATTCGCGAGTGGTGGGCTTTGAAACCTG GAGCCCCTCAACCCAAGGCAAATCAACAACATCAAGACAA CGCTCGAGGTCTTGTGCTTCCGGGTTACAAATACCTTGGACC CGGCAACGGACTCGACAAGGGGGAGCCGGTCAACGCAGCA GACGCGGCGGCCCTCGAGCACGACAAGGCCTACGACCAGC AGCTCAAGGCCGGAGACAACCCGTACCTCAAGTACAACCAC GCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTC TTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAA AGAGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCT AAGACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCAGTCTCC TCAGGAACCGGACTCCTCCGCGGGTATTGGCAAATCGGGTG CACAGCCCGCTAAAAAGAGACTCAATTTCGGTCAGACTGGC GACACAGAGTCAGTCCCAGACCCTCAACCAATCGGAGAACC TCCCGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTTC AGGTGGTGGCGCACCAGTGGCAGACAATAACGAAGGTGCC GATGGAGTGGGTAGTTCCTCGGGAAATTGGCATTGCGATTC CCAATGGCTGGGGGACAGAGTCATCACCACCAGCACCCGAA CCTGGGCCCTGCCCACCTACAACAATCACCTCTACAAGCAA ATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGC CTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGACTTCAA CAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCGAC

		TCATCAACAACAACTGGGGATTCCGGCCTAAGCGACTCAAC TTCAAGCTCTTCAACATTCAGGTCAAAGAGGTTACGGACAA CAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGG TCCAGGTCTTCACGGACTCAGACTATCAGCTCCCGTACGTGC TCGGGTCGGCTCACGAGGGCTGCCTCCCGCCGTTCCCAGCG GACGTTTTCATGATTCCTCAGTACGGGTATCTGACGCTTAAT GATGGAAGCCAGGCCGTGGGTCGTTCGTCCTTTTACTGCCTG GAATATTTCCCGTCGCAAATGCTAAGAACGGGTAACAACTT CCAGTTCAGCTACGAGTTTGAGAACGTACCTTTCCATAGCA GCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATCCA CTCATCGACCAATACTTGTACTATCTCTCAAAGACTATTAAC GGTTCTGGACAGAATCAACAAACGCTAAAATTCAGTGTGGC CGGACCCAGCAACATGGCTGTCCAGGGAAGAAACTACATAC CTGGACCCAGCTACCGACAACAACGTGTCTCAACCACTGTG ACTCAAAACAACAACAGCGAATTTGCTTGGCCTGGAGCTTC TTCTTGGGCTCTCAATGGACGTAATAGCTTGATGAATCCTGG ACCTGCTATGGCCAGCCACAAAGAAGGAGAGGACCGTTTCT TTCCTTTGTCTGGATCTTTAATTTTTGGCAAACAAGGAACTG GAAGAGACAACGTGGATGCGGACAAAGTCATGATAACCAA CGAAGAAGAAATTAAAACTACTAACCCGGTAGCAACGGAG TCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAACA GGCGGTTAGGACGTCTTTGGCACAGGCGCAGACCGGCTGGG TTCAAAACCAAGGAATACTTCCGGGTATGGTTTGGCAGGAC AGAGATGTGTACCTGCAAGGACCCATTTGGGCCAAAATTCC TCACACGGACGGCAACTTTCACCCTTCTCCGCTGATGGGAG GGTTTGGAATGAAGCACCCGCCTCCTCAGATCCTCATCAAA AACACACCTGTACCTGCGGATCCTCCAACGGCCTTCAACAA GGACAAGCTGAACTCTTTCATCACCCAGTATTCTACTGGCCA AGTCAGCGTGGAGATCGAGTGGGAGCTGCAGAAGGAAAAC AGCAAGCGCTGGAACCCGGAGATCCAGTACACTTCCAACTA TTACAAGTCTAATAATGTTGAATTTGCTGTTAATACTGAAGG TGTATATAGTGAACCCCGCCCCATTGGCACCAGATACCTGA CTCGTAATCTGTAA
9	AAV- PHP.eB	ATGGCTGCCGATGGTTATCTTCCAGATTGGCTCGAGGACAA CCTTAGTGAAGGAATTCGCGAGTGGTGGGCTTTGAAACCTG GAGCCCCTCAACCCAAGGCAAATCAACAACATCAAGACAA CGCTCGAGGTCTTGTGCTTCCGGGTTACAAATACCTTGGACC CGGCAACGGACTCGACAAGGGGGAGCCGGTCAACGCAGCA GACGCGGCGGCCCTCGAGCACGACAAGGCCTACGACCAGC AGCTCAAGGCCGGAGACAACCCGTACCTCAAGTACAACCAC GCCGACGCCGAGTTCCAGGAGCGGCTCAAAGAAGATACGTC TTTTGGGGGCAACCTCGGGCGAGCAGTCTTCCAGGCCAAAA AGAGGCTTCTTGAACCTCTTGGTCTGGTTGAGGAAGCGGCT AAGACGGCTCCTGGAAAGAAGAGGCCTGTAGAGCAGTCTCC

		TCAGGAACCGGACTCCTCCGCGGGTATTGGCAAATCGGGTG CACAGCCCGCTAAAAAGAGACTCAATTTCGGTCAGACTGGC GACACAGAGTCAGTCCCAGACCCTCAACCAATCGGAGAACC TCCCGCAGCCCCCTCAGGTGTGGGATCTCTTACAATGGCTTC AGGTGGTGGCGCACCAGTGGCAGACAATAACGAAGGTGCC GATGGAGTGGGTAGTTCCTCGGGAAATTGGCATTGCGATTC CCAATGGCTGGGGGACAGAGTCATCACCACCAGCACCCGAA CCTGGGCCCTGCCCACCTACAACAATCACCTCTACAAGCAA ATCTCCAACAGCACATCTGGAGGATCTTCAAATGACAACGC CTACTTCGGCTACAGCACCCCCTGGGGGTATTTTGACTTCAA CAGATTCCACTGCCACTTCTCACCACGTGACTGGCAGCGAC TCATCAACAACAACTGGGGATTCCGGCCTAAGCGACTCAAC TTCAAGCTCTTCAACATTCAGGTCAAAGAGGTTACGGACAA CAATGGAGTCAAGACCATCGCCAATAACCTTACCAGCACGG TCCAGGTCTTCACGGACTCAGACTATCAGCTCCCGTACGTGC TCGGGTCGGCTCACGAGGGCTGCCTCCCGCCGTTCCCAGCG GACGTTTTCATGATTCCTCAGTACGGGTATCTGACGCTTAAT GATGGAAGCCAGGCCGTGGGTCGTTCGTCCTTTTACTGCCTG GAATATTTCCCGTCGCAAATGCTAAGAACGGGTAACAACTT CCAGTTCAGCTACGAGTTTGAGAACGTACCTTTCCATAGCA GCTACGCTCACAGCCAAAGCCTGGACCGACTAATGAATCCA CTCATCGACCAATACTTGTACTATCTCTCTAGAACTATTAAC GGTTCTGGACAGAATCAACAAACGCTAAAATTCAGTGTGGC CGGACCCAGCAACATGGCTGTCCAGGGAAGAAACTACATAC CTGGACCCAGCTACCGACAACAACGTGTCTCAACCACTGTG ACTCAAAACAACAACAGCGAATTTGCTTGGCCTGGAGCTTC TTCTTGGGCTCTCAATGGACGTAATAGCTTGATGAATCCTGG ACCTGCTATGGCCAGCCACAAAGAAGGAGAGGACCGTTTCT TTCCTTTGTCTGGATCTTTAATTTTTGGCAAACAAGGTACCG GCAGAGACAACGTGGATGCGGACAAAGTCATGATAACCAA CGAAGAAGAAATTAAAACTACTAACCCGGTAGCAACGGAG TCCTATGGACAAGTGGCCACAAACCACCAGAGTGATGGGAC TTTGGCGGTGCCTTTTAAGGCACAGGCGCAGACCGGTTGGG TTCAAAACCAAGGAATACTTCCGGGTATGGTTTGGCAGGAC AGAGATGTGTACCTGCAAGGACCCATTTGGGCCAAAATTCC TCACACGGACGGCAACTTTCACCCTTCTCCGCTGATGGGAG GGTTTGGAATGAAGCACCCGCCTCCTCAGATCCTCATCAAA AACACACCTGTACCTGCGGATCCTCCAACGGCCTTCAACAA GGACAAGCTGAACTCTTTCATCACCCAGTATTCTACTGGCCA AGTCAGCGTGGAGATCGAGTGGGAGCTGCAGAAGGAAAAC AGCAAGCGCTGGAACCCGGAGATCCAGTACACTTCCAACTA TTACAAGTCTAATAATGTTGAATTTGCTGTTAATACTGAAGG TGTATATAGTGAACCCCGCCCCATTGGCACCAGATACCTGA CTCGTAATCTGTAA

II. METHODS

A. Methods of Producing AAVs

[0170] Disclosed herein are methods of identifying a recombinant AAV (rAAV), such as those disclosed herein. The AAV peptide specific to target *in vivo* environments are identified using multiplexed Cre recombination-based AAV targeted evolution (M-CREATE). **FIG. 1** provides a workflow using M-CREATE. M-CREATE uses an rAAV capsid genome (rAAV-Cap-in-cis-lox or rAAV-ΔCap-in-cis-lox2 as described in Example 2 below) that couples a full-length AAV *Cap* gene, controlled by regulatory elements from the AAV *Rep* gene, with a Cre-invertible switch. The rAAV-ΔCap-in-cis-lox2 backbone has a bi-directional polyA flanked by two Lox sites (lox71 and lox66). The ΔCap backbone is nonfunctional as it is missing a portion of the capsid gene. Upon insertion of a library fragment with mutagenesis at a specific site into the capsid, it then becomes a fully functional vector. In a cell expressing the Cre recombinase, the Cre-Lox recombination facilitates inversion of the polyA in addition to flipping the Lox sites to Lox72 and LoxP. (See **FIGS. 1** and **36**) The randomized 7-mer and 11-mers disclosed herein are generated using PCR, which are then inserted into the rAAV-ΔCap-in-cis-lox to generate virus libraries with randomized insertions or substitutions in the capsid protein sequence (*e.g.,* at the AA588_589). (**FIG. 1**). In a first round of *in vivo* selection, the virus libraries are injected into the blood stream (*e.g.*, intravenously) of transgenic animals expressing Cre recombinase. Tissues obtained from the transgenic animals following injection in *in vivo* environment (*e.g.*, brain/liver). The inverted reporter expression cassette is detected using selective amplification expression of the reporter gene expression product. The rAAVs in the tissues are isolated and the viral genome around the insertion site is sequenced and aligned with an AAV9 template DNA fragment. The 7-mers and 11-mers that were recovered were enriched in the target *in vivo* environment, and were cloned into another rAAV-ΔCap-in-cis-lox2 backbone, and another round of *in vivo* selection is performed. The 7-mers and 11-mers enriched in the target *in vivo* environment, and negatively enriched in an off-target *in vivo* environment are sequenced using suitable methods, such as next generation sequencing. **FIGS. 33-35** provide DNA sequences identified using the methods provided herein.

[0171] Methods comprise providing a rAAV genome comprising an AAV capsid gene, and a recognition sequence for a Cre recombinase. In some cases, the rAAV genome has two recognition sequences for Cre recombinase that flank a reporter expression cassette. The recognition sequences for Cre recombinase (*e.g.,* LoxP) are oriented such that an inversion of the reporter cassette is facilitated in the presence of Cre recombinase in a cell. Methods comprise transfecting a population of cells expressing the Cre recombinase with the rAAV genome. The Cre recombinase induces an inversion (*e.g.,* "flip" of the reporter gene into a genome of the transgenic animal). In some cases, the rate of inversion (*e.g., a level of* expression of the reporter gene in a target cell) may be measured using any suitable method, such as quantitative polymerase chain reaction, or immunohistochemistry. The level of expression of the reporter gene is compared to a reference value, which in some cases is the rate of inversion by a reference AAV (*e.g.,* AAV9). Methods disclosed herein provide that an increase in the rate of inversion is detected in a target *in vivo* environment, as compared to the rate of inversion of a reference AAV. In some cases, a decrease in a rate of inversion is detected in an off-target cell, as compared to the rate of inversion of a reference AAV. The rAAV genome recovered using the methods described herein encodes for an AAV capsid particle (*e.g.,* capsid protein, capsid) with an increased specificity for the target cell, and a decreased specificity for the off-target cell.

[0172] Disclosed herein are methods of producing a rAAV disclosed herein. In some instances, all elements that are required for AAV production in target cell (*e.g.*, HEK293cells) are transiently transfected into the target cell using suitable methods known in the art. For example, the rAAV of the present disclosure can be product by co-transfecting three plasmid vectors, a first vector with ITR-containing plasmid carrying the transgene (*e.g.*, therapeutic nucleic acid), a second vector that carries the AAV Rep and Cap genes; and (3), a third vector that provides the helper genes isolated from adenovirus. The methods described herein generate high-titer AAV vectors that are free of adenovirus. The Cap gene disclosed here comprises any one of SEQ ID NOS: 10-434, 860-863, 868-949, 1068-5661, 14841-14880, and 14961-15053 which are DNA sequences encoding the modified AAV capsid protein portions of the present disclosure. In some cases, rAAVs of the present disclosure are generated using the methods described in Challis, R. C. et al. Systemic AAV vectors for widespread and targeted gene delivery in rodents. Nat. Protoc. 14, 379 (2019), which is hereby incorporated by reference in its

entirety. Briefly, triple transfection of HEK293T cells (ATCC) using polyethylenimine (PEI) is performed, viruses are collected after 120 hours from both cell lysates and media, and purified over iodixanol.

[0173] Disclosed herein, are methods comprising: (a) introducing into a cell a nucleic acid comprising: (1) a first nucleic acid sequence encoding a therapeutic gene expression product; (2) a second nucleic acid sequence encoding viral genome components comprising: (i) a Replication (*Rep*) gene encoding a Rep protein; and (ii) a modified capsid (*Cap*) gene encoding a modified AAV capsid protein described herein, and (3) a third nucleic acid sequence encoding a genome of an AAV helper virus; and (b) assembling a recombinant AAV (rAAV) capsid encapsidating the first nucleic acid, the rAAV capsid comprising a tropism with an increased specificity for a target *in vivo* environment in a subject and a decreased specificity for an off-target *in vivo* environment, relative to a tropism of a corresponding parental AAV capsid protein. In some instances, the methods further comprise packing the first nucleic acid sequence encoding the therapeutic gene expression product such that it becomes encapsidated by the modified AAV capsid protein. In some embodiments, the rAAV particles are isolated, concentrated, and purified using suitable viral purification methods, such as those described herein.

[0174] In a non-limiting example, the rAAVs are generated by triple transfection of precursor cells (*e.g.*, HEK293T) cells using a standard transfection protocol (*e.g.*, PEI). Viral particles are harvested from the media after a period of time (*e.g.*, 72 h post transfection) and from the cells and media at a later point in time (*e.g.*, 120 h post transfection). Virus present in the media is concentrated by precipitation with 8% poly(ethylene glycol) and 500 mM sodium chloride and the precipitated virus is added to the lysates prepared from the collected cells. The viruses are purified over iodixanol (Optiprep, Sigma) step gradients (15%, 25%, 40% and 60%). Viruses are concentrated and formulated in PBS. Virus titers are determined by measuring the number of DNaseI-resistant vector genome copies (VGs) using qPCR and the linearized genome plasmid as a control.

[0175] The Rep protein can be selected from the group consisting of Rep78, Rep68, Rep52, and Rep40. The genome of the AAV helper virus comprises an AAV helper gene selected from the group consisting of E2, E4, and VA. The second nucleic acid and the first nucleic acid can be in trans. The second nucleic acid and the first nucleic acid can be in cis.

[0176] The cell can be selected from a group consisting of a human, a primate, a murine, a feline, a canine, a porcine, an ovine, a bovine, an equine, an epine, a caprine and a lupine host cell. In some instances, the cell is a progenitor or precursor cell, such as a stem cell. In some instances, the stem cell is a mesenchymal cell, embryonic stem cell, induced pluripotent stem cell (iPSC), fibroblast or other tissue specific stem cell. The cell can be immortalized. In some cases, the immortalized cell is a HEK293cell. In some instances, the cell is a differentiated cell. Based on the disclosure provided, it is expected that this system can be used in conjunction with any transgenic line expressing a recombinase in the target cell type of interest to develop AAV capsids that more efficiently transduce that target cell population.

B. Methods of rAAV-Mediated Delivery of a Heterologous Nucleic Acid

[0177] Disclosed herein are methods of delivering a heterologous nucleic acid (*e.g.*, therapeutic nucleic acid or transgene disclosed herein) to subject in need thereof. The transgene may be encapsidated by a recombinant AAV (rAAV) capsid protein or rAAV particle such as those described herein.

[0178] Methods may be *ex vivo*, *e.g.*, scientific research purposes or for producing adoptive cellular therapies. The subject may be a human primary cell or a mature cell, or cell line. The subject may be a cell from a monkey, hamster, or mouse. In either case, delivery may include contacting the composition with the cell or cell line.

[0179] Methods may be *in vivo*, *e.g.*, treating a disease or a condition in a subject in need thereof. In some instances, the subject may be mammal, such as a human or non-human primate, in which case delivery of the composition may comprise administering the composition to the subject. In some embodiments, delivery of the heterologous nucleic acid comprises administering to the subject the composition using any one of the routes of administration described herein.

[0180] In some embodiments, methods of increasing transduction of a heterologous nucleic acid in a target *in vivo* environment comprise delivering a rAAV particle described herein, the rAAV engineered to have an increased transduction efficiency in a target *in vivo* environment (*e.g.*, tissue or cell type). In some instances, the increased transduction efficiency comprises a 1-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, 16-fold, 17-fold, 18-fold, 19-fold, 20-fold, 21-fold, 22-fold, 23-fold, 24-

fold, 25-fold, 26-fold, 27-fold, 28-fold, 29-fold, 30-fold, 31-fold, 32-fold, 33-fold, 34-fold, 35-fold, 36-fold, 37-fold, 38-fold, 39-fold, 40-fold, 41-fold, 42-fold, 43-fold, 44-fold, 45-fold, 46-fold, 47-fold, 48-fold, 49-fold, 50-fold, 75-fold, or 100-fold increase, or more, relative to a reference AAV. In some instances, the increased transduction efficiency is at least 30-fold. In some instances, the increased transduction efficiency is at least 40-fold. In some instances, the increased transduction efficiency is at least 50-fold. In some instances, the increased transduction efficiency is at least 60-fold. In some instances, the increased transduction efficiency is at least 80-fold. In some instances, the increased transduction efficiency is at least 90-fold. In some instances, the increased transduction efficiency is at least 100-fold.

[0181] Methods of delivering a heterologous nucleic acid to a target *in vivo* environment are also provided comprising delivering the rAAV particle described herein that has been engineered to have an increased specificity in a target *in vivo* environment (*e.g.*, tissue or cell type), as compared to a reference AAV. Methods, in some cases, comprise detecting whether a rAAV possesses more specificity for a target *in vivo* environment than a reference AAV, includes measuring a level of gene expression product (*e.g.*, RNA or protein) expressed from the heterologous nucleic acid encapsidated by the rAAV in a tissue sample obtained from the target *in vivo* environment in a subject; and comparing the measured level to a control level (such as, for *e.g.*, the gene expression product expressed from a heterologous nucleic acid encapsidated by a reference AAV (*e.g.*, AAV9)). Suitable methods for measuring expression of a gene expression product luciferase reporter assay and quantitative polymerase chain reaction (qPCR).

[0182] In some instances, the reference AAV has a serotype selected from the group consisting of AAV1, AAV2, AAV3, AAV4, AAV5, AAV6, AAV7, AAV8, AAV9, AAV10, AAV11, AAV12, or variant thereof. For example, the reference AAV can have a serotype selected from the group consisting of AAV-PHP.B, AAV-PHP.eB, and AAV-PHP.S.

[0183] ***Delivery to the CNS***

[0184] Provided herein are methods of delivering a heterologous nucleic acid to a target *in vivo* environment comprising delivering a composition to the target *in vivo* environment selected from the group consisting of a central nervous system (CNS) in a subject, the composition comprising a rAAV particle with a rAAV capsid protein, the rAAV capsid protein encapsidating a viral vector encoding a heterologous nucleic acid (*e.g.,* therapeutic nucleic acid). In some

embodiments, the rAAV particle encapsidating the heterologous nucleic acid comprises a rAAV capsid protein engineered with an increased specificity and, in some cases, transduction efficiency when measured in the CNS or the PNS of the subject, even when administered to the subject systemically, as compared to a reference AAV.

[0185] Methods comprise delivering a rAAV particle comprising an rAAV capsid protein with increased specificity and/or transduction efficiency when measured in the CNS in the subject, as compared to a reference AAV (*e.g.,* AAV9). In some embodiments, delivery is systemic. Alternatively, delivery is direct (*e.g.*, into the affected area of the CNS).

[0186] The rAAV capsid protein may comprise a substitution of at least one, two, three, four, five, six, seven, eight, nine, ten, or eleven amino acids provided in an amino acid sequence provided in any one of **Tables 2-3**, in an amino acid sequence of a parental AAV. In some instances, X1 is selected from the group consisting of A, E, D, G, R, S and T. In some instances, the insertion further comprises two amino acids, wherein X2 is selected from the group consisting of A, G, I, L, M, N, Q, R, T, and Y. In some instances, the insertion further comprises three amino acids, wherein X3 is selected from the group consisting of E, K, L, T, and Q. In some instances, the insertion further comprises at least four amino acids, wherein X1 is selected from the group consisting of A, E, D, G, R, S and T, X2 is selected from the group consisting of A, G, I, L, M, N, Q, R, T, and Y, X3 is selected from the group consisting of E, K, L, T, and Q, and X4 is selected from the group consisting of G, I, K, L, M, R, T, and V. In some instances, the insertion further comprises five amino acids wherein X5 is selected from the group consisting of A, D, G, P, L, Q, and V. In some instances, the insertion further comprises at least six amino acids, wherein X6 is selected from the group consisting of F, K, L, N, P, Q, S, and V. In some instances, the insertion further comprises at least seven amino acids, wherein X7 is selected from the group consisting of I, K, L, P, S, and V.

[0187] Disclosed herein are methods comprising delivering a rAAV particle encapsidating a heterologous nucleic acid to a CNS in a subject, the rAAV particle comprising (i) an increased specificity and/or transduction efficiency of the heterologous nucleic acid for the CNS, wherein the rAAV particle has an rAAV capsid protein comprising an insertion of at least or about three, four, five, six, or seven amino acids of an amino acid sequence TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, or RYQGDSV, or any amino acid sequence provided in **Tables 2-3 or**

FIG. 33, at an amino acid position 588_589 in a parental AAV capsid protein. In some embodiments, the delivering is systemic. In some embodiments, the delivery is direct (*e.g.,* injected into the *in vivo* environment). In some embodiments, the parental AAV capsid protein is AAV9 capsid protein (for *e.g.,* provided in SEQ ID NO: 1). In some embodiments, delivery is more specific than a delivery of the heterologous nucleic acid by a reference AAV, *e.g.,* AAV9. In some embodiments, the delivery is systemic (*e.g.,* intravenous). In some embodiments, the subject is a mammal. In some embodiments, the subject is a human.

[0188] ***Delivery to the Liver***

[0189] In some cases, the methods of delivering a heterologous nucleic acid comprise delivering to a target *in vivo* environment in a subject a composition, the composition comprising a rAAV particle with a rAAV capsid protein, the rAAV capsid protein encapsidating a viral vector encoding a heterologous nucleic acid (*e.g.,* therapeutic nucleic acid). In some cases, the target *in vivo* environment is the liver. In some embodiments, the rAAV particle encapsidating the heterologous nucleic acid comprises a rAAV capsid protein engineered with an increased specificity and, in some cases, transduction efficiency when measured in the target *in vivo* environment of the subject, even when administered to the subject systemically.

[0190] In some embodiments, methods comprise delivering a rAAV particle comprising an rAAV capsid protein with increased specificity and/or transduction efficiency of the heterologous nucleic acid for the liver in the subject, as compared to a reference AAV (*e.g.,* AAV9). In some embodiments, rAAVs optimized for targeting the liver have amino acid sequences that comprise an amino acid sequence provided in SEQ ID NOS: 950-1031 and 15054-15146 (**FIG. 35**).

[0191] The rAAV capsid protein suitable for delivery of the heterologous nucleic acid to the liver can comprise an insertion of at least one amino acid in a parental AAV capsid protein. In some instances, the insertion comprises at least one, two, three, four, five, six, seven, eight, nine, ten, or eleven amino acids provided in an amino acid sequence provided in **Table 4**, or **FIG. 35**.

[0192] Disclosed herein are methods comprising delivering a rAAV particle encapsidating a heterologous nucleic acid to the target *in vivo* environment selected from the group consisting of the liver in a subject, the rAAV particle comprising an increased specificity and/or transduction efficiency of the heterologous nucleic acid for the target *in vivo* environment, wherein the rAAV

particle has an rAAV capsid protein comprising an insertion of at least or about three, four, five, six, seven, eight, nine, ten, or eleven amino acids of an amino acid sequence provided in **Table 4**, or **FIG. 35**. In some embodiments, delivery is more specific than a delivery of the heterologous nucleic acid by a reference AAV, *e.g.,* AAV9. In some embodiments, methods further comprise reducing or ablating delivery of the heterologous nucleic acid in an off-target *in vivo* environment, such as the liver, compared to a reference AAV. In some embodiments, delivery is characterized by an increase in efficiency of transduction (*e.g.,* of the heterologous nucleic acid) in the target *in vivo* environment than a transduction efficiency in the target *in vivo* environment of the reference AAV. In some embodiments, the delivery is systemic (*e.g.,* intravenous). In some embodiments, the subject is a mammal. In some cases, the mammal is a human.

C. Methods of Treatment

[0193] Disclosed herein are methods of treating a disease or condition, or a symptom of the disease or condition, in a subject, comprising administrating of therapeutically effective amount of one or more compositions (*e.g.,* rAAV particle, AAV vector, pharmaceutical composition) disclosed herein to the subject. In some embodiments, the composition is a rAAV capsid protein described herein. In some embodiments, the composition is an isolated and purified rAAV capsid protein described herein. In some embodiments, the rAAV particle encapsidates an AAV vector comprising a transgene (*e.g.,* therapeutic nucleic acid). In some embodiments, the composition is a rAAV capsid protein described herein conjugated with a therapeutic agent disclosed herein. In some embodiments, the composition is a pharmaceutical composition comprising the rAAV particle and a pharmaceutically acceptable carrier. In some embodiments, the one or more compositions are administered to the subject alone (*e.g.*, standalone therapy). In some embodiments, the one or more compositions are administered in combination with an additional agent. In some embodiments, the composition is a first-line therapy for the disease or condition. In some embodiments, the composition is a second-line, third-line, or fourth-line therapy, for the disease or condition.

[0194] Provided herein are methods of treating a disease or a condition, or a symptom of the disease or condition, in a subject, comprising: (a) diagnosing a subject with a disease or a condition affecting a target *in vivo* environment; and (b) treating the disease or the condition by

administering to the subject a therapeutically effective amount of a composition disclosed herein (*e.g.,* rAAV particle, AAV vector, pharmaceutical composition), wherein the composition is engineered with an increased specificity for the target *in vivo* environment.

[0195] Disclosed herein are methods of treating a disease or a condition, or a symptom of the disease or the condition, afflicting a target *in vivo* environment in a subject comprising: (a) administering to the subject a composition (*e.g.,* rAAV particle, AAV vector, pharmaceutical composition); and (b) expressing the therapeutic nucleic acid into a target *in vivo* environment in the subject with an increased specificity and/or transduction efficiency, as compared to a reference AAV. In some cases, the reference AAV is AAV9, or a variant thereof.

[0196] Methods of treating a disease or condition affecting the central nervous system (CNS) comprise administering a rAAV particle to a CNS in a subject, the rAAV particle comprising an rAAV capsid protein comprising an insertion of at least or about three, four, five, six, seven, eight, nine, ten, or eleven amino acids of an amino acid sequence TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, RYQGDSV, or TTLKPFS, or any amino acid sequence provided in **Tables 2-3,** or **FIG. 33,** at an amino acid position 588_589 in a parental AAV capsid protein. In some cases, the insertion is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW. In some embodiments, the parental AAV capsid protein is AAV9 capsid protein (for *e.g.,* provided in SEQ ID NO: 1. In some instances, the parental AAV capsid protein comprises an amino acid sequence that is at least 95%, 96%, 96.1, 96.2%, 96.3%, 96.4%, 96.5%, 96.6%, 96.7%, 96.8%, 96.9%, 97.0%, 97.1%, 97.2%, 97.3%, 97.4%, 97.5%, 97.6%, 97.7%, 97.8%, 97.9%, 98.0%, 98.1%, 98.2%, 98.3%, 98.4%, 98.5%, 98.6%, 98.7%, 98.7%, 98.8%, 98.9%, 99.0%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100.0% identical to SEQ ID NO: 1. In some embodiments, delivery is more specific than a delivery of the heterologous nucleic acid by a reference AAV, *e.g.,* AAV9. In some embodiments, the delivery is systemic (*e.g.,* intravenous). In some embodiments, the subject is a human or a non-human primate.

[0197] Methods of treating a disease or a condition afflicting a target *in vivo* environment comprising a liver comprise administering a rAAV particle to the target *in vivo* environment in a subject, the rAAV particle comprising an rAAV capsid protein comprising a substitution of at least or about three, four, five, six, seven, eight, nine, ten, or eleven, amino acids of an amino

acid sequence provided in any one of SEQ ID NOS: 950-1031 and 15054-15146 (**FIG. 35**). In some embodiments, methods comprise delivering a rAAV particle comprising an rAAV capsid protein with increased specificity for the liver in the subject, as compared to a reference AAV (*e.g.,* AAV9). In some embodiments, rAAVs optimized for targeting the liver have amino acid sequences comprising an amino acid sequence KAYSVQV, PSGSARS, and RTANALG at an amino acid position 588_589 in a parental AAV capsid protein. In some embodiments, the parental AAV capsid protein is AAV9 capsid protein (for *e.g.,* provided in SEQ ID NO: 1). In some instances, the parental AAV capsid protein comprises an amino acid sequence that is at least 95%, 96%, 96.1, 96.2%, 96.3%, 96.4%, 96.5%, 96.6%, 96.7%, 96.8%, 96.9%, 97.0%, 97.1%, 97.2%, 97.3%, 97.4%, 97.5%, 97.6%, 97.7%, 97.8%, 97.9%, 98.0%, 98.1%, 98.2%, 98.3%, 98.4%, 98.5%, 98.6%, 98.7%, 98.7%, 98.8%, 98.9%, 99.0%, 99.1%, 99.2%, 99.3%, 99.4%, 99.5%, 99.6%, 99.7%, 99.8%, 99.9%, or 100.0% identical to SEQ ID NO: 1. In some embodiments, delivery is more specific than a delivery of the heterologous nucleic acid by a reference AAV, *e.g.,* AAV9. In some embodiments, the delivery is systemic (*e.g.,* intravenous or intranasal). In some embodiments, the subject is a human or a non-human primate.

[0198] Also provided are methods of modulating a target gene expression product, the methods comprising administering to a subject in need thereof a composition (*e.g.,* rAAV particle, AAV vector, pharmaceutical composition) disclosed herein. For example, methods provided herein comprise administering to a subject a rAAV with a rAAV capsid protein encapsidating a viral vector comprising a heterologous nucleic acid that modulates the expression or the activity of the target gene expression product. In some embodiments, the disease or the condition is characterized by an increased or enhanced expression or activity of a gene or gene expression product thereof, as compared to a normal individual. In some cases, administering the therapeutically effective amount of the composition restores the expression or the activity of the gene or gene expression product thereof to a level that is typical in a normal individual. The term "normal individual" refers to an individual that is not afflicted with the disease or the condition characterized by the variation in expression or activity of the gene or gene expression product thereof.

[0199] Non-limiting examples of genes involved in central nervous system (CNS) diseases or disorders include Sarcoglycan Alpha (SGCA), glutamic acid decarboxylase 65 (GAD65),

glutamic acid decarboxylase 67 (GAD67), CLN2 gene, Nerve Growth Factor (NGF), glial cell derived neurotrophic factor (GDNF), Neurturin, Survival Of Motor Neuron 1, Telomeric (SMN1), β-Glucocerebrosidase (GCase), Frataxin (FXN), Huntingtin (HTN), methyl-CpG binding protein 2 (MECP2), peroxisomal biogenesis factor (PEX), progranulin (GRN), an antitubulin agent, copper-zinc superoxide dismutase (SOD1), Glucosylceramidase Beta (GBA), NPC Intracellular Cholesterol Transporter 1 (NPC1), and NPS3. In some embodiments, the peroxisomal biogenesis factor (PEX) is selected from the group consisting of PEX1, PEX2, PEX3, PEX4, PEX5, PEX6, PEX7, PEX10, PEX11β, PEX12, PEX13, PEX14, PEX16, PEX19, and PEX26. Non-limiting examples of genes implicated in disease or disorder of a particular organ (*e.g.*, lung, heart, liver, muscle, eye) include Cystic Fibrosis Transmembrane Conductance Regulator (CFTR), Factor X (FIX), RPE65, Retinoid Isomerohydrolase (RPE65), Sarcoglycan Alpha (SGCA), and sarco/endoplasmic reticulum Ca2+-ATPase (SERCA2a). In some instances, the expression of a gene or expression or activity of a gene expression product is inhibited by the administration of the composition to the subject. In some instances, the expression of a gene or the expression or the activity of a gene expression product is enhanced by the administration of the composition to the subject.

[0200] In some cases, the composition is administered at dosage levels sufficient to deliver from about 0.0001 mg/kg to about 100 mg/kg, from about 0.001 mg/kg to about 0.05 mg/kg, from about 0.005 mg/kg to about 0.05 mg/kg, from about 0.001 mg/kg to about 0.005 mg/kg, from about 0.05 mg/kg to about 0.5 mg/kg, from about 0.01 mg/kg to about 50 mg/kg, from about 0.1 mg/kg to about 40 mg/kg, from about 0.5 mg/kg to about 30 mg/kg, from about 0.01 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 10 mg/kg, or from about 1 mg/kg to about 25 mg/kg, of subject body weight per day, one or more times a day, to obtain the desired therapeutic effect.

[0201] In some cases, the viral genome (vg) concentration of the composition that is administered is between 1.0 $x10^{11}$ vg per kilogram (kg) and 1.0 $x10^{16}$vg/kg. In some cases, the concentration of infectious particles of at least or about 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, or 10^{17}. In some cases, the concentration of infectious particles is $2x10^7$, $2x10^8$, $2x10^9$, $2x10^{10}$, $2x10^{11}$, $2x10^{12}$, $2x10^{13}$, $2x10^{14}$, $2x10^{15}$, $2x10^{16}$, or $2x10^{17}$. In some cases, the concentration of the infectious particles $3x10^7$, $3x10^8$, $3x10^9$, $3x10^{10}$, $3x10^{11}$, $3x10^{12}$, $3x10^{13}$,

$3x10^{14}$, $3x10^{15}$, $3x10^{16}$, or $3x10^{17}$. In some cases, the concentration of the infectious particles $4x10^{7}$, $4x10^{8}$, $4x10^{9}$, $4x10^{10}$, $4x10^{11}$, $4x10^{12}$, $4x10^{13}$, $4x10^{14}$, $4x10^{15}$, $4x10^{16}$, or $4x10^{17}$. In some cases, the concentration of the infectious particles $5x10^{7}$, $5x10^{8}$, $5x10^{9}$, $5x10^{10}$, $5x10^{11}$, $5x10^{12}$, $5x10^{13}$, $5x10^{14}$, $5x10^{15}$, $5x10^{16}$, or $5x10^{17}$. In some cases, the concentration of the infectious particles $6x10^{7}$, $6x10^{8}$, $6x10^{9}$, $6x10^{10}$, $6x10^{11}$, $6x10^{12}$, $6x10^{13}$, $6x10^{14}$, $6x10^{15}$, $6x10^{16}$, or $6x10^{17}$. In some cases, the concentration of the infectious particles $7x10^{7}$, $7x10^{8}$, $7x10^{9}$, $7x10^{10}$, $7x10^{11}$, $7x10^{12}$, $7x10^{13}$, $7x10^{14}$, $7x10^{15}$, $7x10^{16}$, or $7x10^{17}$. In some cases, the concentration of the infectious particles $8x10^{7}$, $8x10^{8}$, $8x10^{9}$, $8x10^{10}$, $8x10^{11}$, $8x10^{12}$, $8x10^{13}$, $8x10^{14}$, $8x10^{15}$, $8x10^{16}$, or $8x10^{17}$. In some cases, the concentration of the infectious particles $9x10^{7}$, $9x10^{8}$, $9x10^{9}$, $9x10^{10}$, $9x10^{11}$, $9x10^{12}$, $9x10^{13}$, $9x10^{14}$, $9x10^{15}$, $9x10^{16}$, or $9x10^{17}$.

[0202] In some embodiments, the administering of step is performed once. Alternatively, the administering of step is repeated at least twice. The administering of step may be performed once daily. In some cases, the administering of step comprises intravenous administration. In some cases, the administering comprises pulmonary administration. In some cases, the administering comprises intranasal administration (such as a spray). In some cases, the administering of step comprises injecting the composition into a target *in vivo* environment. In some cases, the administering of step does not comprise injecting the composition into the target *in vivo* environment.

[0203] ***Subject***

[0204] Disclosed herein methods of delivering at least one of an AAV particle and viral vector to a subject, for example – to treat or prevent a disease or condition in a subject. The subject, in some cases, is a mammal. Non-limiting examples of a mammal include a mouse, rat, guinea pig, rabbit, chimpanzee, or farm animal. In some instances, the mammal is a non-human primate. In some instances, the subject is human. The subject of the present disclosure may not be diagnosed with a disease or condition. Alternatively, the subject may be a patient that is diagnosed with a disease or disorder, or suspected of having the disease or the disorder.

[0205] ***Disease or Condition***

[0206] Disclosed herein are methods of treating a disease or condition in a subject by administering a composition comprising a rAAV such as those disclosed herein. At least one advantage of the rAAVs disclosed herein, is that the rAAV may be used to treat virtually any

disease or condition that would benefit from a transgene therapy, including but not limited to spinal muscular atrophy (SMA), amyotrophic lateral sclerosis (ALS), Parkinson's disease, Pompe disease, Huntington's disease, Alzheimer's disease, Battens disease, lysosomal storage disorders, glioblastoma multiforme, Rett syndrome, Leber's congenital amaurosis, Late infantile neuronal ceroid lipofuscinosis (LINCL), chronic pain, stroke, spinal cord injury, traumatic brain injury and lysosomal storage disorders.

[0207] The disease or the condition may, in some embodiments, be characterized by a reduced or ablated expression or activity of a gene or gene expression product thereof, as compared to a normal individual. In some embodiments, be characterized by an increased or enhanced expression or activity of a gene or gene expression product thereof, as compared to a normal individual.

[0208] In some cases, the disease or condition is localized to a particular *in vivo* environment in the subject, *e.g.,* the brain or the liver. The compositions of the present disclosure are particularly useful for the treatment of the diseases or conditions described herein because they specifically target the *in vivo* environment and deliver a therapeutic nucleic acid engineered to modulate the activity or the expression of a target gene expression product involved with the pathogenesis or pathology of the disease or condition.

[0209] In some instances, the disease or condition comprises a disease or condition of the central nervous system (CNS). Non-limiting examples of disease of the CNS include Absence of the Septum Pellucidum, Acid Lipase Disease, Acid Maltase Deficiency, Acquired Epileptiform Aphasia, Acute Disseminated Encephalomyelitis, Attention Deficit-Hyperactivity Disorder (ADHD), Adie's Pupil, Adie's Syndrome, Adrenoleukodystrophy, Agenesis of the Corpus Callosum, Agnosia, Aicardi Syndrome, Aicardi-Goutieres Syndrome Disorder, AIDS - Neurological Complications, Alexander Disease, Alpers' Disease, Alternating Hemiplegia, Alzheimer's Disease, Amyotrophic Lateral Sclerosis (ALS), Anencephaly, Aneurysm, Angelman Syndrome, Angiomatosis, Anoxia, Antiphospholipid Syndrome, Aphasia, Apraxia, Arachnoid Cysts, Arachnoiditis, Arnold-Chiari Malformation, Arteriovenous Malformation, Asperger Syndrome, Ataxia, Ataxia Telangiectasia, Ataxias and Cerebellar or Spinocerebellar Degeneration, Atrial Fibrillation and Stroke, Attention Deficit-Hyperactivity Disorder, Autism Spectrum Disorder, Autonomic Dysfunction, Back Pain, Barth Syndrome, Batten Disease,

Becker's Myotonia, Behcet's Disease, Bell's Palsy, Benign Essential Blepharospasm, Benign Focal Amyotrophy, Benign Intracranial Hypertension, Bernhardt-Roth Syndrome, Binswanger's Disease, Blepharospasm, Bloch-Sulzberger Syndrome, Brachial Plexus Birth Injuries, Brachial Plexus Injuries, Bradbury-Eggleston Syndrome, Brain and Spinal Tumors, Brain Aneurysm, Brain Injury, Brown-Sequard Syndrome, Bulbospinal Muscular Atrophy, Cerebral Autosomal Dominant Arteriopathy with Subcortical Infarcts and Leukoencephalopathy (CADASIL), Canavan Disease, Carpal Tunnel Syndrome, Causalgia, Cavernomas, Cavernous Angioma, Cavernous Malformation, Central Cervical Cord Syndrome, Central Cord Syndrome, Central Pain Syndrome, Central Pontine Myelinolysis, Cephalic Disorders, Ceramidase Deficiency, Cerebellar Degeneration, Cerebellar Hypoplasia, Cerebral Aneurysms, Cerebral Arteriosclerosis, Cerebral Atrophy, Cerebral Beriberi, Cerebral Cavemous Malformation, Cerebral Gigantism, Cerebral Hypoxia, Cerebral Palsy, Cerebro-Oculo-Facio-Skeletal Syndrome (COFS), Charcot-Marie-Tooth Disease, Charcot-Marie-Tooth syndrome, classical rhizomelic chondrodysplasia punctata (RCDP), Chiari Malformation, Cholesterol Ester Storage Disease, Chorea, Choreoacanthocytosis, Chronic Inflammatory Demyelinating Polyneuropathy (CIDP), Chronic Orthostatic Intolerance, Chronic Pain, Cockayne Syndrome Type II, Coffin Lowry Syndrome, Colpocephaly, Coma, Complex Regional Pain Syndrome, Congenital Facial Diplegia, Congenital Myasthenia, Congenital Myopathy, Congenital Vascular Cavernous Malformations, Corticobasal Degeneration, Cranial Arteritis, Craniosynostosis, Cree encephalitis, Creutzfeldt-Jakob Disease, Cumulative Trauma Disorders, Cushing's Syndrome, Cytomegalic Inclusion Body Disease, Cytomegalovirus Infection, Dancing Eyes-Dancing Feet Syndrome, Dandy-Walker Syndrome, Dawson Disease, Deafness, De Morsier's Syndrome, Dejerine-Klumpke Palsy, Dementia, Dementia -Multi -Infarct, Dementia - Semantic, Dementia -Subcortical, Dementia With Lewy Bodies, Dentate Cerebellar Ataxia, Dentatorubral Atrophy, Dermatomyositis, Developmental Dyspraxia, Devic's Syndrome, Diabetic Neuropathy, Diffuse Sclerosis, Dravet Syndrome, Duchenne muscular dystrophy, Dysautonomia, Dysgraphia, Dyslexia, Dysphagia, Dyspraxia, Dyssynergia Cerebellaris Myoclonica, Dyssynergia Cerebellaris Progressiva, Dystonias, Early Infantile Epileptic Encephalopathy, Empty Sella Syndrome, Encephalitis, Encephalitis Lethargica, Encephaloceles, Encephalopathy, Encephalopathy (familial infantile), Encephalotrigeminal Angiomatosis, Epilepsy, Epileptic

Hemiplegia, Erb's Palsy, Erb-Duchenne and Dejerine-Klumpke Palsies, Essential Tremor, Extrapontine Myelinolysis, Fabry Disease, Fahr's Syndrome, Fainting, Familial Dysautonomia, Familial Hemangioma, Familial Idiopathic Basal Ganglia Calcification, Familial Periodic Paralyses, Familial Spastic Paralysis, Farber's Disease, Febrile Seizures, Fibromuscular Dysplasia, Fisher Syndrome, Floppy Infant Syndrome, Foot Drop, Friedreich's Ataxia, Frontotemporal Dementia, Gaucher Disease, Generalized Gangliosidoses, Gerstmann's Syndrome, Gerstmann-Straussler-Scheinker Disease, Giant Axonal Neuropathy, Giant Cell Arteritis, Giant Cell Inclusion Disease, glioblastoma, Globoid Cell Leukodystrophy, Glossopharyngeal Neuralgia, Glycogen Storage Disease, Guillain-Barre Syndrome, Hallervorden-Spatz Disease, Head Injury, Headache, Hemicrania Continua, Hemifacial Spasm, Hemiplegia Alterans, Hereditary Neuropathies, Hereditary Spastic Paraplegia, Heredopathia Atactica Polyneuritiformis, Herpes Zoster, Herpes Zoster Oticus, Hirayama Syndrome, Holmes-Adie syndrome, Holoprosencephaly, HTLV-1 Associated Myelopathy, Hughes Syndrome, Huntington's Disease, Hydranencephaly, Hydrocephalus, Hydrocephalus - Normal Pressure, Hydromyelia, Hypercortisolism, Hypersomnia, Hypertonia, Hypotonia, Hypoxia, Immune-Mediated Encephalomyelitis, Inclusion Body Myositis, Incontinentia Pigmenti, Infantile Hypotonia, Infantile Neuroaxonal Dystrophy, Infantile Phytanic Acid Storage Disease, Infantile Refsum Disease, Infantile Spasms, Inflammatory Myopathies, Iniencephaly, Intestinal Lipodystrophy, Intracranial Cysts, Intracranial Hypertension, Isaacs' Syndrome, Joubert Syndrome, Kearns-Sayre Syndrome, Kennedy's Disease, Kinsbourne syndrome, Kleine-Levin Syndrome, Klippel-Feil Syndrome, Klippel-Trenaunay Syndrome (KTS), Kliiver-Bucy Syndrome, Korsakoff s Amnesic Syndrome, Krabbe Disease, Kugelberg-Welander Disease, Kuru, Lambert-Eaton Myasthenic Syndrome, Landau-Kleffner Syndrome, Lateral Femoral Cutaneous Nerve Entrapment, Lateral Medullary Syndrome, Learning Disabilities, Leigh's Disease, Lennox-Gastaut Syndrome, Lesch-Nyhan Syndrome, Leukodystrophy, Levine-Critchley Syndrome, Lewy Body Dementia, Lipid Storage Diseases, Lipoid Proteinosis, Lissencephaly, Locked-In Syndrome, Lou Gehrig's Disease, Lupus -Neurological Sequelae, Lyme Disease - Neurological Complications, Machado- Joseph Disease, Macrencephaly, Megalencephaly, Melkersson-Rosenthal Syndrome, Meningitis, Meningitis and Encephalitis, Menkes Disease, Meralgia Paresthetica, Metachromatic Leukodystrophy, Microcephaly,

Migraine, Miller Fisher Syndrome, Mini Stroke, Mitochondrial Myopathy, Moebius Syndrome, Monomelic Amyotrophy, Motor Neuron Diseases, Moyamoya Disease, Mucolipidoses, Mucopolysaccharidoses, Multi-Infarct Dementia, Multifocal Motor Neuropathy, Multiple Sclerosis, Multiple System Atrophy, Multiple System Atrophy with Orthostatic Hypotension, Muscular Dystrophy, Myasthenia -Congenital, Myasthenia Gravis, Myelinoclastic Diffuse Sclerosis, Myoclonic Encephalopathy of Infants, Myoclonus, Myopathy, Myopathy- Congenital, Myopathy -Thyrotoxic, Myotonia, Myotonia Congenita, Narcolepsy, Neuroacanthocytosis, Neurodegeneration with Brain Iron Accumulation, Neurofibromatosis, Neuroleptic Malignant Syndrome, Neurological Complications of AIDS, Neurological Complications of Lyme Disease, Neurological Consequences of Cytomegalovirus Infection, Neurological Manifestations of Pompe Disease, Neurological Sequelae Of Lupus, Neuromyelitis Optica, Neuromyotonia, Neuronal Ceroid Lipofuscinosis, Neuronal Migration Disorders, Neuropathy- Hereditary, Neurosarcoidosis, Neurosyphilis, Neurotoxicity, Nevus Cavernosus, Niemann-Pick Disease, O'Sullivan-McLeod Syndrome, Occipital Neuralgia, Ohtahara Syndrome, Olivopontocerebellar Atrophy, Opsoclonus Myoclonus, Orthostatic Hypotension, Overuse Syndrome, Pain -Chronic, Pantothenate Kinase-Associated Neurodegeneration, Paraneoplastic Syndromes, Paresthesia, Parkinson's Disease, Paroxysmal Choreoathetosis, Paroxysmal Hemicrania, Parry -Romberg, Pelizaeus-Merzbacher Disease, Pena Shokeir II Syndrome, Perineural Cysts, Periodic Paralyses, Peripheral Neuropathy, Periventricular Leukomalacia, Persistent Vegetative State, Pervasive Developmental Disorders, Phytanic Acid Storage Disease, Pick's Disease, Pinched Nerve, Piriformis Syndrome, Pituitary Tumors, Polymyositis, Pompe Disease, Porencephaly, Post-Polio Syndrome, Postherpetic Neuralgia, Postinfectious Encephalomyelitis, Postural Hypotension, Postural Orthostatic Tachycardia Syndrome, Postural Tachycardia Syndrome, Primary Dentatum Atrophy, Primary Lateral Sclerosis, Primary Progressive Aphasia, Prion Diseases, Progressive Hemifacial Atrophy, Progressive Locomotor Ataxia, Progressive Multifocal Leukoencephalopathy, Progressive Sclerosing Poliodystrophy, Progressive Supranuclear Palsy, Prosopagnosia, Pseudo-Torch syndrome, Pseudotoxoplasmosis syndrome, Pseudotumor Cerebri, Psychogenic Movement, Ramsay Hunt Syndrome I, Ramsay Hunt Syndrome II, Rasmussen's Encephalitis, Reflex Sympathetic Dystrophy Syndrome, Refsum Disease, Refsum Disease - Infantile, Repetitive Motion Disorders, Repetitive Stress Injuries, Restless Legs Syndrome,

Retrovirus-Associated Myelopathy, Rett Syndrome, Reye's Syndrome, Rheumatic Encephalitis, Riley-Day Syndrome, Sacral Nerve Root Cysts, Saint Vitus Dance, Salivary Gland Disease, Sandhoff Disease, Schilder's Disease, Schizencephaly, Seitelberger Disease, Seizure Disorder, Semantic Dementia, Septo-Optic Dysplasia, Severe Myoclonic Epilepsy of Infancy (SMEI), Shaken Baby Syndrome, Shingles, Shy-Drager Syndrome, Sjogren's Syndrome, Sleep Apnea, Sleeping Sickness, Sotos Syndrome, Spasticity, Spina Bifida, Spinal Cord Infarction, Spinal Cord Injury, Spinal Cord Tumors, Spinal Muscular Atrophy, Spinocerebellar Atrophy, Spinocerebellar Degeneration, Steele-Richardson-Olszewski Syndrome, Stiff-Person Syndrome, Striatonigral Degeneration, Stroke, Sturge-Weber Syndrome, Subacute Sclerosing Panencephalitis, Subcortical Arteriosclerotic Encephalopathy, Short-lasting, Unilateral, Neuralgiform (SUNCT) Headache, Swallowing Disorders, Sydenham Chorea, Syncope, Syphilitic Spinal Sclerosis, Syringohydromyelia, Syringomyelia, Systemic Lupus Erythematosus, Tabes Dorsalis,Tardive Dyskinesia, Tarlov Cysts, Tay-Sachs Disease, Temporal Arteritis, Tethered Spinal Cord Syndrome, Thomsen's Myotonia, Thoracic Outlet Syndrome, Thyrotoxic Myopathy, Tic Douloureux, Todd's Paralysis, Tourette Syndrome, Transient Ischemic Attack, Transmissible Spongiform Encephalopathies, Transverse Myelitis, Traumatic Brain Injury, Tremor, Trigeminal Neuralgia, Tropical Spastic Paraparesis, Troyer Syndrome, Tuberous Sclerosis, Vascular Erectile Tumor, Vasculitis Syndromes of the Central and Peripheral Nervous Systems, Von Economo's Disease, Von Hippel-Lindau Disease (VHL), Von Recklinghausen's Disease, Wallenberg's Syndrome, Werdnig-Hoffman Disease, Wernicke-Korsakoff Syndrome, West Syndrome, Whiplash, Whipple's Disease, Williams Syndrome, Wilson Disease, Wolman's Disease, and X-Linked Spinal and Bulbar Muscular Atrophy.

[0210] In some instances, the disease or condition comprises a liver disease or disorder, or is associated with a liver disease or disorder. Non-limiting examples include disorders of bile acid synthesis (*e.g.,* Wilson disease, Progressive familial intrahepatic cholestasis type 3), disorders of carbohydrate metabolism (*e.g.,* Hereditary fructose intolerance, Glycogen storage disease type IV), disorders of amino acids metabolism (*e.g.,* tyrosinemia type I), Urea cycle disorders (*e.g.,* argininosuccinate lyase deficiency, citrin deficiency (CTLN2, NICCD)), disorders of lipid metabolism (*e.g.,* cholesteryl ester storage disease), and others including but not limited to

Alpha-1 antitrypsin deficiency, cystic fibrosis, hereditary hemochromatosis, Alström syndrome, and congenital hepatic fibrosis.

[0211] In some instances, the disease or condition is a disease or condition is of the liver. Non-limiting examples of liver diseases or disorders include Alagille Syndrome, Alcohol-Related Liver Disease, Alpha-1 Antitrypsin Deficiency, Autoimmune Hepatitis, Benign Liver Tumors, Biliary Atresia, Cirrhosis, Crigler-Najjar Syndrome, Galactosemia, Gilbert Syndrome, Hemochromatosis, Hepatic Encephalopathy, Hepatitis A, Hepatitis B, Hepatitis C, Hepatorenal Syndrome, Intrahepatic Cholestasis of Pregnancy (ICP), Lysosomal Acid Lipase Deficiency (LAL-D), Liver Cysts, Liver Cancer, Newborn Jaundice, Non-Alcoholic Fatty Liver Disease, Primary Biliary Cholangitis (PBC), Primary Sclerosing Cholangitis (PSC), Reye Syndrome, Type I Glycogen Storage Disease, and Wilson Disease.

[0212] Provided here, are methods of treating a disease or a condition associated with an aberrant expression or activity of a target gene or gene expression product thereof, the method comprising modulating the expression or the activity of a target gene or gene expression product in a subject by administering a rAAV encapsidating a heterologous nucleic acid of the present disclosure. In some instances, administration is systemic administration. In some instances, the expression or the activity of the target gene or gene expression product is decreased, relative to that in a normal (non-diseased) individual; and administering the rAAV to the subject is sufficient to increase the expression of the activity of the target gene or gene expression product to that of a normal individual. In some instances, the expression or the activity of the gene or gene expression product is increased, relative to that in a normal individual; and administering the rAAV to the subject is sufficient to decrease the expression or the activity of the target gene or gene expression product. In a non-limiting example, a subject diagnosed with Alzheimer's disease, which is caused, in some cases, by a gain-of-function of a Presenilin 1 and/or Presenilin 2 (encoded by the gene PSEN1 and PSEN2, respectively) is administered a rAAV disclosed herein encapsidating a therapeutic nucleic acid that is a silencing RNA (siRNA), or other RNAi with a loss-of-function effect on PSEN1 mRNA.

[0213] Also provided are methods of treating or preventing a disease or condition disclosed herein in a subject comprising administering to the subject a therapeutically effective amount of an AAV vector comprising a nucleic acid sequence encoding a therapeutic gene expression

product described herein. The AAV vector may be encapsidated in the modified capsid protein or AAV viral particle described herein. In some instances, the therapeutic gene expression product is effective to modulate the activity or expression of a target gene or gene expression product.

[0214] ***Formulations, Dosages, and Routes of Administration***

[0215] In general, methods disclosed herein comprise administering a therapeutic rAAV composition by systemic administration. In some instances, methods comprise administering a therapeutic rAAV composition by oral administration. In some instances, methods comprise administering a therapeutic rAAV composition by intraperitoneal injection. In some instances, methods comprise administering a therapeutic rAAV composition in the form of an anal suppository. In some instances, methods comprise administering a therapeutic rAAV composition by intravenous ("i.v.") administration. It is conceivable that one may also administer therapeutic rAAV compositions disclosed herein by other routes, such as subcutaneous injection, intramuscular injection, intradermal injection, transdermal injection percutaneous administration, intranasal administration, intralymphatic injection, rectal administration intragastric administration, intraocular administration, intracerebro-ventricularl administration, intrathecally, or any other suitable parenteral administration. In some instances, methods comprise administering a therapeutic rAAV composition by topical administration, example, by brushing or otherwise contacting the rAAV composition to a region of the subject (*e.g.,* eardrum, bladder). In some embodiments, routes for local delivery closer to site of injury or inflammation are preferred over systemic routes. Routes, dosage, time points, and duration of administrating therapeutics may be adjusted. In some embodiments, administration of therapeutics is prior to, or after, onset of either, or both, acute and chronic symptoms of the disease or condition.

[0216] An effective dose and dosage of pharmaceutical compositions to prevent or treat the disease or condition disclosed herein is defined by an observed beneficial response related to the disease or condition, or symptom of the disease or condition. Beneficial response comprises preventing, alleviating, arresting, or curing the disease or condition, or symptom of the disease or condition. In some embodiments, the beneficial response may be measured by detecting a measurable improvement in the presence, level, or activity, of biomarkers, transcriptomic risk

profile, or intestinal microbiome in the subject. An "improvement," as used herein refers to shift in the presence, level, or activity towards a presence, level, or activity, observed in normal individuals (*e.g.* individuals who do not suffer from the disease or condition). In instances wherein the therapeutic rAAV composition is not therapeutically effective or is not providing a sufficient alleviation of the disease or condition, or symptom of the disease or condition, then the dosage amount and/or route of administration may be changed, or an additional agent may be administered to the subject, along with the therapeutic rAAV composition. In some embodiments, as a patient is started on a regimen of a therapeutic rAAV composition, the patient is also weaned off (*e.g.*, step-wise decrease in dose) a second treatment regimen.

[0217] In some embodiments, pharmaceutical compositions in accordance with the present disclosure may be administered at dosage levels sufficient to deliver from about 0.0001 mg/kg to about 100 mg/kg, from about 0.001 mg/kg to about 0.05 mg/kg, from about 0.005 mg/kg to about 0.05 mg/kg, from about 0.001 mg/kg to about 0.005 mg/kg, from about 0.05 mg/kg to about 0.5 mg/kg, from about 0.01 mg/kg to about 50 mg/kg, from about 0.1 mg/kg to about 40 mg/kg, from about 0.5 mg/kg to about 30 mg/kg, from about 0.01 mg/kg to about 10 mg/kg, from about 0.1 mg/kg to about 10 mg/kg, or from about 1 mg/kg to about 25 mg/kg, of subject body weight per day, one or more times a day, to obtain the desired therapeutic, diagnostic, or prophylactic, effect. It will be understood that the above dosing concentrations may be converted to vg or viral genomes per kg or into total viral genomes administered by one of skill in the art.

[0218] In some cases, a dose of the pharmaceutical composition may comprise a concentration of infectious particles of at least or about 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, 10^{14}, 10^{15}, 10^{16}, or 10^{17}. In some cases, the concentration of infectious particles is $2x10^7$, $2x10^8$, $2x10^9$, $2x10^{10}$, $2x10^{11}$, $2x10^{12}$, $2x10^{13}$, $2x10^{14}$, $2x10^{15}$, $2x10^{16}$, or $2x10^{17}$. In some cases, the concentration of the infectious particles is $3x10^7$, $3x10^8$, $3x10^9$, $3x10^{10}$, $3x10^{11}$, $3x10^{12}$, $3x10^{13}$, $3x10^{14}$, $3x10^{15}$, $3x10^{16}$, or $3x10^{17}$. In some cases, the concentration of the infectious particles is $4x10^7$, $4x10^8$, $4x10^9$, $4x10^{10}$, $4x10^{11}$, $4x10^{12}$, $4x10^{13}$, $4x10^{14}$, $4x10^{15}$, $4x10^{16}$, or $4x10^{17}$. In some cases, the concentration of the infectious particles is $5x10^7$, $5x10^8$, $5x10^9$, $5x10^{10}$, $5x10^{11}$, $5x10^{12}$, $5x10^{13}$, $5x10^{14}$, $5x10^{15}$, $5x10^{16}$, or $5x10^{17}$. In some cases, the concentration of the infectious particles is $6x10^7$, $6x10^8$, $6x10^9$, $6x10^{10}$, $6x10^{11}$, $6x10^{12}$, $6x10^{13}$, $6x10^{14}$, $6x10^{15}$, $6x10^{16}$, or $6x10^{17}$. In some cases, the concentration of the infectious particles is $7x10^7$, $7x10^8$, $7x10^9$,

$7x10^{10}$, $7x10^{11}$, $7x10^{12}$, $7x10^{13}$, $7x10^{14}$, $7x10^{15}$, $7x10^{16}$, or $7x10^{17}$. In some cases, the concentration of the infectious particles is $8x10^{7}$, $8x10^{8}$, $8x10^{9}$, $8x10^{10}$, $8x10^{11}$, $8x10^{12}$, $8x10^{13}$, $8x10^{14}$, $8x10^{15}$, $8x10^{16}$, or $8x10^{17}$. In some cases, the concentration of the infectious particles is $9x10^{7}$, $9x10^{8}$, $9x10^{9}$, $9x10^{10}$, $9x10^{11}$, $9x10^{12}$, $9x10^{13}$, $9x10^{14}$, $9x10^{15}$, $9x10^{16}$, or $9x10^{17}$.

[0219] Disclosed herein, in some embodiments are formulations of pharmaceutically-acceptable excipients and carrier solutions suitable for delivery of the rAAV compositions described herein, as well as suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens. In some embodiments, the amount of therapeutic gene expression product in each therapeutically-useful composition may be prepared is such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable. In some instances, the rAAV compositions are suitably formulated pharmaceutical compositions disclosed herein, to be delivered either intraocularly, intravitreally, parenterally, subcutaneously, intravenously, intracerebro-ventricularly, intramuscularly, intrathecally, orally, intraperitoneally, by oral or nasal inhalation, or by direct injection to one or more cells, tissues, or organs by direct injection.

[0220] In some embodiments, the pharmaceutical forms of the AAV-based viral compositions suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the

injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

[0221] In some cases, for administration of an injectable aqueous solution, for example, the solution may be suitably buffered, if necessary, and the liquid diluent first rendered isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

[0222] Disclosed herein are sterile injectable solutions comprising the rAAV compositions disclosed herein, which are prepared by incorporating the rAAV compositions disclosed herein in the required amount in the appropriate solvent with several of the other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof. Injectable solutions may be advantageous for systemic administration, for example by intravenous administration.

[0223] Also provided herein are formulations in a neutral or salt form. Pharmaceutically-acceptable salts include the acid addition salts (formed with the free amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is

therapeutically effective. The formulations are easily administered in a variety of dosage forms such as injectable solutions, drug-release capsules, and the like.

[0224] Pulmonary administration may be advantageously achieved via the buccal administration. In some embodiments, formulations may comprise dry particles comprising active ingredients. In such embodiments, dry particles may have a diameter in the range from about 0.5 nm to about 7 nm or from about 1 nm to about 6 nm. In some embodiments, formulations may be in the form of dry powders for administration using devices comprising dry powder reservoirs to which streams of propellant may be directed to disperse such powder. In some embodiments, self-propelling solvent/powder dispensing containers may be used. In such embodiments, active ingredients may be dissolved and/or suspended in low-boiling propellant in sealed containers. Such powders may comprise particles wherein at least 98% of the particles by weight have diameters greater than 0.5 nm and at least 95% of the particles by number have diameters less than 7 nm. Alternatively, at least 95% of the particles by weight have a diameter greater than 1 nm and at least 90% of the particles by number have a diameter less than 6 nm. Dry powder compositions may include a solid fine powder diluent such as sugar and are conveniently provided in a unit dose form. Low boiling propellants generally include liquid propellants having a boiling point of below 65 °F at atmospheric pressure. Generally, propellants may constitute 50% to 99.9% (w/w) of the composition, and active ingredient may constitute 0.1% to 20% (w/w) of the composition. Propellants may further comprise additional ingredients such as liquid non-ionic and/or solid anionic surfactant and/or solid diluent (which may have particle sizes of the same order as particles comprising active ingredients).

[0225] Pharmaceutical compositions formulated for pulmonary delivery may provide active ingredients in the form of droplets of solution and/or suspension. Such formulations may be prepared, packaged, and/or sold as aqueous and/or dilute alcoholic solutions and/or suspensions, optionally sterile, comprising active ingredients, and may conveniently be administered using any nebulization and/or atomization device. Such formulations may further comprise one or more additional ingredients including, but not limited to, a flavoring agent such as saccharin sodium, a volatile oil, a buffering agent, a surface-active agent, and/or a preservative such as methylhydroxybenzoate. Droplets provided by this route of administration may have an average diameter in the range from about 0.1 nm to about 200 nm. Formulations described herein useful

for pulmonary delivery may also be useful for intranasal delivery. In some embodiments, formulations for intranasal administration comprise a coarse powder comprising the active ingredient and having an average particle size from about 0.2 μm to 500 μm. Such formulations are administered in the manner in which snuff is taken, i.e. by rapid inhalation through the nasal passage from a container of the powder held close to the nose.

[0226] Formulations suitable for nasal administration may, for example, comprise from about as little as 0.1% (w/w) and as much as 100% (w/w) of active ingredient, and may comprise one or more of the additional ingredients described herein. A pharmaceutical composition may be prepared, packaged, and/or sold in a formulation suitable for buccal administration. Such formulations may, for example, be in the form of tablets and/or lozenges made using conventional methods, and may, for example, comprise 0.1% to 20% (w/w) active ingredient, the balance comprising an orally dissolvable and/or degradable composition and, optionally, one or more of the additional ingredients described herein. Alternately, formulations suitable for buccal administration may comprise powders and/or an aerosolized and/or atomized solutions and/or suspensions comprising active ingredients. Such powdered, aerosolized, and/or aerosolized formulations, when dispersed, may comprise average particle and/or droplet sizes in the range of from about 0.1 nm to about 200 nm, and may further comprise one or more of any additional ingredients described herein.

[0227] Suitable dose and dosage administrated to a subject is determined by factors including, but not limited to, the particular therapeutic rAAV composition, disease condition and its severity, the identity (*e.g.*, weight, sex, age) of the subject in need of treatment, and can be determined according to the particular circumstances surrounding the case, including, *e.g.*, the specific agent being administered, the route of administration, the condition being treated, and the subject or host being treated.

[0228] The amount of AAV compositions and time of administration of such compositions will be within the purview of the skilled artisan having benefit of the present teachings. It is likely, however, that the administration of therapeutically-effective amounts of the disclosed compositions may be achieved by a single administration, example, a single injection of sufficient numbers of infectious particles to provide therapeutic benefit to the patient undergoing

such treatment. This is made possible, at least in part, by the fact that certain target cells (*e.g.*, neurons) do not divide, obviating the need for multiple or chronic dosing.

[0229] Alternatively, in some circumstances, it may be desirable to provide multiple, or successive administrations of the AAV vector compositions, either over a relatively short, or a relatively prolonged period of time, as may be determined by the medical practitioner overseeing the administration of such compositions. For example, the number of infectious particles administered to a mammal may be on the order of about 10^7, 10^8, 10^9, 10^{10}, 10^{11}, 10^{12}, 10^{13}, or even higher, infectious particles/ml given either as a single dose, or divided into two or more administrations as may be required to achieve therapy of the particular disease or disorder being treated. In fact, in certain embodiments, it may be desirable to administer two or more different AAV vector compositions, either alone, or in combination with one or more other therapeutic drugs to achieve the desired effects of a particular therapy regimen. In various embodiments, the daily and unit dosages are altered depending on a number of variables including, but not limited to, the activity of the therapeutic rAAV composition used, the disease or condition to be treated, the mode of administration, the requirements of the individual subject, the severity of the disease or condition being treated, and the judgment of the practitioner.

[0230] In some embodiments, the administration of the therapeutic rAAV composition is hourly, once every 2 hours, 3 hours, 4 hours, 5 hours, 6 hours,7 hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours 22 hours, 23 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, 11 days, 12 days, 13 days, 14 days, 15 days, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 1 year, 2 years, 3 years, 4 years, or 5 years, or 10 years. The effective dosage ranges may be adjusted based on subject's response to the treatment. Some routes of administration will require higher concentrations of effective amount of therapeutics than other routes.

[0231] Although not anticipated given the advantages of the present disclosure, in certain embodiments wherein the patient's condition does not improve, upon the doctor's discretion the administration of therapeutic rAAV composition is administered chronically, that is, for an extended period of time, including throughout the duration of the patient's life in order to ameliorate or otherwise control or limit the symptoms of the patient's disease or condition. In

certain embodiments wherein a patient's status does improve, the dose of therapeutic rAAV composition being administered may be temporarily reduced or temporarily suspended for a certain length of time (i.e., a "drug holiday"). In specific embodiments, the length of the drug holiday is between 2 days and 1 year, including by way of example only, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 12 days, 15 days, 20 days, 28 days, or more than 28 days. The dose reduction during a drug holiday is, by way of example only, by 10%-100%, including by way of example only 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, and 100%. In certain embodiments, the dose of drug being administered may be temporarily reduced or temporarily suspended for a certain length of time (i.e., a "drug diversion"). In specific embodiments, the length of the drug diversion is between 2 days and 1 year, including by way of example only, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 12 days, 15 days, 20 days, 28 days, or more than 28 days. The dose reduction during a drug diversion is, by way of example only, by 10%-100%, including by way of example only 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, and 100%. After a suitable length of time, the normal dosing schedule is optionally reinstated.

[0232] In some embodiments, once improvement of the patient's conditions has occurred, a maintenance dose is administered if necessary. Subsequently, in specific embodiments, the dosage or the frequency of administration, or both, is reduced, as a function of the symptoms, to a level at which the improved disease, disorder or condition is retained. In certain embodiments, however, the patient requires intermittent treatment on a long-term basis upon any recurrence of symptoms.

[0233] Toxicity and therapeutic efficacy of such therapeutic regimens are determined by standard pharmaceutical procedures in cell cultures or experimental animals, including, but not limited to, the determination of the LD50 and the ED50. The dose ratio between the toxic and therapeutic effects is the therapeutic index and it is expressed as the ratio between LD50 and ED50. In certain embodiments, the data obtained from cell culture assays and animal studies are used in formulating the therapeutically effective daily dosage range and/or the therapeutically effective unit dosage amount for use in mammals, including humans. In some embodiments, the dosage amount of the therapeutic rAAV composition described herein lies within a range of

circulating concentrations that include the ED50 with minimal toxicity. In certain embodiments, the daily dosage range and/or the unit dosage amount varies within this range depending upon the dosage form employed and the route of administration utilized.

[0234] ***Additional Therapeutic***

[0235] A therapeutic nucleic acid may be used alone or in combination with an additional therapeutic agent (together, "therapeutic agents"). In some cases, an "additional therapeutic agent" as used herein is administered alone. The therapeutic agent may be administered together or sequentially in a combination therapy. The combination therapy may be administered within the same day, or may be administered one or more days, weeks, months, or years apart. In some cases, a therapeutic nucleic acid provided herein is administered if the subject is determined to be non-responsive to a first line of therapy.

[0236] The additional therapeutic agent can comprise a small molecule. The additional therapeutic agent can comprise an antibody, or antigen-binding fragment. The additional therapeutic agent can comprise a cell-based therapy. Exemplary cell-based therapies include without limitation immune effector cell therapy, chimeric antigen receptor T-cell (CAR-T) therapy, natural killer cell therapy and chimeric antigen receptor natural killer (NK) cell therapy. Either NK cells, or CAR-NK cells, or a combination of both NK cells and CAR-NK cells can be used in combination with the methods disclosed herein. In some embodiments, the NK cells and CAR-NK cells are derived from human induced pluripotent stem cells (iPSC), umbilical cord blood, or a cell line. The NK cells and CAR-NK cells can comprise a cytokine receptor and a suicide gene. The cell-based therapy can comprises a stem cell therapy. The stem cell therapy may be embryonic or somatic stem cells. The stem cells may be isolated from a donor (allogeneic) or isolated from the subject (autologous). The stem cells may be expanded adipose-derived stem cells (eASCs), hematopoietic stem cells (HSCs), mesenchymal stem (stromal) cells (MSCs), or induced pluripotent stem cells (iPSCs) derived from the cells of the subject.

III. KITS

[0237] Disclosed herein are kits comprising compositions disclosed herein. Also disclosed herein are kits for the treatment or prevention of a disease or conditions of the central nervous system (CNS), or target organ or environment (*e.g.*, liver). In some instances, the disease or

condition is cancer, a pathogen infection, pulmonary disease or condition, neurological disease, muscular disease, or an immune disorder, such as those described herein. In one embodiment, a kit can include a therapeutic or prophylactic composition containing an effective amount of a composition of a rAAV particle encapsidating a recombinant AAV vector encoding a therapeutic nucleic acid (*e.g.*, therapeutic nucleic acid) and a recombinant AAV (rAAV) capsid protein of the present disclosure. In another embodiment, a kit can include a therapeutic or prophylactic composition containing an effective amount of cells modified by the rAAV described herein ("modified cell"), in unit dosage form that express therapeutic nucleic acid. In some embodiments, a kit comprises a sterile container which can contain a therapeutic composition; such containers can be boxes, ampules, bottles, vials, tubes, bags, pouches, blister-packs, or other suitable container forms known in the art. Such containers can be made of plastic, glass, laminated paper, metal foil, or other materials suitable for holding medicaments.

[0238] In some cases, rAAV are provided together with instructions for administering the rAAV to a subject having or at risk of developing the disease or condition (*e.g.*, disease of the CNS, PNS, liver, and the like). Instructions can generally include information about the use of the composition for the treatment or prevention of the disease or condition.

[0239] In some cases, a kit can include allogenic cells. In some cases, a kit can include cells that can comprise a genomic modification. In some cases, a kit can comprise "off-the-shelf" cells. In some cases, a kit can include cells that can be expanded for clinical use. In some cases, a kit can contain contents for a research purpose.

[0240] In some cases, the instructions include at least one of the following: description of the therapeutic rAAV composition; dosage schedule and administration for treatment or prevention of the disease or condition disclosed herein; precautions; warnings; indications; counter-indications; overdosage information; adverse reactions; animal pharmacology; clinical studies; and/or references. The instructions can be printed directly on the container (when present), or as a label applied to the container, or as a separate sheet, pamphlet, card, or folder supplied in or with the container. In some cases, instructions provide procedures for administering the rAAV to the subject alone. In some cases, instructions provide procedures for administering the rAAV to the subject at least about 1 hour (hr), 2 hr, 3 hr, 4 hr, 5 hr, 6 hr, 7 hr, 8 hr, 9 hr,10 hr, 11 hr, 12 hr, 13 hr, 14 hr, 15 hr, 16 hr, 17 hr, 18 hr, 19 hr, 20 hr, 21 hr, 22 hr, 23 hr, 24 hr, 25 hr, 26 hr, 27 hr,

28 hr, 29 hr, 30 hr, or up to 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days after or before administering an additional therapeutic agent disclosed herein. In some instances, the instructions provide that the rAAV is formulated for intravenous injection.

IV. DEFINITIONS

[0241] The terminology used herein is for the purpose of describing particular cases only and is not intended to be limiting. As used herein, the singular forms "a", "an" and "the" are intended to include the plural forms as well, unless the context clearly indicates otherwise. Furthermore, to the extent that the terms "including", "includes", "having", "has", "with", or variants thereof are used in either the detailed description and/or the claims, such terms are intended to be inclusive in a manner similar to the term "comprising."

[0242] The term "about" or "approximately" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, *e.g.*, the limitations of the measurement system. For example, "about" can mean within 1 or more than 1 standard deviation, per the practice in the given value. Where particular values are described in the application and claims, unless otherwise stated the term "about" should be assumed to mean an acceptable error range for the particular value.

[0243] As used herein "consisting essentially of" when used to define compositions and methods, shall mean excluding other elements of any essential significance to the combination for the stated purpose. Thus, a composition consisting essentially of the elements as defined herein would not exclude other materials or steps that do not materially affect the basic and novel characteristic(s) of the claimed disclosure, such as compositions for treating skin disorders like acne, eczema, psoriasis, and rosacea.

[0244] The terms "homologous," "homology," or "percent homology" are used herein to generally mean an amino acid sequence or a nucleic acid sequence having the same, or similar sequence to a reference sequence. Percent homology of sequences can be determined using the most recent version of BLAST, as of the filing date of this application.

[0245] The terms "increased," or "increase" are used herein to generally mean an increase by a statically significant amount. In some embodiments, the terms "increased," or "increase," mean

an increase of at least 10% as compared to a reference level, for example an increase of at least about 10%, at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% increase or any increase between 10-100% as compared to a reference level, standard, or control. Other examples of "increase" include an increase of at least 2-fold, at least 5-fold, at least 10-fold, at least 20-fold, at least 50-fold, at least 100-fold, at least 1000-fold or more as compared to a reference level.

[0246] The terms, "decreased" or "decrease" are used herein generally to mean a decrease by a statistically significant amount. In some embodiments, "decreased" or "decrease" means a reduction by at least 10% as compared to a reference level, for example a decrease by at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% decrease (*e.g.*, absent level or non-detectable level as compared to a reference level), or any decrease between 10-100% as compared to a reference level. In the context of a marker or symptom, by these terms is meant a statistically significant decrease in such level. The decrease can be, for example, at least 10%, at least 20%, at least 30%, at least 40% or more, and is preferably down to a level accepted as within the range of normal for an individual without a given disease.

[0247] The terms "subject" is any organism. In some instances, the organism is a mammal. Non-limiting examples of mammal include, any member of the mammalian class: humans, non–human primates such as chimpanzees, and other apes and monkey species; farm animals such as cattle, horses, sheep, goats, swine; domestic animals such as rabbits, dogs, and cats; laboratory animals including rodents, such as rats, mice and guinea pigs, and the like. In one aspect, the mammal is a human. The term "animal" as used herein comprises human beings and non–human animals. In one embodiment, a "non–human animal" is a mammal, for example a rodent such as rat or a mouse. In some instances, the subject is a patient, which as used herein, may refer to a subject diagnosed with a particular disease or disorder.

[0248] The term "gene," as used herein, refers to a segment of nucleic acid that encodes an individual protein or RNA (also referred to as a "coding sequence" or "coding region"),

optionally together with associated regulatory region such as promoter, operator, terminator and the like, which may be located upstream or downstream of the coding sequence.

[0249] The term "adeno-associated virus," or "AAV" as used herein refers to the adeno-associated virus or derivatives thereof. Non-limited examples of AAV's include AAV type 1 (AAV1), AAV type 2 (AAV2), AAV type 3 (AAV3), AAV type 4 (AAV4), AAV type 5 (AAV5), AAV type 6 (AAV6), AAV type 7 (AAV7), AAV type 8 (AAV8), AAV type 9 (AAV9), AAV type 10 (AAV10), AAV type 11 (AAV11), AAV type 12 (AAV12), avian AAV, bovine AAV, canine AAV, equine AAV, primate AAV, non-primate AAV, and ovine AAV. In some instances, the AAV is described as a "Primate AAV," which refers to AAV that infect primates. Likewise an AAV may infect bovine animals (*e.g.*, "bovine AAV", and the like). In some instances, the AAV is wildtype, or naturally occurring. In some instances, the AAV is recombinant.

[0250] The term "AAV capsid" as used herein refers to a capsid protein or peptide of an adeno-associated virus. In some instances, the AAV capsid protein is configured to encapsidate genetic information (*e.g.*, a transgene, therapeutic nucleic acid, viral genome). In some instances, the AAV capsid of the instant disclosure is a modified AAV capsid, relative to a corresponding parental AAV capsid protein.

[0251] The term "tropism" as used herein refers to a quality or characteristic of the AAV capsid that may include specificity for, and/or an increase or a decrease in efficiency of, expressing the encapsidated genetic information into one in *in vivo* environment, relative to a second *in vivo* environment. An *in vivo* environment, in some instances, is a cell-type. An *in vivo* environment, in some instances, is an organ or organ system.

[0252] The term "AAV vector" as used herein refers to nucleic acid polymer encoding genetic information related to the virus. The AAV vector may be a recombinant AAV vector (rAAV), which refers to an AAV vector generated using recombinatorial genetics methods. In some instances, the rAAV vector comprises at least one heterologous polynucleotide (*e.g.* a polynucleotide other than a wild-type or naturally occurring AAV genome such as a transgene).

[0253] The term "AAV particle" as used herein refers to an AAV virus, virion, AAV capsid protein or component thereof. In some cases, the AAV particle is modified relative to a parental AAV particle.

[0254] The term "gene product" of "gene expression product" refers to an expression product of a polynucleotide sequence such as, for *e.g.*, a polypeptide, peptide, protein or RNA, including interfering RNA (*e.g.*, siRNA, miRNA, shRNA) and messenger RNA (mRNA).

[0255] The terms "operatively linked" or "operably linked" refers to a location of two or more elements being close together, and in some cases, next to one other (*e.g.*, genetic elements such as a promoter, enhancer, termination signal sequence, polyadenylation sequence, and the like) that enables a functional relationship between the two or more elements. In one non-limiting example, a promoter that is operatively linked to a coding region enables the initiation of transcription of the coding sequence.

[0256] The term "heterologous" as used herein refers to a genetic element (*e.g.*, coding region) or gene expression product (*e.g.*, RNA, protein) that is derived from a genotypically distinct entity from that of the rest of the entity to which it is being compared.

[0257] The term "endogenous" as used herein refers to a genetic element (*e.g.*, coding region) or gene expression product (*e.g.*, RNA, protein) that is naturally occurring in or associated with an organism or a particular cell within the organism.

[0258] A "detectable moiety" as used herein refers to a moiety that can be covalently or noncovalently attached to a compound or biomolecule that can be detected for instance, using techniques known in the art. In embodiments, the detectable moiety is covalently attached. The detectable moiety may provide for imaging of the attached compound or biomolecule. The detectable moiety may indicate the contacting between two compounds. Exemplary detectable moieties are fluorophores, antibodies, reactive dies, radio-labeled moieties, magnetic contrast agents, and quantum dots. Exemplary fluorophores include fluorescein, rhodamine, GFP, coumarin, FITC, Alexa fluor, Cy3, Cy5, BODIPY, and cyanine dyes. Exemplary radionuclides include Fluorine-18, Gallium-68, and Copper-64. Exemplary magnetic contrast agents include gadolinium, iron oxide and iron platinum, and manganese.

[0259] The terms "treat," "treating," and "treatment" as used herein refers to alleviating or abrogating a disorder, disease, or condition; or one or more of the symptoms associated with the disorder, disease, or condition; or alleviating or eradicating a cause of the disorder, disease, or condition itself. Desirable effects of treatment can include, but are not limited to, preventing occurrence or recurrence of disease, alleviation of symptoms, diminishing any direct or indirect

pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state and remission or improved prognosis.

[0260] The term "therapeutically effective amount" refers to the amount of a compound or therapy that, when administered, is sufficient to prevent development of, or alleviate to some extent, one or more of the symptoms of a disorder, disease, or condition of the disease; or the amount of a compound that is sufficient to elicit biological or medical response of a cell, tissue, system, animal, or human that is being sought by a researcher, veterinarian, medical doctor, or clinician.

[0261] The term "pharmaceutically acceptable carrier," "pharmaceutically acceptable excipient," "physiologically acceptable carrier," or "physiologically acceptable excipient" refers to a pharmaceutically acceptable material, composition, or vehicle, such as a liquid or solid filler, diluent, excipient, solvent, or encapsulating material. A component can be "pharmaceutically acceptable" in the sense of being compatible with the other ingredients of a pharmaceutical formulation. It can also be suitable for use in contact with the tissue or organ of humans and animals without excessive toxicity, irritation, allergic response, immunogenicity, or other problems or complications, commensurate with a reasonable benefit/risk ratio. See, Remington: The Science and Practice of Pharmacy, 21st Edition; Lippincott Williams & Wilkins: Philadelphia, PA, 2005; Handbook of Pharmaceutical Excipients, 5th Edition; Rowe et al., Eds., The Pharmaceutical Press and the American Pharmaceutical Association: 2005; and Handbook of Pharmaceutical Additives, 3rd Edition; Ash and Ash Eds., Gower Publishing Company: 2007; Pharmaceutical Preformulation and Formulation, Gibson Ed., CRC Press LLC: Boca Raton, FL, 2004).

[0262] The term "pharmaceutical composition" refers to a mixture of a compound disclosed herein with other chemical components, such as diluents or carriers. The pharmaceutical composition can facilitate administration of the compound to an organism. Multiple techniques of administering a compound exist in the art including, but not limited to, oral, injection, aerosol, parenteral, and topical administration.

[0263] Non-limiting examples of "sample" include any material from which nucleic acids and/or proteins can be obtained. As non-limiting examples, this includes whole blood, peripheral blood, plasma, serum, saliva, mucus, urine, semen, lymph, fecal extract, cheek swab, cells or

other bodily fluid or tissue, including but not limited to tissue obtained through surgical biopsy or surgical resection. In various embodiments, the sample comprises tissue from the large and/or small intestine. In various embodiments, the large intestine sample comprises the cecum, colon (the ascending colon, the transverse colon, the descending colon, and the sigmoid colon), rectum and/or the anal canal. In some embodiments, the small intestine sample comprises the duodenum, jejunum, and/or the ileum. Alternatively, a sample can be obtained through primary patient derived cell lines, or archived patient samples in the form of preserved samples, or fresh frozen samples.

[0264] The term "*in vivo*" is used to describe an event that takes place in a subject's body.

[0265] The term "*ex vivo*" is used to describe an event that takes place outside of a subject's body. An *ex vivo* assay is not performed on a subject. Rather, it is performed upon a sample separate from a subject. An example of an *ex vivo* assay performed on a sample is an "*in vitro*" assay.

[0266] The term "*in vitro*" is used to describe an event that takes places contained in a container for holding laboratory reagent such that it is separated from the biological source from which the material is obtained. *In vitro* assays can encompass cell-based assays in which living or dead cells are employed. *In vitro* assays can also encompass a cell-free assay in which no intact cells are employed.

[0267] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

V. EXAMPLES

[0268] **Example 1. Method of Producing an rAAV**

[0269] A recombinant AAV (rAAV) is produced. Three plasmid vectors are triple-transfected into an immortalized HEK293 using a standard transfection protocol (*e.g.,* with PEI). The first vector contains a transgene cassette flanked by inverted terminal repeat (ITR) sequences from a parental AAV virus. The transgene cassette has a promoter sequence and that drives transcription of a heterologous nucleic acid in the nucleus of the target cell. The second vector contains nucleic acids encoding the AAV *Rep* gene, as well as a modified *Cap* gene *e.g.*, AAV2/9 REP-AAP-ΔCap). Modified *Cap* gene comprises any one of the DNA sequences

provided in **FIGS. 33-35**, which are the DNA sequences encoding the modified AAV capsid proteins of the present disclosure. The third vector contains nucleic acids encoding helper virus proteins needed for viral assembly, and packaging of the heterologous nucleic acid into the modified capsid structure.

[0270] Viral particles are harvested from the media after 72 h post transfection and from the cells and media at 120 h post transfection. Virus present in the media is concentrated by precipitation with 8% poly(ethylene glycol) and 500 mM sodium chloride and the precipitated virus is added to the lysates prepared from the collected cells. The viruses are purified over iodixanol (Optiprep, Sigma) step gradients (15%, 25%, 40% and 60%). Viruses are concentrated and formulated in PBS. Virus titers are determined by measuring the number of DNaseI-resistant vector genome copies (VGs) using qPCR and the linearized genome plasmid as a control.

[0271] **Example 2. Methods of Identifying Variant AAV Capsid Proteins**

[0272] ***Plasmid***

[0273] Library generation. The rAAV-ΔCap-in-cis-Lox2 plasmid (FIG. 36) is a modification of the rAAV-ΔCap-in-cis-Lox plasmid. For *7-mer-i* library fragment generation, the pCRII-9Cap-XE plasmid was used as a template. The AAV2/9 REP-AAP-ΔCap plasmid (FIG. 36) was modified from the AAV2/9 REP-AAP plasmid.

[0274] The rAAV-ΔCap-in-cis-Lox2 plasmid consists of three major elements that are flanked by AAV2 ITRs. (i) UBC ubiquitous promoter driving the expression of fluorescent protein, mNeongreen, followed by a synthetic polyadenylation sequence. The mCherry expression cassette of the previous version of the plasmid was replaced by mNeonGreen cassette. (ii) A portion of AAV2 rep gene that has the splicing sequences and AAV5 p41 promoter (1680-1974 residues of GenBank AF085716.1) followed by AAV9 cap gene. The prior version of this plasmid, rAAV-ΔCap-in-cis-Lox, has a short 12 bp sequence between restriction sites XbaI and AgeI at AA 450 and 592 of the AAV9 Cap gene. This was replaced by a 723 bp sequence of mRuby2 gene in-frame (acts as filler DNA) in the newer version of the plasmid. (iii) SV40 polyadenylation sequence that is flanked by lox71 and lox66 sites. The minor changes were introduced to the prior version of the plasmid to facilitate ease of cloning and to visualize mammalian cell transfection. The Lox sites in these rAAV plasmids show modest levels of Cre-independent flipping. This was minimized during PCR-based capsid recovery by lowering the

number of amplification cycles to a point where we cannot recover any rAAV capsids from the control DNA extracted from wild-type mice (i.e., lacking Cre expression) that were injected with the library. The pCRII-9Cap-XE plasmid contains the AAV9 capsid gene sequence from AAs 450-592 and is flanked by XbaI and AgeI restriction sites.

[0275] The AAV2/9 REP-AAP-ΔCap plasmid has the five previously existing stop codons of AAV2/9 REP-AAP in addition to the deletion of AAs 450-592 of the AAV9 capsid sequence. These modifications did not affect vector production. The deletion of the overlapping fragment between the REP-AAP and rAAV-ΔCap-in-cis-Lox2 plasmids minimizes recombination between plasmids that could potentially generate AAV9 wild-type capsids during co-transfection in vector production.

[0276] ***Capsid characterization***

[0277] AAV capsids. The AAV capsid variants with 7-mer insertions or 11-mer substitutions were made between positions 587-597 of AAV-PHP.B capsid using the pUCmini-iCAP-PHP.B backbone (Addgene ID: 103002).

[0278] ssAAV genomes. To characterize the AAV capsid variants, the single stranded (ss) rAAV genomes were used. Genomes such as pAAV:CAG-mNeonGreen27 (equivalent plasmid, pAAV: CAG-eYFP35; Addgene ID: 104055), pAAV:CAG-NLS-EGFP26 (equivalent version with one NLS is on Addgene ID 104061), pAAV:CAG-DIO-EYFP35 (Addgene ID: 104052), pAAV: GfABC1D-2xNLS-mTurquoise235 (Addgene ID: 104053), and pAAV-Ple261-iCre30 (Addgene ID 49113) were used.

[0279] pAAV:CAG-mNeonGreen2 genome consists of a ubiquitous CMV-β-Actin-intron-β-Globin (CAG) hybrid promoter driving the expression of a fluorescent protein, mNeonGreen (equivalent plasmid, pAAV: CAG-eYFP3; Addgene ID: 104055). pAAV:CAG-NLS-EGFP1 consists of NLS sequences at the N- and C-termini of EGFP and is driven by the CAG promoter. An equivalent version with one NLS is on Addgene (ID 104061). pAAV:CAG-DIO-EYFP3 (Addgene ID: 104052) consists of a EYFP gene built in the reverse direction of the CAG promoter, and it is flanked by a pair of Cre-Lox sites (Lox P and Lox 2272) on either ends.

[0280] In cells expressing Cre, the Cre-lox pair inverts EYFP enabling transcription and translation, followed by excision in the lox site to prevent re-inversion. pAAV: GfABC1D-2xNLS-mTurquoise23, referred to elsewhere as pAAV:GFAP-2xNLS-mTurquoise2 (Addgene

ID: 104053), consists of NLS sequences at the N- and C-termini of mTurquoise2 and is driven by the astrocyte-specific promoter GfABC1D4. pAAV:Ple261-iCre5 (Addgene ID 49113) contains an endothelial-cell-specific promoter driving the expression of iCre.

[0281] pAAV:CAG-XFP (mNeongreen) was packaged for characterizing AAV variants. However, when performing quantification of cell-types: neurons, astrocytes and oligodendrocytes, CAG-NLS-EGFP was used to restrict the expression to nucleus for easier quantification using microscope images. GFAP-NLS-mTurq2 is used to quantify astrocytes. CAG-DIO-EYFP is used for Cre driver lines, due to the presence of lox sites in this plasmid.

[0282] The self-complementary genome from Dr. Guangping Gao, scAAV:CB6-EGFP genome has a hybrid ubiquitous CB6 promoter (975 bp) comprising a CMV enhancer (cytomegalovirus immediate early enhancer), a chicken-β-actin promoter and hybrid intron, that drives the expression of EGFP. The genome has a rabbit globin poly A (127 bp) following the EGFP gene. The scAAV:CAG-EGFP (Addgene ID:83279), vector uses a ubiquitous CMV-β-Actin-intron-β-Globin (CAG) hybrid promoter to drive the expression of EGFP.

[0283] ***Round-1 AAV capsid library generation***

[0284] Mutagenesis strategy. The 7-mer randomized insertion was designed using the NNK saturation mutagenesis strategy, involving degenerate primers (from Integrated DNA Technologies, Inc.) containing mixed bases. N can be A, C, G, or T bases and K can be G, or T. Using this strategy, combinations of all 20 AAs at each position of the 7-mer peptide using 33 codons were obtained, resulting in a library size of 1.28 billion at the level of AA combinations. The mutagenesis strategy for the *3-mer-s* PHP.B library is described in Chan, K. Y. *et al.* Engineered AAVs for efficient noninvasive gene delivery to the central and peripheral nervous systems. *Nat. Neurosci.* 20, 1172–1179 (2017).

[0285] Library cloning. The 480 bp AAV capsid fragment (450–592 AAs) with the 7-mer random insertion between AAs 588 and 589 was generated by conventional PCR methods with a mixed base degenerate primer. The library fragment was amplified from the pCRII-9Cap-XE template by Q5 Hot Start High-Fidelity 2X Master Mix (NEB; M0494S) with forward primer, XF: 5'-ACTCATCGACCAATACTTGTACTATCTCTCTAGAAC-3' and reverse primer, 7xMNN-588i: 5'-
GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCMNNMNNMNNMNNMNN

MNNMNNTTGGGCACTCTGGTGGTTTGTG-3'. To avoid PCR-induced biases resulting from point mutations, recombination, and template switching, PCR amplification was limited to 15 – 20 cycles and the reactions were scaled up to get the required yield. The resulting PCR products were run on a 1% agarose gel and extracted with a Zymoclean Gel DNA Recovery kit (Zymo Research; D4007). It is critical to avoid AAV contamination during this step by taking precautionary measures like using a clean gel-running box and freshly prepared 1× TAE buffer.

[0286] rAAV-ΔCap-in-cis-Lox2 plasmid (6960 bp) was linearized with the restriction enzymes AgeI and XbaI by following the NEB recommended protocol for double digestion. The digested plasmid was run on a 0.8% – 1% agarose gel to extract the linearized backbone (6237 bp) with a Zymoclean Gel DNA Recovery kit.

[0287] The amplified library fragment was assembled into the linearized vector with the NEBuilder HiFi DNA Assembly Master Mix (NEB; E2621S) and a 1:2 molar ratio of vector to insert, to assemble at 50°C for 60 min.

[0288] Library purification. The assembled library was then subjected to Plasmid Safe (PS) DNase (Epicentre; E3105K) treatment to purify the assembled product by degrading the un-assembled DNA fragments from the mixture. For the R1 library, around 3U of PS DNase per 1 µg of input DNA was used in a 30 min reaction at 37°C. Alternatively, Exonuclease V (RecBCD) was used following the NEB recommended protocol (NEB; M0345S). Both procedures yielded comparable results. The resulting mixture was further purified with a DNA Clean and Concentrator kit (Zymo Research; D4013).

[0289] Library yield. With an assembly efficiency of 15% – 20% post-PS treatment, a yield of about 15 – 20 ng per 100 ng of input DNA per 20 µL reaction was obtained. For building the *7-mer-i* DNA library, approximately 5 – 6 µg of input DNA was used to obtain around 800 ng of assembled library.

[0290] Quality control. To validate successful assembly of the library, 1 ng of the final assembled library was transformed into *E. coli* SURE 2 Supercompetent Cells (Integrated Sciences; 200152). Colonies on an LB/Agar plate containing carbenicillin antibiotic after overnight incubation at 37°C were identified. The DNA library was sequenced around the insertion site (Laragen; Sanger Sequencing). A non-biased library shows multiple nucleotide peaks of equal diversity (25% each of A, T, G, C) across every base position of the diversified

region. To verify that the ITRs were intact, SmaI digestion was carried out as per the NEB recommended protocol (NEB; R0141S). To validate successful transfection and assess the vector-production yield per 150 mm dish, 10 ng of *7-mer-i* library was used to transfect HEK293 producer cells. Uniform expression of mNeonGreen protein across HEK cells was observed, and an average yield of 0.1 – $1x10^{11}$ vg was obtained per 150 mm dish. Using the average yield per dish, the vector production for *in vivo* selection was scaled up (See FIG. 45).

[0291] ***Round-2 AAV capsid DNA library***

[0292] PCR pool design. To maintain proportionate pooling, the fraction of each sample/library that needs to be pooled based on an individual library's diversity was mathematically determined. This process involved estimation of the diversity precluding noise and consideration of amplification of this diversity across samples by determining the area under the curve for the interval of high-confidence variants that falls in the higher RC range. The area under the curve (AUC) was estimated using the composite Simpson's rule by plotting all the recovered variants in a library (X-coordinate) to their read counts (RCs or copy number from deep sequencing data, Y-coordinate) (see FIG. 40). To determine the definite intervals for AUC, the data was sorted based on the decreasing order of the RCs. Noticeably, the distribution has two phases, with a steadier slope of variants in the higher RC range, followed by a steep drop in the slope of the curve (~50-1000 fold lower RCs). By observation, this steeper side of the curve is predominant in sequencing errors/ PCR mutations, hence this error dominant slope otherwise called noise from was precluded from the AUC estimation. When comparing composite Simpson's rule with another function, such as composite trapezoidal rule, the difference was miniscule.

[0293] This area is then used to determine the fraction of an individual library that needs to be pooled into PCR pool library using the formula: [Area under the curve/ total number of libraries pooled].

[0294] The pooled sample was used as a template for further amplification with 12 cycles of 98°C for 10 s, 60°C for 20 s, and 72°C for 30 s by Q5 polymerase, using the primers 588-R2lib-F: 5'-CACTCATCGACCAATACTTGTACTATCTCTCT-3' and 588-R2lib-R: 5'-GTATTCCTTGGTTTTGAACCCAACCG-3'. Similar to R1 library generation, the PCR product was assembled into the rAAV-ΔCap-in-cis-Lox2 plasmid and the virus was produced.

[0295] The R1 libraries used to build R2 were the Cre-Lox flipped rAAV DNA from half of the mouse brains (~0.3 g) and portion of spinal cords (0.1-0.2g) from all Cre lines. The amount of tissue processed here was sufficient for complete capsid library recovery. The differentially pooled and amplified libraries (by *PCR pool* or *synthetic pool*) were assembled using gibson assembly with a follow-up PS or Exonuclease V treatment (as described in R1 library generation). Successful library generation was validated by transformation, Sanger sequencing, and an ITR SmaI digest.

[0296] For vector production, about 10 ng of the purified and assembled library was used to transfect each 150 mm dish of 293T cells, and a yield of about 6×10^{11} vg per 150 mm dish was obtained (i.e. the R2 yield was six times that of R1, unsurprisingly given these sequences have already produced well enough to survive R1 selection).

[0297] *Synthetic pool* design. As described in the PCR pool strategy, high-confidence variants were chosen with RCs above the error-dominant noise slope from the plot of library distribution (see FIG. 40). This came to about 9000 sequences from all brain and spinal cord samples of all Cre lines. A similar primer design as mentioned in the description of the R1 library generation was used. Primers XF: 5'-ACTCATCGACCAATACTTGTACTATCTCTCTAGAAC-3' and 11-mer-588i: 5'-GTATTCCTTGGTTTTGAACCCAACCGGTCTGCGCXXXXXXMNNMNNMNNMNNMNNMNNMNNXXXXXXACTCTGGTGGTTTGTG-3', where "XXXXXXMNNMNNMNNMNNMNNMNNMNNXXXXXX" was replaced with unique nucleotide sequence of a 7-mer tissue recovered variant (7xMNN) along with modification of two adjacent codons flanking on either end of the 7-mer insertion site (6xX), which are residues 587-588 "AQ" and residues 589-590 "AQ" on AAV9 capsid. To select sequences for synthesis, the R1 brain and spinal cord libraries were chosen and used the same threshold limit for RC as described in the *PCR pool* strategy. This came to about 9000 sequences from all brain and spinal cord samples of all Cre lines. Since *spike-in* library has 11-mer mutated variants, the same primer design where "XXXXXXMNNMNNMNNMNNMNNMNNMNNXXXXXX" was replaced with a specific nucleotide sequence of a 11-mer variant. A duplicate of each sequence in this library was designed with different codons optimized for mammals. The primers were designed using a custom built python based script (code will be made available in Github). The

custom-designed oligopool was synthesized in an equimolar ratio by Twist Biosciences. The oligopool was used to amplify the pCRII-XE Cap9 template over 13 cycles of 98°C for 10 s, 60°C for 20 s, and 72°C for 30 s. To obtain a higher yield for large-scale library preparation, the product of the first PCR was used as a template for the second PCR using the primers XF and 588-R2lib-R (described above) and amplified for 13 cycles. As described in the description of the R1 library generation, the PCR product was assembled into an rAAV backbone and processed and purified for virus production. About 10 ng per 150 mm dish of HEK293 cells produced about 6×10^{11} vg of virus library.

[0298] ***AAV viral library production and purification***

[0299] To prevent capsid mosaic formation of the *7-mer-i* library in HEK293 producer cells, only 10 ng of assembled library per 150 mm dish were transfected along with other required reagents for AAV vector production. In addition to the 10 ng of library transfection per 150 mm dish of 293T producer cells, three plasmids were transfected: AAV2/9 REP-AAP-ΔCap, pUC18 and pHelper (genes encoding adenoviral proteins for AAV replication) at a ratio of 1:1:2. The plasmid pUC18 acts as a filler DNA to compensate for the low amount of library DNA in order to maintain the N:P ratio required for optimal transfection using polyethylenimine (PEI, Polysciences; 24765-1) transfection). The cells and culture media were harvested at 60 h post-transfection to collect the viral particles. rAAV harvest and purification were performed as per the protocol. The small amount of library DNA per plate and early cell harvest time are critical for reducing the possibility of mosaic capsid assemblies during vector production (similar considerations seen in prior reports).

[0300] For *7-mer-i* library, the production was scaled up to 60 dishes (~$1.8\text{x}10^7$ cells/dish) and with ~10% transfected with the library, resulted in ~$1\text{x}10^8$ total transformants. For an NNK 7mer library with ~$1\text{x}10^8$ total transformants, the number of unique variants is $9.99\text{x}10^7$.

[0301] For the rAAV DNA extraction from purified rAAV viral library, ~10% of the purified viral library was used to extract the viral genome by proteinase K treatment. In order to degrade any contaminating DNA from the purified library, it was treated with DNase I enzyme (5 µl of 10 U/µl) (Sigma-Aldrich; 4716728001) in 100 µl of DNase I buffer and incubated for 1 h at 37°C. The enzyme was inactivated by adding 5 µl of 0.5 M EDTA at 70°C for 10 min. Following DNase I treatment, the capsid protein shell was digested by adding 120 µl of

proteinase solution containing 5 µl of 20 µg/µl of proteinase K and incubated at 50°C overnight. To inactivate the proteinase K, the mixture was boiled at 95°C. The extracted rAAV library DNA was then concentrated and purified using phenol chloroform and ethanol. An equal volume of Phenol:Chloroform:Isoamyl Alcohol 25:24:1, pH8.0 (~250 µl; ThermoFisher Scientific; 15593031) was added and vortexed for 30 s. The mixture is incubated for 5 min at room temperature (RT) before centrifugation at 15,000 rpm for 10 min at 4°C. The upper aqueous phase was separated and mixed with an equal volume of chloroform and vortexed for 30 s. Following 5 min incubation at RT, centrifuge at 15,000 rpm for 10 min at 4°C. The upper aqueous phase was separated and one-tenth volume of 3M sodium acetate (pH 5.2) along with 2 µl Co-Precipitant Pink (Bioline; BIO-37075) and 2.5 volumes of ice cold 100% ethanol was added before vortexing for 30 s. The mixture was incubated for at least 1 hr at -20°C before centrifugation at 15,000 rpm for 15 min at 4°C. The pellet was air dried and resuspended in TE buffer. The DNA concentration was determined using the Qubit ssDNA assay.

[0302] ***Animals***

[0303] All animal procedures performed in this study were approved by the California Institute of Technology Institutional Animal Care and Use Committee (IACUC). C57BL/6J (000664), Tek-Cre (8863), SNAP25-Cre (23525), GFAP-Cre (012886), Syn1-Cre (3966), and Ai14 (007908) mice lines used in this study were purchased from the Jackson Laboratory (JAX). For *in vivo* library selection, 6- to 8-week-old adult male and female mice were intravenously injected with the viral libraries. Both genders were used for capsid selection to recover capsid variants with minimal gender bias. The IV injection of rAAVs was into the retro-orbital sinus of adult mice. For testing the transduction phenotypes of rAAVs, 6- to 8-week-old C57BL/6J or Tek-Cre or Ai14 adult male mice were randomly assigned. The experimenter was not blinded for any of the experiments performed in this study.

[0304] ***In vivo* selection**

[0305] The *7-mer-i* viral library selections were carried out in different lines of Cre transgenic adult mice: Tek-Cre, SNAP25-Cre, and GFAP-Cre for the R1 selections, and those three plus Syn1-Cre for the R2 selections. Male and female adult mice were intravenously administered with a viral vector dose of 2×10^{11} vg/mouse for the R1 selection, and a dose of 1×10^{12} vg/mouse for the R2 selection. The dose was determined based on the virus yield which

was different across selection rounds (FIG. 45). Both genders were used to recover capsid variants with minimal gender bias. Two weeks post-injection, mice were euthanized and all organs including brain were collected, snap frozen on dry ice, and stored at −80°C.

[0306] ***rAAV genome extraction from tissue***

[0307] Optimization. For rAAV genome extraction from tissues, both the Trizol method (Life Technologies; 15596) and the QIAprep Spin Miniprep kit (Qiagen, Inc; 27104) were used according to the manufacturers' recommended protocols, and found the Trizol method to be more efficient. The total rAAV genome recovery from 0.1 g of mouse liver was quantified by quantitative PCR using the primers mNeonGreen-F: 5'-CGACACATGAGTTACACATCTTTGGCTC-3' and mNeonGreen-R: 5'-GGAGGTCACCCTTGGTGGACTTC-3', which binds to the mNeonGreen gene of the ssAAV-ΔCap-in-cis-Lox2 genome. As an internal control, the amount of mitochondrial DNA (a measure of the recovery of smaller genomes) was quantified using primers Mito-F: 5'-CCCAGCTACTACCATCATTCAAGT-3' and Mito-R: 5'-GATGGTTTGGGAGATTGGTTGATGT-3'. Although the percentage of viral DNA per 1 ng total extracted DNA was about 1.5 fold higher with the QIAprep kit than with the Trizol method, the overall recovery was lower with the QIAprep kit.

[0308] The extracted viral genome was digested with a restriction enzyme, such as SmaI (found within the ITRs), to improve rAAV genome recovery by PCR. This was analyzed by quantitative PCR with Cre+ primers, CapF-56: 5'-ATTGGCACCAGATACCTG ACTCGTAA-3', Cre+R-58: 5'-CAAGTAAAACCTCTACAAATGTGGTAAAATCG-3' and Cre– primers, CapF-56 (see above) and Cre-R-57: 5'-GTCCAAACTCATCAATGTATCTTATCATGTCTG-3'.

[0309] rAAV genome extraction with the Trizol method. Half of a frozen brain hemisphere (0.3 g approx.) was homogenized with a 2 ml glass homogenizer (Sigma Aldrich; D8938) or a motorized plastic pestle (Fisher Scientific;12-141-361, 12-141-363) (for smaller tissues) and processed as described in prior work. The extracted DNA was then treated with 3 – 6 µl of 10 µg/µl RNase Cocktail Enzyme Mix (ThermoFisher Scientific; AM2286) to remove RNA and digested with SmaI restriction enzyme. The treated mixture was then purified with a Zymo DNA

Clean and Concentrator kit (D4033). From deep sequencing data analysis, it was observed that the amount of tissue processed for rAAV genome recovery is sufficient.

[0310] rAAV genome recovery by Cre-dependent PCR. rAAV genomes with Lox sites flipped by Cre recombination were selectively recovered and amplified using PCR with primers that yield a PCR product only if the Lox sites are flipped (See FIG. 37). The primers 71F: 5'-CTTCCAGTTCAGCTACGAGTTTGAGAAC-3' and CDF/R: 5'-CAAGTAAAACCTCTACAAATGTGGTAAAATCG-3' were used and amplified the Cre-recombined genomes over 25 cycles of 98°C for 10 s, 58°C for 30 s, and 72°C for 1 min, using Q5 DNA polymerase

[0311] Total rAAV genome recovery by PCR (Cre-independent). To recover all rAAV genomes from a tissue, the primers XF (5'-ACTCATCGACCAATACTTGTACTATCTCTCTAGAAC-3') and 588-R2lib-R (5'-GTATTCCTTGGTTTTGAACCCAACCG-3') were used to amplify the genomes over 25 cycles of 98°C for 10 s, 60°C for 30 s, and 72°C for 30 min, using Q5 DNA polymerase.

[0312] ***Sample preparation for NGS***

[0313] To analyze selections using deep sequencing, the DNA library was processed, the virus library, and the tissue libraries post-*in vivo* selection to add flow cell adaptors around the diversified 7-mer insertion region (See FIG. 37).

[0314] Preparation of rAAV DNA and Viral DNA library. The Gibson-assembled rAAV DNA library and the DNA extracted from the viral library were amplified by Q5 DNA polymerase using the primers 588i-lib-PCR1-6bpUID-F: 5'-CACGACGCTCTTCCGATCTAANNNNNNAGTCCTATGGACAAGTGGCCACA-3' and 588i-lib-PCR1-R: 5'-GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTCCTTGGTTTTGAACCCAACCG-3' that are positioned around 50 bases from the randomized 7-mer insertion on the capsid, and that contain the Read1 and Read2 flow cell sequences on the 5' end.

[0315] The primer, 588i-lib-PCR1-6bpUID-F: 5' CACGACGCTCTTCCGATCTAANNNNNNAGTCCTATGGACAAGTGGCCACA-3' used to minimally amplify DNA and virus libraries for NGS has 6 nucleotides long UID (unique identifier) "NNNNNN" that sits after 19 nucleotides of Read-1 sequence used in NGS "5'-

CACGACGCTCTTCCGATCT" and linker "AA". The sequence after UID "AGTCCTATGGACAAGTGGCCACA" is the region that anneals to the AAV9 capsid. UID is an optional feature for NGS data analysis to identify potential PCR amplification errors. However, this feature wasn't utilized in the NGS data analysis in this study to maintain consistency with the primers used in rAAV genome recovery from tissues which lacks this UID feature (primers 71F: 5'-CTTCCAGTTCAGCTACGAGTTTGAGAAC-3' and CDF/R: 5'-CAAGTAAAACCTCTACAAATGTGGTAAAATCG-3'). The UID or any kind of overhangs seemed to affect the PCR based recovery from tissue. Presumably, the primer thermostability has a key role to play in very low amount of extracted rAAV genomes from tissues.

[0316] Using 5 –10 ng of template DNA in a 50 µl reaction, the DNA was minimally amplified for 4 cycles of 98°C for 10 s, 60°C for 30 s, and 72°C for 10 s. The mixture was then purified with a PCR purification kit. The eluted DNA was then used as a template in a second PCR to add the unique indices (single or dual) via the recommended primers (NEB; E7335S, E7500S, E7600S) in a 12-cycle reaction using the same temperature cycle as described above. The samples were then sent for deep sequencing following additional processing and validation.

[0317] The PCR products post indices addition were run on a freshly prepared 2% low-melting-point agarose gel (ThermoFisher Scientific; 16520050) for better separation and recovery of the approx. 120 bp DNA band on the gel. Before sending the sample for NGS, the nucleotide diversity at the randomized 7-mer position was verified by Sanger sequencing. If needed, an optional PCR was carried out to send sufficient sample for Sanger sequencing using 15 – 20 cycles of 98°C for 10 s, 60°C for 30 s, and 72°C for 10 s with the primers NGS-QC-F: 5'- AATGATACGGCGACCACCGAG-3' and NGS-QC-R: 5'-CAAGCAGAAGACGGCATACGA-3'. Upon validation, the libraries were sent for deep sequencing using the Illumina HiSeq 2500 System (Millard and Muriel Jacobs Genetics and Genomics Laboratory, Caltech; Integrative Genomics Core, City of Hope).

[0318] Preparation of rAAV tissue DNA library. The PCR-amplified rAAV DNA library from tissue (see section: *In vivo* selection (i) (c)) was further amplified with a 1:100 dilution of this DNA as a template to the primers 1527: 5'-ACACTCTTTCCCTACACGACGCTCTTCCGATCTGACAAGTGGCCACAAACCACCAG-3' and 1532: 5'-

GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCCTTGGTTTTGAACCCAACCG-3' that are positioned around 50 bases from the randomized 7-mer insertion on the capsid, and that contain the Read1 and Read2 sequences on the 5' end. The DNA was amplified by Q5 Hot Start High-Fidelity 2X Master Mix or NEBNext Ultra II Q5 Master Mix (NEB; M0544) for 10 cycles of 98°C for 10 s, 59°C for 30 s, and 72°C for 10 s. The mixture was purified with a PCR purification kit. The eluted DNA was then used as a template in a second PCR to add the unique indices (single or dual) using the recommended primers (NEB; E7335S, E7500S, E7600S) in a 10-cycle reaction with the same temperature cycle as described above (for DNA and virus library preparation). The extracted DNA was validated by Sanger sequencing and sent for deep sequencing as described in the previous section.

[0319] ***In vivo*** **characterization of AAV vectors**

[0320] Cloning AAV capsid variants. The AAV capsid variants were cloned into a pUCmini-iCAP-PHP.B backbone (Addgene ID: 103002) using overlapping forward and reverse primers with 11-mer substitution (in case of 7-mer-i variants, the flanking amino acids from AAV9 capsid AA587-588 "AQ" and AA589-590 "AQ" were subjected to codon modification) that spans from the MscI site (at position 581 AA) to the AgeI site (at position 600 AA) on the pUCmini plasmid. The primers were designed for all capsid variants using a custom python script (Code will be made available on github), and since they cover the entire fragment insertion, these primers are self-annealed and amplified using PCR to create a dsDNA fragment without the use of a template DNA. They are amplified by Q5 Hot Start High-Fidelity 2X Master Mix for 20 cycles of 98°C for 10 s, 60°C for 30 s, and 72°C for 10 s. This fragment was then assembled into the MscI/AgeI digested pUCmini-iCAP-PHP.B backbone by the Gibson assembly method. There is a second MscI site on the backbone; however, this was blocked by methylation. The assembled plasmids were then transformed into NEB Stable Competent *E. coli* (New England Biolabs, Inc; C3040H), and colonies were selected on carbenicillin/ampicillin-LB agar plates.

[0321] List of primers used to clone AAV-PHP variants: The variants from 7-mer-i and 3-mer-s libraries were cloned as 11-mer substitution.

[0322] **TABLE 6. Primers For AAV-PHP Variants**

Variant	Amino	Nucleoti	Forward primer	Reverse primer (5'-3')

Name	acid	de sequence	(5'-3')	
AAV-PHP.V1	AQTALKPFLAQ	GCCCAAACCGCCCTCAAACCCTTCCTCGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAACCGCCCTCAAACCC (SEQ ID NO: 1032)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCGAGGAAGGGTTTGAGGGCGGTTTGGGC (SEQ ID NO: 1047)
AAV-PHP.V2	AQTTLKPFLAQ	GCCCAAACCACCCTCAAACCCTTCCTCGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAACCACCCTCAAACCC (SEQ ID NO: 1033)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCGAGGAAGGGTTTGAGGGTGGTTTGGGC (SEQ ID NO: 1048)
AAV-PHP.B4	AQTLQIPFKAQ	GCCCAAACGTTGCAGATTCCTTTTAAGGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAACGTTGCAGATTCCT (SEQ ID NO: 1034)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCCTTAAAAGGAATCTGCAACGTTTGGGC (SEQ ID NO: 1049)
AAV-PHP.B5	AQTLQLPFKAQ (SEQ ID NO: 1062)	GCCCAAACCCTCCAACTCCCCTTCAAAGCCCAA (SEQ ID NO: 1068)	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAACCCTCCAACTCCCC (SEQ ID NO: 1035)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCTTGGGCTTTGAAGGGGAGTTGGAGGGTTTGGGC (SEQ ID NO: 1050)
AAV-PHP.B6	AQTLQQPFKAQ	GCCCAAACTTTGCAG	GGAGTCCTATGGACAAGTGGCCACAAA	TTCCTTGGTTTTGAACCCAACCGGTCTGCGC

	(SEQ ID NO: 1063)	CAGCCGTTTAAGGCACAG (SEQ ID NO: 1069)	CCACCAGAGTGCCCAAACTTTGCAGCAGCCG (SEQ ID NO: 1036)	CTGTGCCTTAAACGGCTGCTGCAAAGTTTGGGC (SEQ ID NO: 1051)
AAV-PHP.B7	AQSIERPFKAQ	GCCCAAAGCATCGAAAGACCCTTCAAAGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAAGCATCGAAAGACCC (SEQ ID NO: 1037)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCTTTGAAGGGTCTTTCGATGCTTTGGGC (SEQ ID NO: 1052)
AAV-PHP.B8	AQTMQKPFIAQ	GCCCAAACCATGCAAAAACCCTTCATCGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAACCATGCAAAAACCC (SEQ ID NO: 1038)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCGATGAAGGGTTTTTGCATGGTTTGGGC (SEQ ID NO: 1053)
AAV-PHP.C1	AQRYQGDSVAQ	GCCCAAAGGTATCAGGGTGATTCTGTTGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAAGGTATCAGGGTGAT (SEQ ID NO: 1039)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCAACAGAATCACCCTGATACCTTTGGGC (SEQ ID NO: 1054)
AAV-PHP.C2	AQWSTNAGYAQ	GCCCAATGGTCGACAAACGCTGGTTACGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAATGGTCGACAAACGCT (SEQ ID NO: 1040)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCGTAACCAGCGTTTGTCGACCATTGGGC (SEQ ID NO: 1055)

AAV-PHP.C3	AQERVGFAQAQ	GCCCAAGAGCGTGTAGGTTTCGCACAGGCACAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAGAGCGTGTAGGTTTC (SEQ ID NO: 1041)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCCTGTGCGAAACCTACACGCTCTTGGGC (SEQ ID NO: 1056)
AAV-PHP.N	AQTLAVPFSNP (SEQ ID NO: 1064)	GCGCAGACCCTAGCTGTCCCTTTTTCGAACCCT (SEQ ID NO: 1070)	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCGCAGACCCTAGCTGTCCCT (SEQ ID NO: 1042)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCAGGGTTCGAAAAAGGGACAGCTAGGGTCTGCGC (SEQ ID NO: 1057)
AAV-PHP.X1	AQARQMDLSAQ (SEQ ID NO: 1065)	GCCCAAGCCAGACAAATGGACCTCAGCGCACAG (SEQ ID NO: 1071)	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAGCCAGACAAATGGAC (SEQ ID NO: 1043)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCGCTGAGGTCCATTTGTCTGGCTTGGGC (SEQ ID NO: 1058)
AAV-PHP.X2	AQTNKVGNIAQ (SEQ ID NO: 1066)	GCCCAAACCAACAAAGTCGGCAACATCGCACAG (SEQ ID NO: 1072)	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGCCCAAACCAACAAAGTCGGC (SEQ ID NO: 1044)	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCGATGTTGCCGACTTTGTTGGTTTGGGC (SEQ ID NO: 1059)
AAV-PHP.X3	AQQNVTKGVAQ	GCCCAACAGAACGTAACGAAG	GGAGTCCTATGGACAAGTGGCCACAAACCACCAGAGTGC	TTCCTTGGTTTTGAACCCAACCGGTCTGCGCCTGTGCCACACCCT

		GGTGTGG CACAG	CCAACAGAACGTA ACGAAG (SEQ ID NO: 1045)	TCGTTACGTTCTGTT GGGC (SEQ ID NO: 1060)
AAV-PHP.X4	AQLNAIK NIAQ (SEQ ID NO: 1067)	GCCCAAC TCAACGC TATCAAG AACATCG CACAG (SEQ ID NO: 1073)	GGAGTCCTATGGA CAAGTGGCCACAA ACCACCAGAGTGC CCAACTCAACGCT ATCAAG (SEQ ID NO: 1046)	TTCCTTGGTTTTGAA CCCAACCGGTCTGCG CCTGTGCGATGTTCT TGATAGCGTTGAGTT GGGC (SEQ ID NO: 1061)

[0323] AAV vector production. Using an optimized protocol, AAV vectors were produced from 5 –10 150 mm plates, which yielded sufficient amounts for administration to adult mice.

[0324] AAV vector administration. AAV vectors were administered intravenously to adult male mice (6 – 8 weeks of age) via retro-orbital injection at doses of 1 - 10×10^{11} vg. The AAV doses are determined by the experimental needs. CAG-NLS-GFP related experiments for quantification were done at medium dose of $1x10^{11}$ vg given this was the dose previously determined for AAV-PHP.eB characterization. Otherwise, the non-NLS genome related experiments were done at $3x10^{11}$ vg, with the exception of Cre-driver lines (GFAP-Cre or Tek-Cre), or a lower strength promoter containing genome (GFAP-NLS-mTurq) where the dose was $1x10^{12}$ vg. The high dose was chosen to understand the full potential of the new vectors in these systems.

[0325] All experiments with vectors carrying CAG, a strong ubiquitous promoter, were incubated for 3 weeks. The 4 week incubations are those that involved expression from Cre driver lines or cell-type specific promoter where it is generally recommended for a longer wait time. The 2 week incubations are those where the vectors carried self-complementary genomes with strong ubiquitous promoters.

[0326] Tissue processing. After 3 weeks of expression (unless noted otherwise), the mice were anesthetized with Euthasol (pentobarbital sodium and phenytoin sodium solution, Virbac AH) and transcardially perfused with 30 – 50 mL of 0.1 M phosphate buffered saline (PBS) (pH 7.4), followed by 30 – 50 ml of 4% paraformaldehyde (PFA) in 0.1 M PBS. After this procedure,

all organs were harvested and post-fixed in 4% PFA at 4°C overnight. The tissues were then washed and stored at 4°C in 0.1 M PBS and 0.05% sodium azide. All solutions used for this procedure were freshly prepared. For the brain and liver, 100-µm thick sections were cut on a Leica VT1200 vibratome.

[0327] For vascular labeling, the mice were anesthetized and transcardially perfused with 20 mL of ice-cold PBS, followed by 10 mL of ice-cold PBS containing Texas Red-labeled Lycopersicon Esculentum (Tomato) Lectin (1:100, Vector laboratories, TL-1176), and then placed in 30 mL of ice-cold 4% PFA for fixation.

[0328] Immunohistochemistry. Tissue sections – typically 100-µm thick – were first incubated in blocking buffer (10% normal donkey serum, 0.1% Triton X-100, and 0.01% sodium azide in 0.1 M PBS, pH 7.4) with primary antibodies at appropriate dilutions for 24 h at room temperature on a rocker. The primary antibodies used in this study were rabbit S100 (1:400, Abcam, ab868), rabbit Olig2 (1:400; Abcam, ab109186), rabbit NeuN (1:400, Abcam, ab177487), and rabbit GLUT-1 (1:400; Millipore Sigma, 07-1401). After primary antibody incubation, the tissues were washed 1 – 3 times with wash buffer 1 (0.1% Triton X-100 in 0.1 M PBS buffer, pH 7.4) over a period of 5 – 6 h in total. The tissues were then incubated in blocking buffer with the secondary antibodies at appropriate dilutions for 12 – 24 h at room temperature and then washed in three times in 0.1 M PBS, pH 7.4 over a total duration of 5 – 6 h. The secondary antibody used in this study was Alexa Fluor 647 AffiniPure donkey anti-rabbit IgG (H+L) (Jackson ImmunoResearch Lab, 711-605-152). When performing nuclear staining, 4′,6-Diamidine-2′-phenylindole dihydrochloride (DAPI, Sigma Aldrich, 10236276001) is used at a 1:1000 dilution in 0.1 M PBS, pH 7.4 and incubated with tissues for 15 minutes followed by a single wash for 10 minutes in 0.1 M PBS, pH 7.4. The DAPI and/or antibody-stained tissue sections were mounted with ProLong Diamond Antifade Mountant (ThermoFisher Scientific, P36970).

[0329] Hybridization chain reaction (HCR) based RNA labeling in tissues. Fluorescence *in situ* hybridization chain reaction (FITC-HCR) was used to label excitatory neurons with VGLUT1 and inhibitory neurons with GAD1 to characterize the AAV capsid variant AAV-PHP.N in brain tissue using an adapted third-generation HCR protocol. To characterize the AAV capsid variant AAV-PHP.N in brain tissue, HCR method was sought to label excitatory

and inhibitory neurons. Fluorescence in situ hybridization chain reaction (FITC-HCR) was used to label excitatory neurons with VGLUT1 and inhibitory neurons with GAD1. Adapting the third-generation HCR, 13 probe sets were designed for each target by using custom-made software (https://github.com/GradinaruLab/HCRprobe). After 3 weeks of expression, the mice were transcardially perfused and fixed as described earlier (Section D. Tissue processing). To minimize RNase enzyme exposure in fixed tissues, following overnight fixation in 4% PFA, the tissues were washed and stored at 4°C in 0.1 M RNase-free PBS and 0.05% sodium azide. The harvested brains were henceforth handled with care to avoid exposure to RNase using reagents such as RNAlater stabilization solution/RNase-free PBS/ RNaseZap (ThermoFisher Scientific, AM7021, AM9624, AM9780). Once the harvested brains were sagittally sliced to 100-µm thick sections, FITC-HCR was performed to detect both genes. Tissue slices were permeabilized with 0.1% Triton X-100 in 0.1 M RNase-free PBS for 1 h at RT and pre-hybridized in hybridization solution (10% dextran sulfate and 10% ethylene carbonate in 2xSSC buffer (saline-sodium citrate)) for >30 min at 37°C. The designed probes were diluted in hybridization solution to get a final concentration of 2 nM. The tissue sections were then subjected to hybridization with the probes overnight at 37°C. Following this, the sections were washed with pre-warmed wash buffer (10% ethylene carbonate in 2xSSC) at 37°C for 30 min twice, followed by 2xSSC at RT for 30 min twice. Amplification with hairpin pairs (Molecular Technologies, CA) were performed in amplification buffer (10x dextran sulfate in 2xSSC); hairpins were snap-cooled at 95°C for 90 s, followed by RT for 30 min, and diluted with amplification buffer (60 nM). Tissues were then incubated in this amplification buffer with hairpins overnight at RT with gentle agitation. Once the amplification was done, samples were briefly washed with 2xSSC and mounted in Prolong Diamond for imaging.

[0330] Imaging and image processing. All images in this study were acquired either with a Zeiss LSM 880 confocal microscope using the objectives Fluar 5× 0.25 M27, Plan-Apochromat 10× 0.45 M27 (working distance 2.0 mm), and Plan-Apochromat 25× 0.8 Imm Corr DIC M27 multi-immersion; or with a Keyence BZ-X700 microscope. The acquired images were processed in Zen Black 2.3 SP1 (Zeiss), BZ-X Analyzer (Keyence), Illustrator CC 2018 (Adobe), Photoshop CC 2018 (Adobe), and Imaris (Bitplane). To prevent any imaging artifacts resulting from multiple fluorescence spectral overlap, the fluorescence excitation and emission spectra

were kept distinct following the recommended linear unmixed acquisition of individual colors. A far-red fluorescent dye was chosen for any additional marker staining to keep the imaging parameters distinct from in vivo fluorescent expression thereby preventing any spectral overlap across detector channels. The tissues were routinely monitored for auto fluorescence or imaging artifacts before acquisition, and imaging parameters were adjusted if needed. The imaging parameters were cross-checked with tissues lacking in vivo transduction to avoid any imaging artifacts. The regions used for the images were closely matched across experimental groups to minimize bias during comparisons.

[0331] Tissue clearing and imaging of thick tissues. To demonstrate the ability of PHP.V1 to transduce the vasculature across thick tissues, such as half of a mouse-brain hemisphere or a femur bone, tissue from Tek-Cre mice was assessed after 4 weeks' of expression.

[0332] The brain hemisphere was stained with the primary antibody, Anti-GFP (Aves Labs, GFP-1020), and the secondary antibody, goat anti-Chicken IgY, Alexa Fluor 633 (ThermoFisher Scientific, A-21103), and cleared via the iDISCO protocol[38]. For imaging, a commercial light-sheet microscope (Lavision BioTec) with a custom objective lens (4×) was used. The resulting image files were reorganized by a custom MATLAB script to allow stitching with TeraStitcher. For 3-D visualization, Imaris (Bitplane) was used.

[0333] To image the mouse femur bone, the bones were sectioned to 300-μm thickness for antibody penetration and stained with the primary antibody, Anti-GFP, and the secondary antibody, Alexa Fluor 488 donkey anti-chicken IgY (Jackson ImmunoResearch Lab, 703-545-155), and then cleared via the TDE (2-2′-thiodiethanol) clearing method[41]. The images were acquired with a confocal microscope (Zeiss LSM 880) and visualized in Imaris software.

[0334] Tissue processing and imaging for quantification of rAAV transduction *in vivo*. For quantification of rAAV transduction, 6- to 8-week-old male mice were intravenously injected with the virus, which was allowed to express for 3 weeks (unless specified otherwise). The mice were randomly assigned to groups and the experimenter was not blinded. The mice were perfused and the organs were fixed in PFA. The brains and livers were cut into 100-μm thick sections and immunostained with different cell-type-specific antibodies, as described above. The images were acquired either with a 25× objective on a Zeiss LSM 880 confocal microscope or

with a Keyence BZ-X700 microscope; images that are compared directly across groups were acquired and processed with the same microscope and settings.

[0335] For quantification of PHP.B-family variant transduction in tissues, the images were acquired using 25x objective with 1x digital zoom on a Zeiss LSM 880 confocal microscope. With n=3 mice per variant, images were acquired across 4 brain regions – cortex, striatum, ventral midbrain and thalamus, and tissues were stained with 3 cell type markers (NeuN, Olig2, and S100). For each mouse, 2 images per brain region per cell type marker were acquired, and the mean were plotted.

[0336] For PHP.N transduction analysis, the images were acquired using 20x objective on Keyence BZ-X700 microscope. With n=3 mice, images across 4 brain regions - cortex, striatum, ventral midbrain and thalamus were acquired to cover the entire brain regions for 3 cell type markers (NeuN, Olig2, and S100). This involved 6-8 images to cover cortex, thalamus and striatum, and 2 images to cover ventral midbrain per mouse per cell-type marker. For each mouse, across each region, the mean from the images were plotted.

[0337] For PHP.V GLUT1$^+$ transduction analysis, the images were acquired using 25x objective with 1x digital zoom on a Zeiss LSM 880 confocal microscope. Each distinct blood vessel in the image with GLUT1$^+$ staining and XFP expression was determined as positive for transduction. Quantification of expression from the CAG-mNeonGreen vector was performed across the cortex (n = 3 per group). Each data point is drawn from the mean of 3-2 images per mouse. Different brain regions were quantified for Tek-Cre and Ai14 mouse experiments with n = 2 per group. For cortex, cerebellum, striatum and ventral midbrain, the mean was plotted from 3-4 images per mouse per region.

[0338] ***In vitro* characterization of AAV vectors**

[0339] Human Brain Microvascular Endothelial Cells (HBMEC) (ScienCell Research Laboratories, Cat. 1000) were cultured as per the instructions provided by the vendor. HBMEC were cultured from a frozen stock vial in fibronectin-coated T-75 flask (7000-9000 cells/cm^2 seeding density) using the Endothelial Cell Medium (Cat. 1001). The cells were subcultured in fibronectin-coated 48-well plates (0.95 cm^2 growth area) at the recommended seeding density and incubated at 37^{o}C for ~ 24-48 h till the cells were completely adherent with ~ 70-80% confluence. The viral vectors packaging pAAV-CAG-mNeongreen were added to the cell

culture at a dose of either $1x10^8$ or $1x10^{10}$ vg per well (3 wells per dose per vector). The media was changed 24 hours later and the culture was assessed for fluorescence expression at 3 days' post infection. Per vendor recommendation, the culture media was changed every other day to maintain the cell culture.

[0340] ***Data analysis***

[0341] Quantification of rAAV vector transduction in mouse tissue. Manual counting was performed with the Adobe Photoshop CC 2018 Count Tool for cell types in which expression and/or antibody staining covered the whole cell morphology. The Keyence Hybrid Cell Count software (BZ-H3C) was used where the software could reliably detect distinct cells in an entire dataset. To maintain consistency in counting across different markers and groups, one person was assigned to quantify across all groups in all brain areas.

[0342] Manual counting was performed for GLUT-1-stained blood vessels and expression of the ssAAV:CAG-mNeonGreen and ssAAV:CAG-DIO-EYFP, where the efficiency was calculated as the percentage of XFP+ vessels relative to the GLUT-1 staining. Manual counting was also performed to quantify nuclear or soma stained cells, including NeuN-, Olig2-, and S100-stained cells. The efficiency was calculated as the percentage of XFP+ cells relative to cell-marker+ cells.

[0343] Keyence Hybrid Cell Count software (BZ-H3C) was used to quantify expression of nuclear localized AAV genomes in liver hepatocytes that co-localized with the DNA stain, DAPI; and also for the study involving ssAAV:GFAP-2xNLS-mTurquoise2 genomes with S100 cell marker.

[0344] The mean fluorescence intensity across microscopic images were quantified using ImageJ software. The images were processed for background subtraction and using the Threshold operation, the mean fluorescence intensity was measured.

[0345] NGS data alignment and processing. The raw fastq files from NGS runs were processed with custom built scripts (codes will be made available on Github) that align the data to AAV9 template DNA fragment containing the diversified region 7xNNK (for R1) or 11xNNN (for R2 since it was synthesized as 11xNNN). The pipeline to process these datasets involved filtering the dataset to remove the low-quality reads by using the deep sequencing quality score for each sequence. The variant sequences were then recovered from the sequencing reads by

searching for the flanking template sequences, and extracting the nucleotides of the diversified region (perfect string match algorithm). The quality of the aligned data was further investigated to remove any erroneous sequences (such as ones with stop codons). The raw data was plotted (as shown in Supplementary Fig. 1e) to study the quality of recovery across every library. Based on the RC distribution, we adapted a thresholding method to remove plausible erroneous mutants that may have resulted from PCR or NGS based errors. The assumption is that if there is a PCR mutation or NGS error on the recovered parent sequence, the parent must have existed at least one round earlier than the erroneous sequence, and thus a difference in RCs should exist.

[0346] For R1 tissue libraries, a steep drop was observed in the slope of the distribution curve following a long tail of low count sequences, and were found to be rich in sequences that are variations of the parents in the higher counts range. A threshold for RCs was manually set to remove such erroneous mutants. The thresholded data were then processed differently based on the experimental needs as described elsewhere using custom Python based scripts.

[0347] For R2 tissue libraries from *PCR pool* and *synthetic pool*, given the smaller library size compared to R1, the data was thresholded in two steps. Only the tissue recovered sequences that were present in the respective input DNA and virus library were considered (after removing lower count variants from input libraries following the same principle as R1 tissue libraries). This step partially removed the long tail of low count reads. As a second step, the thresholding that was described for R1 tissue libraries was applied.

[0348] While it is plausible that true variants may be lost during thresholding, this method minimized false positives as the low count mutants in tissue and virus libraries often seemed to have very high enrichment score (as RCs are normalized to input library). In other words, thresholding allowed selective investigation on positively and negatively enriched variants that had a higher-confidence in their NGS RCs.

[0349] As an alternative to the manual thresholding method, an optional error correction method called "Collapsing" was built to further validate the outcome from filtered datasets. This method starts at the lowest count variants (variants of count 1) and searches for potential parent variants that are off by one nucleotide but have at least 2-fold higher counts (fold change = $(2^{\Delta CT})$ where CT is PCR cycle threshold). This error correction method then transfers the counts of these potential erroneous sequences to their originating sequences and repeats recursively until

all sequences have been considered. On applying this error correction to the thresholded data, an additional ~0.002-0.03% of sequences were captured (compared to >19% captured by thresholding), confirming that the thresholding strategy was largely successful.

[0350] NGS data analysis. The aligned data were then further processed via a custom data-processing pipeline, with scripts written in Python (available on Github). The enrichment scores of variants (Total = N) across different libraries were calculated from the read counts (RCs) according to the following formula: ***Enrichment score = log10 [(Variant 1 RC in tissue library1/ Sum of variants N RC in library1) / (Variant 1 RC in virus library/ Sum of variants N RC in virus library)]***

[0351] To consistently represent library recovery between R1 and R2 selected variants, the enrichment score of the variants in R1 selection was estimated. The standard score of variants in a specific library was calculated using this formula: Standard score = (read count_i – mean)/standard deviation. Where read count_i is raw copy number of a variant i, Mean is the mean of read counts of all variants across a specific library, Standard deviation is the standard deviation of read counts of all variants across a specific library.

[0352] Since the DNA and virus libraries were not completely sampled unlike the tissue libraries, we assigned an estimated RC for variants that were not present in the input library but were present in the output library. For instance, R1 virus library is the input library to the R1 tissue libraries. The estimated RC is defined as a number that is lower than the lowest RC in the library with the assumption that these variants were found at a relatively lower abundance than the variants recovered from the deep sequencing. In virus libraries, since RC of 1.0 was the lowest, we assigned all missing variants an estimated RC of 0.9. We use this method to calculate the enrichment score of the R1 tissue libraries which is normalized to R1 virus library (Fig. 1d). This was done to represent libraries across two selection rounds consistently. Although, the individual enrichment score among R1 variants didn't add a significant value to the variants selected for R2 selection as described in the criteria to separate signal vs noise in R1 using the RCs.

[0353] Heatmap generation. The relative AA distributions of the diversified regions are plotted as heatmaps. The plots were generated using the Python Plotly plotting library. The heatmap values were generated from custom scripts written in Python, using functions in the

custom "pepars" Python package. Each heatmap uses both an expected (input) distribution of amino acid sequences and an output distribution. The output distribution must be a list of sequences and their count, and the input distribution can be either a list of sequences and their count, or an expected amino acid frequency from a template, such as NNK. For both input and output, the total count of amino acids in each position is tallied in accordance to each sequence's count and then divided by the total sum of counts, giving a frequency of each amino acid at each position. Then, the log2 fold change is calculated between the output and the input. For amino acids with a count of 0 in either the input or output, no calculation is performed. In order to distinguish between statistically significant amino acid biases, a statistical test was performed using the statsmodels Python library. For the case where there are two amino acid counts, a two-sided, two-proportion z-test was performed; for comparing the output amino acid count to an expected input frequency from a template, a one-proportion z-test was performed. All p-values were then corrected for multiple comparisons using Bonferroni correction. Only bias differences below a significance threshold of 1e-4 are then outlined on the heatmap; all other (insignificant) squares are left empty.

[0354] Clustering analysis. Using custom scripts written in MATLAB (version R2017b; MathWorks) the reverse Hamming distances representing the number of shared AAs between two peptides was determined. Cytoscape (version 3.7.1[53]) software was then used to cluster the variants. The AA frequency plot representing the highlighted cluster was created using Weblogo (Version 2.8.2). The reverse Hamming distances (representing the number of shared AAs between two peptides) was determined for all unique capsid variants with greater than 10 count and greater than 2.5-fold enrichment after R2 selection. This process iteratively compares each variant with all other variants within the group. Capsid variants were then clustered by their reverse Hamming distances using Cytoscape. The minimum reverse Hamming distance for visualization was chosen manually based on sequence similarity.

[0355] For the amino acid frequency plots, the number on the bottom represents the position of the diversified motif starting from 1. The size of the amino acid in the stack reflects the proportion of unique clones in which the AA appears at that specific position in the motif. The color code is based on the AA properties. The positively charged residues K, R, and H are in blue. The negatively charged residues D and E are in red. The amide containing polar residues Q,

and N are in magenta. The polar residues T, and S, are in green. The hydrophobic residues A, L, V, I, P, F, M, and W are in black.

[0356] **Example 3. Multiplexed-CREATE allows detailed characterization of the capsid libraries during Round-1 selection.**

[0357] To identify variants that enrich in specific cell types or organs parallel selections across multiple targets were performed, and the enrichment or depletion of each capsid variant across those targets was mapped.

[0358] During DNA and virus library generation there is potential for accumulation of biases that over-represent certain capsid variants, obscuring their true enrichment during *in vivo* selection. These biases may result from PCR amplification bias in the DNA library or sequence bias in the efficiency of virus production across various steps: capsid assembly, genome packaging and stability during purification. This was investigated with the *7-mer-i* library, a randomized 7-mer library inserted between positions 588-589 of AAV9 (FIGS. 1 and 2) in rAAV-ΔCap9-in-cis-Lox2 plasmid (FIG. 36). Sequencing libraries after DNA assembly and virus purification to a depth of 10 – 20 million (M) reads was adequate to capture the bias among variants during virus production (Fig. 3; despite ~1% variant overlap among these libraries; FIGS. 38 and 39), demonstrating that even permissive sites like 588-589 will impose biological constraints on sampled sequence space. The DNA library had a uniform distribution of 9.6 M unique variants within ~10 M total reads (read count (RC) mean = 1.0, S.D. = 0.074), indicating minimal bias. In contrast, the virus library had 3.6 M unique variants within ~20 M depth (RC mean = 4.59, S.D. = 11.15) indicating enrichment of a subset of variants during viral production.

[0359] For *in vivo* selection, the *7-mer-i* viral library was intravenously injected at a dose of $2x10^{11}$ vg per adult transgenic mouse expressing Cre in different brain cell types: GFAP-Cre mice for astrocytes, SNAP25-Cre mice for neurons, and Tek-Cre mice for endothelial cells (n = 2 mice per Cre transgenic line, see Methods). Two weeks after intravenous (IV) injection, the brain and liver tissues were harvested, with the latter serving as a control organ since AAV9 transduces it with high efficiency. The rAAV genomes were extracted from tissues and the capsids that transduced Cre-expressing cells were selectively amplified (FIGS. 40-44). Upon deep sequencing, ~$8x10^4$ unique nucleotide variants recovered from brain tissues and < 50 variants in spinal cords (~48% of which were identified in virus library) were observed across

the transgenic lines, and each variant was represented with an enrichment score reflecting the

Design Parameters	*Synthetic pool* design	*PCR pool* design

change in relative abundance between the brain and the starting virus library (FIG. 4).

[0360] Two features of this dataset stand out. First, the recovered variants in brain tissue were disproportionately represented among the fraction of the transformed capsid library observed by sequencing after viral production demonstrating how production biases skew selection results. Second, the distribution of capsid read counts (RCs) revealed that more than half of the unique recovered variants after selection appear at remarkably low read counts. These variants may either be unintended mutants from experimental manipulation or AAV9-like variants with low basal level of CNS transduction (FIG. 40).

[0361] **Example 4. A novel Round-2 library design improves the selection outcome**

[0362] Concerned that the sequence bias during viral production and recovery would propagate across selection rounds despite post-hoc enrichment scoring, an unbiased library was designed based on the round-1 (R1) output (*synthetic pool* library) via oligo pools (Twist Bioscience). This library was compared to a library PCR amplified directly from the recovered R1 DNA (*PCR pool* library) (FIG. 5, Table 7).

[0363] Table 7: Comparison between the two methods for R2 selection. The table summarizes the pros and cons of selection design parameters by the synthetic pool and PCR pool R2 selection methods.

Carryover of R1 selection bias among variants	No, likelihood of false positives is low	Yes, potential to minimize by normalization
Carryover of R1 selection induced mutants	No	Yes
Confidence in library performance	High, using alternate codon replicates	Low
Customize library or add internal controls	Yes, in an unbiased manner	Yes, with greater risk of bias
Control library size	Yes, without reducing libraries or pooling	Yes, with libraries reduced for pooling
Cost for R2 library generation	High	Low

[0364] The *synthetic pool* library design comprised: (1) equimolar amounts of ~8950 capsid variants present at high read counts in at least one of the R1 selections from brain and spinal cord (FIG. 40); (2) alternative codon replicates of those ~8950 variants (optimized for mammalian codons) to reduce false positives; and (3) a "*spike-in*" library of controls (FIGS. 74 and 75), resulting in a total library size of 18,000 nucleotide variants.

[0365] As anticipated, both round-2 (R2) virus libraries produced a high titer (~$6x10^{11}$ vg per 10 ng of R2 DNA library per 150 mm dish; FIG. 45), and ~99% of variants from the R2 DNA were found after viral production (FIG. 6). However, the distribution of the DNA and virus libraries from both designs differed significantly. The *PCR pool* library carries forward the R1 selection biases (FIGS. 7, 46, and 47) where the abundance reflects prior enrichment across tissues in R1 as well as bias from viral production and sample mixing. Comparatively, the *synthetic pool* DNA library is more evenly distributed, minimizing bias amplification across selection rounds.

[0366] For in vivo selection, a dose of $1x10^{12}$ vg per adult transgenic mouse was administered into three of the previously used lines (n = 2 mice per Cre transgenic line – GFAP, SNAP25, Tek), as well as the Syn-Cre line (for neurons). Two weeks after IV injection, rAAV genomes from brain samples were extracted, selectively amplified, and deep sequenced (as in R1). The synthetic pool library produced a greater number of positively enriched capsid variants than the PCR pool brain library (e.g. ~1700 versus ~700 variants/tissue library at amino acid (AA) level in GFAP-Cre) (FIGS. 8 and 48). In the synthetic pool, ~90% of the variants from the spike-in library were positively enriched as expected (FIG. 48, middle panel; FIG. 74).

[0367] The degree of correlation for enrichment scores of variants recovered from both PCR and synthetic pool libraries varies in each Cre transgenic line, demonstrating the presence of noise within experiments (FIG. 49). The synthetic pool's codon replicate feature addresses this predicament by pinpointing the level of enrichment needed within each selection to rise above noise (FIGS. 9, 50, and 51). This is a significant advantage over the PCR pool design, allowing researchers to confidently interpret enrichment scores in a given selection.

[0368] The degree of enrichment at which correlation breaks down appears to vary with Cre-line. A downside of PCR pool is that there is no way to tell whether it or synthetic pool is the more 'true' enrichment score or even that there may be cause for concern regarding certain enrichment values. The correlation among positively enriched variants between the two methods was found to improve with the magnitude of positive enrichment. For each experiment there is a level of enrichment below which the scores become irreproducible, or noisy. FIG. 50 demonstrates that neither PCR pool nor Synthetic pool is inherently more 'true' at lower enrichment scores. This is because Synthetic pool methodology with its codon replicates has a self-contained control to determine an enrichment level below which enrichment value has no further predictive power. The term 'noise' has been used herein to refer to regions of enrichment in a particular experiment below which values lose their reproducibility and predictive power. Being able to experimentally determine enrichment signal above noise allows researchers to focus their attention and data analyses on enrichment levels that are internally reproducible and thereby avoid selecting false positive variants or drawing invalid conclusions.

[0369] Thus, if one is interested in only the highest enriched variants for a particular tissue, PCR pool design coupled with enrichment normalization to virus library may not drastically

differ from synthetic pool design over one additional round of selection for a subset of in vivo selections (such as Tek-Cre or SNAP-Cre). Without additional validation, however, it is difficult to predict whether a given in vivo system will perform akin to Tek-Cre. This becomes critical in a multiplexed selection study where target-specific variants may not garner the highest enrichments in one particular in vivo selection.

[0370] **Example 5. Analysis of AAV capsid libraries after Round-2 selections**

[0371] Whereas the AA distribution of the DNA library closely matched the Oligopool design, virus production selected for a motif with Asn (N) at position 2, β-branched AAs (I, T, V) at position 4, and positively charged AAs (K, R) at position 5 (FIGS. 10, 52). Fitness for BBB crossing resulted in a very different pattern. In comparison to the R2 virus library, highly enriched variants share preferences, for example, proline (P) in position 5, and phenylalanine (F) in position 6.

[0372] The distribution of the positively enriched variants from brain across all peripheral organs was then determined (FIG. 11, left). About 60 variants that are highly enriched in brain are comparatively depleted across all other organs (FIG. 11, middle). Encouraged by the expected behavior of spike-in control variants (AAV9, PHP.B, PHP.eB), eleven novel variants were chosen for further validation (FIG. 11, right), including several that would have been overlooked if the choice had been based on PCR pool or CREATE (Table 8).

[0373] Table 8: Ranking of AAV-PHP capsids across methods.Ranks of selected variants among all capsids recovered from R2 Tek-Cre selection by *synthetic pool* enrichment score (representing M-CREATE), *PCR pool* enrichment score (representing closer to M-CREATE), or *PCR pool* read counts (representing CREATE), the highest ranks of which starts from 1, and "Not recovered" represent absence of the variant from R2 sequencing data.

AAV Variants	*Synthetic pool* enrichment rank	*PCR pool* enrichment rank	*PCR pool* read count rank
PHP.V1	1	4	3

PHP.V2	2	1	1
PHP.B4	4	10	56
PHP.B7	6	13	36
PHP.B8	3	7	23
PHP.C1	13	34	74
PHP.C2	12	20	293
PHP.C3	16	Not recovered	Not recovered

[0374] These variants were chosen due to their enrichments and where they fall in sequence space. The positively enriched variants were found to cluster into distinct families based on sequence similarity. In agreement with the heatmaps discussed above, the most enriched variants form a distinct family across selections that share a common motif: T in position 1, L in position 2, P in positive 5, F in position 6, and K or L in position 7 (FIGS. 12, 53). This AA pattern closely resembles the previously identified variant, AAV-PHP.B – TLAVPFK. Given the sequence similarity among members, we predicted that they may similarly cross the BBB and target the central nervous system.

[0375] The ability to twice recover the AAV-PHP.B sequence family from completely independently constructed and selected libraries confirms that the viral library's sequence space coverage was broad enough to recover a family of variants sharing a common motif. Unlike CREATE which identified only one variant, AAV-PHP.B, M-CREATE yielded a diverse PHP.B-like family that hints toward important chemical features of this motif. The sequence diversity within this family suggests that isolating AAV-PHP.B was not simply good fortune in previous experiments (considering a theoretical starting library size of ~1.3 billion), and that this is a dominant family for this particular experiment.

[0376] **Example 6. Capsid recovery from Round-2 selection yields a pool of AAV9 variants with enhanced BBB entry and CNS transduction**

[0377] Given the dominance of the PHP.B-family in this particular selection, the most enriched member was tested: TALKPFL (FIGS. 12 and 13) henceforth referred to as AAV-PHP.V1. Somewhat surprisingly given its sequence similarity to AAV.PHP.B, the tropism of AAV-PHP.V1 is biased toward transducing brain vascular cells (FIGS. 14, 54). When delivered intravenously, AAV-PHP.V1 carrying a fluorescent reporter under the control of the ubiquitous CAG promoter transduces ~60% of $GLUT1^+$ cortical brain vasculature compared to ~20% with AAV-PHP.eB and almost no transduction with AAV9 (FIGS. 14 and 16). In addition to the vasculature, AAV-PHP.V1 also transduced ~60% of cortical $S100^+$ astrocytes (FIG. 17). However, AAV-PHP.V1 is not as efficient for astrocyte transduction as the previously reported AAV-PHP.eB (when packaged with an astrocyte specific GfABC1D promoter, FIG. 55).

[0378] For applications requiring endothelial cell-restricted transduction via intravenous delivery, AAV-PHP.V1 vectors can be used in three different systems: (1) in endothelial cell-type specific Tek-Cre mice with a Cre-dependent expression vector (FIG. 15 (left) and FIG. 18), (2) in fluorescent reporter mice where Cre is delivered with an endothelial cell-type specific MiniPromoter (Ple261) (FIG. 15 (right) and FIGS. 19 and 56 through the left column of FIG. 58), and (3) in wild-type mice by packaging a self-complementary genome (scAAV) containing a ubiquitous promoter (Right column of FIG. 58). The mechanism of endothelial cell-specific transduction by AAV-PHP.V1 using scAAV genomes is unclear, but shifts in vector tropism when packaging scAAV genomes have been reported for another capsid.

[0379] Given the dramatic difference in tropism between AAV-PHP.V1 and AAV-PHP.B/eB, we tested several additional variants within the PHP.B-like family. One variant, AAV-PHP.V2 – TTLKPFL, differed by only one AA from AAV-PHP.V1, has a similar tropism (FIGS. 59-61). AAV-PHP.V2 was found at high abundance in R1 selection across all brain libraries and was highly enriched in R2 (FIGS. 4, 11 (right panel), 12, 13, and 40). Given its sequence similarity, similar tropism was expected to that of AAV-PHP.V1. This was validated *in vivo* in C57BL/6J adult mice (ssAAV-PHP.V2:CAG-mNeongreen genome, $3x10^{11}$ vg dose per adult mice, n = 3, FIG. 59), in Tek-Cre mice (ssAAV-PHP.V2:CAG-DIO-EYFP genome, 1×10^{12} vg dose per adult mouse, n = 2, FIG. 60), and in GFAP-Cre mice (ssAAV-PHP.V2:CAG-DIO-EYFP, 1×10^{12} vg dose per adult mouse, n = 2, FIG. 61).

[0380] Three other variants with sequences of roughly equal deviation from both AAV.PHP.V1 and AAV.PHP.B, AAV-PHP.B4 – TLQIPFK, AAV-PHP.B7 – SIERPFK, and AAV-PHP.B8 – TMQKPFI (FIGS. 12, 13, 20, and 21), have PHP.B-like tropism with biased transduction toward neurons and astrocytes (FIGS. 21 and 62-64). Similar variants among the spike-in library, AAV-PHP.B5 – TLQLPFK and AAV-PHP.B6 – TLQQPFK, also shared this tropism (FIGS. 13, 20, 21, and 62).

[0381] To evaluate the performance of the spike-in library, two highly enriched variants similarly placed in sequence space were chosen: AAV-PHP.B6 – TLQLPFK and AAV-PHP.B7 – TLQQPFK (FIGS. 48 (middle panel), and 53) that were previously identified in the 3-mer-s PHP.B library but never validated in vivo. At a modest dose of $1x10^{11}$ vg in C57BL/6J adult mice, these variants also display PHP.B-like tropism (FIGS. 20-21 and 62).

[0382] A series of variants selected to verify M-CREATE's predictive power outside this family were then investigated: (1) A highly enriched variant with a completely unrelated sequence, AAV-PHP.C1 – RYQGDSV (FIGS. 12, 13, 20, and 21), transduced astrocytes at a similar efficiency and neurons at lower efficiency compared to other tested variants from B-family (FIG. 21). (2) Two variants found in high abundance in the R2 *synthetic pool* virus library and negatively enriched in brain (with both codon replicates in agreement), AAV-PHP.X1 – ARQMDLS and AAV-PHP.X2 – TNKVGNI (FIG. 46, right), poorly transduced the CNS (FIG. 63). (3) Two variants that were found in higher abundance in brain libraries from the *PCR pool* R2, AAV-PHP.X3 – QNVTKGV and AAV-PHP.X4 - LNAIKNI also failed to outperform AAV9 in the brain (FIG. 65).

[0383] Collectively, the characterization of these AAV variants demonstrates several key points. First, within a diverse sequence family, there is room for both functional redundancy and the emergence of novel tropisms. Second, highly enriched sequences outside the dominant family are also likely to possess enhanced function. Third, buoyed by codon replicate agreement in the synthetic pool, a variant's enrichment across tissues may be predictive. Fourth, while the *synthetic pool* R2 library contains a subset of the sequences that are in the *PCR pool* R2 and may thereby lack some enhanced variants, the excluded *PCR pool* population is enriched in false positives.

[0384] The ability to confidently predict *in vivo* transduction from a pool of 18,000 variants across mice is a significant advance in the selection process and demonstrates the power of M-CREATE for the evolution of individual vectors.

[0385] **Example 7: Re-investigation of capsid selection that yielded AAV.PHP.eB reveals variant that specifically transduces neurons**

[0386] Using NGS, a *3-mer-s (s-substitution)* PHP.B library generated by the prior CREATE methodology that yielded AAV-PHP.eB[27] was reinvestigated (FIG. 24). The brain libraries were deep sequenced using Cre-dependent PCR and a R2 liver library from wild-type mice (processed via PCR for all capsid sequences regardless of Cre-mediated inversion) and identified 150 – 200 positively enriched capsids in brain tissue (FIGS. 25, 66, and 67). Briefly, the re-investigated 3-mer-s PHP.B library diversified positions 587-597 of the AAV-PHP.B capsid (equivalent of 587-590 AA on AAV9) in portions of three consecutive AAs, (~40,000 total variants) (FIG. 24). Selections were performed in three Cre-transgenic lines: Vglut2-IRES-Cre for glutamatergic neurons, Vgat-IRES-Cre for GABAergic neurons, and GFAP-Cre for astrocytes.

[0387] Variants that were positively enriched in brain and negatively enriched in liver show a significant bias towards certain AAs: G, D, E at position 1; G, S at position 2 (which includes the AAV-PHP.eB motif, DG); and S, N, P at position 9, 10, 11 (FIGS. 26 and 68). Variants that were positively enriched in the brain were clustered according to their sequence similarities and ranked by their negative enrichment in liver (represented by node size in clusters). A distinct family referred to as N emerged with a common motif "SNP" at positions 9-11 on PHP.B backbone (FIGS. 27 and 69).

[0388] The core variant of the N-family cluster: AQTLAVPFSNP was found in high abundance in R1 and R2 selections, had higher enrichment score in Vglut2 and Vgat brain tissues compared to GFAP, and had negative enrichment in liver tissue (FIGS. 25 and 66-69). Unlike AAV-PHP.eB, this variant (AAV-PHP.N) specifically transduced $NeuN^+$ neurons even when packaged with a ubiquitous CAG promoter, although the transduction efficiency varied across brain regions (from ~10-70% in $NeuN^+$ neurons, including both $VGLUT1^+$ excitatory and $GAD1^+$ inhibitory neurons, FIGS. 28, 29, 70, and 71).

[0389] Thus, by re-examining the *3-mer-s* library several novel variants were identified, including one with notable cell-type-specific tropism. While Vglut2-Cre and Vgat-Cre mice were used for in vivo selection, no variants stood out for neuronal subtype-specific transduction of excitatory and inhibitory populations from initial investigations on the NGS dataset. It is possible that a biological solution to this (stringent) selection was not present in the library.

[0390] **Example 8. Investigation of capsid families beyond C57BL/6J mouse strain**

[0391] The enhanced CNS tropism of AAV-PHP.eB is absent in a subset of mouse strains. It is highly efficient in C57BL/6J, FVB/NCrl, DBA/2, and SJL/J, with intermediate enhancement in 129S1/SvimJ, and no enhancement in BALB/cJ and several additional strains. This pattern holds for the two newly identified variants from the PHP.B family, AAV-PHP.V1 and AAV-PHP.N (FIG. 30, Table 9), which did not transduce the CNS in BALB/cJ, yet transduced the FVB/NJ strain (FIG. 31). AAV-PHP.V1 transduced Human Brain Microvascular Endothelial Cell (HBMEC) culture, resulting in increased mean fluorescent intensity compared to AAV9 and AAV-PHP.eB (FIG. 72) however, suggesting the potential for mechanistic complexity.

[0392] Table 9: AAV-PHP vectors identified by CREATE and M-CREATE. The table provides a summary of the variants that have been identified so far using CREATE and M-CREATE, along with their tropism and the evolutionary steps from the parent capsid that was involved in their discovery.

AAV Variants	Reference / Selection method	Tropism	Production	Rounds of evolution from parent capsid
PHP.B, B2, B3	Deverman et al, 2016 / CREATE	**B**road CNS transduction	Good	1 round from AAV9
PHP.A	Deverman et al, 2016 / CREATE	**A**strocyte transduction	Poor; prone to precipitate upon storage at 4°C.	1 round from AAV9
PHP.eB	Chan et al, 2017 / CREATE	**E**nhanced **B**road CNS transduction	Good	2 rounds from AAV9 or

				1 round from PHP.B
PHP.S	Chan et al, 2017 / CREATE	**S**ensory neuron transduction	Good	1 round from AAV9
PHP.V1, V2	Current study / M-CREATE	BBB **V**ascular cells and astrocytes transduction	Good	1 round from AAV9
PHP.B4, B7, B8,	Current study / M-CREATE	**B**road CNS transduction	Good	1 round from AAV9
PHP.B5, B6	Current study / M-CREATE and CREATE	**B**road CNS transduction	Good	2 rounds from AAV9 or 1 round from PHP.B
PHP.C1, C2, C3	Current study / M-CREATE	Broad **C**NS transduction across mouse strains	Good; PHP.C1 prone to precipitate upon storage at 4°C.	1 round from AAV9
PHP.N	Current study / M-CREATE and CREATE	**N**euron transduction	Average	2 rounds from AAV9 or 1 round from PHP.B

[0393] Importantly, M-CREATE revealed many non-PHP.B-like sequence families that enriched through selection for transduction of cells in the CNS. We tested the previously mentioned AAV-PHP.C1: RYQGDSV, as well as AAV-PHP.C2: WSTNAGY, and AAV-PHP.C3: ERVGFAQ (FIG. 30). These showed enhanced BBB crossing irrespective of mouse strain, with roughly equal CNS transduction in BALB/cJ and C57BL/6J (FIGS. 32 and 73). Collectively, these preliminary studies suggest that M-CREATE is capable of finding capsid variants with diverse mechanisms of BBB entry that lack strain-specificity.

[0394] **Example 8. Exemplary Insertion of Variant AAV Capsid Protein Sequence**

[0395] Demonstration of 7 amino acid peptide insertion in AAV capsid: Peptide sequence "TLQIPFK" (SEQ ID: 435) is positioned between AA 588-589 of AAV capsid. The insertion sequence is underlined and **bold**.

MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGYKYLGPG
NGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKEDTSFGG
NLGRAVFQAKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQPAKKRL
NFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSSSGNWH
CDSQWLGDRVITTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWGYFDFN
RFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTSTVQVFT
DSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDGSQAVGRSSFYCLEYFPSQML
RTGNNFQFSYEFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQTLKFSV
AGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALNGRNSLMNPGP
AMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADKVMITNEEEIKTTNPVATESYGQVA
TNHQSAQ**TLQIPFK**AQAQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHTDGNFHP
SPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEWELQKEN
SKRWNPEIQYTSNYYKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL

[0396] Demonstration of 11 amino acid peptide insertion in AAV capsid:

[0397] Peptide sequence "DGTTLKPFLAQ" (SEQ ID: 867) is positioned by replacing AA 587- 590 of AAV capsid. The inserted sequence is underlined and highlighted.

[0398] MAADGYLPDWLEDNLSEGIREWWALKPGAPQPKANQQHQDNARGLVLPGY
KYLGPGNGLDKGEPVNAADAAALEHDKAYDQQLKAGDNPYLKYNHADAEFQERLKE
DTSFGGNLGRAVFQAKKRLLEPLGLVEEAAKTAPGKKRPVEQSPQEPDSSAGIGKSGAQ
PAKKRLNFGQTGDTESVPDPQPIGEPPAAPSGVGSLTMASGGGAPVADNNEGADGVGSS
SGNWHCDSQWLGDRVITTSTRTWALPTYNNHLYKQISNSTSGGSSNDNAYFGYSTPWG
YFDFNRFHCHFSPRDWQRLINNNWGFRPKRLNFKLFNIQVKEVTDNNGVKTIANNLTST
VQVFTDSDYQLPYVLGSAHEGCLPPFPADVFMIPQYGYLTLNDGSQAVGRSSFYCLEYF
PSQMLRTGNNFQFSYEFENVPFHSSYAHSQSLDRLMNPLIDQYLYYLSRTINGSGQNQQ
TLKFSVAGPSNMAVQGRNYIPGPSYRQQRVSTTVTQNNNSEFAWPGASSWALNGRNSL

MNPGPAMASHKEGEDRFFPLSGSLIFGKQGTGRDNVDADKVMITNEEEIKTTNPVATES
YGQVATNHQS**DGTTLKPFLAQ**AQTGWVQNQGILPGMVWQDRDVYLQGPIWAKIPHT
DGNFHPSPLMGGFGMKHPPPQILIKNTPVPADPPTAFNKDKLNSFITQYSTGQVSVEIEW
ELQKENSKRWNPEIQYTSNYYKSNNVEFAVNTEGVYSEPRPIGTRYLTRNL.

[0399] **Example 9. Treating Huntington's Disease (HD)**

[0400] A subject having Huntington's disease is identified. The subject is then systemically administered a first amount of a viral vector that includes a polynucleotide that encodes for a Zinc finger protein (ZFP) engineered to represses the transcription of the Huntingtin (HTT) gene. The vector will be encapsidated by a modified AAV capsid protein with an amino acid sequence provided in **FIG. 33** or provided in **Tables 2-4**, so as to allow proper targeting of the ZFP to the nervous system, among other organs. If needed, the subject is administered a second or third dose of the vector, until a therapeutically effective amount of the ZFP is expressed in the subject in the nervous system.

[0401] **Example 10. Phase 1A Clinical Trial**

[0402] A phase 1A clinical trial is performed to evaluate the safety, tolerability, pharmacokinetics, and pharmacodynamics of an one-time intravenous injection of test composition comprising viral vector encapsidated by a modified capsid protein with any of the amino acid sequences provided in **FIG. 33** or **Tables 2-4**, in subjects with late Huntington's Disease (HD). Eligible subjects are men and women between 21 and 65 years of age.

[0403] **Inclusion Criteria:** Eligible subjects are men and women between 21 and 65 years of age. Subjects that (i) sign and date Sign and date International Classification of Functioning, Disability and Health (ICF); (2) male or female participant aged ≥ 21 and ≤ 65; (3) participants who submit medical report (PCR) attesting Huntington's disease with a number of CAG repeats on chromosome 4, greater than or equal to 40 and less than or equal to 50 (if the participant has not performed the examination and/or if he does not have the report available, a new exam should be done); (4) Score 5 points or more in motor assessment UHDRS scale (Unified Huntington's Disease Rating Scale) at the time of enrollment; (5) Score between 8 and 11 points in the functional capacity of the UHDRS scale at the time of enrollment.

[0404] **Exclusion Criteria: (1)** Any medical observation data (clinical and physical) that medical research judge as a risk for subject if enrollment at the study; (2) any laboratory exam

data that medical research judge as a risk for subject if enrollment at the study; (4) history of epilepsy; (5) diagnostic of major cognitive impairment; (6) active decompensated psychiatric disease; (7) current or prior history of neoplasia; (8) current history of gastrointestinal, hepatic, renal, endocrine, pulmonary, hematologic, immune, metabolic pathology or severe and uncontrolled cardiovascular disease; (8) diagnostic of any active infection, be it viral, bacterial, fungal, or caused by another pathogen; (9) participants who have contraindication to undergo any of the tests performed in this study, for example, have pacemakers or surgical clip; (10) history of alcohol or illegal drugs abusers; (11) history of 1 or more episodes of suicide in the two years before Visit V-4; (12) active smoker or have stopped smoking less than six months prior to enrollment; (13) test positive in at least one of the serological tests: HIV 1 and 2 (Anti-HIV-1,2), HTLV I and II, HBV (HBsAg, anti-HBc), HCV (anti-HCV-Ab) and VDRL (Treponema pallidum); (14) history of drug allergy, including contrasts for imaging, or bovine products; (15) in use or expected use of immunosuppressive drugs or prohibited medicines for the first three months after the first administration of the investigational product; (16) any clinical changes that is interpreted by the medical researcher as a risk to participant's enrollment.

[0405] **Experimental:**

[0406] Placebo. One-time injection of placebo at Week 0.

[0407] Test High Dose. One-time injection of test composition 2 x 10^10 vg at Week 0.

[0408] Test Middle Dose. One-time injection of test composition 6 x 10^9 vg at Week 0.

[0409] Test Low Dose. One-time injection of test composition 2x 10^9 vg at Week 0.

[0410] Test Lowest Dose. One-time injection of test composition 2 x 10^8 vg at Week 0.

[0411] **Primary Outcome Measures:** Safety of the test composition by periodic monitoring changes at adverse events, vital signs, laboratory tests, ECG and incidence of benign and malignant neoplasms [Time Frame: five years]. The safety of the investigational product will be evaluated in detail from periodic evaluations contemplating monitoring changes of: (1) adverse events including type, frequency, intensity, seriousness, severity, and action taken related to the investigational product study; (2) vital signs (BP, HR, axillary temperature), physical and medical examination (BMI, weight, height, medical condition - cardiovascular, pulmonary, digestive, musculoskeletal and peripheral, with emphasis on the neurological assessment and others); (2) laboratory tests included hematologic, biochemical, urologic and serological

analysis; (3) electrocardiogram (ECG) of 12 derivations; (4) and incidence and classification of benign and malignant neoplasms in the following organs/systems: CNS, lung, liver, spleen, pancreas, prostate, testicle, urinary, hematological and skeletal system through the laboratory tests, magnetic resonance imaging, computerized tomography and ultrasonography.

[0412] **Secondary Outcome Measures:** Preliminary efficacy of Cellavita HD by global clinical response (CIBIS) and UHDRS improvement [Time Frame: five years] will be evaluated by statistical comparison of the results of each UHDRS scale component: motor, cognitive and behavior. The global clinical response will be assessed by statistical comparison between baseline score observed by the Investigator before and after Cellavita HD treatment. Preliminary efficacy of Cellavita HD by comparison of the inflammatory markers [Time Frame: one year] will be evaluated by statistical comparison of the inflammatory markers included IL-4, IL-6, IL-10 (interleukin IL) and TNF-alpha (tumoral necrosis factor alpha). Immunological Response of Cellavita HD [Time Frame: one year]. The immunological response induced by Cellavita HD will be evaluated by statistical comparison between baseline results of CD4+ and CD8+ proliferation and the other evaluated times. Preliminary efficacy of Cellavita HD by comparison of the CNS assessment [Time Frame: one year]. Will be evaluated by statistical comparison of the CNS assessment through magnetic resonance image at cortical thickness measurements, volumes of different brain structures, especially the basal ganglia, with special attention to caudate and metabolic changes identified in proton spectroscopy. Risk of suicidal ideation by Hamilton Depression Rating Scale (HDRS) [Time Frame: five years] will be evaluated by suicidal domain. The classificatory pontuation may correspond to mild depression (score: 8 to 13), moderate depression (score: 19 - 22) and severe depression (score: > 23).

[0413] While preferred instances of the present examples have been shown and described herein, it will be obvious to those skilled in the art that such instances are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the disclosure. It should be understood that various alternatives to the instances of the disclosure described herein may be employed in practicing the disclosure. It is intended that the following claims define the scope of the disclosure and that methods and structures within the scope of these claims and their equivalents be covered thereby.

[0414] While preferred embodiments of the present invention have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

CLAIMS

1. An AAV capsid comprising:
    a) an AAV capsid protein comprising:
        i. a first amino acid sequence that is at least 98% identical to amino acid 217 to amino acid 736 of SEQ ID NO: 1; and
        ii. a second amino acid sequence at least 57.1% identical to an amino acid sequence provided in Tables 2-3 or FIG. 33 inserted at an amino acid position 588_589 within SEQ ID NO: 1, wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a central nervous system (CNS) in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1.
2. The AAV capsid of claim 1, wherein the second amino acid sequence is at least 71.4% identical to the amino acid sequence provided in Tables 2-3 or FIG. 33.
3. The AAV capsid of claim 1, wherein the second amino acid sequence is at least 86.7% identical to the amino acid sequence provided in Tables 2-3 or FIG. 33.
4. The AAV capsid of claim 1, wherein the second amino acid sequence is selected from the group consisting of TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, SIERPFK, RYQGDSV, and TTLKPFS.
5. The AAV capsid of claim 1, wherein the AAV capsid protein is present in VP1, VP2, and VP3 of the AAV capsid.
6. The AAV capsid of claim 1, wherein the AAV capsid is chimeric.
7. The AAV capsid of claim 1, wherein 60 copies of the AAV capsid protein are assembled into the AAV capsid.
8. The AAV capsid protein of claim 1, wherein the CNS comprises a cell-type selected from the group consisting of a neuron, an oligodendrocyte, an astrocyte, and a brain vascular cell.
9. The AAV capsid of claim 1, wherein the CNS comprises a tissue that is selected from the group consisting of a brain, a thalamus, a cortex, a striatum, a ventral midbrain, and a spinal cord.

10. The AAV capsid of claim 1, wherein the AAV capsid protein further comprises an amino acid substitution A587D or Q588G.
11. The AAV capsid protein of claim 1, wherein the AAV capsid protein further comprises an amino acid substitution A589N or Q590P.
12. The AAV capsid of claim 1, wherein the second amino acid sequence at the amino acid position 588_589 within SEQ ID NO: 1 is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW.
13. The AAV capsid of claim 1 that is isolated and purified.
14. The AAV capsid of claim 1 formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the CNS, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier.
15. The AAV capsid of claim 14, wherein the pharmaceutical formulation further comprises a therapeutic agent.
16. An AAV capsid comprising an AAV capsid protein comprising a seven-amino-acid insertion (X1-X2-X3-X4-X5-X6-X7) between amino acid 588 and amino acid 589 in an amino acid sequence of the AAV capsid protein provided in SEQ ID NO: 1, wherein:

    X1 is an amino acid selected from the group consisting of E, D, G, R, S and T;

    X2 is an amino acid selected from the group consisting of A, G, I, L, M, N, Q, T, and Y;

    X3 is an amino acid selected from the group consisting of E, K, L, T, and Q; and

    X4 is an amino acid selected from the group consisting of G, I, K, L, R, T, and V.

17. The AAV capsid protein of claim 16, wherein X5 is an amino acid selected from the group consisting of A, D, G, P, L, Q, and V.
18. The AAV capsid protein of claim 17, wherein X6 is an amino acid selected from the group consisting of F, K, N, P, Q, S, and V.
19. The AAV capsid protein of claim 18, wherein X7 is an amino acid selected from the group consisting of I, K, L, P, and V.

20. The AAV capsid of claim 16, wherein the seven-amino-acid insertion is selected from the group consisting of TALKPFL, TTLKPFL, TLQIPFK, TMQKPFI, SIERPFK, RYQGDSV, and TTLKPFS.
21. The AAV capsid of claim 16, wherein the AAV capsid protein is present in VP1, VP2, and VP3 of the AAV capsid.
22. The AAV capsid of claim 16, wherein the AAV capsid is chimeric.
23. The AAV capsid of claim 16, wherein 60 copies of the AAV capsid protein are assembled into the AAV capsid.
24. The AAV capsid of claim 16, wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a central nervous system (CNS) in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1
25. The AAV capsid protein of claim 24, wherein the CNS comprises a cell-type selected from the group consisting of a neuron, a glial cell, an oligodendrocyte, an ependymal cell, an astrocyte, a Schwann cell, a satellite cell, and an enteric glial cell.
26. The AAV capsid of claim 24, wherein the CNS comprises a tissue that is selected from the group consisting of a brain, a thalamus, a cortex, a striatum, a ventral midbrain, and a spinal cord.
27. The AAV capsid of claim 16, wherein the AAV capsid protein further comprises an amino acid substitution comprising A587D or Q588G.
28. The AAV capsid protein of claim 16, wherein the AAV capsid protein further comprises an amino acid substitution comprising A589N or Q590P.
29. The AAV capsid of claim 16, wherein the seven-amino-acid insertion is not TLAVPFK, KFPVALT, SVSKPFL, FTLTTPK, MNATKNV, NGGTSSS, TRTNPEA, or YTLSQGW.
30. The AAV capsid of claim 16 that is isolated and purified.
31. The AAV capsid of claim 16 formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the CNS, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier.
32. The AAV capsid of claim 31, wherein the pharmaceutical formulation further comprises a therapeutic agent.

33. An AAV capsid comprising:
    a) an AAV capsid protein comprising:
        i. a first amino acid sequence that is at least 98% identical to amino acid 217 to amino acid 736 of SEQ ID NO: 1; and
        ii. a second amino acid sequence at least 57.1% identical to an amino acid sequence provided in Table 4 or FIG. 35 at an amino acid position 588_589 within SEQ ID NO: 1, wherein the AAV capsid protein is characterized by at least one of an increased specificity and an increased transduction efficiency when measured in a liver in a subject when delivered to the subject systemically, relative to a native AAV capsid protein provided in SEQ ID NO: 1.
34. The AAV capsid of claim 33, wherein the second amino acid sequence is at least 71.4% identical to the amino acid sequence provided in Table 4 or FIG. 35.
35. The AAV capsid of claim 33, wherein the second amino acid sequence is at least 86.7% identical to the amino acid sequence provided in Table 4 or FIG. 35.
36. The AAV capsid of claim 33, wherein the second amino acid sequence is selected from the group consisting of KAYSVQV, PSGSARS, and RTANALG.
37. The AAV capsid of claim 33, wherein the AAV capsid protein is present in VP1, VP2, and VP3 of the AAV capsid.
38. The AAV capsid of claim 33, wherein the AAV capsid is chimeric.
39. The AAV capsid of claim 33, wherein 60 copies of the AAV capsid protein are assembled into the AAV capsid.
40. The AAV capsid of claim 33 that is isolated and purified.
41. The AAV capsid of claim 33 formulated as a pharmaceutical formulation for intravenous administration to treat a disease or a condition of the liver, the pharmaceutical formulation further comprising a pharmaceutically acceptable carrier.
42. The AAV capsid of claim 41, wherein the pharmaceutical formulation further comprises a therapeutic agent.
43. A recombinant vector comprising a nucleic acid encoding the AAV capsid protein of any one of claims 1-42.

44. A kit comprising:
    a) a first vector comprising the recombinant vector of claim 43;
    b) a second vector encoding a helper virus protein; and
    c) a third vector comprising a therapeutic nucleic acid encoding a therapeutic gene expression product.
45. A method of treating a disease or condition in a subject comprising administering a therapeutically effective amount of a pharmaceutical formulation comprising the AAV capsid protein of any one of claims 1-42.
46. The method of claim 45, wherein the disease or the condition is a disease or a condition of a central nervous system or a liver of the subject.
47. A method of manufacturing a recombinant AAV particle from the AAV capsid of any one of claims 1-42, the method comprising:
    a) introducing into a cell a nucleic acid comprising:
        i. a first nucleic acid sequence encoding a therapeutic gene expression product;
        ii. a second nucleic acid sequence encoding a recombinant viral genome comprising a capsid (*Cap*) gene modified to express the AAV capsid of any one of claims 1-42; and
        iii. a third nucleic acid sequence encoding an AAV helper virus genome; and
    b) assembling the recombinant AAV particle, the recombinant AAV particle comprising the AAV capsid encapsidating the first nucleic acid.
48. A method of manufacturing a recombinant AAV particle, the method comprising:
    a) providing a recombinant AAV genome comprising:
        i. an AAV capsid gene, and
        ii. a recognition sequence for a Cre recombinase, wherein the recognition sequence facilitates a recombinase-dependent change that is detectable, and wherein the recombinase recognition sequence comprises two Cre-recognition sites;
    b) transfecting a population of cells expressing the Cre recombinase with the recombinant AAV genome, whereby the Cre recombinase induces a

recombination event to generate the recombinase-dependent change in the recombinant AAV genome, and wherein the recombinase-dependent change comprises an inversion of the sequence that is flanked by the Cre-recognition sites;

c) detecting an increased rate of the recombinase-dependent change a target cell in the population of cells;

d) detecting a decreased rate of the recombinase-dependent change in an off-target cell in the population of cells; and

e) identifying a recombinant AAV genome generated by the recombinase-dependent change, wherein said identified rAAV genome comprises the inversion, and wherein said identified recombinant AAV genome encodes an AAV capsid particle characterized having an increased specificity for the target cell and a decreased specificity for the off-target cell.

49. The method of claim 48, wherein the off-target cell is a hepatocyte.

50. The method of claim 48, wherein the target cell is a cell selected from the group consisting of a neuron, a glial cell, an oligodendrocyte, an ependymal cell, an astrocyte, a Schwann cell, a satellite cell, and an enteric glial cell.

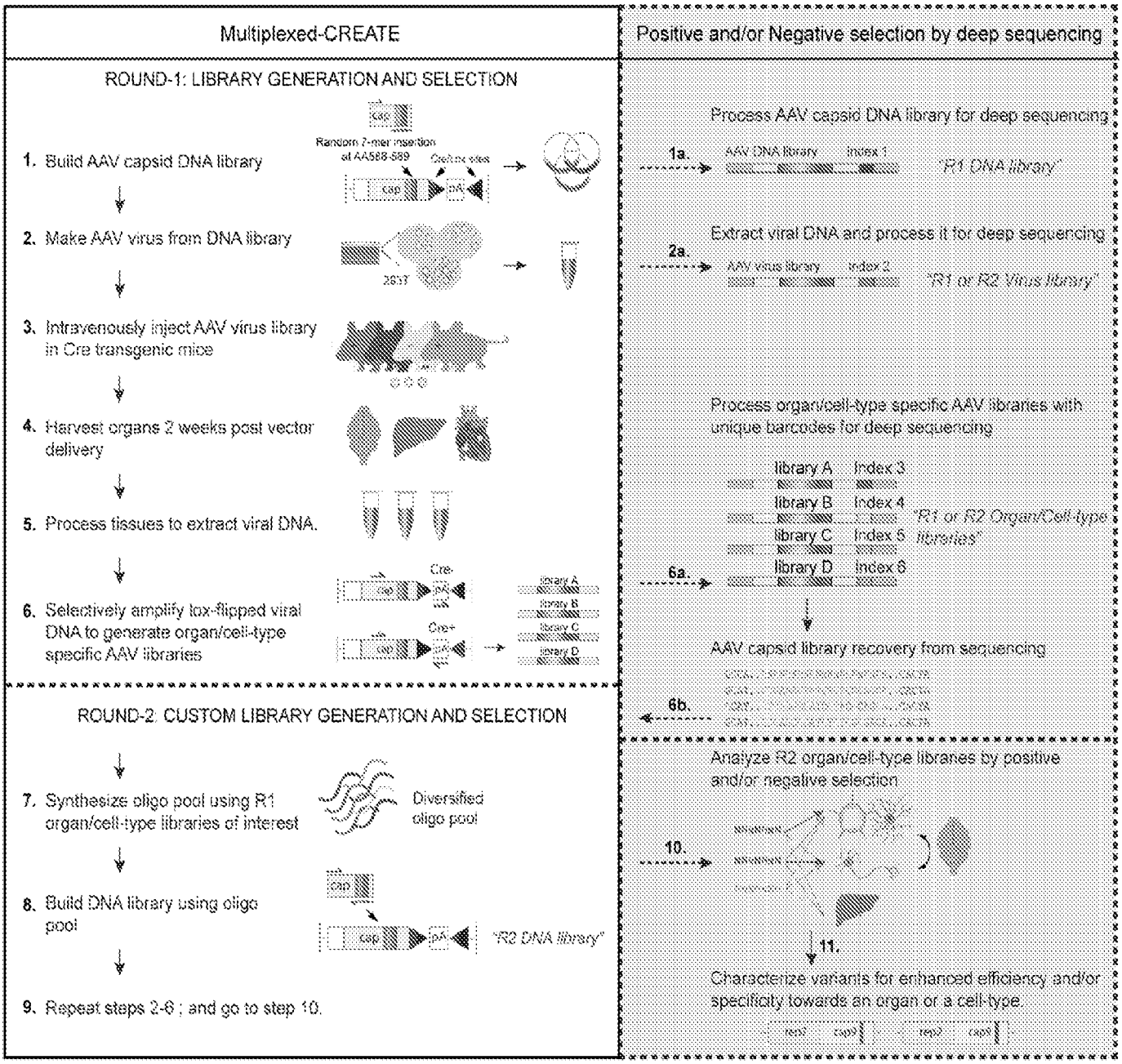

Multiplexed-CREATE
ROUND-1: LIBRARY GENERATION AND SELECTION
1. Build AAV capsid DNA library
Random 7-mer insertion at AA588-589
Cre/lox sites
cap
pA
2. Make AAV virus from DNA library
293T
3. Intravenously inject AAV virus library in Cre transgenic mice
4. Harvest organs 2 weeks post vector delivery
5. Process tissues to extract viral DNA.
6. Selectively amplify lox-flipped viral DNA to generate organ/cell-type specific AAV libraries
Cre-
Cre+
library A
library B
library C
library D
ROUND-2: CUSTOM LIBRARY GENERATION AND SELECTION
7. Synthesize oligo pool using R1 organ/cell-type libraries of interest
Diversified oligo pool
8. Build DNA library using oligo pool
"R2 DNA library"
9. Repeat steps 2-6 ; and go to step 10.
Positive and/or Negative selection by deep sequencing
Process AAV capsid DNA library for deep sequencing
1a.
AAV DNA library
Index 1
"R1 DNA library"
Extract viral DNA and process it for deep sequencing
2a.
AAV virus library
Index 2
"R1 or R2 Virus library"
Process organ/cell-type specific AAV libraries with unique barcodes for deep sequencing
library A Index 3
library B Index 4
library C Index 5
library D Index 6
"R1 or R2 Organ/Cell-type libraries"
6a.
AAV capsid library recovery from sequencing
6b.
Analyze R2 organ/cell-type libraries by positive and/or negative selection
10.
11.
Characterize variants for enhanced efficiency and/or specificity towards an organ or a cell-type.
rep2
cap2

FIG. 1

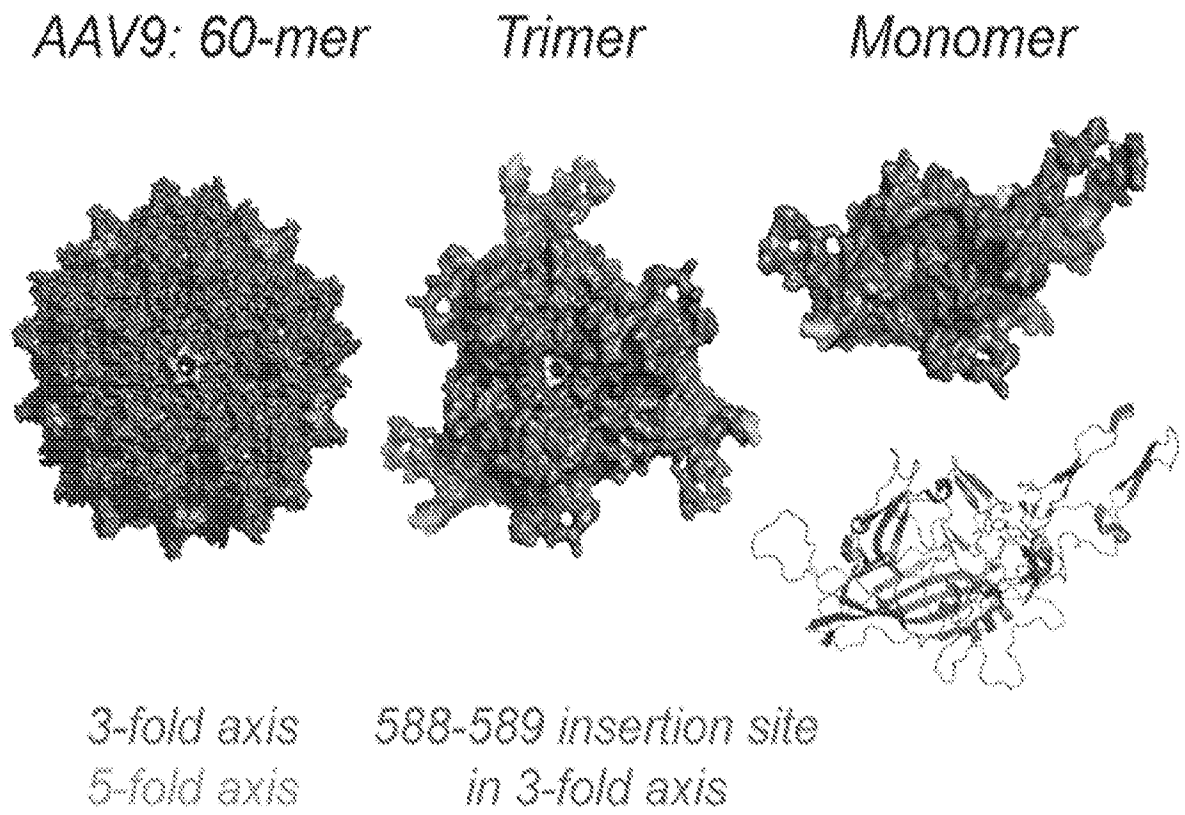

AAV9: 60-mer
Trimer
Monomer
3-fold axis
5-fold axis
588-589 insertion site
in 3-fold axis

FIG. 2

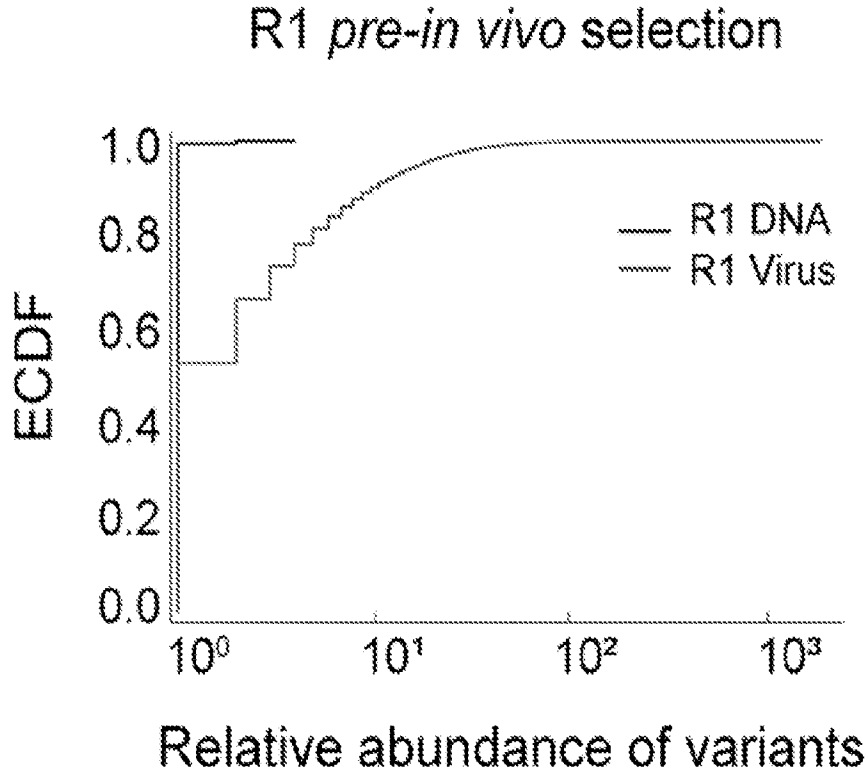

R1 pre-in vivo selection
1.0
0.8
0.6
0.4
0.2
0.0
ECDF
R1 DNA
R1 Virus
10⁰
10¹
10²
10³
Relative abundance of variants

FIG. 3

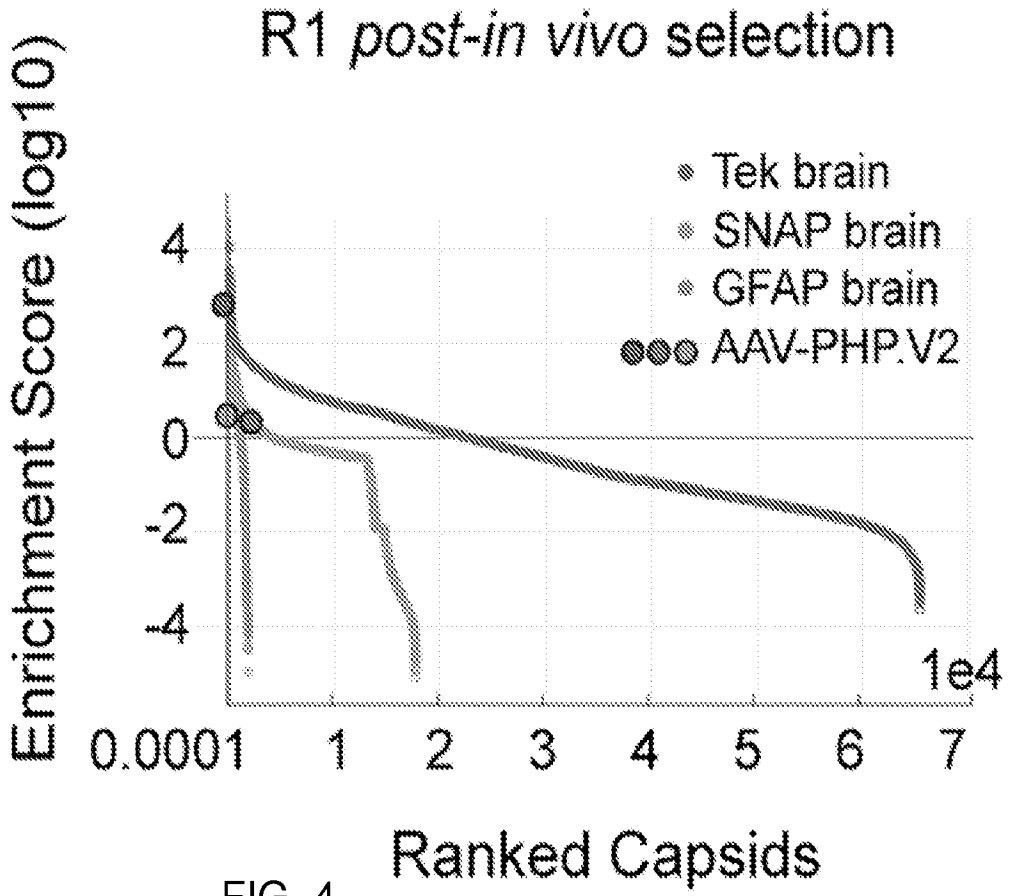

R1 post-in vivo selection
Enrichment Score (log10)
Tek brain
SNAP brain
GFAP brain
AAV-PHP.V2
4
2
0
-2
-4
0.0001
1
2
3
4
5
6
7
1e4
Ranked Capsids

FIG. 4

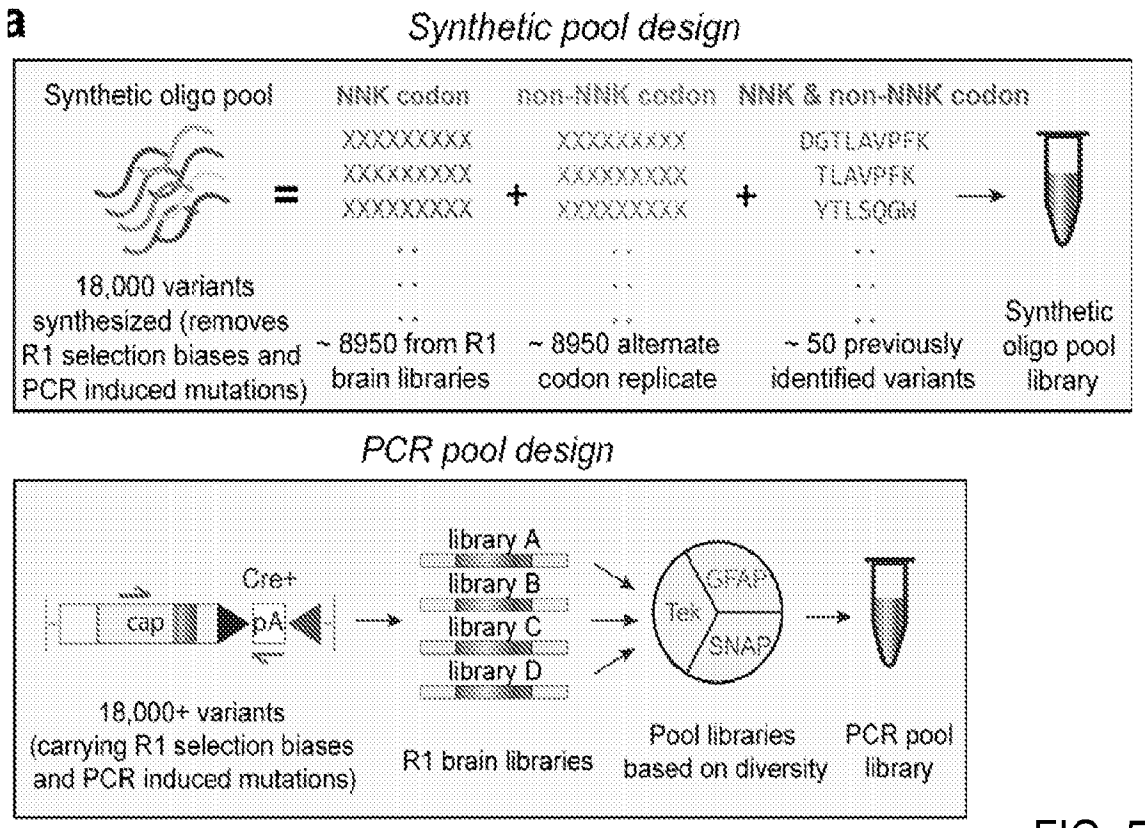

a
Synthetic pool design
Synthetic oligo pool
NNK codon
non-NNK codon
NNK & non-NNK codon
XXXXXXXXX
DGTLAVPFK
TLAVPFK
YTLSQGW
18,000 variants synthesized (removes R1 selection biases and PCR induced mutations)
~ 8950 from R1 brain libraries
~ 8950 alternate codon replicate
~ 50 previously identified variants
Synthetic oligo pool library
PCR pool design
Cre+
cap
pA
library A
library B
library C
library D
Tek
GFAP
SNAP
18,000+ variants (carrying R1 selection biases and PCR induced mutations)
R1 brain libraries
Pool libraries based on diversity
PCR pool library

FIG. 5

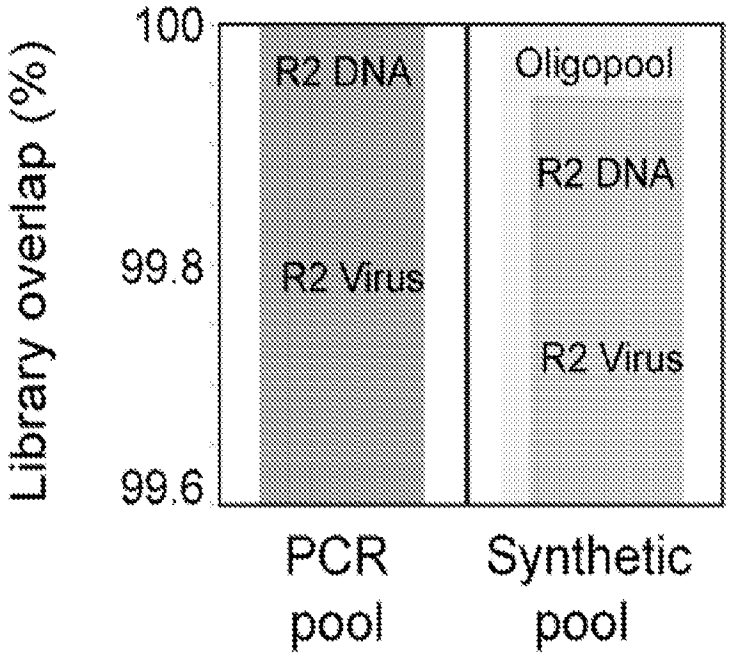

Library overlap (%)
100
99.8
99.6
R2 DNA
R2 Virus
Oligopool
R2 DNA
R2 Virus
PCR pool
Synthetic pool

FIG. 6

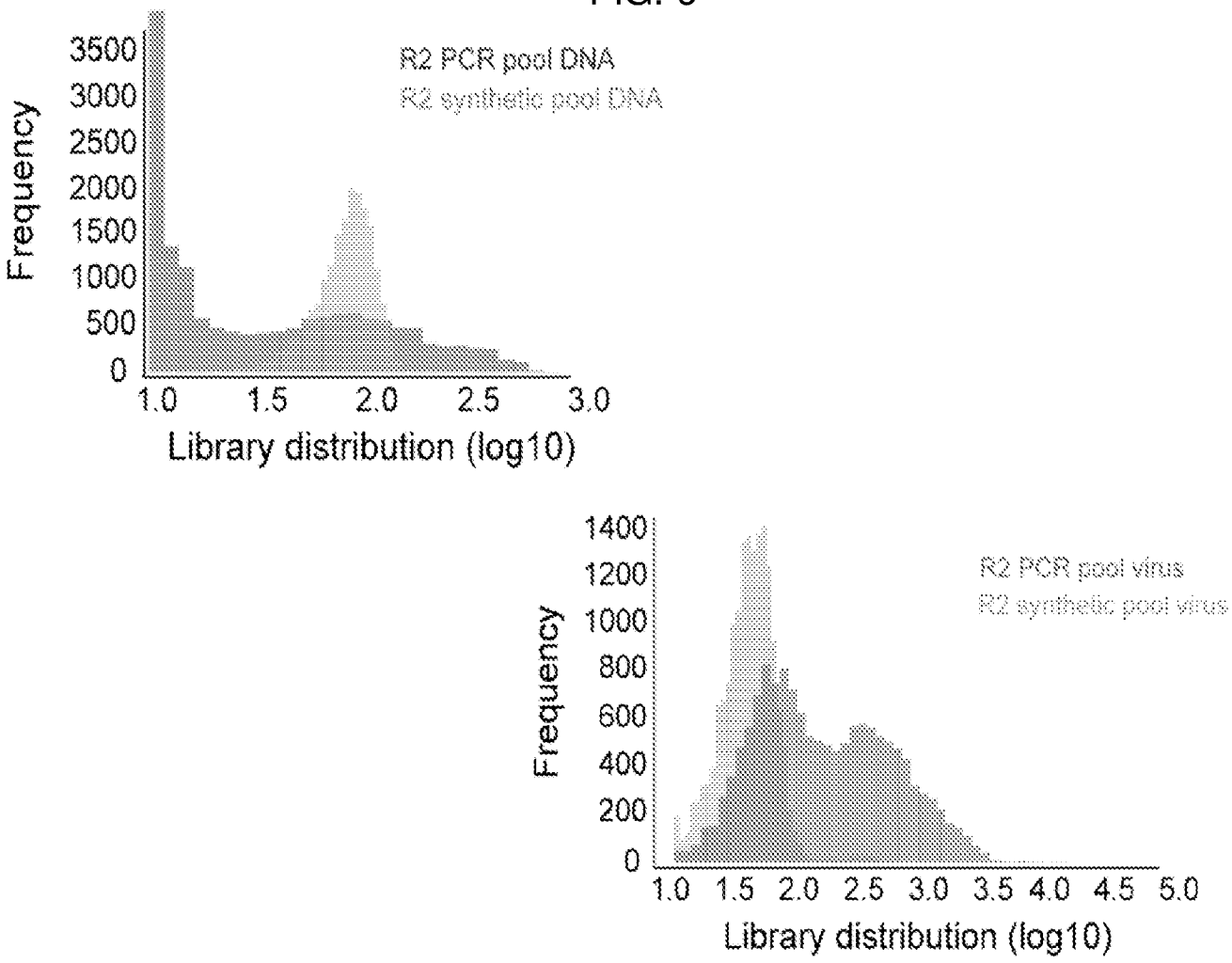

Frequency
3500
3000
2500
2000
1500
1000
500
0
1.0
1.5
2.0
2.5
3.0
Library distribution (log10)
R2 PCR pool DNA
R2 synthetic pool DNA
1400
1200
1000
800
600
400
200
0
1.0
1.5
2.0
2.5
3.0
3.5
4.0
4.5
5.0
Library distribution (log10)
R2 PCR pool virus
R2 synthetic pool virus

FIG. 7

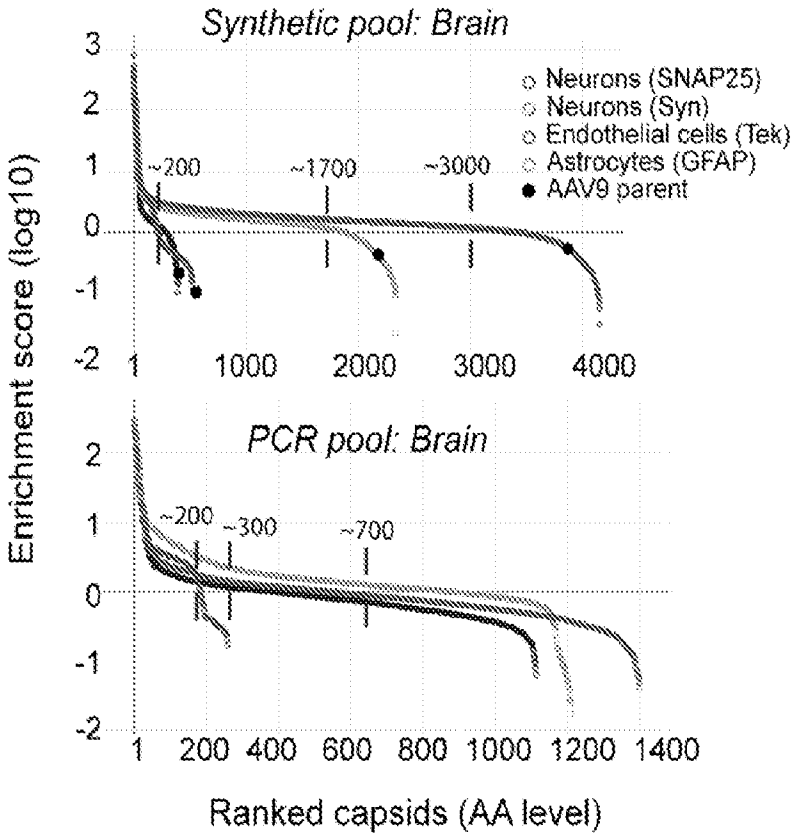

Synthetic pool: Brain
Neurons (SNAP25)
Neurons (Syn)
Endothelial cells (Tek)
Astrocytes (GFAP)
AAV9 parent
~200
~1700
~3000
Enrichment score (log10)
PCR pool: Brain
~200
~300
~700
Ranked capsids (AA level)

FIG. 8

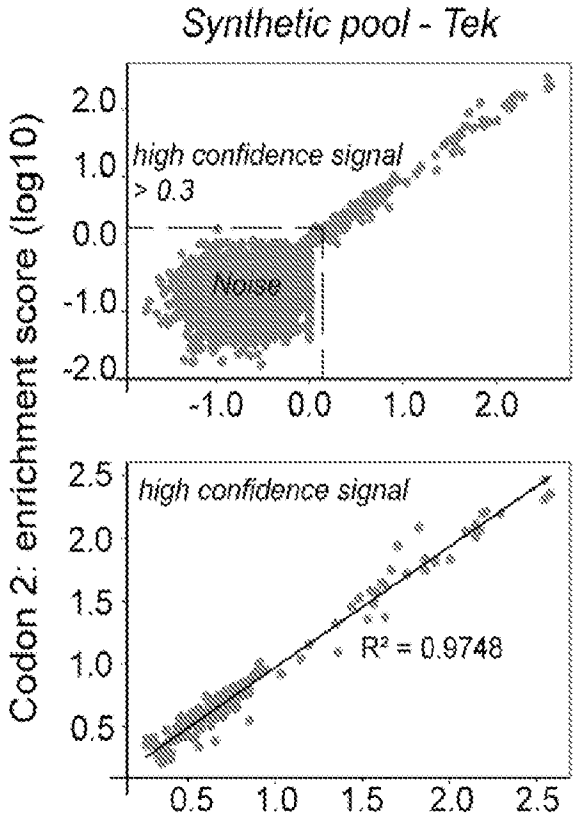

Synthetic pool - Tek
high confidence signal
> 0.3
noise
high confidence signal
R² = 0.9748
Codon 2: enrichment score (log10)
Codon 1: enrichment score (log10)

FIG. 9

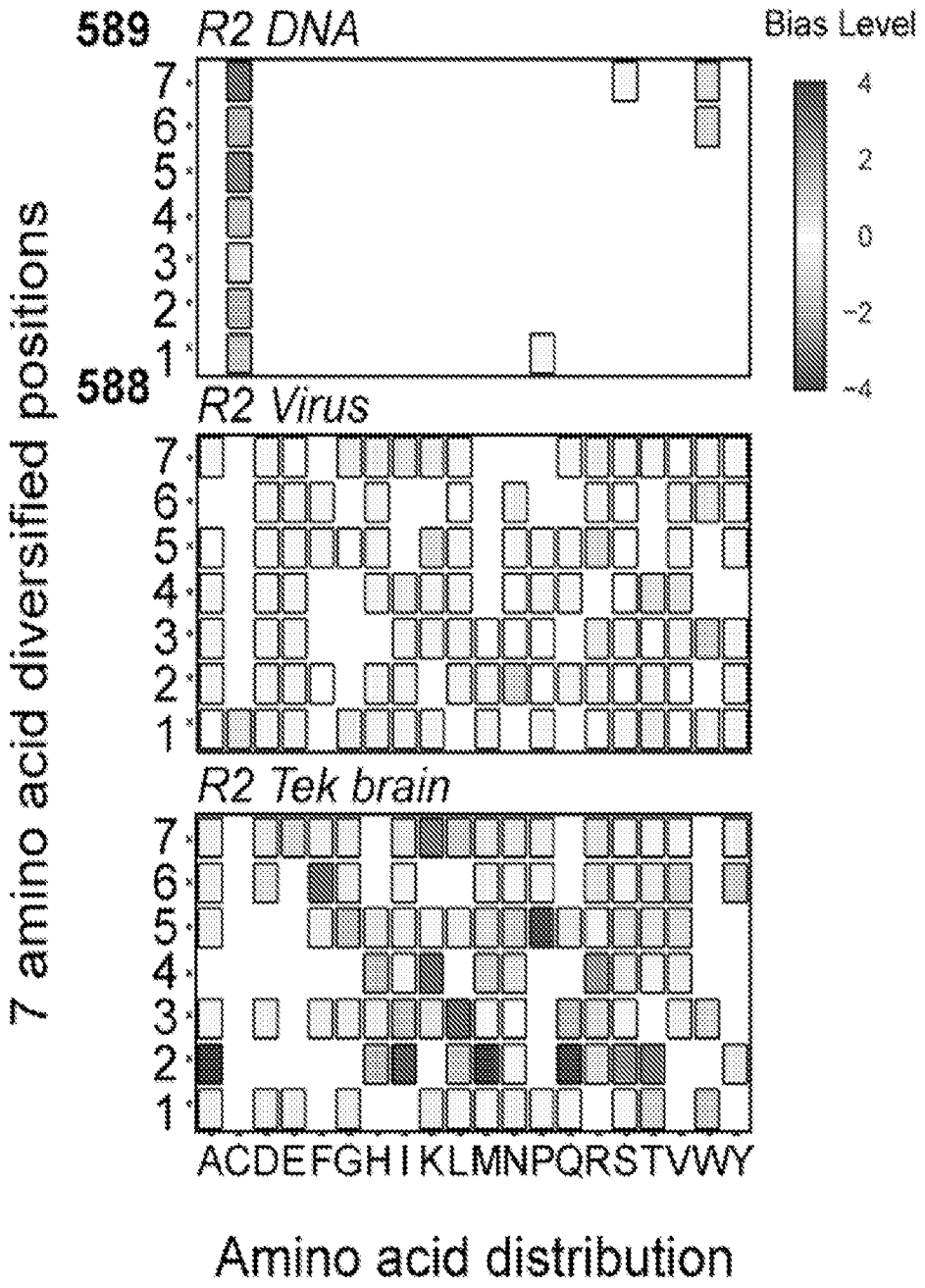
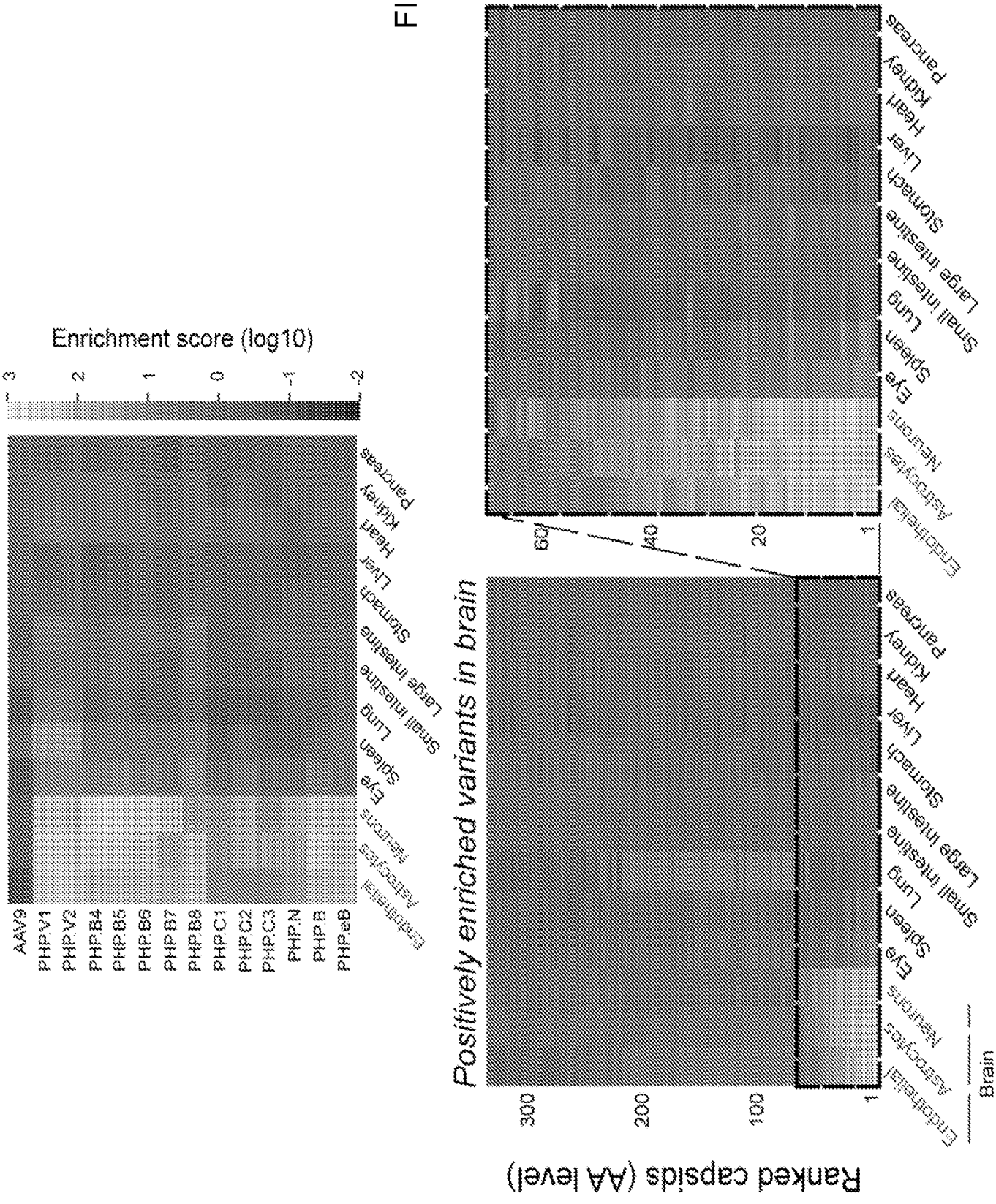

589
R2 DNA
588
R2 Virus
R2 Tek brain
Bias Level
4
2
0
-2
-4
7 amino acid diversified positions
7
6
5
4
3
2
1
ACDEFGHIKLMNPQRSTVWY
Amino acid distribution

FIG. 10

FIG. 11


Enrichment score (log10)
3
2
1
0
-1
-2
AAV9
PHP.V1
PHP.V2
PHP.B4
PHP.B5
PHP.B6
PHP.B7
PHP.B8
PHP.C1
PHP.C2
PHP.C3
PHP.N
PHP.B
PHP.eB
Endothelial
Astrocytes
Neurons
Eye
Spleen
Lung
Small intestine
Large intestine
Stomach
Liver
Heart
Kidney
Pancreas
Positively enriched variants in brain
Ranked capsids (AA level)
300
200
100
1
60
40
20
1
Brain

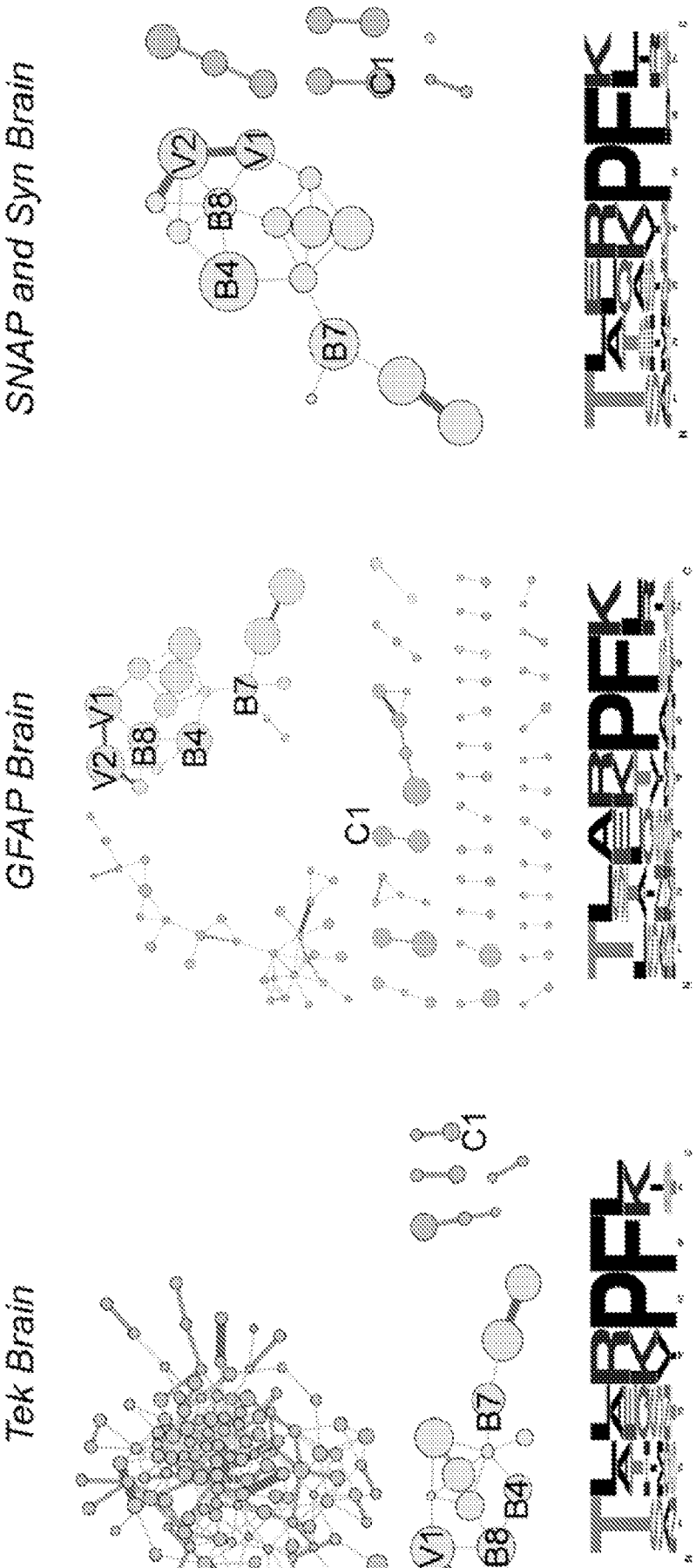


FIG. 12

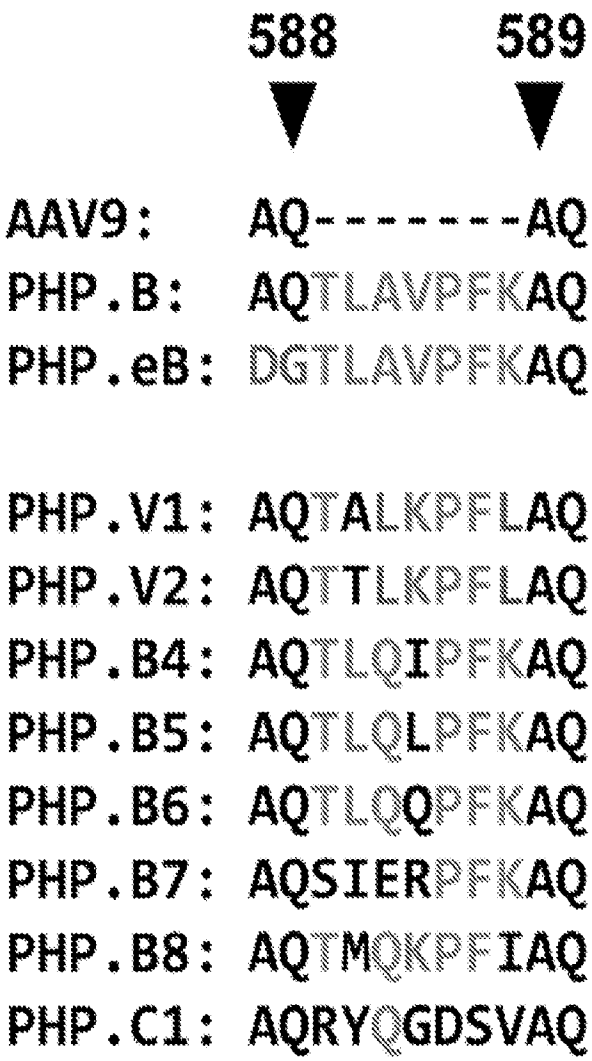

588
589
AAV9: AQ-------AQ
PHP.B: AQTLAVPFKAQ
PHP.eB: DGTLAVPFKAQ
PHP.V1: AQTALKPFLAQ
PHP.V2: AQTTLKPFLAQ
PHP.B4: AQTLQIPFKAQ
PHP.B5: AQTLQLPFKAQ
PHP.B6: AQTLQQPFKAQ
PHP.B7: AQSIERPFKAQ
PHP.B8: AQTMQKPFIAQ
PHP.C1: AQRYQGDSVAQ

FIG. 13

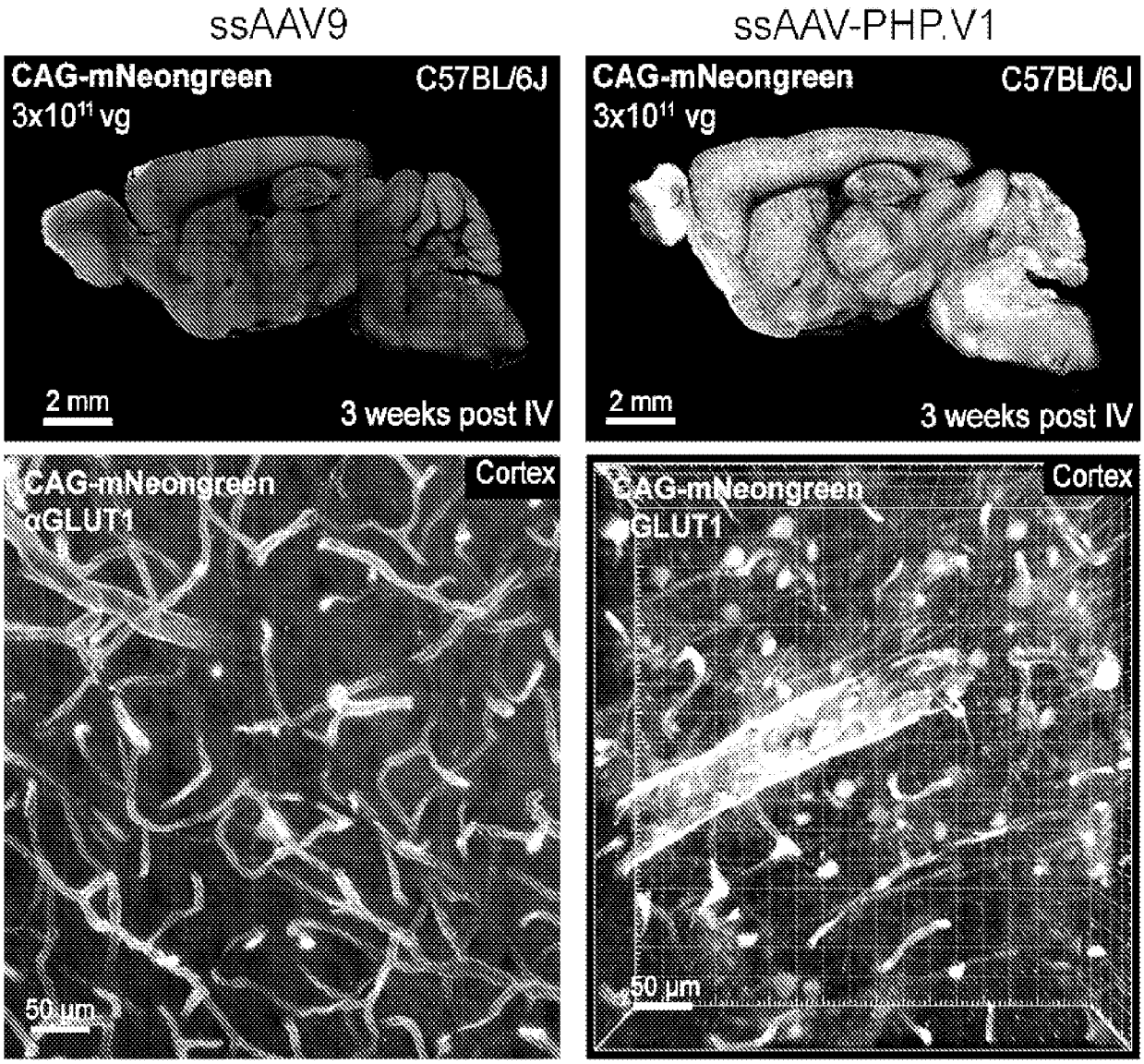

ssAAV9
ssAAV-PHP.V1
CAG-mNeongreen
C57BL/6J
3x10^11 vg
2 mm
3 weeks post IV
CAG-mNeongreen
C57BL/6J
3x10^11 vg
2 mm
3 weeks post IV
CAG-mNeongreen
αGLUT1
Cortex
50 µm
CAG-mNeongreen
GLUT1
Cortex
50 µm

FIG. 14

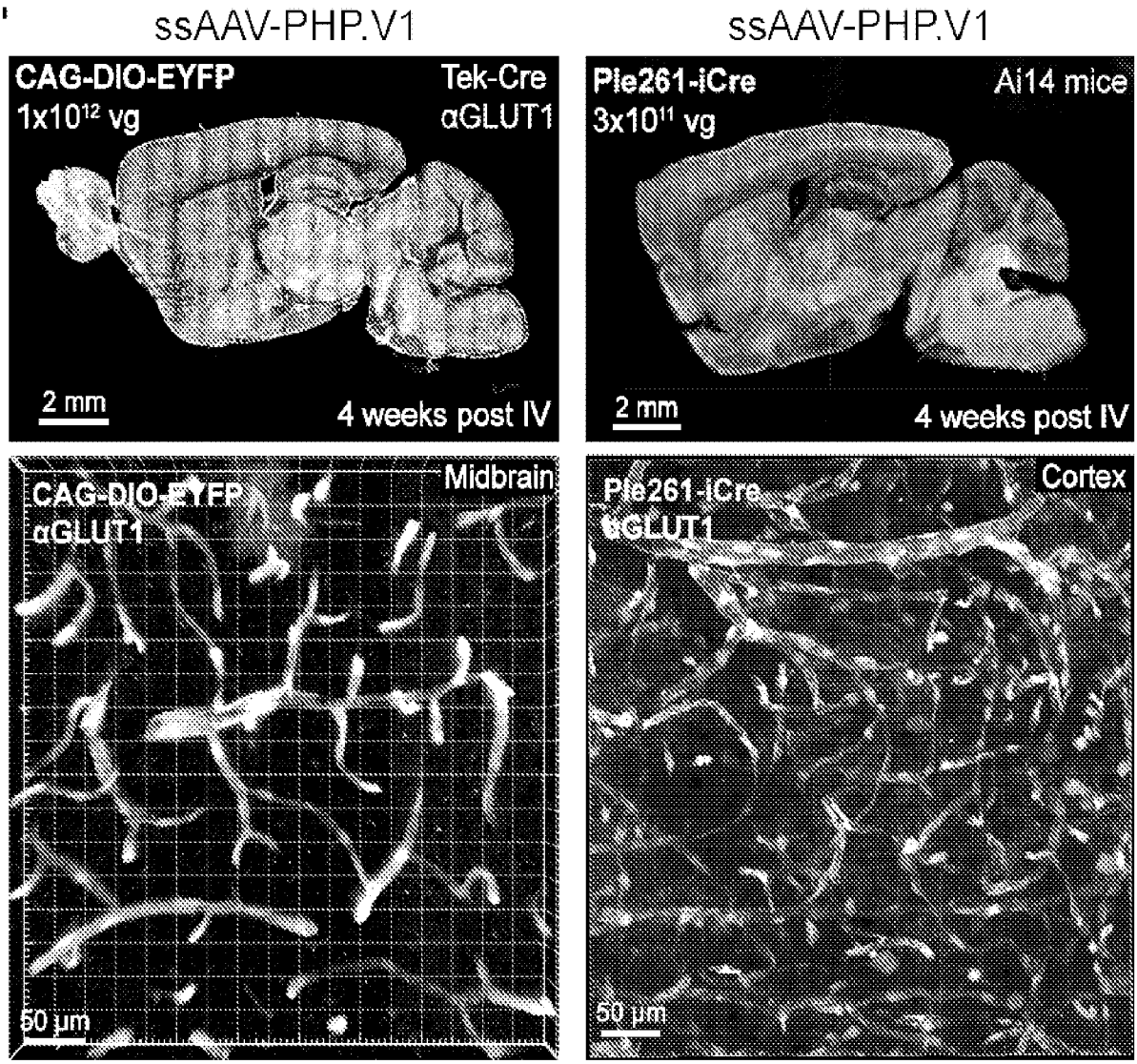

ssAAV-PHP.V1
CAG-DIO-EYFP
1x10^12 vg
Tek-Cre
αGLUT1
2 mm
4 weeks post IV
ssAAV-PHP.V1
Ple261-iCre
3x10^11 vg
Ai14 mice
2 mm
4 weeks post IV
CAG-DIO-EYFP
αGLUT1
Midbrain
50 µm
Ple261-iCre
αGLUT1
Cortex
50 µm

FIG. 15

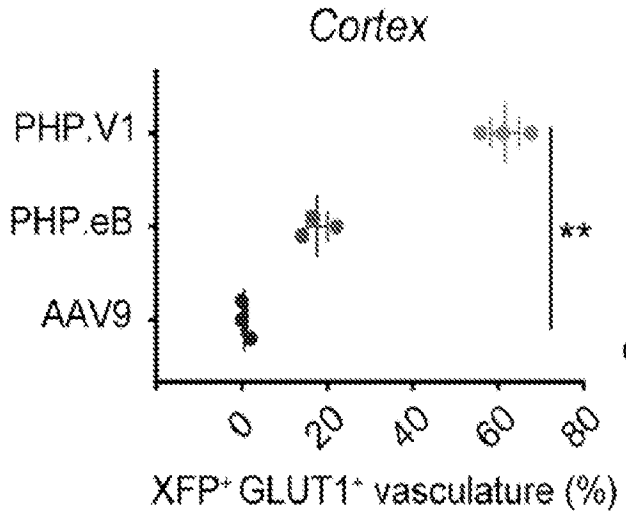


FIG. 16

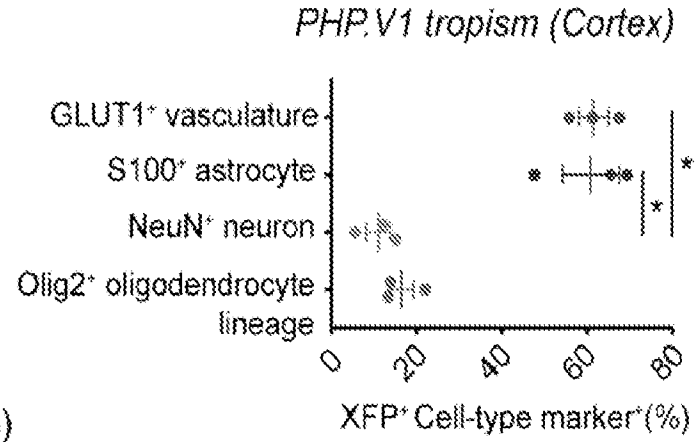


FIG. 17

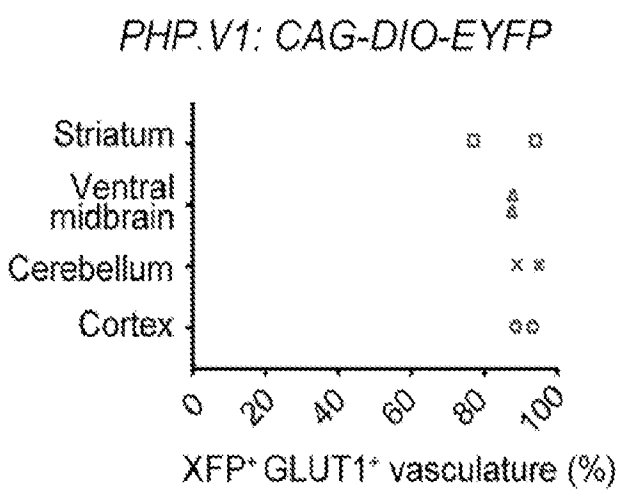


FIG. 18

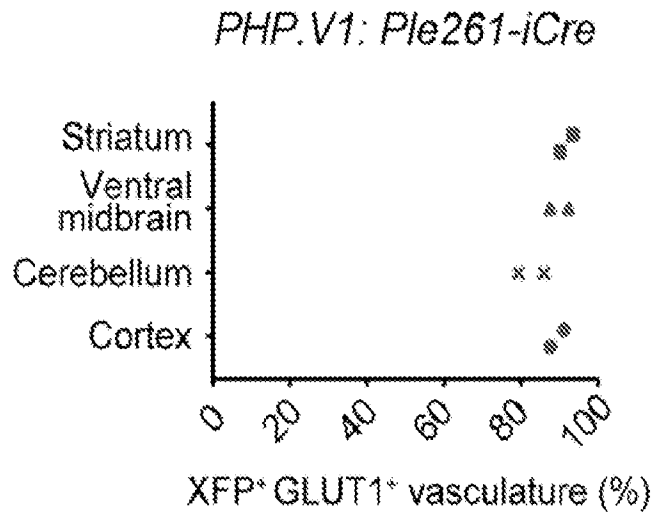


FIG. 19

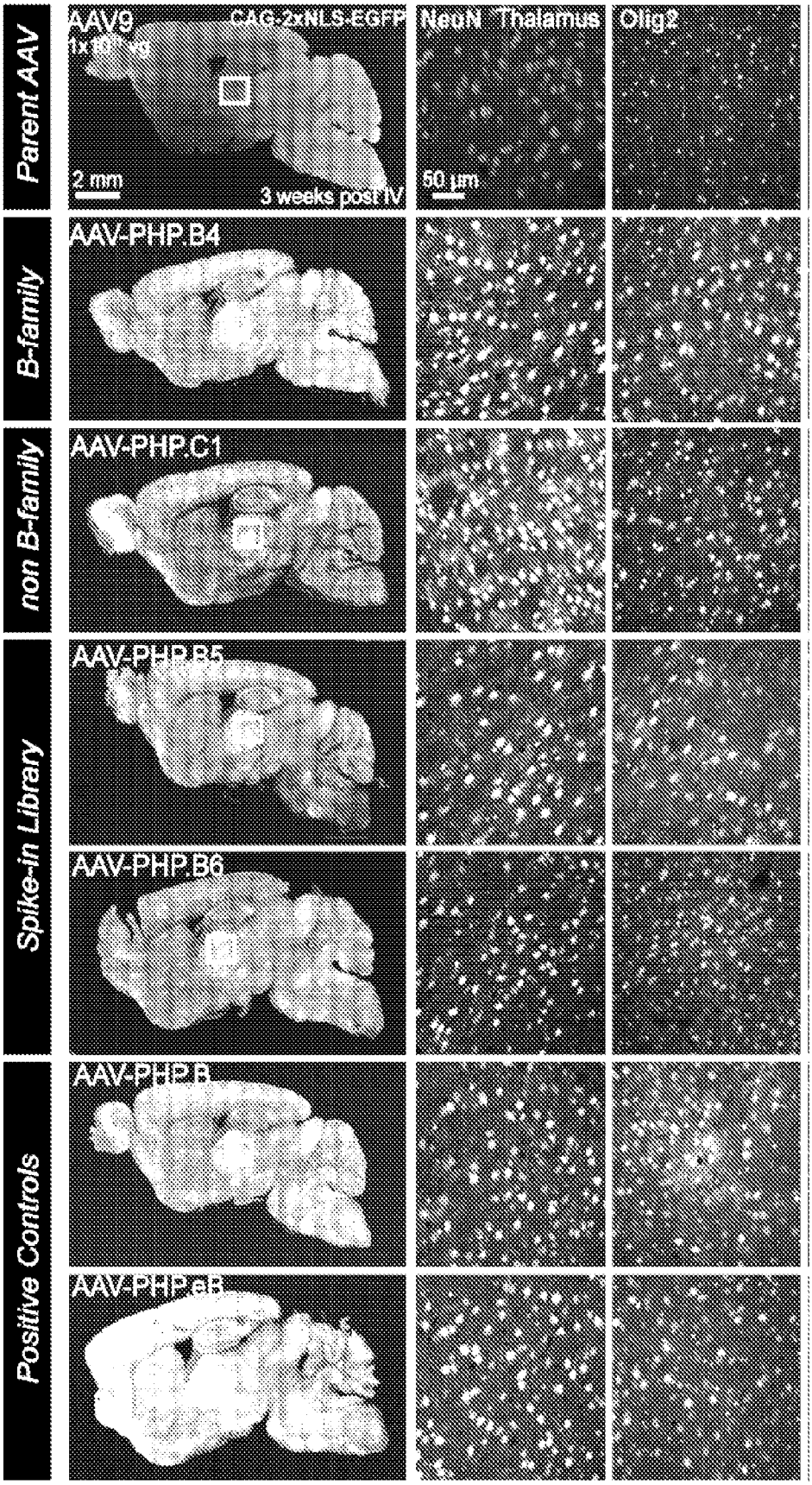

Parent AAV
B-family
non B-family
Spike-in Library
Positive Controls
AAV9
CAG-2xNLS-EGFP
1 x 10^11 vg
2 mm
3 weeks post IV
NeuN Thalamus
Olig2
50 µm
AAV-PHP.B4
AAV-PHP.C1
AAV-PHP.B5
AAV-PHP.B6
AAV-PHP.B
AAV-PHP.eB

FIG. 20

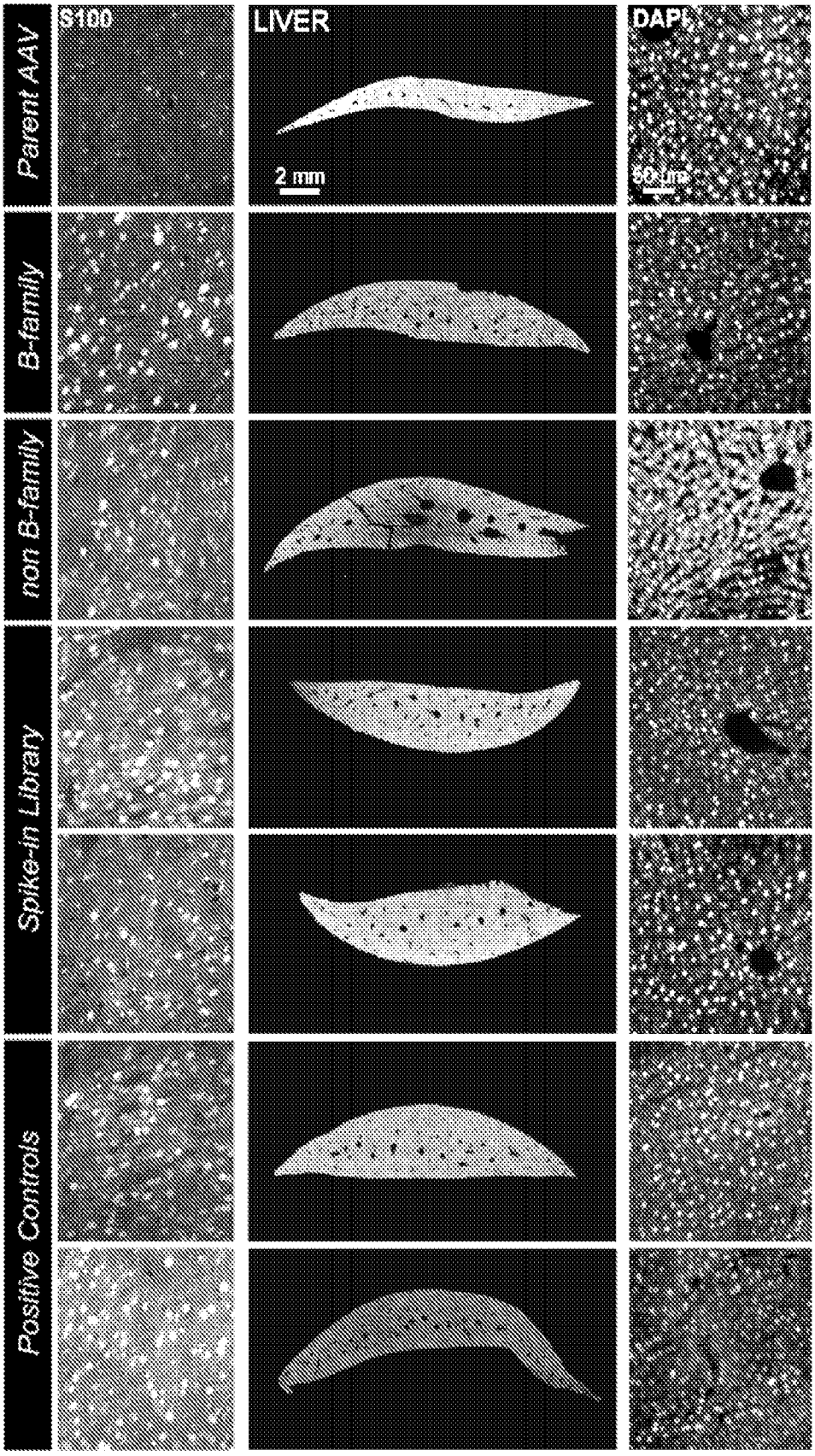


FIG. 20 (Continued)

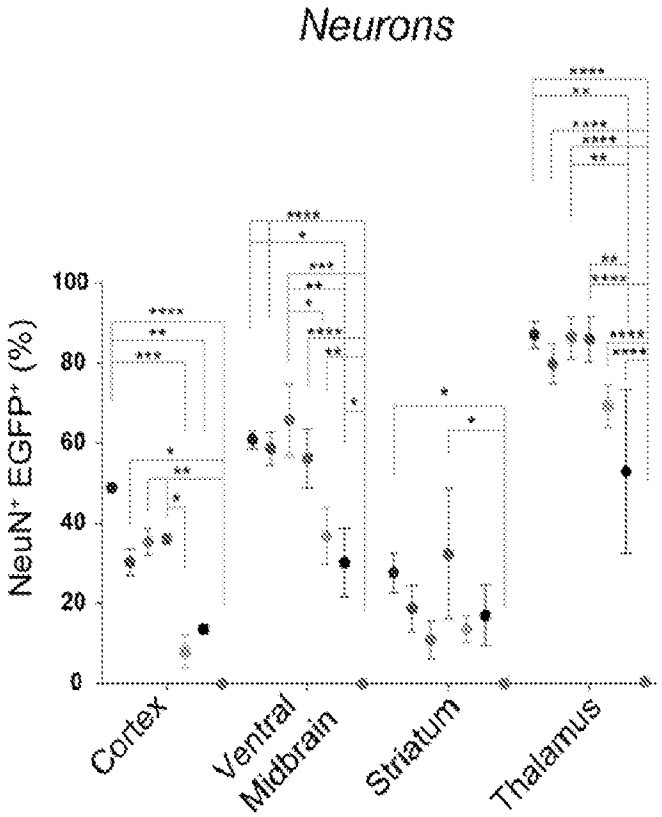

Neurons
NeuN⁺ EGFP⁺ (%)
100
80
60
40
20
0
Cortex
Ventral Midbrain
Striatum
Thalamus

FIG. 21

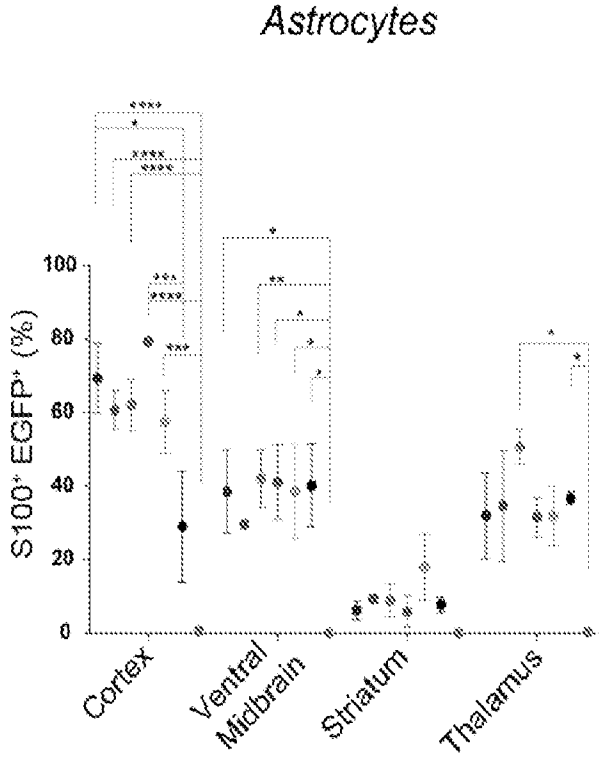

Astrocytes
S100⁺ EGFP⁺ (%)
100
80
60
40
20
0
Cortex
Ventral Midbrain
Striatum
Thalamus

FIG. 22

Oligodendrocyte lineage cells

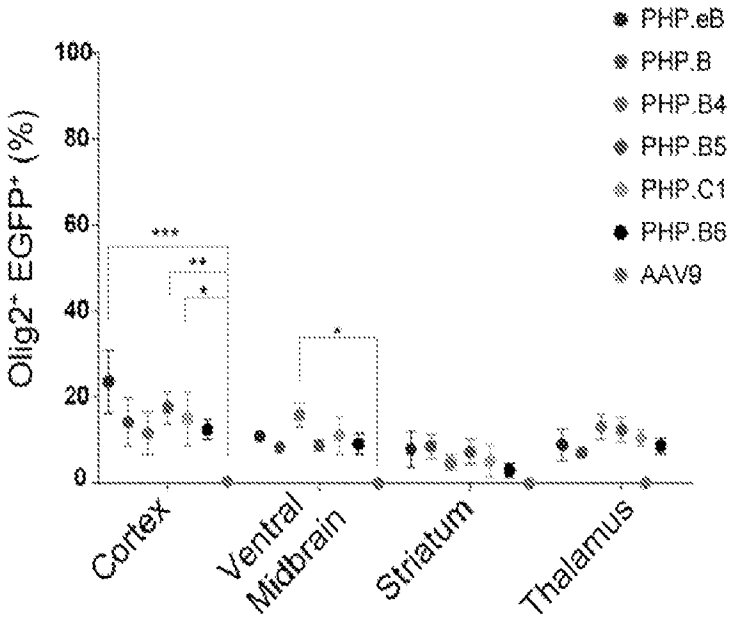


FIG. 23

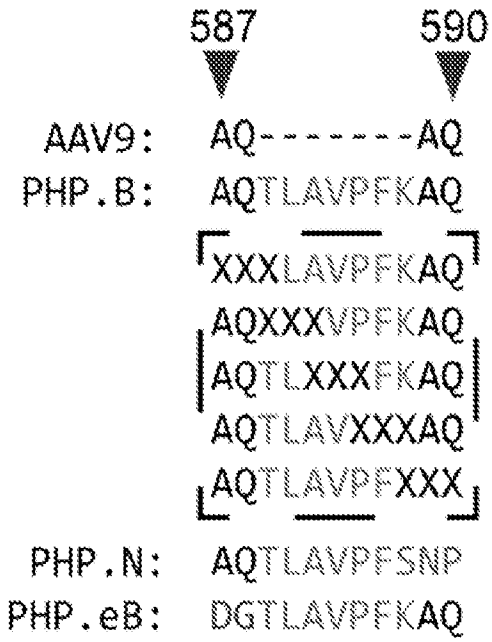


FIG. 24

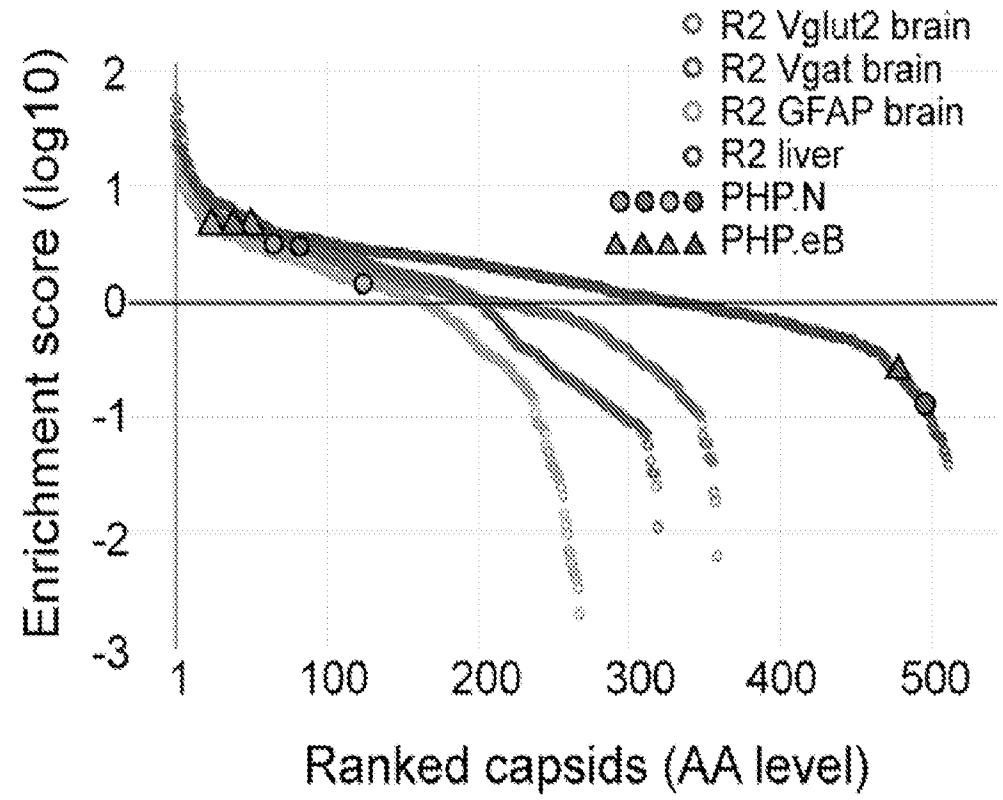

R2 Vglut2 brain
R2 Vgat brain
R2 GFAP brain
R2 liver
PHP.N
PHP.eB
Enrichment score (log10)
2
1
0
-1
-2
-3
1
100
200
300
400
500
Ranked capsids (AA level)

FIG. 25

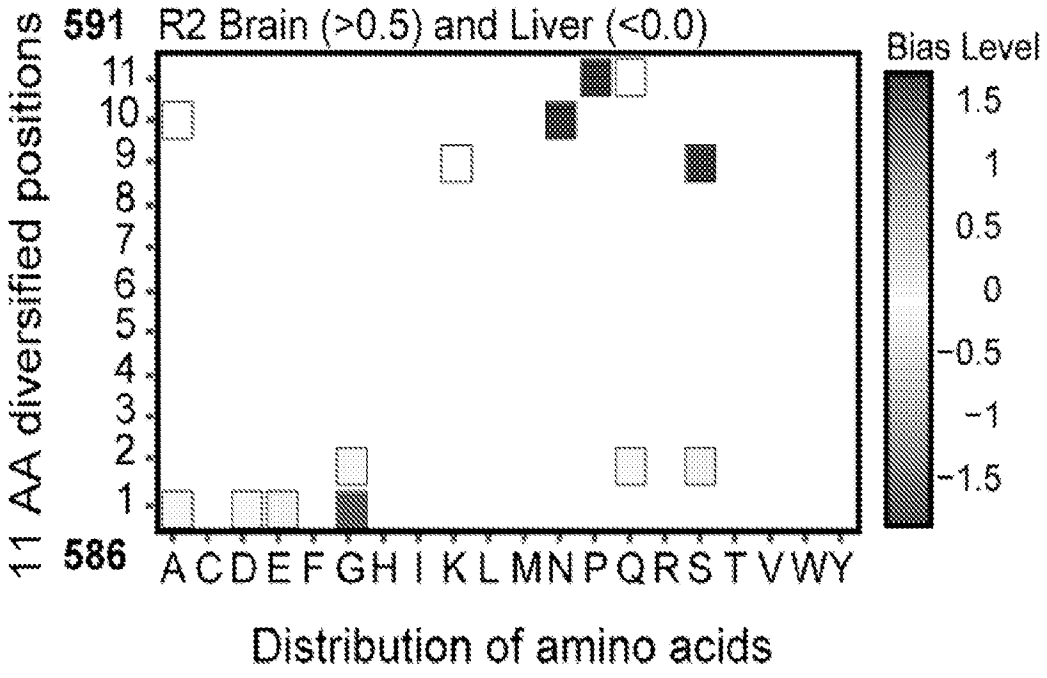

591
R2 Brain (>0.5) and Liver (<0.0)
Bias Level
1.5
1
0.5
0
-0.5
-1
-1.5
11 AA diversified positions
11
10
9
8
7
6
5
4
3
2
1
586
A C D E F G H I K L M N P Q R S T V W Y
Distribution of amino acids

FIG. 26

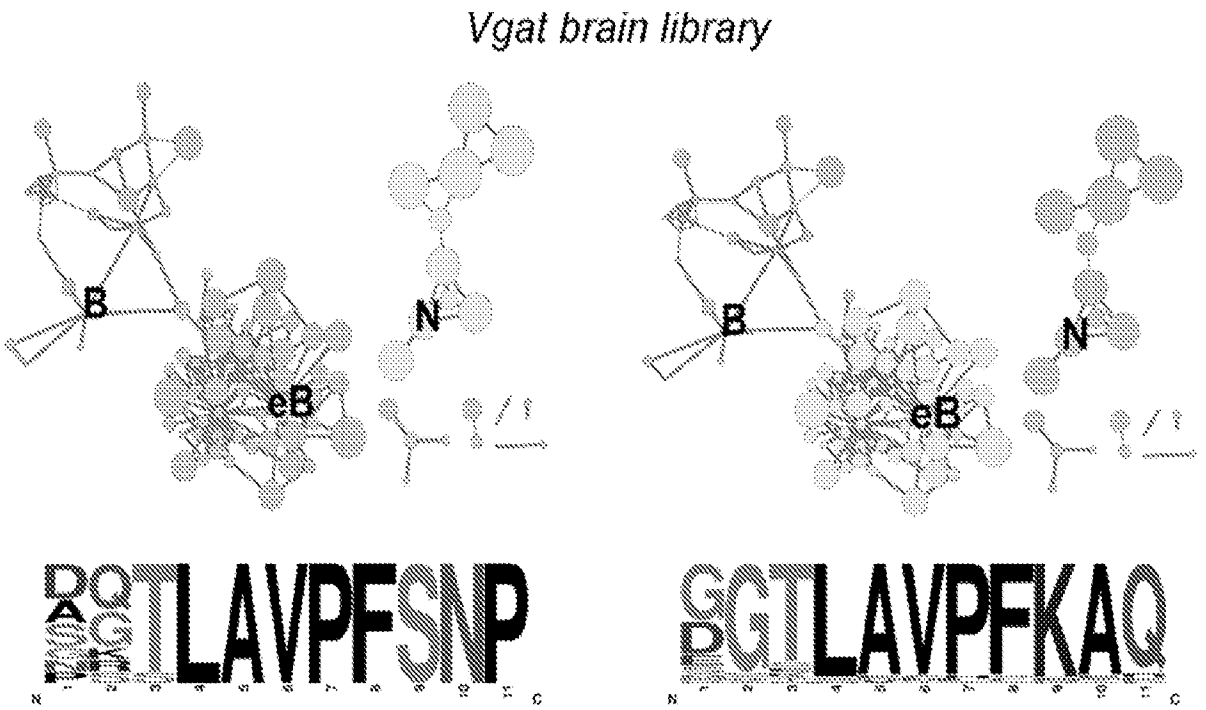

Vgat brain library
B
eB
N
B
eB
N
TLAVPFSNP
GTLAVPFKAQ

FIG. 27

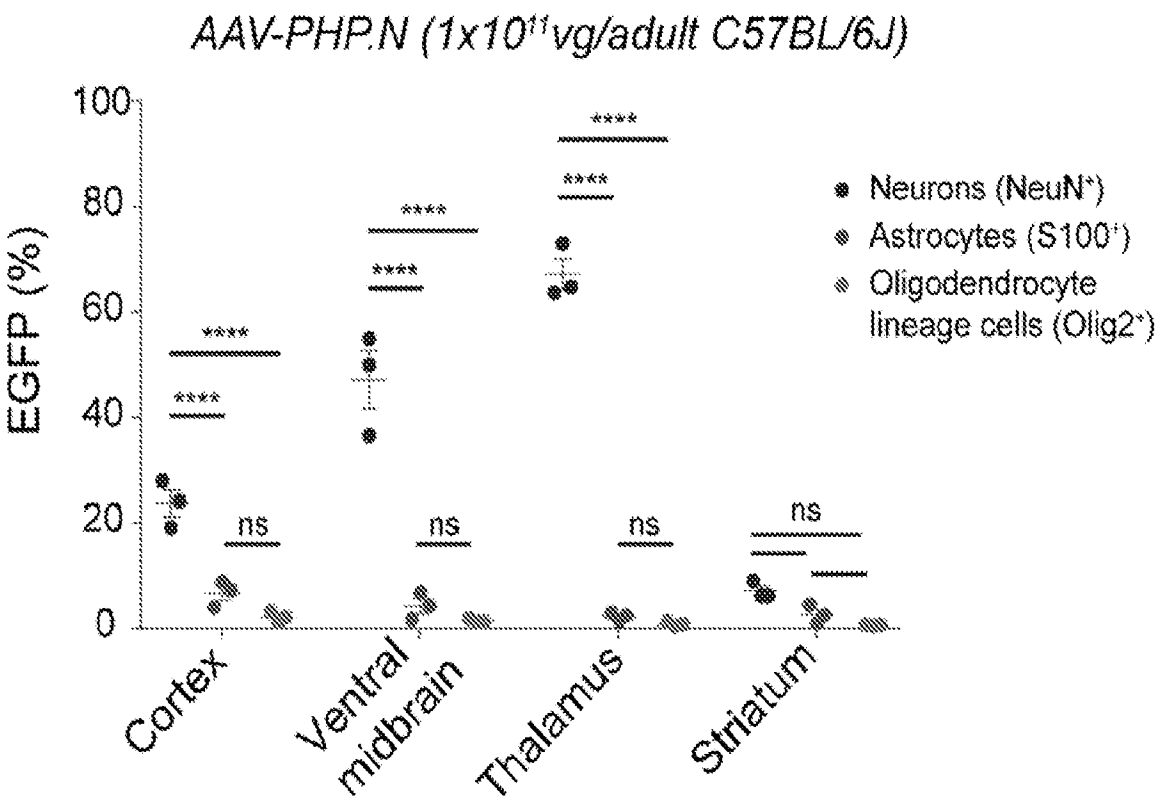

AAV-PHP.N (1x10^11vg/adult C57BL/6J)
EGFP (%)
100
80
60
40
20
0
****
****
****
****
****
****
ns
ns
ns
ns
Cortex
Ventral midbrain
Thalamus
Striatum
Neurons (NeuN+)
Astrocytes (S100+)
Oligodendrocyte lineage cells (Olig2+)

FIG. 28

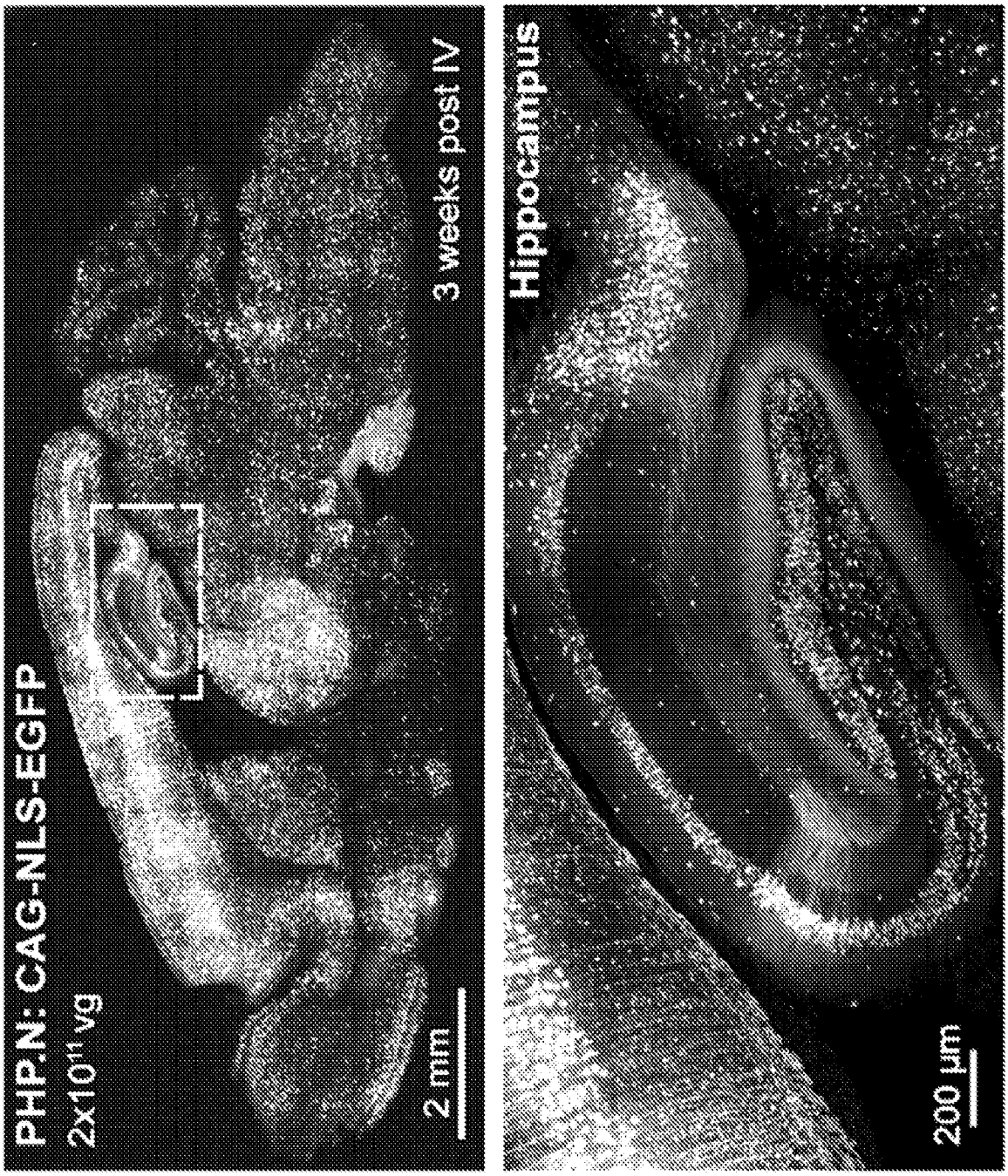

PHP.N: CAG-NLS-EGFP
2x10^11 vg
3 weeks post IV
2 mm
Hippocampus
200 µm

FIG. 29

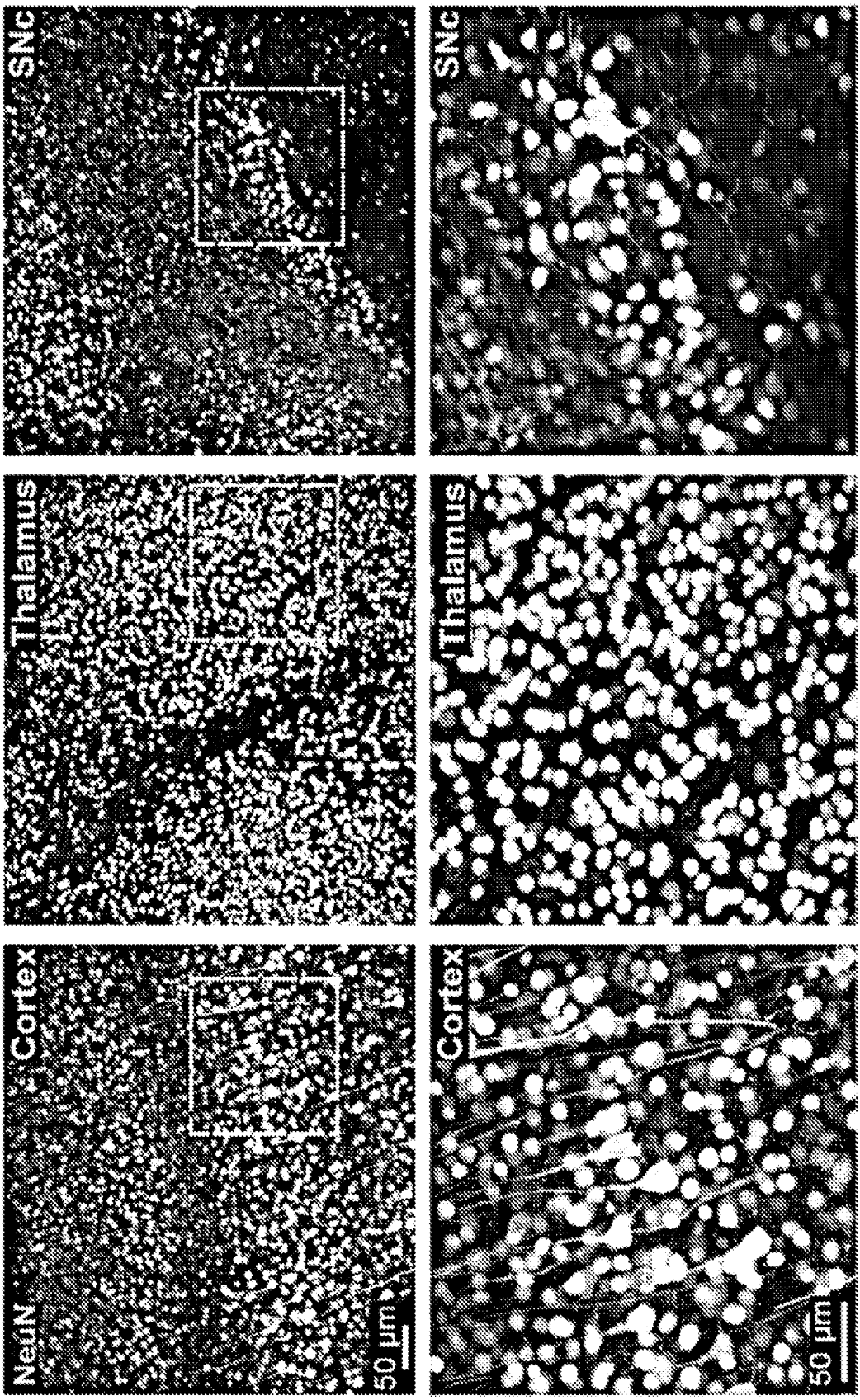
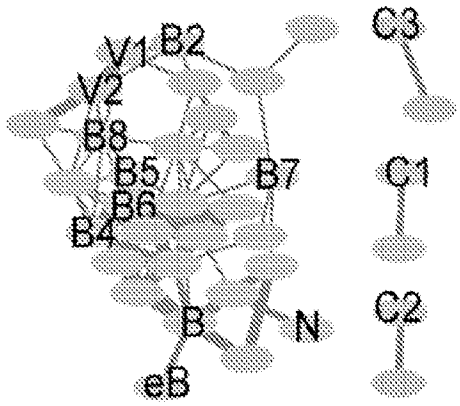


FIG. 29 (Continued)



	B3	588	589
AAV9:		AQ	AQ
PHP.V1:		AQTALKPFLAQ	
PHP.V2:		AQTTLKPFLAQ	
PHP.N:		AQTLAVPFSNP	
PHP.eB:		DGTLAVPFKAQ	
PHP.B:		AQTLAVPFKAQ	
PHP.B2:		AQSVSKPFLAQ	
PHP.B3:		AQFTLTTPKAQ	
PHP.B4:		AQTLQIPFKAQ	
PHP.B5:		AQTLQLPFKAQ	
PHP.B6:		AQTLQQPFKAQ	
PHP.B7:		AQSIERPFKAQ	
PHP.B8:		AQTMQKPFIAQ	
PHP.C1:		AQRYQGDSVAQ	
PHP.C2:		AQWSTNAGYAQ	
PHP.C3:		AQERVGFAQAQ	

FIG. 30

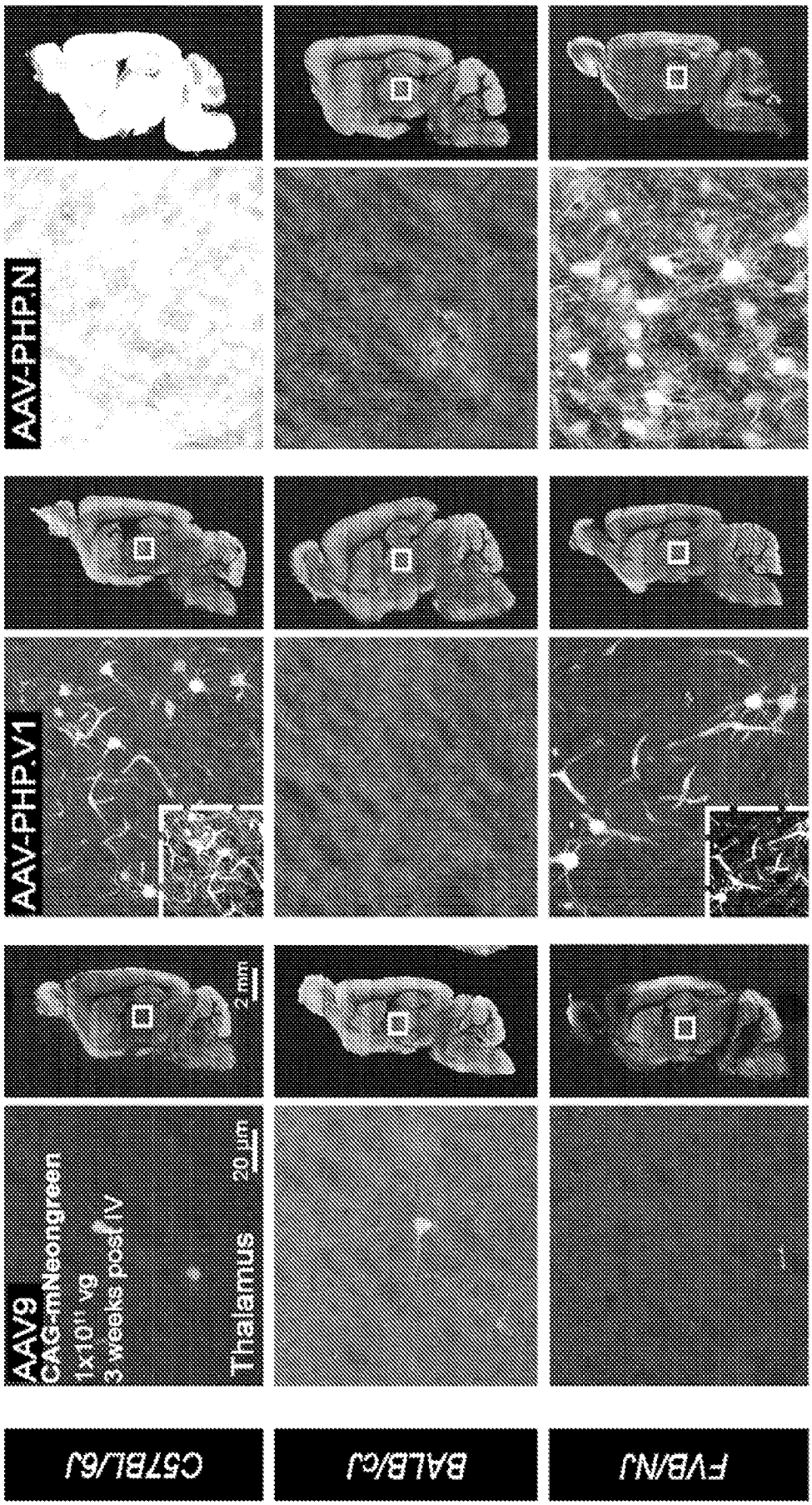

AAV9
CAG-mNeongreen
1x10^11 vg
3 weeks post IV
Thalamus
20 µm
2 mm
AAV-PHP.V1
AAV-PHP.N
C57BL/6J
BALB/cJ
FVB/NJ

FIG. 31

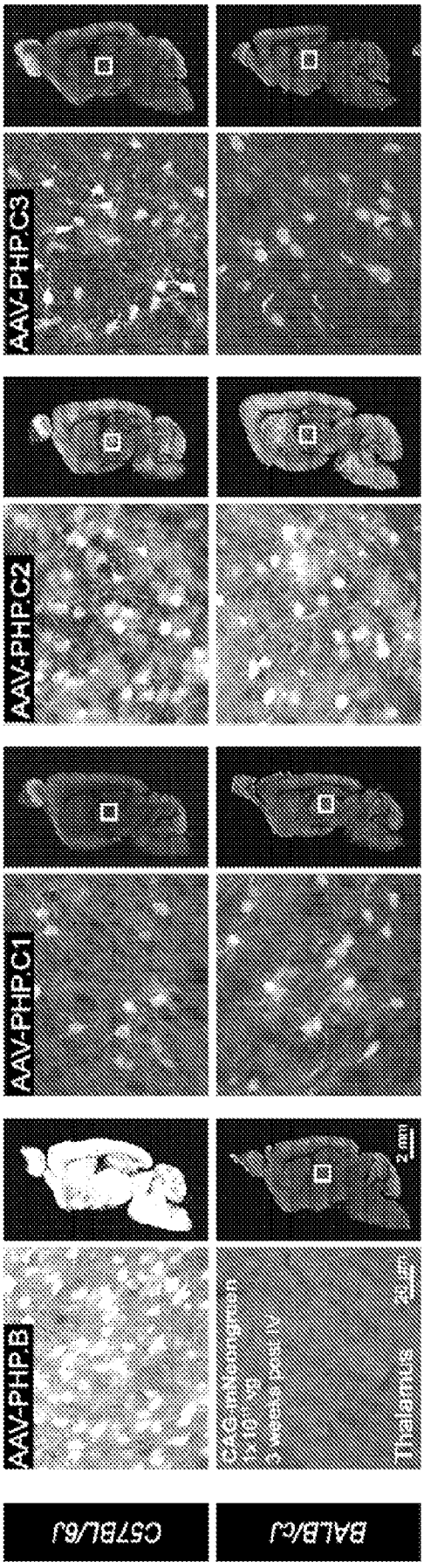

C57BL/6J
BALB/cJ
AAV-PHP.B
AAV-PHP.C1
AAV-PHP.C2
AAV-PHP.C3
2 mm
Thalamus

FIG. 32

Enrich_ rank (within libraries)	SEQ ID NO:	Sequence (for 11 mer AA)	SEQ ID NO:	11 mer Amino Acid	SEQ ID NO:	7 mer Amino acid	Brain-mean-enrichment score (log10)	Brain-mean-standardized-read count
SyS1	1074	GCCCAAACGTTGCAGATTCCTTTTAAGGCACAG	5663	AQTLQIPFKAQ	10252	TLQIPFK	2.730563	26.96166
TS1	1075	GCCCAAACCGCCCTCAAACCCTTCCTCGCACAG	5664	AQTALKPFLAQ	10253	TALKPFL	2.536397	6.252175
TS2	1076	GCCCAAACCACCCTCAAACCCTTCCTCGCACAG	5665	AQTTLKPFLAQ	10254	TTLKPFL	2.513839	10.4831
SyS2	1077	GCCCAAAGCATCGAAAGACCCTTCAAAGCACAG	5666	AQSIERPFKAQ	10255	SIERPFK	2.357132	30.18586
GS4	1078	GCCCAAACCCAAAACAGACCCTTCCTCGCACAG	5667	AQTQNRPFLAQ	10256	TQNRPFL	2.22812	8.911382
TS3	1079	GCCCAAACCATGCAAAAACCCTTCATCGCACAG	5668	AQTMQKPFIAQ	10257	TMQKPFI	2.165359	12.68417
GS5	1080	GCCCAAACTAGTACGCGGCCGTTTTTGGCACAG	5669	AQTSTRPFLAQ	10258	TSTRPFL	2.14357	7.139476
SyS5	1081	GCCCAAGGCACCTTCGTCCCCCCCACCGCACAG	5670	AQGTFVPPTAQ	10259	GTFVPPT	2.110151	7.82868
SyS6	1082	GCCCAATGGTCGACTAATGCGGGTTATGCACAG	5671	AQWSTNAGYAQ	10260	WSTNAGY	1.979177	10.16316
SyS9	1083	GCCCAAACCCTCGAAAGACCCTTCACCGCACAG	5672	AQTLERPFTAQ	10261	TLERPFT	1.892846	9.19788
SP1	1084	GCCCAAACTGCTGCTAAGCCGTTTCTGGCACAG	5673	AQTAAKPFLAQ	10262	TAAKPFL	1.863541	0.239884
GS8	1085	GCCCAAATTAGGATTGGTTATTCGCAGGCACAG	5674	AQIRIGYSQAQ	10263	IRIGYSQ	1.835644	2.556906
SyS10	1086	GCCCAAGAGCGTGTGGGTTTTGCTCAGGCACAG	5675	AQERVGFAQAQ	10264	ERVGFAQ	1.73803	5.438205
SyS12	1087	GCCCAAGCCGACCTCCTCAACTACAGAGCACAG	5676	AQADLLNYRAQ	10265	ADLLNYR	1.599571	1.410457
SyS13	1088	GCCCAACTCGTCGCCGGCTTCAGCCAAGCACAG	5677	AQLVAGFSQAQ	10266	LVAGFSQ	1.591793	6.106031
SyP5	1089	GCCCAATCGTCTCTGAAGCCTTTTCTGGCACAG	5678	AQSSLKPFLAQ	10267	SSLKPFL	1.574365	-0.00792
TS8	1090	GCCCAAACGCATTCTAGGCCGTTTATTGCACAG	5679	AQTHSRPFIAQ	10268	THSRPFI	1.566468	1.399717
GP3	1091	GCCCAACCTTTTCCTGGTTATTCTGCGGCACAG	5680	AQPFPGYSAAQ	10269	PFPGYSA	1.555967	0.122481
SyP6	1092	GCCCAAATTATTGTTGGGTATAGTCAGGCACAG	5681	AQIIVGYSQAQ	10270	IIVGYSQ	1.515858	-0.03845
SS12	1093	GCCCAAAGGTATCAGGGTGATTCTGTTGCACAG	5682	AQRYQGDSVAQ	10271	RYQGDSV	1.486197	2.200634
GS13	1094	GCCCAAAGGTATGCTGGGGATTCTATTGCACAG	5683	AQRYAGDSIAQ	10272	RYAGDSI	1.456352	2.513518
SyS15	1095	GCCCAAAAGACGATTGGGGAGCATTGGGCACAG	5684	AQKTIGEHWAQ	10273	KTIGEHW	1.44094	1.156576
SyS16	1096	GCCCAATGGATGACGCATGGTTCTGCGGCACAG	5685	AQWMTHGSAAQ	10274	WMTHGSA	1.432726	5.12209
GS16	1097	GCCCAAGCTGCTTCGAGGCCGTTTCTTGCACAG	5686	AQAASRPFLAQ	10275	AASRPFL	1.3791	1.903527

FIG. 33

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TP5	1098	GCCCAAACTACTTCTAGGCCGTTTCTTGCACAG	5687	AQTTSRPFLAQ	10276	TTSRPFL	1.353519	-0.09501
SyS17	1099	GCCCAAGCTCGTGTGGGTTTGGCTCAGGCACAG	5688	AQARVGLAQAQ	10277	ARVGLAQ	1.345499	1.982916
GP5	1100	GCCCAAGGGACTAGTCCGAATCTTGCGGCACAG	5689	AQGTSPNLAAQ	10278	GTSPNLA	1.306429	0.315395
SyS19	1101	GCCCAAGTGCGTACGGGGTATAGTTCTGCACAG	5690	AQVRTGYSSAQ	10279	VRTGYSS	1.302979	4.055383
SyS20	1102	GCCCAAATTCGGGTGGGGTATAGTTCTGCACAG	5691	AQIRVGYSSAQ	10280	IRVGYSS	1.286795	1.856458
TP6	1103	GCCCAAACTACTTTGCGTCCGTTTATTGCACAG	5692	AQTTLRPFIAQ	10281	TTLRPFI	1.284391	-0.12323
SyP9	1104	GCCCAAGGTATTACGTCTCTGTTTAAGGCACAG	5693	AQGITSLFKAQ	10282	GITSLFK	1.251837	0.032947
SyS21	1105	GCCCAAACCACCCAAACCCCCTTCAGAGCACAG	5694	AQTTQTPFRAQ	10283	TTQTPFR	1.192121	2.176002
TP8	1106	GCCCAAACTGTGTCGAGGCCGTTTTTGGCACAG	5695	AQTVSRPFLAQ	10284	TVSRPFL	1.171604	-0.12785
SyP11	1107	GCCCAATATGGGACGAATCCGTTTCGTGCACAG	5696	AQYGTNPFRAQ	10285	YGTNPFR	1.13664	-0.03961
SyS25	1108	GCCCAACCCACCATGGTCGACAGCAGCGCACAG	5697	AQPTMVDSSAQ	10286	PTMVDSS	1.099202	0.266059
GP9	1109	GCCCAAAATAAGGCTAGTTCTCAGAATGCACAG	5698	AQNKASSQNAQ	10287	NKASSQN	1.084711	0.150465
GP10	1110	GCCCAAACTTTTCGTAGTTCGAATGATGCACAG	5699	AQTFRSSNDAQ	10288	TFRSSND	1.032118	0.297543
GP11	1111	GCCCAACTGCCGGATCGTTATCCTAATGCACAG	5700	AQLPDRYPNAQ	10289	LPDRYPN	1.019382	0.311223
GP12	1112	GCCCAACAGAATGTTACGAAGGGTGTTGCACAG	5701	AQQNVTKGVAQ	10290	QNVTKGV	1.000865	0.069558
SyS26	1113	GCCCAAGCTCAGTCTCCGATTCTTCGGGCACAG	5702	AQAQSPILRAQ	10291	AQSPILR	0.979922	0.194304
SyS27	1114	GCCCAAGTGGCTACTGGTTATTCTTCGGCACAG	5703	AQVATGYSSAQ	10292	VATGYSS	0.978116	1.060347
GP13	1115	GCCCAATTGAATTCGAATCGGCCTAATGCACAG	5704	AQLNSNRPNAQ	10293	LNSNRPN	0.9672	0.275423
GP14	1116	GCCCAAACGATTCGTAATAATACGATTGCACAG	5705	AQTIRNNTIAQ	10294	TIRNNTI	0.959641	0.134651
SyP21	1117	GCCCAAGATCTTAGTCGTATTTTTAAGGCACAG	5706	AQDLSRIFKAQ	10295	DLSRIFK	0.950386	0.011306
SyS28	1118	GCCCAACTCAGCAACAGCGCCAGCCAAGCACAG	5707	AQLSNSASQAQ	10296	LSNSASQ	0.941212	0.142825
SyS29	1119	GCCCAACTCGAAAACATGGTCATGAGCGCACAG	5708	AQLENMVMSAQ	10297	LENMVMS	0.937552	0.152227
SyS30	1120	GCCCAATTGACTCAGCAGACGGATGTTGCACAG	5709	AQLTQQTDVAQ	10298	LTQQTDV	0.936974	0.055201
SyS31	1121	GCCCAAGCCGGCCTCGCCCACGCCACCGCACAG	5710	AQAGLAHATAQ	10299	AGLAHAT	0.936046	0.0038
SyS32	1122	GCCCAAAATGCTCATACTGCGCTGGATGCACAG	5711	AQNAHTALDAQ	10300	NAHTALD	0.933184	0.121259
TP14	1123	GCCCAATGGCCGATTCTTCGGGCTGATGCACAG	5712	AQWPILRADAQ	10301	WPILRAD	0.931545	-0.12619
GP15	1124	GCCCAAGCGCTGGCTGGTCTGTCTCTGGCACAG	5713	AQALAGLSLAQ	10302	ALAGLSL	0.930454	0.12621
GS21	1125	GCCCAACGTATTGATATGCCTTTTAAGGCACAG	5714	AQRIDMPFKAQ	10303	RIDMPFK	0.920205	0.015073
GP16	1126	GCCCAAACGATGTCGTTGAGTAGTAGTGCACAG	5715	AQTMSLSSSAQ	10304	TMSLSSS	0.919718	0.304165
GS23	1127	GCCCAACAAAACGTCGCCAAAAACCTCGCACAG	5716	AQQNVAKNLAQ	10305	QNVAKNL	0.916602	0.813873
SyS33	1128	GCCCAATTCGACAACCCCAACAACGTCGCACAG	5717	AQFDNPNNVAQ	10306	FDNPNNV	0.915503	0.086072
GS24	1129	GCCCAAGTCCTCATGAGAGAAAGCCTCGCACAG	5718	AQVLMRESLAQ	10307	VLMRESL	0.914386	0.141782

FIG. 33 (Continued)

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SyS34	1130	GCCCAACACCACGACACCGGCAGCGCCGCACAG	5719	AQHHDTGSAAQ	10308	HHDTGSA	0.912951	-0.01452
GP17	1131	GCCCAAGATGCGCCGAATAGTGTGGATGCACAG	5720	AQDAPNSVDAQ	10309	DAPNSVD	0.901999	0.074694
GP18	1132	GCCCAAACTGCGAGTAGGGATGCTAAGGCACAG	5721	AQTASRDAKAQ	10310	TASRDAK	0.889552	0.305208
TS16	1133	GCCCAAACTAATTATACGAAGCAGATTGCACAG	5722	AQTNYTKQIAQ	10311	TNYTKQI	0.889024	1.292832
GP20	1134	GCCCAACCTCATAATGCTTCTGTGTTGGCACAG	5723	AQPHNASVLAQ	10312	PHNASVL	0.864707	0.119015
TS17	1135	GCCCAAACCAACAACACCAGAAACATCGCACAG	5724	AQTNNTRNIAQ	10313	TNNTRNI	0.862873	3.066317
GP21	1136	GCCCAAATGGTTCCTAATCATTCTGGTGCACAG	5725	AQMVPNHSGAQ	10314	MVPNHSG	0.859604	0.10671
SyS36	1137	GCCCAACCGGTGCCGCAGTCTGAGCATGCACAG	5726	AQPVPQSEHAQ	10315	PVPQSEH	0.852761	0.005712
SyS37	1138	GCCCAACTCTACCACGGCGGCAGCACCGCACAG	5727	AQLYHGGSTAQ	10316	LYHGGST	0.851158	1.723386
GP22	1139	GCCCAAATGATTCATACTAGGGAGACGGCACAG	5728	AQMIHTRETAQ	10317	MIHTRET	0.850116	0.21081
TS18	1140	GCCCAAACTAATAATACGAAGCCTCTTGCACAG	5729	AQTNNTKPLAQ	10318	TNNTKPL	0.849557	1.523
TS20	1141	GCCCAACTCAACACCACCAGAAACACCGCACAG	5730	AQLNTTRNTAQ	10319	LNTTRNT	0.839304	2.098399
GP24	1142	GCCCAAGCTTTGCATAATTCTCAGAATGCACAG	5731	AQALHNSQNAQ	10320	ALHNSQN	0.827469	0.061402
TS21	1143	GCCCAAGTGAATAGTACGAGGAATGTTGCACAG	5732	AQVNSTRNVAQ	10321	VNSTRNV	0.826565	1.260315
GP25	1144	GCCCAAGGTGTTGGGGTTGTTACGAAGGCACAG	5733	AQGVGVVTKAQ	10322	GVGVVTK	0.820556	0.292663
GP26	1145	GCCCAAGTTTTGTCGAAGCAGTTGGCTGCACAG	5734	AQVLSKQLAAQ	10323	VLSKQLA	0.816495	0.216922
SyS38	1146	GCCCAATCTAAGTCTCTGCAGCCGTTGGCACAG	5735	AQSKSLQPLAQ	10324	SKSLQPL	0.815502	-0.01826
TS22	1147	GCCCAATCGAATTCTACGCGGTTGGTTGCACAG	5736	AQSNSTRLVAQ	10325	SNSTRLV	0.815119	1.172623
TS23	1148	GCCCAACTCAACCAAACCAAACAAATCGCACAG	5737	AQLNQTKQIAQ	10326	LNQTKQI	0.811665	0.576331
TS24	1149	GCCCAAAACAACAGCGTCAGACAACTCGCACAG	5738	AQNNSVRQLAQ	10327	NNSVRQL	0.806765	2.286879
SyS40	1150	GCCCAAATGTCGGGGTATTCGCATACTGCACAG	5739	AQMSGYSHTAQ	10328	MSGYSHT	0.804194	-0.01048
GS26	1151	GCCCAAGTCAAAGTCCCCATCATCACCGCACAG	5740	AQVKVPIITAQ	10329	VKVPIIT	0.799412	-0.10413
TS25	1152	GCCCAAGGGAATAATACTCGGGCGGTGGCACAG	5741	AQGNNTRAVAQ	10330	GNNTRAV	0.797634	1.315071
TS26	1153	GCCCAACAGAATCAGATTAAGAATATTGCACAG	5742	AQQNQIKNIAQ	10331	QNQIKNI	0.797303	0.74103
TS27	1154	GCCCAAACCAACATGACCAAACCCCTCGCACAG	5743	AQTNMTKPLAQ	10332	TNMTKPL	0.791064	0.75073
TS28	1155	GCCCAAAACAACAGCACCAGACTCAGCGCACAG	5744	AQNNSTRLSAQ	10333	NNSTRLS	0.790429	1.381045
SyS41	1156	GCCCAAAGCATGCTCACCAGCATCGTCGCACAG	5745	AQSMLTSIVAQ	10334	SMLTSIV	0.790252	0.060228
SyS42	1157	GCCCAACTCAACGCCACCGCCAGCAGAGCACAG	5746	AQLNATASRAQ	10335	LNATASR	0.785269	1.621315
SyS43	1158	GCCCAAAATACTGGGGTGCAGGTTAGGGCACAG	5747	AQNTGVQVRAQ	10336	NTGVQVR	0.785026	-0.11955
TS29	1159	GCCCAAACCAACACCGTCAGACCCATCGCACAG	5748	AQTNTVRPIAQ	10337	TNTVRPI	0.780569	1.015192
SyP24	1160	GCCCAACAGTCTACGCCGGGGGCTACTGCACAG	5749	AQQSTPGATAQ	10338	QSTPGAT	0.779842	-0.03057
SP19	1161	GCCCAAGGTCATTCTGAGAATTCTCGTGCACAG	5750	AQGHSENSRAQ	10339	GHSENSR	0.778724	-0.03149

FIG. 33 (Continued)

SyS44	1162	GCCCAACTCCCCACCCAAACCCTCAGAGCACAG	5751	AQLPTQTLRAQ	10340	LPTQTLR	0.773756	0.51102
GS27	1163	GCCCAAAAGAATGCTCCGATGCCTGATGCACAG	5752	AQKNAPMPDAQ	10341	KNAPMPD	0.772397	0.130152
TS31	1164	GCCCAAAGCAACAGCACCAAACCCACCGCACAG	5753	AQSNSTKPTAQ	10342	SNSTKPT	0.768053	2.108136
SyS45	1165	GCCCAACCTATTATTACTATGCCTGCTGCACAG	5754	AQPIITMPAAQ	10343	PIITMPA	0.767318	-0.10299
GS28	1166	GCCCAACCCCTCAAAGGCATCGGCAGCGCACAG	5755	AQPLKGIGSAQ	10344	PLKGIGS	0.767253	-0.07052
GS29	1167	GCCCAAGTCCTCAGCGTCAACCACCTCGCACAG	5756	AQVLSVNHLAQ	10345	VLSVNHL	0.765014	0.050802
SyS46	1168	GCCCAAAGTGTGGCTGCTGTGCATATGGCACAG	5757	AQSVAAVHMAQ	10346	SVAAVHM	0.764013	0.277236
TS32	1169	GCCCAAAGCAACAGCATCAGACTCGTCGCACAG	5758	AQSNSIRLVAQ	10347	SNSIRLV	0.763114	1.058208
TS33	1170	GCCCAACATAATGATACTCGTCCTCTTGCACAG	5759	AQHNDTRPLAQ	10348	HNDTRPL	0.759962	-0.04126
GS31	1171	GCCCAACCTCCGGTGAGGTCTACGGCTGCACAG	5760	AQPPVRSTAAQ	10349	PPVRSTA	0.755777	-0.09946
TS34	1172	GCCCAAATGAACACCGTCAGAAACCTCGCACAG	5761	AQMNTVRNLAQ	10350	MNTVRNL	0.754463	1.394996
GS32	1173	GCCCAATTGACGGATGGTCATCGGATTGCACAG	5762	AQLTDGHRIAQ	10351	LTDGHRI	0.754429	0.32562
TS35	1174	GCCCAAACGAATGCGGTGAAGCTGACTGCACAG	5763	AQTNAVKLTAQ	10352	TNAVKLT	0.752766	1.157992
SyS48	1175	GCCCAACGTGTGGATGCGGTTTTGAGTGCACAG	5764	AQRVDAVLSAQ	10353	RVDAVLS	0.750458	0.650222
TS36	1176	GCCCAAACCAACGCCGTCAAAAGCACCGCACAG	5765	AQTNAVKSTAQ	10354	TNAVKST	0.749271	1.812411
SyS49	1177	GCCCAAATGCTCAACACCACCGCCAGAGCACAG	5766	AQMLNTTARAQ	10355	MLNTTAR	0.747921	2.456673
TS37	1178	GCCCAAGGCAACAACACCAGACCCACCGCACAG	5767	AQGNNTRPTAQ	10356	GNNTRPT	0.747523	1.945144
GP29	1179	GCCCAACAGTCTGGGGGTAGTGCGTTGGCACAG	5768	AQQSGGSALAQ	10357	QSGGSAL	0.744332	0.320051
SyS50	1180	GCCCAAGTGATTGCTTTGTCTACTATGGCACAG	5769	AQVIALSTMAQ	10358	VIALSTM	0.743901	-0.08342
TS38	1181	GCCCAACTGAATACGATTCGGAATGTGGCACAG	5770	AQLNTIRNVAQ	10359	LNTIRNV	0.743811	0.509953
TS39	1182	GCCCAAAGCAACGCCACCAGAAGCGTCGCACAG	5771	AQSNATRSVAQ	10360	SNATRSV	0.740235	2.030618
TS40	1183	GCCCAAGGCAACGGCACCAAATTCATCGCACAG	5772	AQGNGTKFIAQ	10361	GNGTKFI	0.736944	0.870325
TS41	1184	GCCCAAAGCAACACCATCAGACCCGTCGCACAG	5773	AQSNTIRPVAQ	10362	SNTIRPV	0.736197	0.921801
TS42	1185	GCCCAAAGCAACAGCACCAGAGCCATCGCACAG	5774	AQSNSTRAIAQ	10363	SNSTRAI	0.734716	1.769995
SyS51	1186	GCCCAATTTCATTTGACTGATAGGGGTGCACAG	5775	AQFHLTDRGAQ	10364	FHLTDRG	0.733831	-0.11858
GS33	1187	GCCCAACCGATTAGGTCGGATACTGTGGCACAG	5776	AQPIRSDTVAQ	10365	PIRSDTV	0.731286	-0.03233
GS34	1188	GCCCAAGCCAACCAAATCCACAACACCGCACAG	5777	AQANQIHNTAQ	10366	ANQIHNT	0.730071	1.693251
TS44	1189	GCCCAATCGAATACGGTTCGGAATACTGCACAG	5778	AQSNTVRNTAQ	10367	SNTVRNT	0.727807	1.688407
SyS52	1190	GCCCAAACCAGCCTCGGCTACAGCAGCGCACAG	5779	AQTSLGYSSAQ	10368	TSLGYSS	0.727167	0.736367
SyS53	1191	GCCCAAATCAGCGGCGTCCAAACCAGAGCACAG	5780	AQISGVQTRAQ	10369	ISGVQTR	0.724309	-0.03855
TS45	1192	GCCCAATCGAATGCTGTTAGGCAGACTGCACAG	5781	AQSNAVRQTAQ	10370	SNAVRQT	0.72361	1.522098
SyS54	1193	GCCCAATCTCTTTCTGAGCTTAGGATTGCACAG	5782	AQSLSELRIAQ	10371	SLSELRI	0.723061	-0.02338

FIG. 33 (Continued)

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SyS55	1194	GCCCAAAGTACTGAGAAGAGGGATGAGGCACAG	5783	AQSTEKRDEAQ	10372	STEKRDE	0.721349	0.390249
SyS56	1195	GCCCAAAACCTCGTCGGCACCCTCATCGCACAG	5784	AQNLVGTLIAQ	10373	NLVGTLI	0.72103	-0.05799
TS46	1196	GCCCAAGGCAACAACATCAGACTCACCGCACAG	5785	AQGNNIRLTAQ	10374	GNNIRLT	0.719643	1.815768
SyS57	1197	GCCCAAGCCGTCCCCACCGGCCTCAGAGCACAG	5786	AQAVPTGLRAQ	10375	AVPTGLR	0.717951	0.29549
SyS58	1198	GCCCAAGGTGATAATAGTCTGACTAGGGCACAG	5787	AQGDNSLTRAQ	10376	GDNSLTR	0.717624	0.075033
SyS59	1199	GCCCAACACGCCGACAACAGACTCAAAGCACAG	5788	AQHADNRLKAQ	10377	HADNRLK	0.714815	-0.04579
TS47	1200	GCCCAAAGCAACGCCACCAGAAACTTCGCACAG	5789	AQSNATRNFAQ	10378	SNATRNF	0.714052	1.193285
TS48	1201	GCCCAAGGGAATACGACTAGGGGGCTGGCACAG	5790	AQGNTTRGLAQ	10379	GNTTRGL	0.713945	1.078842
SyS60	1202	GCCCAACTCAACCTCACCGCCACCAACGCACAG	5791	AQLNLTATNAQ	10380	LNLTATN	0.71358	0.152602
SyS61	1203	GCCCAAAGCGGCGTCAGCACCACCGACGCACAG	5792	AQSGVSTTDAQ	10381	SGVSTTD	0.711249	-0.01534
GP31	1204	GCCCAATATGCTAAGACGTTGGCTATGGCACAG	5793	AQYAKTLAMAQ	10382	YAKTLAM	0.710703	0.312387
TS49	1205	GCCCAAATGAACCACACCAAACCCACCGCACAG	5794	AQMNHTKPTAQ	10383	MNHTKPT	0.710702	1.058209
TS50	1206	GCCCAAGCTAATGCTACGAGGAATTCTGCACAG	5795	AQANATRNSAQ	10384	ANATRNS	0.707423	0.724059
TS51	1207	GCCCAACAAAACCAAACCAAATCACCGCACAG	5796	AQQNQTKITAQ	10385	QNQTKIT	0.707235	1.179467
TS52	1208	GCCCAATCTAATGCTATTAAGGCTACGGCACAG	5797	AQSNAIKATAQ	10386	SNAIKAT	0.70699	0.910476
SyS62	1209	GCCCAATATCCTGATAATTATGGTAAGGCACAG	5798	AQYPDNYGKAQ	10387	YPDNYGK	0.706343	0.147368
TS53	1210	GCCCAAGGCAACACCACCATCAGAAGCGCACAG	5799	AQGNTTIRSAQ	10388	GNTTIRS	0.705947	1.078768
SyP28	1211	GCCCAACTGGGTCTTACGGGTGCGGTTGCACAG	5800	AQLGLTGAVAQ	10389	LGLTGAV	0.705628	-0.04044
TS54	1212	GCCCAAGCGAATAGTACGCGTATTCTGGCACAG	5801	AQANSTRILAQ	10390	ANSTRIL	0.704068	1.203143
TS55	1213	GCCCAAGATAATGCGATTCGTGCGCAGGCACAG	5802	AQDNAIRAQAQ	10391	DNAIRAQ	0.703945	0.267003
TS56	1214	GCCCAAACGAATTATACTAAGCTTATGGCACAG	5803	AQTNYTKLMAQ	10392	TNYTKLM	0.702916	0.470577
GS38	1215	GCCCAACATAATAGTCCTAGTAGTTATGCACAG	5804	AQHNSPSSYAQ	10393	HNSPSSY	0.70154	-0.08846
TS57	1216	GCCCAAGAGAATATGGTTCGGTCTGTGGCACAG	5805	AQENMVRSVAQ	10394	ENMVRSV	0.700139	0.554646
TS58	1217	GCCCAAACCAACAACATCAAAAGCTACGCACAG	5806	AQTNNIKSYAQ	10395	TNNIKSY	0.698201	1.233802
TS59	1218	GCCCAAACTAATTCGACGAGAGGCCTGTGGCACAG	5807	AQTNSTRPVAQ	10396	TNSTRPV	0.696679	0.516411
GP34	1219	GCCCAACATACGGCTCCGCCTCATCCTGCACAG	5808	AQHTAPPHPAQ	10397	HTAPPHP	0.695156	-0.01516
SyS63	1220	GCCCAAGCCCTCAGCCAAAACACCAGCGCACAG	5809	AQALSQNTSAQ	10398	ALSQNTS	0.692869	0.222209
TS60	1221	GCCCAACCGAATGTGACTAAGAATGCTGCACAG	5810	AQPNVTKNAAQ	10399	PNVTKNA	0.692038	-0.01089
GP36	1222	GCCCAACTTGATACGCTGACGGGTTATGCACAG	5811	AQLDTLTGYAQ	10400	LDTLTGY	0.690142	0.248937
TS61	1223	GCCCAACCTAATAGTGTGCGTTCTGTTGCACAG	5812	AQPNSVRSVAQ	10401	PNSVRSV	0.689082	0.294508
SyS64	1224	GCCCAAACCAGCAGCCACCTCCCCCACGCACAG	5813	AQTSSHLPHAQ	10402	TSSHLPH	0.688469	0.465642
GS40	1225	GCCCAAGTTCTTCATGGTGGTAATGATGCACAG	5814	AQVLHGGNDAQ	10403	VLHGGND	0.687991	0.121136

FIG. 33 (Continued)

TS62	1226	GCCCAAAGCAACTACGTCAAAAGCGCCGCACAG	5815	AQSNYVKSAAQ	10404	SNYVKSA	0.687276	0.620002
TS63	1227	GCCCAAGACAACAACAGCACCAGATGGGCACAG	5816	AQDNNSTRWAQ	10405	DNNSTRW	0.687057	0.34274
GP37	1228	GCCCAAACTGTGATGAAGGGTTTTACTGCACAG	5817	AQTVMKGFTAQ	10406	TVMKGFT	0.687036	0.307342
SyS65	1229	GCCCAAAGCCACACCCTCAGCACCCTCGCACAG	5818	AQSHTLSTLAQ	10407	SHTLSTL	0.686592	0.104749
SyS66	1230	GCCCAACCTGGTCCTCAGCAGGCGAAGGCACAG	5819	AQPGPQQAKAQ	10408	PGPQQAK	0.685365	0.364455
GS41	1231	GCCCAAACTTTTGGGACGTCTAAGTTGGCACAG	5820	AQTFGTSKLAQ	10409	TFGTSKL	0.684153	0.041123
SyS67	1232	GCCCAAAGCAACGCCGTCACCAACAGAGCACAG	5821	AQSNAVTNRAQ	10410	SNAVTNR	0.683838	2.350107
GP38	1233	GCCCAATTGTCTATGTCGACGGTGCCTGCACAG	5822	AQLSMSTVPAQ	10411	LSMSTVP	0.682136	0.463832
GS42	1234	GCCCAAAGGCGTTATGATGGTAGGGAGGCACAG	5823	AQRRYDGREAQ	10412	RRYDGRE	0.681722	-0.04926
TS64	1235	GCCCAAACCAACAGCACCAAAAACATCGCACAG	5824	AQTNSTKNIAQ	10413	TNSTKNI	0.678439	2.312433
GS43	1236	GCCCAAATTAATGCTCAGTGGTCTGCGGCACAG	5825	AQINAQWSAAQ	10414	INAQWSA	0.672085	0.020513
SyS68	1237	GCCCAAGCCCAAACCAGCAACGACCCCGCACAG	5826	AQAQTSNDPAQ	10415	AQTSNDP	0.669325	0.289379
TS65	1238	GCCCAAACGAATGAGACTAGGATGGTGGCACAG	5827	AQTNETRMVAQ	10416	TNETRMV	0.669307	0.50614
TS66	1239	GCCCAAGCCAACGCCACCAGAGGCGTCGCACAG	5828	AQANATRGVAQ	10417	ANATRGV	0.667153	0.206293
SyS69	1240	GCCCAAGCGGATGTGAATGCTTCGGGTGCACAG	5829	AQADVNASGAQ	10418	ADVNASG	0.666574	-0.04779
GP39	1241	GCCCAACTTAGTGAGCGGAATTATGTGGCACAG	5830	AQLSERNYVAQ	10419	LSERNYV	0.665675	0.088761
GP40	1242	GCCCAAAGTGGTGAGCTTGCGCGGGCGGCACAG	5831	AQSGELARAAQ	10420	SGELARA	0.663381	0.117091
TS67	1243	GCCCAAGGGAATACTGCTAAGAATATTGCACAG	5832	AQGNTAKNIAQ	10421	GNTAKNI	0.662988	0.420415
TS68	1244	GCCCAAGACAACGCCGTCAGACCCCTCGCACAG	5833	AQDNAVRPLAQ	10422	DNAVRPL	0.662435	0.259838
SyS70	1245	GCCCAAATGATGCTCAGCGGCCTCAACGCACAG	5834	AQMMLSGLNAQ	10423	MMLSGLN	0.660837	0.004421
TS70	1246	GCCCAACCCAACACCATCAGAAACGTCGCACAG	5835	AQPNTIRNVAQ	10424	PNTIRNV	0.660528	0.629407
TS71	1247	GCCCAAGAGAATTTGACGCGTGGGGTGGCACAG	5836	AQENLTRGVAQ	10425	ENLTRGV	0.659884	0.188249
GP41	1248	GCCCAATTTAGTGCTCGGAGTACGGGGGCACAG	5837	AQFSARSTGAQ	10426	FSARSTG	0.659095	0.105157
TS72	1249	GCCCAAGAAAACGCCACCAGAACCTACGCACAG	5838	AQENATRTYAQ	10427	ENATRTY	0.657305	1.105462
TS73	1250	GCCCAAGGCAACAGCACCAGAATGAACGCACAG	5839	AQGNSTRMNAQ	10428	GNSTRMN	0.656999	0.923491
TS74	1251	GCCCAAGGGAATTCTACTAAGTCTCCTGCACAG	5840	AQGNSTKSPAQ	10429	GNSTKSP	0.656908	0.716749
GS44	1252	GCCCAAATGCAAACCACCCTCCACCTCGCACAG	5841	AQMQTTLHLAQ	10430	MQTTLHL	0.656525	-0.09797
SyS71	1253	GCCCAAAACCCCACCCTCATCACCCTCGCACAG	5842	AQNPTLITLAQ	10431	NPTLITL	0.655924	0.146275
SyS72	1254	GCCCAACTTATTTCTGGTCATGCGCAGGCACAG	5843	AQLISGHAQAQ	10432	LISGHAQ	0.655121	0.171881
SyS73	1255	GCCCAATTCAACCAAGTCAGAAGCCTCGCACAG	5844	AQFNQVRSLAQ	10433	FNQVRSL	0.65493	0.025869
GS45	1256	GCCCAAATGAACATCCTCAGAGAAGTCGCACAG	5845	AQMNILREVAQ	10434	MNILREV	0.654097	-0.09985
GP42	1257	GCCCAAAGTGCTATGATGCGTGGTGTTGCACAG	5846	AQSAMMRGVAQ	10435	SAMMRGV	0.653566	-0.06697

FIG. 33 (Continued)

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SyS74	1258	GCCCAACCCATGCTCAGCAGCCCCAGCGCACAG	5847	AQPMLSSPSAQ	10436	PMLSSPS	0.652269	-0.07485
TS75	1259	GCCCAACAGAATAATACGCTTAGGTCGGCACAG	5848	AQQNNTLRSAQ	10437	QNNTLRS	0.651653	0.733737
GS46	1260	GCCCAAAGGCATTCGGATCCGGTGGAGGCACAG	5849	AQRHSDPVEAQ	10438	RHSDPVE	0.65144	-0.07331
GS47	1261	GCCCAAGTGAATACGACGTTTTCTACGGCACAG	5850	AQVNTTFSTAQ	10439	VNTTFST	0.65142	-0.00755
TS76	1262	GCCCAAATCAACAGCACCAGAGGCATCGCACAG	5851	AQINSTRGIAQ	10440	INSTRGI	0.650374	0.746658
TS77	1263	GCCCAAACCAACGCCGTCAGAGACCTCGCACAG	5852	AQTNAVRDLAQ	10441	TNAVRDL	0.649865	0.608962
TS78	1264	GCCCAATCTAATAGTACTAGGCTGTCGGCACAG	5853	AQSNSTRLSAQ	10442	SNSTRLS	0.649567	1.213202
SyS75	1265	GCCCAAACGTCTATTGCTGGGTCGTTTGCACAG	5854	AQTSIAGSFAQ	10443	TSIAGSF	0.647793	0.065679
SS27	1266	GCCCAACTCGGCAGCACCTACCCCAGAGCACAG	5855	AQLGSTYPRAQ	10444	LGSTYPR	0.644533	-0.23408
SyS76	1267	GCCCAAGCCAACGTCACCACCCAAAGAGCACAG	5856	AQANVTTQRAQ	10445	ANVTTQR	0.643299	0.597905
TS79	1268	GCCCAAAGCAACAGCGTCAGACTCAGCGCACAG	5857	AQSNSVRLSAQ	10446	SNSVRLS	0.641635	0.657122
GS48	1269	GCCCAAGCTACGAATGAGCCTGATCGGGCACAG	5858	AQATNEPDRAQ	10447	ATNEPDR	0.641008	-0.06388
GS49	1270	GCCCAAAGAATGAACCCCGAACAAAGCGCACAG	5859	AQRMNPEQSAQ	10448	RMNPEQS	0.640866	0.123792
GS50	1271	GCCCAATCGGTTAGTGGTTCGGCTAATGCACAG	5860	AQSVSGSANAQ	10449	SVSGSAN	0.640362	-0.07276
GS51	1272	GCCCAACCGAGTAATAGTACTACGCGTGCACAG	5861	AQPSNSTTRAQ	10450	PSNSTTR	0.639664	0.069013
GP43	1273	GCCCAACTTTTTCATGGTACGCATGAGGCACAG	5862	AQLFHGTHEAQ	10451	LFHGTHE	0.639176	0.186361
SyS77	1274	GCCCAACCCCAACTCGGCAGCACCAAAGCACAG	5863	AQPQLGSTKAQ	10452	PQLGSTK	0.638022	0.187838
SyS78	1275	GCCCAACCCATCAGCGCCAACAGACTCGCACAG	5864	AQPISANRLAQ	10453	PISANRL	0.637814	-0.06902
SyS79	1276	GCCCAAAATTCGGGTAATCTTTCTATGGCACAG	5865	AQNSGNLSMAQ	10454	NSGNLSM	0.637206	0.248456
SyS80	1277	GCCCAAAAGGTTGAGGCTATTGGGATGGCACAG	5866	AQKVEAIGMAQ	10455	KVEAIGM	0.63585	0.196256
SyS81	1278	GCCCAAAAGACTTTGCTTAATAGTGTTGCACAG	5867	AQKTLLNSVAQ	10456	KTLLNSV	0.635567	-0.07329
GS52	1279	GCCCAAAATGCTATGGATCTTAAGGTGGCACAG	5868	AQNAMDLKVAQ	10457	NAMDLKV	0.633592	-0.04013
SyS82	1280	GCCCAAATGATGGGTAATGGGTCTTCGGCACAG	5869	AQMMGNGSSAQ	10458	MMGNGSS	0.632846	-0.04467
TS80	1281	GCCCAAAGCAACAGCACCAAAGCCCTCGCACAG	5870	AQSNSTKALAQ	10459	SNSTKAL	0.630646	1.07834
TS81	1282	GCCCAATCTAATAGTACGCGGGGTACGGCACAG	5871	AQSNSTRGTAQ	10460	SNSTRGT	0.630359	1.275033
GS53	1283	GCCCAAAGCCTCAGCAGCCTCCACGTCGCACAG	5872	AQSLSSLHVAQ	10461	SLSSLHV	0.629137	-0.08892
SyS83	1284	GCCCAAACCCTCAGCGGCGCCCTCACCGCACAG	5873	AQTLSGALTAQ	10462	TLSGALT	0.628275	0.306806
TS82	1285	GCCCAACCGAATACGGTGAGGAATAATGCACAG	5874	AQPNTVRNNAQ	10463	PNTVRNN	0.627943	1.035691
TS83	1286	GCCCAAAATAATAATGTGAAGATGACTGCACAG	5875	AQNNNVKMTAQ	10464	NNNVKMT	0.627302	0.23573
GP46	1287	GCCCAATCTGTTGCTAAGCCTTTTATGGCACAG	5876	AQSVAKPFMAQ	10465	SVAKPFM	0.627075	0.17477
SyP29	1288	GCCCAAACGCAGACGACTCGGCTTTCGGCACAG	5877	AQTQTTRLSAQ	10466	TQTTRLS	0.625657	-0.04236
TS84	1289	GCCCAAAATAATGCGACTCGGGGTGGGGCACAG	5878	AQNNATRGGAQ	10467	NNATRGG	0.622765	0.76061

FIG. 33 (Continued)

TS85	1290	GCCCAAACCAACACCACCGCCAGAATCGCACAG	5879	AQTNTTARIAQ	10468	TNTTARI	0.621665	0.649749
TS86	1291	GCCCAAGAGAATAGTATTCGGACTATTGCACAG	5880	AQENSIRTIAQ	10469	ENSIRTI	0.619021	0.750947
GS55	1292	GCCCAAATTAGGGAGACTTCTGGGAAGGCACAG	5881	AQIRETSGKAQ	10470	IRETSGK	0.618732	-0.00781
SyS84	1293	GCCCAAAGCATCTACTACCACACCGAAGCACAG	5882	AQSIYYHTEAQ	10471	SIYYHTE	0.618441	-0.07907
SyS85	1294	GCCCAAGTCCTCGACAACAGCGGCCAAGCACAG	5883	AQVLDNSGQAQ	10472	VLDNSGQ	0.618183	-0.1396
GS56	1295	GCCCAAAGCCACACAACATGACCATCAGAGCACAG	5884	AQSHNMTIRAQ	10473	SHNMTIR	0.614114	0.473069
SyS86	1296	GCCCAAACCATCCCCAGCGCCGGCAAAGCACAG	5885	AQTIPSAGKAQ	10474	TIPSAGK	0.612816	0.150798
SyP30	1297	GCCCCACCTAGGCATACTTTGAGTCAGGCACAG	5886	APPRHTLSQAQ	10475	PRHTLSQ	0.60799	-0.00929
SyS87	1298	GCCCAATCGCTTAATGTGCAGGATGTGGCACAG	5887	AQSLNVQDVAQ	10476	SLNVQDV	0.607203	0.057645
GP48	1299	GCCCAATATCAGTCTCTGGCTAATCCGGCACAG	5888	AQYQSLANPAQ	10477	YQSLANP	0.607005	0.036857
GS58	1300	GCCCAAATTCTGAATATGTCTACGGATGCACAG	5889	AQILNMSTDAQ	10478	ILNMSTD	0.606834	-0.1435
SyS88	1301	GCCCAAGTCCTCCACCTCGGCCACAGCGCACAG	5890	AQVLHLGHSAQ	10479	VLHLGHS	0.605932	0.104512
SyS89	1302	GCCCAAGGTGTTACTCAGACTCCGCGTGCACAG	5891	AQGVTQTPRAQ	10480	GVTQTPR	0.6059	0.243764
TS88	1303	GCCCAAACCAACGACACCAGAAGAATCGCACAG	5892	AQTNDTRRIAQ	10481	TNDTRRI	0.604587	1.419603
SyS90	1304	GCCCAACAAACCGACCACACCAGCAGAGCACAG	5893	AQQTDHTSRAQ	10482	QTDHTSR	0.604031	0.279435
TS90	1305	GCCCAAAAGAATGAGATTAAGAATGTGGCACAG	5894	AQKNEIKNVAQ	10483	KNEIKNV	0.603838	0.384157
GP49	1306	GCCCAATGGACTGGTAATGAGAGGCTTGCACAG	5895	AQWTGNERLAQ	10484	WTGNERL	0.603412	-0.0735
SyS91	1307	GCCCAAGGTAAGAGTGATGCTATGCGGGCACAG	5896	AQGKSDAMRAQ	10485	GKSDAMR	0.603322	0.227787
TS91	1308	GCCCAAGGGAATGCGACTCGTACTTATGCACAG	5897	AQGNATRTYAQ	10486	GNATRTY	0.602016	0.746216
SyS92	1309	GCCCAAGCCAGCAACCTCGGCCTCCCCGCACAG	5898	AQASNLGLPAQ	10487	ASNLGLP	0.600647	0.212421
SyS93	1310	GCCCAAAGCAGCCTCAGCGGCAGCCCCGCACAG	5899	AQSSLSGSPAQ	10488	SSLSGSP	0.599424	0.229985
SyS94	1311	GCCCAAGCCGCCGTCAACCAAGGCGTCGCACAG	5900	AQAAVNQGVAQ	10489	AAVNQGV	0.599283	0.365845
GS60	1312	GCCCAAGACCAAAACCAACCCAGAGAAGCACAG	5901	AQDQNQPREAQ	10490	DQNQPRE	0.59872	-0.04719
GS61	1313	GCCCAACTCACCCAAGACAAACAAGCCGCACAG	5902	AQLTQDKQAAQ	10491	LTQDKQA	0.59843	0.025835
SyS95	1314	GCCCAATTCGGCAGCAACGAACACACAACGCACAG	5903	AQFGSNEHNAQ	10492	FGSNEHN	0.59773	0.246632
GS62	1315	GCCCAACTGAATCAGCCGAATGTGCGGGCACAG	5904	AQLNQPNVRAQ	10493	LNQPNVR	0.59703	-0.00684
TS92	1316	GCCCAAATGAATACTACGCGTAATCTGGCACAG	5905	AQMNTTRNLAQ	10494	MNTTRNL	0.596819	0.171297
TS93	1317	GCCCAAACTAATTCTACTAGGACGAGTGCACAG	5906	AQTNSTRTSAQ	10495	TNSTRTS	0.596817	0.587886
SyS96	1318	GCCCAATTTGAGCTTTCGCATGTGCCTGCACAG	5907	AQFELSHVPAQ	10496	FELSHVP	0.595373	0.012267
SyS97	1319	GCCCAAGAAGGCCTCGGCAACGCCGCCGCACAG	5908	AQEGLGNAAAQ	10497	EGLGNAA	0.59339	-0.02116
SyS98	1320	GCCCAACTCACCGTCACCCTCAACCACGCACAG	5909	AQLTVTLNHAQ	10498	LTVTLNH	0.593104	0.120283
SyS99	1321	GCCCAATTTGGGAATGCGATTCAGTCTGCACAG	5910	AQFGNAIQSAQ	10499	FGNAIQS	0.593063	0.321334

FIG. 33 (Continued)

SyS100	1322	GCCCAACCGGGTGGGGGTTTGACTCCGGCACAG	5911	AQPGGGLTPAQ	10500	PGGGLTP	0.591748	-0.07925
TS94	1323	GCCCAACCCAACATGACCAGAAGCCTCGCACAG	5912	AQPNMTRSLAQ	10501	PNMTRSL	0.591633	-0.10147
SyS101	1324	GCCCAAAGTCAGCTGCATAGGTTGCAGGCACAG	5913	AQSQLHRLQAQ	10502	SQLHRLQ	0.588997	-0.13052
SyS102	1325	GCCCAAAATGATCCTGTGCTGACTGTGGCACAG	5914	AQNDPVLTVAQ	10503	NDPVLTV	0.587622	-0.01116
TS96	1326	GCCCAAGAAAACAGCGTCAGAACCACCGCACAG	5915	AQENSVRTTAQ	10504	ENSVRTT	0.586872	0.975538
SyS103	1327	GCCCAAGATCGTGTGACTAATCCGAAGGCACAG	5916	AQDRVTNPKAQ	10505	DRVTNPK	0.585898	0.111333
GS63	1328	GCCCAACTCAACACCGGCCAAATGAGAGCACAG	5917	AQLNTGQMRAQ	10506	LNTGQMR	0.584482	-0.02938
SyS105	1329	GCCCAAATTAGTCCTTCTCAGGTGAAGGCACAG	5918	AQISPSQVKAQ	10507	ISPSQVK	0.583565	-0.06248
GS64	1330	GCCCAATACAGCGCCGACAAAACCACCGCACAG	5919	AQYSADKTTAQ	10508	YSADKTT	0.583168	0.057165
SyS106	1331	GCCCAAATTGATAGTGCGGGGATGGCGGCACAG	5920	AQIDSAGMAAQ	10509	IDSAGMA	0.582726	0.096381
GS65	1332	GCCCAAAGCAACAACATCAAACTCAACGCACAG	5921	AQSNNIKLNAQ	10510	SNNIKLN	0.582501	0.297073
GP50	1333	GCCCAACTTGAGACGCAGCCTAGGACTGCACAG	5922	AQLETQPRTAQ	10511	LETQPRT	0.582054	0.032491
SyS107	1334	GCCCAAAATTTGCATAGTAATGTGCTGGCACAG	5923	AQNLHSNVLAQ	10512	NLHSNVL	0.581653	-0.14757
SyS108	1335	GCCCAAATGGTCAAAGACACCCAACTCGCACAG	5924	AQMVKDTQLAQ	10513	MVKDTQL	0.581409	0.291903
SyS109	1336	GCCCAACTCATGCACCTCACCAACCCCGCACAG	5925	AQLMHLTNPAQ	10514	LMHLTNP	0.579725	0.107144
GS66	1337	GCCCAAGTCGCCAGCCCCGACAAAAGAGCACAG	5926	AQVASPDKRAQ	10515	VASPDKR	0.579259	0.01036
SyS110	1338	GCCCAAGTCGTCGCCGTCCTCACCAGCGCACAG	5927	AQVVAVLTSAQ	10516	VVAVLTS	0.578391	-0.03811
SyS111	1339	GCCCAAAACATCATGGTCAACGTCCCCGCACAG	5928	AQNIMVNVPAQ	10517	NIMVNVP	0.578008	0.047622
GS67	1340	GCCCAACCGTATAGTGGGCAGCGGACTGCACAG	5929	AQPYSGQRTAQ	10518	PYSGQRT	0.577882	-0.09575
SyS112	1341	GCCCAACCTCTGCTTAAGACGAATACTGCACAG	5930	AQPLLKTNTAQ	10519	PLLKTNT	0.575523	-0.05536
TS97	1342	GCCCAAGGGAATACTACGGTGCGTGGGGCACAG	5931	AQGNTTVRGAQ	10520	GNTTVRG	0.574402	0.890696
TS98	1343	GCCCAAACCAACAAAGTCAGAGACGACGCACAG	5932	AQTNKVRDDAQ	10521	TNKVRDD	0.573889	1.07775
SyS113	1344	GCCCAACCCAGCACCGCCCTCCTCGTCGCACAG	5933	AQPSTALLVAQ	10522	PSTALLV	0.573034	-0.04799
SyS114	1345	GCCCAAATCCAAAGCATCACCCTCAAAGCACAG	5934	AQIQSITLKAQ	10523	IQSITLK	0.572783	0.036592
SyS115	1346	GCCCAACCCCTCCACGCCAACATGAGCGCACAG	5935	AQPLHANMSAQ	10524	PLHANMS	0.570881	0.092035
SyS116	1347	GCCCAAACCGCCCACGCCGAAGCCAGAGCACAG	5936	AQTAHAEARAQ	10525	TAHAEAR	0.570572	0.139128
SyS117	1348	GCCCAAACGAATACGGATTCGTATCGTGCACAG	5937	AQTNTDSYRAQ	10526	TNTDSYR	0.569365	0.111126
SyS118	1349	GCCCAAACCCACGTCAGCCTCGACAGAGCACAG	5938	AQTHVSLDRAQ	10527	THVSLDR	0.569228	0.375899
SyS119	1350	GCCCAATTTAGTACGAAGGATCATGTTGCACAG	5939	AQFSTKDHVAQ	10528	FSTKDHV	0.568654	0.276408
SyS120	1351	GCCCAAGACAACACCCAAACCGCCCCCGCACAG	5940	AQDNTQTAPAQ	10529	DNTQTAP	0.568553	0.088871
TS99	1352	GCCCAAAGCAACAGAATCATCAGCGGCGCACAG	5941	AQSNRIISGAQ	10530	SNRIISG	0.568551	0.92316
TS100	1353	GCCCAAACTAATTCTGTTAGGAATAATGCACAG	5942	AQTNSVRNNAQ	10531	TNSVRNN	0.568237	1.153418

FIG. 33 (Continued)

TS101	1354	GCCCAAAGCAACGAAGTCAGAAACATGGCACAG	5943	AQSNEVRNMAQ	10532	SNEVRNM	0.567847	0.744396
SyS121	1355	GCCCAAGAACTCTACAAACCCAGCAGAGCACAG	5944	AQELYKPSRAQ	10533	ELYKPSR	0.567258	-0.07221
GS69	1356	GCCCAATGGATTACGGGGGGTGCGAGTGCACAG	5945	AQWITGGASAQ	10534	WITGGAS	0.567159	0.345096
TS102	1357	GCCCAAAACAACAGCGTCAGACCCACCGCACAG	5946	AQNNSVRPTAQ	10535	NNSVRPT	0.566945	0.624336
GS70	1358	GCCCAACACACCGCCGTCCTCAGAACCGCACAG	5947	AQHTAVLRTAQ	10536	HTAVLRT	0.565911	-0.03197
SyS122	1359	GCCCAAAATACTTTGTCTCTTGCTCCTGCACAG	5948	AQNTLSLAPAQ	10537	NTLSLAP	0.564955	0.155579
SyS123	1360	GCCCAACCCAACGCCAGCGTCAACAGCGCACAG	5949	AQPNASVNSAQ	10538	PNASVNS	0.564885	0.097515
GS71	1361	GCCCAAGTTACTGGTGGGAATACTTATGCACAG	5950	AQVTGGNTYAQ	10539	VTGGNTY	0.564099	-0.05591
SyS124	1362	GCCCAAGTCAACGAAAACCTCATCGAAGCACAG	5951	AQVNENLIEAQ	10540	VNENLIE	0.563902	-0.13408
SyS125	1363	GCCCAAGTTTTGACGACTCATTCGAATGCACAG	5952	AQVLTTHSNAQ	10541	VLTTHSN	0.563552	-0.14541
GS72	1364	GCCCAACACACCCAACTCCCCCTCACCGCACAG	5953	AQHTQLPLTAQ	10542	HTQLPLT	0.562802	-0.07685
SyS126	1365	GCCCAACGGCAGTCTCTTGAGGCGTTGGCACAG	5954	AQRQSLEALAQ	10543	RQSLEAL	0.562715	-0.07009
SyS127	1366	GCCCAACCCGACGTCACCGAAGGCAGAGCACAG	5955	AQPDVTEGRAQ	10544	PDVTEGR	0.560929	-0.0307
SyS128	1367	GCCCAACCGACTAATATTATGCTTGATGCACAG	5956	AQPTNIMLDAQ	10545	PTNIMLD	0.560313	-0.07894
SyS129	1368	GCCCAACCCAACATGAGCGCCATGATCGCACAG	5957	AQPNMSAMIAQ	10546	PNMSAMI	0.559451	0.270198
SyS130	1369	GCCCAAATTATGAATGGTCAGGCTCTGGCACAG	5958	AQIMNGQALAQ	10547	IMNGQAL	0.558677	0.015194
TS103	1370	GCCCAAAATAATAATTCGACGCGTTTTGCACAG	5959	AQNNNSTRFAQ	10548	NNNSTRF	0.558656	0.432697
TS104	1371	GCCCAAGCCAACGTCACCAGAAGCACCGCACAG	5960	AQANVTRSTAQ	10549	ANVTRST	0.558653	0.70621
SyS131	1372	GCCCAACAGAATCTTGGTCTTAATGTGGCACAG	5961	AQQNLGLNVAQ	10550	QNLGLNV	0.558202	-0.12084
SyS132	1373	GCCCAACAAGCCCAAATGAGCAGCGCCGCACAG	5962	AQQAQMSSAAQ	10551	QAQMSSA	0.557238	0.147605
SyS133	1374	GCCCAACTCACCATGGCCACCAACGTCGCACAG	5963	AQLTMATNVAQ	10552	LTMATNV	0.556779	0.286866
SyS134	1375	GCCCAAGATCGTGATTCTGTGCAGAATGCACAG	5964	AQDRDSVQNAQ	10553	DRDSVQN	0.55654	-0.05483
GS73	1376	GCCCAAGTCAACCCCACCAACAACCTCGCACAG	5965	AQVNPTNNLAQ	10554	VNPTNNL	0.555076	-0.00968
GP51	1377	GCCCAACCGTCTTTTACGACTATGAGTGCACAG	5966	AQPSFTTMSAQ	10555	PSFTTMS	0.554811	0.065283
GS74	1378	GCCCAAAGGGAGACGCCTATTCCTAAGGCACAG	5967	AQRETPIPKAQ	10556	RETPIPK	0.553803	-0.0639
SyS135	1379	GCCCAAAGCCTCAACTTCACCACCGCCGCACAG	5968	AQSLNFTTAAQ	10557	SLNFTTA	0.553055	0.475212
SyS136	1380	GCCCAAGGTATGAGTGGGGTTGCTCAGGCACAG	5969	AQGMSGVAQAQ	10558	GMSGVAQ	0.552736	-0.0578
GP52	1381	GCCCAAAAGGTTGATGCGGCTCAGAGTGCACAG	5970	AQKVDAAQSAQ	10559	KVDAAQS	0.552569	0.100209
GS75	1382	GCCCAACATATTACGACTAATGTGTCTGCACAG	5971	AQHITTNVSAQ	10560	HITTNVS	0.552479	0.112469
SyP32	1383	GCCCAAGAGCGGGAGTCGGCTCGTCTTGCACAG	5972	AQERESARLAQ	10561	ERESARL	0.551876	-0.04251
TS106	1384	GCCCAAGATAATAGGACTCAGAGGACGGCACAG	5973	AQDNRTQRTAQ	10562	DNRTQRT	0.551636	0.853173
SyS137	1385	GCCCAATCTGCGCCTAATGTGACTATTGCACAG	5974	AQSAPNVTIAQ	10563	SAPNVTI	0.551278	0.041441

FIG. 33 (Continued)

TS107	1386	GCCCAAGAAAACGGCACCAGAAACACCGCACAG	5975	AQENGTRNTAQ	10564	ENGTRNT	0.55012	0.5646
SyS138	1387	GCCCAAGGCACCGCCGTCTTCACCGCCGCACAG	5976	AQGTAVFTAAQ	10565	GTAVFTA	0.549912	0.15966
SyS139	1388	GCCCAAGCCAACAACATGAGCCAAACCGCACAG	5977	AQANNMSQTAQ	10566	ANNMSQT	0.549519	0.239635
TS108	1389	GCCCAAGGTAATCATACTTATAATCTGGCACAG	5978	AQGNHTYNLAQ	10567	GNHTYNL	0.549264	-0.25467
GP53	1390	GCCCAACTGAGTCCTTCGAATTCTAATGCACAG	5979	AQLSPSNSNAQ	10568	LSPSNSN	0.549019	-0.07079
SyS140	1391	GCCCAAATGGGCGCCGACCACAGAACCGCACAG	5980	AQMGADHRTAQ	10569	MGADHRT	0.548749	0.159265
TS109	1392	GCCCAAAGTAATTCGACGCGTGGTTCTGCACAG	5981	AQSNSTRGSAQ	10570	SNSTRGS	0.548705	0.187139
SyS141	1393	GCCCAAAATACTTCTGGTGTGCCTAAGGCACAG	5982	AQNTSGVPKAQ	10571	NTSGVPK	0.548579	-0.08828
GS78	1394	GCCCAAATCAACACCGCCGTCGTCAGCGCACAG	5983	AQINTAVVSAQ	10572	INTAVVS	0.54846	-0.10485
SyS142	1395	GCCCAAATGGGGGTTCAGGCTTATGTGGCACAG	5984	AQMGVQAYVAQ	10573	MGVQAYV	0.54845	-0.12925
TS110	1396	GCCCAAGGGAATTTTGTTAAGCCGAATGCACAG	5985	AQGNFVKPNAQ	10574	GNFVKPN	0.547942	0.278497
TS111	1397	GCCCAAGTGAATTCGGTGAGGATGATTGCACAG	5986	AQVNSVRMIAQ	10575	VNSVRMI	0.547171	0.096718
GS79	1398	GCCCAACACGACAGCGCCCAACAGCAGAGCACAG	5987	AQHDSANSRAQ	10576	HDSANSR	0.54671	-0.08012
SyS143	1399	GCCCAACTCGGCGTCAGAGACGACAGCGCACAG	5988	AQIGVRDDSAQ	10577	LGVRDDS	0.545708	-0.07131
TS113	1400	GCCCAAAGCAACGCCGTCAGAGCCAACGCACAG	5989	AQSNAVRANAQ	10578	SNAVRAN	0.545674	0.453866
SyS144	1401	GCCCAACCCGTCCTCGCCGCCACCATGGCACAG	5990	AQPVLAATMAQ	10579	PVLAATM	0.545458	-0.13314
GP54	1402	GCCCAAAATAAGCCTGTGTCTGGTAATGCACAG	5991	AQNKPVSGNAQ	10580	NKPVSGN	0.544076	0.079545
SyS145	1403	GCCCAAGTCGGCCTCGCCAGCCACACCGCACAG	5992	AQVGLASHTAQ	10581	VGLASHT	0.541637	-0.04601
SyS146	1404	GCCCAAGGCAGCAACACCAACATGAAAGCACAG	5993	AQGSNTNMKAQ	10582	GSNTNMK	0.540634	0.026539
GS81	1405	GCCCAAGTTGCTACTACTGTGCATAATGCACAG	5994	AQVATTVHNAQ	10583	VATTVHN	0.540191	-0.11662
GS82	1406	GCCCAAAACACCCTCGACAGCAGAGTCGCACAG	5995	AQNTLDSRVAQ	10584	NTLDSRV	0.539923	-0.05177
SyS147	1407	GCCCAAAGGGAGGCTAATTTGCAGGCGGCACAG	5996	AQREANLQAAQ	10585	REANLQA	0.539717	0.293254
SyS148	1408	GCCCAAGTCGACGCCCTCAGCCACATGGCACAG	5997	AQVDALSHMAQ	10586	VDALSHM	0.539694	0.216373
GS83	1409	GCCCAACTTCGTCTTGCTGGTCTTGCTGCACAG	5998	AQLRLAGLAAQ	10587	LRLAGLA	0.539525	-0.09739
GP55	1410	GCCCAAATTACGGTGACTAATTATTCGGCACAG	5999	AQITVTNYSAQ	10588	ITVTNYS	0.539447	0.273677
SyS149	1411	GCCCAATGGGACAGCGGCAGCGGCGAAGCACAG	6000	AQWDSGSGEAQ	10589	WDSGSGE	0.539198	-0.07979
SyS150	1412	GCCCAATTCGCCAGCGAAACCGTCGCCGCACAG	6001	AQFASETVAAQ	10590	FASETVA	0.537906	-0.02698
SyS151	1413	GCCCAACAGAATGTTACGGGGACGAGGGCACAG	6002	AQQNVTGTRAQ	10591	QNVTGTR	0.537867	0.272466
SyS152	1414	GCCCAACTTAATGGGTTGAATGTGTCTGCACAG	6003	AQLNGLNVSAQ	10592	LNGLNVS	0.537505	-0.02999
GS84	1415	GCCCAAAATATGCTTAAGCAGAGTGAGGCACAG	6004	AQNMLKQSEAQ	10593	NMLKQSE	0.537354	-0.06179
SyS153	1416	GCCCAATTTAATGAGGTTCCGAAGGCGGCACAG	6005	AQFNEVPKAAQ	10594	FNEVPKA	0.537144	-0.03003
SyS154	1417	GCCCAACTCGGCGACATCACCGGCTTCGCACAG	6006	AQLGDITGFAQ	10595	LGDITGF	0.537047	-0.10198

FIG. 33 (Continued)

SyS155	1418	GCCCAAATTTCGGCTTCTCATTCTCGTGCACAG	6007	AQISASHSRAQ	10596	ISASHSR	0.536983	-0.06923
SyS156	1419	GCCCAAAGTCAGACGCAGATTGCTCTTGCACAG	6008	AQSQTQIALAQ	10597	SQTQIAL	0.53684	-0.07569
SyS157	1420	GCCCAAAATATGGCTACTCAGATGAAGGCACAG	6009	AQNMATQMKAQ	10598	NMATQMK	0.536747	-0.11797
SyS158	1421	GCCCAAGTCAACCACAACATCAGACTCGCACAG	6010	AQVNHNIRLAQ	10599	VNHNIRL	0.53652	-0.01096
SyS159	1422	GCCCAAAACGCCCTCCAAGTCCCCGTCGCACAG	6011	AQNALQVPVAQ	10600	NALQVPV	0.536474	0.059794
SyS160	1423	GCCCAAAATTCGACGGGTATTGATACGGCACAG	6012	AQNSTGIDTAQ	10601	NSTGIDT	0.53526	-0.06524
SyS161	1424	GCCCAAGTTGTTGCTGGGCATCTTAATGCACAG	6013	AQVVAGHLNAQ	10602	VVAGHLN	0.534827	-0.11989
SyS162	1425	GCCCAACGGAATGATGCGATTCTGAATGCACAG	6014	AQRNDAILNAQ	10603	RNDAILN	0.53456	0.251531
GS85	1426	GCCCAAAATCGGGTTGATTCGCGGGCTGCACAG	6015	AQNRVDSRAAQ	10604	NRVDSRA	0.53408	0.01415
GS86	1427	GCCCAATCGACGCATTCTACTTATGTGGCACAG	6016	AQSTHSTYVAQ	10605	STHSTYV	0.533753	-0.09066
SyS164	1428	GCCCAAAGTGGGCATGGGACTCTGCGGGCACAG	6017	AQSGHGTLRAQ	10606	SGHGTLR	0.532267	-0.1652
SyS165	1429	GCCCAACCCAACAGCACCACCCTCAGCGCACAG	6018	AQPNSTTLSAQ	10607	PNSTTLS	0.531723	-0.01811
GS87	1430	GCCCAAGACACCCAAACCCACCACACCGCACAG	6019	AQDTKPTNTAQ	10608	DTKPTNT	0.531589	0.18326
SyS166	1431	GCCCAAAACAGAGACACCATCAACAACGCACAG	6020	AQNRDTINNAQ	10609	NRDTINN	0.531212	0.532142
GS88	1432	GCCCAACCCAGAACCCTCAGCGACGGCGCACAG	6021	AQPRTLSDGAQ	10610	PRTLSDG	0.530962	0.113902
GS89	1433	GCCCAAACCAAAGACGTCACCACCAGCGCACAG	6022	AQTKDVTTSAQ	10611	TKDVTTS	0.53023	-0.05088
SS31	1434	GCCCAACTGGGTAATCCTACGCCTTCTGCACAG	6023	AQLGNPTPSAQ	10612	LGNPTPS	0.529624	-0.27772
GP56	1435	GCCCAATATCAGGCGATGTATAGGGATGCACAG	6024	AQYQAMYRDAQ	10613	YQAMYRD	0.528592	0.013767
GS90	1436	GCCCAAAGCGGCGTCCAAGAATTCGACGCACAG	6025	AQSGVQEFDAQ	10614	SGVQEFD	0.528493	-0.16214
SyS167	1437	GCCCAATCTAATCATCTGTCGACGGTTGCACAG	6026	AQSNHLSTVAQ	10615	SNHLSTV	0.528046	0.269982
SyS168	1438	GCCCAACACGACGAAAGAGCCAACATGGCACAG	6027	AQHDERANMAQ	10616	HDERANM	0.526932	0.005367
TS114	1439	GCCCAAACGAATAGTACTCGGTCGCCTGCACAG	6028	AQTNSTRSPAQ	10617	TNSTRSP	0.526707	0.094198
SP27	1440	GCCCAACCGACGGATAAGTCTTATCCGGCACAG	6029	AQPTDKSYPAQ	10618	PTDKSYP	0.525687	-0.03596
SyS170	1441	GCCCAAATGACCGAACAAAGAACCGCCGCACAG	6030	AQMTEQRTAAQ	10619	MTEQRTA	0.524729	0.151606
GS92	1442	GCCCAAACCAACGCCACCCACAGCAAAGCACAG	6031	AQTNATHSKAQ	10620	TNATHSK	0.523113	0.600566
GP58	1443	GCCCAAAATCGGGGTACTTTTAGTGCGGCACAG	6032	AQNRGTFSAAQ	10621	NRGTFSA	0.522986	-0.0735
TS115	1444	GCCCAAAACACCACCAAATTCAACACCGCACAG	6033	AQNTTKFNTAQ	10622	NTTKFNT	0.522899	0.168453
SyS171	1445	GCCCAAGGGATTCCGCCTTTGACTAAGGCACAG	6034	AQGIPPLTKAQ	10623	GIPPLTK	0.522659	0.148866
SyS172	1446	GCCCAAACCGCCAACAGCACCCAAAGAGCACAG	6035	AQTANSTQRAQ	10624	TANSTQR	0.522626	0.365056
SyS173	1447	GCCCAAACTCAGGGTCCGGGTCCGAAGGCACAG	6036	AQTQGPGPKAQ	10625	TQGPGPK	0.522239	0.297383
TS116	1448	GCCCAAATGAATACTACGCGGAATTATGCACAG	6037	AQMNTTRNYAQ	10626	MNTTRNY	0.522193	0.354477
GS94	1449	GCCCAACTCAGAGAAGGCACCTTCATGGCACAG	6038	AQLREGTFMAQ	10627	LREGTFM	0.521554	-0.02029

FIG. 33 (Continued)

SyS174	1450	GCCCAAAACATCAGCAGCACCGACAGAGCACAG	6039	AQNISSTDRAQ	10628	NISSTDR	0.521154	0.307406
SyP33	1451	GCCCAATCGGTTAGTCGGCCGTTTCAGGCACAG	6040	AQSVSRPFQAQ	10629	SVSRPFQ	0.520365	-0.03773
GS96	1452	GCCCAACCTATGTCTGCTAATGGGAAGGCACAG	6041	AQPMSANGKAQ	10630	PMSANGK	0.518792	-0.0464
SyS175	1453	GCCCAAGAAGTCAGAGGCAACACCTTCGCACAG	6042	AQEVRGNTFAQ	10631	EVRGNTF	0.518514	0.312168
GS97	1454	GCCCAATCGCAGAAGGGTCTGTCTGTGGCACAG	6043	AQSQKGLSVAQ	10632	SQKGLSV	0.518477	-0.04267
SyS176	1455	GCCCAAATTGCTGAGAATCTGAGTGCTGCACAG	6044	AQIAENLSAAQ	10633	IAENLSA	0.517935	-0.10864
SyS177	1456	GCCCAATTCAGCAACATGAACCTCAAAGCACAG	6045	AQFSNMNLKAQ	10634	FSNMNLK	0.517734	-0.05191
GP59	1457	GCCCAACCTCGTGAGCGGACTTATACTGCACAG	6046	AQPRERTYTAQ	10635	PRERTYT	0.516835	0.003871
GS99	1458	GCCCAATGGTCGCATAATCCGGATTCTGCACAG	6047	AQWSHNPDSAQ	10636	WSHNPDS	0.516248	-0.11545
GP60	1459	GCCCAAGGTCTTCAGACTCTGATTACGGCACAG	6048	AQGLQTLITAQ	10637	GLQTLIT	0.516123	0.282215
TS117	1460	GCCCAAAGCAACAGAACCAAAGACATCGCACAG	6049	AQSNRTKDIAQ	10638	SNRTKDI	0.515515	0.733669
SyS179	1461	GCCCAAGTGACTGAGACGATTCTTAAGGCACAG	6050	AQVTETILKAQ	10639	VTETILK	0.515459	-0.16223
GS100	1462	GCCCAATATGTTACGCGTAGTGGTCTGGCACAG	6051	AQYVTRSGLAQ	10640	YVTRSGL	0.515319	-0.09386
SS32	1463	GCCCAAATGAACGCCAACATCCTCGTCGCACAG	6052	AQMNANILVAQ	10641	MNANILV	0.514679	-0.31431
GP61	1464	GCCCAAACTACGAATCGGGTGGGTACGGCACAG	6053	AQTTNRVGTAQ	10642	TTNRVGT	0.51427	-0.05638
GS101	1465	GCCCAAGTCCTCAAAAGCCACCTCCAAGCACAG	6054	AQVLKSHLQAQ	10643	VLKSHLQ	0.51406	-0.01612
SyS180	1466	GCCCAAAGCGACGGCCTCAGAACCCAAGCACAG	6055	AQSDGLRTQAQ	10644	SDGLRTQ	0.514048	-0.0323
TS118	1467	GCCCAACTCAACAGCGTCAAACCCAACGCACAG	6056	AQLNSVKPNAQ	10645	LNSVKPN	0.513525	-0.03938
SS33	1468	GCCCAAAGCCAAGCCATCGCCCCCAAAGCACAG	6057	AQSQAIAPKAQ	10646	SQAIAPK	0.51343	-0.30374
TS119	1469	GCCCAATCTAATAATGTTCGTGCTCCGGCACAG	6058	AQSNNVRAPAQ	10647	SNNVRAP	0.513257	0.427193
SyS182	1470	GCCCAAATCAGCCACCTCAGCGAAAGCGCACAG	6059	AQISHLSESAQ	10648	ISHLSES	0.511503	0.085806
SyS183	1471	GCCCAACTCCTCCCCGGCATGAGATTCGCACAG	6060	AQLLPGMRFAQ	10649	LLPGMRF	0.5114	-0.16587
GS102	1472	GCCCAACTTCTTGCGTCGGCTACGAAGGCACAG	6061	AQLLASATKAQ	10650	LLASATK	0.510718	0.025387
SS34	1473	GCCCAAAACCACAACGGCATGGTCAGCGCACAG	6062	AQNHNGMVSAQ	10651	NHNGMVS	0.510709	-0.38341
GS103	1474	GCCCAACACAGCGGCGAACTCAACAACGCACAG	6063	AQHSGELNNAQ	10652	HSGELNN	0.510488	-0.05547
GS104	1475	GCCCAACTTTCTGCGCCTAAGGATACTGCACAG	6064	AQLSAPKDTAQ	10653	LSAPKDT	0.509967	-0.10921
SyS184	1476	GCCCAAATTGGGACTCATGTGGGGACGGCACAG	6065	AQIGTHVGTAQ	10654	IGTHVGT	0.509748	-0.17337
SyS185	1477	GCCCAAGCCGTCGCCCTCGCCAGCGCCGCACAG	6066	AQAVALASAAQ	10655	AVALASA	0.509614	-0.02018
SyS186	1478	GCCCAAATTACTCTTCAGTCTAATGCTGCACAG	6067	AQITLQSNAAQ	10656	ITLQSNA	0.509556	0.125675
SyS187	1479	GCCCAAGTCGACCACAGCCTCACCAGCGCACAG	6068	AQVDHSLTSAQ	10657	VDHSLTS	0.509193	-0.04316
SyS188	1480	GCCCAAGGCAACGAAGCCACCAGCCTCGCACAG	6069	AQGNEATSLAQ	10658	GNEATSL	0.508729	-0.04706
SyS189	1481	GCCCAACCCGTCAGCAGCACCACCCTCGCACAG	6070	AQPVSSTTLAQ	10659	PVSSTTL	0.507682	0.051712

FIG. 33 (Continued)

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SyS190	1482	GCCCAACCCTACCAAACCAGCAGCGCCGCACAG	6071	AQPYQTSSAAQ	10660	PYQTSSA	0.507351	-0.04626
GS105	1483	GCCCAAACCAGCGTCGTCAGCGCCTTCGCACAG	6072	AQTSVVSAFAQ	10661	TSVVSAF	0.507058	-0.11758
SyS191	1484	GCCCAAAACGGCGTCCCCGACACAACAACGCACAG	6073	AQNGVPDNNAQ	10662	NGVPDNN	0.50693	0.070537
SyS192	1485	GCCCAAAGCACCCAAACCATCGGCTTCGCACAG	6074	AQSTQTIGFAQ	10663	STQTIGF	0.505905	0.112417
GP62	1486	GCCCAAATTCGGAGTTCTGATCTTGCGGCACAG	6075	AQIRSSDLAAQ	10664	IRSSDLA	0.505273	0.288145
GS106	1487	GCCCAAAACACCCAAAGCGCCAAATACGCACAG	6076	AQNTQSAKYAQ	10665	NTQSAKY	0.504002	-0.02585
GS107	1488	GCCCAAAGTCTTGAGTCGTCTAGGCAGGCACAG	6077	AQSLESSRQAQ	10666	SLESSRQ	0.503575	-0.02602
GS108	1489	GCCCAACTCAACCTCGCCAGCGGCAGAGCACAG	6078	AQLNLASGRAQ	10667	LNLASGR	0.503463	0.027635
GS110	1490	GCCCAAATGCAGGAGCGTCGGGAGTATGCACAG	6079	AQMQERREYAQ	10668	MQERREY	0.503055	-0.00468
GS111	1491	GCCCAATGGCTCCTCAAAGACGGCTACGCACAG	6080	AQWLLKDGYAQ	10669	WLLKDGY	0.502893	-0.11186
GS112	1492	GCCCAAGGCAGATACCAAACCACCAGCGCACAG	6081	AQGRYQTTSAQ	10670	GRYQTTS	0.502776	0.049992
TS120	1493	GCCCAAAATACGACGAAGTTTCCGTTTGCACAG	6082	AQNTTKFPFAQ	10671	NTTKFPF	0.502408	-0.33072
SyS193	1494	GCCCAAATGAGCAACGGCATCAGCAGAGCACAG	6083	AQMSNGISRAQ	10672	MSNGISR	0.501897	0.448521
GP65	1495	GCCCAACCGATTCGGGATCCGGAGAAGGCACAG	6084	AQPIRDPEKAQ	10673	PIRDPEK	0.501479	-0.07322
SyS194	1496	GCCCAAAGTACGCTGAGTCCGCATGTTGCACAG	6085	AQSTLSPHVAQ	10674	STLSPHV	0.501315	0.165485
GS113	1497	GCCCAATTCATGCCCATCAGCAGCGCCGCACAG	6086	AQFMPISSAAQ	10675	FMPISSA	0.50124	-0.12446
SS35	1498	GCCCAAAGAAGCGACACCCAAAGCAGCGCACAG	6087	AQRSDTQSSAQ	10676	RSDTQSS	0.500462	-0.28596
GS114	1499	GCCCAAGATAATCATGTTATGGCTCGTGCACAG	6088	AQDNHVMARAQ	10677	DNHVMAR	0.499435	0.39719
GS115	1500	GCCCAAAATCTGTCTTCTAAGAGTTGGGCACAG	6089	AQNLSSKSWAQ	10678	NLSSKSW	0.499211	-0.15138
SyS195	1501	GCCCAATCTACGATTCTGAAGGATACTGCACAG	6090	AQSTILKDTAQ	10679	STILKDT	0.499066	-0.11454
GS116	1502	GCCCAACCTACTCATCAGTCTAAGCCGGCACAG	6091	AQPTHQSKPAQ	10680	PTHQSKP	0.498305	-0.04153
SyS196	1503	GCCCAAACGGAGGTGACTCAGAATAAGGCACAG	6092	AQTEVTQNKAQ	10681	TEVTQNK	0.498059	-0.01173
SyS197	1504	GCCCAACACCTCGACAGCAACGGCAGCGCACAG	6093	AQHLDSNGSAQ	10682	HLDSNGS	0.496498	-0.10873
GP66	1505	GCCCAAAATACTGATTCTCGTGTGGGGGCACAG	6094	AQNTDSRVGAQ	10683	NTDSRVG	0.496267	0.009692
SyS198	1506	GCCCAAAGCATGGGCCTCAAAGAAAAAGCACAG	6095	AQSMGLKEKAQ	10684	SMGLKEK	0.495749	-0.04266
SyS199	1507	GCCCAATTGAGTACGTCGTATACTCGGGCACAG	6096	AQLSTSYTRAQ	10685	LSTSYTR	0.495598	0.048715
SyS200	1508	GCCCAATCTGGGATGAGTAATAATCATGCACAG	6097	AQSGMSNNHAQ	10686	SGMSNNH	0.494806	-0.1025
GS117	1509	GCCCAAACCAACTACGACCTCAGAGCCGCACAG	6098	AQTNYDLRAAQ	10687	TNYDLRA	0.494623	-0.03099
SyS201	1510	GCCCAAACCCCCCCAAGCCAAGAAATGGCACAG	6099	AQTPQSQEMAQ	10688	TPQSQEM	0.494147	0.127468
SyS202	1511	GCCCAAAATAGTAATATGGTTACGCCTGCACAG	6100	AQNSNMVTPAQ	10689	NSNMVTP	0.493868	-0.16466
SyS203	1512	GCCCAATCGGCTGTTCCGAATGTTAAGGCACAG	6101	AQSAVPNVKAQ	10690	SAVPNVK	0.493528	0.157825
SyS204	1513	GCCCAAGTCCTCGTCGCCGGCAGCAGAGGCACAG	6102	AQVLVAGSRAQ	10691	VLVAGSR	0.492961	0.099713

FIG. 33 (Continued)

TS122	1514	GCCCAAGGCAACAACAGCAGAAACATGGCACAG	6103	AQGNNSRNMAQ	10692	GNNSRNM	0.492799	1.174147
GP67	1515	GCCCAAATGCCTAGGGGTCATGTTTCGGCACAG	6104	AQMPRGHVSAQ	10693	MPRGHVS	0.492205	-0.07405
SyS205	1516	GCCCAATGGAGCCACAGCGAAAACAGCGCACAG	6105	AQWSHSENSAQ	10694	WSHSENS	0.492196	-0.02126
SyS206	1517	GCCCAATTTGAGAAGGATCCTGTGGCTGCACAG	6106	AQFEKDPVAAQ	10695	FEKDPVA	0.492179	-0.15574
GS119	1518	GCCCAAATTACTCAGGCTACTCCTAGTGCACAG	6107	AQITQATPSAQ	10696	ITQATPS	0.491986	-0.03869
SyS207	1519	GCCCAAGCCAACCTCAGCCACCTCCACGCACAG	6108	AQANLSHLHAQ	10697	ANLSHLH	0.491822	0.025681
SyS208	1520	GCCCAAGGCATCACCAACAGCACCATCGCACAG	6109	AQGITNSTIAQ	10698	GITNSTI	0.491721	0.067512
SyS209	1521	GCCCAACCGTCTCAGCAGCCTACTAGGGCACAG	6110	AQPSQQPTRAQ	10699	PSQQPTR	0.491643	-0.04338
GP68	1522	GCCCAACAGCAGACGCATGAGGATATTGCACAG	6111	AQQQTHEDIAQ	10700	QQTHEDI	0.491168	0.319954
GS120	1523	GCCCAACAGGTTAATGTGTCTCCGGATGCACAG	6112	AQQVNVSPDAQ	10701	QVNVSPD	0.491095	-0.10138
GS121	1524	GCCCAAAAAGCCGTCGTCACCCAAACCGCACAG	6113	AQKAVVTQTAQ	10702	KAVVTQT	0.490849	0.028741
GS122	1525	GCCCAAAATACTGTGAGGTCGTCGACTGCACAG	6114	AQNTVRSSTAQ	10703	NTVRSST	0.4904	-0.06069
SyS210	1526	GCCCAAAACGCCAGCAGCCACCTCCTCGCACAG	6115	AQNASSHLLAQ	10704	NASSHLL	0.490369	0.136447
SyS211	1527	GCCCAATACATCAAAGACAGCACCCCCGCACAG	6116	AQYIKDSTPAQ	10705	YIKDSTP	0.490186	0.300211
GS123	1528	GCCCAAAGCAGCGAAAGCACCAACCTCGCACAG	6117	AQSSESTNLAQ	10706	SSESTNL	0.490052	-0.11765
SyS212	1529	GCCCAAAAAGAAAACGTCGAAGGCAACGCACAG	6118	AQKENVEGNAQ	10707	KENVEGN	0.489872	-0.03302
GS124	1530	GCCCAAAACAACGTCCTCGGCACCCCCGCACAG	6119	AQNNVLGTPAQ	10708	NNVLGTP	0.488512	-0.01901
SyS213	1531	GCCCAACAGAATGTTAGTATTTTGGATGCACAG	6120	AQQNVSILDAQ	10709	QNVSILD	0.48837	-0.0119
SyS214	1532	GCCCAACCTCTGAATTCTGAGAATAATGCACAG	6121	AQPLNSENNAQ	10710	PLNSENN	0.48837	-0.05918
SyS215	1533	GCCCAAACGATTAATCTGGTTGGGTATGCACAG	6122	AQTINLVGYAQ	10711	TINLVGY	0.48837	-0.12222
SyS216	1534	GCCCAACCGGCGTTGGCTGCTCAGGCTGCACAG	6123	AQPALAAQAAQ	10712	PALAAQA	0.48837	-0.18527
SyS217	1535	GCCCAAACTTTGCAGAATTCGATTACGGCACAG	6124	AQTLQNSITAQ	10713	TLQNSIT	0.488231	0.404837
SyS218	1536	GCCCAATTGGGTGGGACGGATGGTCATGCACAG	6125	AQLGGTDGHAQ	10714	LGGTDGH	0.488086	0.359793
SyS219	1537	GCCCAAGCCGGCCCCATCAACAACACCGCACAG	6126	AQAGPINNTAQ	10715	AGPINNT	0.487009	-0.04018
SyS220	1538	GCCCAACATGTTCTTACGCAGTCGGTTGCACAG	6127	AQHVLTQSVAQ	10716	HVLTQSV	0.486848	-0.08758
SyS221	1539	GCCCAAACCACCATCCCCAGCCACCAAGCACAG	6128	AQTTIPSHQAQ	10717	TTIPSHQ	0.486769	0.226515
SyS222	1540	GCCCAACACGACGGCCTCCTCAGCAGAGCACAG	6129	AQHDGLLSRAQ	10718	HDGLLSR	0.4866	-0.01772
SyS223	1541	GCCCAAAGCATCCACACCGGCCTCACCGCACAG	6130	AQSIHTGLTAQ	10719	SIHTGLT	0.486103	0.205807
TS123	1542	GCCCAAGGGAATATGACTAAGTTTACTGCACAG	6131	AQGNMTKFTAQ	10720	GNMTKFT	0.486051	0.259785
SyS224	1543	GCCCAATATGCTTTGAGTACTGATACGGCACAG	6132	AQYALSTDTAQ	10721	YALSTDT	0.485653	-0.07425
SyS225	1544	GCCCAAACCCAAGCCGACAACCTCAAAGCACAG	6133	AQTQADNLKAQ	10722	TQADNLK	0.485417	0.113729
SyS226	1545	GCCCAATGGTACAAAACCCTCGACGCCGCACAG	6134	AQWYKTLDAAQ	10723	WYKTLDA	0.485398	-0.10234

FIG. 33 (Continued)

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GS126	1546	GCCCAACCCCAATACGCCAAAATCAGCGCACAG	6135	AQPQYAKISAQ	10724	PQYAKIS	0.485373	-0.12737
SyS227	1547	GCCCAACTCGCCACCGACAACAAAAGCGCACAG	6136	AQLATDNKSAQ	10725	LATDNKS	0.485187	0.216017
SyS228	1548	GCCCAACTCAGCGTCGTCATCACCAGCGCACAG	6137	AQLSVVITSAQ	10726	LSVVITS	0.484761	-0.14162
SyS229	1549	GCCCAAAATGTGCCGACTTCGCCGCGGGCACAG	6138	AQNVPTSPRAQ	10727	NVPTSPR	0.484481	-0.00571
SyS230	1550	GCCCAAGCCAGACCCGACCTCAAACTCGCACAG	6139	AQARPDLKLAQ	10728	ARPDLKL	0.484242	0.080867
SyS231	1551	GCCCAAAGCGCCCTCGCCAACACCCTCGCACAG	6140	AQSALANTLAQ	10729	SALANTL	0.483363	0.057201
SyS232	1552	GCCCAACTCATGGACTTCAGCAACCCCGCACAG	6141	AQLMDFSNPAQ	10730	LMDFSNP	0.483298	0.044546
SyS233	1553	GCCCAACCTCGGACGGAGTTGATTAGTGCACAG	6142	AQPRTELISAQ	10731	PRTELIS	0.483008	0.271785
SyS234	1554	GCCCAAACCAGCGACATCAAAAGCAAAGCACAG	6143	AQTSDIKSKAQ	10732	TSDIKSK	0.482661	0.009004
GS127	1555	GCCCAAAGCAACGCCACCATGAGATTCGCACAG	6144	AQSNATMRFAQ	10733	SNATMRF	0.482544	0.332692
SyS235	1556	GCCCAAGTCCAAAGCCCCGCCCTCCAAGCACAG	6145	AQVQSPALQAQ	10734	VQSPALQ	0.482506	-0.10268
SS37	1557	GCCCAAACCGCCAACACCACCAGCAGAGCACAG	6146	AQTANTTSRAQ	10735	TANTTSR	0.481309	-0.14344
GS128	1558	GCCCAACAACACATGACCAGCCAAATCGCACAG	6147	AQQHMTSQIAQ	10736	QHMTSQI	0.481226	0.067575
GS129	1559	GCCCAAAGTAATATGTCGTTGAGTAGTGCACAG	6148	AQSNMSLSSAQ	10737	SNMSLSS	0.481136	-0.01785
SyS237	1560	GCCCAAATTACGGGGATTCCGACGTCGGCACAG	6149	AQITGIPTSAQ	10738	ITGIPTS	0.480328	0.061154
GS130	1561	GCCCAATTTACTAATAATGTGAGGGATGCACAG	6150	AQFTNNVRDAQ	10739	FTNNVRD	0.480193	0.04554
SyS238	1562	GCCCAAAACAGCAACGCCGGCGGCAAAGCACAG	6151	AQNSNAGGKAQ	10740	NSNAGGK	0.479053	0.658688
SyS239	1563	GCCCAATACAACACCGACATCACCAAAGCACAG	6152	AQYNTDITKAQ	10741	YNTDITK	0.478109	0.317854
SyS240	1564	GCCCAATTTTCGAATCCGGATAAGATGGCACAG	6153	AQFSNPDKMAQ	10742	FSNPDKM	0.477665	-0.02779
SyS241	1565	GCCCAACTCATGACCACCAGCACCATCGCACAG	6154	AQLMTTSTIAQ	10743	LMTTSTI	0.476766	0.149339
TS124	1566	GCCCAAACGAATAGTACTCTTAGGCAGGCACAG	6155	AQTNSTLRQAQ	10744	TNSTLRQ	0.476574	0.068959
TS125	1567	GCCCAATCGAATTATACTAAGATTATTGCACAG	6156	AQSNYTKIIAQ	10745	SNYTKII	0.475873	0.12486
GS132	1568	GCCCAATCTGCTGGGCTTATTTCTTCGGCACAG	6157	AQSAGLISSAQ	10746	SAGLISS	0.475737	-0.10204
SyS242	1569	GCCCAAAAGCAGGGTCCGATGCTGTCTGCACAG	6158	AQKQGPMLSAQ	10747	KQGPMLS	0.475731	-0.02565
SyS243	1570	GCCCAAGTGAGGACTCCGGGTGTGCAGGCACAG	6159	AQVRTPGVQAQ	10748	VRTPGVQ	0.475278	0.173488
SyS244	1571	GCCCAAACTCCTGATCATCGGGAGCGGGCACAG	6160	AQTPDHRERAQ	10749	TPDHRER	0.473388	-0.13798
SyS245	1572	GCCCAAATGAATGCTACTGTTCCTTCTGCACAG	6161	AQMNATVPSAQ	10750	MNATVPS	0.472837	0.213593
SyS246	1573	GCCCAACTCCACAGCATGCTCGCCCCCGCACAG	6162	AQLHSMLAPAQ	10751	LHSMLAP	0.472535	0.03056
SyS247	1574	GCCCAAGACATGCACCACAGCCAACCCGCACAG	6163	AQDMHHSQPAQ	10752	DMHHSQP	0.472429	0.422194
GS133	1575	GCCCAAAAACCCCTCCCCACCACCTACGCACAG	6164	AQKPLPTTYAQ	10753	KPLPTTY	0.472296	-0.09564
GS134	1576	GCCCAAGCCATGCAAGTCACCCTCAGCGCACAG	6165	AQAMQVTLSAQ	10754	AMQVTLS	0.471652	-0.13615
GS135	1577	GCCCAAAGCCCCACCCACGACGCCAGAGCACAG	6166	AQSPTHDARAQ	10755	SPTHDAR	0.471243	-0.00229

FIG. 33 (Continued)

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SyS248	1578	GCCCAAGCGCTTTCTGTTAAGGAGCTTGCACAG	6167	AQALSVKELAQ	10756	ALSVKEL	0.470954	-0.13187
GP70	1579	GCCCAACCGTCTCGTGTGCCGACTCAGGCACAG	6168	AQPSRVPTQAQ	10757	PSRVPTQ	0.470688	-0.07252
SyS250	1580	GCCCAAGGCAGCCTCGGCCTCGGCAAAGCACAG	6169	AQGSLGLGKAQ	10758	GSLGLGK	0.470335	0.013558
SyS251	1581	GCCCAACATAGTTCGTATTCGTCGAAGGCACAG	6170	AQHSSYSSKAQ	10759	HSSYSSK	0.469692	-0.15617
GS136	1582	GCCCAACCGAATCCTAGTAATCCTTCTGCACAG	6171	AQPNPSNPSAQ	10760	PNPSNPS	0.469689	-0.12006
GP71	1583	GCCCAAACTAAGAATGGTGTTGCGCAGGCACAG	6172	AQTKNGVAQAQ	10761	TKNGVAQ	0.469615	0.072268
GP72	1584	GCCCAAGGTAGTACGAGTAGTGCTTATGCACAG	6173	AQGSTSSAYAQ	10762	GSTSSAY	0.469559	0.258704
SyS253	1585	GCCCAAAGAAGCACCCACGAAAACACCGCACAG	6174	AQRSTHENTAQ	10763	RSTHENT	0.467377	0.19944
SyS254	1586	GCCCAATCTGGTCATGATCGTGATGCTGCACAG	6175	AQSGHDRDAAQ	10764	SGHDRDA	0.466417	0.040229
SyS255	1587	GCCCAAAATACTCAGTCTTATACTAGTGCACAG	6176	AQNTQSYTSAQ	10765	NTQSYTS	0.466373	-0.08867
SyS256	1588	GCCCAAGATCGTGTTCCGCATTTGCGGGCACAG	6177	AQDRVPHLRAQ	10766	DRVPHLR	0.466296	-0.16397
SyS257	1589	GCCCAAAATAATCCGCCTCATATGCGGGGCACAG	6178	AQNNPPHMRAQ	10767	NNPPHMR	0.465834	-0.1254
SyS258	1590	GCCCAAAGAAGCCTCCAAAGCCAATTCGCACAG	6179	AQRSLQSQFAQ	10768	RSLQSQF	0.465601	-0.06774
SyS259	1591	GCCCAAATTCGTGATGATCGGTCTTTGGCACAG	6180	AQIRDDRSLAQ	10769	IRDDRSL	0.465259	0.094784
GS137	1592	GCCCAAATGTTGTCTGCTCCGCTGCCGGCACAG	6181	AQMLSAPLPAQ	10770	MLSAPLP	0.465145	-0.10658
SyS260	1593	GCCCAAACTTCGAGTATTTTGACTACGGCACAG	6182	AQTSSILTTAQ	10771	TSSILTT	0.465093	0.037804
SyS261	1594	GCCCAACGTGAGCAGATGAATCTTGTGGCACAG	6183	AQREQMNLVAQ	10772	REQMNLV	0.464872	-0.01918
SyS262	1595	GCCCAAAAGACGCAGAGTTTGAGTAATGCACAG	6184	AQKTQSLSNAQ	10773	KTQSLSN	0.464418	0.284303
SyS263	1596	GCCCAATTGAAGACTGCTGAGTATACTGCACAG	6185	AQLKTAEYTAQ	10774	LKTAEYT	0.464287	0.205827
SyS264	1597	GCCCAATCGAGTGAGAAGCCGTTTCGGGCACAG	6186	AQSSEKPFRAQ	10775	SSEKPFR	0.464115	0.348084
SyS265	1598	GCCCAACCCACCAGCGGCGTCTTCGGCGCACAG	6187	AQPTSGVFGAQ	10776	PTSGVFG	0.464095	-0.13314
SyS266	1599	GCCCAAGGCCCCAGCATCGTCACCATGGCACAG	6188	AQGPSIVTMAQ	10777	GPSIVTM	0.464061	0.018407
SyS267	1600	GCCCAAACGAGTGATAAGAGTTCGCTTGCACAG	6189	AQTSDKSSLAQ	10778	TSDKSSL	0.463586	0.196158
SyS268	1601	GCCCAAAATACTATTACTATGGCTAAGGCACAG	6190	AQNTITMAKAQ	10779	NTITMAK	0.46346	0.027199
GS139	1602	GCCCAACGGAATCAGCCTGTTCCGAGTGCACAG	6191	AQRNQPVPSAQ	10780	RNQPVPS	0.463054	-0.12521
SyS269	1603	GCCCAAAGCGTCCACCTCAACCTCCAAGCACAG	6192	AQSVHLNLQAQ	10781	SVHLNLQ	0.463008	-0.15411
SyS270	1604	GCCCAATATAATCTGACGATGGTTAGTGCACAG	6193	AQYNLTMVSAQ	10782	YNLTMVS	0.462794	-0.10646
GS140	1605	GCCCAAACCGCCGACAGCCACCCCAGAGCACAG	6194	AQTADSHPRAQ	10783	TADSHPR	0.462708	-0.06423
SyS271	1606	GCCCAATTGCTTGGTGAGAAGGTGATGGCACAG	6195	AQLLGEKVMAQ	10784	LLGEKVM	0.462387	0.138902
SyS272	1607	GCCCAATGGGATCTGACTGCTCCGCAGGCACAG	6196	AQWDLTAPQAQ	10785	WDLTAPQ	0.462376	-0.1489
SyS273	1608	GCCCAAGTGCTTGCTGATCGTCTTCCGGCACAG	6197	AQVLADRLPAQ	10786	VLADRLP	0.461956	-0.00299
SyS274	1609	GCCCAATCTCGTGCGCTGCCGAATTCGGCACAG	6198	AQSRALPNSAQ	10787	SRALPNS	0.461886	-0.05729

FIG. 33 (Continued)

SyS276	1610	GCCCAAAGCAGCCTCAACATGCCCAGAGCACAG	6199	AQSSLNMPRAQ	10788	SSLNMPR	0.461752	0.063904
GS141	1611	GCCCAACAGAAGGTTTCGATTTTGGCTGCACAG	6200	AQQKVSILAAQ	10789	QKVSILA	0.461267	-0.03269
GS142	1612	GCCCAAAGAGGCGACAACAGCAGACTCGCACAG	6201	AQRGDNSRLAQ	10790	RGDNSRL	0.461258	-0.08034
SyS277	1613	GCCCAAAGAATCGACCTCGGCAGCCAAGCACAG	6202	AQRIDLGSQAQ	10791	RIDLGSQ	0.461247	0.339499
SyS278	1614	GCCCAAGCGTCGCTGGGTCTTCGGGCTGCACAG	6203	AQASLGLRAAQ	10792	ASLGLRA	0.461166	-0.04662
GS143	1615	GCCCAATCGATGCAGAATGGTCTTCGGGCACAG	6204	AQSMQNGLRAQ	10793	SMQNGLR	0.460831	-0.12628
SyS279	1616	GCCCAAACGTTGGCTGTGGGGATTGCGGCACAG	6205	AQTLAVGIAAQ	10794	TLAVGIA	0.46068	0.081823
SyS280	1617	GCCCAAGGGCAGACTGTGACGGGGGCGGCACAG	6206	AQGQTVTGAAQ	10795	GQTVTGA	0.460554	0.339252
SyS281	1618	GCCCAACATGCTTTGAGTCCTTCTCCGGCACAG	6207	AQHALSPSPAQ	10796	HALSPSP	0.459785	0.442724
GS144	1619	GCCCAAGTCAGCAGCGTCTTCACCGAAGCACAG	6208	AQVSSVFTEAQ	10797	VSSVFTE	0.459264	-0.12544
GS145	1620	GCCCAATACGGCGCCGGCGCCGTCAAAGCACAG	6209	AQYGAGAVKAQ	10798	YGAGAVK	0.459168	-0.15792
GS146	1621	GCCCAAAAAGAAACCCTCCCCAACGCCGCACAG	6210	AQKETLPNAAQ	10799	KETLPNA	0.458924	0.031664
GS147	1622	GCCCAAATCCCCAGCCAAACCCCCCTCGCACAG	6211	AQIPSQTPLAQ	10800	IPSQTPL	0.458515	0.02063
SyS282	1623	GCCCAAAGCGCCATCAGCACCTTCGTCGCACAG	6212	AQSAISTFVAQ	10801	SAISTFV	0.458157	0.041708
SyS283	1624	GCCCAAGTCAACAGCACCAGCAGCACCGCACAG	6213	AQVNSTSSTAQ	10802	VNSTSST	0.458101	0.362297
GS148	1625	GCCCAACCTACGCGTGATTATAAGGAGGCACAG	6214	AQPTRDYKEAQ	10803	PTRDYKE	0.457355	-0.10546
GS149	1626	GCCCAAAACAACCCCGCCAGCACCCAAGCACAG	6215	AQNNPASTQAQ	10804	NNPASTQ	0.457315	-0.17195
SyS284	1627	GCCCAAGTGACGCAGACGTCTGTTAATGCACAG	6216	AQVTQTSVNAQ	10805	VTQTSVN	0.456877	0.386968
SyS285	1628	GCCCAATGGGCCGGCACCACCAGCCACGCACAG	6217	AQWAGTTSHAQ	10806	WAGTTSH	0.45637	0.26665
SyS286	1629	GCCCAAGTCACCGCCGGCTTCAGCGCCGCACAG	6218	AQVTAGFSAAQ	10807	VTAGFSA	0.455591	0.020831
SyS287	1630	GCCCAATTGCATTCTCCTTCTATGCAGGCACAG	6219	AQLHSPSMQAQ	10808	LHSPSMQ	0.454973	-0.08509
GS151	1631	GCCCAATTTCCTACGCAGCCTTCGATGGCACAG	6220	AQFPTQPSMAQ	10809	FPTQPSM	0.454886	-0.05716
SyS288	1632	GCCCAAGCCCAAAGCGTCAACGACGGCGCACAG	6221	AQAQSVNDGAQ	10810	AQSVNDG	0.454548	-0.14283
SyS289	1633	GCCCAAGTCGCCAGCACCACCTACACCGCACAG	6222	AQVASTTYTAQ	10811	VASTTYT	0.454439	0.100393
SyS290	1634	GCCCAACTGGGGGGGTTGAATTCGGTGGCACAG	6223	AQLGGLNSVAQ	10812	LGGLNSV	0.454111	0.166066
SyS291	1635	GCCCAAGCCGGCGCCCCCAGCCTCAGCGCACAG	6224	AQAGAPSLSAQ	10813	AGAPSLS	0.452883	-0.02402
TS126	1636	GCCCAAAGTAATAGGAAGATTGATGATGCACAG	6225	AQSNRKIDDAQ	10814	SNRKIDD	0.452682	0.231949
GP73	1637	GCCCAATCTCCTAATAATAGGGCTGTGGCACAG	6226	AQSPNNRAVAQ	10815	SPNNRAV	0.452479	0.244087
SyS293	1638	GCCCAAGTTTTGAGGGAGGATCAGTCGGCACAG	6227	AQVLREDQSAQ	10816	VLREDQS	0.452095	-0.02524
SyS294	1639	GCCCAACTTCTTGCGACTGGGCTTAAGGCACAG	6228	AQLLATGLKAQ	10817	LLATGLK	0.452095	-0.17193
GS152	1640	GCCCAAGTCCACCTCAGAAGCCAAATCGCACAG	6229	AQVHLRSQIAQ	10818	VHLRSQI	0.451987	-0.18149
GS153	1641	GCCCAAAGTGCGAATTCGAATTTGAAGGCACAG	6230	AQSANSNLKAQ	10819	SANSNLK	0.451973	0.020578

FIG. 33 (Continued)

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SyS295	1642	GCCCAAAGCAAAGCCGGCGAAGGCAACGCACAG	6231	AQSKAGEGNAQ	10820	SKAGEGN	0.451948	0.034237
SyS296	1643	GCCCAAGTCAGCAACCCCGCCATGAAAGCACAG	6232	AQVSNPAMKAQ	10821	VSNPAMK	0.451812	0.252408
GS154	1644	GCCCAAATCAACGGCAACAACCAAAGAGCACAG	6233	AQINGNNQRAQ	10822	INGNNQR	0.451801	0.154055
SP30	1645	GCCCAATATAAGTCGACGACTCTTTCTGCACAG	6234	AQYKSTTLSAQ	10823	YKSTTLS	0.451779	-0.05333
SyS297	1646	GCCCAAAAAGAAGGCCTCGTCAGCAGAGCACAG	6235	AQKEGLVSRAQ	10824	KEGLVSR	0.451637	0.196029
GS155	1647	GCCCAACACCTCAAAGTCATGACCATCGCACAG	6236	AQHLKVMTIAQ	10825	HLKVMTI	0.451183	-0.16304
SyS298	1648	GCCCAAAGAACCAACGACCACAGCAGCGCACAG	6237	AQRTNDHSSAQ	10826	RTNDHSS	0.45114	0.269153
SyS299	1649	GCCCAACTGCCTTCTCAGTCTGCTAAGGCACAG	6238	AQLPSQSAKAQ	10827	LPSQSAK	0.450976	-0.15061
GS156	1650	GCCCAAATTACGCTGAGGCATTTGCAGGCACAG	6239	AQITLRHLQAQ	10828	ITLRHLQ	0.45092	-0.16814
SyS300	1651	GCCCAACAAATGATCGCCAACATCCCCGCACAG	6240	AQQMIANIPAQ	10829	QMIANIP	0.450647	0.113255
SyS301	1652	GCCCAAAGTTCTTCGACTGATCAGCATGCACAG	6241	AQSSSTDQHAQ	10830	SSSTDQH	0.450468	-0.09886
SyS302	1653	GCCCAAAGAAGCACCGACTTCACCCCCGCACAG	6242	AQRSTDFTPAQ	10831	RSTDFTP	0.450431	-0.13428
SyS303	1654	GCCCAACAGCATGCGTCTATTTCTGCTGCACAG	6243	AQQHASISAAQ	10832	QHASISA	0.450427	0.019295
GS157	1655	GCCCAAAACATCAGCAGCATGCAAATGGCACAG	6244	AQNISSMQMAQ	10833	NISSMQM	0.450075	-0.06541
GS158	1656	GCCCAATCGGGGAATGTTGTGGGGCGGGCACAG	6245	AQSGNVVGRAQ	10834	SGNVVGR	0.449772	-0.03169
SyS304	1657	GCCCAAAGCAAAGGCGACACCAGCGCCGCACAG	6246	AQSKGDTSAAQ	10835	SKGDTSA	0.449763	0.203441
SyS306	1658	GCCCAACTGCTGAATACGGGGACTAAGGCACAG	6247	AQLLNTGTKAQ	10836	LLNTGTK	0.448254	0.095948
GS159	1659	GCCCAAGGTACTGGGGCTAGTATGAATGCACAG	6248	AQGTGASMNAQ	10837	GTGASMN	0.448204	-0.05716
SyS307	1660	GCCCAACGTCTTGATGCGAATTCTACGGCACAG	6249	AQRLDANSTAQ	10838	RLDANST	0.448191	0.242147
GS161	1661	GCCCAACTCCCCGAAAGACCCAACAGCGCACAG	6250	AQLPERPNSAQ	10839	LPERPNS	0.448013	-0.01858
SyS308	1662	GCCCAAGCCAGAGAAATCCTCAACCACGCACAG	6251	AQAREILNHAQ	10840	AREILNH	0.447539	-0.01147
GS162	1663	GCCCAAAACTTCAAAACCACCAACAGCGCACAG	6252	AQNFKTTNSAQ	10841	NFKTTNS	0.447528	0.230441
GS163	1664	GCCCAAGGCAGAACCGTCCAAGACAGAGCACAG	6253	AQGRTVQDRAQ	10842	GRTVQDR	0.447505	0.075102
GS164	1665	GCCCAAGGTATGAATCAGACGACGACTGCACAG	6254	AQGMNQTTTAQ	10843	GMNQTTT	0.446073	-0.05268
SyS309	1666	GCCCAAGTCGGCAAAGACGGCGTCCTCGCACAG	6255	AQVGKDGVLAQ	10844	VGKDGVL	0.445922	0.442273
GS165	1667	GCCCAAGTCACCAGAGACGGCGCCAAAGCACAG	6256	AQVTRDGAKAQ	10845	VTRDGAK	0.444855	0.06699
GS166	1668	GCCCAAGGTACTGCTACGTATGGTAAGGCACAG	6257	AQGTATYGKAQ	10846	GTATYGK	0.444487	-0.00843
SyS310	1669	GCCCAAATGTTGGGTGCTGAGGGGTATGCACAG	6258	AQMLGAEGYAQ	10847	MLGAEGY	0.444372	-0.08881
SyS311	1670	GCCCAAGTCACCCAACAAAACCACCACGCACAG	6259	AQVTQQNHHAQ	10848	VTQQNHH	0.444284	0.142962
SyS312	1671	GCCCAAACCGTCAACGCCGACCAACTCGCACAG	6260	AQTVNADQLAQ	10849	TVNADQL	0.444272	0.091137
GS167	1672	GCCCAACAGATGCAGAATAGTCCTATTGCACAG	6261	AQQMQNSPIAQ	10850	QMQNSPI	0.443818	-0.13896
SyS313	1673	GCCCAAGGGACGCTGGCGAGTTCGAAGGCACAG	6262	AQGTLASSKAQ	10851	GTLASSK	0.443282	0.256025

FIG. 33 (Continued)

GS169	1674	GCCCAATCTAATGTGACGATTGCGCATGCACAG	6263	AQSNVTIAHAQ	10852	SNVTIAH	0.442526	-0.12177
GS170	1675	GCCCAAGCGAATAATTCTCGTCCGTTTGCACAG	6264	AQANNSRPFAQ	10853	ANNSRPF	0.442454	0.419078
SyS314	1676	GCCCAAATTGCGACGGCGGGTGGTCCTGCACAG	6265	AQIATAGGPAQ	10854	IATAGGP	0.441873	0.058602
SyS315	1677	GCCCAAGCCTTCAGCGGCCCCAGCAGAGCACAG	6266	AQAFSGPSRAQ	10855	AFSGPSR	0.441659	0.035379
SyS316	1678	GCCCAACTCACCAACCTCGTCAGCAGAGCACAG	6267	AQLTNLVSRAQ	10856	LTNLVSR	0.441549	0.067167
SyS317	1679	GCCCAAGCCGGCCAACACCTCGCCCTCGCACAG	6268	AQAGQHLALAQ	10857	AGQHLAL	0.441104	-0.01578
SyS318	1680	GCCCAAAGTGTTGTGGCGTCTGCGAATGCACAG	6269	AQSVVASANAQ	10858	SVVASAN	0.441056	0.010976
SyS319	1681	GCCCAAGAGACTGTTTCGACTAGTCTTGCACAG	6270	AQETVSTSLAQ	10859	ETVSTSL	0.441048	-0.09691
SyS320	1682	GCCCAAATCCTCGCCGCCCTCACCGGCGCACAG	6271	AQILAALTGAQ	10860	ILAALTG	0.440956	-0.10525
SyS321	1683	GCCCAAACGACGGATAAGGCTGCGCTTGCACAG	6272	AQTTDKAALAQ	10861	TTDKAAL	0.440639	0.0093
SyS322	1684	GCCCAATACCTCGACAAACCCGGCGCCGCACAG	6273	AQYLDKPGAAQ	10862	YLDKPGA	0.43977	0.043522
SyS323	1685	GCCCAACCCAACCTCAGCAACCTCATGGCACAG	6274	AQPNLSNLMAQ	10863	PNLSNLM	0.439343	0.188183
SyS324	1686	GCCCAAATTAATGCGCCTACGGCTAGTGCACAG	6275	AQINAPTASAQ	10864	INAPTAS	0.439282	0.11633
SyS325	1687	GCCCAACATGGTGGTACGAGTCTGGCTGCACAG	6276	AQHGGTSLAAQ	10865	HGGTSLA	0.439114	0.231778
SyS326	1688	GCCCAAAATATTCAGTTGTCTCTTGCTGCACAG	6277	AQNIQLSLAAQ	10866	NIQLSLA	0.438906	-0.04774
SyS327	1689	GCCCAAACTCTTCATATGTCTAGTAAGGCACAG	6278	AQTLHMSSKAQ	10867	TLHMSSK	0.438887	-0.06151
GS171	1690	GCCCAAGCCATCATCAACCCCCACAGCGCACAG	6279	AQAIINPHSAQ	10868	AIINPHS	0.438571	-0.07991
SyS328	1691	GCCCAAAATACTCTGATTAATGTTAGTGCACAG	6280	AQNTLINVSAQ	10869	NTLINVS	0.438518	-0.09555
SyS329	1692	GCCCAAAACAGCGTCGTCCTCGCCATGGCACAG	6281	AQNSVVLAMAQ	10870	NSVVLAM	0.438471	-0.12176
SyS330	1693	GCCCAAAATATGGCTTCTTTGTCGGCGGCACAG	6282	AQNMASLSAAQ	10871	NMASLSA	0.438292	0.417265
GS172	1694	GCCCAAAGCAGCACCCACCTCCTCGCCGCACAG	6283	AQSSTHLLAAQ	10872	SSTHLLA	0.438222	-0.05576
SyS331	1695	GCCCAAGACAACAGCCAAAGCGACAAAGCACAG	6284	AQDNSQSDKAQ	10873	DNSQSDK	0.437981	-0.03541
GS173	1696	GCCCAAGGCATCACCACCAACGCCCACGCACAG	6285	AQGITTNAHAQ	10874	GITTNAH	0.437698	0.041733
SyS332	1697	GCCCAATCTAGTACTATTAATGGGTATGCACAG	6286	AQSSTINGYAQ	10875	SSTINGY	0.437133	-0.0969
SyS333	1698	GCCCAAAATCATACGCGGATGAATGAGGCACAG	6287	AQNHTRMNEAQ	10876	NHTRMNE	0.436984	0.166362
GS174	1699	GCCCAAGGCAACCAACAAAAAAACCTCGCACAG	6288	AQGNQQKNLAQ	10877	GNQQKNL	0.436441	-0.03233
GS175	1700	GCCCAAGGTACGAGTGATCGGCAGCAGGCACAG	6289	AQGTSDRQQAQ	10878	GTSDRQQ	0.436147	0.02699
GS176	1701	GCCCAAAGCGACAGCGAATACAAACCCGCACAG	6290	AQSDSEYKPAQ	10879	SDSEYKP	0.435589	-0.08679
SyS334	1702	GCCCAAACGGCTGCGCATGTTAGTTATGCACAG	6291	AQTAAHVSYAQ	10880	TAAHVSY	0.435197	-0.16291
SyS335	1703	GCCCAAATGGCCACCACCCACGCCGCCGCACAG	6292	AQMATTHAAAQ	10881	MATTHAA	0.434993	0.274299
TS128	1704	GCCCAAAACAGCGTCAGACAAAGCCTCGCACAG	6293	AQNSVRQSLAQ	10882	NSVRQSL	0.434805	-0.16564
SyS336	1705	GCCCAATCGGGTAGTGGTGTTAGTAGTGCACAG	6294	AQSGSGVSSAQ	10883	SGSGVSS	0.434548	0.291222

FIG. 33 (Continued)

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SyS337	1706	GCCCAACCCACCACCAGAATCACCGACGCACAG	6295	AQPTTRITDAQ	10884	PTTRITD	0.434069	0.294752
SyS338	1707	GCCCAAAGTCATGAGGCGAAGAATCCTGCACAG	6296	AQSHEAKNPAQ	10885	SHEAKNP	0.433539	-0.031
SyS339	1708	GCCCAACCGTATAGTACTGCTGATCGGGCACAG	6297	AQPYSTADRAQ	10886	PYSTADR	0.433522	-0.04024
GS177	1709	GCCCAAATGCTCAGCAACACCAACCACGCACAG	6298	AQMLSNTNHAQ	10887	MLSNTNH	0.433305	0.052866
GS178	1710	GCCCAAAGCCTCGGCCTCGGCGGCAGCGCACAG	6299	AQSLGLGGSAQ	10888	SLGLGGS	0.433248	-0.04395
GS179	1711	GCCCAAAACGCCATGAACATGCCCGTCGCACAG	6300	AQNAMNMPVAQ	10889	NAMNMPV	0.433136	-0.04434
GS180	1712	GCCCAAATGCTTGGGCATATTGCGAATGCACAG	6301	AQMLGHIANAQ	10890	MLGHIAN	0.432465	-0.11638
SyS341	1713	GCCCAAAAAGGCCAAACCGTCAGCGAAGCACAG	6302	AQKGQTVSEAQ	10891	KGQTVSE	0.432458	0.072331
GS181	1714	GCCCAAATGGATAATCGTAATAATTGGGCACAG	6303	AQMDNRNNWAQ	10892	MDNRNNW	0.43156	-0.1586
GP76	1715	GCCCAACTGTTGCATAGGAATGATGTTGCACAG	6304	AQLLHRNDVAQ	10893	LLHRNDV	0.431521	-0.0735
SyS342	1716	GCCCAAGCTAATCTGGTTTCGGCGAAGGCACAG	6305	AQANLVSAKAQ	10894	ANLVSAK	0.431404	-0.07004
GS182	1717	GCCCAAAGTCTGACGAGGGATCTGAAGGCACAG	6306	AQSLTRDLKAQ	10895	SLTRDLK	0.431179	-0.08846
SyS343	1718	GCCCAAGGTGGGCAGATTGTGTCGCGTGCACAG	6307	AQGGQIVSRAQ	10896	GGQIVSR	0.430648	-0.00826
SyS344	1719	GCCCAAAATTATACTCCTGATAAGAGGGCACAG	6308	AQNYTPDKRAQ	10897	NYTPDKR	0.430568	-0.16745
SyS345	1720	GCCCAACTCTACGCCAACCACCACAGCGCACAG	6309	AQLYANHHSAQ	10898	LYANHHS	0.430452	-0.081
SyS346	1721	GCCCAAGAGAGTGTGGCTGGGCATATGGCACAG	6310	AQESVAGHMAQ	10899	ESVAGHM	0.430163	-0.1063
GP77	1722	GCCCAAGAGCCTCGTCAGGATGCGCATGCACAG	6311	AQEPRQDAHAQ	10900	EPRQDAH	0.43013	0.337418
SyS347	1723	GCCCAAAGCGTCGGCGGCACCACCCAAGCACAG	6312	AQSVGGTTQAQ	10901	SVGGTTQ	0.430117	0.05114
SyS348	1724	GCCCAACAACCCGCCATGTTCAACGGCGCACAG	6313	AQQPAMFNGAQ	10902	QPAMFNG	0.430117	-0.15374
GS184	1725	GCCCAAGTCAAACAAACCGTCATGAGCGCACAG	6314	AQVKQTVMSAQ	10903	VKQTVMS	0.429804	-8.09E-05
SyS349	1726	GCCCAACTTTATGAGCAGGCTTCTAAGGCACAG	6315	AQLYEQASKAQ	10904	LYEQASK	0.429754	0.124383
SyS350	1727	GCCCAAATTAATGCGGCGATTGCTCTGGCACAG	6316	AQINAAIALAQ	10905	INAAIAL	0.429581	-0.21436
SyS351	1728	GCCCAACTCGAACTCAGCCACAGCAGAGCACAG	6317	AQLELSHSRAQ	10906	LELSHSR	0.429244	0.25293
GP78	1729	GCCCAAAGTGTGAAGAGTATTATGAATGCACAG	6318	AQSVKSIMNAQ	10907	SVKSIMN	0.428562	-0.07287
SyS352	1730	GCCCAAGTGCCGAATCGTGAGCCTAAGGCACAG	6319	AQVPNREPKAQ	10908	VPNREPK	0.428373	0.228979
SyP35	1731	GCCCAAATTGCTTCTTTGCTGTCGCGTGCACAG	6320	AQIASLLSRAQ	10909	IASLLSR	0.428365	-0.04133
SyS353	1732	GCCCAAGCCAACAACGTCGCCGACAGAGCACAG	6321	AQANNVADRAQ	10910	ANNVADR	0.42829	0.331604
SyS354	1733	GCCCAAAGCGTCGACAGAGCCGAAAGAGCACAG	6322	AQSVDRAERAQ	10911	SVDRAER	0.428286	0.009172
SyS355	1734	GCCCAAGTCCTCGCCGACAGAGTCCCCGCACAG	6323	AQVLADRVPAQ	10912	VLADRVP	0.428185	0.109096
SyS356	1735	GCCCAACGGACTGATTCGTCTCATCCGGCACAG	6324	AQRTDSSHPAQ	10913	RTDSSHP	0.42814	0.164627
GS185	1736	GCCCAAATTCTTGGTACTGGTGGGCAGGCACAG	6325	AQILGTGGQAQ	10914	ILGTGGQ	0.427671	-0.15048
SyS357	1737	GCCCAATCTACTGCGCAGGCTAGTTATGCACAG	6326	AQSTAQASYAQ	10915	STAQASY	0.427624	0.14248

FIG. 33 (Continued)

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SyS358	1738	GCCCAAGTCGGCCCCATCAACACCGTCGCACAG	6327	AQVGPINTVAQ	10916	VGPINTV	0.427596	0.270593
SyS359	1739	GCCCAACAAACCAACAACACCGTCAGAGCACAG	6328	AQQTNNTVRAQ	10917	QTNNTVR	0.427534	0.514292
TS129	1740	GCCCAAGGCAACGCCGTCAGAAGCACCGCACAG	6329	AQGNAVRSTAQ	10918	GNAVRST	0.427529	1.114857
SyS360	1741	GCCCAACAGAATTTGACTAAGGGTCAGGCACAG	6330	AQQNLTKGQAQ	10919	QNLTKGQ	0.427304	0.307102
GS186	1742	GCCCAAAAACAACTCAGCAAAGACTACGCACAG	6331	AQKQLSKDYAQ	10920	KQLSKDY	0.427204	0.142161
SyS361	1743	GCCCAAATGGTTCAGAATGGTCTGATTGCACAG	6332	AQMVQNGLIAQ	10921	MVQNGLI	0.426778	0.092359
SyS362	1744	GCCCAAATCGTCGAACACATGCCCCTCGCACAG	6333	AQIVEHMPLAQ	10922	IVEHMPL	0.426165	-0.1101
GS187	1745	GCCCAATACGACACCACCAGCATCTTCGCACAG	6334	AQYDTTSIFAQ	10923	YDTTSIF	0.425436	-0.10346
GS188	1746	GCCCAAAATAGTATTTCGTCTTCGGCTGCACAG	6335	AQNSISSSAAQ	10924	NSISSSA	0.425239	0.069039
SyS364	1747	GCCCAAGGCGGCAACAACAGCCTCCACGCACAG	6336	AQGGNNSLHAQ	10925	GGNNSLH	0.425087	0.214382
SyS365	1748	GCCCAAATTTCTGGTGCGTCTCTTATGGCACAG	6337	AQISGASLMAQ	10926	ISGASLM	0.424892	-0.11822
GP79	1749	GCCCAAGCTACTCTTTCGAGGAATGTTGCACAG	6338	AQATLSRNVAQ	10927	ATLSRNV	0.424839	-0.0735
SyS366	1750	GCCCAACTGGCTAATAATGTTCCGCTTGCACAG	6339	AQLANNVPLAQ	10928	LANNVPL	0.424655	-0.08052
SyS367	1751	GCCCAATGGAGCGACCCCAGCGACCTCGCACAG	6340	AQWSDPSDLAQ	10929	WSDPSDL	0.424504	-0.17072
SyS368	1752	GCCCAAAGCAGCCTCACCGACCAACCCGCACAG	6341	AQSSLTDQPAQ	10930	SSLTDQP	0.424278	0.005071
SyS369	1753	GCCCAATACGTCCCCGACCACACCAGAGCACAG	6342	AQYVPDHTRAQ	10931	YVPDHTR	0.424216	0.056561
SyS370	1754	GCCCAAAATAATACGGAGGGTAAGGCGGCACAG	6343	AQNNTEGKAAQ	10932	NNTEGKA	0.423868	0.141109
TS130	1755	GCCCAAGGTAATAGTGTTAGGTTGATTGCACAG	6344	AQGNSVRLIAQ	10933	GNSVRLI	0.423672	-0.10341
SyS371	1756	GCCCAAATTGCGCAGTCGAATACTCTTGCACAG	6345	AQIAQSNTLAQ	10934	IAQSNTL	0.423532	0.211326
GS189	1757	GCCCAACACGACAACGCCACCAAATACGCACAG	6346	AQHDNATKYAQ	10935	HDNATKY	0.423515	0.078962
SyS372	1758	GCCCAAACTAAGGCTAATGAGATGCAGGCACAG	6347	AQTKANEMQAQ	10936	TKANEMQ	0.423482	0.265014
GS190	1759	GCCCAATATTTGGGTACGGTTGTTGCGGCACAG	6348	AQYLGTVVAAQ	10937	YLGTVVA	0.423467	-0.07819
SyS373	1760	GCCCAACCTTCGATTGAGCTTAAGCCTGCACAG	6349	AQPSIELKPAQ	10938	PSIELKP	0.423417	-0.09703
SyS374	1761	GCCCAAGCTGCGGGGAATGTTCTTATGGCACAG	6350	AQAAGNVLMAQ	10939	AAGNVLM	0.423413	0.035242
SyS375	1762	GCCCAAACGTCTGTGGCTAATTTGCGTGCACAG	6351	AQTSVANLRAQ	10940	TSVANLR	0.422924	0.030491
GS191	1763	GCCCAATTTTCGCGTGAGCCGAAGCCTGCACAG	6352	AQFSREPKPAQ	10941	FSREPKP	0.422561	-0.02217
SyS376	1764	GCCCAAACCCCCAGAGAAAACTGGGGCGCACAG	6353	AQTPRENWGAQ	10942	TPRENWG	0.422534	-0.00948
SyS377	1765	GCCCAATCGCAGAATGTTGGTACTAAGGCACAG	6354	AQSQNVGTKAQ	10943	SQNVGTK	0.422488	-0.06393
GS192	1766	GCCCAATATCTGGATAAGGGGAGGACTGCACAG	6355	AQYLDKGRTAQ	10944	YLDKGRT	0.422461	-0.04855
GP80	1767	GCCCAAACGAGTACGACGCCTTTTCTTGCACAG	6356	AQTSTTPFLAQ	10945	TSTTPFL	0.422363	-0.0737
SyS378	1768	GCCCAACGGCAGGATAATCTGGAGCTGGCACAG	6357	AQRQDNLELAQ	10946	RQDNLEL	0.422343	-0.03114
SyS379	1769	GCCCAAATCAGCGACAGCAGAGTCCACGCACAG	6358	AQISDSRVHAQ	10947	ISDSRVH	0.421868	0.204338

FIG. 33 (Continued)

GS193	1770	GCCCAAAGTCAGAGTAGTCATTATAAGGCACAG	6359	AQSQSSHYKAQ	10948	SQSSHYK	0.421689	-0.11747
SyS380	1771	GCCCAATTGAATCGGGTGGTTTCGCAGGCACAG	6360	AQLNRVVSQAQ	10949	LNRVVSQ	0.421684	-0.17314
SyS381	1772	GCCCAAATGGCCCTCGACAACAGCAGAGCACAG	6361	AQMALDNSRAQ	10950	MALDNSR	0.421593	0.010591
SyS382	1773	GCCCAACTCATCCAAAGCATGGCCAAAGCACAG	6362	AQLIQSMAKAQ	10951	LIQSMAK	0.42118	-0.0049
SyS383	1774	GCCCAAGCGGGTGAGCCTAATTCTAGGGCACAG	6363	AQAGEPNSRAQ	10952	AGEPNSR	0.421075	-0.13064
SyS384	1775	GCCCAAAGTAATCAGTCTACTGTTCGGGCACAG	6364	AQSNQSTVRAQ	10953	SNQSTVR	0.420949	0.206664
SyS385	1776	GCCCAAACCAGCAACCTCAGCGAAAGAGCACAG	6365	AQTSNLSERAQ	10954	TSNLSER	0.420166	0.187613
TS132	1777	GCCCAATCGAATTCTACTTCTCGTGCTGCACAG	6366	AQSNSTSRAAQ	10955	SNSTSRA	0.420136	0.455929
GS194	1778	GCCCAAATGCAGCAGCAGTTTCCTTCGGCACAG	6367	AQMQQQFPSAQ	10956	MQQQFPS	0.419987	-0.07715
SyS386	1779	GCCCAATTCAACACCCTCGCCGAAGTCGCACAG	6368	AQFNTLAEVAQ	10957	FNTLAEV	0.419845	0.023739
SyS387	1780	GCCCAACCGGGGGTTACGGTTATTAGTGCACAG	6369	AQPGVTVISAQ	10958	PGVTVIS	0.419723	-0.08635
SyS388	1781	GCCCAACTCCAAAACGTCCACGACAGCGCACAG	6370	AQLQNVHDSAQ	10959	LQNVHDS	0.419505	0.029624
SyS389	1782	GCCCAAAATTCGGTTATTGGTGGGTCGGCACAG	6371	AQNSVIGGSAQ	10960	NSVIGGS	0.41915	0.135501
SyS390	1783	GCCCAAAACGAAGGCGTCAGACCCCTCGCACAG	6372	AQNEGVRPLAQ	10961	NEGVRPL	0.418827	0.007496
GS197	1784	GCCCAATCGGTGAATCCTAGTGTGGTTGCACAG	6373	AQSVNPSVVAQ	10962	SVNPSVV	0.418691	-0.08801
SyS391	1785	GCCCAAATGAGTACGACGTCTGAGGATGCACAG	6374	AQMSTTSEDAQ	10963	MSTTSED	0.418589	-0.10689
SyS392	1786	GCCCAAATTCATAGTGGGCTTCCGAAGGCACAG	6375	AQIHSGLPKAQ	10964	IHSGLPK	0.418094	0.165287
SyS393	1787	GCCCAAGGTATGAATGGTTATCCGAAGGCACAG	6376	AQGMNGYPKAQ	10965	GMNGYPK	0.417434	-0.02328
SyS394	1788	GCCCAAAGTATTCGGGATTCTGTGAAGGCACAG	6377	AQSIRDSVKAQ	10966	SIRDSVK	0.417384	0.095996
SyS395	1789	GCCCAAATGCTTAAGCCGGATAATGTTGCACAG	6378	AQMLKPDNVAQ	10967	MLKPDNV	0.417215	-0.01225
SyS396	1790	GCCCAAGCTTTTACGTCGTCTCTTGGGGCACAG	6379	AQAFTSSLGAQ	10968	AFTSSLG	0.41715	-0.08384
SyS397	1791	GCCCAAATGCTGGATAAGTCTTCGTCGGCACAG	6380	AQMLDKSSSAQ	10969	MLDKSSS	0.416677	0.230852
GS198	1792	GCCCAAAAGACTCAGAATACTCAGATGGCACAG	6381	AQKTQNTQMAQ	10970	KTQNTQM	0.416523	0.092678
SyS398	1793	GCCCAAGGGACTACTAGTTCGATGGCTGCACAG	6382	AQGTTSSMAAQ	10971	GTTSSMA	0.416405	0.279218
GS199	1794	GCCCAAGGCAGCGCCGCCAGCCAAGCCGCACAG	6383	AQGSAASQAAQ	10972	GSAASQA	0.416298	-0.04868
SyS399	1795	GCCCAAGCCCACAGCAACATCGACAGCGCACAG	6384	AQAHSNIDSAQ	10973	AHSNIDS	0.416158	0.134486
SyS400	1796	GCCCAAGGCAGCGCCAGCAGCCTCCTCGCACAG	6385	AQGSASSLLAQ	10974	GSASSLL	0.41564	-0.02039
SyS401	1797	GCCCAATTGAGTCCTAATTCTAGTTTTGCACAG	6386	AQLSPNSSFAQ	10975	LSPNSSF	0.415615	0.029121
SyS402	1798	GCCCAAGGGCATTCTGTTACTCCGTCTGCACAG	6387	AQGHSVTPSAQ	10976	GHSVTPS	0.415423	0.010986
SyS403	1799	GCCCAAAAAGGCGGCAACAGCATCGACGCACAG	6388	AQKGGNSIDAQ	10977	KGGNSID	0.415013	0.279789
SyS404	1800	GCCCAACTCGGCCCCAGCCCCAGCGCCGCACAG	6389	AQLGPSPSAAQ	10978	LGPSPSA	0.41486	-0.19011
SyS405	1801	GCCCAACAGCTGCCTATGCTTAATGCTGCACAG	6390	AQQLPMLNAAQ	10979	QLPMLNA	0.414768	0.206951

FIG. 33 (Continued)

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SyS407	1802	GCCCAAGCTACGAATATTCTTACTGCGGCACAG	6391	AQATNILTAAQ	10980	ATNILTA	0.413225	-0.04554
GS201	1803	GCCCAACTCATGCAAAACGGCCAAAAAGCACAG	6392	AQlMQNGQKAQ	10981	LMQNGQK	0.413036	0.001705
SyS408	1804	GCCCAACATAATAATGGGCAGGCTTTGGCACAG	6393	AQHNNGQALAQ	10982	HNNGQAL	0.412853	-0.18614
SyS409	1805	GCCCAATCTATTACTCAGACTCTTTCTGCACAG	6394	AQSITQTLSAQ	10983	SITQTLS	0.412719	0.059774
TS135	1806	GCCCAAGGGAATAGGATTAGTAATACGGCACAG	6395	AQGNRISNTAQ	10984	GNRISNT	0.412694	0.198634
SyS410	1807	GCCCAAGGTCCTCAGAATGATCCGCCGGCACAG	6396	AQGPQNDPPAQ	10985	GPQNDPP	0.41264	-0.03615
GS202	1808	GCCCAAATCAACGGCATGGGCCCCAACGCACAG	6397	AQINGMGPNAQ	10986	INGMGPN	0.412563	0.028973
SyS411	1809	GCCCAAACTGGGAATGCGCATCCTAATGCACAG	6398	AQTGNAHPNAQ	10987	TGNAHPN	0.412504	-0.09192
SyS412	1810	GCCCAATATGCTGTGAATCTGAATAATGCACAG	6399	AQYAVNLNNAQ	10988	YAVNLNN	0.412504	-0.15859
GS203	1811	GCCCAAGCGTTGATTTCTAATAGTACGGCACAG	6400	AQALISNSTAQ	10989	ALISNST	0.412484	-0.03295
SyS413	1812	GCCCAATCTCATGTTTCTACTACTATGGCACAG	6401	AQSHVSTTMAQ	10990	SHVSTTM	0.412469	0.018515
SyS414	1813	GCCCAACTGGATGATTTTGTGAGGCCGGCACAG	6402	AQLDDFVRPAQ	10991	LDDFVRP	0.41244	-0.19203
GS204	1814	GCCCAAAATAATACTGCGCGGTCTGTTGCACAG	6403	AQNNTARSVAQ	10992	NNTARSV	0.412149	-0.09946
SyS415	1815	GCCCAAAACAAATACCCCCAACCCAGCGCACAG	6404	AQNKYPQPSAQ	10993	NKYPQPS	0.412005	-0.11816
SyS416	1816	GCCCAATATGCGTCGGAGTTGTTTGTTGCACAG	6405	AQYASELFVAQ	10994	YASELFV	0.411713	-0.19254
GS205	1817	GCCCAATTCTACACCGCCAACGCCAGCGCACAG	6406	AQFYTANASAQ	10995	FYTANAS	0.411179	-0.07392
GP83	1818	GCCCAATTTACGAAGTCGAATGCGACTGCACAG	6407	AQFTKSNATAQ	10996	FTKSNAT	0.411133	-0.07308
SyS417	1819	GCCCAACTCGCCGTCAGCCAAATGAGAGCACAG	6408	AQLAVSQMRAQ	10997	LAVSQMR	0.411001	-0.03857
SyS418	1820	GCCCAAAGGAATGGTCAGCTGATTGTGGCACAG	6409	AQRNGQLIVAQ	10998	RNGQLIV	0.410978	0.234351
SyS419	1821	GCCCAAGACACCGCCAACACCGCCAGAGCACAG	6410	AQDTANTARAQ	10999	DTANTAR	0.410859	0.147093
GS207	1822	GCCCAAAAACCCACCGAAGTCCAACACGCACAG	6411	AQKPTEVQHAQ	11000	KPTEVQH	0.410623	-0.02471
SyS420	1823	GCCCAACTTACTAATGCGGCGACTTATGCACAG	6412	AQLTNAATYAQ	11001	LTNAATY	0.410298	0.266975
SyS421	1824	GCCCAAATCAGCAACGTCCAAGCCAACGCACAG	6413	AQISNVQANAQ	11002	ISNVQAN	0.410249	0.422795
SyS422	1825	GCCCAAGAGAGTCGTAATAATGGGTTTGCACAG	6414	AQESRNNGFAQ	11003	ESRNNGF	0.410147	-0.09761
SyS423	1826	GCCCAAAGCACCGGCCCCACCATGCACGCACAG	6415	AQSTGPTMHAQ	11004	STGPTMH	0.409836	0.093513
SyS424	1827	GCCCAAACGCCTGGTGAGTCGCATAAGGCACAG	6416	AQTPGESHKAQ	11005	TPGESHK	0.409786	-0.15011
GS208	1828	GCCCAAAGCGTCAGCATCGCCAGCAGCGCACAG	6417	AQSVSIASSAQ	11006	SVSIASS	0.409517	-0.03488
SyS425	1829	GCCCAAAATGGTGTTACGCAGTCTAAGGCACAG	6418	AQNGVTQSKAQ	11007	NGVTQSK	0.409482	-0.08464
GS209	1830	GCCCAAGCTAAGAATACGTATGCTTCTGCACAG	6419	AQAKNTYASAQ	11008	AKNTYAS	0.409391	-0.06675
SyS426	1831	GCCCAAGGTACTTCGGATGGTCATAGGGCACAG	6420	AQGTSDGHRAQ	11009	GTSDGHR	0.408706	-0.00891
SP33	1832	GCCCAATGGTCTCAGAATAAGGGGTATGCACAG	6421	AQWSQNKGYAQ	11010	WSQNKGY	0.408567	-0.04954
SyS427	1833	GCCCAAGGTCAGTTGGCGCGGTCTGTTGCACAG	6422	AQGQLARSVAQ	11011	GQLARSV	0.408524	-0.00072

FIG. 33 (Continued)

GS210	1834	GCCCAAATCGGCGGCGGCGCCCAAAAAGCACAG	6423	AQIGGGAQKAQ	11012	IGGGAQK	0.408472	0.032961
GS211	1835	GCCCAAGCCGGCAACGCCAGCCACACCGCACAG	6424	AQAGNASHTAQ	11013	AGNASHT	0.408162	-0.12162
SyS428	1836	GCCCAATTCAACCAAGTCGGCAAAATGGCACAG	6425	AQFNQVGKMAQ	11014	FNQVGKM	0.407791	0.16513
SyS429	1837	GCCCAAACGAGGGATACTCTGTATAAGGCACAG	6426	AQTRDTLYKAQ	11015	TRDTLYK	0.407466	-0.16866
SyS430	1838	GCCCAAAACGGCAGCCCCAGCTACAACGCACAG	6427	AQNGSPSYNAQ	11016	NGSPSYN	0.407246	-0.15253
SyS431	1839	GCCCAATTGGCTGAGGCGCATGCTCGTGCACAG	6428	AQLAEAHARAQ	11017	LAEAHAR	0.407096	-0.17435
SyS432	1840	GCCCAACCTATGTCTAATTCGGAGCGTGCACAG	6429	AQPMSNSERAQ	11018	PMSNSER	0.407062	0.211218
SyS434	1841	GCCCAACACGTCACCAGCCTCAACGACGCACAG	6430	AQHVTSLNDAQ	11019	HVTSLND	0.406789	0.247538
GS212	1842	GCCCAAGGGGCTCCGCATGTTTCGAGGGCACAG	6431	AQGAPHVSRAQ	11020	GAPHVSR	0.406617	-0.07068
SyS435	1843	GCCCAAAATACTAATGGGAATAGTGCGGCACAG	6432	AQNTNGNSAAQ	11021	NTNGNSA	0.405996	0.106612
SyS436	1844	GCCCAAAACGAACTCACCGGCATGCTCGCACAG	6433	AQNELTGMLAQ	11022	NELTGML	0.405204	-0.12222
SyS437	1845	GCCCAAAGTTCTCTTTTGCCTGCTGCTGCACAG	6434	AQSSLLPAAAQ	11023	SSLLPAA	0.404837	-0.11667
SyS438	1846	GCCCAACCGGTTGGTCAGTCGTTGACTGCACAG	6435	AQPVGQSLTAQ	11024	PVGQSLT	0.404833	-0.00463
SyS439	1847	GCCCAATTGACTGCTGCGAAGGGTCTTGCACAG	6436	AQLTAAKGLAQ	11025	LTAAKGL	0.404775	-0.07979
GP85	1848	GCCCAACTGATTGGGCGGCTGACTTCTGCACAG	6437	AQLIGRLTSAQ	11026	LIGRLTS	0.404569	-0.07322
GP86	1849	GCCCAAGCTAAGCATAATGATAATATTGCACAG	6438	AQAKHNDNIAQ	11027	AKHNDNI	0.404338	0.076246
SyS440	1850	GCCCAATTGCGTAGTGGTGATGAGATGGCACAG	6439	AQLRSGDEMAQ	11028	LRSGDEM	0.404093	-0.0112
SyS441	1851	GCCCAACCCCAAAACAGCACCACCGCCGCACAG	6440	AQPQNSTTAAQ	11029	PQNSTTA	0.404089	-0.04125
GS213	1852	GCCCAACTGGCTACTGGGCCTCTTTTTGCACAG	6441	AQLATGPLFAQ	11030	LATGPLF	0.403608	-0.16394
SyS442	1853	GCCCAAGCGTCTGCTGTGAGTCAGAAGGCACAG	6442	AQASAVSQKAQ	11031	ASAVSQK	0.403527	0.110544
SyS443	1854	GCCCAAGCGCCTGTTAGTTCTGCGTTGGCACAG	6443	AQAPVSSALAQ	11032	APVSSAL	0.40338	-0.15617
SyS444	1855	GCCCAAACGATGCCGAGTCTGGATAGTGCACAG	6444	AQTMPSLDSAQ	11033	TMPSLDS	0.403287	-0.20951
GS215	1856	GCCCAACATATGAATTTTCCGAATCCGGCACAG	6445	AQHMNFPNPAQ	11034	HMNFPNP	0.403183	-0.14779
SP34	1857	GCCCAAGCGTCTGCGAGGATGGATGCGGCACAG	6446	AQASARMDAAQ	11035	ASARMDA	0.402718	-0.05379
SyS445	1858	GCCCAAACCGTCATCGTCGGCGGCAGAGCACAG	6447	AQTVIVGGRAQ	11036	TVIVGGR	0.402646	-0.15534
SyS446	1859	GCCCAAAGTAGTCAGAGTCAGACTGTTGCACAG	6448	AQSSQSQTVAQ	11037	SSQSQTV	0.40259	-0.00826
GS216	1860	GCCCAAATCAACACCACCAGCCAAAAAGCACAG	6449	AQINTTSQKAQ	11038	INTTSQK	0.402505	0.195122
SyS447	1861	GCCCAAGCTGGGGCGCGTGTTACGGAGGCACAG	6450	AQAGARVTEAQ	11039	AGARVTE	0.402225	0.012345
GS217	1862	GCCCAACCCGCCCCCCACAGCGGCAGCGCACAG	6451	AQPAPHSGSAQ	11040	PAPHSGS	0.402189	-0.18099
SyS448	1863	GCCCAACTCAACGTCATGTACAACCCCGCACAG	6452	AQLNVMYNPAQ	11041	LNVMYNP	0.402132	-0.11495
GS218	1864	GCCCAAGGGCATGCTCAGACTCTTTATGCACAG	6453	AQGHAQTLYAQ	11042	GHAQTLY	0.402085	-0.07242
GS219	1865	GCCCAAACTCCTAATCTGTCTACTCATGCACAG	6454	AQTPNLSTHAQ	11043	TPNLSTH	0.401391	-0.11638

FIG. 33 (Continued)

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SyS449	1866	GCCCAAAGCGCCGAAAGAACCAACGTCGCACAG	6455	AQSAERTNVAQ	11044	SAERTNV	0.40125	0.211168
TS136	1867	GCCCAAAACAACCTCAGACCCGTCTACGCACAG	6456	AQNNLRPVYAQ	11045	NNLRPVY	0.401221	-0.16565
SyS450	1868	GCCCAAAATCAGCAGTCTGCTTATACGGCACAG	6457	AQNQQSAYTAQ	11046	NQQSAYT	0.400966	0.20764
SyS451	1869	GCCCAAGTCGTCGACGGCAAAACCCAAGCACAG	6458	AQVVDGKTQAQ	11047	VVDGKTQ	0.400944	0.002558
SyS452	1870	GCCCAACCCCTCCCCCAACAACTCGACGCACAG	6459	AQPLPQQLDAQ	11048	PLPQQLD	0.40087	-0.04961
SyS453	1871	GCCCAAGTCGCCGAAATCGTCCAACTCGCACAG	6460	AQVAEIVQLAQ	11049	VAEIVQL	0.400846	-0.19011
SS41	1872	GCCCAAGACAGAAACACCACCGTCAGAGCACAG	6461	AQDRNTTVRAQ	11050	DRNTTVR	0.40065	-0.05681
SyS454	1873	GCCCAAAATATGATGAAGACGGGGATGGCACAG	6462	AQNMMKTGMAQ	11051	NMMKTGM	0.400506	0.125092
SyS455	1874	GCCCAAGTCCAATTCAACACCAGCAAAGCACAG	6463	AQVQFNTSKAQ	11052	VQFNTSK	0.400373	0.028343
SyS456	1875	GCCCAACCTGGGAATGCTAGTATTCGTGCACAG	6464	AQPGNASIRAQ	11053	PGNASIR	0.400324	-0.16951
SyS457	1876	GCCCAACTCGGCGGCATCCTCAGCGCCGCACAG	6465	AQLGGILSAAQ	11054	LGGILSA	0.400238	-0.08048
SyS458	1877	GCCCAACAGACGGATCATTCGCATCTTGCACAG	6466	AQQTDHSHLAQ	11055	QTDHSHL	0.400082	-0.00343
SyS459	1878	GCCCAAACGCTGCATGCTGAGTTTAGTGCACAG	6467	AQTLHAEFSAQ	11056	TLHAEFS	0.399977	-0.08783
GP87	1879	GCCCAACTGTCGGATCGTCTGAATGCGGCACAG	6468	AQLSDRLNAAQ	11057	LSDRLNA	0.399921	0.343918
GS222	1880	GCCCAACTGAATGAGCGTATTGGTGGGGCACAG	6469	AQLNERIGGAQ	11058	LNERIGG	0.399725	0.141871
SyS460	1881	GCCCAAACTTTGAATTCGACGGCGTCGGCACAG	6470	AQTLNSTASAQ	11059	TLNSTAS	0.399702	-0.02669
GS223	1882	GCCCAATCTGGGCGGGTTGTTGCGCAGGCACAG	6471	AQSGRVVAQAQ	11060	SGRVVAQ	0.399629	-0.09114
TS137	1883	GCCCAAAATAATCGTACGACTAATAATGCACAG	6472	AQNNRTTNNAQ	11061	NNRTTNN	0.399086	0.311194
SS42	1884	GCCCAAAACGTCCCCAGCAGCACCTACGCACAG	6473	AQNVPSSTYAQ	11062	NVPSSTY	0.39867	-0.28456
SyS461	1885	GCCCAAGTCCCCAGCACCGCCCTCAAAGCACAG	6474	AQVPSTALKAQ	11063	VPSTALK	0.3985	0.103803
SyS462	1886	GCCCAACCTCCTAATACTCAGAGTCTGGCACAG	6475	AQPPNTQSLAQ	11064	PPNTQSL	0.398398	-0.08905
TS138	1887	GCCCAAACGAATACGACGCGGGCGATGGCACAG	6476	AQTNTTRAMAQ	11065	TNTTRAM	0.397943	0.551742
TS139	1888	GCCCAAAGCAACAGAACCGTCAGAGAAGCACAG	6477	AQSNRTVREAQ	11066	SNRTVRE	0.397876	0.454359
SyS463	1889	GCCCAAGCTTCGACTCAGATTATGAGGGCACAG	6478	AQASTQIMRAQ	11067	ASTQIMR	0.397639	-0.12339
SyS464	1890	GCCCAAACGGTGATTAGTTCTAGTCGTGCACAG	6479	AQTVISSSRAQ	11068	TVISSSR	0.397266	-0.01675
GS226	1891	GCCCAAGTCTACAGCCCCCAAGGCACCGCACAG	6480	AQVYSPQGTAQ	11069	VYSPQGT	0.397151	0.052156
SyS465	1892	GCCCAAGGCAGCCCCACCCAAAGCATGGCACAG	6481	AQGSPTQSMAQ	11070	GSPTQSM	0.396853	0.092045
SyS466	1893	GCCCAAGCGGTGTCGTCGGAGGCTCGTGCACAG	6482	AQAVSSEARAQ	11071	AVSSEAR	0.396674	-0.15767
SyS467	1894	GCCCAAGGTTCGGTTGCGACTCTTACTGCACAG	6483	AQGSVATLTAQ	11072	GSVATLT	0.396673	0.012454
SyS468	1895	GCCCAAAGCGCCAACACCGGCACCGGCGCACAG	6484	AQSANTGTGAQ	11073	SANTGTG	0.396431	-0.10276
SyS469	1896	GCCCAAATTGTTCAGGGGACTAGTATGGCACAG	6485	AQIVQGTSMAQ	11074	IVQGTSM	0.39631	0.142036
GS227	1897	GCCCAAACTCCTTCGCTTGGTGTTCTTGCACAG	6486	AQTPSLGVLAQ	11075	TPSLGVL	0.395938	-0.05178

FIG. 33 (Continued)

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SyS470	1898	GCCCAACCCAACATGATGGGCAGCAGCGCACAG	6487	AQPNMMGSSAQ	11076	PNMMGSS	0.395744	-0.10497
GS228	1899	GCCCAACTCACCCAAAGCCCCGCCCCCGCACAG	6488	AQLTQSPAPAQ	11077	LTQSPAP	0.395705	-0.03746
GS229	1900	GCCCAAAAAGGCAGCAACAGCACCCTCGCACAG	6489	AQKGSNSTLAQ	11078	KGSNSTL	0.395617	0.158094
SyS471	1901	GCCCAACCCATGGCCGCCGCCCCCAGAGCACAG	6490	AQPMAAAPRAQ	11079	PMAAAPR	0.394928	-0.11822
GS230	1902	GCCCAAGTTACGACGGGTCCGAGTCGTGCACAG	6491	AQVTTGPSRAQ	11080	VTTGPSR	0.39486	-0.05507
GS231	1903	GCCCAAGTCGTCAGCCCCCCTCAGCTACGCACAG	6492	AQVVSPLSYAQ	11081	VVSPLSY	0.394822	-0.12073
SyS472	1904	GCCCAAGTGACGGGTTCTGTGCAGAAGGCACAG	6493	AQVTGSVQKAQ	11082	VTGSVQK	0.394696	-0.04095
GS232	1905	GCCCAAGGCGGCACCACCGTCCAAACCGCACAG	6494	AQGGTTVQTAQ	11083	GGTTVQT	0.39469	-0.06883
SyS473	1906	GCCCAAAACAGCGCCCAAATCAACATGGCACAG	6495	AQNSAQINMAQ	11084	NSAQINM	0.394642	0.174839
GS234	1907	GCCCAACCCGGCACCCAAAAACCCACCGCACAG	6496	AQPGTQKPTAQ	11085	PGTQKPT	0.394239	-0.04567
GP88	1908	GCCCAAGGGAAGGCTAGTCATTATCCTGCACAG	6497	AQGKASHYPAQ	11086	GKASHYP	0.394204	-0.07412
GP89	1909	GCCCAATATAATAGTGTTCCGTCGGCGGCACAG	6498	AQYNSVPSAAQ	11087	YNSVPSA	0.393949	0.00863
SyS474	1910	GCCCAAGTTTATGAGCGGGTTTCTCATGCACAG	6499	AQVYERVSHAQ	11088	VYERVSH	0.393656	0.020329
SyS475	1911	GCCCAAGATGTGAATAATAGGTCTATGGCACAG	6500	AQDVNNRSMAQ	11089	DVNNRSM	0.393538	-0.20588
GS235	1912	GCCCAACCTCATGCGGTTTCTATGCTTGCACAG	6501	AQPHAVSMLAQ	11090	PHAVSML	0.392826	-0.1747
GP90	1913	GCCCAAGGGATGCCTGCTCCTCTTGGTGCACAG	6502	AQGMPAPLGAQ	11091	GMPAPLG	0.392659	-0.07169
SyS476	1914	GCCCAACAGCTTCAGATTAATCCGGCTGCACAG	6503	AQQLQINPAAQ	11092	QLQINPA	0.392185	-0.12586
SyS477	1915	GCCCAAACTATGGATCTGTCGCCGCCGGCACAG	6504	AQTMDLSPPAQ	11093	TMDLSPP	0.392185	-0.12586
SyS478	1916	GCCCAAACCACCGACCTCCACGCCAAAGCACAG	6505	AQTTDLHAKAQ	11094	TTDLHAK	0.392056	-0.00463
GS236	1917	GCCCAACACCACACCACCCAAACCACCGCACAG	6506	AQHHTTQTTAQ	11095	HHTTQTT	0.39199	-0.07609
SyS479	1918	GCCCAACCGAGTTCTAATTCTACTAATGCACAG	6507	AQPSSNSTNAQ	11096	PSSNSTN	0.391964	-0.12824
SyS480	1919	GCCCAAACCAGATACAACGTCGACCCCCGCACAG	6508	AQTRYNVDPAQ	11097	TRYNVDP	0.391808	0.095996
SyS481	1920	GCCCAAAGCGTCGTCAGCCTCAGCCCCCGCACAG	6509	AQSVVSLSPAQ	11098	SVVSLSP	0.391603	0.006038
SyS482	1921	GCCCAAGAAAAAAGTCGACCAACTCAGAGCACAG	6510	AQEKVDQLRAQ	11099	EKVDQLR	0.391412	-0.13677
SyS483	1922	GCCCAAAGCGACAGCAGACAAACCCTCGCACAG	6511	AQSDSRQTLAQ	11100	SDSRQTL	0.391412	-0.13677
SyS484	1923	GCCCAAACTTATCCTGCTACGAGTGATGCACAG	6512	AQTYPATSDAQ	11101	TYPATSD	0.391335	0.284964
GS237	1924	GCCCAAAGCATGAACGTCGGCAGCGCCGCACAG	6513	AQSMNVGSAAQ	11102	SMNVGSA	0.391048	-0.05003
GS238	1925	GCCCAACTTGAGTCTAGTAATGCTATTGCACAG	6514	AQLESSNAIAQ	11103	LESSNAI	0.3905	-0.13061
GP91	1926	GCCCAATCTCCGACGAATCATGCTCCTGCACAG	6515	AQSPTNHAPAQ	11104	SPTNHAP	0.389815	0.121844
SyS486	1927	GCCCAAGCGCATGAGGGGATGGTTAAGGCACAG	6516	AQAHEGMVKAQ	11105	AHEGMVK	0.389656	0.111097
SyS487	1928	GCCCAAGTTGATACTTTGTTGTCGAAGGCACAG	6517	AQVDTLLSKAQ	11106	VDTLLSK	0.389333	-0.13837
GS240	1929	GCCCAAACCGCCGGCCAACTCACCTGGGCACAG	6518	AQTAGQLTWAQ	11107	TAGQLTW	0.38913	-0.16432

FIG. 33 (Continued)

SyS488	1930	GCCCAAATGGGCATGGACGGCCAAATCGCACAG	6519	AQMGMDGQIAQ	11108	MGMDGQI	0.38907	-0.16766
SyS489	1931	GCCCAAGAGCTGGAGAATGGTCGTCGTGCACAG	6520	AQELENGRRAQ	11109	ELENGRR	0.38896	-0.14888
GS241	1932	GCCCAACTCGACCTCAGCGTCAGCAGAGCACAG	6521	AQLDLSVSRAQ	11110	LDLSVSR	0.388881	-0.12807
SyS490	1933	GCCCAATCTCAGCATCCGAATATGACGGCACAG	6522	AQSQHPNMTAQ	11111	SQHPNMT	0.388765	0.328765
SyS491	1934	GCCCAATATCATGAGGTGTCGGAGCATGCACAG	6523	AQYHEVSEHAQ	11112	YHEVSEH	0.388683	-0.07979
GS242	1935	GCCCAAATGCGGTCGCCGCCTCCTACGGCACAG	6524	AQMRSPPPTAQ	11113	MRSPPPT	0.388551	-0.14906
GS243	1936	GCCCAAGGTAGTGGTAGTTCGACGATTGCACAG	6525	AQGSGSSTIAQ	11114	GSGSSTI	0.388493	-0.05911
SyS492	1937	GCCCAAGGTGGTGATGCTGGGAGGTGGGCACAG	6526	AQGGDAGRWAQ	11115	GGDAGRW	0.388134	-0.0507
SyS493	1938	GCCCAAAAGGCTGAGGCGATGGTTATTGCACAG	6527	AQKAEAMVIAQ	11116	KAEAMVI	0.387828	-0.0246
SyS494	1939	GCCCAAGCCAACAAAGACCTCGGCGTCGCACAG	6528	AQANKDLGVAQ	11117	ANKDLGV	0.387437	0.102738
SyS495	1940	GCCCAAACGTCGTCGGAGAATAGGACTGCACAG	6529	AQTSSENRTAQ	11118	TSSENRT	0.387311	-0.10606
GS244	1941	GCCCAAGGCCCCGACAGAACCGCCGCCGCACAG	6530	AQGPDRTAAAQ	11119	GPDRTAA	0.387298	-0.02676
SyS496	1942	GCCCAAGGCAGCACCGTCGTCCACCTCGCACAG	6531	AQGSTVVHLAQ	11120	GSTVVHL	0.386932	0.060317
SyS497	1943	GCCCAAACTGCGGTGGTGGTGCCTCAGGCACAG	6532	AQTAVVVPQAQ	11121	TAVVVPQ	0.386787	0.055989
SyS498	1944	GCCCAAGCGGTTAATATTGCTAATGCGGCACAG	6533	AQAVNIANAAQ	11122	AVNIANA	0.386669	-0.05398
SyS499	1945	GCCCAATTGCTGTCTCAGAGTGGGGTGGCACAG	6534	AQLLSQSGVAQ	11123	LLSQSGV	0.386652	-0.15808
SyS500	1946	GCCCAACACACCGGCGAAGGCAAACTCGCACAG	6535	AQHTGEGKLAQ	11124	HTGEGKL	0.386636	0.213701
SyS501	1947	GCCCAAAGCAACGGCAACAACATCAGAGCACAG	6536	AQSNGNNIRAQ	11125	SNGNNIR	0.386253	0.22344
GS245	1948	GCCCAAGAAGTCACCCTCATGCACACAAAGCACAG	6537	AQEVTLMHKAQ	11126	EVTLMHK	0.386174	-0.15766
GP92	1949	GCCCAACTTACTACTACGGGGAGTAATGCACAG	6538	AQLTTTGSNAQ	11127	LTTTGSN	0.385682	0.152692
GS247	1950	GCCCAAGACATCAGCGGCAAAATCGCCGCACAG	6539	AQDISGKIAAQ	11128	DISGKIA	0.385274	-0.05387
GS249	1951	GCCCAAATTTCGCCGAATGTTTATAGTGCACAG	6540	AQISPNVYSAQ	11129	ISPNVYS	0.384876	0.050202
GS250	1952	GCCCAATATAATAAGCTTGTTGATGGTGCACAG	6541	AQYNKLVDGAQ	11130	YNKLVDG	0.38484	-0.16146
GS251	1953	GCCCAATTTCATACGCATCCTACGAGTGCACAG	6542	AQFHTHPTSAQ	11131	FHTHPTS	0.384812	-0.07443
GP93	1954	GCCCAACCTACTCTGGAGGCTACGAGTGCACAG	6543	AQPTLEATSAQ	11132	PTLEATS	0.384801	0.117964
SyS503	1955	GCCCAAGAACTCGGCAGAAACGGCCCCGCACAG	6544	AQELGRNGPAQ	11133	ELGRNGP	0.38437	0.084485
SyS504	1956	GCCCAAGTCGACAAAGTCGAAAGACTCGCACAG	6545	AQVDKVERLAQ	11134	VDKVERL	0.384245	-0.07403
SyS505	1957	GCCCAAACCACCACCATGACCCCCCAGAGCACAG	6546	AQTTTMTPRAQ	11135	TTTMTPR	0.384195	0.082987
SyS506	1958	GCCCAACTCCAACAAATCCCCACCCCCGCACAG	6547	AQLQQIPTPAQ	11136	LQQIPTP	0.384174	-0.14405
SyS507	1959	GCCCAAACCGACAGCAACAGCCTCCAAGCACAG	6548	AQTDSNSLQAQ	11137	TDSNSLQ	0.384026	-0.11495
GS252	1960	GCCCAAGACGACAGAAGCGTCAGATTCGCACAG	6549	AQDDRSVRFAQ	11138	DDRSVRF	0.384013	-0.08841
GS253	1961	GCCCAACTTGCTACTCAGAATGCTTCGGCACAG	6550	AQLATQNASAQ	11139	LATQNAS	0.383747	-0.11907

FIG. 33 (Continued)

GS254	1962	GCCCAAGTCGGCACCCACATCCACAGCGCACAG	6551	AQVGTHIHSAQ	11140	VGTHIHS	0.383741	-0.07376
SyS508	1963	GCCCAAAGCGAAAGAAGCAGCGTCAAAGCACAG	6552	AQSERSSVKAQ	11141	SERSSVK	0.38368	-0.04815
GS255	1964	GCCCAAGGCTACGCCCACAGCATGATCGCACAG	6553	AQGYAHSMIAQ	11142	GYAHSMI	0.383633	-0.16718
GS256	1965	GCCCAACCGTTGAGTGGGGGTGTTCGTGCACAG	6554	AQPLSGGVRAQ	11143	PLSGGVR	0.383535	-0.18245
GS257	1966	GCCCAACTCACCTACGTCGCCAGCAGCGCACAG	6555	AQLTYVASSAQ	11144	LTYVASS	0.383535	-0.18245
GS258	1967	GCCCAAGTCGACAAAACCCTCAGCAGAGCACAG	6556	AQVDKTLSRAQ	11145	VDKTLSR	0.383399	0.00026
SyS509	1968	GCCCAACCCAACCTCGTCGGCGTCCCCGCACAG	6557	AQPNLVGVPAQ	11146	PNLVGVP	0.383392	-0.17259
SS45	1969	GCCCAAACCAAAATCGACACCGTCAGAGCACAG	6558	AQTKIDTVRAQ	11147	TKIDTVR	0.383311	-0.33355
SyS510	1970	GCCCAAAGCGGCGGCACCCAAGCCAGAGCACAG	6559	AQSGGTQARAQ	11148	SGGTQAR	0.383037	0.132131
SyS511	1971	GCCCAACATAGTACGCCGCTGGTGTCGGCACAG	6560	AQHSTPLVSAQ	11149	HSTPLVS	0.382943	0.058414
SyS512	1972	GCCCAACATTCGGGGACGAATCTTCGTGCACAG	6561	AQHSGTNLRAQ	11150	HSGTNLR	0.382943	-0.13556
SyS513	1973	GCCCAAGCGCAGCCTAGGCTGGTGACTGCACAG	6562	AQAQPRLVTAQ	11151	AQPRLVT	0.382943	-0.13556
SyS514	1974	GCCCAACCTCTTGGTGCGCATGGTTCGGCACAG	6563	AQPLGAHGSAQ	11152	PLGAHGS	0.382943	-0.16466
SyS515	1975	GCCCAAATCAGCGACGCCAGCGTCCTCGCACAG	6564	AQISDASVLAQ	11153	ISDASVL	0.382943	-0.16466
SyS516	1976	GCCCAAATGAGCGTCGGCGTCAAAACCGCACAG	6565	AQMSVGVKTAQ	11154	MSVGVKT	0.382941	0.297777
GS259	1977	GCCCAAAACATCGCCGAAGGCCTCAGCGCACAG	6566	AQNIAEGLSAQ	11155	NIAEGLS	0.382807	-0.14958
SyS517	1978	GCCCAATCGTCGAATTCTGATGGGATTGCACAG	6567	AQSSNSDGIAQ	11156	SSNSDGI	0.382517	-0.12782
SyS518	1979	GCCCAAGTCGGCCAAACCACCAACAGCGCACAG	6568	AQVGQTTNSAQ	11157	VGQTTNS	0.382475	0.202682
SyS519	1980	GCCCAAGAGTCGAAGCGGCCTTTTCTTGCACAG	6569	AQESKRPFLAQ	11158	ESKRPFL	0.382336	-0.02035
SyP37	1981	GCCCAAAGTCAGGAGAATAGTCGTACTGCACAG	6570	AQSQENSRTAQ	11159	SQENSRT	0.382175	-0.03831
SyS520	1982	GCCCAAAATACTGGGACTGATCATCCGGCACAG	6571	AQNTGTDHPAQ	11160	NTGTDHP	0.382096	0.093385
TS140	1983	GCCCAAGGGAATTGGGTTAAGGATATTGCACAG	6572	AQGNWVKDIAQ	11161	GNWVKDI	0.382083	0.231014
SyS521	1984	GCCCAAAGACTCACCGAAACCGTCACCGCACAG	6573	AQRLTETVTAQ	11162	RLTETVT	0.381934	-0.02213
SyS522	1985	GCCCAAGGCGAAATCGGCGTCCTCTACGCACAG	6574	AQGEIGVLYAQ	11163	GEIGVLY	0.381809	-0.12707
SyS523	1986	GCCCAACTGGCTCCGGAGCCGCTTAAGGCACAG	6575	AQLAPEPLKAQ	11164	LAPEPLK	0.38143	-0.18527
SyS524	1987	GCCCAAAACAAACTCCCCCCCGCCCTCGCACAG	6576	AQNKLPPALAQ	11165	NKLPPAL	0.381262	0.008029
SyS525	1988	GCCCAAAATATTGGGACTCGGGATGCGGCACAG	6577	AQNIGTRDAAQ	11166	NIGTRDA	0.38124	-0.20466
GS262	1989	GCCCAAACCGTCAGAGAACTCCAACCCGCACAG	6578	AQTVRELQPAQ	11167	TVRELQP	0.380962	-0.03275
SyS526	1990	GCCCAAGAGAATCATGGTACGACTAGTGCACAG	6579	AQENHGTTSAQ	11168	ENHGTTS	0.380821	0.0704
GS263	1991	GCCCAACACACCGACAGAAACTACGTCGCACAG	6580	AQHTDRNYVAQ	11169	HTDRNYV	0.380666	-0.06073
SyS528	1992	GCCCAAACTGTTGGTCCGACGTCTCATGCACAG	6581	AQTVGPTSHAQ	11170	TVGPTSH	0.380499	0.283908
SyS529	1993	GCCCAAGGCCTCGTCAAAGACCACCCCGCACAG	6582	AQGLVKDHPAQ	11171	GLVKDHP	0.380297	0.060613

FIG. 33 (Continued)

SUBSTITUTE SHEET (RULE 26)

SyS530	1994	GCCCAAATCAACGCCCTCACCAACGGCGCACAG	6583	AQINALTNGAQ	11172	INALTNG	0.380078	0.380078	0.298241
SyS531	1995	GCCCAACCCCTCGACAGCAACAGAGACGCACAG	6584	AQPLDSNRDAQ	11173	PLDSNRD	0.380007	0.380007	-0.00615
GP94	1996	GCCCAACTTAAGGTGACGAAGATTGATGCACAG	6585	AQLKVTKIDAQ	11174	LKVTKID	0.379542	0.379542	-0.07197
GS264	1997	GCCCAACATAATAGTAATCCTGGGTTGGCACAG	6586	AQHNSNPGLAQ	11175	HNSNPGL	0.379381	0.379381	-0.02297
GS265	1998	GCCCAAACCACCGTCATCCTCAAAACCGCACAG	6587	AQTTVILKTAQ	11176	TTVILKT	0.379349	0.379349	-0.13952
GS266	1999	GCCCAACTTGGTAAGGGTATGACTGCGGCACAG	6588	AQLGKGMTAAQ	11177	LGKGMTA	0.379294	0.379294	0.02198
SyS532	2000	GCCCAATTCAGCATCAGCGACCTCAAAGCACAG	6589	AQFSISDLKAQ	11178	FSISDLK	0.379031	0.379031	-0.02524
SyS533	2001	GCCCAAAGTACGGATACTCATCTTCCTGCACAG	6590	AQSTDTHLPAQ	11179	STDTHLP	0.378372	0.378372	-0.01675
TS141	2002	GCCCAATTGAATGCTGTTAAGAATGTTGCACAG	6591	AQLNAVKNVAQ	11180	LNAVKNV	0.378181	0.378181	0.632673
GP95	2003	GCCCAACGTTCGACTCCGAATACGATTGCACAG	6592	AQRSTPNTIAQ	11181	RSTPNTI	0.377505	0.377505	0.34596
GP96	2004	GCCCAATTGAGTATTAAGTTGCAGAATGCACAG	6593	AQLSIKLQNAQ	11182	LSIKLQN	0.377502	0.377502	-0.02247
SyS534	2005	GCCCAAAGTCTTGCGATTACTAGTAGTGCACAG	6594	AQSLAITSSAQ	11183	SLAITSS	0.37731	0.37731	-0.04258
GS270	2006	GCCCAACGGCAGGATATTACTATTGCTGCACAG	6595	AQRQDITIAAQ	11184	RQDITIA	0.377132	0.377132	-0.06485
GS271	2007	GCCCAAGGTAATGCTACGCCTCGGTCTGCACAG	6596	AQGNATPRSAQ	11185	GNATPRS	0.377091	0.377091	0.192946
SyS536	2008	GCCCAAAGCCTCGTCGGCACCACCAGCGCACAG	6597	AQSLVGTTSAQ	11186	SLVGTTS	0.376972	0.376972	0.04223
GS272	2009	GCCCAATGGCAGACTCAGGATAAGGAGGCACAG	6598	AQWQTQDKEAQ	11187	WQTQDKE	0.376959	0.376959	-0.16753
SyS537	2010	GCCCAAACGCCTAATGTGCCGTCTCCGGCACAG	6599	AQTPNVPSPAQ	11188	TPNVPSP	0.376726	0.376726	-0.06646
SyS539	2011	GCCCAAATTAATACTATTAGTCCGAAGGCACAG	6600	AQINTISPKAQ	11189	INTISPK	0.376382	0.376382	-0.16102
SyS541	2012	GCCCAACCCCTCGGCACCAGCAACACCGCACAG	6601	AQPLGTSNTAQ	11190	PLGTSNT	0.376355	0.376355	0.102187
SyS542	2013	GCCCAAAGCCAAGTCAACGGCGGCAAAGCACAG	6602	AQSQVNGGKAQ	11191	SQVNGGK	0.37633	0.37633	0.282579
SyS543	2014	GCCCAACCGATTAATGATAAGGTGATGGCACAG	6603	AQPINDKVMAQ	11192	PINDKVM	0.376049	0.376049	0.017194
SyS545	2015	GCCCAAAACGTCAGCAGCAGCATCCTCGCACAG	6604	AQNVSSSILAQ	11193	NVSSSIL	0.375885	0.375885	0.134279
GS273	2016	GCCCAACAGGCGAATTGGACTGCGTCTGCACAG	6605	AQQANWTASAQ	11194	QANWTAS	0.375563	0.375563	-0.10129
SyS546	2017	GCCCAAAGACCCGAAAACCACAGCAGCGCACAG	6606	AQRPENHSSAQ	11195	RPENHSS	0.375415	0.375415	0.065176
GS274	2018	GCCCAAACTAGGAATTTGGATGTTCATGCACAG	6607	AQTRNLDVHAQ	11196	TRNLDVH	0.374612	0.374612	-0.17829
SyS547	2019	GCCCAAATTAATAGTTCGTTTTCTAAGGCACAG	6608	AQINSSFSKAQ	11197	INSSFSK	0.374256	0.374256	-0.0095
SyS548	2020	GCCCAATCTATTCAGGGGTCTCAGCGGGCACAG	6609	AQSIQGSQRAQ	11198	SIQGSQR	0.374054	0.374054	0.007566
SyS549	2021	GCCCAAGTTGTGGCGGTTGGTCAGTTTGCACAG	6610	AQVVAVGQFAQ	11199	VVAVGQF	0.373702	0.373702	-0.13556
TS143	2022	GCCCAAGTCAACAAAGTCAGAGACGTCGCACAG	6611	AQVNKVRDVAQ	11200	VNKVRDV	0.373538	0.373538	-0.18383
SyS550	2023	GCCCAAAAGCCTAATGCTCAGATTCAGGCACAG	6612	AQKPNAQIQAQ	11201	KPNAQIQ	0.373406	0.373406	-0.06161
SyS551	2024	GCCCAAATGTCTATTGGTACGGGTTCGGCACAG	6613	AQMSIGTGSAQ	11202	MSIGTGS	0.373384	0.373384	0.053851
GS276	2025	GCCCAAGGGCTGCAGGCGACGTATTCTGCACAG	6614	AQGLQATYSAQ	11203	GLQATYS	0.373212	0.373212	-0.09754

FIG. 33 (Continued)

SyS552	2026	GCCCAACAAACCCTCAGCGCCAGCAGCGCACAG	6615	AQQTLSASSAQ	11204	QTLSASS	0.373145	-0.04342
GS277	2027	GCCCAAGACCCCCCCCAACAAATTCCCCGCACAG	6616	AQDPPNKFPAQ	11205	DPPNKFP	0.373042	0.030997
SyS554	2028	GCCCAAAGAATCAGCACCCTCGGCCTCGCACAG	6617	AQRISTLGLAQ	11206	RISTLGL	0.373026	-0.22891
SyS555	2029	GCCCAAAATTCGGATCGTTCGGTTAGTGCACAG	6618	AQNSDRSVSAQ	11207	NSDRSVS	0.372705	-0.18284
GP97	2030	GCCCAATATAATCTGCGTCTTGGGGGGGGCACAG	6619	AQYNLRLGGAQ	11208	YNLRLGG	0.37241	-0.00505
SyS556	2031	GCCCAAGTTCAGGATCGGGCGATGACTGCACAG	6620	AQVQDRAMTAQ	11209	VQDRAMT	0.37233	0.095998
SyS557	2032	GCCCAAAGCAGCAGCACCCTCCCCAGAGCACAG	6621	AQSSSTLPRAQ	11210	SSSTLPR	0.37218	0.075239
SyS558	2033	GCCCAAGGCGGCGTCCAAACCGACACAGCGCACAG	6622	AQGGVQTDSAQ	11211	GGVQTDS	0.371805	-0.08222
SS48	2034	GCCCAATTGTTGTCTAATAATACTCGGGCACAG	6623	AQLLSNNTRAQ	11212	LLSNNTR	0.371753	-0.20449
SyS559	2035	GCCCAATATCATGCTGCTCAGGCTGTTGCACAG	6624	AQYHAAQAVAQ	11213	YHAAQAV	0.371353	0.02988
GP98	2036	GCCCAAATGAGTGGTGTGGGTAGTTCGGCACAG	6625	AQMSGVGSSAQ	11214	MSGVGSS	0.371229	0.337397
SyS560	2037	GCCCAACTCACCGGCCAAGTCCTCGTCGCACAG	6626	AQLTGQVLVAQ	11215	LTGQVLV	0.370851	-0.08343
SyS561	2038	GCCCAAGCGGTTAATAGGCTGCCTATTGCACAG	6627	AQAVNRLPIAQ	11216	AVNRLPI	0.370811	-0.12454
SyS562	2039	GCCCAAAGTTCTCAGATGCCGTTGCGGGCACAG	6628	AQSSQMPLRAQ	11217	SSQMPLR	0.370795	-0.05174
GS279	2040	GCCCAAAGCAGCAACATCGCCGACAGCGCACAG	6629	AQSSNIADSAQ	11218	SSNIADS	0.370754	-0.10675
SyS563	2041	GCCCAAGTTGTTACGCCGCAGATTAGTGCACAG	6630	AQVVTPQISAQ	11219	VVTPQIS	0.37058	-0.15746
GS280	2042	GCCCAAGATTCTAAGAAGATGAGTTGGGCACAG	6631	AQDSKKMSWAQ	11220	DSKKMSW	0.370419	-0.09553
SyS564	2043	GCCCAAGAGACGTATAAGACTACTCTGGCACAG	6632	AQETYKTTLAQ	11221	ETYKTTL	0.370166	-0.03857
SyS565	2044	GCCCAACTTACTATGGGTAATTCTCTGGCACAG	6633	AQLTMGNSLAQ	11222	LTMGNSL	0.36988	0.014405
SyS566	2045	GCCCAATTTAAGGTTAGTATTCAGCAGGCACAG	6634	AQFKVSIQQAQ	11223	FKVSIQQ	0.369779	-0.20345
SyS567	2046	GCCCAAGATGGTCATGCTCATCTTCCGGCACAG	6635	AQDGHAHLPAQ	11224	DGHAHLP	0.369646	-0.11191
SyS568	2047	GCCCAAACCGCCGTCAGCCTCAGCAACGCACAG	6636	AQTAVSLSNAQ	11225	TAVSLSN	0.369523	-0.01275
SyS569	2048	GCCCAAAGCCAAAACCAAATGCAAACCGCACAG	6637	AQSQNQMQTAQ	11226	SQNQMQT	0.369507	-0.13071
SyS570	2049	GCCCAACAGAGTGTGACTACGCAGCATGCACAG	6638	AQQSVTTQHAQ	11227	QSVTTQH	0.369126	0.146422
SyS571	2050	GCCCAACTCAGCACCGCCCTCACCGTCGCACAG	6639	AQLSTALTVAQ	11228	LSTALTV	0.369039	-0.00037
SyS572	2051	GCCCAACTCGCCAACGCCGTCACCAAAGCACAG	6640	AQLANAVTKAQ	11229	LANAVTK	0.368954	0.183009
GS281	2052	GCCCAAACCGGCCACGTCCACGAAAACGCACAG	6641	AQTGHVHENAQ	11230	TGHVHEN	0.368935	-0.08669
SyS573	2053	GCCCAATCGATTTCGGATACGGCTTCTGCACAG	6642	AQSISDTASAQ	11231	SISDTAS	0.368929	-0.0313
GS282	2054	GCCCAACCCGTCGTCCAAAGCGTCGGCGCACAG	6643	AQPVVQSVGAQ	11232	PVVQSVG	0.368793	-0.15766
GS283	2055	GCCCAACAACACCTCAGCACCGTCAACGCACAG	6644	AQQHLSTVNAQ	11233	QHLSTVN	0.368559	-0.15574
SyS575	2056	GCCCAACTGAGTCATAATACGACGCATGCACAG	6645	AQLSHNTTHAQ	11234	LSHNTTH	0.368528	0.093848
SyS576	2057	GCCCAACCTTCGAATTTTTCGAATTCTGCACAG	6646	AQPSNFSNSAQ	11235	PSNFSNS	0.368509	0.141011

FIG. 33 (Continued)

SyS577	2058	GCCCAATTTGATAAGTCTGTTCCTAGTGCACAG	6647	AQFDKSVPSAQ	11236	FDKSVPS	0.368326	-0.04816
GS284	2059	GCCCAAACCCAAGCCACCGAAAAAGACGCACAG	6648	AQTQATEKDAQ	11237	TQATEKD	0.368256	-0.09754
SyS578	2060	GCCCAATTGAGTGCGAAGGCTAGTCAGGCACAG	6649	AQLSAKASQAQ	11238	LSAKASQ	0.368184	0.299581
SyS579	2061	GCCCAATCGGTTCAGCCTGCGGTGTCGGCACAG	6650	AQSVQPAVSAQ	11239	SVQPAVS	0.367991	0.197439
SyS580	2062	GCCCAAAGTTTGATGCATGGGACGCCTGCACAG	6651	AQSLMHGTPAQ	11240	SLMHGTP	0.367985	0.049386
GS285	2063	GCCCAACCCACCATCAGAACCAACACCGCACAG	6652	AQPTIRTNTAQ	11241	PTIRTNT	0.367694	-0.04787
SyS581	2064	GCCCAAAATGATTCGCTTAAGGTTAATGCACAG	6653	AQNDSLKVNAQ	11242	NDSLKVN	0.367645	-0.2268
SyS582	2065	GCCCAAAGCACCCAACCCGTCAACAGAGCACAG	6654	AQSTQPVNRAQ	11243	STQPVNR	0.367609	-0.15981
GS286	2066	GCCCAATCTTCGGATAAGCATAATCCTGCACAG	6655	AQSSDKHNPAQ	11244	SSDKHNP	0.367604	0.108588
SyS583	2067	GCCCAATTCCTCGAAAACGCCAAAATCGCACAG	6656	AQFLENAKIAQ	11245	FLENAKI	0.367535	0.026006
SyS584	2068	GCCCAAGTGTCTACTGGTACTCTTAAGGCACAG	6657	AQVSTGTLKAQ	11246	VSTGTLK	0.367523	-0.07858
GS287	2069	GCCCAACGTGATGCGTCTTTGAGTACTGCACAG	6658	AQRDASLSTAQ	11247	RDASLST	0.36722	-0.14238
SyS585	2070	GCCCAAAAGGGTACTGAGATTAAGCTTGCACAG	6659	AQKGTEIKLAQ	11248	KGTEIKL	0.367015	-0.01863
SyS586	2071	GCCCAAATTATGAATCAGCTGGGTGATGCACAG	6660	AQIMNQLGDAQ	11249	IMNQLGD	0.36699	-0.08828
SyS587	2072	GCCCAACCTAGTAATAATACTCAGATTGCACAG	6661	AQPSNNTQIAQ	11250	PSNNTQI	0.366851	-0.10646
SyS588	2073	GCCCAAACTTCGAGTAGTATTACGACTGCACAG	6662	AQTSSSITTAQ	11251	TSSSITT	0.366832	0.041648
SyS589	2074	GCCCAAAGGGATCTGAATGCGCATAATGCACAG	6663	AQRDLNAHNAQ	11252	RDLNAHN	0.366746	0.001434
SyS590	2075	GCCCAAACCGGCTTCGCCAGAAGCGAAGCACAG	6664	AQTGFARSEAQ	11253	TGFARSE	0.366503	-0.14283
GS288	2076	GCCCAACTCGAACAACTCGCCCCCAAAGCACAG	6665	AQLEQLAPKAQ	11254	LEQLAPK	0.36606	-0.18054
SyS591	2077	GCCCAAGCCGCCATGCAAAGCGAAAGAGCACAG	6666	AQAAMQSERAQ	11255	AAMQSER	0.365747	0.085313
GS290	2078	GCCCAACAGCTTAATTATGAGGCGCATGCACAG	6667	AQQLNYEAHAQ	11256	QLNYEAH	0.36537	-0.15497
SyS592	2079	GCCCAAGCCAACCCCGGCAGCCTCCTCGCACAG	6668	AQANPGSLLAQ	11257	ANPGSLL	0.365151	0.332343
GS291	2080	GCCCAACTTAGGCATATTGAGACGCCTGCACAG	6669	AQLRHIETPAQ	11258	LRHIETP	0.365122	-0.10472
SS49	2081	GCCCAACTTCCTCAGAATTCGGCGAAGGCACAG	6670	AQLPQNSAKAQ	11259	LPQNSAK	0.36494	-0.2215
SyS593	2082	GCCCAAGCCGGCAGCCCCATCAGCAGAGCACAG	6671	AQAGSPISRAQ	11260	AGSPISR	0.364661	0.254221
SyS594	2083	GCCCAAAGAGCCACCAACGTCGAAGTCGCACAG	6672	AQRATNVEVAQ	11261	RATNVEV	0.364602	0.350302
SyS595	2084	GCCCAACCCCAACCCAACACAGAGGCGCACAG	6673	AQPQPNNRGAQ	11262	PQPNNRG	0.364568	0.149339
SyS596	2085	GCCCAATCTCCTTCGACGCCTCATCTTGCACAG	6674	AQSPSTPHLAQ	11263	SPSTPHL	0.364561	-0.038
SyS597	2086	GCCCAACTTTCGAATACTTTGACTAATGCACAG	6675	AQLSNTLTNAQ	11264	LSNTLTN	0.364377	-0.02217
GS292	2087	GCCCAATCGAATAGGGAGGGTTTGATGGCACAG	6676	AQSNREGLMAQ	11265	SNREGLM	0.364262	-0.06434
SyS598	2088	GCCCAAGTCGCCCACAGCCCCCCCCAGCGCACAG	6677	AQVAHSPPSAQ	11266	VAHSPPS	0.364259	0.059626
GS293	2089	GCCCAAAGCGTCAAAAACATGCTCACCGCACAG	6678	AQSVKNMLTAQ	11267	SVKNMLT	0.364054	-0.01456

FIG. 33 (Continued)

GS294	2090	GCCCAAGGGCTTTCGACTGGTCTTGCTGCACAG	6679	AQGLSTGLAAQ	11268	GLSTGLA	0.36383	-0.09664
GS295	2091	GCCCAAGCCATGAGCAGACCCGAACTCGCACAG	6680	AQAMSRPELAQ	11269	AMSRPEL	0.363746	-0.09205
SyS599	2092	GCCCAAGCCATGGACCTCAAACTCCAAGCACAG	6681	AQAMDLKLQAQ	11270	AMDLKLQ	0.363654	-0.13677
SyS600	2093	GCCCAAGCCGTCGCCGGCCCCACCAAAGCACAG	6682	AQAVAGPTKAQ	11271	AVAGPTK	0.363564	0.026302
SyS601	2094	GCCCAACCTACTCTTGGGTCGCGTACTGCACAG	6683	AQPTLGSRTAQ	11272	PTLGSRT	0.363533	0.006254
SyS602	2095	GCCCAAAGTGAGAATCCTATTGATCCGGCACAG	6684	AQSENPIDPAQ	11273	SENPIDP	0.363529	-0.19011
SyS603	2096	GCCCAAACCAACAACAGCCCCGGCACCGCACAG	6685	AQTNNSPGTAQ	11274	TNNSPGT	0.36339	0.163927
SyS604	2097	GCCCAACACACCAGCCCCACCAGCCTCGCACAG	6686	AQHTSPTSLAQ	11275	HTSPTSL	0.363168	0.036859
GS297	2098	GCCCAAAACAACGCCGGCATCAGCATGGCACAG	6687	AQNNAGISMAQ	11276	NNAGISM	0.362679	-0.08459
GS298	2099	GCCCAACTCGTCTACAGCAACAACACCGCACAG	6688	AQLVYSNNTAQ	11277	LVYSNNT	0.362616	-0.14524
SyS605	2100	GCCCAACCGGCGAGTCAGTCTACGACTGCACAG	6689	AQPASQSTTAQ	11278	PASQSTT	0.362362	0.055989
SyS606	2101	GCCCAAGTTCAGGTTGGGCATCCTCTTGCACAG	6690	AQVQVGHPLAQ	11279	VQVGHPL	0.362247	-0.16466
SyS607	2102	GCCCAAGACGCCAGCTACACCGGCACCGCACAG	6691	AQDASYTGTAQ	11280	DASYTGT	0.361961	-0.19133
SyS608	2103	GCCCAAGGGATTACTACTGAGGCGCGGGCACAG	6692	AQGITTEARAQ	11281	GITTEAR	0.361378	-0.11715
SyS609	2104	GCCCAATCTATGCCTCAGCATGCTATTGCACAG	6693	AQSMPQHAIAQ	11282	SMPQHAI	0.361137	-0.01957
SyS610	2105	GCCCAACTCCAAAGCGCCCTCCAAAACGCACAG	6694	AQLQSALQNAQ	11283	LQSALQN	0.361126	-0.20951
SyS611	2106	GCCCAAAAAAGCAGCGACAGCACCAGCGCACAG	6695	AQKSSDSTSAQ	11284	KSSDSTS	0.360758	0.203964
GS300	2107	GCCCAAAAAAGCCCCGCCGGCGCCCTCGCACAG	6696	AQKSPAGALAQ	11285	KSPAGAL	0.360597	-0.10382
SyS613	2108	GCCCAAACCGAAATGAGCCTCACCAGCGCACAG	6697	AQTEMSLTSAQ	11286	TEMSLTS	0.360316	-0.1489
SyS614	2109	GCCCAATTGAATAGTGAGACTTTTCCTGCACAG	6698	AQLNSETFPAQ	11287	LNSETFP	0.360064	-0.18405
SyS615	2110	GCCCAAAGCGCCCTCAGCCAACAATACGCACAG	6699	AQSALSQQYAQ	11288	SALSQQY	0.359961	-0.08871
GP99	2111	GCCCAACGTTCGGTGGCTAATGTGCCGGCACAG	6700	AQRSVANVPAQ	11289	RSVANVP	0.359888	0.151036
SyS616	2112	GCCCAAAGCAGCGGCGCCACCCTCCAAGCACAG	6701	AQSSGATLQAQ	11290	SSGATLQ	0.359857	0.069108
SyS617	2113	GCCCAACTCAACGGCGGCGCCGCCAGCGCACAG	6702	AQLNGGAASAQ	11291	LNGGAAS	0.359832	-0.13192
SyS619	2114	GCCCAAAGCCACCAAACCACCCCCCACCGCACAG	6703	AQSHQTTPTAQ	11292	SHQTTPT	0.359233	-0.10135
GS301	2115	GCCCAATATGAGAATAGTAGTAGTTTGGCACAG	6704	AQYENSSSLAQ	11293	YENSSSL	0.359035	-0.14003
SyS620	2116	GCCCAAATTCAGACTTCTGCTCATACTGCACAG	6705	AQIQTSAHTAQ	11294	IQTSAHT	0.358854	0.06834
SyS621	2117	GCCCAAAGAGAAATCCAAAAAATGAGCGCACAG	6706	AQREIQKMSAQ	11295	REIQKMS	0.358714	-0.09495
SyS622	2118	GCCCAAAGCGCCGGCATGATCAGCCACGCACAG	6707	AQSAGMISHAQ	11296	SAGMISH	0.358383	0.117139
SyS623	2119	GCCCAAATGAGAAGCACCGACAGCGAAGCACAG	6708	AQMRSTDSEAQ	11297	MRSTDSE	0.358219	0.15208
SyS624	2120	GCCCAAAGCCACCCCCCAAGGCGACAGCGCACAG	6709	AQSHPQGDSAQ	11298	SHPQGDS	0.358104	-0.12208
SyS625	2121	GCCCAACTCATCGACACCAAAATCAGCGCACAG	6710	AQLIDTKISAQ	11299	LIDTKIS	0.358044	0.03053

FIG. 33 (Continued)

SyS626	2122	GCCCAAACCCACCTCAAAGACCTCCTCGCACAG	6711	AQTHLKDLLAQ	11300	THLKDLL	0.357945	0.035942
GS302	2123	GCCCAAGGTACTTCGAGTGTGCTGATTGCACAG	6712	AQGTSSVLIAQ	11301	GTSSVLI	0.357908	0.009233
SyS627	2124	GCCCAACCTTTGGTTACGAATGAGCCTGCACAG	6713	AQPLVTNEPAQ	11302	PLVTNEP	0.357827	-0.06917
GS303	2125	GCCCAAAGAGACCTCAGCCACAACAGCGCACAG	6714	AQRDLSHNSAQ	11303	RDLSHNS	0.357777	-0.14151
SyS628	2126	GCCCAATATGATAATGAGCATAGGCCGGCACAG	6715	AQYDNEHRPAQ	11304	YDNEHRP	0.3577	0.184576
SyP39	2127	GCCCAAGTTGGGAGTCATACTATGACGGCACAG	6716	AQVGSHTMTAQ	11305	VGSHTMT	0.357557	-0.04335
SyS629	2128	GCCCAAGGGCATACGAGTGTGTCTCTGGCACAG	6717	AQGHTSVSLAQ	11306	GHTSVSL	0.357531	-0.06038
SyS630	2129	GCCCAACTCGACCTCAAAAACCAAAGAGCACAG	6718	AQLDLKNQRAQ	11307	LDLKNQR	0.357396	0.14998
SyS631	2130	GCCCAACCCGTCGCCAAAATCACCAGCGCACAG	6719	AQPVAKITSAQ	11308	PVAKITS	0.357222	-0.08463
GS305	2131	GCCCAACTTGAGAATGGGAAGCCTAAGGCACAG	6720	AQLENGKPKAQ	11309	LENGKPK	0.356969	-0.1617
GS306	2132	GCCCAAGACCTCGCCAGAGCCACCCTCGCACAG	6721	AQDLARATLAQ	11310	DLARATL	0.356925	-0.11281
GS307	2133	GCCCAAAAGGTTCGTGATGATAAGCCTGCACAG	6722	AQKVRDDKPAQ	11311	KVRDDKP	0.356843	0.02987
SS50	2134	GCCCAACACAACGTCGCCATCACCCCCGCACAG	6723	AQHNVAITPAQ	11312	HNVAITP	0.356745	-0.25276
GS308	2135	GCCCAAACCTTCAACGCCACCTACGCCGCACAG	6724	AQTFNATYAAQ	11313	TFNATYA	0.35665	-0.07129
SyS632	2136	GCCCAAGGCAGCCAAGGCACCATCAGAGCACAG	6725	AQGSQGTIRAQ	11314	GSQGTIR	0.356647	0.346418
GS309	2137	GCCCAAAGCCTCGGCCACGACGCCAGAGCACAG	6726	AQSLGHDARAQ	11315	SLGHDAR	0.356616	-0.07956
SyS633	2138	GCCCAACGTAGTGGGCCGGATTCTTCTGCACAG	6727	AQRSGPDSSAQ	11316	RSGPDSS	0.356605	0.13964
SyS634	2139	GCCCAAGCTATGAATCTTCAGAATTTGGCACAG	6728	AQAMNLQNLAQ	11317	AMNLQNL	0.355956	-0.06641
SyP40	2140	GCCCAACTTCGGGCTGGTCCGGGTGTGGCACAG	6729	AQLRAGPGVAQ	11318	LRAGPGV	0.355879	-0.04263
SyS636	2141	GCCCAAACCGTCATGAGCAGCAGCAGCGCACAG	6730	AQTVMSSSSAQ	11319	TVMSSSS	0.355682	0.155451
GS313	2142	GCCCAACATACTTCTCCTGTGGGTTATGCACAG	6731	AQHTSPVGYAQ	11320	HTSPVGY	0.355451	-0.07506
SyP41	2143	GCCCAATGGACTTCTCAGGCTACGGCGGCACAG	6732	AQWTSQATAAQ	11321	WTSQATA	0.355301	-0.03985
SyS637	2144	GCCCAAACGATGAATTCTGTTCCTCGTGCACAG	6733	AQTMNSVPRAQ	11322	TMNSVPR	0.355114	-0.10975
GS315	2145	GCCCAAGTCAACGGCGGCATGGTCAACGCACAG	6734	AQVNGGMVNAQ	11323	VNGGMVN	0.3551	-0.17381
GS316	2146	GCCCAAACTAATGCTAGGATGAATACTGCACAG	6735	AQTNARMNTAQ	11324	TNARMNT	0.354728	-0.01679
SyS638	2147	GCCCAAATCAGCGGCAACATGCACAGCGCACAG	6736	AQISGNMHSAQ	11325	ISGNMHS	0.354683	0.134397
GS317	2148	GCCCAAAGCGTCGGCGGCGCCAGCTTCGCACAG	6737	AQSVGGASFAQ	11326	SVGGASF	0.354664	-0.04069
GS318	2149	GCCCAAACCAGCGAAAGCCCCTACAAAGCACAG	6738	AQTSESPYKAQ	11327	TSESPYK	0.354593	-0.18278
SyS639	2150	GCCCAAGGTCATTTTGGTACTATGTCGGCACAG	6739	AQGHFGTMSAQ	11328	GHFGTMS	0.354408	-0.06031
SyS640	2151	GCCCAACTTACGACTAGTGGTCTGAAGGCACAG	6740	AQLTTSGLKAQ	11329	LTTSGLK	0.354396	0.01345
GS319	2152	GCCCAAAGGATTAATTCGTCTACGTATGCACAG	6741	AQRINSSTYAQ	11330	RINSSTY	0.354303	-0.18727
GP100	2153	GCCCAACTGACTGGTAGTTCGTTGACTGCACAG	6742	AQLTGSSLTAQ	11331	LTGSSLT	0.354102	-0.07405

FIG. 33 (Continued)

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SyS641	2154	GCCCAACCGATTCGGGGTACTATTTATGCACAG	6743	AQPIRGTIYAQ	11332	PIRGTIY	0.354066	-0.08153
GS320	2155	GCCCAAACCACCAGCAACAACACCCACGCACAG	6744	AQTTSNNTHAQ	11333	TTSNNTH	0.354066	0.118932
SyS642	2156	GCCCAACAGGTGACTACTAATTTGGATGCACAG	6745	AQQVTTNLDAQ	11334	QVTTNLD	0.353947	-0.09555
SyS643	2157	GCCCAAGCTTTGGATTCTAGTGAGCCGGCACAG	6746	AQALDSSEPAQ	11335	ALDSSEP	0.353947	-0.1889
SyS644	2158	GCCCAATACCCCAAAAACGTCGCCTGGGCACAG	6747	AQYPKNVAWAQ	11336	YPKNVAW	0.353947	-0.20588
SyS645	2159	GCCCAATCTACTACTGGGCGGAATCTGGCACAG	6748	AQSTTGRNLAQ	11337	STTGRNL	0.353947	-0.21436
SyS646	2160	GCCCAAACGAAGCTTATGCAGTCTAATGCACAG	6749	AQTKLMQSNAQ	11338	TKLMQSN	0.353941	0.01478
SyS647	2161	GCCCAAAACAGCTACGGCGACGCCGCCGCACAG	6750	AQNSYGDAAAQ	11339	NSYGDAA	0.3539	-0.07546
SyS648	2162	GCCCAAGAGCATACGGGTGCGCCTGCTGCACAG	6751	AQEHTGAPAAQ	11340	EHTGAPA	0.353742	-0.18861
SyS649	2163	GCCCAACTGCGGACTGAGACGGCGAATGCACAG	6752	AQLRTETANAQ	11341	LRTETAN	0.353402	-0.03968
SyS650	2164	GCCCAAGTCCTCGACGTCAACACCCTCGCACAG	6753	AQVLDVNTLAQ	11342	VLDVNTL	0.353275	-0.15041
SyS651	2165	GCCCAAGACAGAGGCAACGACAAACTCGCACAG	6754	AQDRGNDKLAQ	11343	DRGNDKL	0.353216	0.297443
GS321	2166	GCCCAAAGCTTCACCAACAGCACCCACGCACAG	6755	AQSFTNSTHAQ	11344	SFTNSTH	0.352987	0.109223
SyS652	2167	GCCCAACTCGCCCACAGCAGCCTCAGCGCACAG	6756	AQLAHSSLSAQ	11345	LAHSSLS	0.352724	-0.00659
GS323	2168	GCCCAAAGACTCGTCGACCCCATCCCCGCACAG	6757	AQRLVDPIPAQ	11346	RLVDPIP	0.352703	-0.09391
SyS653	2169	GCCCAATGGGGCGACAAAGAAACCTTCGCACAG	6758	AQWGDKETFAQ	11347	WGDKETF	0.352651	-0.15617
SyS654	2170	GCCCAAAGAGACGACAACCTCAGCACCGCACAG	6759	AQRDDNLSTAQ	11348	RDDNLST	0.352538	-0.05395
SyS655	2171	GCCCAATCTAAGCAGTTGATTGATACTGCACAG	6760	AQSKQLIDTAQ	11349	SKQLIDT	0.352442	-0.22803
GS325	2172	GCCCAATTTCAGAATCAGACTGTTGGTGCACAG	6761	AQFQNQTVGAQ	11350	FQNQTVG	0.352245	-0.04999
SyS656	2173	GCCCAAGTCTTCAGCAGCGACAGCCTCGCACAG	6762	AQVFSSDSLAQ	11351	VFSSDSL	0.352214	0.031487
SyS657	2174	GCCCAATATGCGCAGCAGTTGCCTGTGGCACAG	6763	AQYAQQLPVAQ	11352	YAQQLPV	0.352069	-0.06517
SyS658	2175	GCCCAAATTGTGACTGGTACTACGCAGGCACAG	6764	AQIVTGTTQAQ	11353	IVTGTTQ	0.351501	-0.17505
SyS659	2176	GCCCAAAGCAAAATCACCGAAAGCAACGCACAG	6765	AQSKITESNAQ	11354	SKITESN	0.351451	0.084909
SyS660	2177	GCCCAAATTGCTGGGCAGGTGGGGGCGGCACAG	6766	AQIAGQVGAAQ	11355	IAGQVGA	0.351384	0.33939
SyS661	2178	GCCCAAGGTTATAGTCAGACGCCTCATGCACAG	6767	AQGYSQTPHAQ	11356	GYSQTPH	0.351298	0.03403
GS326	2179	GCCCAAGGTTTGGCGTTGCGTCCTGATGCACAG	6768	AQGLALRPDAQ	11357	GLALRPD	0.35125	-0.09087
SyS662	2180	GCCCAAAACGCCGTCAGCAACAACACCGCACAG	6769	AQNAVSNNTAQ	11358	NAVSNNT	0.351208	0.221429
SyS663	2181	GCCCAAAACCAAAGCACCCTCCCCACCGCACAG	6770	AQNQSTLPTAQ	11359	NQSTLPT	0.351121	0.2934
GS328	2182	GCCCAAACCAGCATCCCCGACAAACCCGCACAG	6771	AQTSIPDKPAQ	11360	TSIPDKP	0.351033	-0.02153
SyS664	2183	GCCCAAGGCAGCAGCACCGCCAGCCTCGCACAG	6772	AQGSSTASLAQ	11361	GSSTASL	0.350993	0.260874
GS329	2184	GCCCAAAGAATCATCGGCACCGCCACCGCACAG	6773	AQRIIGTATAQ	11362	RIIGTAT	0.350979	-0.11461
GP101	2185	GCCCAAAGTTTGAATGGGGGTCGGACGGCACAG	6774	AQSLNGGRTAQ	11363	SLNGGRT	0.35082	0.208517

FIG. 33 (Continued)

GS330	2186	GCCCAACCGGTGAAGACTGTTGGGATTGCACAG	6775	AQPVKTVGIAQ	11364	PVKTVGI	0.350777	-0.15669
GS331	2187	GCCCAACAGCCGTCTGCGATTCCGAATGCACAG	6776	AQQPSAIPNAQ	11365	QPSAIPN	0.350511	-0.03818
SyS666	2188	GCCCAATTCGCCAGCAGCGTCAGCGCCGCACAG	6777	AQFASSVSAAQ	11366	FASSVSA	0.35031	-0.00733
SyS667	2189	GCCCAAGAAGGCAACCTCACCAAACTCGCACAG	6778	AQEGNLTKLAQ	11367	EGNLTKL	0.350039	-0.17629
GS333	2190	GCCCAATTGGGGACTAGGACTACTTCTGCACAG	6779	AQLGTRTTSAQ	11368	LGTRTTS	0.349926	0.147471
GS334	2191	GCCCAAACTCATCGTGATTTTTCTCCTGCACAG	6780	AQTHRDFSPAQ	11369	THRDFSP	0.349916	-0.17201
SyS668	2192	GCCCAAACCGGCGTCAGCACCGGCGTCGCACAG	6781	AQTGVSTGVAQ	11370	TGVSTGV	0.349619	-0.05108
SyS669	2193	GCCCAAGTGCCGAATAATTCGCAGCGGGCACAG	6782	AQVPNNSQRAQ	11371	VPNNSQR	0.349519	-0.04801
GS335	2194	GCCCAAATGCCCAGCGGCGTCCCCGTCGCACAG	6783	AQMPSGVPVAQ	11372	MPSGVPV	0.349514	-0.10759
GS336	2195	GCCCAAAACGCCCTCCCCAGACCCAACGCACAG	6784	AQNALPRPNAQ	11373	NALPRPN	0.349247	-0.07734
SyS670	2196	GCCCAACGGACGGATCATTCTCAGATTGCACAG	6785	AQRTDHSQIAQ	11374	RTDHSQI	0.349055	0.104306
GS337	2197	GCCCAACAAACCCTCAAAAGCGCCTACGCACAG	6786	AQQTLKSAYAQ	11375	QTLKSAY	0.349045	-0.12676
GS338	2198	GCCCAAAAGGAGGAGCATACGCGGGGGGGCACAG	6787	AQKEEHTRGAQ	11376	KEEHTRG	0.349029	-0.12253
SyS671	2199	GCCCAACTCCCCGCCGCCCCCAGATACGCACAG	6788	AQLPAAPRYAQ	11377	LPAAPRY	0.348993	-0.20103
SyS672	2200	GCCCAACTGGATAAGGCGCATTTTGCTGCACAG	6789	AQLDKAHFAAQ	11378	LDKAHFA	0.348667	0.240412
SyS673	2201	GCCCAACACGCCATCGACGCCGTCAAAGCACAG	6790	AQHAIDAVKAQ	11379	HAIDAVK	0.348532	-0.11859
GS340	2202	GCCCAACCGATTCTTACGGCTGTGCCGGCACAG	6791	AQPILTAVPAQ	11380	PILTAVP	0.348418	-0.18547
GS341	2203	GCCCAAACCGTCCAACAAAGCGCCATGGCACAG	6792	AQTVQQSAMAQ	11381	TVQQSAM	0.348333	0.005294
GS342	2204	GCCCAATCGGAGGGGATTGGTGGTCGTGCACAG	6793	AQSEGIGGRAQ	11382	SEGIGGR	0.348134	-0.14524
SyS674	2205	GCCCAAATGGGTTCTACTGTTACTCGTGCACAG	6794	AQMGSTVTRAQ	11383	MGSTVTR	0.348015	0.199144
SyS675	2206	GCCCAAAGCGTCAGAAGCCCCACCAAAGCACAG	6795	AQSVRSPTKAQ	11384	SVRSPTK	0.347898	-0.14405
SyS676	2207	GCCCAAACTACGCGTGATGTTACTACGGCACAG	6796	AQTTRDVTTAQ	11385	TTRDVTT	0.347689	-0.08907
GS343	2208	GCCCAATCGGCGGCTGGGAAGACTTATGCACAG	6797	AQSAAGKTYAQ	11386	SAAGKTY	0.347647	-0.11818
SyS677	2209	GCCCAAACGACGCCGAGTACTGTTCGTGCACAG	6798	AQTTPSTVRAQ	11387	TTPSTVR	0.347437	0.192531
SyS678	2210	GCCCAAGTTGCTCTGACGACGACGGTTGCACAG	6799	AQVALTTTVAQ	11388	VALTTTV	0.347428	-0.14068
SyS679	2211	GCCCAAGATACGCAGCTTCCGCTGAGTGCACAG	6800	AQDTQLPLSAQ	11389	DTQLPLS	0.347386	-0.16102
SS52	2212	GCCCAAAACGCCGTCAGCAACCCCCTCGCACAG	6801	AQNAVSNPLAQ	11390	NAVSNPL	0.347346	-0.29875
GS344	2213	GCCCAAATGGAACTCAAATACCAAAGAGCACAG	6802	AQMELKYQRAQ	11391	MELKYQR	0.347339	-0.07279
GS345	2214	GCCCAAAACAGCCTCCACGGCCACGCCGCACAG	6803	AQNSLHGHAAQ	11392	NSLHGHA	0.347161	-0.15227
SyS680	2215	GCCCAACACAGCCCCAGCCTCAGCGACGCACAG	6804	AQHSPSLSDAQ	11393	HSPSLSD	0.347084	-0.08881
SyS681	2216	GCCCAAGGCAGCGTCACCAGCCTCGGCGCACAG	6805	AQGSVTSLGAQ	11394	GSVTSLG	0.346855	-0.16397
SyS682	2217	GCCCAAAGAGAAGTCAGCAGCACCACCGCACAG	6806	AQREVSSTTAQ	11395	REVSSTT	0.346744	0.143514

FIG. 33 (Continued)

GS346	2218	GCCCAAGGTAAGGCGACGCTTGATACTGCACAG	6807	AQGKATLDTAQ	11396	GKATLDT	0.346704	-0.12044
GS347	2219	GCCCAACTTAATCCTCCTTTGAATAATGCACAG	6808	AQLNPPLNNAQ	11397	LNPPLNN	0.346683	-0.15676
SyS683	2220	GCCCAAACTTCTGGGCATTCGCCGTCGGCACAG	6809	AQTSGHSPSAQ	11398	TSGHSPS	0.346676	0.010364
SyS684	2221	GCCCAAGACGTCACCGCCACCGCCCCCGCACAG	6810	AQDVTATAPAQ	11399	DVTATAP	0.346433	-0.18648
GS349	2222	GCCCAACACCAAAACACCGGCAGCGTCGCACAG	6811	AQHQNTGSVAQ	11400	HQNTGSV	0.346357	-0.01619
SyS686	2223	GCCCAAGATCTTACGCATACTTTTGATGCACAG	6812	AQDLTHTFDAQ	11401	DLTHTFD	0.34605	-0.19496
GS350	2224	GCCCAATACCTCCCCAACAAAGAAAGAGCACAG	6813	AQYLPNKERAQ	11402	YLPNKER	0.345987	-0.05272
SyS687	2225	GCCCAAGTGGATGGTACGTATACGGTGGCACAG	6814	AQVDGTYTVAQ	11403	VDGTYTV	0.345915	-0.0622
SyS688	2226	GCCCAATACCTCACCAGCGGCGGCTACGCACAG	6815	AQYLTSGGYAQ	11404	YLTSGGY	0.345752	-0.13798
SyS689	2227	GCCCAAGCCAGCCTCGTCGTCGCCGCACAG	6816	AQASLVVVAAQ	11405	ASLVVVA	0.3457	-0.17072
SyS690	2228	GCCCAATTTGATGCTAATTCGAAGATTGCACAG	6817	AQFDANSKIAQ	11406	FDANSKI	0.345431	-0.14647
SyS691	2229	GCCCAATACCTCACCGAAAGCCCCGGCGCACAG	6818	AQYLTESPGAQ	11407	YLTESPG	0.345425	-0.15781
GS351	2230	GCCCAAAGAAACGCCAGCCTCGACCCCGCACAG	6819	AQRNASLDPAQ	11408	RNASLDP	0.345339	-0.0446
GP103	2231	GCCCAAGCGGGGAGTCCTCGTGCGGGTGCACAG	6820	AQAGSPRAGAQ	11409	AGSPRAG	0.345002	-0.07336
SyS692	2232	GCCCAAAGAGTCGAAAAACTCACCCCCGCACAG	6821	AQRVEKLTPAQ	11410	RVEKLTP	0.344773	-0.07567
SyS693	2233	GCCCAAAGAACCACCGGCGACAACACCGCACAG	6822	AQRTTGDNTAQ	11411	RTTGDNT	0.344747	0.190402
SyS694	2234	GCCCAACCCGCCGCCACCAGCGGCTTCGCACAG	6823	AQPAATSGFAQ	11412	PAATSGF	0.344706	-0.16344
SyS695	2235	GCCCAAATTCTTACGATTCATACGCATGCACAG	6824	AQILTIHTHAQ	11413	ILTIHTH	0.344626	-0.22042
GS354	2236	GCCCAAATCAACATCAGCAGCCACGTCGCACAG	6825	AQINISSHVAQ	11414	INISSHV	0.34453	-0.03881
GS355	2237	GCCCAACCCAGCGGCAGCGCCAGAAGCGCACAG	6826	AQPSGSARSAQ	11415	PSGSARS	0.344116	-0.15192
SyS696	2238	GCCCAAAGTACGATGCCGACTAGGCTGGCACAG	6827	AQSTMPTRLAQ	11416	STMPTRL	0.344089	-0.10729
SyS697	2239	GCCCAACTCTACGCCAGCGCCGGCGTCGCACAG	6828	AQLYASAGVAQ	11417	LYASAGV	0.34374	-0.13192
GP104	2240	GCCCAATTGGTTCAGACGGGGCTGCTGGCACAG	6829	AQLVQTGLLAQ	11418	LVQTGLL	0.343691	-0.07266
GS357	2241	GCCCAAGTCAGCCTCAACAGAACCGAAGCACAG	6830	AQVSLNRTEAQ	11419	VSLNRTE	0.343359	-0.01647
SyP42	2242	GCCCAAGGTGGGAGGGAGAGTTCTTTGGCACAG	6831	AQGGRESSLAQ	11420	GGRESSL	0.343358	-0.04339
GS358	2243	GCCCAAGTGGAGAGGATGCCGAGGATGGCACAG	6832	AQVERMPRMAQ	11421	VERMPRM	0.343043	-0.03534
SyS699	2244	GCCCAACCCCAAATCGGCATCCCCGACGCACAG	6833	AQPQIGIPDAQ	11422	PQIGIPD	0.342946	-0.05619
GS359	2245	GCCCAAGCTACGGTGAAGTCGAGTACTGCACAG	6834	AQATVKSSTAQ	11423	ATVKSST	0.342874	0.027178
SyS700	2246	GCCCAAGGCGGCAACGTCCAAGCCATCGCACAG	6835	AQGGNVQAIAQ	11424	GGNVQAI	0.342847	-0.0119
SyS701	2247	GCCCAAACTATTGTTAATGTTACTAGTGCACAG	6836	AQTIVNVTSAQ	11425	TIVNVTS	0.342809	-0.19739
SyS702	2248	GCCCAAGGCGACCCCGCCCAAAGCAGCGCACAG	6837	AQGDPAQSSAQ	11426	GDPAQSS	0.342651	-0.10889
SyS703	2249	GCCCAAACTAAGAATACTGATTTTCAGGCACAG	6838	AQTKNTDFQAQ	11427	TKNTDFQ	0.34251	-0.02105

FIG. 33 (Continued)

GS361	2250	GCCCAAAGACACACCGACGCCGTCATCGCACAG	6839	AQRHTDAVIAQ	11428	RHTDAVI	0.342481	-0.12298
SyS704	2251	GCCCAAAGCGTCCACACCGCCGTCAGAGCACAG	6840	AQSVHTAVRAQ	11429	SVHTAVR	0.342291	-0.02887
SyS705	2252	GCCCAAATCACCAGCCTCATGAGCGGCGCACAG	6841	AQITSLMSGAQ	11430	ITSLMSG	0.342264	-0.11737
SyS706	2253	GCCCAAGACCACAACCAAATCAGCCTCGCACAG	6842	AQDHNQISLAQ	11431	DHNQISL	0.341991	-0.16587
GS362	2254	GCCCAACAAGGCCAAAGCGCCCTCAAAGCACAG	6843	AQQGQSALKAQ	11432	QGQSALK	0.341744	0.009075
TS146	2255	GCCCAAAACAACGCCACCAGATACACCGCACAG	6844	AQNNATRYTAQ	11433	NNATRYT	0.34159	0.011557
SyS707	2256	GCCCAATCGCGTAATACGACTTCGTGGGCACAG	6845	AQSRNTTSWAQ	11434	SRNTTSW	0.341535	-0.21436
GS364	2257	GCCCAACCTAGTAATTCGAAGCTGATTGCACAG	6846	AQPSNSKLIAQ	11435	PSNSKLI	0.341264	-0.05716
SyS709	2258	GCCCAAAAAACCGTCAGCCTCAACGACGCACAG	6847	AQKTVSLNDAQ	11436	KTVSLND	0.341072	0.177223
SyS710	2259	GCCCAAACCCCCCTCCCCAGAGTCAGCGCACAG	6848	AQTPLPRVSAQ	11437	TPLPRVS	0.340871	-0.18284
GS365	2260	GCCCAACAGACTATTGCGAGTGCTTTGGCACAG	6849	AQQTIASALAQ	11438	QTIASAL	0.340714	-0.14779
GS366	2261	GCCCAACCTATTATGAAGACGACGGTTGCACAG	6850	AQPIMKTTVAQ	11439	PIMKTTV	0.340641	-0.111
SyS711	2262	GCCCAAAGTGCGGTTATTCAGGGGCATGCACAG	6851	AQSAVIQGHAQ	11440	SAVIQGH	0.340621	-0.08096
SyS712	2263	GCCCAACCGCTGTATGGTACGATGTCTCACAG	6852	AQPLYGTMSAQ	11441	PLYGTMS	0.34044	-0.21325
TS147	2264	GCCCAAGCGAATCGGACTAAGGATTATGCACAG	6853	AQANRTKDYAQ	11442	ANRTKDY	0.34043	0.212101
SyS713	2265	GCCCAAGTTATTCCGCAGACGGAGAGGGCACAG	6854	AQVIPQTERAQ	11443	VIPQTER	0.34041	-0.15132
SS53	2266	GCCCAAATCGTCAACGGCCACATCAGAGCACAG	6855	AQIVNGHIRAQ	11444	IVNGHIR	0.340404	-0.39357
SyS714	2267	GCCCAAAGCAGACCCAACGAAACCACCGCACAG	6856	AQSRPNETTAQ	11445	SRPNETT	0.340281	0.437826
SyS716	2268	GCCCAAGGGTATACTCCGGTTTCGAGGGCACAG	6857	AQGYTPVSRAQ	11446	GYTPVSR	0.34003	-0.22803
SyS717	2269	GCCCAACCTCTGCAGAGGACTATTGGGGCACAG	6858	AQPLQRTIGAQ	11447	PLQRTIG	0.340023	-0.17557
GS367	2270	GCCCAAAGCACCGGCAGCCCCACCATCGCACAG	6859	AQSTGSPTIAQ	11448	STGSPTI	0.339967	-0.092
SyS718	2271	GCCCAAAGTACTATGACGGGGCTGATTGCACAG	6860	AQSTMTGLIAQ	11449	STMTGLI	0.339737	-0.05431
GS368	2272	GCCCAAATCCACGCCGTCGGCGCCGAAGCACAG	6861	AQIHAVGAEAQ	11450	IHAVGAE	0.33972	-0.18099
SyS719	2273	GCCCAAACCGCCCAACGTCAGCGAACTCGCACAG	6862	AQTANVSELAQ	11451	TANVSEL	0.33963	-0.05039
SyS720	2274	GCCCAAAACAAAAGCGACATGCCCCCACGCACAG	6863	AQNKSDMPHAQ	11452	NKSDMPH	0.339521	0.149221
SyS721	2275	GCCCAAAGCAACTACAACACCCACGACGCACAG	6864	AQSNYNTHDAQ	11453	SNYNTHD	0.339506	0.012789
SyS722	2276	GCCCAACCGAGTGTTACTCATCATCCGGCACAG	6865	AQPSVTHHPAQ	11454	PSVTHHP	0.339089	0.133746
GS369	2277	GCCCAAAATTTGAGTCTTAAGCCGCTGGCACAG	6866	AQNLSLKPLAQ	11455	NLSLKPL	0.338682	-0.1774
TS148	2278	GCCCAACTTTATTCGAATAAGAGTAATGCACAG	6867	AQLYSNKSNAQ	11456	LYSNKSN	0.338445	-0.09092
SyS725	2279	GCCCAAGATAATGGTCTGGTTCATAGGGCACAG	6868	AQDNGLVHRAQ	11457	DNGLVHR	0.337855	-0.05918
SyS726	2280	GCCCAAATGGGCACCCTCACCATCAGCGCACAG	6869	AQMGTLTISAQ	11458	MGTLTIS	0.337855	-0.20103
GS370	2281	GCCCAAACTTTTCAGTCTGATGAGAGGGCACAG	6870	AQTFQSDERAQ	11459	TFQSDER	0.337719	-0.16573

FIG. 33 (Continued)

GS371	2282	GCCCAAATCGTCACCGGCGCCTACAGAGCACAG	6871	AQIVTGAYRAQ	11460	IVTGAYR	0.337298	-0.16814
SyS727	2283	GCCCAAACCGTCGTCAACCCCAGCAGCGCACAG	6872	AQTVVNPSSAQ	11461	TVVNPSS	0.337204	0.129144
GP105	2284	GCCCAAGATAATAATGTTAGGCATACGGCACAG	6873	AQDNNVRHTAQ	11462	DNNVRHT	0.33706	0.231989
GS373	2285	GCCCAAGATCGTTCGCAGAATTCGTTGGCACAG	6874	AQDRSQNSLAQ	11463	DRSQNSL	0.337028	0.002952
SyS728	2286	GCCCAACATCCTCCTGTGCCGGCGTCTGCACAG	6875	AQHPPVPASAQ	11464	HPPVPAS	0.336942	0.072962
SyS729	2287	GCCCAAAAATACATCACCCCCAGCAGCGCACAG	6876	AQKYITPSSAQ	11465	KYITPSS	0.336738	-0.12344
GS374	2288	GCCCAAGTGCCGGATAAGCAGGCGATGGCACAG	6877	AQVPDKQAMAQ	11466	VPDKQAM	0.336567	-0.02576
SyS730	2289	GCCCAAGTTATTGCGAAGACTGAGTATGCACAG	6878	AQVIAKTEYAQ	11467	VIAKTEY	0.33656	-0.04584
SyS731	2290	GCCCAAGGGGGGCAGGCGGAGGCGCGGGCACAG	6879	AQGGQAEARAQ	11468	GGQAEAR	0.336557	-0.04446
SyS732	2291	GCCCAACAACCCGTCCTCAACCAACCCGCACAG	6880	AQQPVLNQPAQ	11469	QPVLNQP	0.336549	0.089177
GS375	2292	GCCCAAAATAATACTAATGAGAATCTTGCACAG	6881	AQNNTNENLAQ	11470	NNTNENL	0.336205	-0.15048
SyS733	2293	GCCCAAACTAATCTGTCTCTGTCGTCGGCACAG	6882	AQTNLSLSSAQ	11471	TNLSLSS	0.336067	0.24816
SyS734	2294	GCCCAAGGTCAGTCGAGTGATGAGCGGGCACAG	6883	AQGQSSDERAQ	11472	GQSSDER	0.336014	0.211316
GS376	2295	GCCCAAACCCACGCCACCACCTTCGCCGCACAG	6884	AQTHATTFAAQ	11473	THATTFA	0.335849	-0.02171
SyS736	2296	GCCCAAACCAGCCAACAAGACAGAAGCGCACAG	6885	AQTSQQDRSAQ	11474	TSQQDRS	0.335683	-0.02651
GS377	2297	GCCCAAGCGTTGTTGCATCGTGAGGCGGCACAG	6886	AQALLHREAAQ	11475	ALLHREA	0.335641	-0.13881
SyS737	2298	GCCCAAAATCCGAGTGTTACTGCTCTTGCACAG	6887	AQNPSVTALAQ	11476	NPSVTAL	0.335537	-0.07068
GS378	2299	GCCCAAGTCGCCAACCTCAACAGCAGAGCACAG	6888	AQVANLNSRAQ	11477	VANLNSR	0.335302	-0.03973
SyS739	2300	GCCCAAACCATGCTCCTCGAACCCAAAGCACAG	6889	AQTMLLEPKAQ	11478	TMLLEPK	0.335297	-0.20955
SyS740	2301	GCCCAAAATGTTAGGCCTTCGACTTATGCACAG	6890	AQNVRPSTYAQ	11479	NVRPSTY	0.335144	-0.11737
GS379	2302	GCCCAAGTGATTCATATTACGAATACGGCACAG	6891	AQVIHITNTAQ	11480	VIHITNT	0.334532	-0.12797
SyS741	2303	GCCCAAAGCAACCCCAGCCTCCTCACCGCACAG	6892	AQSNPSLLTAQ	11481	SNPSLLT	0.334488	-0.16466
SyS742	2304	GCCCAATATCAGGATAATGCTAGGCTTGCACAG	6893	AQYQDNARLAQ	11482	YQDNARL	0.33435	-0.22434
SyS743	2305	GCCCAAATCCAAGGCCTCACCAGCCACGCACAG	6894	AQIQGLTSHAQ	11483	IQGLTSH	0.334337	0.418222
GP106	2306	GCCCAAACTTATAATCAGGGTAAGCAGGCACAG	6895	AQTYNQGKQAQ	11484	TYNQGKQ	0.334287	-0.07398
GS380	2307	GCCCAAGCTCCTACGGGGATGAAGCATGCACAG	6896	AQAPTGMKHAQ	11485	APTGMKH	0.334244	-0.16753
SyS745	2308	GCCCAAATGAGTGGTGAGCTTATTCGTGCACAG	6897	AQMSGELIRAQ	11486	MSGELIR	0.333966	-0.05676
GS381	2309	GCCCAAAGACTCAACACCAGCCACCTCGCACAG	6898	AQRLNTSHLAQ	11487	RLNTSHL	0.33391	0.026856
SyS746	2310	GCCCAAGCGACGGCTCTGGCGGCGGGTGCACAG	6899	AQATALAAGAQ	11488	ATALAAG	0.333841	-0.19618
SyS747	2311	GCCCAACCTATTTCGGGGCTTAAGTCGGCACAG	6900	AQPISGLKSAQ	11489	PISGLKS	0.333712	-0.18245
SyS748	2312	GCCCAAGAGCGTACTTTTAATCCGGCTGCACAG	6901	AQERTFNPAAQ	11490	ERTFNPA	0.333392	-0.01544
SyS749	2313	GCCCAAATGAGTAATATTTCTAGTGTGGCACAG	6902	AQMSNISSVAQ	11491	MSNISSV	0.333354	0.062249

FIG. 33 (Continued)

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GS382	2314	GCCCAAAGAGACGCCAGACTCAGCCCCGCACAG	6903	AQRDARLSPAQ	11492	RDARLSP	0.332845	-0.01943
SyS750	2315	GCCCAAGACCACTACGTCAACACCAGAGCACAG	6904	AQDHYVNTRAQ	11493	DHYVNTR	0.332785	-0.19723
SyS752	2316	GCCCAACCTGGGACTGCTGTTCGTCTGGCACAG	6905	AQPGTAVRLAQ	11494	PGTAVRL	0.332711	-0.18163
SyS753	2317	GCCCAAGACAAAGGCACCCTCAGCGAAGCACAG	6906	AQDKGTLSEAQ	11495	DKGTLSE	0.332541	-0.08949
GS383	2318	GCCCAATCGATTCCTAGGACGGATAATGCACAG	6907	AQSIPRTDNAQ	11496	SIPRTDN	0.332462	-0.00974
SyS754	2319	GCCCAAGAGCCGGTTCTTCATACTGTTGCACAG	6908	AQEPVLHTVAQ	11497	EPVLHTV	0.332214	-0.19739
GS385	2320	GCCCAAGACAGAGCCATCCTCAACAGCGCACAG	6909	AQDRAILNSAQ	11498	DRAILNS	0.332175	-0.04121
SyS755	2321	GCCCAAGAAATCGGCAGCCTCAGACAAGCACAG	6910	AQEIGSLRQAQ	11499	EIGSLRQ	0.332133	-0.16273
SyS756	2322	GCCCAAGCCTTCGTCGGCGCCACCCCCGCACAG	6911	AQAFVGATPAQ	11500	AFVGATP	0.332091	-0.0026
GS386	2323	GCCCAATTCGTCCAAACAAAGACGCCGCACAG	6912	AQFVQNKDAAQ	11501	FVQNKDA	0.332078	-0.07421
SyS758	2324	GCCCAAAGGGATAAGGCGGGGCCTACGGCACAG	6913	AQRDKAGPTAQ	11502	RDKAGPT	0.331877	0.088605
GS387	2325	GCCCAACTCCTCCCCACCGCCCACAACGCACAG	6914	AQLLPTAHNAQ	11503	LLPTAHN	0.331739	0.074733
SyS759	2326	GCCCAACCCAACGGCATCACCAGCACCGCACAG	6915	AQPNGITSTAQ	11504	PNGITST	0.330938	-0.07827
GP108	2327	GCCCAATCGGGTGTGACGAAGGGTAGTGCACAG	6916	AQSGVTKGSAQ	11505	SGVTKGS	0.330938	-0.07433
SyS760	2328	GCCCAAATGAACAGCACCATCAGCCACGCACAG	6917	AQMNSTISHAQ	11506	MNSTISH	0.330866	0.28997
GS389	2329	GCCCAATACAAAAGCGACGTCGGCAGCGCACAG	6918	AQYKSDVGSAQ	11507	YKSDVGS	0.330858	-0.10092
GS390	2330	GCCCAACCGGTGACGCGTGTTAATCTTGCACAG	6919	AQPVTRVNLAQ	11508	PVTRVNL	0.330856	-0.18099
SyS761	2331	GCCCAAAGAAACGTCGCCGACGGCCTCGCACAG	6920	AQRNVADGLAQ	11509	RNVADGL	0.330693	0.111344
GS391	2332	GCCCAAGCTTCGGCTACTTCGATTACTGCACAG	6921	AQASATSITAQ	11510	ASATSIT	0.330598	-0.15766
SyS762	2333	GCCCAAAGCGGCACCGCCAGCAACGTCGCACAG	6922	AQSGTASNVAQ	11511	SGTASNV	0.330558	-0.00713
SyS763	2334	GCCCAACGGCAGGATCTTGGTAGTACTGCACAG	6923	AQRQDLGSTAQ	11512	RQDLGST	0.330378	0.022044
SyS764	2335	GCCCAAGACAGCGCCCTCATCAGCAAAGCACAG	6924	AQDSALISKAQ	11513	DSALISK	0.330309	-0.10674
SyS765	2336	GCCCAAAACAACGGCCTCAACAGCGCCGCACAG	6925	AQNNGLNSAAQ	11514	NNGLNSA	0.329752	0.087826
SyS766	2337	GCCCAAGCTGCGAGTGAGCGTCGGATGGCACAG	6926	AQAASERRMAQ	11515	AASERRM	0.32966	-0.15374
GS393	2338	GCCCAACGTCATTCTGCTGTGCCTGAGGCACAG	6927	AQRHSAVPEAQ	11516	RHSAVPE	0.329584	-0.11663
GS394	2339	GCCCAATATCAGGATACGAAGGGGCAGGCACAG	6928	AQYQDTKGQAQ	11517	YQDTKGQ	0.329332	-0.01392
SyS767	2340	GCCCAAAAGACTGGGTCGCTGCCTGTGGCACAG	6929	AQKTGSLPVAQ	11518	KTGSLPV	0.329312	-0.0962
SyS768	2341	GCCCAAATTGCGCGGAGTGTGTCTATGGCACAG	6930	AQIARSVSMAQ	11519	IARSVSM	0.32924	0.053318
SyS769	2342	GCCCAACCCAGCAGCAAACTCCCCCTCGCACAG	6931	AQPSSKLPLAQ	11520	PSSKLPL	0.329108	-0.01365
SyS770	2343	GCCCAAATCAACGACCAAAGAATCAGCGCACAG	6932	AQINDQRISAQ	11521	INDQRIS	0.328822	-0.05944
GS396	2344	GCCCAAGGTATTTCTGAGAAGACTTCTGCACAG	6933	AQGISEKTSAQ	11522	GISEKTS	0.328727	-0.03473
GS397	2345	GCCCAAACTAGTGCTTATACTTCGGTGGCACAG	6934	AQTSAYTSVAQ	11523	TSAYTSV	0.328529	-0.09069

FIG. 33 (Continued)

SyS771	2346	GCCCAAGGCACCCTCCACAGCAGCGCCGCACAG	6935	AQGTLHSSAAQ	11524	GTLHSSA	0.328517	0.041441
SyS772	2347	GCCCAAGCCCCCAGAGACGCCGCCAGCGCACAG	6936	AQAPRDAASAQ	11525	APRDAAS	0.328496	-0.12465
GS398	2348	GCCCAAAATAATACTGCTATGAGTCTTGCACAG	6937	AQNNTAMSLAQ	11526	NNTAMSL	0.328406	-0.11076
SyS774	2349	GCCCAAATCCTCAGAGTCGCCGACGCCGCACAG	6938	AQILRVADAAQ	11527	ILRVADA	0.328209	0.007753
SyS775	2350	GCCCAAGCCAGCGTCGCCGGCGCCAGCGCACAG	6939	AQASVAGASAQ	11528	ASVAGAS	0.328202	-0.18527
SyS776	2351	GCCCAAAGCGTCCTCAACGGCAGCAAAGCACAG	6940	AQSVLNGSKAQ	11529	SVLNGSK	0.328132	0.135186
SyS777	2352	GCCCAAATTTATCAGACGGCTTCTGCGGCACAG	6941	AQIYQTASAAQ	11530	IYQTASA	0.328046	0.09508
SyS778	2353	GCCCAAACCAGCGAAAGAACCCAATTCGCACAG	6942	AQTSERTQFAQ	11531	TSERTQF	0.327984	0.021394
SyS780	2354	GCCCAAAGCACCGTCGCCCTCACCAGCGCACAG	6943	AQSTVALTSAQ	11532	STVALTS	0.327951	0.008571
SyP45	2355	GCCCAAGGGAATACGGTGATTAATGCGGCACAG	6944	AQGNTVINAAQ	11533	GNTVINA	0.32791	-0.03915
SyS781	2356	GCCCAACCCCTCGGCAGCATCGTCACCGCACAG	6945	AQPLGSIVTAQ	11534	PLGSIVT	0.327886	-0.17799
GS399	2357	GCCCAACTCAGAATGAGCGACAGCTTCGCACAG	6946	AQLRMSDSFAQ	11535	LRMSDSF	0.327847	-0.16304
GS400	2358	GCCCAAACCAGCGCAAAGCGGCACCCTCGCACAG	6947	AQTSESGTLAQ	11536	TSESGTL	0.327847	-0.16304
SyS782	2359	GCCCAAGAGGCGACGCGGCCTGTTCGGGCACAG	6948	AQEATRPVRAQ	11537	EATRPVR	0.327835	-0.14041
SyS783	2360	GCCCAAAATAAGCAGTTTTTGGCTGATGCACAG	6949	AQNKQFLADAQ	11538	NKQFLAD	0.327749	-0.0825
SyS784	2361	GCCCAACTCACCATCAGAGACAACGTCGCACAG	6950	AQLTIRDNVAQ	11539	LTIRDNV	0.327594	-0.05797
SyS785	2362	GCCCAAGTTGGGTCTGGGCTTGCTAAGGCACAG	6951	AQVGSGLAKAQ	11540	VGSGLAK	0.327594	-0.13314
GS401	2363	GCCCAACAAAACGCCACCAACCTCATGGCACAG	6952	AQQNATNLMAQ	11541	QNATNLM	0.327526	-0.04297
GS402	2364	GCCCAATCTATGTATGCTGGGCATGAGGCACAG	6953	AQSMYAGHEAQ	11542	SMYAGHE	0.327425	-0.18637
SyS786	2365	GCCCAAATGGTCAACAGCGAAAAAGCCGCACAG	6954	AQMVNSEKAAQ	11543	MVNSEKA	0.327321	0.005673
GP109	2366	GCCCAACGTATGAGTATGCGGTCTGATGCACAG	6955	AQRMSMRSDAQ	11544	RMSMRSD	0.327321	-0.07169
SyS787	2367	GCCCAAAGCAGCAGCGGCCTCAACAAAGCACAG	6956	AQSSSGLNKAQ	11545	SSSGLNK	0.327268	0.120372
SyS788	2368	GCCCAACAAAGCAGCGTCCTCACCCCCGCACAG	6957	AQQSSVLTPAQ	11546	QSSVLTP	0.327119	0.083873
SyS790	2369	GCCCAAACTCCTAATTTGGAGACTAGTGCACAG	6958	AQTPNLETSAQ	11547	TPNLETS	0.326877	-0.12871
GS406	2370	GCCCAAATGCGTGGTACTCTTTCGATGGCACAG	6959	AQMRGTLSMAQ	11548	MRGTLSM	0.326812	-0.15383
SyS791	2371	GCCCAAGATCATGGTGCTAGTCTTCCTGCACAG	6960	AQDHGASLPAQ	11549	DHGASLP	0.326678	-0.18648
SyS792	2372	GCCCAATCTCATTTGGCGACGCCGAAGGCACAG	6961	AQSHLATPKAQ	11550	SHLATPK	0.326626	-0.14162
SyS793	2373	GCCCAATCTGATGCGTCGCATCGGCAGGCACAG	6962	AQSDASHRQAQ	11551	SDASHRQ	0.326591	-0.09677
SyS794	2374	GCCCAAACCGGCACCGAAAGACTCAGCGCACAG	6963	AQTGTERLSAQ	11552	TGTERLS	0.326591	-0.09677
SyS795	2375	GCCCAAGCCGTCGGCCACGTCGGCCCCGCACAG	6964	AQAVGHVGPAQ	11553	AVGHVGP	0.326533	-0.06025
SyS796	2376	GCCCAACAAAGCCAACAAGGCGTCAAAGCACAG	6965	AQQSQQGVKAQ	11554	QSQQGVK	0.326127	0.155451
SyS798	2377	GCCCAAAATCTTACGATTAGTAATCGGGCACAG	6966	AQNLTISNRAQ	11555	NLTISNR	0.325983	-0.18861

FIG. 33 (Continued)

SyS799	2378	GCCCAAGTCAGCAGCGGCTACGAAACCGCACAG	6967	AQVSSGYETAQ	11556	VSSGYET	0.325948	-0.01693
SyS800	2379	GCCCAATCGATTTCTCCTCCTCGTACGGCACAG	6968	AQSISPPRTAQ	11557	SISPPRT	0.325816	-0.0841
SyS801	2380	GCCCAACCCTACAACCAAAGCCCCAGCGCACAG	6969	AQPYNQSPSAQ	11558	PYNQSPS	0.325728	-0.10729
GS411	2381	GCCCAAACGATGTCGTATAATACTAATGCACAG	6970	AQTMSYNTNAQ	11559	TMSYNTN	0.325719	-0.16035
GS412	2382	GCCCAAGGCGCCTACAACACCGTCAGCGCACAG	6971	AQGAYNTVSAQ	11560	GAYNTVS	0.32537	-0.10423
GS413	2383	GCCCAATCGAAGGTTACGCCTCCTCTGGCACAG	6972	AQSKVTPPLAQ	11561	SKVTPPL	0.325307	-0.111
SyS803	2384	GCCCAAAGATTCAGAGAAAACGACCACGCACAG	6973	AQRFRENDHAQ	11562	RFRENDH	0.325231	0.023208
SyS804	2385	GCCCAATTGGATACTGGGCAGCCGACGGCACAG	6974	AQLDTGQPTAQ	11563	LDTGQPT	0.325094	-0.12829
GS414	2386	GCCCAACTTCCGTCGACTCCGCAGAATGCACAG	6975	AQLPSTPQNAQ	11564	LPSTPQN	0.325044	-0.06588
SyS805	2387	GCCCAAACCCTCAGCTACGTCACCAGCGCACAG	6976	AQTLSYVTSAQ	11565	TLSYVTS	0.324951	-0.18042
SyS806	2388	GCCCAAAGCACCACCGTCCTCCCCGTCGCACAG	6977	AQSTTVLPVAQ	11566	STTVLPV	0.324892	-0.0659
SyS807	2389	GCCCAAATGACGCATACGCTTTTGAGTGCACAG	6978	AQMTHTLLSAQ	11567	MTHTLLS	0.324713	-0.08142
GS415	2390	GCCCAAAGCACCTACAACAAAACCTTCGCACAG	6979	AQSTYNKTFAQ	11568	STYNKTF	0.324696	-0.13571
GS416	2391	GCCCAAGCGACGTCGAGTCATACGCTGGCACAG	6980	AQATSSHTLAQ	11569	ATSSHTL	0.324696	-0.13571
SyS808	2392	GCCCAAAGACTCAACGGCACCGAACCCGCACAG	6981	AQRLNGTEPAQ	11570	RLNGTEP	0.32462	0.318751
SS55	2393	GCCCAACAAGCCAACACCCCCACCAAAGCACAG	6982	AQQANTPTKAQ	11571	QANTPTK	0.324608	-0.31402
SyS809	2394	GCCCAAAGCGCCGTCATCAACAGCAGCGCACAG	6983	AQSAVINSSAQ	11572	SAVINSS	0.324458	0.174798
SyS810	2395	GCCCAAAACCACGGCAACGAAGTCAAAGCACAG	6984	AQNHGNEVKAQ	11573	NHGNEVK	0.324286	0.277768
GS417	2396	GCCCAAAAGCATCTGTCGCATGATCCGGCACAG	6985	AQKHLSHDPAQ	11574	KHLSHDP	0.324246	-0.0337
GP110	2397	GCCCAATTGGGGTCGGGTAGGATGGCTGCACAG	6986	AQLGSGRMAAQ	11575	LGSGRMA	0.324054	0.229744
GS418	2398	GCCCAAAGCAACCAAATCACCATCGTCGCACAG	6987	AQSNQITIVAQ	11576	SNQITIV	0.324029	-0.0065
SyS811	2399	GCCCAAGGTGGTAGGGGTGTGGGTATGGCACAG	6988	AQGGRGVGMAQ	11577	GGRGVGM	0.323942	-0.12991
SyS812	2400	GCCCAATTCGTCACCGAAAGCAAAAGCGCACAG	6989	AQFVTESKSAQ	11578	FVTESKS	0.323852	-0.0172
SyS813	2401	GCCCAAAACAGCGTCCACAACGACCTCGCACAG	6990	AQNSVHNDLAQ	11579	NSVHNDL	0.323841	-0.12222
SyS814	2402	GCCCAAAGCCCCCAACAAAGCAGATACGCACAG	6991	AQSPQQSRYAQ	11580	SPQQSRY	0.323644	-0.10768
SyS815	2403	GCCCAAACTCAGCCTAATCATGATTCTGCACAG	6992	AQTQPNHDSAQ	11581	TQPNHDS	0.323393	-0.13686
SyS816	2404	GCCCAAACGAGGCTGAATGAGGTGACTGCACAG	6993	AQTRLNEVTAQ	11582	TRLNEVT	0.323308	0.334916
GP111	2405	GCCCAAACGGCGCAGCGTACTAATGTTGCACAG	6994	AQTAQRTNVAQ	11583	TAQRTNV	0.323198	-0.07405
GS419	2406	GCCCAACCCGGCAGAAGCCCCACCACCGCACAG	6995	AQPGRSPTTAQ	11584	PGRSPTT	0.322786	0.116763
SyS817	2407	GCCCAAGCCTACAGCGTCGTCAGAGGCGCACAG	6996	AQAYSVVRGAQ	11585	AYSVVRG	0.322605	-0.20462
SyS819	2408	GCCCAAGTTGGTCCGGTGCTTTCTAGGGCACAG	6997	AQVGPVLSRAQ	11586	VGPVLSR	0.322462	-0.09823
GS420	2409	GCCCAAACCAAAATGGGCACCCCCAACGCACAG	6998	AQTKMGTPNAQ	11587	TKMGTPN	0.322339	-0.18099

FIG. 33 (Continued)

SyS820	2410	GCCCAAACCACACCCCAACCTCAACCCCGCACAG	6999	AQTTPNLNPAQ	11588	TTPNLNP	0.322176	0.074234
SyS821	2411	GCCCAAACCAGCGGCACCGACGGCATCGCACAG	7000	AQTSGTDGIAQ	11589	TSGTDGI	0.321888	0.01477
SyS822	2412	GCCCAACCGATGCCTAATATGCCGTCGGCACAG	7001	AQPMPNMPSAQ	11590	PMPNMPS	0.321861	0.022044
SyS823	2413	GCCCAAGCCGACGCCCTCAGCAACAGAGGCACAG	7002	AQADALSNRAQ	11591	ADALSNR	0.321783	0.322733
SyS824	2414	GCCCAACTCCAAACCAGCAGCCACACCGCACAG	7003	AQLQTSSHTAQ	11592	LQTSSHT	0.321651	0.18026
SyS825	2415	GCCCAAACCAGCATGCAAGGCGTCTACGCACAG	7004	AQTSMQGVYAQ	11593	TSMQGVY	0.321563	-0.10563
SyS826	2416	GCCCAACAGACTACTGTTTTGAATAAGGCACAG	7005	AQQTTVLNKAQ	11594	QTTVLNK	0.321543	-0.16225
SyS827	2417	GCCCAAATCATCCCCGTCAACAGCACCGCACAG	7006	AQIIPVNSTAQ	11595	IIPVNST	0.321508	0.144707
GS422	2418	GCCCAAATTGCTACTGTTACTTCTAGTGCACAG	7007	AQIATVTSSAQ	11596	IATVTSS	0.321299	-0.05443
GS423	2419	GCCCAATTGGAGACGCCGGGTCGTATGGCACAG	7008	AQLETPGRMAQ	11597	LETPGRM	0.320829	-0.09575
GS424	2420	GCCCAAATCGCCACCAGCGTCGGCAGCGCACAG	7009	AQIATSVGSAQ	11598	IATSVGS	0.320659	-0.18547
SyS829	2421	GCCCAAGTCAGAGAACACGAAGCCCTCGCACAG	7010	AQVREHEALAQ	11599	VREHEAL	0.320474	-0.00948
SyS830	2422	GCCCAACCCCTCACCAACGTCCAAGGCGCACAG	7011	AQPLTNVQGAQ	11600	PLTNVQG	0.320474	-0.0313
SyS831	2423	GCCCAACGTGATATGGTGCAGACTATGGCACAG	7012	AQRDMVQTMAQ	11601	RDMVQTM	0.320474	-0.04585
SyS832	2424	GCCCAAAGACTCGGCTTCGCCACCAACGCACAG	7013	AQRLGFATNAQ	11602	RLGFATN	0.320474	-0.11859
SyS833	2425	GCCCAAATGTCTCAGGTGACGACTGAGGCACAG	7014	AQMSQVTTEAQ	11603	MSQVTTE	0.320474	-0.13314
SyS834	2426	GCCCAAAGTGTGCTTCCGAATGCTATTGCACAG	7015	AQSVLPNAIAQ	11604	SVLPNAI	0.320474	-0.16223
GS425	2427	GCCCAAAAATTCAGCCCCACCCTCGCCGCACAG	7016	AQKFSPTLAAQ	11605	KFSPTLA	0.320006	-0.04848
SyS835	2428	GCCCAAAACATCGGCAACATGGTCCTCGCACAG	7017	AQNIGNMVLAQ	11606	NIGNMVL	0.319937	-0.23296
SyP46	2429	GCCCAAAGTCTTCTTACTGTTTTGAGTGCACAG	7018	AQSLLTVLSAQ	11607	SLLTVLS	0.319922	-0.044
SyS836	2430	GCCCAAAACAGCAACCCCAGCATGCTCGCACAG	7019	AQNSNPSMLAQ	11608	NSNPSML	0.319815	0.040229
GS427	2431	GCCCAAATTACTGCGGCTGTGCGTGATGCACAG	7020	AQITAAVRDAQ	11609	ITAAVRD	0.319761	-0.17672
SyS837	2432	GCCCAAGCCTACACCAGCAACGACAGAGGCACAG	7021	AQAYTSNDRAQ	11610	AYTSNDR	0.319729	0.012799
SyS838	2433	GCCCAAAACAGCGTCGGCAGCATGAAAGCACAG	7022	AQNSVGSMKAQ	11611	NSVGSMK	0.319621	0.189219
SyS839	2434	GCCCAAAGACTCGACACCACCTGGGTCGCACAG	7023	AQRLDTTWVAQ	11612	RLDTTWV	0.319493	-0.0907
SyS840	2435	GCCCAAATTGCTGAGGCGGGGGGTCGTGCACAG	7024	AQIAEAGGRAQ	11613	IAEAGGR	0.319466	-0.09798
SyS841	2436	GCCCAAAGCAAAACCAACCTCCAACTCGCACAG	7025	AQSKTNLQLAQ	11614	SKTNLQL	0.319422	0.140853
SyS842	2437	GCCCAATTTTCGAAGGATGATGCTGTTGCACAG	7026	AQFSKDDAVAQ	11615	FSKDDAV	0.31934	-0.12707
SyS843	2438	GCCCAACTCACCAGCCACAGCCTCACCGCACAG	7027	AQLTSHSLTAQ	11616	LTSHSLT	0.319284	0.082661
GS428	2439	GCCCAACACGTCCAACTCCAATACCCCGCACAG	7028	AQHVQLQYPAQ	11617	HVQLQYP	0.319263	-0.16753
SyS844	2440	GCCCAAAACCACACCAACCCAGCGCCGCACAG	7029	AQNHNQPSAAQ	11618	NHNQPSA	0.319177	-0.15617
SyS845	2441	GCCCAAACTGAGGGTGCGCGGAGTTTGGCACAG	7030	AQTEGARSLAQ	11619	TEGARSL	0.319062	-0.05481

FIG. 33 (Continued)

SyS846	2442	GCCCAAAACCAAAGCGACAGCAAAGTCGCACAG	7031	AQNQSDSKVAQ	11620	NQSDSKV	0.319021	0.002646
SyS847	2443	GCCCAAGTGAGTCTTCCGCTGGCTCCGGCACAG	7032	AQVSLPLAPAQ	11621	VSLPLAP	0.319021	-0.17799
GS429	2444	GCCCAAAACAACACCAACCTCAGCAGAGCACAG	7033	AQNNTNLSRAQ	11622	NNTNLSR	0.318597	0.099602
GP113	2445	GCCCAATATTCGAATAGTAATAATCATGCACAG	7034	AQYSNSNNHAQ	11623	YSNSNNH	0.31847	-0.07259
SyS848	2446	GCCCAAGGCCTCGAAACCAGACTCCACGCACAG	7035	AQGLETRLHAQ	11624	GLETRLH	0.318311	-0.01832
SyS849	2447	GCCCAACTGACTACTACTGAGTCTAAGGCACAG	7036	AQLTTTESKAQ	11625	LTTTESK	0.318126	-0.13556
SyS850	2448	GCCCAAATGGGCGCCAGAATGCCCCTCGCACAG	7037	AQMGARMPLAQ	11626	MGARMPL	0.317628	0.100846
SyS851	2449	GCCCAAAGTCATGATCATATGCTTATTGCACAG	7038	AQSHDHMLIAQ	11627	SHDHMLI	0.317559	-0.1792
SyS852	2450	GCCCAACGTACTGAGGGTTCGGATAATGCACAG	7039	AQRTEGSDNAQ	11628	RTEGSDN	0.317519	-0.08748
SyS853	2451	GCCCAAAATTTTCAGCGTGATGGGCCGGCACAG	7040	AQNFQRDGPAQ	11629	NFQRDGP	0.317429	-0.00904
SyS854	2452	GCCCAACTTTCGAATATTAATCCGCATGCACAG	7041	AQLSNINPHAQ	11630	LSNINPH	0.317372	-0.0216
SyS855	2453	GCCCAAAGCAGCAACCACACCAGCAGAGCACAG	7042	AQSSNHTSRAQ	11631	SSNHTSR	0.317335	0.288709
SyS856	2454	GCCCAAATGCACGTCAACGCCAGCCCCCGCACAG	7043	AQMHVNASPAQ	11632	MHVNASP	0.317257	0.128729
SyS857	2455	GCCCAATGGGATTCGTTGGCTGCGCCGGCACAG	7044	AQWDSLAAPAQ	11633	WDSLAAP	0.317054	-0.1295
SyS858	2456	GCCCAACTGGATGGTGCGCATAATGCGGCACAG	7045	AQLDGAHNAAQ	11634	LDGAHNA	0.316943	-0.13677
GS436	2457	GCCCAATCGATTAGGAGTCCGCCTCCTGCACAG	7046	AQSIRSPPPAQ	11635	SIRSPPP	0.31688	-0.15407
GS437	2458	GCCCAAAATGGGACGCTGAAGGGGTTGGCACAG	7047	AQNGTLKGLAQ	11636	NGTLKGL	0.316732	-0.08754
SyS859	2459	GCCCAATTTTATCAGGAGCAGTCTTTGGCACAG	7048	AQFYQEQSLAQ	11637	FYQEQSL	0.316697	-0.15132
SyS860	2460	GCCCAATACGACCAAAAAAGCCTCGCCGCACAG	7049	AQYDQKSLAAQ	11638	YDQKSLA	0.316591	-0.02956
GP114	2461	GCCCAACTGTCGACGAATCGTACTTTTGCACAG	7050	AQLSTNRTFAQ	11639	LSTNRTF	0.31655	-0.07398
GS439	2462	GCCCAAAAACAAACCCAAGACAGCAGCGCACAG	7051	AQKQTQDSSAQ	11640	KQTQDSS	0.316176	-0.04007
GS440	2463	GCCCAATATGAGCGGGGGCCTCAGATGGCACAG	7052	AQYERGPQMAQ	11641	YERGPQM	0.315854	-0.17291
SyS862	2464	GCCCAAACCCACGCCAACAGCGTCAGAGCACAG	7053	AQTHANSVRAQ	11642	THANSVR	0.315781	-0.07488
GS441	2465	GCCCAAAGTATGAATACTAATGCTTCTGCACAG	7054	AQSMNTNASAQ	11643	SMNTNAS	0.315733	-0.12336
SyS863	2466	GCCCAACTTGATAATGAGAAGGGGAGGGGCACAG	7055	AQLDNEKGRAQ	11644	LDNEKGR	0.315543	0.058188
GS442	2467	GCCCAACTCGGCCAACTCCTCCAAAGCGCACAG	7056	AQLGQLLQSAQ	11645	LGQLLQS	0.315509	-0.16214
SyS864	2468	GCCCAAATGCGGATGCCTGTTAATATGGCACAG	7057	AQMRMPVNMAQ	11646	MRMPVNM	0.315482	-0.20224
GS443	2469	GCCCAAGGCACCAGCAACCTCCCCAGCGCACAG	7058	AQGTSNLPSAQ	11647	GTSNLPS	0.314909	-0.13702
GS444	2470	GCCCAAGAGGGGGGAGATGAAGTCTCCGGCACAG	7059	AQEGEMKSPAQ	11648	EGEMKSP	0.31482	-0.1646
SyS865	2471	GCCCAACAGCTGGGGCATGATAATCGGGCACAG	7060	AQQLGHDNRAQ	11649	QLGHDNR	0.314814	-0.11961
SyS866	2472	GCCCAACTGGATGATTCTGCGGGGAGGGCACAG	7061	AQLDDSAGRAQ	11650	LDDSAGR	0.314701	-0.11941
SyS867	2473	GCCCAAACTGGTGCTGGTAATGGGCGGGGCACAG	7062	AQTGAGNGRAQ	11651	TGAGNGR	0.314656	-0.01667

FIG. 33 (Continued)

SyS868	2474	GCCCAAAACACCGGCGCCGCCATGATGGCACAG	7063	AQNTGAAMMAQ	11652	NTGAAMM	0.314631	0.055763
GS446	2475	GCCCAAATGGGGGCGAATACGTCTGTTGCACAG	7064	AQMGANTSVAQ	11653	MGANTSV	0.314385	-0.08188
SyS869	2476	GCCCAACCCAGCACCCACGGCGGCAGCGCACAG	7065	AQPSTHGGSAQ	11654	PSTHGGS	0.314357	-0.1889
SyS870	2477	GCCCAAATGCCTCAGTCGCAGCCGAATGCACAG	7066	AQMPQSQPNAQ	11655	MPQSQPN	0.31424	0.015982
SyS871	2478	GCCCAATCTACTCAGGCTAGGCTGACGGCACAG	7067	AQSTQARLTAQ	11656	STQARLT	0.314143	-0.15374
SyS872	2479	GCCCAAAGCGAATACCTCCTCAACCCCGCACAG	7068	AQSEYLLNPAQ	11657	SEYLLNP	0.314087	-0.19618
SyS873	2480	GCCCAAACTACTGGTCCTGGGCTGAATGCACAG	7069	AQTTGPGLNAQ	11658	TTGPGLN	0.314048	0.103567
GS449	2481	GCCCAACCTGGGAGTTCTGTGTCTTATGCACAG	7070	AQPGSSVSYAQ	11659	PGSSVSY	0.313645	-0.14868
GS450	2482	GCCCAATATTTTGGGTCGGCGCAGGAGGCACAG	7071	AQYFGSAQEAQ	11660	YFGSAQE	0.313586	-0.17958
GS451	2483	GCCCAAGCCGTCATCAACAACGCCACCGCACAG	7072	AQAVINNATAQ	11661	AVINNAT	0.313428	-0.0842
SyS874	2484	GCCCAAGTCGCCATGCAAGACAAAAAAGCACAG	7073	AQVAMQDKKAQ	11662	VAMQDKK	0.313354	-0.14041
SyS875	2485	GCCCAAGCGGATAAATATGAATATTAAGGCACAG	7074	AQADNMNIKAQ	11663	ADNMNIK	0.313295	-0.07009
GP115	2486	GCCCAAGGGCGGGCGACGACTGATTCTGCACAG	7075	AQGRATTDSAQ	11664	GRATTDS	0.313279	-0.07065
SyS876	2487	GCCCAAATGAACCTCCACCTCAAAGGCGCACAG	7076	AQMNLHLKGAQ	11665	MNLHLKG	0.313136	0.083677
TS152	2488	GCCCAATCGAATCAGATTCGTGATTCGGCACAG	7077	AQSNQIRDSAQ	11666	SNQIRDS	0.313116	-0.32301
SyS877	2489	GCCCAAGTTAATGGTCAGAGTACGCCTGCACAG	7078	AQVNGQSTPAQ	11667	VNGQSTP	0.313037	-0.00962
SyS878	2490	GCCCAAATTCTTCCTCAGTTGAATTCGGCACAG	7079	AQILPQLNSAQ	11668	ILPQLNS	0.312954	-0.03559
SyS879	2491	GCCCAAGTCCAAGACAGCCTCCACTTCGCACAG	7080	AQVQDSLHFAQ	11669	VQDSLHF	0.312874	0.083873
SyS880	2492	GCCCAAGACGTCAGCAACAGAAACACAACGCACAG	7081	AQDVSNRNNAQ	11670	DVSNRNN	0.312493	-0.15411
GP116	2493	GCCCAAGATGCTAGTCATGGTTCTAGTGCACAG	7082	AQDASHGSSAQ	11671	DASHGSS	0.312276	-0.07391
SyS881	2494	GCCCAACGGGCGAGTGCTCATCCGCCGGCACAG	7083	AQRASAHPPAQ	11672	RASAHPP	0.312043	-0.11646
SyS882	2495	GCCCAACCCAGCCTCAGAGCCCTCGACGCACAG	7084	AQPSLRALDAQ	11673	PSLRALD	0.311957	-0.17678
SyS883	2496	GCCCAAGATAAGACGCCTCCGGTTGCTGCACAG	7085	AQDKTPPVAAQ	11674	DKTPPVA	0.311957	-0.17678
SyS884	2497	GCCCAACTTAATGATGTTACGACTAGGGCACAG	7086	AQLNDVTTRAQ	11675	LNDVTTR	0.311619	-0.20586
SyS885	2498	GCCCAAGGCGCCAGCAACGCCCAAGCCGCACAG	7087	AQGASNAQAAQ	11676	GASNAQA	0.311537	0.290108
SyS886	2499	GCCCAAAATGGGTCGCGGGATGCGTTGGCACAG	7088	AQNGSRDALAQ	11677	NGSRDAL	0.311371	0.125773
GS452	2500	GCCCAATACGGCGTCGAAAGAATGAGCGCACAG	7089	AQYGVERMSAQ	11678	YGVERMS	0.311356	-0.04604
GS453	2501	GCCCAAGCCAAAGTCGCCAGCAGCTTCGCACAG	7090	AQAKVASSFAQ	11679	AKVASSF	0.311335	-0.04098
SyS887	2502	GCCCAACATAAGCAGATTCTGTTGGATGCACAG	7091	AQHKQILLDAQ	11680	HKQILLD	0.311304	-0.10069
SyS888	2503	GCCCAAGACAGAGCCAACGACAGAATCGCACAG	7092	AQDRANDRIAQ	11681	DRANDRI	0.311232	0.08751
GS454	2504	GCCCAAAAAATGAGCACCACCATGCTCGCACAG	7093	AQKMSTTMLAQ	11682	KMSTTML	0.31117	-0.1003
SyS889	2505	GCCCAAGGCGGCGAAAACGGCGTCATCGCACAG	7094	AQGGENGVIAQ	11683	GGENGVI	0.310602	-0.15011

FIG. 33 (Continued)

SyS890	2506	GCCCAAGTTACGCAGACTCTGATTTCGGCACAG	7095	AQVTQTLISAQ	11684	VTQTLIS	0.310505	-0.17799
SyS891	2507	GCCCAACTGTATACTAAGGCTCTGATTGCACAG	7096	AQLYTKALIAQ	11685	LYTKALI	0.310465	-0.10161
GS455	2508	GCCCAAACCCTCCCCGGCCACACAGAGCACAG	7097	AQTLPGHNRAQ	11686	TLPGHNR	0.310262	-0.1756
SyS892	2509	GCCCAAAGTAAGTCTGGGCTTGTGGGTGCACAG	7098	AQSKSGLVGAQ	11687	SKSGLVG	0.310236	0.168736
GS456	2510	GCCCAACTTACTTTGAAGGATACTAGTGCACAG	7099	AQLTLKDTSAQ	11688	LTLKDTS	0.310122	-0.18278
SyS893	2511	GCCCAATGGAACGGCACCGGCGTCAGCGCACAG	7100	AQWNGTGVSAQ	11689	WNGTGVS	0.310096	-0.0119
SS58	2512	GCCCAACTCGTCCAAAACAACACCATGGCACAG	7101	AQLVQNNTMAQ	11690	LVQNNTM	0.310057	-0.30263
SyS894	2513	GCCCAACTCGCCGACAGAGGCAGCGCCGCACAG	7102	AQLADRGSAAQ	11691	LADRGSA	0.310018	-0.08828
GS459	2514	GCCCAATTGGCTTCGACGGGTGCGAATGCACAG	7103	AQLASTGANAQ	11692	LASTGAN	0.309525	-0.13094
GS460	2515	GCCCAACTTGGGCGGAATGATACTCTTGCACAG	7104	AQLGRNDTLAQ	11693	LGRNDTL	0.3095	-0.05896
GS461	2516	GCCCAAAGAAGCACCAACGGCGAAGCCGCACAG	7105	AQRSTNGEAAQ	11694	RSTNGEA	0.309188	-0.01679
GS462	2517	GCCCAAGGCGCCACCTACCAAAGAACCGCACAG	7106	AQGATYQRTAQ	11695	GATYQRT	0.309152	-0.12526
SyS895	2518	GCCCAAGGCAAAAGCCAACTCCTCATGGCACAG	7107	AQGKSQLLMAQ	11696	GKSQLLM	0.309137	-0.07057
SyS896	2519	GCCCAAAATACTGCTACGTTTTCTTCGGCACAG	7108	AQNTATFSSAQ	11697	NTATFSS	0.309129	-0.04787
GS463	2520	GCCCAATATTCGACGACGATTTCTCCGGCACAG	7109	AQYSTTISPAQ	11698	YSTTISP	0.30904	-0.07316
SyS897	2521	GCCCAACCCAGACACAGCGTCCAAGACGCACAG	7110	AQPRHSVQDAQ	11699	PRHSVQD	0.308961	-0.20314
GP117	2522	GCCCAAAATAATAATACGAAGATGAATGCACAG	7111	AQNNNTKMNAQ	11700	NNNTKMN	0.30893	-0.03193
GS464	2523	GCCCAACTCACCGGCCACCACACCAAAGCACAG	7112	AQLTGHHTKAQ	11701	LTGHHTK	0.308925	-0.15855
SyS899	2524	GCCCAAAACGTCAGCAGCGGCCAAAGAGCACAG	7113	AQNVSSGQRAQ	11702	NVSSGQR	0.308694	0.425634
SS60	2525	GCCCAAAGCCTCCAAGACGCCAGACTCGCACAG	7114	AQSLQDARLAQ	11703	SLQDARL	0.308634	-0.29859
SyS900	2526	GCCCAACTTAATAGGGATGGGTCGGTGGCACAG	7115	AQLNRDGSVAQ	11704	LNRDGSV	0.308572	-0.18648
SyS901	2527	GCCCAAAACAGCACCGAAAACAGCACCGCACAG	7116	AQNSTENSTAQ	11705	NSTENST	0.308538	-0.07217
SyS903	2528	GCCCAAAGCCTCGTCGCCCAACCCGTCGCACAG	7117	AQSLVAQPVAQ	11706	SLVAQPV	0.308428	-0.08008
SyS904	2529	GCCCAACATGCTGCTACGGTGAGTCATGCACAG	7118	AQHAATVSHAQ	11707	HAATVSH	0.308062	0.032955
SyS905	2530	GCCCAAAATGTGTCTGGTGCGCGTTTGGCACAG	7119	AQNVSGARLAQ	11708	NVSGARL	0.308062	-0.04948
GS466	2531	GCCCAAAGAGCCGACAAATTCGACTACGCACAG	7120	AQRADKFDYAQ	11709	RADKFDY	0.308023	-0.02692
SyS906	2532	GCCCAAAGCCAACCCGACGTCACCTACGCACAG	7121	AQSQPDVTYAQ	11710	SQPDVTY	0.307992	-0.127
SyS907	2533	GCCCAAGTTCTTACTCAGCAGACTCATGCACAG	7122	AQVLTQQTHAQ	11711	VLTQQTH	0.307679	0.0148
SyS908	2534	GCCCAAACCGACAACAGCACCACCACAGAGCACAG	7123	AQTDNSTTRAQ	11712	TDNSTTR	0.307679	0.131421
SyS909	2535	GCCCAATATAATACTCGGTATGATGCTGCACAG	7124	AQYNTRYDAAQ	11713	YNTRYDA	0.307506	-0.20103
SyS910	2536	GCCCAAAGCGCCAACGACGCCAGAGTCGCACAG	7125	AQSANDARVAQ	11714	SANDARV	0.307448	-0.03147
SyS911	2537	GCCCAAATCCTCACCCCCGACCTCAGAGCACAG	7126	AQILTPDLRAQ	11715	ILTPDLR	0.307422	-0.08464

FIG. 33 (Continued)

SyS912	2538	GCCCAACCTAATGTGGGTGCGAGTTCGGCACAG	7127	AQPNVGASSAQ	11716	PNVGASS	0.307375	-0.17136
SyS914	2539	GCCCAACTCAGCGCCAGCCACACCATCGCACAG	7128	AQLSASHTIAQ	11717	LSASHTI	0.307038	-0.14672
SS61	2540	GCCCAAACCAAAGTCCTCATCGAAAAAGCACAG	7129	AQTKVLIEKAQ	11718	TKVLIEK	0.306967	-0.36752
SyS915	2541	GCCCAAATGAATACTCTTATTCCTGCGGCACAG	7130	AQMNTLIPAAQ	11719	MNTLIPA	0.306966	-0.05601
SyS916	2542	GCCCAATCTTCGAATGTTGTGACTACTGCACAG	7131	AQSSNVVTTAQ	11720	SSNVVTT	0.306697	0.098037
SyS917	2543	GCCCAAATGAACGTCAGACCCACCACCGCACAG	7132	AQMNVRPTTAQ	11721	MNVRPTT	0.306682	0.085085
SyS918	2544	GCCCAAGATACTGGTCTTAATAATAGGGCACAG	7133	AQDTGLNNRAQ	11722	DTGLNNR	0.306651	0.011783
GS467	2545	GCCCAAACCCTCAACAGAGACCACATGGCACAG	7134	AQTLNRDHMAQ	11723	TLNRDHM	0.306373	-0.09048
GS469	2546	GCCCAACTCCTCCTCAGCCACCACGCCGCACAG	7135	AQLLLSHHAAQ	11724	LLLSHHA	0.306247	-0.18099
SyS919	2547	GCCCAAAACCCCGCCATGGCCACCTTCGCACAG	7136	AQNPAMATFAQ	11725	NPAMATF	0.305992	-0.14768
GS470	2548	GCCCAAATTTCTCAGCGGATTTATGCGGCACAG	7137	AQISQRIYAAQ	11726	ISQRIYA	0.30595	-0.16528
SyS920	2549	GCCCAAACGACTGGGGTTGCTGGTAGTGCACAG	7138	AQTTGVAGSAQ	11727	TTGVAGS	0.305896	0.05663
SyS921	2550	GCCCAATTTGGGACGTTTCCGACGCCTGCACAG	7139	AQFGTFPTPAQ	11728	FGTFPTP	0.305776	-0.10477
SS62	2551	GCCCAAAGAGGCAGCGACTTCGACAGCGCACAG	7140	AQRGSDFDSAQ	11729	RGSDFDS	0.305764	-0.33979
GS472	2552	GCCCAAAGCAAAGCCAGCCTCGACAGCGCACAG	7141	AQSKASLDSAQ	11730	SKASLDS	0.305689	-0.08038
GS473	2553	GCCCAACTTCTTAATAGTCATTCTGCTGCACAG	7142	AQLLNSHSAAQ	11731	LLNSHSA	0.305635	0.015974
GS474	2554	GCCCAAGCTAGTATTCATAAGGATATTGCACAG	7143	AQASIHKDIAQ	11732	ASIHKDI	0.305534	-0.1269
GS475	2555	GCCCAAAGCGACCCCGGCAAATTCATGGCACAG	7144	AQSDPGKFMAQ	11733	SDPGKFM	0.305528	-0.10472
SyS922	2556	GCCCAAGGCACCAGCAGCGCCCAAAGAGCACAG	7145	AQGTSSAQRAQ	11734	GTSSAQR	0.305492	-0.05312
SyS923	2557	GCCCAAAGTACGAATAGTAAGCTGGAGGCACAG	7146	AQSTNSKLEAQ	11735	STNSKLE	0.305492	-0.15496
SyS924	2558	GCCCAAAATTTGCAGACTGTTCCGAATGCACAG	7147	AQNLQTVPNAQ	11736	NLQTVPN	0.305492	-0.15496
GS476	2559	GCCCAAGTCGTCACCCACCTCAACGCCGCACAG	7148	AQVVTHLNAAQ	11737	VVTHLNA	0.305419	-0.13612
SyS925	2560	GCCCAACTCAGCACCAGCAACAACTTCGCACAG	7149	AQLSTSNNFAQ	11738	LSTSNNF	0.305414	0.115059
SyS926	2561	GCCCAAAACAACAGCGGCCACATCAGCGCACAG	7150	AQNNSGHISAQ	11739	NNSGHIS	0.305094	-0.09434
SyS927	2562	GCCCAAGCCTACCAAGTCAACAGCGACGCACAG	7151	AQAYQVNSDAQ	11740	AYQVNSD	0.305066	0.03955
SyS928	2563	GCCCAACAGCAGAATTATTTGAATCATGCACAG	7152	AQQQNYLNHAQ	11741	QQNYLNH	0.304957	-0.16223
GS477	2564	GCCCAATTTGCGACTACGAATACTGGGGCACAG	7153	AQFATTNTGAQ	11742	FATTNTG	0.304891	0.033545
GS478	2565	GCCCAACTTGCGAATAAGATTGCGAATGCACAG	7154	AQLANKIANAQ	11743	LANKIAN	0.304879	-0.01499
GS479	2566	GCCCAACAAAGCTTCCAAAGAGAAGTCGCACAG	7155	AQQSFQREVAQ	11744	QSFQREV	0.304879	-0.14689
SyS930	2567	GCCCAACTGCATATTTCGGAGCCGAGGGCACAG	7156	AQLHISEPRAQ	11745	LHISEPR	0.30455	-0.13556
GS481	2568	GCCCAACGTGTGGGTGAGCGGGAGCAGGCACAG	7157	AQRVGEREQAQ	11746	RVGEREQ	0.304522	-0.17829
SyS931	2569	GCCCAAGTTAATATTATTCAGGCGTCGGCACAG	7158	AQVNIIQASAQ	11747	VNIIQAS	0.304499	-0.05678

FIG. 33 (Continued)

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SyS932	2570	GCCCAAGGCGTCGGCCTCCACAACAAAGCACAG	7159	AQGVGLHNKAQ	11748	GVGLHNK	0.304499	-0.10606
SyS933	2571	GCCCAAAATAATCCTGCGATTCCGATTCGCACAG	7160	AQNNPAIPIAQ	11749	NNPAIPI	0.30426	-0.01336
GP118	2572	GCCCAACGGCTGTCGAGTCAGGCTGTGGCACAG	7161	AQRLSSQAVAQ	11750	RLSSQAV	0.304245	-0.07356
SyS934	2573	GCCCAACACAGCAACGAACTCAGACCCGCACAG	7162	AQHSNELRPAQ	11751	HSNELRP	0.304109	0.131628
SyS935	2574	GCCCAAAGCCTCGGCCCCACCACCAACGCACAG	7163	AQSLGPTTNAQ	11752	SLGPTTN	0.304096	-0.09555
TS154	2575	GCCCAAGGTAATCAGACGAATCGTTCGGCACAG	7164	AQGNQTNRSAQ	11753	GNQTNRS	0.303952	-0.06046
SyS936	2576	GCCCAAAGTAATCCGGTGGGTAATCCGGCACAG	7165	AQSNPVGNPAQ	11754	SNPVGNP	0.303849	0.006491
SyS937	2577	GCCCAACAAGTCCCCCCCCTCGTCCCCGCACAG	7166	AQQVPPLVPAQ	11755	QVPPLVP	0.303762	-0.17678
SyS939	2578	GCCCAACTCAGCACCCCCCCCCACCCAAGCACAG	7167	AQLSTPPTQAQ	11756	LSTPPTQ	0.303367	0.011133
SyS940	2579	GCCCAAGTGGGTACGGAGCCGCTTTCTGCACAG	7168	AQVGTEPLSAQ	11757	VGTEPLS	0.303367	-0.21072
GS483	2580	GCCCAAAGACCCGACGCCACCAGCCACGCACAG	7169	AQRPDATSHAQ	11758	RPDATSH	0.303361	-0.12139
GS485	2581	GCCCAAGTTGAGAAGCAGATGCTTAATGCACAG	7170	AQVEKQMLNAQ	11759	VEKQMLN	0.303278	-0.10651
SyS941	2582	GCCCAATTCAAAAGCGCCCAAGCCACCGCACAG	7171	AQFKSAQATAQ	11760	FKSAQAT	0.303093	-0.09677
SyS942	2583	GCCCAATGGGCTTTGTCTACGGATGGGGCACAG	7172	AQWALSTDGAQ	11761	WALSTDG	0.302822	-0.19969
SyS943	2584	GCCCAACTTGCTGGTCTGGCTACTAATGCACAG	7173	AQLAGLATNAQ	11762	LAGLATN	0.302566	-0.04978
SyS944	2585	GCCCAAACCCTCACCGCCGGCACCCCCCGCACAG	7174	AQTLTAGTPAQ	11763	TLTAGTP	0.302458	0.051682
GS486	2586	GCCCAAATCCCCGTCACCAGCAGAATGGCACAG	7175	AQIPVTSRMAQ	11764	IPVTSRM	0.302322	-0.15669
SyS945	2587	GCCCAAGGGACGGATTATCCTAGGTCTGCACAG	7176	AQGTDYPRSAQ	11765	GTDYPRS	0.302309	-0.17799
SyS946	2588	GCCCAAGTTACGGAGCATAGTAAGTTGGCACAG	7177	AQVTEHSKLAQ	11766	VTEHSKL	0.302301	-0.1054
GS487	2589	GCCCAAAACATGAGCATGCCCGTCAAAGCACAG	7178	AQNMSMPVKAQ	11767	NMSMPVK	0.302291	-0.06614
SyS947	2590	GCCCAAAGCGTCGGCGTCGGCATGAGCGCACAG	7179	AQSVGVGMSAQ	11768	SVGVGMS	0.302147	-0.04842
SyS948	2591	GCCCAACCCAGAACCGACAACGAAGGCGCACAG	7180	AQPRTDNEGAQ	11769	PRTDNEG	0.302129	-0.11889
SyS949	2592	GCCCAATTCAGCAACCCCGACAGAACCGCACAG	7181	AQFSNPDRTAQ	11770	FSNPDRT	0.302103	-0.03523
SyS950	2593	GCCCAAATGCACCTCGTCCCCACCACCGCACAG	7182	AQMHLVPTTAQ	11771	MHLVPTT	0.302085	-0.09798
SyS951	2594	GCCCAAAATGCTCCTCCGGTTTCTTCTGCACAG	7183	AQNAPPVSSAQ	11772	NAPPVSS	0.301938	0.008708
SyS952	2595	GCCCAATCGAATTTGCCTACTTTGGCGGCACAG	7184	AQSNLPTLAAQ	11773	SNLPTLA	0.301914	0.035379
GS490	2596	GCCCAAATCATGCAAGGCATGACCACCGCACAG	7185	AQIMQGMTTAQ	11774	IMQGMTT	0.301878	-0.14272
SyS953	2597	GCCCAAAGTCGTGAGACGACGAGTCCTGCACAG	7186	AQSRETTSPAQ	11775	SRETTSP	0.30158	0.041441
SyS954	2598	GCCCAAAACCCCACCAGCTTCAGCACCGCACAG	7187	AQNPTSFSTAQ	11776	NPTSFST	0.30158	-0.17193
SyS955	2599	GCCCAAAATTTGCAGCATGGTTCGACTGCACAG	7188	AQNLQHGSTAQ	11777	NLQHGST	0.301496	0.225756
GS491	2600	GCCCAAAATTTTCATTCTGGTCATACGGCACAG	7189	AQNFHSGHTAQ	11778	NFHSGHT	0.301283	-0.13881
GS492	2601	GCCCAAACTGAGAGTGTGTATGCGAGGGCACAG	7190	AQTESVYARAQ	11779	TESVYAR	0.301236	-0.15383

FIG. 33 (Continued)

GS493	2602	GCCCAAACTAAGTCTGAGATTCCTAATGCACAG	7191	AQTKSEIPNAQ	11780	TKSEIPN	0.301236	-0.15383
SyS956	2603	GCCCAAACCAGCCTCGCCGACATGAGAGCACAG	7192	AQTSLADMRAQ	11781	TSLADMR	0.301192	-0.01918
GS494	2604	GCCCAAAGACTCAAAGCCGACATCACCGCACAG	7193	AQRLKADITAQ	11782	RLKADIT	0.301085	-0.08801
SyS957	2605	GCCCAACTGAATATGAATGTTCTGGCTGCACAG	7194	AQLNMNVLAAQ	11783	LNMNVLA	0.301014	-0.03968
GS495	2606	GCCCAAAGCCTCAGACCCATCAGCGTCGCACAG	7195	AQSLRPISVAQ	11784	SLRPISV	0.301004	-0.15945
SyS958	2607	GCCCAACTCAGCGTCCAACTCGTCGAAGCACAG	7196	AQLSVQLVEAQ	11785	LSVQLVE	0.300849	-0.14056
SyS959	2608	GCCCAAAGTTTTGAGGGTGTTCTTCCGGCACAG	7197	AQSFEGVLPAQ	11786	SFEGVLP	0.300847	-0.1792
GS496	2609	GCCCAAATCATCGTCGGCCTCCAACCCGCACAG	7198	AQIIVGLQPAQ	11787	IIVGLQP	0.3008	-0.11578
GS497	2610	GCCCAAGTCAGCAGCTACGAAAGACTCGCACAG	7199	AQVSSYERLAQ	11788	VSSYERL	0.300709	-0.12053
SyS960	2611	GCCCAAAGAACCAACGACGCCATCGTCGCACAG	7200	AQRTNDAIVAQ	11789	RTNDAIV	0.300688	0.340159
GS498	2612	GCCCAATTCAGCGAACACAGAGAACTCGCACAG	7201	AQFSEHRELAQ	11790	FSEHREL	0.300668	-0.16304
GS499	2613	GCCCAAAAAGAAGCCACCGCCAACACCGCACAG	7202	AQKEATANTAQ	11791	KEATANT	0.300598	-0.06336
SyS962	2614	GCCCAACTCAGAGCCAGCATCACCGTCGCACAG	7203	AQLRASITVAQ	11792	LRASITV	0.300214	0.025681
SyS963	2615	GCCCAATGGTTGGGTATTACTGAGGCGGCACAG	7204	AQWLGITEAAQ	11793	WLGITEA	0.300198	-0.07373
SyS964	2616	GCCCAAAGCAGCCAAAAAGCCGCCGAAGCACAG	7205	AQSSQKAAEAQ	11794	SSQKAAE	0.300091	-0.02263
GS501	2617	GCCCAAGGGTCGACTCCTGGTCTTGCTGCACAG	7206	AQGSTPGLAAQ	11795	GSTPGLA	0.299731	-0.12625
SyS965	2618	GCCCAAAAGGGGAATGCTAATGATCTTGCACAG	7207	AQKGNANDLAQ	11796	KGNANDL	0.299619	-0.12733
SyS966	2619	GCCCAAACCAGCGCCCCCCTCAAACTCGCACAG	7208	AQTSAPLKLAQ	11797	TSAPLKL	0.299556	-0.03494
SyS967	2620	GCCCAACCTGTGCAGACGAATGGGCATGCACAG	7209	AQPVQTNGHAQ	11798	PVQTNGH	0.299313	-0.06587
SyS968	2621	GCCCAAAGGCCGGCTGTGGATTCGGCTGCACAG	7210	AQRPAVDSAAQ	11799	RPAVDSA	0.299287	-0.04179
SyS969	2622	GCCCAAACCACCCTCAGCCAAAACAGAGCACAG	7211	AQTTLSQNRAQ	11800	TTLSQNR	0.299223	-0.05801
SyS970	2623	GCCCAAGTCATGACCGTCGGCAGCCTCGCACAG	7212	AQVMTVGSLAQ	11801	VMTVGSL	0.299001	-0.07033
SyS971	2624	GCCCAAGCCCTCAACAAAGAAACTGGGCACAG	7213	AQALNKENWAQ	11802	ALNKENW	0.298989	-0.20709
SyS973	2625	GCCCAACATCATCATTTGACGGGGGAATGCACAG	7214	AQHHHLTGNAQ	11803	HHHLTGN	0.298821	-0.17259
GS502	2626	GCCCAAGGGATGCGGACTGTGAATATTGCACAG	7215	AQGMRTVNIAQ	11804	GMRTVNI	0.298627	-0.18099
GS503	2627	GCCCAAACTCTGAATAGTTCGGTGGCTGCACAG	7216	AQTLNSSVAAQ	11805	TLNSSVA	0.298611	-0.08717
GS504	2628	GCCCAATCTGCTTCGACGATTCTTGTTGCACAG	7217	AQSASTILVAQ	11806	SASTILV	0.298566	-0.16753
GP119	2629	GCCCAAGAGATGATTAGGCCTCGTGCGGCACAG	7218	AQEMIRPRAAQ	11807	EMIRPRA	0.298415	0.162495
SyS974	2630	GCCCAAATGTCGGCGGCGAGTTATAAGGCACAG	7219	AQMSAASYKAQ	11808	MSAASYK	0.298381	-0.14302
SyS975	2631	GCCCAACATTTTACGACTGGGTCTGTTGCACAG	7220	AQHFTTGSVAQ	11809	HFTTGSV	0.298366	-0.02828
GS505	2632	GCCCAAGCTTCTCATACTATTGGGCTTGCACAG	7221	AQASHTIGLAQ	11810	ASHTIGL	0.298317	-0.10725
GS506	2633	GCCCAAAGTCGGGAGCATCAGCTGTATGCACAG	7222	AQSREHQLYAQ	11811	SREHQLY	0.298183	-0.11266

FIG. 33 (Continued)

GS507	2634	GCCCAAGCTGGTACGACGGCTCCGCTTGCACAG	7223	AQAGTTAPLAQ	11812	AGTTAPL	0.298135	-0.06321
GS508	2635	GCCCAAGGCAAAGTCAGCGGCGCCATGGCACAG	7224	AQGKVSGAMAQ	11813	GKVSGAM	0.298131	-0.11524
GS509	2636	GCCCAAAAACTCAGCGGCATGAGCGTCGCACAG	7225	AQKLSGMSVAQ	11814	KLSGMSV	0.297895	-0.15574
GS510	2637	GCCCAAGTCCTCCCCAAAGACGACGCCGCACAG	7226	AQVLPKDDAAQ	11815	VLPKDDA	0.297661	-0.1747
SyS976	2638	GCCCAACTCGCCGGCATCCTCACCACCGCACAG	7227	AQLAGILTTAQ	11816	LAGILTT	0.297605	-0.0739
SyS977	2639	GCCCAAGTCGTCCCCGGCGCCCAAACCGCACAG	7228	AQVVPGAQTAQ	11817	VVPGAQT	0.297436	-0.06047
SyS978	2640	GCCCAAGGTCAGCATTCTTATGCGCATGCACAG	7229	AQGQHSYAHAQ	11818	GQHSYAH	0.297408	-0.07737
SyS979	2641	GCCCAACATCATCTGAGTACGTCGATTGCACAG	7230	AQHHLSTSIAQ	11819	HHLSTSI	0.297404	-0.03102
SyS980	2642	GCCCAAACCCTCATCCCCCCCAACCCCCGCACAG	7231	AQTLIPPNPAQ	11820	TLIPPNP	0.297351	-0.14283
GS511	2643	GCCCAAGAGATGCATAATCCTAGGGCGGCGCACAG	7232	AQEMHNPRAAQ	11821	EMHNPRA	0.297287	-0.11417
SyS982	2644	GCCCAAATCGAAAACCCCCCCCAGAGGCGCACAG	7233	AQIENPPRGAQ	11822	IENPPRG	0.297181	-0.0878
SyS983	2645	GCCCAAGGCCAATTCAGCGACGCCAGAGCACAG	7234	AQGQFSDARAQ	11823	GQFSDAR	0.297111	0.032689
SyS984	2646	GCCCAAGCCGAAGCCAGCGCCAGCAGAGCACAG	7235	AQAEASASRAQ	11824	AEASASR	0.297046	-0.07131
SyS985	2647	GCCCAACTTGTTAAGGGGGGATGCGAGGGCACAG	7236	AQLVKGDARAQ	11825	LVKGDAR	0.29699	0.026608
GS512	2648	GCCCAACAGGGTCATACGCATGGGAATGCACAG	7237	AQQGHTHGNAQ	11826	QGHTHGN	0.296975	-0.12903
GS513	2649	GCCCAACAGAAGCCTACGTCTACTTTTGCACAG	7238	AQQKPTSTFAQ	11827	QKPTSTF	0.296937	-0.15288
GS514	2650	GCCCAAAAGCTTGCTGCTTTGGGTGCTGCACAG	7239	AQKLAALGAAQ	11828	KLAALGA	0.296882	-0.17672
SyS986	2651	GCCCAATCGTCTGTGGATCAGATGAAGGCACAG	7240	AQSSVDQMKAQ	11829	SSVDQMK	0.296846	-0.08602
SyS987	2652	GCCCAAGGCATCGTCACCGCCCCCCTCGCACAG	7241	AQGIVTAPLAQ	11830	GIVTAPL	0.296762	-0.16951
GS515	2653	GCCCAACTTTTGAAGATGCCTTCTCCTGCACAG	7242	AQLLKMPSPAQ	11831	LLKMPSP	0.296723	-0.12298
SyS988	2654	GCCCAAAATGTTGCTCATACGGTGCGTGCACAG	7243	AQNVAHTVRAQ	11832	NVAHTVR	0.2967	-0.06524
SyS989	2655	GCCCAACTGATGAGTACGAATGTGAGTGCACAG	7244	AQLMSTNVSAQ	11833	LMSTNVS	0.29667	0.039016
SyS990	2656	GCCCAACTGTCTAATAATAATGCGCTTGCACAG	7245	AQLSNNNALAQ	11834	LSNNNAL	0.296455	-0.22803
SyS991	2657	GCCCAACTCCTCATCGGCCCCACCGGCGCACAG	7246	AQLLIGPTGAQ	11835	LLIGPTG	0.296321	-0.11131
GS517	2658	GCCCAAGTCAGAAACACCATGATCAGCGCACAG	7247	AQVRNTMISAQ	11836	VRNTMIS	0.296311	-0.17201
GS518	2659	GCCCAAGGCGCCACCGGCCACCTCACCGCACAG	7248	AQGATGHLTAQ	11837	GATGHLT	0.296311	-0.17201
GS519	2660	GCCCAAATGACCGTCGGCAACCTCGGCGCACAG	7249	AQMTVGNLGAQ	11838	MTVGNLG	0.29631	-0.06764
SyS992	2661	GCCCAAAGTAATGGTCTGAATGGTTTGGCACAG	7250	AQSNGLNGLAQ	11839	SNGLNGL	0.296065	-0.23419
SyS994	2662	GCCCAACGGAATGAGAATGAGAGTCGTGCACAG	7251	AQRNENESRAQ	11840	RNENESR	0.295831	-0.08635
SyP47	2663	GCCCAAGGGAATGCTCGGGATGCGAGTGCACAG	7252	AQGNARDASAQ	11841	GNARDAS	0.295799	-0.04389
SyS995	2664	GCCCAAATCAGCAAACTCCTCCTCAGCGCACAG	7253	AQISKLLLSAQ	11842	ISKLLLS	0.295612	-0.10947
GS520	2665	GCCCAAAACGACACCACCAACATGAGCGCACAG	7254	AQNDTTNMSAQ	11843	NDTTNMS	0.295587	-0.16718

FIG. 33 (Continued)

SyS996	2666	GCCCAAGGCCTCGAAGCCAACAAAAGCGCACAG	7255	AQGLEANKSAQ	11844	GLEANKS	0.295578	0.033862
SyS998	2667	GCCCAACATTATAGTACTGTTGGGGTGGCACAG	7256	AQHYSTVGVAQ	11845	HYSTVGV	0.295419	-0.19011
SyS999	2668	GCCCAACCTACGATTTCGGTTCTGCCTGCACAG	7257	AQPTISVLPAQ	11846	PTISVLP	0.295257	-0.21694
SyS1000	2669	GCCCAAGTCCAAACCATCGGCCACGAAGCACAG	7258	AQVQTIGHEAQ	11847	VQTIGHE	0.295085	-0.16397
SyS1001	2670	GCCCAAAAACCCGAAACCGCCAGCGACGCACAG	7259	AQKPETASDAQ	11848	KPETASD	0.294946	-0.1036
SS64	2671	GCCCAAACCAACACCCCCACCAGCAGAGCACAG	7260	AQTNTPTSRAQ	11849	TNTPTSR	0.294926	-0.28124
SyS1002	2672	GCCCAAAGTTTGACGCTTAGTTCGCATGCACAG	7261	AQSLTLSSHAQ	11850	SLTLSSH	0.294898	-0.14526
GP120	2673	GCCCAACATTATCATAGTATTCAGGCTGCACAG	7262	AQHYHSIQAAQ	11851	HYHSIQA	0.294855	-0.07232
SyS1003	2674	GCCCAATACCACGGCGAAAACGAAAGAGCACAG	7263	AQYHGENERAQ	11852	YHGENER	0.294846	-0.08758
GS522	2675	GCCCAACTGCCTCATACTGCGCGTGTGGCACAG	7264	AQLPHTARVAQ	11853	LPHTARV	0.294761	-0.14958
SyS1004	2676	GCCCAAACCAGAGAAGGCAGCACCGGCGCACAG	7265	AQTREGSTGAQ	11854	TREGSTG	0.294636	-0.02281
GS525	2677	GCCCAAGTTGATCGTAGGGCGATGCTTGCACAG	7266	AQVDRRAMLAQ	11855	VDRRAML	0.294282	-0.08
SyS1005	2678	GCCCAAACCAGCGTCAGCGCCGTCATGGCACAG	7267	AQTSVSAVMAQ	11856	TSVSAVM	0.29428	-0.21679
SyS1006	2679	GCCCAAAGCCAAAAACTCACCGAAAAAGCACAG	7268	AQSQKLTEKAQ	11857	SQKLTEK	0.294248	-0.04613
SyS1007	2680	GCCCAAAGACTCCCCAGCCTCAGCGTCGCACAG	7269	AQRLPSLSVAQ	11858	RLPSLSV	0.294218	-0.049
SyS1008	2681	GCCCAAAGTGTTAGTGAGGGTAGTAGGGCACAG	7270	AQSVSEGSRAQ	11859	SVSEGSR	0.294121	-0.18245
SyS1009	2682	GCCCAAAGCATCCCCAGCGTCAGCGCCGCACAG	7271	AQSIPSVSAAQ	11860	SIPSVSA	0.294121	-0.13314
GS526	2683	GCCCAAACTACTAATAATGCTAAGAGTGCACAG	7272	AQTTNNAKSAQ	11861	TTNNAKS	0.294054	-0.13141
SyS1010	2684	GCCCAAGCGAGTGGGGAGGCTTCGACTGCACAG	7273	AQASGEASTAQ	11862	ASGEAST	0.293904	-0.11222
SyS1011	2685	GCCCAAGATAATAATTCGAGTATTGCTGCACAG	7274	AQDNNSSIAAQ	11863	DNNSSIA	0.293817	-0.21202
SyS1012	2686	GCCCAAGTCCACGACAACAGCAAACTCGCACAG	7275	AQVHDNSKLAQ	11864	VHDNSKL	0.293384	-0.0119
SyS1013	2687	GCCCAATCTACTTTGGCGGGTTCGGAGGCACAG	7276	AQSTLAGSEAQ	11865	STLAGSE	0.293384	-0.18527
SyS1014	2688	GCCCAACCTGAGAAGAGTCATTCGTCGGCACAG	7277	AQPEKSHSSAQ	11866	PEKSHSS	0.293335	0.032955
GS529	2689	GCCCAACAAATGCTCAGAGCCAGCGTCGCACAG	7278	AQQMLRASVAQ	11867	QMLRASV	0.293248	-0.17022
SyS1015	2690	GCCCAAGCCCTCAGCAACAACATCACCGCACAG	7279	AQALSNNITAQ	11868	ALSNNIT	0.293202	0.023276
SyS1016	2691	GCCCAAAGTTTGGCGAATCAGTTGCCTGCACAG	7280	AQSLANQLPAQ	11869	SLANQLP	0.29314	-0.10658
SyS1017	2692	GCCCAAGAACAAAGCAGACTCCAAACCGCACAG	7281	AQEQSRLQTAQ	11870	EQSRLQT	0.292969	0.059223
SyS1018	2693	GCCCAAAATTTGTCTCAGAATGTTATGGCACAG	7282	AQNLSQNVMAQ	11871	NLSQNVM	0.292952	-0.04783
SyS1019	2694	GCCCAAAGCCACAAACTCAGCAGCAGCGCACAG	7283	AQSHKLSSSAQ	11872	SHKLSSS	0.29295	0.045078
GP122	2695	GCCCAACCTACTAATACTAAGACGGCGGCACAG	7284	AQPTNTKTAAQ	11873	PTNTKTA	0.292879	-0.0737
GS530	2696	GCCCAAATGAATCCGGCTACTGTGGCTGCACAG	7285	AQMNPATVAAQ	11874	MNPATVA	0.29272	-0.03446
SyS1021	2697	GCCCAAAAGATTGAGCGTACGAATTTTGCACAG	7286	AQKIERTNFAQ	11875	KIERTNF	0.292715	-0.1986

FIG. 33 (Continued)

GS532	2698	GCCCAAACTAGTCCTACGTATAAGTTGGCACAG	7287	AQTSPTYKLAQ	11876	TSPTYKL	0.292683	-0.16394
SyS1022	2699	GCCCAAAGGAGTGATCATATTGATTATGCACAG	7288	AQRSDHIDYAQ	11877	RSDHIDY	0.292545	-0.17314
GS533	2700	GCCCAAACTCTTGGTCTGAATACTAATGCACAG	7289	AQTLGLNTNAQ	11878	TLGLNTN	0.29252	-0.08599
GS534	2701	GCCCAACCCCTCAGCAACCACGGCACCGCACAG	7290	AQPLSNHGTAQ	11879	PLSNHGT	0.292259	-0.14779
SyS1023	2702	GCCCAAGCCGTCAGCAGACTCCCCATGGCACAG	7291	AQAVSRLPMAQ	11880	AVSRLPM	0.292237	-0.0617
SyS1024	2703	GCCCAACTCCTCACCGAAAGCAAAATGGCACAG	7292	AQLLTESKMAQ	11881	LLTESKM	0.292116	-0.05872
GS535	2704	GCCCAACATATGAGGACGGATACTGCTGCACAG	7293	AQHMRTDTAAQ	11882	HMRTDTA	0.292093	0.026545
SS65	2705	GCCCAAAGTCTTACGGTTAATGCGGCTGCACAG	7294	AQSLTVNAAAQ	11883	SLTVNAA	0.292051	-0.35371
SyS1025	2706	GCCCAAAACCCCAACGGCGTCACCGTCGCACAG	7295	AQNPNGVTVAQ	11884	NPNGVTV	0.292021	0.126305
GS536	2707	GCCCAAACTACTAAGTTGCCGACTCTTGCACAG	7296	AQTTKLPTLAQ	11885	TTKLPTL	0.291897	-0.16241
GS537	2708	GCCCAAAATTCTACGTCGAAGCAGCTGGCACAG	7297	AQNSTSKQLAQ	11886	NSTSKQL	0.291795	-0.10165
SyS1026	2709	GCCCAAACTTTGGGGTCGTCTAATACTGCACAG	7298	AQTLGSSNTAQ	11887	TLGSSNT	0.29177	0.260145
SyS1027	2710	GCCCAACCGCGTGCGACTGATCCGCAGGCACAG	7299	AQPRATDPQAQ	11888	PRATDPQ	0.291721	-0.15534
SyS1028	2711	GCCCAAAGCCTCCTCAACAAAACCACCGCACAG	7300	AQSLLNKTTAQ	11889	SLLNKTT	0.291681	-0.03372
SyS1029	2712	GCCCAACACAAAAAAGCGACGGCAGCCCCGCACAG	7301	AQQKSDGSPAQ	11890	QKSDGSP	0.291669	-0.06584
SyS1030	2713	GCCCAAACCGTCAGCGGCTTCACCAAAGCACAG	7302	AQTVSGFTKAQ	11891	TVSGFTK	0.291528	-0.16386
SyS1031	2714	GCCCAAACCGTCCTCGTCAAAAGCACCGCACAG	7303	AQTVLVKSTAQ	11892	TVLVKST	0.291496	-0.03529
SyS1032	2715	GCCCAAGGGGGCTCATATTTCTAATCCTGCACAG	7304	AQGAHISNPAQ	11893	GAHISNP	0.291472	-0.05008
SyS1033	2716	GCCCAAGAACCCAGCATCCCCAGACCCGCACAG	7305	AQEPSIPRPAQ	11894	EPSIPRP	0.291443	-0.01064
GS538	2717	GCCCAAGGCACCGTCCAAGCCAGACAAGCACAG	7306	AQGTVQARQAQ	11895	GTVQARQ	0.291432	-0.12617
GS539	2718	GCCCAAAATAATCATAATTATGTGGATGCACAG	7307	AQNNHNYVDAQ	11896	NNHNYVD	0.291265	-0.18099
SyS1034	2719	GCCCAAAGGACGGCGAGTGTTAGTTTGGCACAG	7308	AQRTASVSLAQ	11897	RTASVSL	0.291215	-0.02711
SyS1035	2720	GCCCAAATCAGCATGGACAACCACAGAGCACAG	7309	AQISMDNHRAQ	11898	ISMDNHR	0.291187	-0.14425
GS540	2721	GCCCAAAGTGATGGGCATAATCATTCTGCACAG	7310	AQSDGHNHSAQ	11899	SDGHNHS	0.291146	-0.15288
SyS1036	2722	GCCCAAAGCGCCGGCAGCGGCATCGGCGCACAG	7311	AQSAGSGIGAQ	11900	SAGSGIG	0.290985	-0.22527
GS541	2723	GCCCAAAAAGCCACCCTCAGCGAAAAAGCACAG	7312	AQKATLSEKAQ	11901	KATLSEK	0.290766	-0.1747
GS542	2724	GCCCAAATCCACGCCGGCGGCCAAAGAGCACAG	7313	AQIHAGGQRAQ	11902	IHAGGQR	0.290742	-0.07711
SyS1038	2725	GCCCAACTGACTCCTAGTAGTGCGAATGCACAG	7314	AQLTPSSANAQ	11903	LTPSSAN	0.290681	-0.11131
GS543	2726	GCCCAAGACGGCAAAGCCTACAACCACGCACAG	7315	AQDGKAYNHAQ	11904	DGKAYNH	0.290644	-0.08049
GS544	2727	GCCCAATGGTCGGCGCAGACGATGAATGCACAG	7316	AQWSAQTMNAQ	11905	WSAQTMN	0.290564	-0.15855
TS155	2728	GCCCAAAATAGTACGCGGATTATTGTTGCACAG	7317	AQNSTRIIVAQ	11906	NSTRIIV	0.290552	-0.32039
GS545	2729	GCCCAAAAAAACAGCAGCATGCTCCTCGCACAG	7318	AQKNSSMLLAQ	11907	KNSSMLL	0.290508	-0.18457

FIG. 33 (Continued)

GS546	2730	GCCCAAAGACAAGTCAGCGGCACCAGCGCACAG	7319	AQRQVSGTSAQ	11908	RQVSGTS	0.290227	-0.07752
SyS1039	2731	GCCCAACCCGTCACCGGCAACAGCGACGCACAG	7320	AQPVTGNSDAQ	11909	PVTGNSD	0.290223	-0.13048
GS548	2732	GCCCAAATGTACCCCGACAGACACAGCGCACAG	7321	AQMYPDRHSAQ	11910	MYPDRHS	0.29019	-0.15227
SyS1040	2733	GCCCAAACCTACCAAATCGGCGCCGTCGCACAG	7322	AQTYQIGAVAQ	11911	TYQIGAV	0.29007	-0.19723
GS549	2734	GCCCAAAAAACCGGCAGCCTCAGCGCCGCACAG	7323	AQKTGSLSAAQ	11912	KTGSLSA	0.289983	-0.06165
SyS1041	2735	GCCCAAATCATCCCCGCCAGCAGCCCCCGCACAG	7324	AQIIPASSPAQ	11913	IIPASSP	0.289839	0.121455
GS550	2736	GCCCAAGACAACCAAGGCACCAAACACGCACAG	7325	AQDNQGTKHAQ	11914	DNQGTKH	0.289725	-0.03079
GS551	2737	GCCCAAAGCTACAAAGAAAGCCCCAGCGCACAG	7326	AQSYKESPSAQ	11915	SYKESPS	0.28952	-0.05844
SyS1042	2738	GCCCAAGCCATCATCAGCAACAACAGAGCACAG	7327	AQAIISNNRAQ	11916	AIISNNR	0.289509	-0.09122
SyS1043	2739	GCCCAAACCGACCAAATCAGAACCTACGCACAG	7328	AQTDQIRTYAQ	11917	TDQIRTY	0.289464	-0.12291
SyS1044	2740	GCCCAACACAGCGCCACCAACATCGACGCACAG	7329	AQHSATNIDAQ	11918	HSATNID	0.289436	-0.08891
SyS1045	2741	GCCCAAGGCACCGTCAACATCAGCGCCGCACAG	7330	AQGTVNISAAQ	11919	GTVNISA	0.2894	-0.13798
SyS1046	2742	GCCCAAGCTGTTGTTCCGGCTATGCAGGCACAG	7331	AQAVVPAMQAQ	11920	AVVPAMQ	0.2894	-0.23255
SyS1047	2743	GCCCAAATCCCCAGAAGCGACCCCAGCGCACAG	7332	AQIPRSDPSAQ	11921	IPRSDPS	0.289334	0.133056
GS553	2744	GCCCAAACTAAGTATACGTTGCAGAGTGCACAG	7333	AQTKYTLQSAQ	11922	TKYTLQS	0.28888	-0.06245
SyS1050	2745	GCCCAATCTCTGCGTGAGACGAGTATTGCACAG	7334	AQSLRETSIAQ	11923	SLRETSI	0.288816	-0.08828
SyS1051	2746	GCCCAAGAGGGTGATAATAAGCGGTTGGCACAG	7335	AQEGDNKRLAQ	11924	EGDNKRL	0.288603	-0.16397
SyS1052	2747	GCCCAAATCGTCAGCAGCACCAGCAGCGCACAG	7336	AQIVSSTSSAQ	11925	IVSSTSS	0.28856	0.01345
GS554	2748	GCCCAATTGGTGAATTCTGGGGCGCATGCACAG	7337	AQLVNSGAHAQ	11926	LVNSGAH	0.288432	-0.09841
SyS1053	2749	GCCCAACGTACGTCGGATAATCAGACGGCACAG	7338	AQRTSDNQTAQ	11927	RTSDNQT	0.288338	0.057271
GS555	2750	GCCCAACCCGACGGCAAAAGCCTCGCCGCACAG	7339	AQPDGKSLAAQ	11928	PDGKSLA	0.288271	-0.11074
SyS1054	2751	GCCCAACACAAAAACATGCTCGAAACCGCACAG	7340	AQHKNMLETAQ	11929	HKNMLET	0.288245	-0.17678
GS556	2752	GCCCAACTCAGCCCCGGCGTCACCGCCGCACAG	7341	AQLSPGVTAAQ	11930	LSPGVTA	0.288083	-0.08353
TS156	2753	GCCCAAACCAACCACACCAGAAACACCGCACAG	7342	AQTNHTRNTAQ	11931	TNHTRNT	0.288053	0.024621
SyS1055	2754	GCCCAACTCGGCGACAGCGAAAGAAACGCACAG	7343	AQLGDSERNAQ	11932	LGDSERN	0.288003	-0.13314
SyS1056	2755	GCCCAACTCCTCAAAATCGAACAAATGGCACAG	7344	AQLLKIEQMAQ	11933	LLKIEQM	0.288003	-0.17072
GS557	2756	GCCCAAAGCCACCTCAAAGAACACCCCGCACAG	7345	AQSHLKEHPAQ	11934	SHLKEHP	0.287866	-0.03141
SS68	2757	GCCCAACCCATCGACACAACAGACAATACGCACAG	7346	AQPIDNRQYAQ	11935	PIDNRQY	0.287402	-0.31048
SyS1058	2758	GCCCAAGATATGCATTCGGGGGTGAAGGCACAG	7347	AQDMHSGVKAQ	11936	DMHSGVK	0.287371	-0.10493
SyS1059	2759	GCCCAACCTTCGTCGCCTATTCCGAATGCACAG	7348	AQPSSPIPNAQ	11937	PSSPIPN	0.287367	-0.19353
SyS1061	2760	GCCCAACTCAGCAGCACCCTCGACGACGCACAG	7349	AQLSSTLDDAQ	11938	LSSTLDD	0.287224	-0.19011
SyS1062	2761	GCCCAACCCAACACCGCCCACAGCAGCGCACAG	7350	AQPNTAHSSAQ	11939	PNTAHSS	0.287109	-0.03284

FIG. 33 (Continued)

SyS1063	2762	GCCCAAGCCACCAGAGTCGACGTCATCGCACAG	7351	AQATRVDVIAQ	11940	ATRVDVI	0.28708	0.115394
GS558	2763	GCCCAAAGCACCAACGTCACCACCGTCGCACAG	7352	AQSTNVTTVAQ	11941	STNVTTV	0.287059	-0.10292
SyS1064	2764	GCCCAATATGGTAATAATAGTTTTAGTGCACAG	7353	AQYGNNSFSAQ	11942	YGNNSFS	0.28698	0.020733
SyS1065	2765	GCCCAACCCACCGCCAAACCCATGTACGCACAG	7354	AQPTAKPMYAQ	11943	PTAKPMY	0.28686	-0.0907
SyS1066	2766	GCCCAACTCCCCAACCTCCCCACCATCGCACAG	7355	AQLPNLPTIAQ	11944	LPNLPTI	0.286792	-0.17799
GS560	2767	GCCCAAACTAGGTTGCCGAATATTAGTGCACAG	7356	AQTRLPNISAQ	11945	TRLPNIS	0.286766	-0.17022
GS561	2768	GCCCAACATAAGCATTCTACGCAGGGTGCACAG	7357	AQHKHSTQGAQ	11946	HKHSTQG	0.286766	-0.17022
GS562	2769	GCCCAAAATGGTACGAATGGTTTTACTGCACAG	7358	AQNGTNGFTAQ	11947	NGTNGFT	0.286695	-0.06992
SyS1067	2770	GCCCAAAGCACCGACGCCATCAGATTCGCACAG	7359	AQSTDAIRFAQ	11948	STDAIRF	0.286524	-0.12222
GS563	2771	GCCCAACTGGTTCGTGATCATACGGCGGCACAG	7360	AQLVRDHTAAQ	11949	LVRDHTA	0.286491	-0.11663
SyS1069	2772	GCCCAAATCAGCCTCGGCTACAGCAAAGCACAG	7361	AQISLGYSKAQ	11950	ISLGYSK	0.286475	-0.21557
SyS1070	2773	GCCCAACTTTTTGGTTCTTCGCATACGGCACAG	7362	AQLFGSSHTAQ	11951	LFGSSHT	0.286475	-0.21557
SyS1071	2774	GCCCAAAGCACCATCACCCCCAGACTCGCACAG	7363	AQSTITPRLAQ	11952	STITPRL	0.286416	-0.16587
SyS1072	2775	GCCCAACAGATTACTAATGGGCTGCGTGCACAG	7364	AQQITNGLRAQ	11953	QITNGLR	0.286347	-0.11252
SyS1073	2776	GCCCAAACGACGGAGTATAATATTCGTGCACAG	7365	AQTTEYNIRAQ	11954	TTEYNIR	0.286245	-0.1101
SyS1074	2777	GCCCAAACCGACCTCGGCAGAGGCACCGCACAG	7366	AQTDLGRGTAQ	11955	TDLGRGT	0.286128	0.04021
GS564	2778	GCCCAAGAAAGAAGCCCCACCATCCTCGCACAG	7367	AQERSPTILAQ	11956	ERSPTIL	0.286103	-0.17195
SyS1075	2779	GCCCAACATGGGGATTCTGCGAGGACTGCACAG	7368	AQHGDSARTAQ	11957	HGDSART	0.286062	0.001434
SyS1077	2780	GCCCAATTGAGTGTGCCTAATCAGCAGGCACAG	7369	AQLSVPNQQAQ	11958	LSVPNQQ	0.285811	0.019619
SyS1078	2781	GCCCAAAGCGACGGCCCCGTCCCCAGAGCACAG	7370	AQSDGPVPRAQ	11959	SDGPVPR	0.285737	-0.10136
GS565	2782	GCCCAAAATATGAATCATATTGCTTCTGCACAG	7371	AQNMNHIASAQ	11960	NMNHIAS	0.28572	-0.04994
SyS1079	2783	GCCCAAGTCCCCCAACAGCCCCCCAAAGAGCACAG	7372	AQVPNSPQRAQ	11961	VPNSPQR	0.285696	-0.06754
SS70	2784	GCCCAAGACAGAATGGCCAGCAGCAGAGCACAG	7373	AQDRMASSRAQ	11962	DRMASSR	0.285607	-0.34425
SyS1080	2785	GCCCAATTGCTGTCGAATTCGAGTCAGGCACAG	7374	AQLLSNSSQAQ	11963	LLSNSSQ	0.285424	0.07245
GS567	2786	GCCCAAGAGACGGCGGTGTTGAATCATGCACAG	7375	AQETAVLNHAQ	11964	ETAVLNH	0.285405	-0.14868
GS568	2787	GCCCAAGAACAAAGAACCCCCAGCCCCGCACAG	7376	AQEQRTPSPAQ	11965	EQRTPSP	0.285349	-0.02041
SyS1081	2788	GCCCAACAACACCTCAACGGCAGCATCGCACAG	7377	AQQHLNGSIAQ	11966	QHLNGSI	0.285255	0.080069
SyS1082	2789	GCCCAAAGCGTCCTCCAAGTCGAAGGCGCACAG	7378	AQSVLQVEGAQ	11967	SVLQVEG	0.285245	-0.17259
SyS1083	2790	GCCCAATTTCTGTCGGGTACGACTAAGGCACAG	7379	AQFLSGTTKAQ	11968	FLSGTTK	0.285183	-0.17314
SyS1085	2791	GCCCAAGGTAATCCGAATGATCGGCAGGCACAG	7380	AQGNPNDRQAQ	11969	GNPNDRQ	0.284868	0.038445
SyS1086	2792	GCCCAAACCGACAAAGCCGTCCAAATCGCACAG	7381	AQTDKAVQIAQ	11970	TDKAVQI	0.284813	-0.02105
GS569	2793	GCCCAAGAGAAGTATACGGGTTCGCCTGCACAG	7382	AQEKYTGSPAQ	11971	EKYTGSP	0.284752	-0.08897

FIG. 33 (Continued)

GS570	2794	GCCCAACTCGCCGGCAGCAGAAACCTCGCACAG	7383	AQLAGSRNLAQ	11972	LAGSRNL	0.284402	-0.02848
SyS1087	2795	GCCCAAATGATCCCCAGCACCAACTTCGCACAG	7384	AQMIPSTNFAQ	11973	MIPSTNF	0.28421	-0.0822
GS572	2796	GCCCAACCTTTGACGGGTTCTAGTGCTGCACAG	7385	AQPLTGSSAAQ	11974	PLTGSSA	0.284117	-0.10557
SyS1088	2797	GCCCAAAGCGTCAGCAACGCCTTCAGCGCACAG	7386	AQSVSNAFSAQ	11975	SVSNAFS	0.284101	-0.196
GS573	2798	GCCCAACAGGGGGGTCAGGCGCTTAGGGCACAG	7387	AQQGGQALRAQ	11976	QGGQALR	0.283993	-0.16337
GS574	2799	GCCCAACACCCCGGCCAAACCCTCAGCGCACAG	7388	AQHPGQTLSAQ	11977	HPGQTLS	0.28394	-0.15586
GS575	2800	GCCCAAAAGGAGTATAATACGTATAGTGCACAG	7389	AQKEYNTYSAQ	11978	KEYNTYS	0.283589	-0.1701
SyS1089	2801	GCCCAAACCCACACCGCCCAACCCAGCGCACAG	7390	AQTHTAQPSAQ	11979	THTAQPS	0.283513	-0.14667
SyS1090	2802	GCCCAAATGACGCCGCAGGTTCCTCGTGCACAG	7391	AQMTPQVPRAQ	11980	MTPQVPR	0.283499	-0.15617
SyS1091	2803	GCCCAAACTCGGGTTTCTAGTCTTGCGGCACAG	7392	AQTRVSSLAAQ	11981	TRVSSLA	0.283423	-0.15011
SyS1092	2804	GCCCAACACGCCGACCTCAAAATCGTCGCACAG	7393	AQHADLKIVAQ	11982	HADLKIV	0.283397	-0.05645
SyS1093	2805	GCCCAAAACAGAAACACCGACACCGTCGCACAG	7394	AQNRNTDTVAQ	11983	NRNTDTV	0.283396	-0.01003
SyS1094	2806	GCCCAAGCCCACAAAGACAACCACCTCGCACAG	7395	AQAHKDNHLAQ	11984	AHKDNHL	0.283218	-0.13192
SyS1095	2807	GCCCAATCTGTTCCTGTGCCTGCTGCTGCACAG	7396	AQSVPVPAAAQ	11985	SVPVPAA	0.283166	-0.09997
GS577	2808	GCCCAACAAACCAACAGCGCCCTCATGGCACAG	7397	AQQTNSALMAQ	11986	QTNSALM	0.283146	-0.11549
GS578	2809	GCCCAACTCGGCAGAGACACCGCCTACGCACAG	7398	AQLGRDTAYAQ	11987	LGRDTAY	0.283146	-0.09664
SyP48	2810	GCCCAAAGTTCTGTTGCTCTTGTTGTTGCACAG	7399	AQSSVALVVAQ	11988	SSVALVV	0.282934	-0.04243
GS579	2811	GCCCAAATGAACGCCGCCACCACCCAAGCACAG	7400	AQMNAATTQAQ	11989	MNAATTQ	0.282892	-0.11642
GS581	2812	GCCCAAATGGTTTCTACGGCTAAGGATGCACAG	7401	AQMVSTAKDAQ	11990	MVSTAKD	0.282806	-0.01428
SyS1097	2813	GCCCAACTGGGTCAGATGTATTCTCCGGCACAG	7402	AQLGQMYSPAQ	11991	LGQMYSP	0.28245	-0.19723
GS583	2814	GCCCAAGATTCGAAGGAGAAGCCTAATGCACAG	7403	AQDSKEKPNAQ	11992	DSKEKPN	0.282074	-0.18816
SyS1098	2815	GCCCAAAGCCCCCCCGTCCAAGGCCTCGCACAG	7404	AQSPPVQGLAQ	11993	SPPVQGL	0.28194	-0.10889
SyS1099	2816	GCCCAAACTGCGTCGGATCGTTTGCCGGCACAG	7405	AQTASDRLPAQ	11994	TASDRLP	0.281925	-0.04427
SyS1100	2817	GCCCAAATCTACAGCCCCACCACCGTCGCACAG	7406	AQIYSPTTVAQ	11995	IYSPTTV	0.28173	0.009655
SyS1101	2818	GCCCAAAGTCAGTCTAAGGAGCTGCGGGCACAG	7407	AQSQSKELRAQ	11996	SQSKELR	0.28162	-0.14795
SyS1102	2819	GCCCAAGGCGCCCTCAACGGCGGCGTCGCACAG	7408	AQGALNGGVAQ	11997	GALNGGV	0.28162	-0.09251
GS585	2820	GCCCAAACTATTATTAATTCGAGTAAGGCACAG	7409	AQTIINSSKAQ	11998	TIINSSK	0.281489	-0.18054
GS586	2821	GCCCAACCTGTGAGTGCTCAGCCTGTTGCACAG	7410	AQPVSAQPVAQ	11999	PVSAQPV	0.281416	-0.16663
SyS1103	2822	GCCCAATCTAATGAGGCGGTGACTAATGCACAG	7411	AQSNEAVTNAQ	12000	SNEAVTN	0.281348	-0.11723
SyS1104	2823	GCCCAAGCGAGTATGCAGATGAATCGTGCACAG	7412	AQASMQMNRAQ	12001	ASMQMNR	0.281339	-0.06586
SyS1105	2824	GCCCAAAGCGTCGGCAAAAGCGAACTCGCACAG	7413	AQSVGKSELAQ	12002	SVGKSEL	0.281132	0.014504
SyS1106	2825	GCCCAATCTCAGGTTAATCCTTCTAGTGCACAG	7414	AQSQVNPSSAQ	12003	SQVNPSS	0.280883	-0.06161

FIG. 33 (Continued)

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SyS1107	2826	GCCCAAATTACGACTGATCAGCCTTTTGCACAG	7415	AQITTDQPFAQ	12004	ITTDQPF	0.280883	-0.16466
SyS1109	2827	GCCCAAAATAATGGGTCTGGTTCTTATGCACAG	7416	AQNNGSGSYAQ	12005	NNGSGSY	0.280653	-0.22064
GS587	2828	GCCCAAACCCTCGCCAGAAGCAGCGTCGCACAG	7417	AQTLARSSVAQ	12006	TLARSSV	0.280506	0.024598
GS588	2829	GCCCAAAACGCCAGCACCATGACCAGAGCACAG	7418	AQNASTMTRAQ	12007	NASTMTR	0.280372	-0.01638
GP124	2830	GCCCAAACGAATCAGGTGAGGTATGTTGCACAG	7419	AQTNQVRYVAQ	12008	TNQVRYV	0.280321	-0.06218
GS589	2831	GCCCAAAGCACCCAAAGCCCCAACAGAGCACAG	7420	AQSTQSPNRAQ	12009	STQSPNR	0.280294	-0.0613
GS590	2832	GCCCAAGATACGGGGGCGAGGGGGTTGGCACAG	7421	AQDTGARGLAQ	12010	DTGARGL	0.279908	-0.09508
SyS1110	2833	GCCCAACCTGGTTCTCATGTGGTGGCTGCACAG	7422	AQPGSHVVAAQ	12011	PGSHVVA	0.279813	-0.10701
SyS1112	2834	GCCCAAGCCAACGGCATCGAAACCAAAGCACAG	7423	AQANGIETKAQ	12012	ANGIETK	0.279639	-0.14768
SyS1113	2835	GCCCAAGCGCATGGTCAGGTGCAGGAGGGCACAG	7424	AQAHGQVQEAQ	12013	AHGQVQE	0.279602	-0.15374
SyS1114	2836	GCCCAAGCTCTGAGTCATGATCTTTCGGCACAG	7425	AQALSHDLSAQ	12014	ALSHDLS	0.279563	-0.15981
SyS1115	2837	GCCCAACTCGGCAGCAGCCTCACCGCCGCACAG	7426	AQLGSSLTAAQ	12015	LGSSLTA	0.279545	-0.0211
SS74	2838	GCCCAAGGCAACAACACCGCCAAACTCGCACAG	7427	AQGNNTAKLAQ	12016	GNNTAKL	0.279413	-0.32548
SyS1116	2839	GCCCAAAATTATGCTCAGTCTGCGCTTGCACAG	7428	AQNYAQSALAQ	12017	NYAQSAL	0.279327	-0.19011
GS592	2840	GCCCAAGATTCGCAGAGTAAGACTTTTGCACAG	7429	AQDSQSKTFAQ	12018	DSQSKTF	0.279314	-0.15955
TS157	2841	GCCCAAACTAATCATGTTAAGTTTACGGCACAG	7430	AQTNHVKFTAQ	12019	TNHVKFT	0.279279	-0.09196
GS593	2842	GCCCAAAGCACACCCCACCCACGGCCTCGCACAG	7431	AQSTPTHGLAQ	12020	STPTHGL	0.279226	-0.09374
SyS1117	2843	GCCCAAAGTGTGGGGTTGACGATGGTGGCACAG	7432	AQSVGLTMVAQ	12021	SVGLTMV	0.279206	-0.20224
SyS1118	2844	GCCCAAATTCCGAAGGGTTCTGGGGCGGCACAG	7433	AQIPKGSGAAQ	12022	IPKGSGA	0.279091	0.080236
GS594	2845	GCCCAAACCGCCCAAGCCAGAGTCCTCGCACAG	7434	AQTAQARVLAQ	12023	TAQARVL	0.279047	-0.1122
GS595	2846	GCCCAATGGCACGCCCGGCAGCGTCGGCGCACAG	7435	AQWHAGSVGAQ	12024	WHAGSVG	0.279017	-0.09667
SyS1119	2847	GCCCAATCGCAGTCTCTTTTGGTTGAGGCACAG	7436	AQSQSLLVEAQ	12025	SQSLLVE	0.278987	-0.22042
SyS1120	2848	GCCCAAAATAATAGTGGGCCTTTGAAGGCACAG	7437	AQNNSGPLKAQ	12026	NNSGPLK	0.278922	-0.21078
SyS1121	2849	GCCCAAAGGGATAATGCTATTGAGCATGCACAG	7438	AQRDNAIEHAQ	12027	RDNAIEH	0.278763	-0.17259
GS597	2850	GCCCAAACTATGTCGAATATTACGAGGGGCACAG	7439	AQTMSNITRAQ	12028	TMSNITR	0.278669	0.034782
SyS1122	2851	GCCCAACTCAGCACCCTCAGCCAAATGGCACAG	7440	AQLSTLSQMAQ	12029	LSTLSQM	0.278541	-0.0734
GS598	2852	GCCCAAGTCATGCAAAACTACGGCAGCGCACAG	7441	AQVMQNYGSAQ	12030	VMQNYGS	0.278395	-0.1774
SyS1123	2853	GCCCAAACTCATTCGGCGCAGCAGAATGCACAG	7442	AQTHSAQQNAQ	12031	THSAQQN	0.277996	-0.10236
GS601	2854	GCCCAATCGGTTCCTCCGAATAGGAATGCACAG	7443	AQSVPPNRNAQ	12032	SVPPNRN	0.277804	-0.13857
SyS1125	2855	GCCCAATCTGTTGCGGCGAGTCCTCGTGCACAG	7444	AQSVAASPRAQ	12033	SVAASPR	0.277759	-0.03359
SyS1127	2856	GCCCAAAATAATACTTCGACGCTGCATGCACAG	7445	AQNNTSTLHAQ	12034	NNTSTLH	0.277642	-0.19739
SyS1128	2857	GCCCAAAATCTTTCTGATCATATGCCGGCACAG	7446	AQNLSDHMPAQ	12035	NLSDHMP	0.277561	-0.22803

FIG. 33 (Continued)

GP125	2858	GCCCAAGGTCTGTATGCTACGACTTCTGCACAG	7447	AQGLYATTSAQ	12036	GLYATTS	0.277546	0.324596
SyS1129	2859	GCCCAACGTAATGGTGGTGCGAATGTTGCACAG	7448	AQRNGGANVAQ	12037	RNGGANV	0.277332	0.271066
SyS1130	2860	GCCCAATTCCACAACCTCACCCTCAGCGCACAG	7449	AQFHNLTLSAQ	12038	FHNLTLS	0.277251	-0.09337
SyS1131	2861	GCCCAATGGAAGAGTCCTGCTGCTATTGCACAG	7450	AQWKSPAAIAQ	12039	WKSPAAI	0.277234	-0.14405
SyS1132	2862	GCCCAACCCAAAGGCCTCAGCGGCGAAGCACAG	7451	AQPKGLSGEAQ	12040	PKGLSGE	0.277183	0.248416
GS603	2863	GCCCAATCGCATTATCAGTTGCATCCGGCACAG	7452	AQSHYQLHPAQ	12041	SHYQLHP	0.27717	-0.17005
SyS1133	2864	GCCCAAACCACCTTCAGAAGCGCCCCCGCACAG	7453	AQTTFRSAPAQ	12042	TTFRSAP	0.277074	-0.08464
SyS1134	2865	GCCCAATACGACGCCACCCACAGCGCCGCACAG	7454	AQYDATHSAAQ	12043	YDATHSA	0.27674	-0.16889
GS605	2866	GCCCAAAATCAGTCGGGTCCGTTGAAGGCACAG	7455	AQNQSGPLKAQ	12044	NQSGPLK	0.276624	-0.00392
SyS1135	2867	GCCCAACACACCAACATGACCAGCATGGCACAG	7456	AQHTNMTSMAQ	12045	HTNMTSM	0.276609	0.123822
SyS1136	2868	GCCCAACATATGAAGAGTCAGCTGCCGGCACAG	7457	AQHMKSQLPAQ	12046	HMKSQLP	0.276324	0.098421
GS606	2869	GCCCAAAAACTCCCCACCATGGCCAACGCACAG	7458	AQKLPTMANAQ	12047	KLPTMAN	0.275986	-0.0594
GS607	2870	GCCCAAGTTGGGACTAATGCGAATCATGCACAG	7459	AQVGTNANHAQ	12048	VGTNANH	0.275965	-0.13666
GP126	2871	GCCCAATTGAAGACTGATCCTTTTCTGGCACAG	7460	AQLKTDPFLAQ	12049	LKTDPFL	0.275884	-0.07259
GS608	2872	GCCCAACACCTCCAACAAAACCTCACCGCACAG	7461	AQHLQQNLTAQ	12050	HLQQNLT	0.275812	-0.16146
SyS1137	2873	GCCCAAACTCAGAATAAGAATTCTCATGCACAG	7462	AQTQNKNSHAQ	12051	TQNKNSH	0.275704	-0.04648
SS76	2874	GCCCAACCCAACGCCCAAAGCCAAAGAGCACAG	7463	AQPNAQSQRAQ	12052	PNAQSQR	0.27556	-0.34576
SyS1138	2875	GCCCAAGGTAGTGGTCATTCGACTCTTGCACAG	7464	AQGSGHSTLAQ	12053	GSGHSTL	0.275521	-0.11616
SyS1139	2876	GCCCAATTGACGGGTAGGCTTGAGAAGGCACAG	7465	AQLTGRLEKAQ	12054	LTGRLEK	0.275499	-0.06888
SyS1140	2877	GCCCAACCCAGCAGAAACGCCAGCCTCGCACAG	7466	AQPSRNASLAQ	12055	PSRNASL	0.275483	-0.0216
GS610	2878	GCCCAAGTTTTTAGGACGTCGGATCTTGCACAG	7467	AQVFRTSDLAQ	12056	VFRTSDL	0.275429	-0.12297
GS611	2879	GCCCAAATCGCCAGCACCTACAGCAGCGCACAG	7468	AQIASTYSSAQ	12057	IASTYSS	0.275379	0.042246
SyS1141	2880	GCCCAAACCATCAACCACGCCACCAGCGCACAG	7469	AQTINHATSAQ	12058	TINHATS	0.275307	0.060839
SyS1142	2881	GCCCAAGCTATGAATAATCGTGCTCATGCACAG	7470	AQAMNNRAHAQ	12059	AMNNRAH	0.275089	-0.19723
GS612	2882	GCCCAATCGCATCATGAGCAGGTTTCTGCACAG	7471	AQSHHEQVSAQ	12060	SHHEQVS	0.274982	-0.12807
SyS1143	2883	GCCCAATCGGGGGTTACTAGTAAGCTTGCACAG	7472	AQSGVTSKLAQ	12061	SGVTSKL	0.274938	-0.12208
SyS1144	2884	GCCCAAGTGTTTACTAATGATGTGCCTGCACAG	7473	AQVFTNDVPAQ	12062	VFTNDVP	0.274934	-0.14041
SyS1145	2885	GCCCAAGCTGCGGTGTTGGTGGCTCCGGCACAG	7474	AQAAVLVAPAQ	12063	AAVLVAP	0.274757	-0.22434
GS613	2886	GCCCAACCCACCGCCGGCAGATACCTCGCACAG	7475	AQPTAGRYLAQ	12064	PTAGRYL	0.274712	-0.18816
GS614	2887	GCCCAACATCTTAATTCGCAGAATATGGCACAG	7476	AQHLNSQNMAQ	12065	HLNSQNM	0.274394	-0.04601
SyS1146	2888	GCCCAACCCAACCCCAACGTCGGCAGAGCACAG	7477	AQPNPNVGRAQ	12066	PNPNVGR	0.274299	0.025701
SyS1147	2889	GCCCAAGCTAGTGAGAATCTTCGTTCGGCACAG	7478	AQASENLRSAQ	12067	ASENLRS	0.2742	-0.12824

FIG. 33 (Continued)

GP127	2890	GCCCAAAATAGTCCGATGAGGACTGCTGCACAG	7479	AQNSPMRTAAQ	12068	NSPMRTA	0.273993	-0.07315
SyP49	2891	GCCCAAGTTGCTGGTACGAATCAGCCGGCACAG	7480	AQVAGTNQPAQ	12069	VAGTNQP	0.273896	-0.04327
SyS1149	2892	GCCCAAGGGTCGGAGTCTAGTATGCGGGCACAG	7481	AQGSESSMRAQ	12070	GSESSMR	0.273598	-0.03614
GS616	2893	GCCCAAACGTTGGCGTCTGCTTCGCGGGGCACAG	7482	AQTLASASRAQ	12071	TLASASR	0.273592	-0.14592
SyS1150	2894	GCCCAAATTTCGCAGTCTTGGACTGCTGCACAG	7483	AQISQSWTAAQ	12072	ISQSWTA	0.273499	-0.00996
SyS1151	2895	GCCCAAAGTGGTGATTCGAGGTCTACTGCACAG	7484	AQSGDSRSTAQ	12073	SGDSRST	0.273214	-0.06701
SyS1152	2896	GCCCAACCCAACATCAAAACCGACCTCGCACAG	7485	AQPNIKTDLAQ	12074	PNIKTDL	0.273105	-0.03104
SyS1154	2897	GCCCAATGGCAAGCCACCGACACCGCCGCACAG	7486	AQWQATDTAAQ	12075	WQATDTA	0.273081	-0.15981
GS617	2898	GCCCAAAACAACAACGTCGTCACCTACGCACAG	7487	AQNNNVVTYAQ	12076	NNNVVTY	0.273055	-0.01771
GS618	2899	GCCCAAAAGGCTATTAGTACGGCTAATGCACAG	7488	AQKAISTANAQ	12077	KAISTAN	0.273038	-0.04153
GS619	2900	GCCCAAAGGCAGGAGGTGAGTGGTAATGCACAG	7489	AQRQEVSGNAQ	12078	RQEVSGN	0.273031	-0.13857
SyS1155	2901	GCCCAATGGCAAGACCTCAACGTCGTCGCACAG	7490	AQWQDLNVVAQ	12079	WQDLNVV	0.272986	-0.19496
SyS1157	2902	GCCCAAAGTCGTTCTGATAATCCTCTGGCACAG	7491	AQSRSDNPLAQ	12080	SRSDNPL	0.272715	-0.01048
GP128	2903	GCCCAAATTGGTTCGTCTACTAAGCCTGCACAG	7492	AQIGSSTKPAQ	12081	IGSSTKP	0.272685	-0.07433
SyS1158	2904	GCCCAAAGCCCCCATCATCAACACCAGCGCACAG	7493	AQSPIINTSAQ	12082	SPIINTS	0.272664	-0.00749
GS621	2905	GCCCAAGATAAGGATACTGCTGCTCCTGCACAG	7494	AQDKDTAAPAQ	12083	DKDTAAP	0.272552	-0.17112
SyS1160	2906	GCCCAAAGCAAAGTCGACAGCAGCTACGCACAG	7495	AQSKVDSSYAQ	12084	SKVDSSY	0.272199	0.039017
GS622	2907	GCCCAAACCCTCACCAGAGGCACCCCCGCACAG	7496	AQTLTRGTPAQ	12085	TLTRGTP	0.272157	-0.11459
SyS1161	2908	GCCCAAACCAGAACCAGCCCCATCCAAGCACAG	7497	AQTRTSPIQAQ	12086	TRTSPIQ	0.272145	0.276035
SyS1162	2909	GCCCAACTGACTAGTGCGACTACTAATGCACAG	7498	AQLTSATTNAQ	12087	LTSATTN	0.271967	-0.03654
SyS1163	2910	GCCCAAACGATTAATATTCATTCGGCTGCACAG	7499	AQTINIHSAAQ	12088	TINIHSA	0.271956	0.018437
GS624	2911	GCCCAATCGTTTTCGCCTGAGAATCGTGCACAG	7500	AQSFSPENRAQ	12089	SFSPENR	0.271946	-0.02008
GS625	2912	GCCCAAGGGATGGCTCTGGGGACGGGGGCACAG	7501	AQGMALGTGAQ	12090	GMALGTG	0.271775	-0.1119
SyS1164	2913	GCCCAATACAACGGCACCCAAGGCAGAGCACAG	7502	AQYNGTQGRAQ	12091	YNGTQGR	0.271748	-0.04076
GS626	2914	GCCCAAAACAAACTCCTCGAACACCCCGCACAG	7503	AQNKLLEHPAQ	12092	NKLLEHP	0.271731	-0.12087
SyS1165	2915	GCCCAATATGTTAATAATGTTGCTCCGGCACAG	7504	AQYVNNVAPAQ	12093	YVNNVAP	0.271696	-0.08207
SyS1166	2916	GCCCAATATAGTGTGGTGCATGATAAGGCACAG	7505	AQYSVVHDKAQ	12094	YSVVHDK	0.271642	-0.21921
GS627	2917	GCCCAAGGCCTCGAAACCAGACACATGGCACAG	7506	AQGLETRHMAQ	12095	GLETRHM	0.271626	-0.13881
SyS1167	2918	GCCCAAGCGCCTAATTTGATGGCGGATGCACAG	7507	AQAPNLMADAQ	12096	APNLMAD	0.271598	-0.09085
SyS1168	2919	GCCCAAAACAGCAACGGCATGGCCCCCGCACAG	7508	AQNSNGMAPAQ	12097	NSNGMAP	0.271581	0.042555
SyS1169	2920	GCCCAAAGTTTGAATTATAGTCAGAATGCACAG	7509	AQSLNYSQNAQ	12098	SLNYSQN	0.271519	7.41E-05
SyS1170	2921	GCCCAAACCGAATACGCCAACGGCAGAGCACAG	7510	AQTEYANGRAQ	12099	TEYANGR	0.27145	-0.08881

FIG. 33 (Continued)

GP129	2922	GCCCAACCTCTTGGGCATGTTAGGTCTGCACAG	7511	AQPLGHVRSAQ	12100	PLGHVRS	0.271369	0.161673
GS628	2923	GCCCAACTTCGGGATTCGCCGGGGCTGGCACAG	7512	AQLRDSPGLAQ	12101	LRDSPGL	0.271307	-0.1747
SyS1171	2924	GCCCAAGTTATTAGGTCGAATACTCATGCACAG	7513	AQVIRSNTHAQ	12102	VIRSNTH	0.271216	-0.15781
SyS1172	2925	GCCCAAGCGTCGGTGAGTAATCTTTCGGCACAG	7514	AQASVSNLSAQ	12103	ASVSNLS	0.271028	-0.12012
SyS1173	2926	GCCCAATGGGCCCAAAGAACCAGCCAAGCACAG	7515	AQWAQRTSQAQ	12104	WAQRTSQ	0.271025	-0.17382
GS630	2927	GCCCAAAACGACAAAGGCATGAGCAGAGCACAG	7516	AQNDKGMSRAQ	12105	NDKGMSR	0.270989	-0.07517
GP130	2928	GCCCAACAGAATGATACTCGTAATTATGCACAG	7517	AQQNDTRNYAQ	12106	QNDTRNY	0.270955	-0.07273
SyS1174	2929	GCCCAAGGCGAAGTCGCCGGCAGACTCGCACAG	7518	AQGEVAGRLAQ	12107	GEVAGRL	0.270924	-0.02281
SyS1175	2930	GCCCAAACCACCACCAACACCGTCAGCGCACAG	7519	AQTTTNTVSAQ	12108	TTTNTVS	0.270848	-0.1792
SyS1176	2931	GCCCAACCGGTTATGTCGAATAAGGATGCACAG	7520	AQPVMSNKDAQ	12109	PVMSNKD	0.270622	-0.13314
GS632	2932	GCCCAAAACGGCGGCACCACCTTCATCGCACAG	7521	AQNGGTTFIAQ	12110	NGGTTFI	0.270379	-0.12521
SyS1177	2933	GCCCAAGTTTTGAAGACTACGGCTATTGCACAG	7522	AQVLKTTAIAQ	12111	VLKTTAI	0.270139	-0.19133
SyS1178	2934	GCCCAACCCCCACGGCGTCGGCAGCGCCGCACAG	7523	AQPHGVGSAAQ	12112	PHGVGSA	0.27008	-0.03489
GS635	2935	GCCCAATCTAATGCGCATCCTCTCGGCTGCACAG	7524	AQSNAHPLAAQ	12113	SNAHPLA	0.270011	-0.17958
SyS1179	2936	GCCCAAAAAAGCACCAGCCTCGACCCCGCACAG	7525	AQKSTSLDPAQ	12114	KSTSLDP	0.269961	-0.05312
SyS1180	2937	GCCCAATTCAACAAAACCAACGACATGGCACAG	7526	AQFNKTNDMAQ	12115	FNKTNDM	0.269911	0.039016
SyS1181	2938	GCCCAACACCAAACCAGCGAACTCAGAGCACAG	7527	AQHQTSELRAQ	12116	HQTSELR	0.269505	-0.13316
SyS1182	2939	GCCCAATGGGCCAAAGTCCTCGACAAAGCACAG	7528	AQWAKVLDKAQ	12117	WAKVLDK	0.269376	-0.18042
GS637	2940	GCCCAAATGAGCAGCAACAACAAAAGCGCACAG	7529	AQMSSNNKSAQ	12118	MSSNNKS	0.26924	-0.10804
GS638	2941	GCCCAAGATGGTACTCATTTGAAGCTGGCACAG	7530	AQDGTHLKLAQ	12119	DGTHLKL	0.269216	-0.12903
SyS1183	2942	GCCCAAACGGTTATTAGTGATCAGAGGGCACAG	7531	AQTVISDQRAQ	12120	TVISDQR	0.269208	-0.23296
GS639	2943	GCCCAAATGCACAGCCAACTCCTCCCCGCACAG	7532	AQMHSQLLPAQ	12121	MHSQLLP	0.269185	-0.16394
GP131	2944	GCCCAATCGTCTTATGGGACTGCGGCGGCACAG	7533	AQSSYGTAAAQ	12122	SSYGTAA	0.269078	-0.07134
SyS1184	2945	GCCCAAGTGTTGTCTACGATGGCTGTTGCACAG	7534	AQVLSTMAVAQ	12123	VLSTMAV	0.269054	-0.01394
GS640	2946	GCCCAATCGGCTTCGAATTTTGCGTCTGCACAG	7535	AQSASNFASAQ	12124	SASNFAS	0.268964	-0.14715
GS642	2947	GCCCAAAGTAAGGCTGGTCTGAGTGATGCACAG	7536	AQSKAGLSDAQ	12125	SKAGLSD	0.268902	-0.06703
GS643	2948	GCCCAAATTAATCGGATTGTTAGTGGGGCACAG	7537	AQINRIVSGAQ	12126	INRIVSG	0.268902	-0.0141
SyS1185	2949	GCCCAAAAACTCGACACCCCCGGCAAAGCACAG	7538	AQKLDTPGKAQ	12127	KLDTPGK	0.268816	-0.14647
GS644	2950	GCCCAAATGGATCGTATTGTTAAGATGGCACAG	7539	AQMDRIVKMAQ	12128	MDRIVKM	0.268718	-0.16125
SyS1186	2951	GCCCAAAGAGAAAGAAGCACCGACGCCGCACAG	7540	AQRERSTDAAQ	12129	RERSTDA	0.26861	0.020477
GS645	2952	GCCCAACTCAGAGACAGCACCGGCCACGCACAG	7541	AQLRDSTGHAQ	12130	LRDSTGH	0.268608	-0.08258
SyS1187	2953	GCCCAAATGAGAGGCCAAGGCGTCCACGCACAG	7542	AQMRGQGVHAQ	12131	MRGQGVH	0.268511	0.013557

FIG. 33 (Continued)

GS646	2954	GCCCAAAGCGCCCAAATGATCAGCCCCGCACAG	7543	AQSAQMISPAQ	12132	SAQMISP	0.268303	-0.02348
GP132	2955	GCCCAATGGACGAATGGTGTTGCGAAGGCACAG	7544	AQWTNGVAKAQ	12133	WTNGVAK	0.268192	-0.06433
SyS1189	2956	GCCCAAACCGCCATCAGCATCCAAGTCGCACAG	7545	AQTAISIQVAQ	12134	TAISIQV	0.268061	-0.08809
SyS1190	2957	GCCCAACCGAGTGGTTCGCAGTCGCATGCACAG	7546	AQPSGSQSHAQ	12135	PSGSQSH	0.267911	-0.05043
GS647	2958	GCCCAAAACAGACTCACCCCCGGCAGCGCACAG	7547	AQNRLTPGSAQ	12136	NRLTPGS	0.267734	-0.10327
GS648	2959	GCCCAAATTGCTCTTGAGCATAGGAATGCACAG	7548	AQIALEHRNAQ	12137	IALEHRN	0.267665	-0.12712
SyS1191	2960	GCCCAACCCGCCAGAACCCCCCCCCCAAGCACAG	7549	AQPARTPPQAQ	12138	PARTPPQ	0.267618	-0.20466
SyS1192	2961	GCCCAAATGGGCAAAAGCAACGGCGTCGCACAG	7550	AQMGKSNGVAQ	12139	MGKSNGV	0.267557	0.120243
GS650	2962	GCCCAACCCATCGTCAGAAGCACCAGCGCACAG	7551	AQPIVRSTSAQ	12140	PIVRSTS	0.267482	-0.16484
SyS1193	2963	GCCCAAGTCACCCAACTCAGCCCCAGAGCACAG	7552	AQVTQLSPRAQ	12141	VTQLSPR	0.267246	-0.09677
SyS1194	2964	GCCCAAAAAGCCCTCCTCCCCCTCACCGCACAG	7553	AQKALLPLTAQ	12142	KALLPLT	0.267246	-0.2277
SyS1195	2965	GCCCAAAGCGGCAACAGCAGACTCCAAGCACAG	7554	AQSGNSRLQAQ	12143	SGNSRLQ	0.26719	0.05114
GS652	2966	GCCCAACGTAATCAGAGTGCGCCGCTTGCACAG	7555	AQRNQSAPLAQ	12144	RNQSAPL	0.267054	-0.15048
SyS1196	2967	GCCCAAAACCTCCAAAACATGATCCAAGCACAG	7556	AQNLQNMIQAQ	12145	NLQNMIQ	0.266969	-0.02887
SyS1197	2968	GCCCAATCGTCGTATGATAAGAGTCTTGCACAG	7557	AQSSYDKSLAQ	12146	SSYDKSL	0.266826	0.022044
GS653	2969	GCCCAAGTCCTCGCCAACCAACAAATCGCACAG	7558	AQVLANQQIAQ	12147	VLANQQI	0.266825	-0.06614
GS654	2970	GCCCAACGGACTACGAATGAGCCTACTGCACAG	7559	AQRTTNEPTAQ	12148	RTTNEPT	0.266797	-0.08947
SyS1198	2971	GCCCAAATCGTCAGCAACCAAATGAGCGCACAG	7560	AQIVSNQMSAQ	12149	IVSNQMS	0.266638	-0.17752
GS656	2972	GCCCAAAATGCGACGCATGCTAATGTTGCACAG	7561	AQNATHANVAQ	12150	NATHANV	0.266602	-0.17112
GS657	2973	GCCCAAAAGGGGAATGAGCCGTTGCGGGCACAG	7562	AQKGNEPLRAQ	12151	KGNEPLR	0.266575	-0.1338
SyS1199	2974	GCCCAACTCGGCACCTACCTCAGCCCCGCACAG	7563	AQLGTYLSPAQ	12152	LGTYLSP	0.26632	-0.1489
GS659	2975	GCCCAAACCAACGTCCTCCCCCTCCCCGCACAG	7564	AQTNVLPLPAQ	12153	TNVLPLP	0.266141	-0.11907
SyS1200	2976	GCCCAAAAGCTGTCGCATGAGCCTAGTGCACAG	7565	AQKLSHEPSAQ	12154	KLSHEPS	0.266136	-0.01973
GS660	2977	GCCCAATTCGACAAACAAAACCCCACCGCACAG	7566	AQFDKQNPTAQ	12155	FDKQNPT	0.266099	-0.1328
SyS1201	2978	GCCCAATTTGGGGGTCGTTATGAGAAGGCACAG	7567	AQFGGRYEKAQ	12156	FGGRYEK	0.265902	-0.05312
GS662	2979	GCCCAAACCGTCCAAAACCACACCAACGCACAG	7568	AQTVQNHTNAQ	12157	TVQNHTN	0.265878	-0.05463
SyS1204	2980	GCCCAACCGCTGAAGCCGATGCAGACGGCACAG	7569	AQPLKPMQTAQ	12158	PLKPMQT	0.265871	-0.21941
SyS1205	2981	GCCCAACACAAGGCGAAACCAACCACAGAGCACAG	7570	AQQGETNHRAQ	12159	QGETNHR	0.265871	-0.21941
SyS1206	2982	GCCCAAGCCCACAGCAACATGGTCAACGCACAG	7571	AQAHSNMVNAQ	12160	AHSNMVN	0.26579	0.063826
GS663	2983	GCCCAAGTGAGTGCGAGTAGTAATAAGGCACAG	7572	AQVSASSNKAQ	12161	VSASSNK	0.265618	-0.1774
GS665	2984	GCCCAAACTAATCAGTCGAAGAATTTTGCACAG	7573	AQTNQSKNFAQ	12162	TNQSKNF	0.2653	0.063276
GS666	2985	GCCCAAAAGATGAAGGATATGAGTATTGCACAG	7574	AQKMKDMSIAQ	12163	KMKDMSI	0.265261	-0.17291

FIG. 33 (Continued)

SyS1209	2986	GCCCAACACCCCAGCGGCAGCACCCTCGCACAG	7575	AQHPSGSTLAQ	12164	HPSGSTL	0.265242	-0.09127
SyS1210	2987	GCCCAAATTAAGGATACTGTTTCTGGGGCACAG	7576	AQIKDTVSGAQ	12165	IKDTVSG	0.265119	-0.06613
GS668	2988	GCCCAAATGAACACCCTCACCAACGTCGCACAG	7577	AQMNTLTNVAQ	12166	MNTLTNV	0.264894	-0.09087
SyS1211	2989	GCCCAAACTGATAGTGCTCCGCATCCGGCACAG	7578	AQTDSAPHPAQ	12167	TDSAPHP	0.264791	-0.12222
SyS1212	2990	GCCCAACCCAGACCCGTCAGCAACGGCGCACAG	7579	AQPRPVSNGAQ	12168	PRPVSNG	0.264764	-0.02466
SyS1213	2991	GCCCAATCTGTTGATAGGCGGCCGCAGGCACAG	7580	AQSVDRRPQAQ	12169	SVDRRPQ	0.264728	-0.0604
GS670	2992	GCCCAAATGGATTCTCCTATTAGGAATGCACAG	7581	AQMDSPIRNAQ	12170	MDSPIRN	0.264655	-0.15766
GS671	2993	GCCCAAGCTACGCGTATGAGTATTCCTGCACAG	7582	AQATRMSIPAQ	12171	ATRMSIP	0.264401	-0.16932
SyS1214	2994	GCCCAAAACGTCCCCACCAGCCTCCCCGCACAG	7583	AQNVPTSLPAQ	12172	NVPTSLP	0.264383	0.102058
SyS1215	2995	GCCCAAAGCCTCAGAATCGAAAGCAAAGCACAG	7584	AQSLRIESKAQ	12173	SLRIESK	0.264383	-0.12829
GS673	2996	GCCCAAAACAGCGGCAACACCCTCGGCGCACAG	7585	AQNSGNTLGAQ	12174	NSGNTLG	0.264155	-0.1119
SyS1216	2997	GCCCAACGGTTGGATCATGCTAGTATTGCACAG	7586	AQRLDHASIAQ	12175	RLDHASI	0.264068	-0.07051
SyS1217	2998	GCCCAAAGCCACCTCGTCGTCAGCGCCGCACAG	7587	AQSHLVVSAAQ	12176	SHLVVSA	0.263941	-0.22064
SyS1218	2999	GCCCAACCCGCCAGCCCCAGAAGCCACGCACAG	7588	AQPASPRSHAQ	12177	PASPRSH	0.263752	-0.19618
SyS1219	3000	GCCCAAAACCACACCCTCGTCCCCCCCGCACAG	7589	AQNHTLVPPAQ	12178	NHTLVPP	0.263502	-0.06767
SyS1220	3001	GCCCAAATGCAGATGACGGGGACTGCTGCACAG	7590	AQMQMTGTAAQ	12179	MQMTGTA	0.26338	0.109806
SyS1221	3002	GCCCAAAATACTCAGGCGAATCCGAGGGCACAG	7591	AQNTQANPRAQ	12180	NTQANPR	0.263187	0.026893
GS675	3003	GCCCAAACCAGAGACCTCAACGCCATCGCACAG	7592	AQTRDLNAIAQ	12181	TRDLNAI	0.263161	-0.06205
SyS1222	3004	GCCCAAACCGACGCCAGCAGCCCCTTCGCACAG	7593	AQTDASSPFAQ	12182	TDASSPF	0.263114	-0.20224
SyS1223	3005	GCCCAAGCTGATCAGAGGCAGCCGAAGGCACAG	7594	AQADQRQPKAQ	12183	ADQRQPK	0.263076	-0.0037
SyS1224	3006	GCCCAAGCCGTCAACCCCAACTACGCCGCACAG	7595	AQAVNPNYAAQ	12184	AVNPNYA	0.262974	-0.0907
SyS1225	3007	GCCCAACTGACTGCTACGAATGTTCGGGCACAG	7596	AQLTATNVRAQ	12185	LTATNVR	0.262845	0.030087
SyS1226	3008	GCCCAATTGACTGCGTCTACTTATTCGGCACAG	7597	AQLTASTYSAQ	12186	LTASTYS	0.262777	-0.16344
SyS1227	3009	GCCCAAGGGTCGCGTGATAATTCTGTGGCACAG	7598	AQGSRDNSVAQ	12187	GSRDNSV	0.262777	-0.21921
SyS1228	3010	GCCCAAACTGATACTCAGAATCGGCTTGCACAG	7599	AQTDTQNRLAQ	12188	TDTQNRL	0.262725	-0.15534
GS676	3011	GCCCAAAATAGTACGGTTAATACGGGTGCACAG	7600	AQNSTVNTGAQ	12189	NSTVNTG	0.262505	-0.14811
SyS1229	3012	GCCCAATTGTCTCATGCGATGCGTTCTGCACAG	7601	AQLSHAMRSAQ	12190	LSHAMRS	0.262482	-0.18042
SyS1230	3013	GCCCAACGGCTGCCGATGACTACTATGGCACAG	7602	AQRLPMTTMAQ	12191	RLPMTTM	0.262441	-0.04775
SyS1231	3014	GCCCAACTCTACCACGAAAGCCAAACCGCACAG	7603	AQLYHESQTAQ	12192	LYHESQT	0.262338	-0.18614
SyS1232	3015	GCCCAAATTTTGCATCAGAGTTCGACTGCACAG	7604	AQILHQSSTAQ	12193	ILHQSST	0.262234	0.103448
GS677	3016	GCCCAAACCAGCCTCGCCACCCAAACCGCACAG	7605	AQTSLATQTAQ	12194	TSLATQT	0.262228	-0.11907
GS678	3017	GCCCAAAGAACCCCCACCCTCACCGTCGCACAG	7606	AQRTPTLTVAQ	12195	RTPTLTV	0.262188	-0.1338

FIG. 33 (Continued)

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GS679	3018	GCCCAAGCTACGCGTGAGAGTCGTACGGCACAG	7607	AQATRESRTAQ	12196	ATRESRT	0.262188	-0.1338
SyS1233	3019	GCCCAATTGTCTGAGAGTCTGCGGATTGCACAG	7608	AQLSESLRIAQ	12197	LSESLRI	0.262085	-0.13071
SyS1234	3020	GCCCAAAGCGTCACCGGCGGCATGGTCGCACAG	7609	AQSVTGGMVAQ	12198	SVTGGMV	0.261982	0.275265
SyS1235	3021	GCCCAACCCAGAACCAGCGACAGCAACGCACAG	7610	AQPRTSDSNAQ	12199	PRTSDSN	0.261751	0.100471
GS680	3022	GCCCAAGTTCATTCTACGGTTACGTCGGCACAG	7611	AQVHSTVTSAQ	12200	VHSTVTS	0.261737	-0.09477
SyS1236	3023	GCCCAAGGCACCAACATGAACCACCTCGCACAG	7612	AQGTNMNHLAQ	12201	GTNMNHL	0.261685	-0.07009
SyS1237	3024	GCCCAAATGAAGGCTGAGTTGTATGCGGCACAG	7613	AQMKAELYAAQ	12202	MKAELYA	0.261535	-0.02039
GS681	3025	GCCCAACTCAGAAGCCCCAGCGTCGACGCACAG	7614	AQLRSPSVDAQ	12203	LRSPSVD	0.261426	0.021615
SyS1238	3026	GCCCAAACCAACAGCCCCCCAATTCCCCGCACAG	7615	AQTNSPQFPAQ	12204	TNSPQFP	0.261388	0.019965
TS158	3027	GCCCAAAATAATTCGCTTAGGTCGAATGCACAG	7616	AQNNSLRSNAQ	12205	NNSLRSN	0.261381	-0.10273
GS682	3028	GCCCAAGACAGCCACATGGGCAAATACGCACAG	7617	AQDSHMGKYAQ	12206	DSHMGKY	0.261318	-0.11556
SyS1239	3029	GCCCAAGTTAATTCGATGACGCCGCGGGCACAG	7618	AQVNSMTPRAQ	12207	VNSMTPR	0.261313	0.013095
SyS1240	3030	GCCCAACTCGCCCCCATCAGCCTCAACGCACAG	7619	AQLAPISLNAQ	12208	LAPISLN	0.261307	-0.03736
SyS1241	3031	GCCCAAAATATGCCGAGTATTATGCAGGCACAG	7620	AQNMPSIMQAQ	12209	NMPSIMQ	0.261198	-0.19254
TS159	3032	GCCCAAGGGAATATGATTAAGGTGGCGGCACAG	7621	AQGNMIKVAAQ	12210	GNMIKVA	0.261132	-0.28624
SyS1242	3033	GCCCAAACCGGCGTCAGCCTCCAAGTCGCACAG	7622	AQTGVSLQVAQ	12211	TGVSLQV	0.261129	-0.23133
SyS1243	3034	GCCCAACCTCAGTTTAATACTGCGTCGGCACAG	7623	AQPQFNTASAQ	12212	PQFNTAS	0.261076	-0.14283
SyS1244	3035	GCCCAAACGGAGGCGTATAGGAATACTGCACAG	7624	AQTEAYRNTAQ	12213	TEAYRNT	0.261	-0.18163
SyS1245	3036	GCCCAACTTATGAAGGCTGATACTGTGGCACAG	7625	AQLMKADTVAQ	12214	LMKADTV	0.260947	-0.04342
GS683	3037	GCCCAAAATCATAAGGAGTTTATGCTTGCACAG	7626	AQNHKEFMLAQ	12215	NHKEFML	0.260914	-0.14906
GS684	3038	GCCCAATTGAATGGGACTTTGACTGTGGCACAG	7627	AQLNGTLTVAQ	12216	LNGTLTV	0.26088	-0.1462
GS686	3039	GCCCAAACTGCGAAGATTTTGACGATGGCACAG	7628	AQTAKILTMAQ	12217	TAKILTM	0.260811	-0.17112
SyS1246	3040	GCCCAACTCAGAGACAGCCTCCCCGTCGCACAG	7629	AQLRDSLPVAQ	12218	LRDSLPV	0.260626	0.104246
SyS1247	3041	GCCCAACTCAAAGGCGGCGACAGCTGGGCACAG	7630	AQLKGGDSWAQ	12219	LKGGDSW	0.260615	-0.12208
GS687	3042	GCCCAAAAAACCGTCGACATCATGGGCGCACAG	7631	AQKTVDIMGAQ	12220	KTVDIMG	0.260533	-0.09485
GS688	3043	GCCCAACTCAACATGGGCCAAATGAAAGCACAG	7632	AQLNMGQMKAQ	12221	LNMGQMK	0.260458	-0.09755
SyS1248	3044	GCCCAAAGCGTCCCCAGCCTCGACAGAGCACAG	7633	AQSVPSLDRAQ	12222	SVPSLDR	0.260448	-0.05185
SyS1249	3045	GCCCAACAGCTGTTGGGGACGAGTAAGGCACAG	7634	AQQLLGTSKAQ	12223	QLLGTSK	0.260344	-0.23296
SyS1250	3046	GCCCAAATGAATCCTAAGCATGGTCTGGCACAG	7635	AQMNPKHGLAQ	12224	MNPKHGL	0.260327	-0.18769
SyS1251	3047	GCCCAATCTCCGGAGGGTTCTCTGAAGGCACAG	7636	AQSPEGSLKAQ	12225	SPEGSLK	0.260327	-0.18769
SyS1252	3048	GCCCAAGCGAATATGCCGAATTCTCGGGCACAG	7637	AQANMPNSRAQ	12226	ANMPNSR	0.260318	-0.08035
SyS1253	3049	GCCCAAGCCTACATCAGCAGCGGCGTCGCACAG	7638	AQAYISSGVAQ	12227	AYISSGV	0.260028	-0.08758

FIG. 33 (Continued)

GS690	3050	GCCCAAGAAAGAGGCAGCCAAGCCAACGCACAG	7639	AQERGSQANAQ	12228	ERGSQAN	0.260015	-0.16304
GS691	3051	GCCCAAGGTCATGATAGGCTGAGTCCGGCACAG	7640	AQGHDRLSPAQ	12229	GHDRLSP	0.259905	-0.06434
GS692	3052	GCCCAAACGAGTAATGTGACTGGTACTGCACAG	7641	AQTSNVTGTAQ	12230	TSNVTGT	0.259758	-0.10244
GS693	3053	GCCCAACTCACCCACAACGTCGGCGTCGCACAG	7642	AQLTHNVGVAQ	12231	LTHNVGV	0.259654	-0.0842
GS694	3054	GCCCAAAGGGAGGATGGGGTGGCTAAGGCACAG	7643	AQREDGVAKAQ	12232	REDGVAK	0.2595	-0.1774
SyS1254	3055	GCCCAACCCGCCGACGGCTACAAACTCGCACAG	7644	AQPADGYKLAQ	12233	PADGYKL	0.259383	0.021493
GS697	3056	GCCCAACAACTCGACGCCACCAGAGCCGCACAG	7645	AQQLDATRAAQ	12234	QLDATRA	0.259246	-0.02679
GS698	3057	GCCCAAGTGACTGGTATGACGACTCGTGCACAG	7646	AQVTGMTTRAQ	12235	VTGMTTR	0.259241	-0.1747
SyS1255	3058	GCCCAATCGGATAGTCGGACGTATGAGGCACAG	7647	AQSDSRTYEAQ	12236	SDSRTYE	0.25915	-0.12829
SyS1259	3059	GCCCAAGTTGAGCCGCTGAAGCCGGATGCACAG	7648	AQVEPLKPDAQ	12237	VEPLKPD	0.258734	-0.17799
SyS1260	3060	GCCCAAGGCGTCCTCGCCAGCAACAGAGCACAG	7649	AQGVLASNRAQ	12238	GVLASNR	0.258676	-0.15411
SyS1262	3061	GCCCAAATGGGCGAAAGAATGAGCATCGCACAG	7650	AQMGERMSIAQ	12239	MGERMSI	0.258443	-0.05797
SyS1263	3062	GCCCAATTTACGAAGACTGAGGATTTGGCACAG	7651	AQFTKTEDLAQ	12240	FTKTEDL	0.258323	-0.0551
SyS1264	3063	GCCCAAGTCAAAAACACCGAACTCCTCGCACAG	7652	AQVKNTELLAQ	12241	VKNTELL	0.258283	0.073327
GS700	3064	GCCCAAACTGTTACGAGTACGGTGGTGGCACAG	7653	AQTVTSTVVAQ	12242	TVTSTVV	0.258274	-0.18637
SyS1267	3065	GCCCAAGCCAAATACGGCGACCCCACCGCACAG	7654	AQAKYGDPTAQ	12243	AKYGDPT	0.257892	0.222899
GS701	3066	GCCCAAACCAGCGACAGACTCCTCGGCGCACAG	7655	AQTSDRLLGAQ	12244	TSDRLLG	0.257859	-0.13666
GS702	3067	GCCCAAGCTGTTGGGAATACTAAGATGGCACAG	7656	AQAVGNTKMAQ	12245	AVGNTKM	0.25783	-0.13952
GS704	3068	GCCCAACAGACGTATATAATAAGATGGATGCACAG	7657	AQQTYNKMDAQ	12246	QTYNKMD	0.257666	-0.05596
GS706	3069	GCCCAAGCGTGGGCTAGTCAGTCTTCGGCACAG	7658	AQAWASQSSAQ	12247	AWASQSS	0.25724	-0.14779
SyS1269	3070	GCCCAAAATGCGTTTCTTACTGGTGGGGCACAG	7659	AQNAFLTGGAQ	12248	NAFLTGG	0.257171	-0.20103
SyS1270	3071	GCCCAAAGCATCGGCGACAAATACACCGCACAG	7660	AQSIGDKYTAQ	12249	SIGDKYT	0.257047	-0.09127
GS707	3072	GCCCAATCGAATCATCATCATACTGGGGCACAG	7661	AQSNHHHTGAQ	12250	SNHHHTG	0.256757	-0.11758
GS708	3073	GCCCAAATCACCAACAAACCCATGACCGCACAG	7662	AQITNKPMTAQ	12251	ITNKPMT	0.256656	-0.13702
SS84	3074	GCCCAACTCAGCGGCCAAGTCAGCAACGCACAG	7663	AQLSGQVSNAQ	12252	LSGQVSN	0.256425	-0.35654
GS709	3075	GCCCAAAATAGTATGTCGGGGCATTTGGCACAG	7664	AQNSMSGHLAQ	12253	NSMSGHL	0.256275	-0.14334
SyS1271	3076	GCCCAACCTGCGGTGCATGGTTATGCTGCACAG	7665	AQPAVHGYAAQ	12254	PAVHGYA	0.256274	-0.20709
GS710	3077	GCCCAACTCATGAGAACCAAACAACCCGCACAG	7666	AQLMRTKQPAQ	12255	LMRTKQP	0.256142	-0.14906
SyS1272	3078	GCCCAAAGCAGCCTCGCCGTCAACAAAGCACAG	7667	AQSSLAVNKAQ	12256	SSLAVNK	0.256141	-0.07737
SyS1273	3079	GCCCAAAATACGCAGTCGGAGCCTCGTGCACAG	7668	AQNTQSEPRAQ	12257	NTQSEPR	0.2561	0.127962
SyS1275	3080	GCCCAAGATCATCTGGTTAGTGTTCCTGCACAG	7669	AQDHLVSVPAQ	12258	DHLVSVP	0.256044	-0.19107
SyS1276	3081	GCCCAATGGGCCACCAGCACCCACGACGCACAG	7670	AQWATSTHDAQ	12259	WATSTHD	0.256044	-0.18121

FIG. 33 (Continued)

SyS1277	3082	GCCCAACCCCAACAACAACCCATCGGCGCACAG	7671	AQPQQQPIGAQ	12260	PQQQPIG	0.256044	-0.21571
SyS1278	3083	GCCCAAAGCCTCAGCACCCACAGCGACGCACAG	7672	AQSLSTHSDAQ	12261	SLSTHSD	0.255878	-0.0507
SyS1279	3084	GCCCAAGGCAGCATGGCCGCCAGAAGCGCACAG	7673	AQGSMAARSAQ	12262	GSMAARS	0.2558	-0.12101
GS711	3085	GCCCAAGCCCCCGGCATGACCGCCAGAGCACAG	7674	AQAPGMTARAQ	12263	APGMTAR	0.255662	-0.16623
SyS1280	3086	GCCCAAGTCCTCGCCAACATGACCGCCGCACAG	7675	AQVLANMTAAQ	12264	VLANMTA	0.255612	0.070331
SyS1281	3087	GCCCAACTCACCAAACAAGAAAGCGCCGCACAG	7676	AQLTKQESAAQ	12265	LTKQESA	0.255528	-0.09434
SyS1282	3088	GCCCAAGGCGCCAACAGCGGCGGCGTCGCACAG	7677	AQGANSGGVAQ	12266	GANSGGV	0.255503	0.080739
SyS1283	3089	GCCCAACAGAGTGAGCCGAAGCGTCCTGCACAG	7678	AQQSEPKRPAQ	12267	QSEPKRP	0.255307	-0.11616
SyS1284	3090	GCCCAAGTCCACGGCGAAAGAAGCGTCGCACAG	7679	AQVHGERSVAQ	12268	VHGERSV	0.255229	0.018407
SyS1285	3091	GCCCAAGCGCATCAGACTGCTGCTTCTGCACAG	7680	AQAHQTAASAQ	12269	AHQTAAS	0.255147	-0.17557
GP133	3092	GCCCAAGTTCGGGAGATGCAGACGGCGGCACAG	7681	AQVREMQTAAQ	12270	VREMQTA	0.255121	-0.07329
GS713	3093	GCCCAAGTCGCCCCCAGCGCCCTCCACGCACAG	7682	AQVAPSALHAQ	12271	VAPSALH	0.255035	-0.16842
SyS1286	3094	GCCCAAAGTGTTGGTCATCATAATATGGCACAG	7683	AQSVGHHNMAQ	12272	SVGHHNM	0.254967	-0.18648
SyS1287	3095	GCCCAATTCCTCACCCAAGGCGACGTCGCACAG	7684	AQFLTQGDVAQ	12273	FLTQGDV	0.254933	-0.11838
SyS1288	3096	GCCCAATTCAGCACCCAATTCCAACACGCACAG	7685	AQFSTQFQHAQ	12274	FSTQFQH	0.254806	-0.14302
GP134	3097	GCCCAACAGAATACGACGCGGTCGAATGCACAG	7686	AQQNTTRSNAQ	12275	QNTTRSN	0.254756	0.347693
SyS1289	3098	GCCCAACCCGCCGTCACCAGCATCGCCGCACAG	7687	AQPAVTSIAAQ	12276	PAVTSIA	0.254579	-0.07092
SyS1290	3099	GCCCAAGCCAGCACCAACACCTACGTCGCACAG	7688	AQASTNTYVAQ	12277	ASTNTYV	0.254465	0.185493
SyS1291	3100	GCCCAATCGACGGCTACGCCTACGTCGGCACAG	7689	AQSTATPTSAQ	12278	STATPTS	0.254392	-0.19723
GS714	3101	GCCCAACATTTTAATAGGACGTCGCCTGCACAG	7690	AQHFNRTSPAQ	12279	HFNRTSP	0.254355	-0.04208
SyS1294	3102	GCCCAAAGCGTCGCCGGCATGCTCCCCGCACAG	7691	AQSVAGMLPAQ	12280	SVAGMLP	0.254355	-0.14405
SyS1295	3103	GCCCAACCTATGAGTTCTGAGAGTAGTGCACAG	7692	AQPMSSESSAQ	12281	PMSSESS	0.25434	-0.20216
SyS1296	3104	GCCCAAAGCCTCGCCAGCACCACCGTCGCACAG	7693	AQSLASTTVAQ	12282	SLASTTV	0.254318	-0.00463
SyS1297	3105	GCCCAAACTTCTACTCCTGCTCAGGTTGCACAG	7694	AQTSTPAQVAQ	12283	TSTPAQV	0.254198	0.05736
SyS1298	3106	GCCCAAAGTCTGACGGCGCAGCAGCCTGCACAG	7695	AQSLTAQQPAQ	12284	SLTAQQP	0.254112	-0.01576
GS715	3107	GCCCAAAGTGGTCGTGTGCCTGTGGCTGCACAG	7696	AQSGRVPVAAQ	12285	SGRVPVA	0.254016	-0.18816
GS716	3108	GCCCAACTCGACGCCGCCAAAAGCCTCGCACAG	7697	AQLDAAKSLAQ	12286	LDAAKSL	0.253973	-0.14151
GS717	3109	GCCCAAAACTTCGCCAACAAAAAACGTCGCACAG	7698	AQNFANKNVAQ	12287	NFANKNV	0.25395	0.011201
GS718	3110	GCCCAAGGCCCCCGCCAGCGTCACCCCCCGCACAG	7699	AQGPASVTPAQ	12288	GPASVTP	0.253945	-0.05651
SyS1299	3111	GCCCAATATTCTCGGGAGGCGACGAATGCACAG	7700	AQYSREATNAQ	12289	YSREATN	0.253828	0.015982
SyS1300	3112	GCCCAAACCGGCAGCAGCTTCGCCATGGCACAG	7701	AQTGSSFAMAQ	12290	TGSSFAM	0.25367	-0.1344
SyS1301	3113	GCCCAAGGGATTAAGGGGGATCCGGTTGCACAG	7702	AQGIKGDPVAQ	12291	GIKGDPV	0.253653	-0.05918

FIG. 33 (Continued)

SyS1302	3114	GCCCAAGTCACCAGCACCAGCCACGCCGCACAG	7703	AQVTSTSHAAQ	12292	VTSTSHA	0.253643	0.149339
SyS1303	3115	GCCCAAACCAGCCAAAACAACCTCAGAGCACAG	7704	AQTSQNNLRAQ	12293	TSQNNLR	0.253347	-0.04388
GS719	3116	GCCCAAATGAGACAAGAAGGCCTCAGCGCACAG	7705	AQMRQEGLSAQ	12294	MRQEGLS	0.253321	-0.14238
SyS1304	3117	GCCCAACTCAACCTCAACGCCATCGCCGCACAG	7706	AQLNLNAIAAQ	12295	LNLNAIA	0.253187	-0.10853
SyS1305	3118	GCCCAAAGTAAGAATGAGGGGCCTACTGCACAG	7707	AQSKNEGPTAQ	12296	SKNEGPT	0.253158	-0.05578
SyS1306	3119	GCCCAAGATTCTCGTTCTACGACTAATGCACAG	7708	AQDSRSTTNAQ	12297	DSRSTTN	0.252881	0.072962
SyS1307	3120	GCCCAAAGCACCGGCGACGCCCTCAGAGCACAG	7709	AQSTGDALRAQ	12298	STGDALR	0.252785	0.062357
SyS1308	3121	GCCCAAATTAATAAGCCTGGTACGCCTGCACAG	7710	AQINKPGTPAQ	12299	INKPGTP	0.25278	0.014889
SyS1309	3122	GCCCAAGTTTCGGCTCCTTTGAATATTGCACAG	7711	AQVSAPLNIAQ	12300	VSAPLNI	0.252695	-0.23618
GP135	3123	GCCCAAGTTTCTTTGGGTTCGCTTGCGGCACAG	7712	AQVSLGSLAAQ	12301	VSLGSLA	0.252596	0.083569
SyS1310	3124	GCCCAACTCAACCACATCAACGAAAAAGCACAG	7713	AQLNHINEKAQ	12302	LNHINEK	0.252494	-0.00166
SyS1311	3125	GCCCAAAAGTCGGTGACGATTCTTTCGGCACAG	7714	AQKSVTILSAQ	12303	KSVTILS	0.252487	-0.19375
GS722	3126	GCCCAATCTAATGTGTCGTCGCTTGTTGCACAG	7715	AQSNVSSLVAQ	12304	SNVSSLV	0.252289	-0.12894
GS723	3127	GCCCAATTTTCGCAGACTGTTGGGGGGGCACAG	7716	AQFSQTVGGAQ	12305	FSQTVGG	0.252132	-0.0379
GS724	3128	GCCCAACGTCCGTCTATTACGCATGATGCACAG	7717	AQRPSITHDAQ	12306	RPSITHD	0.252097	-0.13761
SyS1314	3129	GCCCAAAGACAAGAAAGCACCACCCTCGCACAG	7718	AQRQESTTLAQ	12307	RQESTTL	0.252004	-0.07737
SyS1315	3130	GCCCAAGGGCCTTATGTGACTCCTCAGGCACAG	7719	AQGPYVTPQAQ	12308	GPYVTPQ	0.251887	0.023256
SyS1316	3131	GCCCAAAACGGCCTCGTCACCACCGCCGCACAG	7720	AQNGLVTTAAQ	12309	NGLVTTA	0.251887	-0.01918
SyS1317	3132	GCCCAACACGCCGGCAACGTCCCCGGCGCACAG	7721	AQHAGNVPGAQ	12310	HAGNVPG	0.251887	-0.1889
SyS1318	3133	GCCCAACCCATGGGCAACAACCTCGTCGCACAG	7722	AQPMGNNLVAQ	12311	PMGNNLV	0.251827	-0.23296
SyS1319	3134	GCCCAAGTCTACAACGACAGAAGCCACGCACAG	7723	AQVYNDRSHAQ	12312	VYNDRSH	0.251746	-0.03526
GS725	3135	GCCCAAACCCACAAAGAAAGCGGCTACGCACAG	7724	AQTHKESGYAQ	12313	THKESGY	0.251703	-0.06465
SyS1320	3136	GCCCAAGGCATGAACAGCGTCCTCCTCGCACAG	7725	AQGMNSVLLAQ	12314	GMNSVLL	0.25156	-0.15738
GS726	3137	GCCCAATACCTCGAAAACCAATACAGCGCACAG	7726	AQYLENQYSAQ	12315	YLENQYS	0.251521	-0.17291
GP137	3138	GCCCAATCTATTACGTCGAGGCCTAATGCACAG	7727	AQSITSRPNAQ	12316	SITSRPN	0.251405	-0.02611
GS727	3139	GCCCAAAGCCACCAAAACACCGCCAGAGCACAG	7728	AQSHQNTARAQ	12317	SHQNTAR	0.251208	-0.15138
GS728	3140	GCCCAACGTTTGGTTCAGTCTGCGGAGGCACAG	7729	AQRLVQSAEAQ	12318	RLVQSAE	0.251117	-0.12998
SyS1321	3141	GCCCAATACCCCAAAAGCGCCACCAACGCACAG	7730	AQYPKSATNAQ	12319	YPKSATN	0.250939	-0.04706
SyS1322	3142	GCCCAAATTAATTCTTCTCCGCCGCTGGCACAG	7731	AQINSSPPLAQ	12320	INSSPPL	0.250894	-0.20462
GS729	3143	GCCCAAACTCAGAATCTGGCGGGTGGTGCACAG	7732	AQTQNLAGGAQ	12321	TQNLAGG	0.250713	-0.13682
SyS1323	3144	GCCCAATTCCAAGTCGCCAAAGACAGAGCACAG	7733	AQFQVAKDRAQ	12322	FQVAKDR	0.250692	0.020536
GS731	3145	GCCCAACGGCTGAGTGGTAATCAGAATGCACAG	7734	AQRLSGNQNAQ	12323	RLSGNQN	0.250664	0.025382

FIG. 33 (Continued)

SyS1324	3146	GCCCAAACTACGGATCGGGTGTCGCATGCACAG	7735	AQTTDRVSHAQ	12324	TTDRVSH	0.250526	0.007999
SyS1325	3147	GCCCAAACTGCTACTGTGACGGCTCGGGCACAG	7736	AQTATVTARAQ	12325	TATVTAR	0.250464	-0.16039
SyS1326	3148	GCCCAACTCAGCATGATGAGCGACAAAGCACAG	7737	AQLSMMSDKAQ	12326	LSMMSDK	0.250432	-0.15808
GS733	3149	GCCCAAACTCTGATTCAGACTAGTCCGGCACAG	7738	AQTLIQTSPAQ	12327	TLIQTSP	0.250263	-0.14429
SyS1327	3150	GCCCAACCGATGCATATTACGAATGCTGCACAG	7739	AQPMHITNAAQ	12328	PMHITNA	0.250148	-0.22434
GS734	3151	GCCCAAACCGTCGGCCAACCCGCCCACGCACAG	7740	AQTVGQPAHAQ	12329	TVGQPAH	0.25007	-0.08134
SyS1328	3152	GCCCAAGAAGACAAAGACGTCAGACTCGCACAG	7741	AQEDKDVRLAQ	12330	EDKDVRL	0.249926	-0.22926
GS735	3153	GCCCAAATGAAGGTTGCGCAGCCTATGGCACAG	7742	AQMKVAQPMAQ	12331	MKVAQPM	0.249854	-0.12039
SyS1329	3154	GCCCAAGTGGGGGTGCCTAATCTGCCGGCACAG	7743	AQVGVPNLPAQ	12332	VGVPNLP	0.24985	-0.07803
SyS1330	3155	GCCCAAGCGCCGCTGAGTAGTGATCCGGCACAG	7744	AQAPLSSDPAQ	12333	APLSSDP	0.249809	-0.13798
GS737	3156	GCCCAATTCCTCCACGCCAGCGTCGACGCACAG	7745	AQFLHASVDAQ	12334	FLHASVD	0.249673	-0.17919
GS738	3157	GCCCAACCTACTGTGGGGACGTATATTGCACAG	7746	AQPTVGTYIAQ	12335	PTVGTYI	0.249673	-0.1765
GS739	3158	GCCCAAGAGCCTCTGCATAGGAATTCTGCACAG	7747	AQEPLHRNSAQ	12336	EPLHRNS	0.249673	-0.1442
GS740	3159	GCCCAAGCCAGCACCGTCACCGTCGAAGCACAG	7748	AQASTVTVEAQ	12337	ASTVTVE	0.249673	-0.18727
GS741	3160	GCCCAAGCCCCCAGAATCGACAACGCCGCACAG	7749	AQAPRIDNAAQ	12338	APRIDNA	0.249673	-0.05537
GS744	3161	GCCCAATATCGTGATTCGGCTGCTCCTGCACAG	7750	AQYRDSAAPAQ	12339	YRDSAAP	0.249343	-0.13666
SyS1332	3162	GCCCAACTCACCCAAAACGCCAGCGTCGCACAG	7751	AQLTQNASVAQ	12340	LTQNASV	0.249317	-0.0022
SyS1335	3163	GCCCAATTGAGTGCTCGTTTGACGACTGCACAG	7752	AQLSARLTTAQ	12341	LSARLTT	0.24914	-0.09677
SS87	3164	GCCCAAAACGGCAAAAGCAGCGACAAAGCACAG	7753	AQNGKSSDKAQ	12342	NGKSSDK	0.249118	-0.28649
SyS1336	3165	GCCCAAGCGCTGGTGAAGGATACTACTGCACAG	7754	AQALVKDTTAQ	12343	ALVKDTT	0.248993	-0.14405
SyS1337	3166	GCCCAAATGCTCGTCACCACCGGCGAAGCACAG	7755	AQMLVTTGEAQ	12344	MLVTTGE	0.248845	-0.13932
SyS1338	3167	GCCCAAAGCGGCAACCCCAGCTACGCCGCACAG	7756	AQSGNPSYAAQ	12345	SGNPSYA	0.248803	-0.02317
SyS1339	3168	GCCCAAGTCATCACCGGCGGCATGAGCGCACAG	7757	AQVITGGMSAQ	12346	VITGGMS	0.248801	0.075387
SyS1340	3169	GCCCAACTCGAACCCAACGTCCAAACCGCACAG	7758	AQLEPNVQTAQ	12347	LEPNVQT	0.248763	-0.19133
SyS1341	3170	GCCCAAAGATTCAGCGAAGTCACCCCCCGCACAG	7759	AQRFSEVTPAQ	12348	RFSEVTP	0.248692	0.100649
GS745	3171	GCCCAAGATCCGGGGAAGGCGAGTCTGGCACAG	7760	AQDPGKASLAQ	12349	DPGKASL	0.248503	-0.07157
SyS1343	3172	GCCCAAATCGCCCACGAAAGCACCGACGCACAG	7761	AQIAHESTDAQ	12350	IAHESTD	0.248487	-0.15595
GS748	3173	GCCCAATATCCTAGTAATTCTATGCATGCACAG	7762	AQYPSNSMHAQ	12351	YPSNSMH	0.248436	-0.05512
SyS1345	3174	GCCCAAAGCACCACCCCCCCCAGCGGCGCACAG	7763	AQSTTPPSGAQ	12352	STTPPSG	0.248285	-0.18648
SyS1346	3175	GCCCAAGTTGAGCAGAATTCTAAGAATGCACAG	7764	AQVEQNSKNAQ	12353	VEQNSKN	0.248285	-0.18648
GS749	3176	GCCCAAACGATTGCGGGTCGGCTTGTGGCACAG	7765	AQTIAGRLVAQ	12354	TIAGRLV	0.248255	-0.15097
GS750	3177	GCCCAAGCTAGGCATACGGGTGAGATGGCACAG	7766	AQARHTGEMAQ	12355	ARHTGEM	0.24798	-0.11854

FIG. 33 (Continued)

GS751	3178	GCCCAACAGCATCTGCCGAATCATATTGCACAG	7767	AQQHLPNHIAQ	12356	QHLPNHI	0.2479	-0.16932
GS752	3179	GCCCAAACTACTATGGGGACTTATCCTGCACAG	7768	AQTTMGTYPAQ	12357	TTMGTYP	0.247856	-0.17201
SyS1347	3180	GCCCAAACCGAAAGCGTCATGCCCAGAGCACAG	7769	AQTESVMPRAQ	12358	TESVMPR	0.247776	-0.09369
SyS1348	3181	GCCCAAGGCGCCAAACCCAGCAACGACGCACAG	7770	AQGAKPSNDAQ	12359	GAKPSND	0.247643	0.125092
SyS1349	3182	GCCCAAGCCGTCAGCAGCGACATGAGCGCACAG	7771	AQAVSSDMSAQ	12360	AVSSDMS	0.2476	-0.16102
SyS1350	3183	GCCCAACACAGCCCCCAACTCGGCGGCGCACAG	7772	AQHSPQLGGAQ	12361	HSPQLGG	0.247571	-0.12465
SyS1351	3184	GCCCAATTGTATACTAATCCTAATACTGCACAG	7773	AQLYTNPNTAQ	12362	LYTNPNT	0.247527	-0.17382
SyS1352	3185	GCCCAAACCGTCGCCCTCAACATGGCCGCACAG	7774	AQTVALNMAAQ	12363	TVALNMA	0.247496	-0.02465
GS754	3186	GCCCAACAGCGGGTTCCTGCTTATCAGGCACAG	7775	AQQRVPAYQAQ	12364	QRVPAYQ	0.247403	-0.14564
SyS1353	3187	GCCCAAAGTGATGTTTCTAAGGTTTATGCACAG	7776	AQSDVSKVYAQ	12365	SDVSKVY	0.247354	-0.11668
SyS1354	3188	GCCCAATCGAAATACGGGGGAGCAGGTTGCACAG	7777	AQSNTGEQVAQ	12366	SNTGEQV	0.247184	-0.19254
SyS1355	3189	GCCCAATTCACCACCGGCCTCAACCACGCACAG	7778	AQFTTGLNHAQ	12367	FTTGLNH	0.247139	-0.09374
SyS1356	3190	GCCCAAAACGACACCCAATACAAACACGCACAG	7779	AQNDTQYKHAQ	12368	NDTQYKH	0.247109	-0.10786
SyS1357	3191	GCCCAAGTCCACGACGTCAAAGGCATCGCACAG	7780	AQVHDVKGIAQ	12369	VHDVKGI	0.247033	0.063895
GS756	3192	GCCCAATATGGTGGTAGGGATAGTTATGCACAG	7781	AQYGGRDSYAQ	12370	YGGRDSY	0.246964	-0.09066
SyS1358	3193	GCCCAACATAGTACTGCGACTACTCATGCACAG	7782	AQHSTATTHAQ	12371	HSTATTH	0.246866	-0.15132
SyS1360	3194	GCCCAACCTTCGCCTACTACTCGGACTGCACAG	7783	AQPSPTTRTAQ	12372	PSPTTRT	0.246802	-0.21694
SyS1361	3195	GCCCAAGGGCATGCGGAGGCGGCGATGGCACAG	7784	AQGHAEAAMAQ	12373	GHAEAAM	0.246802	-0.16027
SyS1362	3196	GCCCAAAGCCTCAGCACCAGACCCGTCGCACAG	7785	AQSLSTRPVAQ	12374	SLSTRPV	0.24675	-0.01949
GS757	3197	GCCCAATCTCCGGTGCCTGGTAAGCCTGCACAG	7786	AQSPVPGKPAQ	12375	SPVPGKP	0.246636	-0.15138
GS758	3198	GCCCAAACCAGAATCAACAGCCCCCTCGCACAG	7787	AQTRINSPLAQ	12376	TRINSPL	0.246552	-0.07422
SyS1363	3199	GCCCAAGAGTCTACGTATGCGAAGCTGGCACAG	7788	AQESTYAKLAQ	12377	ESTYAKL	0.246443	-0.12586
SyS1364	3200	GCCCAACAAATCAACCAAGGCACCAGAGCACAG	7789	AQQINQGTRAQ	12378	QINQGTR	0.246362	0.115808
GS759	3201	GCCCAAGGCAGCAGAACCGGCAGCATCGCACAG	7790	AQGSRTGSIAQ	12379	GSRTGSI	0.24628	-0.05088
SyS1365	3202	GCCCAAGGGAATGCTTCTTGGTCGGCTGCACAG	7791	AQGNASWSAAQ	12380	GNASWSA	0.246249	0.006225
SyS1366	3203	GCCCAAGCGGCTCATGATATTGGTAAGGCACAG	7792	AQAAHDIGKAQ	12381	AAHDIGK	0.2462	-0.14162
GS760	3204	GCCCAAAAGGATAGGCCTTTTGTGGAGGCACAG	7793	AQKDRPFVEAQ	12382	KDRPFVE	0.246199	-0.16753
SyS1367	3205	GCCCAACTCCCCCCACACCAAACCCTTCGCACAG	7794	AQLPHTKPFAQ	12383	LPHTKPF	0.246181	-0.02281
SyS1368	3206	GCCCAACCTGGGAAGGGTGTGTCTCTTGCACAG	7795	AQPGKGVSLAQ	12384	PGKGVSL	0.246139	0.157066
SyS1369	3207	GCCCAAGACAGACAAAACGCCAGCGCCGCACAG	7796	AQDRQNASAAQ	12385	DRQNASA	0.246065	-0.07979
SyS1370	3208	GCCCAAGTCCAACCCAGCCTCAGCGTCGCACAG	7797	AQVQPSLSVAQ	12386	VQPSLSV	0.246042	-0.08582
SyS1371	3209	GCCCAAAAGCCTACGCCGATTGAGTTTGCACAG	7798	AQKPTPIEFAQ	12387	KPTPIEF	0.246004	-0.1986

FIG. 33 (Continued)

SyS1372	3210	GCCCAACTGCTTCATGATATGAAGAGTGCACAG	7799	AQLLHDMKSAQ	12388	LLHDMKS	0.245942	0.000193
SyS1373	3211	GCCCAAAACAGCGACAGAACCCTCAGCGCACAG	7800	AQNSDRTLSAQ	12389	NSDRTLS	0.245806	-0.17998
SyS1374	3212	GCCCAAAAGGTTGGGCATGGGTTTAATGCACAG	7801	AQKVGHGFNAQ	12390	KVGHGFN	0.24575	-0.23173
GS761	3213	GCCCAAACGAAGCCTGCGGTTAGTTTTGCACAG	7802	AQTKPAVSFAQ	12391	TKPAVSF	0.245736	-0.16051
SyS1375	3214	GCCCAAGCTATGACGAATATTCCGAAGGCACAG	7803	AQAMTNIPKAQ	12392	AMTNIPK	0.245618	-0.13316
GS762	3215	GCCCAATTTTCGCATATGTCTTTGCCGGCACAG	7804	AQFSHMSLPAQ	12393	FSHMSLP	0.245614	-0.18368
SyS1376	3216	GCCCAAGGGTCTGTGCGGGATAATCCGGCACAG	7805	AQGSVRDNPAQ	12394	GSVRDNP	0.245593	-0.19375
GS763	3217	GCCCAAAGTAGTTCGCAGGGGCCGACTGCACAG	7806	AQSSSQGPTAQ	12395	SSSQGPT	0.24552	-0.10423
GP139	3218	GCCCAACTTGTGGGGCGGCCGGTTACGGCACAG	7807	AQLVGRPVTAQ	12396	LVGRPVT	0.245491	-0.07301
SyS1377	3219	GCCCAAATCAACTACGGCGTCCAAAAAGCACAG	7808	AQINYGVQKAQ	12397	INYGVQK	0.245326	0.004509
SyS1378	3220	GCCCAAATTAATAAGGATAATAATCAGGCACAG	7809	AQINKDNNQAQ	12398	INKDNNQ	0.245119	-0.081
SyS1379	3221	GCCCAAAGTGGTCAGTCTTCTGCTATGGCACAG	7810	AQSGQSSAMAQ	12399	SGQSSAM	0.245048	-0.00536
GS765	3222	GCCCAAGAATACAACAGCACCAAACTCGCACAG	7811	AQEYNSTKLAQ	12400	EYNSTKL	0.244968	0.026789
SyS1381	3223	GCCCAATTTATGACGCTGGAGCGGGCGGCACAG	7812	AQFMTLERAAQ	12401	FMTLERA	0.244739	-0.20466
GS766	3224	GCCCAATTCGGCAAAGACTACGTCAACGCACAG	7813	AQFGKDYVNAQ	12402	FGKDYVN	0.244671	-0.06664
SyS1382	3225	GCCCAACTCCTCCTCGGCGGCACCCCCGCACAG	7814	AQLLLGGTPAQ	12403	LLLGGTP	0.244645	-0.15288
GS767	3226	GCCCAAACCACCACCTACACCAGAAACGCACAG	7815	AQTTTYTRNAQ	12404	TTTYTRN	0.244598	-0.0132
GP140	3227	GCCCAAGATCGGGGTATGCGGGGGGCTGCACAG	7816	AQDRGMRGAAQ	12405	DRGMRGA	0.24456	-0.07273
GS769	3228	GCCCAAGCGGTTTCGGGTACGCGTACGGCACAG	7817	AQAVSGTRTAQ	12406	AVSGTRT	0.244519	-0.05607
SS88	3229	GCCCAAAACTTCAGCGGCGTCGCCAAAGCACAG	7818	AQNFSGVAKAQ	12407	NFSGVAK	0.24428	-0.34565
GS770	3230	GCCCAAGATCGGAATAATAGTATTTCGGCACAG	7819	AQDRNNSISAQ	12408	DRNNSIS	0.244033	-0.1765
GS771	3231	GCCCAAATCCCCCCAAAGACCCCTCGACGCACAG	7820	AQIPQRPLDAQ	12409	IPQRPLD	0.244033	-0.1424
GP141	3232	GCCCAACCTGCTGCGAATCAGTATGTTGCACAG	7821	AQPAANQYVAQ	12410	PAANQYV	0.243833	0.318489
GS772	3233	GCCCAATACAGCGGCACCGCCATCAGAGCACAG	7822	AQYSGTAIRAQ	12411	YSGTAIR	0.243671	-0.06766
GS773	3234	GCCCAATGGGTTCAGCGGACTGAGAGTGCACAG	7823	AQWVQRTESAQ	12412	WVQRTES	0.243512	-0.17768
SyS1385	3235	GCCCAACCCAAAGACGGCGGCGCCATCGCACAG	7824	AQPKDGGAIAQ	12413	PKDGGAI	0.243472	-0.17259
SyS1386	3236	GCCCAACTTGCTACTCCGCAGGAGGAGGCACAG	7825	AQLATPQEEAQ	12414	LATPQEE	0.243453	-0.23618
GS774	3237	GCCCAACTGAATAGTCCGGTTATGGCGGCACAG	7826	AQLNSPVMAAQ	12415	LNSPVMA	0.243434	-0.14048
GP142	3238	GCCCAAGGGGCTACTGGGACGAGGGCTGCACAG	7827	AQGATGTRAAQ	12416	GATGTRA	0.243373	-0.01961
SyS1387	3239	GCCCAACGGACGGATGTGCGGACGAATGCACAG	7828	AQRTDVRTNAQ	12417	RTDVRTN	0.243327	-0.18527
SyS1388	3240	GCCCAAAGAAACCTCGCCCACCCCTACGCACAG	7829	AQRNLAHPYAQ	12418	RNLAHPY	0.243327	-0.18527
SyS1389	3241	GCCCAACTCAGCACCAGCTACAGCACCGCACAG	7830	AQLSTSYSTAQ	12419	LSTSYST	0.243288	-0.15981

FIG. 33 (Continued)

SyS1390	3242	GCCCAAGGCGTCAACCAAACCGCCAGAGCACAG	7831	AQGVNQTARAQ	12420	GVNQTAR	0.243276	-0.08615
SyS1391	3243	GCCCAACTTCCGGCTAGTTCGGCTAGGGCACAG	7832	AQLPASSARAQ	12421	LPASSAR	0.243214	-0.08645
SyS1392	3244	GCCCAACAACTCTACAGCGTCAACGCCGCACAG	7833	AQQLYSVNAAQ	12422	QLYSVNA	0.243023	-0.15496
SyS1393	3245	GCCCAAGTTGGGACGTATACTGCTACGGCACAG	7834	AQVGTYTATAQ	12423	VGTYTAT	0.243023	-0.18042
GS775	3246	GCCCAAAGAAGCATGACCGTCATCGAAGCACAG	7835	AQRSMTVIEAQ	12424	RSMTVIE	0.242977	-0.15669
SyS1394	3247	GCCCAATTTGGGCGTGGTGATACGGGTGCACAG	7836	AQFGRGDTGAQ	12425	FGRGDTG	0.242909	0.104483
SyS1395	3248	GCCCAAGCCGCCGGCAGAAGCAACCCCGCACAG	7837	AQAAGRSNPAQ	12426	AAGRSNP	0.242903	0.079024
GS776	3249	GCCCAAATGCCTCAGTCGAGTCTTGCTGCACAG	7838	AQMPQSSLAAQ	12427	MPQSSLA	0.242838	-0.16718
SyS1397	3250	GCCCAACCGTCTAAGCATGAGCGGTATGCACAG	7839	AQPSKHERYAQ	12428	PSKHERY	0.242467	-0.20586
SyS1399	3251	GCCCAATTGTTTGATTCTTCTAAGACTGCACAG	7840	AQLFDSSKTAQ	12429	LFDSSKT	0.242166	-0.06487
GS779	3252	GCCCAAAGCCCCCAACCCAGACTCAGCGCACAG	7841	AQSPQPRLSAQ	12430	SPQPRLS	0.242119	-0.1774
SyS1400	3253	GCCCAAAGAAGACCCGACGTCGAAAACGCACAG	7842	AQRRPDVENAQ	12431	RRPDVEN	0.242029	-0.04446
GS780	3254	GCCCAACCGATGGGTAGTGCGGGTAGTGCACAG	7843	AQPMGSAGSAQ	12432	PMGSAGS	0.241931	-0.10709
GS781	3255	GCCCAATGGAGCACCGGCATGACCAGCGCACAG	7844	AQWSTGMTSAQ	12433	WSTGMTS	0.241931	-0.10709
SyS1401	3256	GCCCAAGGCCTCGTCAGAAACGGCGTCGCACAG	7845	AQGLVRNGVAQ	12434	GLVRNGV	0.241887	0.011133
SyS1402	3257	GCCCAAGAGGGGTCGTATAGTACGTCTGCACAG	7846	AQEGSYSTSAQ	12435	EGSYSTS	0.241562	-0.07279
SyS1403	3258	GCCCAAGCCACCAGCATGCTCACCCACGCACAG	7847	AQATSMLTHAQ	12436	ATSMLTH	0.241541	-0.18163
SyS1404	3259	GCCCAAAGCACCACCGGCCCCCCCCAGCGCACAG	7848	AQSTTGPPSAQ	12437	STTGPPS	0.241416	-0.00061
SyS1405	3260	GCCCAACGTGGGGCGTCGGTGTCTATGGCACAG	7849	AQRGASVSMAQ	12438	RGASVSM	0.241293	-0.17678
SyS1406	3261	GCCCAAGTCCACGAACACGGCGCCAGCGCACAG	7850	AQVHEHGASAQ	12439	VHEHGAS	0.241293	-0.20709
GS783	3262	GCCCAACATTCTCCTTCTCAGCCGAGGGCACAG	7851	AQHSPSQPRAQ	12440	HSPSQPR	0.241239	-0.18816
SyS1407	3263	GCCCAAGGCATCGGCCAAAACACCGCCGCACAG	7852	AQGIGQNTAAQ	12441	GIGQNTA	0.240916	0.12394
SyS1408	3264	GCCCAACACAGAGTCGAAAACAGCTACGCACAG	7853	AQHRVENSYAQ	12442	HRVENSY	0.240897	-0.13677
GS785	3265	GCCCAAACTGAGTTTAAGCCTCCGTCGGCACAG	7854	AQTEFKPPSAQ	12443	TEFKPPS	0.240856	-0.16051
SyS1409	3266	GCCCAATATGGTAATTTGGGGGTTAATGCACAG	7855	AQYGNLGVNAQ	12444	YGNLGVN	0.240623	-0.09677
SyS1410	3267	GCCCAACTCACCAGAGTCCTCACCGGCGCACAG	7856	AQLTRVLTGAQ	12445	LTRVLTG	0.240472	-0.09192
SyS1411	3268	GCCCAAATGAAAAACAGCAACGGCGCCGCACAG	7857	AQMKNSNGAAQ	12446	MKNSNGA	0.240422	-0.05676
GS788	3269	GCCCAAGGCACCCAAACCCACCTCCAAGCACAG	7858	AQGTQTHLQAQ	12447	GTQTHLQ	0.24023	-0.15766
SyS1412	3270	GCCCAAAATGCGCTTGCTAGGACGATGGCACAG	7859	AQNALARTMAQ	12448	NALARTM	0.240048	-0.14768
GS789	3271	GCCCAAAATAATTCTATGCAGACGGTGGCACAG	7860	AQNNSMQTVAQ	12449	NNSMQTV	0.24002	-0.16035
GS790	3272	GCCCAACACAACAAGGCAACGGCAGAAGCGCACAG	7861	AQQQGNGRSAQ	12450	QQGNGRS	0.239981	-0.06255
GS791	3273	GCCCAACTCACCAAAAGCCAAGGCTACGCACAG	7862	AQLTKSQGYAQ	12451	LTKSQGY	0.239958	-0.05367

FIG. 33 (Continued)

SyS1413	3274	GCCCAAGCCCCCGCCGAACCCAAAACCGCACAG	7863	AQAPAEPKTAQ	12452	APAEPKT	0.239917	-0.07252
SyS1415	3275	GCCCAATATAGTAATCAGGTGAGTAATGCACAG	7864	AQYSNQVSNAQ	12453	YSNQVSN	0.23984	-0.17799
GS792	3276	GCCCAAACTCGTACGGGGTTTTCTCCTGCACAG	7865	AQTRTGFSPAQ	12454	TRTGFSP	0.23983	-0.09659
SyS1416	3277	GCCCAACCCGTCTACAAAACCGACGACGCACAG	7866	AQPVYKTDDAQ	12455	PVYKTDD	0.23942	0.109874
SyS1417	3278	GCCCAATCTGATAGGCCGGCTCCTGAGGCACAG	7867	AQSDRPAPEAQ	12456	SDRPAPE	0.239322	-0.20345
GS796	3279	GCCCAAGTTCAGGAGAAGTCGAGGCCTGCACAG	7868	AQVQEKSRPAQ	12457	VQEKSRP	0.239154	-0.05489
SyS1418	3280	GCCCAAAGCGGCGGCCTCACCGAAAGAGCACAG	7869	AQSGGLTERAQ	12458	SGGLTER	0.238974	0.018624
GS797	3281	GCCCAAAGCGGCGGCACCAGAGAAGGCGCACAG	7870	AQSGGTREGAQ	12459	SGGTREG	0.238968	-0.17195
GS798	3282	GCCCAAGCCGTCCCCGGCGAAACCAGAGCACAG	7871	AQAVPGETRAQ	12460	AVPGETR	0.238881	-0.10872
SyS1419	3283	GCCCAACCGCGGCCGGAGAGGATGTATGCACAG	7872	AQPRPERMYAQ	12461	PRPERMY	0.238847	-0.23376
SyS1420	3284	GCCCAAAGCAACGGCAACATCAGCAGAGCACAG	7873	AQSNGNISRAQ	12462	SNGNISR	0.23868	0.07724
GS799	3285	GCCCAAGCCAGAACCGAAAGAAACCAAGCACAG	7874	AQARTERNQAQ	12463	ARTERNQ	0.238676	-0.07152
SyS1421	3286	GCCCAAAGTCCTCAGCAGTTTTCGAAGGCACAG	7875	AQSPQQFSKAQ	12464	SPQQFSK	0.238555	-0.16766
SyS1422	3287	GCCCAAAGCACCGGCCCCTTCCCCCAAGCACAG	7876	AQSTGPFPQAQ	12465	STGPFPQ	0.238506	-0.2268
GS800	3288	GCCCAAGCCAACATCGGCACCAGCACCGCACAG	7877	AQANIGTSTAQ	12466	ANIGTST	0.238473	-0.1462
SyS1423	3289	GCCCAATACAGAGACAACACCAGCGGCGCACAG	7878	AQYRDNTSGAQ	12467	YRDNTSG	0.238378	-0.04463
SyS1424	3290	GCCCAAGTGCAGACTAGGTCTCCGATGGCACAG	7879	AQVQTRSPMAQ	12468	VQTRSPM	0.238378	-0.13435
SyS1425	3291	GCCCAAATCCACACCAGCATCGTCGACGCACAG	7880	AQIHTSIVDAQ	12469	IHTSIVD	0.238378	-0.1792
GS801	3292	GCCCAAATGACTCGGACTAGTAGTGAGGCACAG	7881	AQMTRTSSEAQ	12470	MTRTSSE	0.23833	-0.08134
SyP51	3293	GCCCAACCGTCGAATTTTCCTGGGTCTGCACAG	7882	AQPSNFPGSAQ	12471	PSNFPGS	0.238303	-0.0398
SyS1426	3294	GCCCAAATGATCGGCGGCACCCAAAGCGCACAG	7883	AQMIGGTQSAQ	12472	MIGGTQS	0.238168	-0.21921
SyS1427	3295	GCCCAAAAGCTTGATAAGCATGAGTCTGCACAG	7884	AQKLDKHESAQ	12473	KLDKHES	0.238069	-0.16951
SyS1428	3296	GCCCAACTTACGAGTAGTAATAGTGCTGCACAG	7885	AQLTSSNSAAQ	12474	LTSSNSA	0.23749	-0.09555
GS805	3297	GCCCAAAGTACTCGTGATACTCATTTTGCACAG	7886	AQSTRDTHFAQ	12475	STRDTHF	0.237351	-0.04196
GS808	3298	GCCCAAGATACGTTGAAGGCTGTTAGGGCACAG	7887	AQDTLKAVRAQ	12476	DTLKAVR	0.237261	-0.17201
GS809	3299	GCCCAACAGCGTAATCCGTCGCTTCATGCACAG	7888	AQQRNPSLHAQ	12477	QRNPSLH	0.237261	-0.14151
SyS1430	3300	GCCCAATCGGGTGATGGGAATCGTTCGGCACAG	7889	AQSGDGNRSAQ	12478	SGDGNRS	0.237239	0.28722
SyS1431	3301	GCCCAAGGCGTCTACAAAACCCTCCACGCACAG	7890	AQGVYKTLHAQ	12479	GVYKTLH	0.236906	-0.18042
GS812	3302	GCCCAAATTAATTCGAATCAGGTGAGTGCACAG	7891	AQINSNQVSAQ	12480	INSNQVS	0.236622	-0.1774
SyS1432	3303	GCCCAACACTACAACGAACACATGACCGCACAG	7892	AQHYNEHMTAQ	12481	HYNEHMT	0.236614	-0.05689
SyS1433	3304	GCCCAAACTGTGCAGGTTCGTGATCGGGCACAG	7893	AQTVQVRDRAQ	12482	TVQVRDR	0.236461	-0.06516
TS162	3305	GCCCAAGGCAACGACATCAGAAGCAGAGCACAG	7894	AQGNDIRSRAQ	12483	GNDIRSR	0.236352	0.106582

FIG. 33 (Continued)

SyS1434	3306	GCCCAAGTCAGCGTCAGCATGGGCCCCGCACAG	7895	AQVSVSMGPAQ	12484	VSVSMGP	0.236036	-0.02892
SyS1436	3307	GCCCAATTCAAAACCAACATCAGCGCCGCACAG	7896	AQFKTNISAAQ	12485	FKTNISA	0.235866	-0.12707
SyS1438	3308	GCCCAATTTCCGAAGGTGGAGAGGTATGCACAG	7897	AQFPKVERYAQ	12486	FPKVERY	0.235735	-0.23296
SyS1439	3309	GCCCAACTTAGTAAGTTTCAGACTACGGCACAG	7898	AQLSKFQTTAQ	12487	LSKFQTT	0.235498	-0.19723
SyS1442	3310	GCCCAAAGCCTCATGAACAGCAGAAGCGCACAG	7899	AQSLMNSRSAQ	12488	SLMNSRS	0.235263	-0.09106
SyP52	3311	GCCCAAGGGCGTGGGGTGCTGGAGTCTGCACAG	7900	AQGRGVLESAQ	12489	GRGVLES	0.235143	-0.04392
GS814	3312	GCCCAACCTAATGGGTCGCAGATGATTGCACAG	7901	AQPNGSQMIAQ	12490	PNGSQMI	0.235069	-0.1756
SyS1443	3313	GCCCAACCCACCGTCGGCAACAGCTACGCACAG	7902	AQPTVGNSYAQ	12491	PTVGNSY	0.234983	0.010187
SyS1444	3314	GCCCAAAGCAGCGACATCATGAAAGCCGCACAG	7903	AQSSDIMKAAQ	12492	SSDIMKA	0.234776	-0.13314
GS816	3315	GCCCAACTGATGACTAGTGCTGGTCGTGCACAG	7904	AQLMTSAGRAQ	12493	LMTSAGR	0.234691	-0.17829
SyS1447	3316	GCCCAACCCGCCATGAGCAGCAGAGAGCACAG	7905	AQPAMSSSRAQ	12494	PAMSSSR	0.234552	0.036927
GS817	3317	GCCCAACGTGATAAGGCGATTTCGACGGCACAG	7906	AQRDKAISTAQ	12495	RDKAIST	0.234493	-0.08025
GS818	3318	GCCCAATTGACTTTGAAGCAGGGGATTGCACAG	7907	AQLTLKQGIAQ	12496	LTLKQGI	0.234404	-0.1433
GS819	3319	GCCCAATCTCATGCTAATGGGTTTAGTGCACAG	7908	AQSHANGFSAQ	12497	SHANGFS	0.234293	-0.18099
SyS1449	3320	GCCCAACCGAATTTGAAGGCTCCGCAGGCACAG	7909	AQPNLKAPQAQ	12498	PNLKAPQ	0.233974	-0.18769
SyS1450	3321	GCCCAAAGCTACGGCAGAGAAGTCAGAGCACAG	7910	AQSYGREVRAQ	12499	SYGREVR	0.233931	-0.18284
SyS1451	3322	GCCCAAAACGACACCCAAAGCCCCAAAGCACAG	7911	AQNDTQSPKAQ	12500	NDTQSPK	0.233816	-0.16829
SyS1452	3323	GCCCAAGACGAAAGAGCCCCCAAACACGCACAG	7912	AQDERAPKHAQ	12501	DERAPKH	0.233748	-0.15859
GS820	3324	GCCCAAAACGGCAGACCCATGGGCATGGCACAG	7913	AQNGRPMGMAQ	12502	NGRPMGM	0.233736	-0.12617
GS821	3325	GCCCAACATACTCAGTCTGTGACTATGGCACAG	7914	AQHTQSVTMAQ	12503	HTQSVTM	0.233699	-0.16125
SyS1453	3326	GCCCAAAACAACTTCAACGCCAGCCTCGCACAG	7915	AQNNFNASLAQ	12504	NNFNASL	0.23358	-0.1295
SyS1454	3327	GCCCAAGAATACCTCAAAGGCAGCGCCGCACAG	7916	AQEYLKGSAAQ	12505	EYLKGSA	0.23358	-0.1295
GS822	3328	GCCCAATCTAAGACGCCTGATATGTTGGCACAG	7917	AQSKTPDMLAQ	12506	SKTPDML	0.233472	-0.15138
SyS1455	3329	GCCCAAGTCAACACCGGCCACGTCAGAGCACAG	7918	AQVNTGHVRAQ	12507	VNTGHVR	0.23344	-0.13454
GS823	3330	GCCCAAGGTTCTCAGTCGGATGCGCGTGCACAG	7919	AQGSQSDARAQ	12508	GSQSDAR	0.233353	-0.0985
SyS1456	3331	GCCCAATCTTTGACTTTTTCTAAGGATGCACAG	7920	AQSLTFSKDAQ	12509	SLTFSKD	0.233165	-0.15904
SyS1457	3332	GCCCAAAACGCCCTCGAAAGCAGAATGGCACAG	7921	AQNALESRMAQ	12510	NALESRM	0.233165	-0.18121
SyS1458	3333	GCCCAAAACGGCATCGCCAGAGAACCCGCACAG	7922	AQNGIAREPAQ	12511	NGIAREP	0.233148	0.030787
SyS1459	3334	GCCCAAAACCTCGTCAGCGTCAGCACCGCACAG	7923	AQNLVSVSTAQ	12512	NLVSVST	0.232787	-0.21694
SyS1461	3335	GCCCAAGACATGCTCAGCTACAAACCCGCACAG	7924	AQDMLSYKPAQ	12513	DMLSYKP	0.232747	0.049327
SyS1463	3336	GCCCAAAGAAGCACCGACAGCATGACCGCACAG	7925	AQRSTDSMTAQ	12514	RSTDSMT	0.232649	0.12732
SyS1464	3337	GCCCAAGAGATGAATCATAGTCTTTCTGCACAG	7926	AQEMNHSLSAQ	12515	EMNHSLS	0.232545	-0.18614

FIG. 33 (Continued)

GS827	3338	GCCCAAGCCCTCAGCAAAGAAGCCAGCGCACAG	7927	AQALSKEASAQ	12516	ALSKEAS	0.232439	-0.11949
SyS1465	3339	GCCCAAAACGGCCACAACATGAGCCAAGCACAG	7928	AQNGHNMSQAQ	12517	NGHNMSQ	0.232428	-0.00948
SyS1466	3340	GCCCAAACCACCGCCGAAGCCACCAGAGCACAG	7929	AQTTAEATRAQ	12518	TTAEATR	0.232428	-0.03372
SyS1467	3341	GCCCAAAGAGAAAGCGCCCACCACAACGCACAG	7930	AQRESAHHNAQ	12519	RESAHHN	0.232428	-0.12586
SyS1469	3342	GCCCAAATGTTTACGGGGAATGGGCAGGCACAG	7931	AQMFTGNGQAQ	12520	MFTGNGQ	0.232428	-0.218
SyS1470	3343	GCCCAACATCTTCAGACGCCGCCGGCTGCACAG	7932	AQHLQTPPAAQ	12521	HLQTPPA	0.232331	-0.2305
SyS1471	3344	GCCCAATCGCTTGTGGGTCAGGGTAAGGCACAG	7933	AQSLVGQGKAQ	12522	SLVGQGK	0.232298	-0.09584
SyS1472	3345	GCCCAACTCCCCCTCACCCCCATCGCCGCACAG	7934	AQLPLTPIAAQ	12523	LPLTPIA	0.232279	0.019127
GS828	3346	GCCCAAGCTATGAAGCAGTCGTCTATTGCACAG	7935	AQAMKQSSIAQ	12524	AMKQSSI	0.232051	-0.12341
GS829	3347	GCCCAATATCCTACGAATGTGAAGTCGGCACAG	7936	AQYPTNVKSAQ	12525	YPTNVKS	0.232018	0.099106
SyS1473	3348	GCCCAAAGCAACAGCCTCCCCAGCAGAGCACAG	7937	AQSNSLPSRAQ	12526	SNSLPSR	0.231997	-0.06106
GS830	3349	GCCCAACCGACGGCGGCTACTGGGACGGCACAG	7938	AQPTAATGTAQ	12527	PTAATGT	0.231918	-0.16528
GS831	3350	GCCCAAATCGCCCAAAACGGCCCCGGCGCACAG	7939	AQIAQNGPGAQ	12528	IAQNGPG	0.231887	-0.12998
SyS1475	3351	GCCCAAACTACTCATCAGCTTACTCCGGCACAG	7940	AQTTHQLTPAQ	12529	TTHQLTP	0.231805	0.179914
SyS1476	3352	GCCCAACTTATTCCTGCGAGGGATGTGGCACAG	7941	AQLIPARDVAQ	12530	LIPARDV	0.231788	-0.0519
SyS1477	3353	GCCCAAAAAATCGCCCACGGCGACATCGCACAG	7942	AQKIAHGDIAQ	12531	KIAHGDI	0.231565	-0.05433
SyS1478	3354	GCCCAAGCCAGACCCCAAAGCGACAAAGCACAG	7943	AQARPQSDKAQ	12532	ARPQSDK	0.231506	0.192363
SyS1479	3355	GCCCAACCCAGACCCAACGTCCTCGACGCACAG	7944	AQPRPNVLDAQ	12533	PRPNVLD	0.231372	0.138428
GS833	3356	GCCCAACTCAACAAAGGCAGCAGCAACGCACAG	7945	AQLNKGSSNAQ	12534	LNKGSSN	0.231355	-0.0385
GS834	3357	GCCCAACGGGTTTATAATGGTGATCTGGCACAG	7946	AQRVYNGDLAQ	12535	RVYNGDL	0.231254	-0.14048
SyS1481	3358	GCCCAAACCGTCCCCGCCAACAGCAGCGCACAG	7947	AQTVPANSSAQ	12536	TVPANSS	0.231245	-0.13677
SyS1482	3359	GCCCAAACCAGACACACCAGCCTCACCGCACAG	7948	AQTRHTSLTAQ	12537	TRHTSLT	0.231191	-0.14647
SS95	3360	GCCCAAAATCATGCGGTGACGAATTCTGCACAG	7949	AQNHAVTNSAQ	12538	NHAVTNS	0.231161	-0.29794
SyS1483	3361	GCCCAATTGGCGTCGCATTCTACGCTTGCACAG	7950	AQLASHSTLAQ	12539	LASHSTL	0.231132	-0.15617
GS836	3362	GCCCAAGTCGCCTTCAAAAGCGGCATCGCACAG	7951	AQVAFKSGIAQ	12540	VAFKSGI	0.231125	-0.13792
SyS1484	3363	GCCCAAAGAGTCGGCCCCGAAAGCAGCGCACAG	7952	AQRVGPESSAQ	12541	RVGPESS	0.231067	-0.16587
GS838	3364	GCCCAAGCCCCCAGCAACGTCCACACCGCACAG	7953	AQAPSNVHTAQ	12542	APSNVHT	0.231055	-0.05067
SyS1485	3365	GCCCAAACTAGGTCGGAGGTGATGAAGGCACAG	7954	AQTRSEVMKAQ	12543	TRSEVMK	0.230872	-0.19011
GS839	3366	GCCCAATTGAAGGAGCAGCATGGTGGGGCACAG	7955	AQLKEQHGGAQ	12544	LKEQHGG	0.230779	-0.18009
SP37	3367	GCCCAAAAGGCGGAGTCGCATGCGACGGCACAG	7956	AQKAESHATAQ	12545	KAESHAT	0.230702	-0.0491
SyS1486	3368	GCCCAATATAGGACGGATATGCTGAGTGCACAG	7957	AQYRTDMLSAQ	12546	YRTDMLS	0.230667	-0.20955
GS841	3369	GCCCAAGATACGCAGGGGAGGATGCGGGCACAG	7958	AQDTQGRMRAQ	12547	DTQGRMR	0.230611	-0.10327

FIG. 33 (Continued)

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GS842	3370	GCCCAATGTCTTCCTAAGGGTTGTACGGCACAG	7959	AQCLPKGCTAQ	12548	CLPKGCT	0.230518	-0.15097
SyS1487	3371	GCCCAAGGCAGCCCCACCGTCGTCCACGCACAG	7960	AQGSPTVVHAQ	12549	GSPTVVH	0.230363	-0.07403
SyS1488	3372	GCCCAATTGTCGCTTTCTACGCAGAGGGCACAG	7961	AQLSLSTQRAQ	12550	LSLSTQR	0.230358	-0.10005
GS843	3373	GCCCAAAACATGGCCCAAAACGCCAGAGCACAG	7962	AQNMAQNARAQ	12551	NMAQNAR	0.230121	-0.1462
GS845	3374	GCCCAACTCAGCACCAACGTCCTCCTCGCACAG	7963	AQLSTNVLLAQ	12552	LSTNVLL	0.229919	-0.16573
GS846	3375	GCCCAAACTTCGCCTGTTATTCGTACTGCACAG	7964	AQTSPVIRTAQ	12553	TSPVIRT	0.229823	-0.17386
SyS1490	3376	GCCCAACCTAGTGCTGGTCATGTTTTTGGCACAG	7965	AQPSAGHVLAQ	12554	PSAGHVL	0.229391	-0.18648
GS849	3377	GCCCAACTGTCTGGTACGGCTACTTCGGCACAG	7966	AQLSGTATSAQ	12555	LSGTATS	0.229374	-0.16909
SyS1491	3378	GCCCAAACGGGTAATCCGAATCCGACTGCACAG	7967	AQTGNPNPTAQ	12556	TGNPNPT	0.229306	-0.17998
SyS1492	3379	GCCCAACAATTCGAACACAGCCTCCCCGCACAG	7968	AQQFEHSLPAQ	12557	QFEHSLP	0.229163	-0.03857
SyS1493	3380	GCCCAACTCACCCCCGGCCAAATCAGAGCACAG	7969	AQLTPGQIRAQ	12558	LTPGQIR	0.229124	0.08066
GS850	3381	GCCCAACTGATGAATGCGAAGACGACGGCACAG	7970	AQLMNAKTTAQ	12559	LMNAKTT	0.22906	-0.06983
SyS1494	3382	GCCCAACAAAGAGACACCAACATGGCCGCACAG	7971	AQQRDTNMAAQ	12560	QRDTNMA	0.228811	0.109343
SyS1495	3383	GCCCAAAACCTCCTCGAAATCGGCAGAGCACAG	7972	AQNLLEIGRAQ	12561	NLLEIGR	0.228652	-0.22042
SyS1496	3384	GCCCAAGACGTCAAAGACAAACAAATCGCACAG	7973	AQDVKDKQIAQ	12562	DVKDKQI	0.228561	-0.08214
GS851	3385	GCCCAAGTGACTATTTCGAATAAGCCTGCACAG	7974	AQVTISNKPAQ	12563	VTISNKP	0.228495	-0.06638
SyS1497	3386	GCCCAAAGCACACCCCATCAACAGCAGAGCACAG	7975	AQSTPINSRAQ	12564	STPINSR	0.228369	-0.10161
SyS1499	3387	GCCCAAGGCACCCACGGCCTCACCAGCGCACAG	7976	AQGTHGLTSAQ	12565	GTHGLTS	0.228217	0.021364
SyS1500	3388	GCCCAACAGTCTCCGGGGATGATTCATGCACAG	7977	AQQSPGMIHAQ	12566	QSPGMIH	0.228178	-0.10536
SyS1501	3389	GCCCAACAAACCGGCCCCGTCCTCAGCGCACAG	7978	AQQTGPVLSAQ	12567	QTGPVLS	0.2281	-0.17799
GS853	3390	GCCCAAACTTATGTGTCGTCTGGTCCGGCACAG	7979	AQTYVSSGPAQ	12568	TYVSSGP	0.228034	-0.07561
SyS1502	3391	GCCCAAACCAGCACCCTCCCCAGACTCGCACAG	7980	AQTSTLPRLAQ	12569	TSTLPRL	0.227986	-0.21571
SyS1503	3392	GCCCAATACACCCACAAAGACAACGACGCACAG	7981	AQYTHKDNDAQ	12570	YTHKDND	0.227932	-0.20709
SyS1504	3393	GCCCAACTCGGCGCCCAAAGCACCCTCGCACAG	7982	AQLGAQSTLAQ	12571	LGAQSTL	0.227857	-0.18769
SyS1505	3394	GCCCAATTGGCGCAGGTTAGGCCTGCTGCACAG	7983	AQLAQVRPAAQ	12572	LAQVRPA	0.227792	-0.01727
GS854	3395	GCCCAAGGCAGAGTCGTCGCCAGCAACGCACAG	7984	AQGRVVASNAQ	12573	GRVVASN	0.227751	-0.11202
TS165	3396	GCCCAAAGTAATCGGGTTAGGGATCTTGCACAG	7985	AQSNRVRDLAQ	12574	SNRVRDL	0.227718	-0.09285
SyS1506	3397	GCCCAAGAAAGAGACAGAGAAAAACTCGCACAG	7986	AQERDREKLAQ	12575	ERDREKL	0.227632	-0.12947
GS855	3398	GCCCAAAAGTCTGGGACGAGTTCTACTGCACAG	7987	AQKSGTSSTAQ	12576	KSGTSST	0.227463	-0.16214
SyS1507	3399	GCCCAAGCTGGTCAGAGTACTATTTATGCACAG	7988	AQAGQSTIYAQ	12577	AGQSTIY	0.227436	-0.20224
GS856	3400	GCCCAAGAGTTTTCGCAGCCGAGGCTGGCACAG	7989	AQEFSQPRLAQ	12578	EFSQPRL	0.22738	-0.18245
GS857	3401	GCCCAAACGTATGCGAGGTCGGATAAGGCACAG	7990	AQTYARSDKAQ	12579	TYARSDK	0.227253	-0.11091

FIG. 33 (Continued)

GS859	3402	GCCCAAGGCAAATTCAACGGCCACACCGCACAG	7991	AQGKFNGHTAQ	12580	GKFNGHT	0.227141	-0.07202
GS860	3403	GCCCAACGGTTGATTAGTAATGGGAATGCACAG	7992	AQRLISNGNAQ	12581	RLISNGN	0.227083	-0.13571
GS861	3404	GCCCAATTGAAGGAGTCGTTGGGGCCTGCACAG	7993	AQLKESLGPAQ	12582	LKESLGP	0.226974	-0.14811
GS862	3405	GCCCAAAACAGACACACCCTCGCCGTCGCACAG	7994	AQNRHTLAVAQ	12583	NRHTLAV	0.226794	-0.18188
GS863	3406	GCCCAAAGAGACACCAGACTCAGCGCCGCACAG	7995	AQRDTRLSAAQ	12584	RDTRLSA	0.226714	-0.14334
GS864	3407	GCCCAAGTCAGCAGACTCGGCAGCATCGCACAG	7996	AQVSRLGSIAQ	12585	VSRLGSI	0.226686	-0.12988
GS865	3408	GCCCAATTGACTACGTCGGTGATTTCGGCACAG	7997	AQLTTSVISAQ	12586	LTTSVIS	0.226678	-0.17291
SyS1509	3409	GCCCAATTTAAGGGGGGTGGCTCATATTGCACAG	7998	AQFKGVAHIAQ	12587	FKGVAHI	0.226637	-0.1792
GS866	3410	GCCCAAAAGACGACGGAGGCTCTTCCTGCACAG	7999	AQKTTEALPAQ	12588	KTTEALP	0.226561	-0.15574
SyS1510	3411	GCCCAACGTAATCAGCATGATACTACTGCACAG	8000	AQRNQHDTTAQ	12589	RNQHDTT	0.226461	-0.1307
SyS1511	3412	GCCCAAAATAAGCTTCTGCCTCGTAGTGCACAG	8001	AQNKLLPRSAQ	12590	NKLLPRS	0.226387	-0.15657
GS867	3413	GCCCAAGTCAACAGCCACGAAAGAGCCGCACAG	8002	AQVNSHERAAQ	12591	VNSHERA	0.226374	-0.16814
GS868	3414	GCCCAAGCGAAGGGTAGTCTGAATATGGCACAG	8003	AQAKGSLNMAQ	12592	AKGSLNM	0.22628	-0.08549
SyS1512	3415	GCCCAAGTTAAGACTGATCGGGTTCTGGCACAG	8004	AQVKTDRVLAQ	12593	VKTDRVL	0.226235	-0.04586
SyS1513	3416	GCCCAACCGCGTTCGGATCAGATTAGGGCACAG	8005	AQPRSDQIRAQ	12594	PRSDQIR	0.226105	-0.21694
GS869	3417	GCCCAAAACAGAGTCGGCACCGAAAGAGCACAG	8006	AQNRVGTERAQ	12595	NRVGTER	0.226048	-0.00622
SyS1514	3418	GCCCAAGGCGTCCCCACCGCCGGCACCGCACAG	8007	AQGVPTAGTAQ	12596	GVPTAGT	0.226045	-0.22557
GS870	3419	GCCCAAAGCCTCATGAAACAAAGCCACGCACAG	8008	AQSLMKQSHAQ	12597	SLMKQSH	0.225961	-0.13881
GS871	3420	GCCCAAGGCACCAGCAGCAACATCATGGCACAG	8009	AQGTSSNIMAQ	12598	GTSSNIM	0.225838	-0.14143
SyS1515	3421	GCCCAACTTCGGAGTGATATTAGTACTGCACAG	8010	AQLRSDISTAQ	12599	LRSDIST	0.225835	-0.09082
GS872	3422	GCCCAAATGACCACCGGCAGAGACCTCGCACAG	8011	AQMTTGRDLAQ	12600	MTTGRDL	0.225564	-0.06321
SyS1516	3423	GCCCAAAGTGGTGTTGCGAATAGTTATGCACAG	8012	AQSGVANSYAQ	12601	SGVANSY	0.225464	-0.10606
SyS1517	3424	GCCCAAGCGGTTCCGTCTTATAATAATGCACAG	8013	AQAVPSYNNAQ	12602	AVPSYNN	0.225384	-0.18728
GS873	3425	GCCCAACTCAACGGCGGCAACAGCCCCGCACAG	8014	AQLNGGNSPAQ	12603	LNGGNSP	0.225327	-0.11997
GS874	3426	GCCCAAAACAGCCACACCAGCTGGGCACAG	8015	AQNSHSTSWAQ	12604	NSHSTSW	0.225327	-0.17291
GS875	3427	GCCCAAATGTATCATACGGGGCAGGTGGCACAG	8016	AQMYHTGQVAQ	12605	MYHTGQV	0.22518	-0.15855
GS876	3428	GCCCAAAGAGACAAACTCTACATCGCCGCACAG	8017	AQRDKLYIAAQ	12606	RDKLYIA	0.225179	-0.14429
SyS1518	3429	GCCCAAAGGAAGTCGGAGGCGGTTCTTGCACAG	8018	AQRKSEAVLAQ	12607	RKSEAVL	0.225067	-0.14768
SyP53	3430	GCCCAACATAAGGGTATTCAGGTGATTGCACAG	8019	AQHKGIQVIAQ	12608	HKGIQVI	0.224991	-0.04221
GP146	3431	GCCCAAATTGGGAAGGATGCTCCGAAGGCACAG	8020	AQIGKDAPKAQ	12609	IGKDAPK	0.224985	-0.06655
SyS1519	3432	GCCCAAAGCCTCGCCGGCCTCCAAGACGCACAG	8021	AQSLAGLQDAQ	12610	SLAGLQD	0.22498	0.118922
SyS1520	3433	GCCCAATTTAGGGTGTCTGTTGCTGAGGCACAG	8022	AQFRVSVAEAQ	12611	FRVSVAE	0.22497	-0.2305

FIG. 33 (Continued)

SyS1521	3434	GCCCAAACCCACAAAGAACACAGCATCGCACAG	8023	AQTHKEHSIAQ	12612	THKEHSI	0.2249	-0.06105
SyS1522	3435	GCCCAAAACAGCAACCACACCTACAGAGCACAG	8024	AQNSNHTYRAQ	12613	NSNHTYR	0.224808	-0.22285
SyS1523	3436	GCCCAATTTAATGGGGTTCGTACGGTGGCACAG	8025	AQFNGVRTVAQ	12614	FNGVRTV	0.224692	-0.12465
GS878	3437	GCCCAACACATGGGCATGAGAGACGGCGCACAG	8026	AQHMGMRDGAQ	12615	HMGMRDG	0.22465	-0.16125
SyS1524	3438	GCCCAAGGGCAGCAGTCTATGGCGGTGGCACAG	8027	AQGQQSMAVAQ	12616	GQQSMAV	0.224648	-0.1923
GS879	3439	GCCCAATGGTCGAGTCAGGTTAATCGTGCACAG	8028	AQWSSQVNRAQ	12617	WSSQVNR	0.224293	-0.16432
SyS1525	3440	GCCCAAGGTTCGCATGTTGGGATGCCGGCACAG	8029	AQGSHVGMPAQ	12618	GSHVGMP	0.224189	-0.1392
GP147	3441	GCCCAAAAGGGGTCGTTGACTGCTAGTGCACAG	8030	AQKGSLTASAQ	12619	KGSLTAS	0.224166	-0.06794
SyS1526	3442	GCCCAAGGCGCCCAAAGCAACATCGTCGCACAG	8031	AQGAQSNIVAQ	12620	GAQSNIV	0.224129	-0.07858
GS880	3443	GCCCAAAATGATTATAATCATACGCGTGCACAG	8032	AQNDYNHTRAQ	12621	NDYNHTR	0.224097	-0.18547
GS881	3444	GCCCAACAAATCAACCCCAGCAGCGTCGCACAG	8033	AQQINPSSVAQ	12622	QINPSSV	0.224097	-0.17829
GS882	3445	GCCCAAGCGTTGCGTGGTGCGTCTAATGCACAG	8034	AQALRGASNAQ	12623	ALRGASN	0.224097	-0.17112
SyS1527	3446	GCCCAAAGTGCTTCGACTATGTCGTTTGCACAG	8035	AQSASTMSFAQ	12624	SASTMSF	0.223975	-0.13887
GS883	3447	GCCCAACTCAGCAGCAACAACAACAACGCACAG	8036	AQLSSNNNNAQ	12625	LSSNNNN	0.223961	-0.10614
GS884	3448	GCCCAATCTACGACGCTGGCGTCGAAGGCACAG	8037	AQSTTLASKAQ	12626	STTLASK	0.223954	-0.1411
GS885	3449	GCCCAACACAGAATGCTCGACGGCGTCGCACAG	8038	AQHRMLDGVAQ	12627	HRMLDGV	0.223938	-0.15478
SyS1528	3450	GCCCAAAGCAGCGAAAGCAGCACCCCCGCACAG	8039	AQSSESSTPAQ	12628	SSESSTP	0.223912	-0.17678
GS886	3451	GCCCAATTGTATGATTCTAGTCATAGTGCACAG	8040	AQLYDSSHSAQ	12629	LYDSSHS	0.223828	-0.13594
SyS1529	3452	GCCCAAGGTAATTATAATTTGAGTGTGGCACAG	8041	AQGNYNLSVAQ	12630	GNYNLSV	0.223824	-0.18808
GS887	3453	GCCCAAATGCATAATGTTGCTACGGTGGCACAG	8042	AQMHNVATVAQ	12631	MHNVATV	0.223778	-0.12132
SyS1530	3454	GCCCAAACCAACTACGGCGACAGCGTCGCACAG	8043	AQTNYGDSVAQ	12632	TNYGDSV	0.223637	-0.06038
SyS1531	3455	GCCCAAAATCGTGGGGAGGATGCGCGGGCACAG	8044	AQNRGEDARAQ	12633	NRGEDAR	0.223622	0.017796
GS889	3456	GCCCAATTTGGTAAGACGGCGGCTACTGCACAG	8045	AQFGKTAATAQ	12634	FGKTAAT	0.223612	-0.1451
GS890	3457	GCCCAAAATACGAAGGTTAATACTGAGGCACAG	8046	AQNTKVNTEAQ	12635	NTKVNTE	0.223612	-0.1451
GS891	3458	GCCCAAGTCACCGGCCACCTCAGCAGCGCACAG	8047	AQVTGHLSSAQ	12636	VTGHLSS	0.223553	-0.15945
SyS1532	3459	GCCCAAGTGGCTACTTCGCATTTGAAGGCACAG	8048	AQVATSHLKAQ	12637	VATSHLK	0.223491	-0.21436
SyS1533	3460	GCCCAATACACCCCCGGCAGCGACAGAGCACAG	8049	AQYTPGSDRAQ	12638	YTPGSDR	0.223431	-0.03541
SyS1534	3461	GCCCAAGGCTTCACCACCGTCACCCACGCACAG	8050	AQGFTTVTHAQ	12639	GFTTVTH	0.223406	-0.15859
SyS1535	3462	GCCCAAGCCGCCGCCACCAGCACCACCGCACAG	8051	AQAAATSTTAQ	12640	AAATSTT	0.223334	-0.08247
SyS1536	3463	GCCCAAGCGAATATTCATGTTCATGGTGCACAG	8052	AQANIHVHGAQ	12641	ANIHVHG	0.223187	-0.13556
SyS1537	3464	GCCCAATATAGTTTGCGGGGTAATGATGCACAG	8053	AQYSLRGNDAQ	12642	YSLRGND	0.223187	-0.16344
SyS1538	3465	GCCCAAATTGATCAGATTGTGCAGCGTGCACAG	8054	AQIDQIVQRAQ	12643	IDQIVQR	0.223187	-0.19133

FIG. 33 (Continued)

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SyS1539	3466	GCCCAATTCAACAGCGACCTCGCCATGGCACAG	8055	AQFNSDLAMAQ	12644	FNSDLAM	0.223187	-0.19133
SyS1540	3467	GCCCAAAATATGGAGTCGCAGCGTTATGCACAG	8056	AQNMESQRYAQ	12645	NMESQRY	0.223135	-0.2231
SyP54	3468	GCCCAACCGCTTTCTAGTTCGCTTTCGGCACAG	8057	AQPLSSSLSAQ	12646	PLSSSLS	0.222938	-0.04335
SyS1541	3469	GCCCAACAGGGTACGCTTCATGCTGAGGCACAG	8058	AQQGTLHAEAQ	12647	QGTLHAE	0.222917	-0.19618
SyS1542	3470	GCCCAACCCGACAGAGCCACCGCCCTCGCACAG	8059	AQPDRATALAQ	12648	PDRATAL	0.222911	-0.1344
SyS1543	3471	GCCCAAGCCAACGGCAAAATCCAACTCGCACAG	8060	AQANGKIQLAQ	12649	ANGKIQL	0.22286	0.163533
SyS1545	3472	GCCCAATACAGCAAAGACAGACACGACGCACAG	8061	AQYSKDRHDAQ	12650	YSKDRHD	0.22263	0.135905
SyS1546	3473	GCCCAAGACAGCACCAGCAGAGCCTGGGCACAG	8062	AQDSTSRAWAQ	12651	DSTSRAW	0.222511	-0.22891
SyS1547	3474	GCCCAAGGCCTCAGCGTCGCCATCCCCGCACAG	8063	AQGLSVAIPAQ	12652	GLSVAIP	0.222511	-0.22891
SyS1548	3475	GCCCAATCGTATCTTACTAATCATGTGGCACAG	8064	AQSYLTNHVAQ	12653	SYLTNHV	0.222327	-0.20588
SyS1550	3476	GCCCAAGTTATTACGCATAATATGCCTGCACAG	8065	AQVITHNMPAQ	12654	VITHNMP	0.222221	-0.13192
GS894	3477	GCCCAAAACAGAACCCACGTCCCCCAAGCACAG	8066	AQNRTHVPQAQ	12655	NRTHVPQ	0.222189	-0.10995
GS895	3478	GCCCAACTCCAAACCACCAGAGCCGTCGCACAG	8067	AQLQTTRAVAQ	12656	LQTTRAV	0.222058	0.00505
SyS1551	3479	GCCCAAGCCCCCAACGCCATCGACGTCGCACAG	8068	AQAPNAIDVAQ	12657	APNAIDV	0.222003	-0.13677
GS896	3480	GCCCAAGTCAGAGACAACACCGTCTACGCACAG	8069	AQVRDNTVYAQ	12658	VRDNTVY	0.221995	-0.14143
SyS1552	3481	GCCCAAACTCGTATTGGGACGTCGTTGGCACAG	8070	AQTRIGTSLAQ	12659	TRIGTSL	0.221747	-0.01731
SyS1553	3482	GCCCAAACCCTCACCAGCGGCAACGTCGCACAG	8071	AQTLTSGNVAQ	12660	TLTSGNV	0.221657	0.075338
GS897	3483	GCCCAACATCTTGATACTATGCGGGGGTGCACAG	8072	AQHLDTMRGAQ	12661	HLDTMRG	0.221624	-0.14743
GS898	3484	GCCCAACTCAGCAGCACCACCCTCAACGCACAG	8073	AQLSSTTLNAQ	12662	LSSTTLN	0.221499	-0.10327
TS166	3485	GCCCAAGTTCAGAGTAATAGGACTAATGCACAG	8074	AQVQSNRTNAQ	12663	VQSNRTN	0.221422	-0.26117
SyS1554	3486	GCCCAAAATAATAATATTACGACGTCTGCACAG	8075	AQNNNITTSAQ	12664	NNNITTS	0.221339	-0.15304
GS899	3487	GCCCAAGTCGGCACCGCCGGCAAACTCGCACAG	8076	AQVGTAGKLAQ	12665	VGTAGKL	0.221334	-0.1471
SyS1555	3488	GCCCAACCCGCCATCAGCACCGACCACGCACAG	8077	AQPAISTDHAQ	12666	PAISTDH	0.22129	-0.17435
GP148	3489	GCCCAAAGTAATCTGGGTAATGTGCCGGCACAG	8078	AQSNLGNVPAQ	12667	SNLGNVP	0.22117	-0.04186
SyS1556	3490	GCCCAACAAAACCAAAGCAGATTCACCGCACAG	8079	AQQNQSRFTAQ	12668	QNQSRFT	0.221076	0.133629
GS900	3491	GCCCAAGCTTCTAAGGGTATGACGTTGGCACAG	8080	AQASKGMTLAQ	12669	ASKGMTL	0.221024	-0.11947
SyS1557	3492	GCCCAAGCCACCCGCCCAAGACAAAACCGCACAG	8081	AQATAQDKTAQ	12670	ATAQDKT	0.220998	-0.14056
SS100	3493	GCCCAATGGGACAGCAGCAGCGTCAGAGCACAG	8082	AQWDSSSVRAQ	12671	WDSSSVR	0.220864	-0.36436
SyS1558	3494	GCCCAAACGAATGGTAGTGAGAAGAGTGCACAG	8083	AQTNGSEKSAQ	12672	TNGSEKS	0.220858	-0.11495
SyS1560	3495	GCCCAATCTGCTGAGAATCATACGTATGCACAG	8084	AQSAENHTYAQ	12673	SAENHTY	0.220753	-0.21202
SyS1561	3496	GCCCAAAGCGTCCCCCAAGCCTACCAAGCACAG	8085	AQSVPQAYQAQ	12674	SVPQAYQ	0.220753	-0.23296
SyS1562	3497	GCCCAAAAAGACTACGTCGTCACCAACGCACAG	8086	AQKDYVVTNAQ	12675	KDYVVTN	0.220753	-0.23296

FIG. 33 (Continued)

SyS1563	3498	GCCCAAGTCGTCCAAATGAAACAAACCGCACAG	8087	AQVVQMKQTAQ	12676	VVQMKQT	0.220688	-0.18405
GS901	3499	GCCCAAAGAACCCTCAGCCTCACCGCCGCACAG	8088	AQRTLSLTAAQ	12677	RTLSLTA	0.220684	-0.171
GS902	3500	GCCCAAAACACCGTCGTCGGCAGCAGCGCACAG	8089	AQNTVVGSSAQ	12678	NTVVGSS	0.220539	-0.15192
GS903	3501	GCCCAATCTTTGAATAGTCCGACGACTGCACAG	8090	AQSLNSPTTAQ	12679	SLNSPTT	0.220388	-0.12331
SyS1564	3502	GCCCAAACCACCGGCATGGACGTCAAAGCACAG	8091	AQTTGMDVKAQ	12680	TTGMDVK	0.220289	-0.06566
GS907	3503	GCCCAAAACAACAGAGACACCACCAACGCACAG	8092	AQNNRDTTNAQ	12681	NNRDTTN	0.220068	-0.11907
GS908	3504	GCCCAATGGGGCAACTACACCCCCACCGCACAG	8093	AQWGNYTPTAQ	12682	WGNYTPT	0.220016	-0.16842
SyS1565	3505	GCCCAAGGGATTACGCGTTCTGATACTGCACAG	8094	AQGITRSDTAQ	12683	GITRSDT	0.219828	-0.01242
GS910	3506	GCCCAACACATCCTCAGAACCCCCGAAGCACAG	8095	AQHILRTPEAQ	12684	HILRTPE	0.219735	-0.1756
GS911	3507	GCCCAACGTTCTGCTAGTGTGGAGAATGCACAG	8096	AQRSASVENAQ	12685	RSASVEN	0.219721	-0.14524
SyS1568	3508	GCCCAAAGCCTCAGCCTCGGCAAAGGCGCACAG	8097	AQSLSLGKGAQ	12686	SLSLGKG	0.219525	-0.0022
SyS1570	3509	GCCCAAAAAAGAGAAGTCGTCGGCGACGCACAG	8098	AQKREVVGDAQ	12687	KREVVGD	0.219431	-0.0561
SyS1571	3510	GCCCAAATCCAACCCAGCAACCACGAAGCACAG	8099	AQIQPSNHEAQ	12688	IQPSNHE	0.219421	-0.16223
GS912	3511	GCCCAAATGAATCTGGGTAATGCGCCGGCACAG	8100	AQMNLGNAPAQ	12689	MNLGNAP	0.219412	-0.18278
SyS1572	3512	GCCCAACAGCCGAATAATACTAATAGTGCACAG	8101	AQQPNNTNSAQ	12690	QPNNTNS	0.219392	-0.15739
GS914	3513	GCCCAACTCCAAAGCATGGTCCAAGGCGCACAG	8102	AQLQSMVQGAQ	12691	LQSMVQG	0.219195	-0.14779
SyS1573	3514	GCCCAACATGGTAATACTACTTCGACTGCACAG	8103	AQHGNTTSTAQ	12692	HGNTTST	0.219043	-0.04692
SyS1576	3515	GCCCAAATCCAAAGCACCGTCACCCTCGCACAG	8104	AQIQSTVTLAQ	12693	IQSTVTL	0.218993	-0.14672
SyS1577	3516	GCCCAAGACGACAGACAAGGCCCCAGAGCACAG	8105	AQDDRQGPRAQ	12694	DDRQGPR	0.218992	-0.13071
SyS1578	3517	GCCCAACAGACGGCTACGAATATTCTGGCACAG	8106	AQQTATNILAQ	12695	QTATNIL	0.218912	-0.22649
GS915	3518	GCCCAACGGCAGCATGCGGATACTGTTGCACAG	8107	AQRQHADTVAQ	12696	RQHADTV	0.218828	-0.10831
GS916	3519	GCCCAAACTAGGTCGGAGAGTTCTCTGGCACAG	8108	AQTRSESSLAQ	12697	TRSESSL	0.218795	-0.16718
GS917	3520	GCCCAACGTGGGCATGATCCGGCTGTGGCACAG	8109	AQRGHDPAVAQ	12698	RGHDPAV	0.218795	-0.16718
SyS1579	3521	GCCCAAAGCACCAGCCAAACCGACCTCGCACAG	8110	AQSTSQTDLAQ	12699	STSQTDL	0.218784	-0.10958
SyS1580	3522	GCCCAAGTCAGCACCAGCGCCGTCCTCGCACAG	8111	AQVSTSAVLAQ	12700	VSTSAVL	0.218614	-0.10842
SyS1581	3523	GCCCAAAGCATGCCCCCCGAAAGATTCGCACAG	8112	AQSMPPERFAQ	12701	SMPPERF	0.218531	-0.14302
SS104	3524	GCCCAAGTCACCAGCGCCCACCCCGTCGCACAG	8113	AQVTSAHPVAQ	12702	VTSAHPV	0.218414	-0.35519
SyS1582	3525	GCCCAAACCAGCAGACAAGTCGGCCTCGCACAG	8114	AQTSRQVGLAQ	12703	TSRQVGL	0.218414	-0.08585
SyS1583	3526	GCCCAAACTCCGAAGTTTTCTTATGAGGCACAG	8115	AQTPKFSYEAQ	12704	TPKFSYE	0.218414	-0.23133
GS918	3527	GCCCAAAACAGAATGGCCAGCACCATGGCACAG	8116	AQNRMASTMAQ	12705	NRMASTM	0.218278	-0.15766
SyS1584	3528	GCCCAACTCCTCGACAACACCAGACCCGCACAG	8117	AQLLDNTRPAQ	12706	LLDNTRP	0.218247	0.036592
GS919	3529	GCCCAATTGACGACTATTCCTAGTACTGCACAG	8118	AQLTTIPSTAQ	12707	LTTIPST	0.218243	-0.16932

FIG. 33 (Continued)

TS168	3530	GCCCAAGCCAACAGAATCAGAGACAACGCACAG	8119	AQANRIRDNAQ	12708	ANRIRDN	0.218215	-0.03931
SyS1585	3531	GCCCAACCCAGAGACATCCAAAGAACCGCACAG	8120	AQPRDIQRTAQ	12709	PRDIQRT	0.218142	-0.00772
GP149	3532	GCCCAAATGCCTCATGGGCTTAAGAATGCACAG	8121	AQMPHGLKNAQ	12710	MPHGLKN	0.218113	-0.06725
SyS1586	3533	GCCCAACCTTTTACGCAGAATCATCTTGCACAG	8122	AQPFTQNHLAQ	12711	PFTQNHL	0.218077	-0.16344
SyS1587	3534	GCCCAAAATGCGAATGGTAATACTCGTGCACAG	8123	AQNANGNTRAQ	12712	NANGNTR	0.218042	-0.18163
GS920	3535	GCCCAACTGGCTTATTCTACGTCGGCGGCACAG	8124	AQLAYSTSAAQ	12713	LAYSTSA	0.217974	0.000834
GS921	3536	GCCCAAACCGACAGATACAACATCAAAGCACAG	8125	AQTDRYNIKAQ	12714	TDRYNIK	0.217916	-0.16484
GS922	3537	GCCCAATATGTTACTAGTGCTGAGCATGCACAG	8126	AQYVTSAEHAQ	12715	YVTSAEH	0.217839	-0.1765
GS923	3538	GCCCAAAGTCATCAGCAGACTACGGTTGCACAG	8127	AQSHQQTTVAQ	12716	SHQQTTV	0.217682	-0.10921
SyS1588	3539	GCCCAACTTAATATGCAGACGAGGGGGGGCACAG	8128	AQLNMQTRGAQ	12717	LNMQTRG	0.217651	-0.01433
GS925	3540	GCCCAATACACCCCCCAACTCAAAAGCGCACAG	8129	AQYTPQLKSAQ	12718	YTPQLKS	0.217643	-0.17958
SyS1589	3541	GCCCAACAGATTAATGGTCAGGTTATTGCACAG	8130	AQQINGQVIAQ	12719	QINGQVI	0.217561	-0.20466
GS926	3542	GCCCAAACGCGTGAGGGTGTGTTGCCTGCACAG	8131	AQTREGVLPAQ	12720	TREGVLP	0.217502	-0.13952
SyS1591	3543	GCCCAAGTTCATCAGTCGGTGCCGCTGGCACAG	8132	AQVHQSVPLAQ	12721	VHQSVPL	0.217352	-0.17314
SyS1592	3544	GCCCAACCGTATTCGATGGGGCATCCTGCACAG	8133	AQPYSMGHPAQ	12722	PYSMGHP	0.217352	-0.17314
GS927	3545	GCCCAAGGCACCAAAACCCACAGCCTCGCACAG	8134	AQGTKTHSLAQ	12723	GTKTHSL	0.217339	-0.14906
SyS1595	3546	GCCCAAACGCTGACTACGGGGTCGAAGGCACAG	8135	AQTLTTGSKAQ	12724	TLTTGSK	0.217166	-0.04194
GS928	3547	GCCCAATTTACGATTGGTGTTACGGGGGGCACAG	8136	AQFTIGVTGAQ	12725	FTIGVTG	0.21713	-0.0827
GS930	3548	GCCCAACTCAGCAGCCACAACCACACGCACAG	8137	AQLSSHNHNAQ	12726	LSSHNHN	0.216901	-0.13284
SyS1596	3549	GCCCAAACCGGCAAAATGCCCCTCGAAGCACAG	8138	AQTGKMPLEAQ	12727	TGKMPLE	0.216862	-0.14056
GS931	3550	GCCCAAACTGCGAATCCTCATGCGACTGCACAG	8139	AQTANPHATAQ	12728	TANPHAT	0.216859	-0.04999
SyS1597	3551	GCCCAACACGACAGCGTCGCCAGCAGCGCACAG	8140	AQHDSVASSAQ	12729	HDSVASS	0.216844	-0.154
GS932	3552	GCCCAAACGCGTGCGGATGTGTTGATGGCACAG	8141	AQTRADVLMAQ	12730	TRADVLM	0.216806	-0.13761
GS933	3553	GCCCAAGCTAATCATGCTTCTAATGCGGCACAG	8142	AQANHASNAAQ	12731	ANHASNA	0.216449	-0.09199
SyS1599	3554	GCCCAAAGCCACACATCGTCGGCGTCGAAGCACAG	8143	AQSHIVGVEAQ	12732	SHIVGVE	0.216347	0.074638
GS934	3555	GCCCAATACACCGCCCAAAAAACCAGCGCACAG	8144	AQYTAQKTSAQ	12733	YTAQKTS	0.2162	-0.16573
SyS1600	3556	GCCCAATTGCCTGCTGTGCAGAAGATGGCACAG	8145	AQLPAVQKMAQ	12734	LPAVQKM	0.216175	-0.12465
SyS1601	3557	GCCCAATCTGGTATTCAGACGGCTAAGGCACAG	8146	AQSGIQTAKAQ	12735	SGIQTAK	0.215988	-0.14283
GS935	3558	GCCCAAGATCCGGTGAAGATTGGTCATGCACAG	8147	AQDPVKIGHAQ	12736	DPVKIGH	0.215963	-0.16125
GS936	3559	GCCCAAAGTCAGACTATGAGTAAGAGTGCACAG	8148	AQSQTMSKSAQ	12737	SQTMSKS	0.215809	-0.07639
SyS1602	3560	GCCCAAAGCCTCACCCCCACCAACATCGCACAG	8149	AQSLTPTNIAQ	12738	SLTPTNI	0.215809	-0.0396
GS937	3561	GCCCAATATCTTAATAATACGAATTCTGCACAG	8150	AQYLNNTNSAQ	12739	YLNNTNS	0.215545	-0.18054

FIG. 33 (Continued)

GS938	3562	GCCCAAATGACCAGAATGAGCCAAAACGCACAG	8151	AQMTRMSQNAQ	12740	MTRMSQN	0.215545	-0.18054
GS939	3563	GCCCAAGTCAACCAAAGCCTCAGCAGAGCACAG	8152	AQVNQSLSRAQ	12741	VNQSLSR	0.215514	-0.03828
GS940	3564	GCCCAAAGAACCGTCACCGACACAACAGAGCACAG	8153	AQRTVTDNRAQ	12742	RTVTDNR	0.21543	-0.10655
SyS1603	3565	GCCCAAATTACTGGGGTGTTTGCTAATGCACAG	8154	AQITGVFANAQ	12743	ITGVFAN	0.215212	-0.05959
SyS1604	3566	GCCCAATCGCCTGGGCTGAGTAGGGTTGCACAG	8155	AQSPGLSRVAQ	12744	SPGLSRV	0.215048	-0.09636
GP151	3567	GCCCAAGTGGTGAATCCTCAGACTAGGGCACAG	8156	AQVVNPQTRAQ	12745	VVNPQTR	0.214905	-0.06586
SyS1606	3568	GCCCAATGGAGCCAAAGCCTCAGCGCCGCACAG	8157	AQWSQSLSAAQ	12746	WSQSLSA	0.214764	-0.14405
SyS1607	3569	GCCCAACCCAGAGACGCCAGCAACGACGCACAG	8158	AQPRDASNDAQ	12747	PRDASND	0.214659	-0.20224
GS942	3570	GCCCAATACACCAGCATGACCGAATTCGCACAG	8159	AQYTSMTEFAQ	12748	YTSMTEF	0.214654	-0.17112
SS106	3571	GCCCAAAACAACAGCCCCAGCCCCAGAGCACAG	8160	AQNNSPSPRAQ	12749	NNSPSPR	0.214625	-0.35665
SyS1608	3572	GCCCAAAACAGCCTCAGCCACGGCGACGCACAG	8161	AQNSLSHGDAQ	12750	NSLSHGD	0.21457	-0.10404
SyS1609	3573	GCCCAAAGAGTCGCCGGCGAAATGGCCGCACAG	8162	AQRVAGEMAAQ	12751	RVAGEMA	0.214459	0.040653
GS943	3574	GCCCAAGGTATTGGGTCTAGGGAGCTTGCACAG	8163	AQGIGSRELAQ	12752	GIGSREL	0.214321	-0.1462
SyS1610	3575	GCCCAATATGTTAGTCGTATTCGTGATGCACAG	8164	AQYVSRIRDAQ	12753	YVSRIRD	0.214067	-0.19375
SyS1611	3576	GCCCAATACCCCAGCCCCAACGACAACGCACAG	8165	AQYPSPNDNAQ	12754	YPSPNDN	0.213993	-0.16708
SyS1612	3577	GCCCAACTTCAGAGGACGGCGCATAATGCACAG	8166	AQLQRTAHNAQ	12755	LQRTAHN	0.213963	-0.15374
SyS1613	3578	GCCCAACTCGACAGCCTCAGCAGACACGCACAG	8167	AQLDSLSRHAQ	12756	LDSLSRH	0.213963	-0.15374
GS945	3579	GCCCAAACCAAAATCAGCGCCGGCAGCGCACAG	8168	AQTKISAGSAQ	12757	TKISAGS	0.21391	-0.10628
SyS1614	3580	GCCCAAAAAGACAACAGCCCCGTCGTCGCACAG	8169	AQKDNSPVVAQ	12758	KDNSPVV	0.213893	-0.11374
SyS1615	3581	GCCCAAACCGGCCAAGGCAGCAGCCTCGCACAG	8170	AQTGQGSSLAQ	12759	TGQGSSL	0.213721	-0.16397
SyS1617	3582	GCCCAAGATACGCATCTGAGTCGTCATGCACAG	8171	AQDTHLSRHAQ	12760	DTHLSRH	0.213534	-0.21194
SyS1618	3583	GCCCAAGATATTGTTAGGAGGCAGGCTGCACAG	8172	AQDIVRRQAAQ	12761	DIVRRQA	0.213267	-0.03009
SyS1619	3584	GCCCAAGCTATGAAGTATGCGCAGACTGCACAG	8173	AQAMKYAQTAQ	12762	AMKYAQT	0.213114	-0.15011
SyS1620	3585	GCCCAAAGGCTGGCTGATCAGCATCCGGCACAG	8174	AQRLADQHPAQ	12763	RLADQHP	0.213086	-0.20093
SyS1621	3586	GCCCAAGCTCCTGATAGTACTCGGATGGCACAG	8175	AQAPDSTRMAQ	12764	APDSTRM	0.213044	0.014524
SyS1622	3587	GCCCAAAGTCGGGTTTCTCCTTCTTCGGCACAG	8176	AQSRVSPSSAQ	12765	SRVSPSS	0.213013	0.008275
GS949	3588	GCCCAAGTGCATGGTCAGGGTGAGCCTGCACAG	8177	AQVHGQGEPAQ	12766	VHGQGEP	0.212959	-0.1765
SyS1623	3589	GCCCAAATGAGAGACAGCAGCACCAGAGCACAG	8178	AQMRDSSTRAQ	12767	MRDSSTR	0.21283	0.073268
GS951	3590	GCCCAATGGCCCCAACACACCAACACCGCACAG	8179	AQWPQHTNTAQ	12768	WPQHTNT	0.212527	-0.15855
GS952	3591	GCCCAAGTCGGCAGCTACCCCGTCACCGCACAG	8180	AQVGSYPVTAQ	12769	VGSYPVT	0.21252	0.007456
SyS1625	3592	GCCCAAACTGCGACTCAGGGGGCTAATGCACAG	8181	AQTATQGANAQ	12770	TATQGAN	0.212372	-0.07076
SyS1626	3593	GCCCAAAAGAATAATAGTATGGATAGTGCACAG	8182	AQKNNSMDSAQ	12771	KNNSMDS	0.212366	-0.12084

FIG. 33 (Continued)

SyS1628	3594	GCCCAACACACCAACGCCGTCAAAGAAGCACAG	8183	AQHTNAVKEAQ	12772	HTNAVKE	0.212319	0.211829	
GS953	3595	GCCCAACTTCATTCGGTGACTACGCCGGCACAG	8184	AQLHSVTTPAQ	12773	LHSVTTP	0.212166	-0.0828	
SyS1629	3596	GCCCAAGCCCCCGGCCAACAAAACTTCGCACAG	8185	AQAPGQQNFAQ	12774	APGQQNF	0.212026	0.059715	
GS955	3597	GCCCAATCTTATACTAATCGTACTATGGCACAG	8186	AQSYTNRTMAQ	12775	SYTNRTM	0.211833	-0.0714	
SyS1632	3598	GCCCAATCGGGTCAGAGTAATACGAAGGCACAG	8187	AQSGQSNTKAQ	12776	SGQSNTK	0.211749	-0.18984	
SyS1633	3599	GCCCAAGACAGCTACAGAGCCCAAAGCGCACAG	8188	AQDSYRAQSAQ	12777	DSYRAQS	0.211749	-0.02105	
SyS1634	3600	GCCCAAATGTATAAGCATAATTCTGATGCACAG	8189	AQMYKHNSDAQ	12778	MYKHNSD	0.211732	-0.06767	
GS957	3601	GCCCAAAGCCTCGCCATGGTCAACCCCCGCACAG	8190	AQSLAMVNPAQ	12779	SLAMVNP	0.211678	-0.17768	
SyS1635	3602	GCCCAACCCCTCACCAGCAAAAGCATGGCACAG	8191	AQPLTSKSMAQ	12780	PLTSKSM	0.211599	0.023996	
GS958	3603	GCCCAACTCGGCGCCCAACCCACCCCCGCACAG	8192	AQLGAQPTPAQ	12781	LGAQPTP	0.211205	-0.15955	
GS959	3604	GCCCAAGAAGGCAACCAAAAACCCCAAGCACAG	8193	AQEGNQKPQAQ	12782	EGNQKPQ	0.211139	-0.18637	
SyP56	3605	GCCCAACAGGTTCGGCCGGGTGCTCATGCACAG	8194	AQQVRPGAHAQ	12783	QVRPGAH	0.211056	-0.04396	
GS962	3606	GCCCAAAGCGGCAACATCACCGCCATGGCACAG	8195	AQSGNITAMAQ	12784	SGNITAM	0.210967	-0.16842	
SyS1637	3607	GCCCAAAACGACAGCAAAATCGCCGAAGCACAG	8196	AQNDSKIAEAQ	12785	NDSKIAE	0.210955	-0.2305	
SyS1638	3608	GCCCAAATCATGAAAAACGAACACAACGCACAG	8197	AQIMKNEHNAQ	12786	IMKNEHN	0.210886	-0.16102	
GS963	3609	GCCCAACTTTTGACGAATACTGATCGGGCACAG	8198	AQLLTNTDRAQ	12787	LLTNTDR	0.210857	-0.16432	
SyS1640	3610	GCCCAAGATACGGCGCAGAGTCGTAATGCACAG	8199	AQDTAQSRNAQ	12788	DTAQSRN	0.210588	0.341933	
SyS1641	3611	GCCCAAATTGATCATGGTAAGACGAATGCACAG	8200	AQIDHGKTNAQ	12789	IDHGKTN	0.210574	-0.15253	
GS964	3612	GCCCAAACCAGCCCCAGAAGCCTCCTCGCACAG	8201	AQTSPRSLLAQ	12790	TSPRSLL	0.210515	-0.15764	
GS965	3613	GCCCAATCGAATCCTCGGGATTCTAGTGCACAG	8202	AQSNPRDSSAQ	12791	SNPRDSS	0.210308	-0.12807	
SyS1643	3614	GCCCAAATCATGCAAAGCATCCAAAACGCACAG	8203	AQIMQSIQNAQ	12792	IMQSIQN	0.210287	-0.14405	
GS966	3615	GCCCAAAAAGTCAGCCCCAGCAGCACCGCACAG	8204	AQKVSPSSTAQ	12793	KVSPSST	0.210279	-0.06417	
SyS1645	3616	GCCCAAACCGGCCCCCAGCCCCAGCCTCGCACAG	8205	AQTGPSPSLAQ	12794	TGPSPSL	0.210228	-0.17505	
SyS1646	3617	GCCCAAGGCGCCGCCAGAGCCCAAGCCCGCACAG	8206	AQGAARAQAAQ	12795	GAARAQA	0.210219	0.035379	
GS967	3618	GCCCAAAAGTTTCAGTCTCCTGAGCCTGCACAG	8207	AQKFQSPEPAQ	12796	KFQSPEP	0.210082	-0.18009	
SyS1647	3619	GCCCAAATGGCGACGAATTCGACGGAGGCACAG	8208	AQMATNSTEAQ	12797	MATNSTE	0.210073	-0.15738	
GS968	3620	GCCCAAAACGTCCTCACCAACATCAGCGCACAG	8209	AQNVLTNISAQ	12798	NVLTNIS	0.210069	-0.17386	
SS112	3621	GCCCAAAAGAATGGTATGAATTTGGTGGCACAG	8210	AQKNGMNLVAQ	12799	KNGMNLV	0.210013	-0.32377	
SyS1649	3622	GCCCAAACTCCTACGCAGCCTTCTAGTGCACAG	8211	AQTPTQPSSAQ	12800	TPTQPSS	0.209867	-0.19254	
SyS1650	3623	GCCCAAACTAAGGAGCTTGTTATTCATGCACAG	8212	AQTKELVIHAQ	12801	TKELVIH	0.209867	-0.19254	
SyS1651	3624	GCCCAAATCATGAACCAAAGCGTCCAAGCACAG	8213	AQIMNQSVQAQ	12802	IMNQSVQ	0.209715	-0.03979	
SyS1653	3625	GCCCAAGTGTCTAATGCTAGGGATAAGGCACAG	8214	AQVSNARDKAQ	12803	VSNARDK	0.209549	-0.14041	

FIG. 33 (Continued)

TS169	3626	GCCCAAAGTAATCATACGCGGTCGTATGCACAG	8215	AQSNHTRSYAQ	12804	SNHTRSY	0.20947	-0.21368
GS971	3627	GCCCAACACACCGACAGACTCAACCCCGCACAG	8216	AQHTDRLNPAQ	12805	HTDRLNP	0.209344	-0.14238
SyS1654	3628	GCCCAAGCCGCCCCCAGCATGAGCGACGCACAG	8217	AQAAPSMSDAQ	12806	AAPSMSD	0.209262	-0.17557
GS972	3629	GCCCAATTTTCGAATACGCATGCTTTGGCACAG	8218	AQFSNTHALAQ	12807	FSNTHAL	0.209156	-0.17381
SyS1655	3630	GCCCAAGCTCATGATCTGCATCGTGTGGCACAG	8219	AQAHDLHRVAQ	12808	AHDLHRV	0.209091	-0.17998
SyS1656	3631	GCCCAACTTCAGGTTAATCATGTGGCGGCACAG	8220	AQLQVNHVAAQ	12809	LQVNHVA	0.209057	-0.14526
SyS1657	3632	GCCCAAAGCGGCCCCAACCTCAGCAGAGCACAG	8221	AQSGPNLSRAQ	12810	SGPNLSR	0.209039	0.179343
GS974	3633	GCCCAAACTTATACGTCGACGCCTGGTGCACAG	8222	AQTYTSTPGAQ	12811	TYTSTPG	0.209033	-0.13253
GS975	3634	GCCCAATATGGTACTCCTCCTTCGACGGCACAG	8223	AQYGTPPSTAQ	12812	YGTPPST	0.209029	-0.11621
SyS1658	3635	GCCCAATATGGTGTGAGTTCGGGTAGTGCACAG	8224	AQYGVSSGSAQ	12813	YGVSSGS	0.209	-0.07131
SyS1659	3636	GCCCAACCCACCAGAGACCTCATGAGCGCACAG	8225	AQPTRDLMSAQ	12814	PTRDLMS	0.209	-0.16708
SyS1660	3637	GCCCAAAAGATTGATGCGATGACGCAGGCACAG	8226	AQKIDAMTQAQ	12815	KIDAMTQ	0.208964	-0.12454
GS976	3638	GCCCAAAGAATCGGCACCAGCGAAGTCGCACAG	8227	AQRIGTSEVAQ	12816	RIGTSEV	0.208937	-0.10921
GS977	3639	GCCCAATTTGATCCTCTTCAGTCGTCGGCACAG	8228	AQFDPLQSSAQ	12817	FDPLQSS	0.208624	-0.13472
SyS1662	3640	GCCCAACTCCTCCACCACGTCGAAGTCGCACAG	8229	AQLLHHVEVAQ	12818	LLHHVEV	0.208542	-0.15011
GS978	3641	GCCCAAGTCACCCTCGGCAACAGCGTCGCACAG	8230	AQVTLGNSVAQ	12819	VTLGNSV	0.208389	-0.14524
SyS1663	3642	GCCCAACTCCTCAACGACAGAAGCGTCGCACAG	8231	AQLLNDRSVAQ	12820	LLNDRSV	0.208296	-0.09749
GS979	3643	GCCCAATTCGTCGACAGAAGACCCCAAGCACAG	8232	AQFVDRRPQAQ	12821	FVDRRPQ	0.207955	-0.00471
SyS1664	3644	GCCCAAACGAATGTGACTACGACGACGGCACAG	8233	AQTNVTTTTAQ	12822	TNVTTTT	0.207819	-0.05555
SyS1665	3645	GCCCAAGACGAAACCAACAAAAGATGGGCACAG	8234	AQDETNKRWAQ	12823	DETNKRW	0.207819	-0.20709
SyS1666	3646	GCCCAAACGTCGACGTCTGCTATTCGGGCACAG	8235	AQTSTSAIRAQ	12824	TSTSAIR	0.207608	-0.1626
SyS1668	3647	GCCCAAGGCACCAGCAGAGTCCAAGGCGCACAG	8236	AQGTSRVQGAQ	12825	GTSRVQG	0.207468	0.069325
SyS1669	3648	GCCCAACTCAACACCATGGCCCTCCCCGCACAG	8237	AQLNTMALPAQ	12826	LNTMALP	0.207441	-0.15981
SyS1671	3649	GCCCAAAGTACTCATGCGACTGATAGGGCACAG	8238	AQSTHATDRAQ	12827	STHATDR	0.207437	0.052678
SyS1672	3650	GCCCAACACCACGGCGTCACCAGCGGCGCACAG	8239	AQHHGVTSGAQ	12828	HHGVTSG	0.207346	-0.13809
SyS1674	3651	GCCCAAGGCCTCATGGCCAACAACCCCGCACAG	8240	AQGLMANNPAQ	12829	GLMANNP	0.207257	-0.19723
SyS1675	3652	GCCCAAGGGTCTTCGTCTAATTCGTTTGCACAG	8241	AQGSSSNSFAQ	12830	GSSSNSF	0.207096	-0.03155
GS985	3653	GCCCAAAGAGAAAAAATGACCCTCCTCGCACAG	8242	AQREKMTLLAQ	12831	REKMTLL	0.207031	-0.18368
SyS1676	3654	GCCCAAAGCCCCGTCAGCAGCGACAGCGCACAG	8243	AQSPVSSDSAQ	12832	SPVSSDS	0.206943	-0.18954
SyS1679	3655	GCCCAAGACGTCGCCCACAAAGACAGAGCACAG	8244	AQDVAHKDRAQ	12833	DVAHKDR	0.206739	-0.10729
SyS1680	3656	GCCCAAAGTATGGTTTCTAATATTGCGGCACAG	8245	AQSMVSNIAAQ	12834	SMVSNIA	0.206728	-0.08096
GS986	3657	GCCCAAATGATGCATAATATGCAGTCTGCACAG	8246	AQMMHNMQSAQ	12835	MMHNMQS	0.20664	-0.13284

FIG. 33 (Continued)

GS987	3658	GCCCAAGTGTCGAATTCTTCTCGGATGGCACAG	8247	AQVSNSSRMAQ	12836	VSNSSRM	0.20658	-0.16842
GS988	3659	GCCCAATATACGGCTACTAAGGCGAGTGCACAG	8248	AQYTATKASAQ	12837	YTATKAS	0.206493	-0.1442
GS989	3660	GCCCAAAGCACCAGCGGCGGCGTCAGAGCACAG	8249	AQSTSGGVRAQ	12838	STSGGVR	0.206367	-0.11215
SyS1681	3661	GCCCAATTTACTAGGGCTGAGCCTGCGGCACAG	8250	AQFTRAEPAAQ	12839	FTRAEPA	0.206339	-0.13071
SyS1682	3662	GCCCAACCTATTACGAGGGGTACTATTGCACAG	8251	AQPITRGTIAQ	12840	PITRGTI	0.206234	-0.16951
SyS1683	3663	GCCCAATACCACACAACAGCATGCTCGGCGCACAG	8252	AQYHNSMLGAQ	12841	YHNSMLG	0.206136	-0.11374
GP153	3664	GCCCAAAGTAATAGTCCGGGTAATGCTGCACAG	8253	AQSNSPGNAAQ	12842	SNSPGNA	0.205916	-0.06579
GS990	3665	GCCCAACAAAAAGGCGTCCAACTCCCCGCACAG	8254	AQQKGVQLPAQ	12843	QKGVQLP	0.205912	-0.01992
GS991	3666	GCCCAACGTAGTGAGACTAATAATACTGCACAG	8255	AQRSETNNTAQ	12844	RSETNNT	0.205906	-0.18637
SyS1685	3667	GCCCAAGTGGATCAGATGCTGGCTCCTGCACAG	8256	AQVDQMLAPAQ	12845	VDQMLAP	0.205805	-0.19133
GS992	3668	GCCCAACAAACCAGACACACCAGCATGGCACAG	8257	AQQTRHTSMAQ	12846	QTRHTSM	0.205758	-0.12266
SyS1686	3669	GCCCAAATGCACGCCGACAGAGCCCTCGCACAG	8258	AQMHADRALAQ	12847	MHADRAL	0.205735	-0.12963
GS994	3670	GCCCAATCGACTACGCATGCTCCTAAGGCACAG	8259	AQSTTHAPKAQ	12848	STTHAPK	0.205535	-0.12148
SyS1687	3671	GCCCAATCTAATCAGACTATTATGACGGCACAG	8260	AQSNQTIMTAQ	12849	SNQTIMT	0.205491	-0.16587
GS995	3672	GCCCAAGTTTCTTCGCCTTCTGGTCTGGCACAG	8261	AQVSSPSGLAQ	12850	VSSPSGL	0.205479	-0.14665
SyS1689	3673	GCCCAAAAAAGAGGCGAAGAAATGGTCGCACAG	8262	AQKRGEEMVAQ	12851	KRGEEMV	0.205315	-0.19477
SyS1690	3674	GCCCAACAGGATAGTGGGAATAGTTATGCACAG	8263	AQQDSGNSYAQ	12852	QDSGNSY	0.205249	-0.21315
SyS1691	3675	GCCCAAAGCCACGCCACCACCGGCGGCGCACAG	8264	AQSHATTGGAQ	12853	SHATTGG	0.205059	-0.19618
SyS1693	3676	GCCCAAAAGCTGAGTGAGACGTCTCATGCACAG	8265	AQKLSETSHAQ	12854	KLSETSH	0.205006	-0.21448
SyS1694	3677	GCCCAACTTAATTATAAGGAGGCGCCGGCACAG	8266	AQLNYKEAPAQ	12855	LNYKEAP	0.204978	-0.18769
SyS1695	3678	GCCCAAAGCGTCGACAGCGTCAGACTCGCACAG	8267	AQSVDSVRLAQ	12856	SVDSVRL	0.20496	-0.08842
SyS1697	3679	GCCCAACAACCCAACGTCATCCAAACCGCACAG	8268	AQQPNVIQTAQ	12857	QPNVIQT	0.204872	0.059518
GS996	3680	GCCCAACGTATGACTAATTTGCAGACTGCACAG	8269	AQRMTNLQTAQ	12858	RMTNLQT	0.20474	-0.17863
SyS1698	3681	GCCCAAGCCACACCCCCGGCGGCAGCGGCGCACAG	8270	AQATPGGSGAQ	12859	ATPGGSG	0.204721	-0.15374
SyS1699	3682	GCCCAAGACGTCAACAGCATGAGCAGCGCGCACAG	8271	AQDVNSMSSAQ	12860	DVNSMSS	0.204599	-0.23419
SyS1700	3683	GCCCAATTGCCTCGTAGTCATCTTGATGCACAG	8272	AQLPRSHLDAQ	12861	LPRSHLD	0.204525	-0.13316
SyS1701	3684	GCCCAACCCGCCCCCAGATACGACAAAGCACAG	8273	AQPAPRYDKAQ	12862	PAPRYDK	0.204501	-0.09014
SyS1703	3685	GCCCAAAGAAACTACAGCGACAAAGACGCACAG	8274	AQRNYSDKDAQ	12863	RNYSDKD	0.204317	0.088722
SyS1704	3686	GCCCAAAGTGAGAATCTTTTGAGTCGTGCACAG	8275	AQSENLLSRAQ	12864	SENLLSR	0.204317	-0.20951
GS997	3687	GCCCAAAGTAGTCTTAATATGAAGGATGCACAG	8276	AQSSLNMKDAQ	12865	SSLNMKD	0.204292	-0.11279
GS998	3688	GCCCAAAGCGACAAAGAATACGGCAGAGCACAG	8277	AQSDKEYGRAQ	12866	SDKEYGR	0.204204	-0.15001
GS999	3689	GCCCAATACGTCAGCCAAAGCGGCATGGCACAG	8278	AQYVSQSGMAQ	12867	YVSQSGM	0.204064	-0.17672

FIG. 33 (Continued)

GS1000	3690	GCCCAAAACGTCGTCAGCGTCAGACAAGCACAG	8279	AQNVVSVRQAQ	12868	NVVSVRQ	0.204038	-0.16753
SyS1705	3691	GCCCAAACGGGTAAGGAGGGTCGGACTGCACAG	8280	AQTGKEGRTAQ	12869	TGKEGRT	0.203988	-0.05387
GS1001	3692	GCCCAATTTAAGAATACTGTGGCGACTGCACAG	8281	AQFKNTVATAQ	12870	FKNTVAT	0.203984	-0.13702
SyS1706	3693	GCCCAAGGCAGCAGAGAACCCAGCAGCGCACAG	8282	AQGSREPSSAQ	12871	GSREPSS	0.203966	-0.2268
SyS1707	3694	GCCCAAAGAGAAAAAGTCAGCACCCCCGCACAG	8283	AQREKVSTPAQ	12872	REKVSTP	0.20368	0.088388
GP154	3695	GCCCAACAGGAGCCTGCTAGGCATAATGCACAG	8284	AQQEPARHNAQ	12873	QEPARHN	0.203631	-0.07336
GS1002	3696	GCCCAAACTAGTCATTCGAATGGTCGTGCACAG	8285	AQTSHSNGRAQ	12874	TSHSNGR	0.203484	-0.09149
SyS1708	3697	GCCCAAGACCTCAGCAGCCCCAAAATGGCACAG	8286	AQDLSSPKMAQ	12875	DLSSPKM	0.203432	-0.06161
SyS1709	3698	GCCCAACTCGCCACCACCCCCAAACCCGCACAG	8287	AQLATTPKPAQ	12876	LATTPKP	0.203432	-0.11253
SyS1710	3699	GCCCAAAGCGGCCCCAACGTCAGCCTCGCACAG	8288	AQSGPNVSLAQ	12877	SGPNVSL	0.203432	-0.16344
SyS1711	3700	GCCCAACCCGTCTACAACGCCAGCCCCGCACAG	8289	AQPVYNASPAQ	12878	PVYNASP	0.203401	-0.21941
SyS1712	3701	GCCCAAAATTCTACTACTTTGGTGATGGCACAG	8290	AQNSTTLVMAQ	12879	NSTTLVM	0.203291	-0.10908
SyS1713	3702	GCCCAAAGAAACGCCGTCGTCAGCATGGCACAG	8291	AQRNAVVSMAQ	12880	RNAVVSM	0.203173	-0.1307
SP38	3703	GCCCAAAAGGATCTTCTGGCTAAGCTTGCACAG	8292	AQKDLLAKLAQ	12881	KDLLAKL	0.203052	-0.0513
SyS1715	3704	GCCCAACCCCACGAAGGCAGCAGAGCACAG	8293	AQPHEGSSRAQ	12882	PHEGSSR	0.202954	-0.08343
SyS1716	3705	GCCCAACGGGATACGGTTTCGCGTTATGCACAG	8294	AQRDTVSRYAQ	12883	RDTVSRY	0.20293	-0.15411
SyS1717	3706	GCCCAAGGCCAAGCCGCCCAAGGCCACGCACAG	8295	AQGQAAQGHAQ	12884	GQAAQGH	0.202823	-0.14283
SyS1718	3707	GCCCAAAGGGCTGAGACTGCTCATGTGGCACAG	8296	AQRAETAHVAQ	12885	RAETAHV	0.202798	-0.15132
SyS1720	3708	GCCCAAGAAAACAGAACCGTCCCCACCGCACAG	8297	AQENRTVPTAQ	12886	ENRTVPT	0.202755	0.23929
GS1004	3709	GCCCAAAGTAGTAATGATGCGAGGGTGGCACAG	8298	AQSSNDARVAQ	12887	SSNDARV	0.202721	-0.1747
SyS1721	3710	GCCCAACCCGGCCAAGTCGACAGAAGAGCACAG	8299	AQPGQVDRRAQ	12888	PGQVDRR	0.202674	-0.18527
SyS1723	3711	GCCCAAGGCCCCGGCGCCAACACCACCGCACAG	8300	AQGPGANTTAQ	12889	GPGANTT	0.202623	-0.17752
SyS1724	3712	GCCCAAATGCCCCGAAAACCTCAAAGAAGCACAG	8301	AQMPENLKEAQ	12890	MPENLKE	0.202544	-0.21072
GS1005	3713	GCCCAAACGAATGCGGTGGCTTCTAATGCACAG	8302	AQTNAVASNAQ	12891	TNAVASN	0.202544	-0.12235
GS1006	3714	GCCCAATACGGCAAAATCGAACTCTACGCACAG	8303	AQYGKIELYAQ	12892	YGKIELY	0.202395	-0.17919
SyS1725	3715	GCCCAAAATCCGAATGGTACGGGTTTTGCACAG	8304	AQNPNGTGFAQ	12893	NPNGTGF	0.202346	-0.1784
GS1007	3716	GCCCAATCTCGGAATACTATGGGTTCGGCACAG	8305	AQSRNTMGSAQ	12894	SRNTMGS	0.202244	-0.11377
GS1008	3717	GCCCAACCGAGTCATGGGATTACGGCTGCACAG	8306	AQPSHGITAAQ	12895	PSHGITA	0.202231	-0.10748
SyS1726	3718	GCCCAATTGGAGACGCTGAGGGGGCCTGCACAG	8307	AQLETLRGPAQ	12896	LETLRGP	0.202095	-0.0594
SyS1727	3719	GCCCAAGATCGTTCTCCTGATATTAGGGCACAG	8308	AQDRSPDIRAQ	12897	DRSPDIR	0.202025	-0.19723
SyS1728	3720	GCCCAAAAGGATTTGGCGTCTGCGAAGGCACAG	8309	AQKDLASAKAQ	12898	KDLASAK	0.201927	-0.22803
SyS1729	3721	GCCCAAATCACCAGCCACGGCAACAGCGCACAG	8310	AQITSHGNSAQ	12899	ITSHGNS	0.201888	0.12116

FIG. 33 (Continued)

GS1009	3722	GCCCAACATTCTAAGATGCCTTCTACGGCACAG	8311	AQHSKMPSTAQ	12900	HSKMPST	0.201887	-0.16214
GS1010	3723	GCCCAAATTGCGACTTTTACGACGGCGGCACAG	8312	AQIATFTTAAQ	12901	IATFTTA	0.201795	-0.08442
SyS1730	3724	GCCCAAGCGGCGTCTGGGTATCTTAATGCACAG	8313	AQAASGYLNAQ	12902	AASGYLN	0.201793	-0.1986
SyS1731	3725	GCCCAAGATAGTGTTAGGCCGGCTATTGCACAG	8314	AQDSVRPAIAQ	12903	DSVRPAI	0.201702	-0.20709
SyS1732	3726	GCCCAAAGACTCAGCGAAGAAATGAGAGCACAG	8315	AQRLSEEMRAQ	12904	RLSEEMR	0.201693	-0.22434
SyS1733	3727	GCCCAACTCCCCATCAGCGCCACCGAAGCACAG	8316	AQLPISATEAQ	12905	LPISATE	0.201693	-0.22434
SyS1734	3728	GCCCAATCTAATGTGGCGGCTCAGATGGCACAG	8317	AQSNVAAQMAQ	12906	SNVAAQM	0.2016	-0.21557
SyS1735	3729	GCCCAATATCAGTCGCTGATTTCTGAGGCACAG	8318	AQYQSLISEAQ	12907	YQSLISE	0.2016	-0.21557
SyS1737	3730	GCCCAATATCAGAGTGGGTATGATAAGGCACAG	8319	AQYQSGYDKAQ	12908	YQSGYDK	0.201403	-0.07145
SyS1738	3731	GCCCAACTCAGAACCGGCGAACTCACCGCACAG	8320	AQLRTGELTAQ	12909	LRTGELT	0.201143	-0.02579
SyS1739	3732	GCCCAACCGGCGACGAATAATATGCGGGCACAG	8321	AQPATNNMRAQ	12910	PATNNMR	0.201063	-0.21325
SyS1740	3733	GCCCAAGTCAGCAGCAAATTCAGCGCACAG	8322	AQVSSSKFSAQ	12911	VSSSKFS	0.201033	-0.08585
SyS1741	3734	GCCCAAACTACGCTGCTTGATAAGGCTGCACAG	8323	AQTTLLDKAAQ	12912	TTLLDKA	0.201033	-0.19496
SyS1742	3735	GCCCAAAGCCCCGCCCTCCACCCCAGCGCACAG	8324	AQSPALHPSAQ	12913	SPALHPS	0.201033	-0.19496
SyS1743	3736	GCCCAATTCAACCACAACAGAACCGACGCACAG	8325	AQFNHNRTDAQ	12914	FNHNRTD	0.200936	-0.13686
GS1013	3737	GCCCAAGCCGAAAAAACCGCCAACGGCGCACAG	8326	AQAEKTANGAQ	12915	AEKTANG	0.200841	-0.1756
GS1014	3738	GCCCAAAATCTGCGTGTGACGGCTTCGGCACAG	8327	AQNLRVTASAQ	12916	NLRVTAS	0.200801	-0.08207
GS1015	3739	GCCCAAATGAAGGATGGGTCGCGGATTGCACAG	8328	AQMKDGSRIAQ	12917	MKDGSRI	0.200699	-0.14334
SyS1744	3740	GCCCAAAGAATCGGCGCCAACGCCACCGCACAG	8329	AQRIGANATAQ	12918	RIGANAT	0.200534	0.065728
GS1018	3741	GCCCAAGCCAACCTCACCCCCAACAGAGCACAG	8330	AQANLTPNRAQ	12919	ANLTPNR	0.20043	-0.18009
SyP58	3742	GCCCAATCGGTGTCTGATAAGAGTCATGCACAG	8331	AQSVSDKSHAQ	12920	SVSDKSH	0.200325	-0.03907
SyS1745	3743	GCCCAATACAGCACCCTCCACACCGCCGCACAG	8332	AQYSTLHTAAQ	12921	YSTLHTA	0.200268	0.146915
SyS1747	3744	GCCCAAACGAAGTTTGGTGGTATTCAGGCACAG	8333	AQTKFGGIQAQ	12922	TKFGGIQ	0.200153	0.040003
GS1019	3745	GCCCAAGACATCCCCAAAGGCAGCAGCGCACAG	8334	AQDIPKGSSAQ	12923	DIPKGSS	0.200135	-0.13523
SyS1748	3746	GCCCAAATCCTCCCCAGCAGCAGCCAAGCACAG	8335	AQILPSSSQAQ	12924	ILPSSSQ	0.200107	0.034167
GS1020	3747	GCCCAAGTCAGCCAAACCACCAGCAGCGCACAG	8336	AQVSQTTSSAQ	12925	VSQTTSS	0.200008	-0.11818
SyS1750	3748	GCCCAAACGATTCATCTGCATAAGGATGCACAG	8337	AQTIHLHKDAQ	12926	TIHLHKD	0.199958	-0.13314
SyS1754	3749	GCCCAAGTCACCGACAGAGTCGGCAACGCACAG	8338	AQVTDRVGNAQ	12927	VTDRVGN	0.199795	-0.1792
SyP59	3750	GCCCAACTGCCTGCTCGGGCTGCTAATGCACAG	8339	AQLPARAANAQ	12928	LPARAAN	0.199763	-0.04316
SyS1755	3751	GCCCAACACACCCAAAGCATGACCGTCGCACAG	8340	AQHTQSMTVAQ	12929	HTQSMTV	0.199748	0.113433
SyS1756	3752	GCCCAACTCCTCAACAGCAGCCAACTCGCACAG	8341	AQLLNSSQLAQ	12930	LLNSSQL	0.199713	-0.01322
SyS1757	3753	GCCCAAAGAAACAGCGAACTCAGAGCCGCACAG	8342	AQRNSELRAAQ	12931	RNSELRA	0.199623	-0.1344

FIG. 33 (Continued)

SyS1758	3754	GCCCAACAGAAGTCTCCGAATGGTCTGGCACAG	8343	AQQKSPNGLAQ	12932	QKSPNGL	0.199418	-0.01019
SyS1759	3755	GCCCAAAAAAGCGGCGACCACCTCACCGCACAG	8344	AQKSGDHLTAQ	12933	KSGDHLT	0.199256	-0.10889
TS171	3756	GCCCAAGGGAATCGGACTACGAGTAGTGCACAG	8345	AQGNRTTSSAQ	12934	GNRTTSS	0.199229	-0.1942
SyS1760	3757	GCCCAAATGGTCGCCCTCACCGTCGGCGCACAG	8346	AQMVALTVGAQ	12935	MVALTVG	0.19916	-0.17557
SyS1761	3758	GCCCAACTCAGCAGCAACAGCCCCAGAGCACAG	8347	AQLSSNSPRAQ	12936	LSSNSPR	0.199055	0.023543
SyS1762	3759	GCCCAAGCTTCGAATAATCAGACGTATGCACAG	8348	AQASNNQTYAQ	12937	ASNNQTY	0.199003	-0.05924
GS1025	3760	GCCCAAAACAACATCGTCACCACCAGCGCACAG	8349	AQNNIVTTSAQ	12938	NNIVTTS	0.19875	-0.15317
GS1026	3761	GCCCAACACGACACCAAAAAACCCATGGCACAG	8350	AQHDTKKPMAQ	12939	HDTKKPM	0.198636	-0.1338
SyS1765	3762	GCCCAAATTAATACGGCTAGTTATAAGGCACAG	8351	AQINTASYKAQ	12940	INTASYK	0.198495	-0.10647
SyS1766	3763	GCCCAAAGTGGTATGGTTAGTATGTCGGCACAG	8352	AQSGMVSMSAQ	12941	SGMVSMS	0.19837	-0.10161
SyS1768	3764	GCCCAACTCGTCACCGCCAGCGCCAGAGCACAG	8353	AQLVTASARAQ	12942	LVTASAR	0.198271	-0.12079
GS1028	3765	GCCCAAAGCAGAGCCCCCAGCGCCATGGCACAG	8354	AQSRAPSAMAQ	12943	SRAPSAM	0.198243	-0.1747
SyS1769	3766	GCCCAAAACAACAACCAAAAAGTCTACGCACAG	8355	AQNNNQKVYAQ	12944	NNNQKVY	0.197983	-0.11345
SyS1770	3767	GCCCAAACTAGTGTGGTTGCTAATCCTGCACAG	8356	AQTSVVANPAQ	12945	TSVVANP	0.197975	-0.02461
SyS1771	3768	GCCCAAGGCAACGCCGGCCCCAGCCTCGCACAG	8357	AQGNAGPSLAQ	12946	GNAGPSL	0.197961	-0.17382
SyS1772	3769	GCCCAATACAGCACCAGCCTCGAACTCGCACAG	8358	AQYSTSLELAQ	12947	YSTSLEL	0.197917	-0.23419
SyS1773	3770	GCCCAACCGTCTAATCCGCCTAAGGAGGCACAG	8359	AQPSNPPKEAQ	12948	PSNPPKE	0.197834	-0.10324
SyS1774	3771	GCCCAAACTAATTCTAAGCCTTCGTGGGCACAG	8360	AQTNSKPSWAQ	12949	TNSKPSW	0.197791	-0.2305
SyS1775	3772	GCCCAATCGATTGATCGGCAGCAGCTTGCACAG	8361	AQSIDRQQLAQ	12950	SIDRQQL	0.19771	-0.16273
GS1030	3773	GCCCAAAACAAAGCCGGCCCCGCCAGCGCACAG	8362	AQNKAGPASAQ	12951	NKAGPAS	0.197681	-0.08173
GS1031	3774	GCCCAAAGCATGACCACCAACAGAAGCGCACAG	8363	AQSMTTNRSAQ	12952	SMTTNRS	0.197629	-0.14958
SyS1776	3775	GCCCAAGGCAACAGCGCCGTCCAACTCGCACAG	8364	AQGNSAVQLAQ	12953	GNSAVQL	0.197614	-0.09127
GS1032	3776	GCCCAAAGAAGCAGCGACGTCAACACCGCACAG	8365	AQRSSDVNTAQ	12954	RSSDVNT	0.197531	-0.12807
SyS1777	3777	GCCCAACACACAACGGCGTCCAAAGCGTCGCACAG	8366	AQHNGVQSVAQ	12955	HNGVQSV	0.197468	0.173685
SyS1778	3778	GCCCAAGAAAAAGACCACGGCATGGCCGCACAG	8367	AQEKDHGMAAQ	12956	EKDHGMA	0.197362	-0.12344
SyS1779	3779	GCCCAATACAGACTCCCCGACGGCAGAGCACAG	8368	AQYRLPDGRAQ	12957	YRLPDGR	0.197255	-0.21202
SyS1780	3780	GCCCAAAGCAGCAGAGAACTCAGACTCGCACAG	8369	AQSSRELRLAQ	12958	SSRELRL	0.197138	-0.13192
SyS1782	3781	GCCCAAAACCAAGTCGAAAGCAGAGTCGCACAG	8370	AQNQVESRVAQ	12959	NQVESRV	0.196941	-0.11838
SyS1783	3782	GCCCAAGCCCTCCACAGCGTCCCCAAAGCACAG	8371	AQALHSVPKAQ	12960	ALHSVPK	0.196939	-0.11574
SyS1784	3783	GCCCAAACTGGTCCTAGTACGGTGCCGGCACAG	8372	AQTGPSTVPAQ	12961	TGPSTVP	0.196935	-0.09919
SyS1785	3784	GCCCAAGAACCCCCTCGGCGTCCACCCCGCACAG	8373	AQEPLGVHPAQ	12962	EPLGVHP	0.196915	-0.19723
GS1036	3785	GCCCAAACCAGAACCGACACCACCAACGCACAG	8374	AQTRTDTTNAQ	12963	TRTDTTN	0.196745	-0.08049

FIG. 33 (Continued)

GS1037	3786	GCCCAAAGCCACAACCTCACCGCCGACGCACAG	8375	AQSHNLTADAQ	12964	SHNLTAD	0.196727	-0.15855
SyS1787	3787	GCCCAAAACGTCAGAAGAGACGACACCGCACAG	8376	AQNVRRDDTAQ	12965	NVRRDDT	0.196487	-0.11616
SyS1788	3788	GCCCAATTCGCCGCCAACCTCGTCGCCGCACAG	8377	AQFAANLVAAQ	12966	FAANLVA	0.196427	-0.13677
SyS1790	3789	GCCCAAATCGGCGCCCAAGCCAGAATGGCACAG	8378	AQIGAQARMAQ	12967	IGAQARM	0.19619	-0.15288
SyS1791	3790	GCCCAAAATTCTATGTCTAAGGCTTATGCACAG	8379	AQNSMSKAYAQ	12968	NSMSKAY	0.196153	-0.1986
GS1039	3791	GCCCAAAACGTCAACAAAGACAGAGTCGCACAG	8380	AQNVNKDRVAQ	12969	NVNKDRV	0.196068	-0.1442
GS1040	3792	GCCCAATCTTTTCAGGGTTCGGCTAGGGCACAG	8381	AQSFQGSARAQ	12970	SFQGSAR	0.196025	-0.06362
GS1041	3793	GCCCAAGCCAACAGCGACCACATCCACGCACAG	8382	AQANSDHIHAQ	12971	ANSDHIH	0.196025	-0.13792
GS1042	3794	GCCCAAGTCAGCCTCGCCAGCAAAAGCGCACAG	8383	AQVSLASKSAQ	12972	VSLASKS	0.195985	-0.13164
SyS1793	3795	GCCCAACCCAAAGACAGAGCCACCAGCGCACAG	8384	AQPKDRATSAQ	12973	PKDRATS	0.195973	-0.13314
SyS1794	3796	GCCCAAGTTCGGTCGCAGAGTGATTCGGCACAG	8385	AQVRSQSDSAQ	12974	VRSQSDS	0.195812	-0.12101
SyS1795	3797	GCCCAACTTGGTAATTCGGTGTTTAAGGCACAG	8386	AQLGNSVFKAQ	12975	LGNSVFK	0.195693	-0.10483
SyS1796	3798	GCCCAAAGCACCAAAGAAAGCCCCAAAGCACAG	8387	AQSTKESPKAQ	12976	STKESPK	0.195693	-0.23173
SyS1797	3799	GCCCAACTCCAACCCACCACCTTCAGCGCACAG	8388	AQLQPTTFSAQ	12977	LQPTTFS	0.195693	-0.23173
SyS1798	3800	GCCCAACCCATGCACACCGCCATGGTCGCACAG	8389	AQPMHTAMVAQ	12978	PMHTAMV	0.195687	-0.14162
SyS1799	3801	GCCCAAGTGTTTGCTCATACTGGTCTTGCACAG	8390	AQVFAHTGLAQ	12979	VFAHTGL	0.195535	-0.2277
GS1044	3802	GCCCAACAAAAAGCCACCAGCATCCACGCACAG	8391	AQQKATSIHAQ	12980	QKATSIH	0.195419	-0.1338
SyS1800	3803	GCCCAAGGTTCTAAGTCGGATAATCTGGCACAG	8392	AQGSKSDNLAQ	12981	GSKSDNL	0.195377	-0.15011
SyS1801	3804	GCCCAAAGCGGCACCAACGTCGTCAGCGCACAG	8393	AQSGTNVVSAQ	12982	SGTNVVS	0.195376	-0.20955
SyS1802	3805	GCCCAAACCAAACTCACCACCCTCAGCGCACAG	8394	AQTKLTTLSAQ	12983	TKLTTLS	0.195251	-0.19846
SyS1803	3806	GCCCAACCCATCCTCCACACAACCAAATCGCACAG	8395	AQPILHNQIAQ	12984	PILHNQI	0.195237	-0.13798
SyS1804	3807	GCCCAAGTCACCAACCCCATCAAACCCGCACAG	8396	AQVTNPIKPAQ	12985	VTNPIKP	0.195213	-0.19477
SyS1805	3808	GCCCAAACCAACGCCCTCCACATGAAAGCACAG	8397	AQTNALHMKAQ	12986	TNALHMK	0.195213	-0.19477
SyS1806	3809	GCCCAAGTCGCCCACGCCTACCCCGCCGCACAG	8398	AQVAHAYPAAQ	12987	VAHAYPA	0.195206	0.067049
SyS1807	3810	GCCCAAGCTGAGCATGGTCTTGGTCCTGCACAG	8399	AQAEHGLGPAQ	12988	AEHGLGP	0.195111	-0.20345
GS1045	3811	GCCCAAATGAACAAATACAGCCCCGCCGCACAG	8400	AQMNKYSPAAQ	12989	MNKYSPA	0.195101	-0.14689
SyS1808	3812	GCCCAAACCATGCAAGACAGACTCACCGCACAG	8401	AQTMQDRLTAQ	12990	TMQDRLT	0.19501	-0.12978
SyS1809	3813	GCCCAAGGCGTCAAAATCCTCAACAGCGCACAG	8402	AQGVKILNSAQ	12991	GVKILNS	0.194998	-0.11374
GS1046	3814	GCCCAAGCGCAGAATAAGATGACGAGTGCACAG	8403	AQAQNKMTSAQ	12992	AQNKMTS	0.194978	-0.14048
SyS1810	3815	GCCCAAACCAGCGCCCTCACCGACATCGCACAG	8404	AQTSALTDIAQ	12993	TSALTDI	0.194946	-0.19133
SyS1811	3816	GCCCAAGACCTCAGACACGCCGACATCGCACAG	8405	AQDLRHADIAQ	12994	DLRHADI	0.194916	-0.14647
GP158	3817	GCCCAACAGAATAAGGCGTTGACGGTGGCACAG	8406	AQQNKALTVAQ	12995	QNKALTV	0.194813	-0.07426

FIG. 33 (Continued)

SyS1812	3818	GCCCAAACTCAGGGGATTACGATTGTGGCACAG	8407	AQTQGITIVAQ	12996	TQGITIV	0.194803	-0.1792
GS1047	3819	GCCCAAACGGCGACTATTCTGTCGGGGGGCACAG	8408	AQTATILSGAQ	12997	TATILSG	0.194742	-0.11376
GP159	3820	GCCCAATTTGCGGCGAGTAATATTTCTGCACAG	8409	AQFAASNISAQ	12998	FAASNIS	0.194572	-0.07232
SyS1814	3821	GCCCAACGTAATACTATGGAGACTATGGCACAG	8410	AQRNTMETMAQ	12999	RNTMETM	0.194502	-0.19981
GS1049	3822	GCCCAAAGTTCTGGTACTAGTTATAGTGCACAG	8411	AQSSGTSYSAQ	13000	SSGTSYS	0.194467	-0.1765
SyS1815	3823	GCCCAAGCCAACCACGGCCTCAACGCCGCACAG	8412	AQANHGLNAAQ	13001	ANHGLNA	0.194455	0.086643
GS1050	3824	GCCCAAATGCTGTCGAATTCGCGTAGTGCACAG	8413	AQMLSNSRSAQ	13002	MLSNSRS	0.194307	-0.13666
SyS1816	3825	GCCCAAGCTGCGATTCATGCGACGCCTGCACAG	8414	AQAAIHATPAQ	13003	AAIHATP	0.194234	-0.23255
SyS1817	3826	GCCCAATGGCAGTCGTTTGCGTCGGCGGCACAG	8415	AQWQSFASAAQ	13004	WQSFASA	0.194234	-0.23255
SyS1818	3827	GCCCAAATGGGTGGGAATTCGAGTACGGCACAG	8416	AQMGGNSSTAQ	13005	MGGNSST	0.194111	-0.01311
SyS1819	3828	GCCCAAAAGACGGATTTGGCGCAGCATGCACAG	8417	AQKTDLAQHAQ	13006	KTDLAQH	0.194111	-0.15132
TS172	3829	GCCCAAGTCAACACCACCAGATTCAGCGCACAG	8418	AQVNTTRFSAQ	13007	VNTTRFS	0.19409	-0.31218
SyS1821	3830	GCCCAAAATGTGCATGCTCATCAGGCTGCACAG	8419	AQNVHAHQAAQ	13008	NVHAHQA	0.193921	-0.11495
GS1051	3831	GCCCAAGGCGCCATGAGCATCCAAACCGCACAG	8420	AQGAMSIQTAQ	13009	GAMSIQT	0.193889	-0.10282
GS1052	3832	GCCCAAGCTCGGGGTCCGACGATTGTTGCACAG	8421	AQARGPTIVAQ	13010	ARGPTIV	0.193777	-0.18099
GS1055	3833	GCCCAAACGATGCATAGTAAGTCGGATGCACAG	8422	AQTMHSKSDAQ	13011	TMHSKSD	0.193462	-0.16035
GS1056	3834	GCCCAAACGGTTACGCAGACTACTCAGGCACAG	8423	AQTVTQTTQAQ	13012	TVTQTTQ	0.193371	-0.16663
GS1057	3835	GCCCAAGGCAACACCAACAGCCTCACCGCACAG	8424	AQGNTNSLTAQ	13013	GNTNSLT	0.193295	-0.04686
GS1058	3836	GCCCAAAGAGTCATCGCCAGCGTCAACGCACAG	8425	AQRVIASVNAQ	13014	RVIASVN	0.193253	-0.15001
SyS1823	3837	GCCCAACCCAGCAGCGGCAACAGCGAAGCACAG	8426	AQPSSGNSEAQ	13015	PSSGNSE	0.193165	-0.03781
GS1059	3838	GCCCAACAGCCGCATGGTTTTACGGCTGCACAG	8427	AQQPHGFTAAQ	13016	QPHGFTA	0.19311	-0.08893
GS1060	3839	GCCCAAACCACCGGCACCAACATGAGAGCACAG	8428	AQTTGTNMRAQ	13017	TTGTNMR	0.192999	-0.1586
SyS1825	3840	GCCCAATTCACCAGACTCGAAGACAGAGCACAG	8429	AQFTRLEDRAQ	13018	FTRLEDR	0.192838	-0.12829
GS1061	3841	GCCCAAGACAGAAGCCCCGCCCACACCGCACAG	8430	AQDRSPAHTAQ	13019	DRSPAHT	0.192801	-0.06749
SyS1827	3842	GCCCAACACGTCCACAACACCGTCCCCGCACAG	8431	AQHVHNTVPAQ	13020	HVHNTVP	0.192711	-0.04938
SS118	3843	GCCCAAATGAACACCACCGGCACCAAAGCACAG	8432	AQMNTTGTKAQ	13021	MNTTGTK	0.192667	-0.30576
SyS1828	3844	GCCCAATTCGCCACCCAAACCATCGCCGCACAG	8433	AQFATQTIAAQ	13022	FATQTIA	0.192606	0.020831
GS1062	3845	GCCCAAGTCAGCGGCAACATCCCCGTCGCACAG	8434	AQVSGNIPVAQ	13023	VSGNIPV	0.192554	-0.1774
GS1063	3846	GCCCAAGACGGCAGAAACATCGCCCCCGCACAG	8435	AQDGRNIAPAQ	13024	DGRNIAP	0.192531	-0.10292
SyS1829	3847	GCCCAAATGCTCCCCACCGTCAACAGAGCACAG	8436	AQMLPTVNRAQ	13025	MLPTVNR	0.192494	-0.11361
GS1064	3848	GCCCAACCTACTACTAATGTGCTTGGTGCACAG	8437	AQPTTNVLGAQ	13026	PTTNVLG	0.192456	-0.15676
SyS1830	3849	GCCCAACGGGAGATGCATGGTACTCTTGCACAG	8438	AQREMHGTLAQ	13027	REMHGTL	0.192442	-0.13677

FIG. 33 (Continued)

GS1066	3850	GCCCAATCTCCGTATTCGACTCGTCCGGCACAG	8439	AQSPYSTRPAQ	13028	SPYSTRP	0.192371	-0.15517
SyS1832	3851	GCCCAATACAACATGAACACCGAAATGGCACAG	8440	AQYNMNTEMAQ	13029	YNMNTEM	0.192365	-0.17314
SyS1833	3852	GCCCAAGGGGCGCGTATGGGTCATTCGGCACAG	8441	AQGARMGHSAQ	13030	GARMGHS	0.192225	-0.07252
SyS1834	3853	GCCCAATTCAGCCCCGGCTACGTCCCCGCACAG	8442	AQFSPGYVPAQ	13031	FSPGYVP	0.192168	-0.09677
SyS1835	3854	GCCCAACAGCAGCATATTCCTCCTTCTGCACAG	8443	AQQQHIPPSAQ	13032	QQHIPPS	0.191995	-0.18984
GS1067	3855	GCCCAACTCAGCACCAGCCTCAGCCCCGCACAG	8444	AQLSTSLSPAQ	13033	LSTSLSP	0.191963	-0.10041
SyS1836	3856	GCCCAAGTTAATGGGATTAAGGAGTATGCACAG	8445	AQVNGIKEYAQ	13034	VNGIKEY	0.191891	-0.081
SyP60	3857	GCCCAAGGTGTGCGGACTGAGCCGATGGCACAG	8446	AQGVRTEPMAQ	13035	GVRTEPM	0.191789	-0.0406
SyS1837	3858	GCCCAAAGAAACAACGACAGCCTCACCGCACAG	8447	AQRNNDSLTAQ	13036	RNNDSLT	0.191786	0.1054
SyS1838	3859	GCCCAATTTAATGCGTCTCCTAAGTTGGCACAG	8448	AQFNASPKLAQ	13037	FNASPKL	0.191776	-0.19375
SyS1839	3860	GCCCAAGGCCTCACCACCAGCACCACCGCACAG	8449	AQGLTTSTTAQ	13038	GLTTSTT	0.191776	-0.19375
SyS1840	3861	GCCCAAATGATCAGAGGCACCAGCAGCGCACAG	8450	AQMIRGTSSAQ	13039	MIRGTSS	0.191749	-0.11737
SyS1841	3862	GCCCAAACTAAGCTTGTGGCTACTGTGGCACAG	8451	AQTKLVATVAQ	13040	TKLVATV	0.191661	-0.21941
SyS1842	3863	GCCCAAGTGAGTCGGCAGTTTGAGCCGGCACAG	8452	AQVSRQFEPAQ	13041	VSRQFEP	0.191661	-0.21941
SyS1843	3864	GCCCAAAATGGTGATAGTTTGCGTCCTGCACAG	8453	AQNGDSLRPAQ	13042	NGDSLRP	0.191643	-0.05025
SyS1844	3865	GCCCAAACCCAAAACCTCAGCAGCCACGCACAG	8454	AQTQNLSSHAQ	13043	TQNLSSH	0.191633	0.003465
SyS1845	3866	GCCCAAACCGTCACCGGCAGCCTCGTCGCACAG	8455	AQTVTGSLVAQ	13044	TVTGSLV	0.191556	-0.15374
SyS1846	3867	GCCCAAGGCAGAGGCCCCGAAGCCCAAGCACAG	8456	AQGRGPEAQAQ	13045	GRGPEAQ	0.191398	0.062377
GS1068	3868	GCCCAACCCAGAAACGTCGGCCTCGAAGCACAG	8457	AQPRNVGLEAQ	13046	PRNVGLE	0.191325	-0.0842
SyS1847	3869	GCCCAATTCAACAGCAGCATCCCCACCGCACAG	8458	AQFNSSIPTAQ	13047	FNSSIPT	0.191319	0.002066
SyS1848	3870	GCCCAAGGTAATCAGCAGCATTCTTCTGCACAG	8459	AQGNQQHSSAQ	13048	GNQQHSS	0.191216	0.020615
GS1069	3871	GCCCAACCCATCACCAACGGCAGCTTCGCACAG	8460	AQPITNGSFAQ	13049	PITNGSF	0.191188	-0.13074
GS1070	3872	GCCCAAGTTCAGCGTACTCCGCTTACTGCACAG	8461	AQVQRTPLTAQ	13050	VQRTPLT	0.191121	-0.18054
GS1071	3873	GCCCAAACGCCTTATGCTGGTAGGGCTGCACAG	8462	AQTPYAGRAAQ	13051	TPYAGRA	0.19095	-0.10831
SyS1849	3874	GCCCAACTGGCTCTGTCTAATCGTACGGCACAG	8463	AQLALSNRTAQ	13052	LALSNRT	0.190717	-0.17259
SyS1850	3875	GCCCAAGGTCAGATGGCTACTGGTCTGGCACAG	8464	AQGQMATGLAQ	13053	GQMATGL	0.190704	-0.13866
SyS1852	3876	GCCCAATCTAATCCTGCGACTACTACTGCACAG	8465	AQSNPATTTAQ	13054	SNPATTT	0.190655	-0.11859
GS1074	3877	GCCCAAGGGCGGACTACTAGTGATAGTGCACAG	8466	AQGRTTSDSAQ	13055	GRTTSDS	0.190613	-0.09357
GS1075	3878	GCCCAAAGCAGACTCACCAGCCTCGGCGCACAG	8467	AQSRLTSLGAQ	13056	SRLTSLG	0.19049	-0.12819
SyS1853	3879	GCCCAACATCTTTCTACGCCGGATTTGGCACAG	8468	AQHLSTPDLAQ	13057	HLSTPDL	0.190472	-0.18737
SyS1854	3880	GCCCAAATGCCTCATGCTCCGACTTCGGCACAG	8469	AQMPHAPTSAQ	13058	MPHAPTS	0.190411	-0.14283
GS1076	3881	GCCCAAGTTGCGGGTATGTTGACGCATGCACAG	8470	AQVAGMLTHAQ	13059	VAGMLTH	0.190345	-0.17672

FIG. 33 (Continued)

GS1077	3882	GCCCAAGTCGCCAGCCAAAAACTCAACGCACAG	8471	AQVASQKLNAQ	13060	VASQKLN	0.190288	-0.13094
SyS1856	3883	GCCCAAACCCAAAGCATGACCAGCAGAGCACAG	8472	AQTQSMTSRAQ	13061	TQSMTSR	0.190241	-0.02852
GS1079	3884	GCCCAACCCATCAGCACCATGAGCCTCGCACAG	8473	AQPISTMSLAQ	13062	PISTMSL	0.19008	-0.1765
SyS1857	3885	GCCCAAGCCCAACTCAACAGCGCCGGCGCACAG	8474	AQAQLNSAGAQ	13063	AQLNSAG	0.190056	-0.1392
SyS1858	3886	GCCCAACACCTCCCCAAATACGAACACGCACAG	8475	AQHLPKYEHAQ	13064	HLPKYEH	0.190056	-0.1392
GS1080	3887	GCCCAAGGGGTGCAGGCTGTTGTGGGTGCACAG	8476	AQGVQAVVGAQ	13065	GVQAVVG	0.189947	-0.15647
SyS1859	3888	GCCCAAGGCGACACCCAATACGCCAGAGCACAG	8477	AQGDTQYARAQ	13066	GDTQYAR	0.189923	-0.1792
SyS1860	3889	GCCCAAGCCAGCCCCCTCGTCATGAGCGCACAG	8478	AQASPLVMSAQ	13067	ASPLVMS	0.189788	-0.033
SyS1861	3890	GCCCAAAGCAACGCCGGCATGAGCAAAGCACAG	8479	AQSNAGMSKAQ	13068	SNAGMSK	0.189781	-0.07895
SyS1862	3891	GCCCAAAGAAGCGTCAGCGCCGTCCCCGCACAG	8480	AQRSVSAVPAQ	13069	RSVSAVP	0.189731	-0.22064
SyS1863	3892	GCCCAACCCAGCTACCACAAAAGCCCCCGCACAG	8481	AQPSYHKSPAQ	13070	PSYHKSP	0.189731	-0.15164
GS1081	3893	GCCCAACATCAGTTTACTAGTTCTGCGGCACAG	8482	AQHQFTSSAAQ	13071	HQFTSSA	0.189638	-0.13792
SyS1865	3894	GCCCAAAACCAAAGCCCCATCGGCGCCGCACAG	8483	AQNQSPIGAAQ	13072	NQSPIGA	0.189626	-0.22434
SyS1866	3895	GCCCAAGGTGCGGCTGGGATGTCGCGGGCACAG	8484	AQGAAGMSRAQ	13073	GAAGMSR	0.189609	-0.04299
GS1082	3896	GCCCAAACGGTGAAGACGTATAGTGCGGCACAG	8485	AQTVKTYSAAQ	13074	TVKTYSA	0.189603	0.055302
SyS1867	3897	GCCCAACTCAGCATGACCAGCCAAATGGCACAG	8486	AQLSMTSQMAQ	13075	LSMTSQM	0.189571	-0.09374
SyS1868	3898	GCCCAAGGCCTCAGCCCCACCTTCGGCGCACAG	8487	AQGLSPTFGAQ	13076	GLSPTFG	0.189515	-0.16273
GS1083	3899	GCCCAAATGGACACCGTCATGAAAGGCGCACAG	8488	AQMDTVMKGAQ	13077	MDTVMKG	0.189386	-0.16663
GS1085	3900	GCCCAACGTGATAAGATTTCTACGTATGCACAG	8489	AQRDKISTYAQ	13078	RDKISTY	0.189205	-0.18099
SyS1870	3901	GCCCAAGACAGCAACAGCTACGTCAGAGCACAG	8490	AQDSNSYVRAQ	13079	DSNSYVR	0.189097	-0.18121
SyS1872	3902	GCCCAAAGCCTCAAAAGCAGCCCCCTTCGCACAG	8491	AQSLKSSPFAQ	13080	SLKSSPF	0.189004	-0.19981
GS1088	3903	GCCCAACTTGATCGTACTGCGAAGCCTGCACAG	8492	AQLDRTAKPAQ	13081	LDRTAKP	0.188806	-0.15676
SyS1873	3904	GCCCAACCGTCGAGGGCTCCGGATCCTGCACAG	8493	AQPSRAPDPAQ	13082	PSRAPDP	0.188784	-0.10614
SyS1874	3905	GCCCAATACCTCAACCAAATCAGAAGCGCACAG	8494	AQYLNQIRSAQ	13083	YLNQIRS	0.188662	-0.10889
GS1090	3906	GCCCAACAAAACAGAAGCGTCGTCGAAGCACAG	8495	AQQNRSVVEAQ	13084	QNRSVVE	0.188647	-0.14238
GS1091	3907	GCCCAACAGGAGTCTATGGTTAAGTATGCACAG	8496	AQQESMVKYAQ	13085	QESMVKY	0.188647	-0.17958
GS1092	3908	GCCCAAAAGCTGTCGCAGGAGAGTAATGCACAG	8497	AQKLSQESNAQ	13086	KLSQESN	0.18854	-0.13253
SyS1875	3909	GCCCAACGTGGTACTATGGAGCATGATGCACAG	8498	AQRGTMEHDAQ	13087	RGTMEHD	0.188451	-0.18042
SyS1878	3910	GCCCAACAGTCGGGTCCTGGGATTGTGGCACAG	8499	AQQSGPGIVAQ	13088	QSGPGIV	0.188217	-0.2083
SyS1879	3911	GCCCAACTCAACCAAGGCGACCTCCTCGCACAG	8500	AQLNQGDLLAQ	13089	LNQGDLL	0.188212	-0.21078
SyS1880	3912	GCCCAAGCCAAAACCATCGGCAGCACCGCACAG	8501	AQAKTIGSTAQ	13090	AKTIGST	0.188109	-0.10161
SyS1881	3913	GCCCAAGACAGCGGCAACAGAACCAGCGCACAG	8502	AQDSGNRTSAQ	13091	DSGNRTS	0.187878	-0.11374

FIG. 33 (Continued)

SyS1882	3914	GCCCAACTCAGCCACAGCACCAGCTTCGCACAG	8503	AQLSHSTSFAQ	13092	LSHSTSF	0.187878	-0.11374
GS1094	3915	GCCCAAGGTGATTTTTCGTCGAAGCAGGCACAG	8504	AQGDFSSKQAQ	13093	GDFSSKQ	0.187866	-0.03656
GP160	3916	GCCCAAGATCATAGTAATGCGTATCGTGCACAG	8505	AQDHSNAYRAQ	13094	DHSNAYR	0.187845	-0.07058
SyS1883	3917	GCCCAAGTTCCGACTGATCGTCCTCGTGCACAG	8506	AQVPTDRPRAQ	13095	VPTDRPR	0.187817	-0.22042
SyS1884	3918	GCCCAAAGCATGCAACTCATCAACGAAGCACAG	8507	AQSMQLINEAQ	13096	SMQLINE	0.187817	-0.22042
GS1095	3919	GCCCAATACGCCAACAGCGTCGGCCTCGCACAG	8508	AQYANSVGLAQ	13097	YANSVGL	0.187791	-0.11279
SyS1885	3920	GCCCAAGTCTACCTCGCCAGCGGCGGCGCACAG	8509	AQVYLASGGAQ	13098	VYLASGG	0.187783	-0.22187
SyS1886	3921	GCCCAACTCATCCCCGTCACCAGCGTCGCACAG	8510	AQLIPVTSVAQ	13099	LIPVTSV	0.187768	-0.20466
SyS1888	3922	GCCCAAGGCAACATGAACAGCAGAACCGCACAG	8511	AQGNMNSRTAQ	13100	GNMNSRT	0.18734	-0.07494
SyS1889	3923	GCCCAAAGCCACACAACGACAGAAGCCTCGCACAG	8512	AQSHNDRSLAQ	13101	SHNDRSL	0.18734	-0.13798
SyS1890	3924	GCCCAACATAGGATTCCTACGGCTGGGGCACAG	8513	AQHRIPTAGAQ	13102	HRIPTAG	0.18734	-0.18527
SyS1891	3925	GCCCAAATGGGCAAAGACTACACCCACGCACAG	8514	AQMGKDYTHAQ	13103	MGKDYTH	0.187325	-0.18984
SyS1893	3926	GCCCAATCTCATGCGAGTACTCCTATTGCACAG	8515	AQSHASTPIAQ	13104	SHASTPI	0.18723	-0.16041
GS1098	3927	GCCCAACTCAACAGCCAAACCAGAAGCGCACAG	8516	AQLNSQTRSAQ	13105	LNSQTRS	0.18719	-0.08992
SyS1894	3928	GCCCAACGGACGCTGAGTGATAGTGTGGCACAG	8517	AQRTLSDSVAQ	13106	RTLSDSV	0.187066	-0.11859
SyS1895	3929	GCCCAACTTACGACTGCTAAGACGTTTGCACAG	8518	AQLTTAKTFAQ	13107	LTTAKTF	0.187043	-0.19723
GS1099	3930	GCCCAAAGAATCGTCGGCAGCACCAGCGCACAG	8519	AQRIVGSTSAQ	13108	RIVGSTS	0.187032	-0.05357
SyS1897	3931	GCCCAAACCAAAACCCTCGCCCTCCACGCACAG	8520	AQTKTLALHAQ	13109	TKTLALH	0.187025	-0.15011
SyS1898	3932	GCCCAATGGGAAGTCCCCGCCAGAAACGCACAG	8521	AQWEVPARNAQ	13110	WEVPARN	0.186968	-0.18163
SyS1899	3933	GCCCAAATTTCTAATCCGGCGATTGCTGCACAG	8522	AQISNPAIAAQ	13111	ISNPAIA	0.186968	-0.18163
GS1101	3934	GCCCAATTGGGGGCTTCGCAGACTTCTGCACAG	8523	AQLGASQTSAQ	13112	LGASQTS	0.186895	-0.14143
GS1103	3935	GCCCAACTCAGCACCCACAACAGCGTCGCACAG	8524	AQLSTHNSVAQ	13113	LSTHNSV	0.186848	-0.02926
GS1104	3936	GCCCAAAGACACACCGACATCGACACCGCACAG	8525	AQRHTDIDTAQ	13114	RHTDIDT	0.186832	-0.14779
SyP61	3937	GCCCAAGGGAGGCCGGTTATTGCGGCGGCACAG	8526	AQGRPVIAAAQ	13115	GRPVIAA	0.186825	-0.04411
SyS1900	3938	GCCCAAGCCAACCTCAGAGACGGCGTCGCACAG	8527	AQANLRDGVAQ	13116	ANLRDGV	0.186763	-0.13071
GS1105	3939	GCCCAAGTTCAGTCTCCGTCGATTACGGCACAG	8528	AQVQSPSITAQ	13117	VQSPSIT	0.186748	-0.17201
SyS1901	3940	GCCCAATTCACCAGCGGCAGCCACCTCGCACAG	8529	AQFTSGSHLAQ	13118	FTSGSHL	0.18672	-0.14647
GS1106	3941	GCCCAACCTCTTCAGCAGTCGGGTCATGCACAG	8530	AQPLQQSGHAQ	13119	PLQQSGH	0.186526	-0.09792
SyS1902	3942	GCCCAAGCCAGAGTCGCCACCACCCTCGCACAG	8531	AQARVATTLAQ	13120	ARVATTL	0.186427	-0.14283
GS1108	3943	GCCCAACCCGGCAGACAAAACGACGCCGCACAG	8532	AQPGRQNDAAQ	13121	PGRQNDA	0.186248	-0.1214
SyS1905	3944	GCCCAAAAATACAGCAGCACCGCCATCGCACAG	8533	AQKYSSTAIAQ	13122	KYSSTAI	0.186114	-0.03736
SyS1906	3945	GCCCAACACAGCACCCACTACATCGCCGCACAG	8534	AQHSTHYIAAQ	13123	HSTHYIA	0.186051	-0.15496

FIG. 33 (Continued)

SyS1907	3946	GCCCAACAACCCCTCAACGCCCTCCCCGCACAG	8535	AQQPLNALPAQ	13124	QPLNALP	0.185989	0.064654
GS1109	3947	GCCCAAAAAACCCAAGAAACCGGCAACGCACAG	8536	AQKTQETGNAQ	13125	KTQETGN	0.185973	-0.16035
SyS1908	3948	GCCCAAAGTGAGTTGTCTCGGCATGCGGCACAG	8537	AQSELSRHAAQ	13126	SELSRHA	0.18587	0.08751
GS1110	3949	GCCCAAGGCCCCCAAAACCATCAGCACCGCACAG	8538	AQGPKTISTAQ	13127	GPKTIST	0.18578	-0.09587
GS1111	3950	GCCCAAAGTCATAGTATTGTGAATCCGGCACAG	8539	AQSHSIVNPAQ	13128	SHSIVNP	0.18578	-0.1765
SyS1909	3951	GCCCAACATTCGAATACTGTGAGTTCGGCACAG	8540	AQHSNTVSSAQ	13129	HSNTVSS	0.18577	0.232173
SyS1910	3952	GCCCAAGTCGCCGGCCTCACCGTCCAAGCACAG	8541	AQVAGLTVQAQ	13130	VAGLTVQ	0.185758	0.055989
GS1112	3953	GCCCAAGCCAACCCCGGCCTCGCCAACGCACAG	8542	AQANPGLANAQ	13131	ANPGLAN	0.185473	-0.16663
SyS1912	3954	GCCCAAGCCAGCGTCCAAATGACCCTCGCACAG	8543	AQASVQMTLAQ	13132	ASVQMTL	0.185379	-0.2305
SyS1913	3955	GCCCAACTCGTCACCGCCCAAGGCCCCCGCACAG	8544	AQLVTAQGPAQ	13133	LVTAQGP	0.185303	-0.10115
GP161	3956	GCCCAAACTACGCGTTATACTTCGCCGGCACAG	8545	AQTTRYTSPAQ	13134	TTRYTSP	0.185249	-0.07433
SyS1914	3957	GCCCAAATGGACACCGACAAACCCAGAGCACAG	8546	AQMDTDKPRAQ	13135	MDTDKPR	0.185204	-0.14405
SS121	3958	GCCCAAGGCACCAGCGTCCAAGACAGAGAGCACAG	8547	AQGTSVQDRAQ	13136	GTSVQDR	0.185176	-0.37486
GS1113	3959	GCCCAAAGAGCCAGCCCCCAACAATACGCACAG	8548	AQRASPQQYAQ	13137	RASPQQY	0.185058	-0.15478
SyS1915	3960	GCCCAAGTCAGCAGCGAACACAGAATCGCACAG	8549	AQVSSEHRIAQ	13138	VSSEHRI	0.184992	0.003859
GS1114	3961	GCCCAAAGCAACATGAAAATCCAACCCGCACAG	8550	AQSNMKIQPAQ	13139	SNMKIQP	0.184985	-0.09183
SyS1916	3962	GCCCAAAACCTCAGAATCGAACCCATGGCACAG	8551	AQNLRIEPMAQ	13140	NLRIEPM	0.18494	-0.08585
SyS1917	3963	GCCCAACCCACCGAAAGCCTCAGAGTCGCACAG	8552	AQPTESLRVAQ	13141	PTESLRV	0.184782	-0.20955
GP162	3964	GCCCAAACTAATAGGGGTCTTGCTCTTGCACAG	8553	AQTNRGLALAQ	13142	TNRGLAL	0.184678	-0.05599
SyS1920	3965	GCCCAACATGAGAAGACGGCGTATATATTGCACAG	8554	AQHEKTAYIAQ	13143	HEKTAYI	0.184498	-0.15657
SyS1921	3966	GCCCAAAATGTTATTTCTAAGAATTTGGCACAG	8555	AQNVISKNLAQ	13144	NVISKNL	0.184372	-0.22649
SyP62	3967	GCCCAAGGGACGGCGGGGTTTTCGTCGGCACAG	8556	AQGTAGFSSAQ	13145	GTAGFSS	0.184333	-0.04152
SyS1922	3968	GCCCAAATTGCGCAGATGGGGGTTAAGGCACAG	8557	AQIAQMGVKAQ	13146	IAQMGVK	0.184332	-0.18861
SyS1923	3969	GCCCAAACTTCTAAGGATGTGAAGGATGCACAG	8558	AQTSKDVKDAQ	13147	TSKDVKD	0.184281	-0.18769
SyS1924	3970	GCCCAAATCATCGGCGCCAGAGACATCGCACAG	8559	AQIIGARDIAQ	13148	IIGARDI	0.18425	-0.16829
SyS1925	3971	GCCCAACTTAGGGATACGGGTCTTGGGGCACAG	8560	AQLRDTGLGAQ	13149	LRDTGLG	0.184224	-0.1489
SyS1926	3972	GCCCAACTCAGCAACAGCCTCGGCCAAGCACAG	8561	AQLSNSLGQAQ	13150	LSNSLGQ	0.184171	0.126572
GS1116	3973	GCCCAAAACGTCCTCAACAGCAGAGGCGCACAG	8562	AQNVLNSRGAQ	13151	NVLNSRG	0.18417	-0.17958
GS1117	3974	GCCCAATTTAGGGGGTAGTGGTAGTCCGGCACAG	8563	AQFRGSGSPAQ	13152	FRGSGSP	0.18417	-0.17958
GS1118	3975	GCCCAAAATCCGGAGTTGCCGCGTCAGGCACAG	8564	AQNPELPRQAQ	13153	NPELPRQ	0.184111	-0.16932
GS1119	3976	GCCCAAACGTCTAGTTCGTTTAAGGAGGCACAG	8565	AQTSSSFKEAQ	13154	TSSSFKE	0.184043	-0.14524
SyS1928	3977	GCCCAAAACAGAGAATACATGACCCACGCACAG	8566	AQNREYMTHAQ	13155	NREYMTH	0.183973	-0.18405

FIG. 33 (Continued)

SyP63	3978	GCCCAAACGCCTGGTGTTGCGCATCCTGCACAG	8567	AQTPGVAHPAQ	13156	TPGVAHP	0.183725	-0.04392
SyS1931	3979	GCCCAAACGCAGTCTTCGGAGGGGCCTGCACAG	8568	AQTQSSEGPAQ	13157	TQSSEGP	0.183702	-0.19969
GS1120	3980	GCCCAAAGGGGTGAGCCGATTGTGTCGGCACAG	8569	AQRGEPIVSAQ	13158	RGEPIVS	0.183678	-0.17577
GS1121	3981	GCCCAATCGCTTACGTCTCTGAATTCTGCACAG	8570	AQSLTSLNSAQ	13159	SLTSLNS	0.183678	-0.14143
SyS1933	3982	GCCCAAACGGTGTTGCATACGAGGCAGGCACAG	8571	AQTVLHTRQAQ	13160	TVLHTRQ	0.183603	-0.06701
SyS1934	3983	GCCCAATTGTCGAAGTCGGGTGCGGATGCACAG	8572	AQLSKSGADAQ	13161	LSKSGAD	0.183472	-0.12577
SyS1935	3984	GCCCAAGCCAACGGCAACCAAAGCCTCGCACAG	8573	AQANGNQSLAQ	13162	ANGNQSL	0.183416	0.105951
SyS1936	3985	GCCCAATTCGTCACCAGCAGCGGCGCACAG	8574	AQFVTSSSGAQ	13163	FVTSSSG	0.183382	0.086298
SyP64	3986	GCCCAAGGTGCGAATAATCATACGCGTGCACAG	8575	AQGANNHTRAQ	13164	GANNHTR	0.183354	-0.04236
SyS1937	3987	GCCCAACACGCCCAGCGACGTCAACAACGCACAG	8576	AQHASDVNNAQ	13165	HASDVNN	0.183281	-0.23173
GS1123	3988	GCCCAAGGCCACCACACCAGCGACCCCCGCACAG	8577	AQGHHTSDPAQ	13166	GHHTSDP	0.183067	-0.17381
SyS1939	3989	GCCCAAGACAAAAACCCCGGCGTCCACGCACAG	8578	AQDKNPGVHAQ	13167	DKNPGVH	0.182966	-0.15011
SyS1940	3990	GCCCAATCGAGGAATTCGCATATTGAGGCACAG	8579	AQSRNSHIEAQ	13168	SRNSHIE	0.182829	-0.00548
SyS1941	3991	GCCCAACAGGCGAGTTCTGATCATGTTGCACAG	8580	AQQASSDHVAQ	13169	QASSDHV	0.182736	-0.1889
GS1125	3992	GCCCAACTCAGAGACACCCCCTACAACGCACAG	8581	AQLRDTPYNAQ	13170	LRDTPYN	0.182726	-0.18188
GS1126	3993	GCCCAAAGTTTGGCTGCGACGAGGGATGCACAG	8582	AQSLAATRDAQ	13171	SLAATRD	0.182549	-0.12807
SyS1942	3994	GCCCAAGGCCACGTCAACAACGCCGTCGCACAG	8583	AQGHVNNAVAQ	13172	GHVNNAV	0.182493	-0.12331
SyS1943	3995	GCCCAAATTGGTGGGCTTACGACGCGGGCACAG	8584	AQIGGLTTRAQ	13173	IGGLTTR	0.18241	-0.12143
GS1127	3996	GCCCAAAGCAAAGAAAGAAACGGCCAAGCACAG	8585	AQSKERNGQAQ	13174	SKERNGQ	0.182404	-0.12617
GS1128	3997	GCCCAATTGAATAGTGGTTCTTCTGCTGCACAG	8586	AQLNSGSSAAQ	13175	LNSGSSA	0.182404	-0.16432
SyS1944	3998	GCCCAAACCATGAGCACCACCTACGAAGCACAG	8587	AQTMSTTYEAQ	13176	TMSTTYE	0.182396	-0.10816
GS1129	3999	GCCCAAGGCGCCGACAACAGAATCAGCGCACAG	8588	AQGADNRISAQ	13177	GADNRIS	0.182324	-0.17022
SyS1945	4000	GCCCAAACCCAAAACAACGGCGACGTCGCACAG	8589	AQTQNNGDVAQ	13178	TQNNGDV	0.18227	-0.20466
GP163	4001	GCCCAAAATGGTCCGTCTGTGCTGAGTGCACAG	8590	AQNGPSVLSAQ	13179	NGPSVLS	0.182231	0.090896
SyS1946	4002	GCCCAAACGGCTCTTCGGGATGTGGGTGCACAG	8591	AQTALRDVGAQ	13180	TALRDVG	0.182226	0.09096
SyS1947	4003	GCCCAAAGGACTATGGGGACGACTATGGCACAG	8592	AQRTMGTTMAQ	13181	RTMGTTM	0.182133	0.002686
GS1131	4004	GCCCAAACGAGGGGTACGACTGTGGAGGCACAG	8593	AQTRGTTVEAQ	13182	TRGTTVE	0.182067	0.079797
GS1132	4005	GCCCAAACCGTCAGCAGAGTCCAAGTCGCACAG	8594	AQTVSRVQVAQ	13183	TVSRVQV	0.181971	-0.16842
SyS1948	4006	GCCCAAAGGCTGGATACTAGTGCGGATGCACAG	8595	AQRLDTSADAQ	13184	RLDTSAD	0.181959	-0.1344
GS1133	4007	GCCCAACTCATGACCAAAGGCCTCGTCGCACAG	8596	AQLMTKGLVAQ	13185	LMTKGLV	0.181936	-0.17829
SyS1949	4008	GCCCAACCCATGAGAATGCAAACCGCCGCACAG	8597	AQPMRMQTAAQ	13186	PMRMQTA	0.181912	-0.17998
SyS1950	4009	GCCCAAGTGGTGCTGGGGAGTACTTCTGCACAG	8598	AQVVLGSTSAQ	13187	VVLGSTS	0.181893	-0.13192

FIG. 33 (Continued)

GS1135	4010	GCCCAATCTAATAATGGGAATGGTCATGCACAG	8599	AQSNNGNGHAQ	13188	SNNGNGH	0.181861	-0.17863
SyS1951	4011	GCCCAAAGAGGCCCCGACCTCCTCAACGCACAG	8600	AQRGPDLLNAQ	13189	RGPDLLN	0.181699	-0.12829
SyS1952	4012	GCCCAAGGTTTTAATAGTATGAAGCCTGCACAG	8601	AQGFNSMKPAQ	13190	GFNSMKP	0.181699	-0.17435
SyS1953	4013	GCCCAACTCAACAGCAACCCCATGAACGCACAG	8602	AQLNSNPMNAQ	13191	LNSNPMN	0.181699	-0.17435
GS1136	4014	GCCCAACTCAGCAACAGAGTCCAAAGCGCACAG	8603	AQLSNRVQSAQ	13192	LSNRVQS	0.181602	-0.07962
GS1137	4015	GCCCAAAGCAGAATGGAAGGCACCGTCGCACAG	8604	AQSRMEGTVAQ	13193	SRMEGTV	0.181451	-0.1451
SyS1955	4016	GCCCAAAGCGAACAATACGTCAGAGTCGCACAG	8605	AQSEQYVRVAQ	13194	SEQYVRV	0.181394	-0.16643
GS1138	4017	GCCCAAAGTAATCTTGCGAATCAGCCTGCACAG	8606	AQSNLANQPAQ	13195	SNLANQP	0.1813	-0.16484
GP164	4018	GCCCAAGTGAGTATGCAGAGGCCGACGGCACAG	8607	AQVSMQRPTAQ	13196	VSMQRPT	0.181294	-0.06864
SyS1956	4019	GCCCAATTTCATGGTCAGGGTATGTCTGCACAG	8608	AQFHGQGMSAQ	13197	FHGQGMS	0.181291	-0.14405
SyS1959	4020	GCCCAAACCGGCGCCATCAACGCCCCCGCACAG	8609	AQTGAINAPAQ	13198	TGAINAP	0.181162	-0.21202
SyS1960	4021	GCCCAAACGCTGTTTAAGAATGGTCCTGCACAG	8610	AQTLFKNGPAQ	13199	TLFKNGP	0.181097	-0.21315
SyS1961	4022	GCCCAAGTGGTGCCTATTTCGACGAATGCACAG	8611	AQVVPISTNAQ	13200	VVPISTN	0.181026	-0.16344
GS1140	4023	GCCCAAGCCAAAGGCACCGCCCTCGTCGCACAG	8612	AQAKGTALVAQ	13201	AKGTALV	0.180981	-0.16304
SyS1962	4024	GCCCAAAGGGATACTGTGCAGGTGTATGCACAG	8613	AQRDTVQVYAQ	13202	RDTVQVY	0.180851	-0.21571
GS1141	4025	GCCCAACTCGGCACCAAAGCCACCCACGCACAG	8614	AQLGTKATHAQ	13203	LGTKATH	0.180672	-0.16125
SyS1964	4026	GCCCAAGACAACGTCAGAGTCACCGCCGCACAG	8615	AQDNVRVTAAQ	13204	DNVRVTA	0.180658	0.019619
SP40	4027	GCCCAAACGAGGCCTGGGTCGCATACTGCACAG	8616	AQTRPGSHTAQ	13205	TRPGSHT	0.180609	-0.05314
SyS1965	4028	GCCCAAGCTCAGTTGGCTCCTCGTGCGGCACAG	8617	AQAQLAPRAAQ	13206	AQLAPRA	0.180606	-0.19846
GP165	4029	GCCCAATCTACTATGCGGACGTCGCTGGCACAG	8618	AQSTMRTSLAQ	13207	STMRTSL	0.1806	0.12275
SP41	4030	GCCCAAATGAATCAGACTTCTGCTAAGGCACAG	8619	AQMNQTSAKAQ	13208	MNQTSAK	0.180557	-0.05178
SyS1966	4031	GCCCAAAGCAGAAGCAGCCCCCACCATCGCACAG	8620	AQSRSSPTIAQ	13209	SRSSPTI	0.180499	-0.01734
GS1142	4032	GCCCAAAGCGCCCTCAACCAATACCCCGCACAG	8621	AQSALNQYPAQ	13210	SALNQYP	0.180451	-0.08545
GS1143	4033	GCCCAAATCAGCACCACCACCAGAAACGCACAG	8622	AQISTTTRNAQ	13211	ISTTTRN	0.180379	-0.13952
GS1144	4034	GCCCAATCTCGTGATACGCCGAGTGGTGCACAG	8623	AQSRDTPSGAQ	13212	SRDTPSG	0.18029	-0.0879
SyS1967	4035	GCCCAAAACTTCAACAAACAAGGCCTCGCACAG	8624	AQNFNKQGLAQ	13213	NFNKQGL	0.180248	-0.06663
SyS1968	4036	GCCCAACCTAGTAATACGTCTTCGGTTGCACAG	8625	AQPSNTSSVAQ	13214	PSNTSSV	0.180178	-0.2231
SS127	4037	GCCCAAACTGTTAGTACGAATGCGAGGGCACAG	8626	AQTVSTNARAQ	13215	TVSTNAR	0.180153	-0.35824
GS1145	4038	GCCCAAAACATGAGCCAAACCGTCGCCGCACAG	8627	AQNMSQTVAAQ	13216	NMSQTVA	0.180083	-0.15766
GS1146	4039	GCCCAAATTGGGAAGAGTTCTACTCCTGCACAG	8628	AQIGKSSTPAQ	13217	IGKSSTP	0.179902	-0.11877
GS1147	4040	GCCCAAAGAGAAACCGAAACCGGCAGAGCACAG	8629	AQRETETGRAQ	13218	RETETGR	0.179896	-0.13189
SyS1969	4041	GCCCAACCTTATACTCCGCTGACTGGTGCACAG	8630	AQPYTPLTGAQ	13219	PYTPLTG	0.179831	-0.19496

FIG. 33 (Continued)

SyS1970	4042	GCCCAAGCCGAATACAACACCGGCGTCGCACAG	8631	AQAEYNTGVAQ	13220	AEYNTGV	0.179673	-0.16466
SyS1971	4043	GCCCAAGGCAGAAACGCCGAAACCAGAGCACAG	8632	AQGRNAETRAQ	13221	GRNAETR	0.17963	-0.04562
GS1149	4044	GCCCAAACGTTTAATCATACTACTGATGCACAG	8633	AQTFNHTTDAQ	13222	TFNHTTD	0.179619	-0.17768
GS1150	4045	GCCCAAACCCACCTCAGCACCCTCGGCGCACAG	8634	AQTHLSTLGAQ	13223	THLSTLG	0.179495	-0.06913
GS1151	4046	GCCCAACTTAAGGGTATTAGTCAGCATGCACAG	8635	AQLKGISQHAQ	13224	LKGISQH	0.17936	-0.12235
SyS1974	4047	GCCCAATATTCTAGTGGTATGACTACGGCACAG	8636	AQYSSGMTTAQ	13225	YSSGMTT	0.17933	-0.09037
SyS1975	4048	GCCCAAACGGCTATTACGATGACTAGTGCACAG	8637	AQTAITMTSAQ	13226	TAITMTS	0.179201	-0.00948
SyS1976	4049	GCCCAAAGAGGCAACGAACTCAACACCGCACAG	8638	AQRGNELNTAQ	13227	RGNELNT	0.179161	-0.06646
SyS1977	4050	GCCCAAGTCGTCAGCAGCCAAATGGCCGCACAG	8639	AQVVSSQMAAQ	13228	VVSSQMA	0.179109	-0.03159
SyS1978	4051	GCCCAACACCAACACGAAAAACATGGTCGCACAG	8640	AQHQHENMVAQ	13229	HQHENMV	0.179092	-0.15927
SyS1980	4052	GCCCAAAGCTTCGGCGGCGTCCCCAAAGCACAG	8641	AQSFGGVPKAQ	13230	SFGGVPK	0.179027	-0.08158
GS1153	4053	GCCCAATTGATGCGTGATAGTAAGTCTGCACAG	8642	AQLMRDSKSAQ	13231	LMRDSKS	0.17901	-0.11654
GS1154	4054	GCCCAAATGAGAACCAACCTCAGCATGGCACAG	8643	AQMRTNLSMAQ	13232	MRTNLSM	0.179008	-0.17381
SyS1981	4055	GCCCAACCGAATAATCCTGTGGTGCCTGCACAG	8644	AQPNNPVVPAQ	13233	PNNPVVP	0.179008	-0.18042
GP167	4056	GCCCAAAGGGTTAGTCAGTCTATGGGTGCACAG	8645	AQRVSQSMGAQ	13234	RVSQSMG	0.17897	-0.07391
SyS1982	4057	GCCCAAGCTGAGGGTCCTCAGAAGACGGCACAG	8646	AQAEGPQKTAQ	13235	AEGPQKT	0.178923	-0.05601
SyS1983	4058	GCCCAACTTAATTCTGTGGTTCATACGGCACAG	8647	AQLNSVVHTAQ	13236	LNSVVHT	0.17892	-0.01781
GS1155	4059	GCCCAACTGTTGACGTTGAATTCGGCTGCACAG	8648	AQLLTLNSAAQ	13237	LLTLNSA	0.178886	-0.16814
SyS1985	4060	GCCCAAACGCTTGCTCCTCGGAGGGATGCACAG	8649	AQTLAPRRDAQ	13238	TLAPRRD	0.178476	-0.16951
GS1159	4061	GCCCAAAGAGTCGCCAACCCCGCCACCGCACAG	8650	AQRVANPATAQ	13239	RVANPAT	0.178389	-0.12177
SyS1986	4062	GCCCAATTGCCGGATCCTAGGTTGCAGGCACAG	8651	AQLPDPRLQAQ	13240	LPDPRLQ	0.178351	-0.1063
SyS1987	4063	GCCCAAAAAATGGACGTCGGCGAAGCCGCACAG	8652	AQKMDVGEAAQ	13241	KMDVGEA	0.178194	-0.22434
SyS1988	4064	GCCCAAGGTCCGTCTCCTATGGTTATGGCACAG	8653	AQGPSPMVMAQ	13242	GPSPMVM	0.178194	-0.22434
GS1160	4065	GCCCAAGGCACCAACAAAGCCACCGCCGCACAG	8654	AQGTNKATAAQ	13243	GTNKATA	0.178061	-0.05206
GS1161	4066	GCCCAACTCAGCGCCCACGGCACCACCGCACAG	8655	AQLSAHGTTAQ	13244	LSAHGTT	0.178024	-0.18009
GS1162	4067	GCCCAAACCAGCAGATACAACAGCGCCGCACAG	8656	AQTSRYNSAAQ	13245	TSRYNSA	0.177853	-0.16663
SyS1989	4068	GCCCAAGGCCCCAACAGCAGCTTCAAAGCACAG	8657	AQGPNSSFKAQ	13246	GPNSSFK	0.177775	-0.16273
GS1163	4069	GCCCAAAGTGTTGGGAGGGCTCCGATTGCACAG	8658	AQSVGRAPIAQ	13247	SVGRAPI	0.177653	-0.14715
SyS1990	4070	GCCCAATTTCAGGGTGAGAAGACGTGGGCACAG	8659	AQFQGEKTWAQ	13248	FQGEKTW	0.177633	-0.06462
SyS1991	4071	GCCCAAACCAGCAGCGCCAGAACCATCGCACAG	8660	AQTSSARTIAQ	13249	TSSARTI	0.177546	-0.07616
SyS1992	4072	GCCCAAGCTGAGCGTACTGGGACTGCGGCACAG	8661	AQAERTGTAAQ	13250	AERTGTA	0.177482	-0.16643
GS1164	4073	GCCCAACTCAACCTCGGCACCCCCAAAGCACAG	8662	AQLNLGTPKAQ	13251	LNLGTPK	0.177441	-0.17672

FIG. 33 (Continued)

GP168	4074	GCCCAAGCTGCGCCGGTTGGGTCTAGGGCACAG	8663	AQAAPVGSRAQ	13252	AAPVGSR	0.177438	0.019689
GS1165	4075	GCCCAAATGAGACAAGCCAACCACCCCGCACAG	8664	AQMRQANHPAQ	13253	MRQANHP	0.177418	-0.10804
SyS1993	4076	GCCCAAGAGCAGCAGCGTGATGTGCTGGCACAG	8665	AQEQQRDVLAQ	13254	EQQRDVL	0.177373	-0.18368
SyS1994	4077	GCCCAACCCAAAAGCGACGAACTCACCGCACAG	8666	AQPKSDELTAQ	13255	PKSDELT	0.177331	-0.23173
SyS1995	4078	GCCCAAAATGCTCGTGTTCAGGAGACTGCACAG	8667	AQNARVQETAQ	13256	NARVQET	0.177294	0.036888
SyS1996	4079	GCCCAAACTACGGTTGCTACTCAGTCGGCACAG	8668	AQTTVATQSAQ	13257	TTVATQS	0.177266	-0.08132
SyS1997	4080	GCCCAAACCGAAGTCAGCCACAGACCCGCACAG	8669	AQTEVSHRPAQ	13258	TEVSHRP	0.177079	-0.13314
SyS1998	4081	GCCCAAAGCAGCACCGTCAAAAACGTCGCACAG	8670	AQSSTVKNVAQ	13259	SSTVKNV	0.177072	0.041757
SyS1999	4082	GCCCAAATCGACAGCCACCTCAACAGAGCACAG	8671	AQIDSHLNRAQ	13260	IDSHLNR	0.176954	-0.05133
SyS2000	4083	GCCCAAGGTTCGACTCAGCTGAGTCTGGCACAG	8672	AQGSTQLSLAQ	13261	GSTQLSL	0.17695	-0.03737
GS1170	4084	GCCCAAGACGGCAGCCCCGCCACCAAAGCACAG	8673	AQDGSPATKAQ	13262	DGSPATK	0.17691	-0.18637
SyS2001	4085	GCCCAACAAACCGGCAACAGCCAAGCCGCACAG	8674	AQQTGNSQAAQ	13263	QTGNSQA	0.176685	-0.02351
SyS2002	4086	GCCCAAAGACAAGACGTCAACGTCAGCGCACAG	8675	AQRQDVNVSAQ	13264	RQDVNVS	0.176645	-0.22187
GS1172	4087	GCCCAACTCGACTACGGCGTCAAAAGCGCACAG	8676	AQLDYGVKSAQ	13265	LDYGVKS	0.176625	-0.01607
SyS2003	4088	GCCCAAGGTTCTCGTCCTGAGGCGCCGGCACAG	8677	AQGSRPEAPAQ	13266	GSRPEAP	0.176327	-0.1489
SyS2004	4089	GCCCAATGGAGCAACATGACCGCCGCCGCACAG	8678	AQWSNMTAAAQ	13267	WSNMTAA	0.176285	0.188706
GP171	4090	GCCCAAACTAATACTACTCGGATTTCTGCACAG	8679	AQTNTTRISAQ	13268	TNTTRIS	0.176104	0.234131
SyS2007	4091	GCCCAACCTTATGCGGAGAGGCAGGCTGCACAG	8680	AQPYAERQAAQ	13269	PYAERQA	0.175875	-0.12869
SyS2008	4092	GCCCAAACCAGCAGCGCCACCGTCCTCGCACAG	8681	AQTSSATVLAQ	13270	TSSATVL	0.175872	-0.08332
SyS2009	4093	GCCCAAGCGCAGACTGATTTTAGGCAGGCACAG	8682	AQAQTDFRQAQ	13271	AQTDFRQ	0.175789	-0.17557
GS1173	4094	GCCCAAAACAGCGGCAACGAACACAGCGCACAG	8683	AQNSGNEHSAQ	13272	NSGNEHS	0.175772	-0.17919
SyS2010	4095	GCCCAAAAGCCGCTGATTAATGCTACTGCACAG	8684	AQKPLINATAQ	13273	KPLINAT	0.175674	-0.17193
SyS2011	4096	GCCCAAATGGGGAGTTCGTCGGCGTTTGCACAG	8685	AQMGSSSAFAQ	13274	MGSSSAF	0.175674	-0.17193
GS1174	4097	GCCCAAATTGGTAATAAGACGAGTCTGGCACAG	8686	AQIGNKTSLAQ	13275	IGNKTSL	0.175642	-0.13523
SyS2012	4098	GCCCAAGCCGCCAACACCGCCCCCCAAAGCACAG	8687	AQAANTAPKAQ	13276	AANTAPK	0.17558	-0.10142
GS1175	4099	GCCCAACTCGTCGACCAAAGAGCCACCGCACAG	8688	AQLVDQRATAQ	13277	LVDQRAT	0.175514	-0.1774
SyS2015	4100	GCCCAACAAGTCAAACTCGGCAGCACCGCACAG	8689	AQQVKLGSTAQ	13278	QVKLGST	0.175457	-0.21315
GS1176	4101	GCCCAACTCACCAGCAACACCCACGTCGCACAG	8690	AQLTSNTHVAQ	13279	LTSNTHV	0.175385	-0.05777
GS1177	4102	GCCCAAGTCTACAGCGCCATCAACAAAGCACAG	8691	AQVYSAINKAQ	13280	VYSAINK	0.175251	-0.17386
SyS2017	4103	GCCCAAAGAGCCAACGGCAGCGACCTCGCACAG	8692	AQRANGSDLAQ	13281	RANGSDL	0.17502	0.012701
SyS2018	4104	GCCCAAAACCTCAAAAGCCAAACCGAAGCACAG	8693	AQNLKSQTEAQ	13282	NLKSQTE	0.174966	-0.12454
SyS2019	4105	GCCCAAAGCTACGGCAACGAAATCAGAGCACAG	8694	AQSYGNEIRAQ	13283	SYGNEIR	0.174809	0.068074

FIG. 33 (Continued)

SyS2020	4106	GCCCAACTCACCAGAGGCGCCATCGGCGCACAG	8695	AQLTRGAIGAQ	13284	LTRGAIG	0.174654	-0.13192
GS1178	4107	GCCCAACCCATCAGAACCGTCGACACCGCACAG	8696	AQPIRTVDTAQ	13285	PIRTVDT	0.174634	-0.12446
SyS2021	4108	GCCCAACGGAGTATGCCTGATGGTTCGGCACAG	8697	AQRSMPDGSAQ	13286	RSMPDGS	0.174629	-0.18769
GS1179	4109	GCCCAAACCGCCCACACCGGCCCCCTCGCACAG	8698	AQTAHTGPLAQ	13287	TAHTGPL	0.174581	-0.15288
SP42	4110	GCCCAATCGCAGGGGAGTCCGCTTTCGGCACAG	8699	AQSQGSPLSAQ	13288	SQGSPLS	0.174469	-0.0526
SyS2022	4111	GCCCAACTCCAAGCCATCGCCCACAGCGCACAG	8700	AQLQAIAHSAQ	13289	LQAIAHS	0.174346	-0.17678
SyS2024	4112	GCCCAAGGCAACAGCCTCAGCACCAGCGCACAG	8701	AQGNSLSTSAQ	13290	GNSLSTS	0.174173	-0.2268
GS1180	4113	GCCCAACTCACCCACAGAGAAGCCGAAGCACAG	8702	AQLTHREAEAQ	13291	LTHREAE	0.174167	-0.06761
GS1181	4114	GCCCAAACGTTGCATCTGGCGAAGGAGGCACAG	8703	AQTLHLAKEAQ	13292	TLHLAKE	0.174141	-0.16663
GS1182	4115	GCCCAAAACATCAGCAGCAGCGGCAAAGCACAG	8704	AQNISSSGKAQ	13293	NISSSGK	0.174056	-0.08647
SyS2026	4116	GCCCAAGGCAGACACATGGTCATGGAAGCACAG	8705	AQGRHMVMEAQ	13294	GRHMVME	0.173999	-0.09555
GS1183	4117	GCCCAAGGTGAGAGGTTTGGGGGGCCTGCACAG	8706	AQGERFGGPAQ	13295	GERFGGP	0.173807	-0.18009
SyS2027	4118	GCCCAATATAGTGGGTCTTCTACTAAGGCACAG	8707	AQYSGSSTKAQ	13296	YSGSSTK	0.173744	-0.09789
SyS2028	4119	GCCCAAAAGGAGTCTCTGTTAGTGCGAATGCACAG	8708	AQKESVSANAQ	13297	KESVSAN	0.173712	-0.006
SyS2030	4120	GCCCAAATTACGAGTGATGGGAAGCCGGCACAG	8709	AQITSDGKPAQ	13298	ITSDGKP	0.173449	0.031329
SyS2031	4121	GCCCAAGGTCATGATGCGCGTGTGGTTGCACAG	8710	AQGHDARVVAQ	13299	GHDARVV	0.173427	0.011182
SyS2032	4122	GCCCAAACCAGCAGCAACGGCGTCAGAGCACAG	8711	AQTSSNGVRAQ	13300	TSSNGVR	0.173427	0.042989
GS1184	4123	GCCCAAAATCATCAGAATCGGTCTTTGGCACAG	8712	AQNHQNRSLAQ	13301	NHQNRSL	0.173427	-0.18245
GS1185	4124	GCCCAACGGGTTCCGGAGCAGAATGTGGCACAG	8713	AQRVPEQNVAQ	13302	RVPEQNV	0.173385	-0.18054
GS1186	4125	GCCCAAAGCGCCCAACTCAGAAGCAGCGCACAG	8714	AQSAQLRSSAQ	13303	SAQLRSS	0.173344	-0.17863
GS1187	4126	GCCCAACACGCCAAAAGCGAAACCTACGCACAG	8715	AQHAKSETYAQ	13304	HAKSETY	0.173305	-0.17672
SyS2033	4127	GCCCAACTCCTCACCCAAGTCGAAACCGCACAG	8716	AQLLTQVETAQ	13305	LLTQVET	0.173298	-0.12503
SyS2034	4128	GCCCAAACCAAAACCGCCGACACCTACGCACAG	8717	AQTKTADTYAQ	13306	TKTADTY	0.173226	0.171999
SyS2035	4129	GCCCAAGTTATGCCTGCTACGTTGAGTGCACAG	8718	AQVMPATLSAQ	13307	VMPATLS	0.173152	-0.19254
GS1188	4130	GCCCAATACCAAGCCAACAACCTCATCGCACAG	8719	AQYQANNLIAQ	13308	YQANNLI	0.17301	-0.15955
SyS2036	4131	GCCCAAGTCAGAGTCCCCGACAGCAGCGCACAG	8720	AQVRVPDSSAQ	13309	VRVPDSS	0.172979	-0.09411
SyS2037	4132	GCCCAACACCAAACCGGCAGCGGCTTCGCACAG	8721	AQHQTGSGFAQ	13310	HQTGSGF	0.172861	-0.04462
SyS2038	4133	GCCCAAAGTGCTACGTTGAGTGGGTATGCACAG	8722	AQSATLSGYAQ	13311	SATLSGY	0.172673	-0.16344
GS1189	4134	GCCCAAAATGGTTCTGCGACGTATTCTGCACAG	8723	AQNGSATYSAQ	13312	NGSATYS	0.172618	0.021489
GS1190	4135	GCCCAAAGCACCAGACCCACCCTCACCGCACAG	8724	AQSTRPTLTAQ	13313	STRPTLT	0.172526	-0.15048
SyS2039	4136	GCCCAAAGACCCGCCGACGTCAGCCAAGCACAG	8725	AQRPADVSQAQ	13314	RPADVSQ	0.172441	-0.14526
GS1191	4137	GCCCAAAGCCACCTCAGCAGCACCGGCGCACAG	8726	AQSHLSSTGAQ	13315	SHLSSTG	0.172433	-0.18637

FIG. 33 (Continued)

GS1192	4138	GCCCAAGCTAATCAGTCTTATGATCGGGCACAG	8727	AQANQSYDRAQ	13316	ANQSYDR	0.172433	-0.18637
SyS2040	4139	GCCCAAAGCAGCGGCGACAGAACCGCCGCACAG	8728	AQSSGDRTAAQ	13317	SSGDRTA	0.172372	-0.21448
SyS2041	4140	GCCCAAGGCAGCGTCCCCGGCCTCAACGCACAG	8729	AQGSVPGLNAQ	13318	GSVPGLN	0.172134	-0.22803
SyS2043	4141	GCCCAACTCGTCACCATCCACAGCGCCGCACAG	8730	AQLVTIHSAAQ	13319	LVTIHSA	0.171906	-0.22285
SyS2044	4142	GCCCAACCTCAGCATGAGACTACGCTGGCACAG	8731	AQPQHETTLAQ	13320	PQHETTL	0.171807	-0.21557
SyS2046	4143	GCCCAACCGACGAAGTCGGCGCAGTATGCACAG	8732	AQPTKSAQYAQ	13321	PTKSAQY	0.171667	-0.11931
GS1194	4144	GCCCAAAAAAAAAGACCCCGTCCTCGGCGCACAG	8733	AQKKDPVLGAQ	13322	KKDPVLG	0.171636	-0.17919
SyS2047	4145	GCCCAATTTAGGGTTGGTCCGTCTGCTGCACAG	8734	AQFRVGPSAAQ	13323	FRVGPSA	0.171598	-0.19739
SyS2048	4146	GCCCAAACCAGCAGCGGCCACGCCGTCGCACAG	8735	AQTSSGHAVAQ	13324	TSSGHAV	0.17151	-0.12824
SyS2049	4147	GCCCAACGTGTTGGTGAGGCTAGGATGGCACAG	8736	AQRVGEARMAQ	13325	RVGEARM	0.171462	-0.18284
SyS2050	4148	GCCCAACGTGTTACGTCGCCTTCTAAGGCACAG	8737	AQRVTSPSKAQ	13326	RVTSPSK	0.171402	-0.17557
SyS2051	4149	GCCCAAGATAGGATGCCTTCTACGATTGCACAG	8738	AQDRMPSTIAQ	13327	DRMPSTI	0.171373	-0.17193
SyS2052	4150	GCCCAACAAGGCGACACCAGCAAACACGCACAG	8739	AQQGDTSKHAQ	13328	QGDTSKH	0.171295	-0.16102
GS1195	4151	GCCCAAAGCACCAGCAGCAACAGAGCCGCACAG	8740	AQSTSSNRAAQ	13329	STSSNRA	0.171266	-0.12044
GS1196	4152	GCCCAAAAGGTGCCTACGGGTTATACGGCACAG	8741	AQKVPTGYTAQ	13330	KVPTGYT	0.171266	-0.14334
SyS2053	4153	GCCCAATTCAAAGGCCAAAGAAACGACGCACAG	8742	AQFKGQRNDAQ	13331	FKGQRND	0.171225	-0.15011
SyS2055	4154	GCCCAAGGTAATCATTTGGGGAATGAGGCACAG	8743	AQGNHLGNEAQ	13332	GNHLGNE	0.170544	-0.18245
SyS2056	4155	GCCCAAGCCAGCAAAAGCTTCGAACTCGCACAG	8744	AQASKSFELAQ	13333	ASKSFEL	0.170464	-0.08466
SyS2057	4156	GCCCAAACCGTCAGAGACACCACCAGAGCACAG	8745	AQTVRDTTRAQ	13334	TVRDTTR	0.170442	0.262057
GS1199	4157	GCCCAAAAGGTTAGTCCGAATACTCTTGCACAG	8746	AQKVSPNTLAQ	13335	KVSPNTL	0.170349	-0.16484
GS1201	4158	GCCCAAGGCAGAACCCCCGAAAGCTACGCACAG	8747	AQGRTPESYAQ	13336	GRTPESY	0.16998	-0.18368
SyS2058	4159	GCCCAACAGGTGTCGGGGGTTAGGACGGCACAG	8748	AQQVSGVRTAQ	13337	QVSGVRT	0.169959	-0.11859
SyS2059	4160	GCCCAATACACCGGCATCAGCACCAGCGCACAG	8749	AQYTGISTSAQ	13338	YTGISTS	0.169959	-0.13314
SyS2060	4161	GCCCAACAAACCGCCGAACCCCACACAAAGCACAG	8750	AQQTAEPHKAQ	13339	QTAEPHK	0.169959	-0.16223
SyS2061	4162	GCCCAACTTGGTCCTGTGGGTTCTCCGGCACAG	8751	AQLGPVGSPAQ	13340	LGPVGSP	0.169959	-0.16587
SyS2062	4163	GCCCAAGCCAGAGACGACAGCACCGACGCACAG	8752	AQARDDSTDAQ	13341	ARDDSTD	0.169959	-0.22042
SyS2063	4164	GCCCAAAATTTTAAGCATAGTGAGGTGGCACAG	8753	AQNFKHSEVAQ	13342	NFKHSEV	0.169959	-0.22042
GS1202	4165	GCCCAAATTACTACTCCTCTGCAGGCGGCACAG	8754	AQITTPLQAAQ	13343	ITTPLQA	0.169823	-0.18188
SyS2066	4166	GCCCAACCCATGAGCAGCAGAGAAAGAGCACAG	8755	AQPMSSRERAQ	13344	PMSSRER	0.169722	-0.10113
GS1204	4167	GCCCAAGTCGAAAACGGCAAAGGCCTCGCACAG	8756	AQVENGKGLAQ	13345	VENGKGL	0.169651	-0.13239
SyS2067	4168	GCCCAAACCAGCAACAGCGGCCTCGCCGCACAG	8757	AQTSNSGLAAQ	13346	TSNSGLA	0.169432	-0.02428
SyS2068	4169	GCCCAAGGCAACAGCCTCGCCAACCCCGCACAG	8758	AQGNSLANPAQ	13347	GNSLANP	0.169287	-0.15041

FIG. 33 (Continued)

SS131	4170	GCCCAAGCCAGCAACGAAGCCCACGCCGCACAG	8759	AQASNEAHAAQ	13348	ASNEAHA	0.169245	-0.37022
GS1207	4171	GCCCAAGGCCTCGCCGGCAGCACCCCCCGCACAG	8760	AQGLAGSTPAQ	13349	GLAGSTP	0.169127	-0.18245
SyS2069	4172	GCCCAAGTCCCCGCCCCCGGCAGATACGCACAG	8761	AQVPAPGRYAQ	13350	VPAPGRY	0.169081	-0.19353
GS1208	4173	GCCCAAGCCAGCGACAGACTCATCGCCGCACAG	8762	AQASDRLIAAQ	13351	ASDRLIA	0.168842	-0.14151
GS1209	4174	GCCCAAATCAGCACCTGGCAAACCCAAGCACAG	8763	AQISTWQTQAQ	13352	ISTWQTQ	0.168829	-0.1447
SyS2070	4175	GCCCAAATCACCAGCGGCGCCACCGTCGCACAG	8764	AQITSGATVAQ	13353	ITSGATV	0.168795	-0.1344
GS1210	4176	GCCCAACTTGCGAAGGCGAGTAATGTTGCACAG	8765	AQLAKASNVAQ	13354	LAKASNV	0.168765	-0.10613
SyS2071	4177	GCCCAACCGCAGGGGACGTTTGGGAGTGCACAG	8766	AQPQGTFGSAQ	13355	PQGTFGS	0.168707	-0.1489
SyS2072	4178	GCCCAAATTGTTCGGCCGCCGAATAGTGCACAG	8767	AQIVRPPNSAQ	13356	IVRPPNS	0.168685	-0.15253
SyS2073	4179	GCCCAAACCAGCCACCTCACCAGCGCCGCACAG	8768	AQTSHLTSAAQ	13357	TSHLTSA	0.16862	-0.07746
SyS2075	4180	GCCCAACTCCACCCCGAAACCATGAGAGCACAG	8769	AQLHPETMRAQ	13358	LHPETMR	0.168589	-0.16708
SyS2076	4181	GCCCAAGTCCTCCACGACACCAGATACGCACAG	8770	AQVLHDTRYAQ	13359	VLHDTRY	0.168547	-0.14967
SS132	4182	GCCCAAGTCAGCAACCCCCCCCAGAGGCGCACAG	8771	AQVSNPPRGAQ	13360	VSNPPRG	0.168542	-0.36117
GS1211	4183	GCCCAAGAGCCTCTGATGACTAGGCCTGCACAG	8772	AQEPLMTRPAQ	13361	EPLMTRP	0.168414	-0.16214
GS1212	4184	GCCCAAGACAGAGTCAGCAGCAGCCACGCACAG	8773	AQDRVSSSHAQ	13362	DRVSSSH	0.168392	0.004781
GP175	4185	GCCCAAACTAAGACTGGTCATTCGAGTGCACAG	8774	AQTKTGHSSAQ	13363	TKTGHSS	0.168367	-0.07287
GS1213	4186	GCCCAATCGTCGTATTCTCCTGTTACTGCACAG	8775	AQSSYSPVTAQ	13364	SSYSPVT	0.168316	-0.08904
GS1214	4187	GCCCAAAAACCCAACCTCCAAAACAACGCACAG	8776	AQKPNLQNNAQ	13365	KPNLQNN	0.168309	-0.10113
SyS2077	4188	GCCCAACTCAAAAGCCCCCCCCGGCATCGCACAG	8777	AQLKSPPGIAQ	13366	LKSPPGI	0.168269	-0.20345
SyS2078	4189	GCCCAAGGGATGCAGCTGGGGATGCCGGCACAG	8778	AQGMQLGMPAQ	13367	GMQLGMP	0.168244	-0.00148
SyS2079	4190	GCCCAACATCAGGCGAATCTTACGTTGGCACAG	8779	AQHQANLTLAQ	13368	HQANLTL	0.168142	-0.21436
GS1215	4191	GCCCAAACTGGTCATCCTACGACTGCGGCACAG	8780	AQTGHPTTAAQ	13369	TGHPTTA	0.168138	-0.09841
GS1216	4192	GCCCAATTCATCGGCAGCCACCTCGGCGCACAG	8781	AQFIGSHLGAQ	13370	FIGSHLG	0.168096	-0.14906
SyS2081	4193	GCCCAAAGGAATGAGAGTAATGGGCCGGCACAG	8782	AQRNESNGPAQ	13371	RNESNGP	0.167998	-0.2305
SyS2082	4194	GCCCAAAAGATTGAGACGAATGGTAATGCACAG	8783	AQKIETNGNAQ	13372	KIETNGN	0.167998	-0.21078
SyS2083	4195	GCCCAATATCTTCAGAATGGTGTTGTTGCACAG	8784	AQYLQNGVVAQ	13373	YLQNGVV	0.167795	-0.04255
SyS2084	4196	GCCCAAAGACCCGGCATGCTCGGCACCGCACAG	8785	AQRPGMLGTAQ	13374	RPGMLGT	0.167685	-0.12829
SyS2085	4197	GCCCAATTGACGCAGATTGGGACTGCTGCACAG	8786	AQLTQIGTAAQ	13375	LTQIGTA	0.167589	-0.03508
GS1218	4198	GCCCAAAACGAAGACGTCCAAAGAGCCGCACAG	8787	AQNEDVQRAAQ	13376	NEDVQRA	0.1675	-0.13213
SyS2086	4199	GCCCAACATTTGGCTGATCAGAGTCGTGCACAG	8788	AQHLADQSRAQ	13377	HLADQSR	0.167422	-0.00573
SyS2087	4200	GCCCAATTGGGTAATGATACGGTGAGGGCACAG	8789	AQLGNDTVRAQ	13378	LGNDTVR	0.167404	-0.15374
SyS2091	4201	GCCCAAAACAACCACCACGTCCCCCCCGCACAG	8790	AQNNHHVPPAQ	13379	NNHHVPP	0.167167	0.019492

FIG. 33 (Continued)

GS1220	4202	GCCCAAGACAAAGCCGGCACCCTCAGCGCACAG	8791	AQDKAGTLSAQ	13380	DKAGTLS	0.167139	-0.12171
SyS2093	4203	GCCCAACGTACTAAGAATGAGTCGATGGCACAG	8792	AQRTKNESMAQ	13381	RTKNESM	0.167044	-0.1792
SyS2094	4204	GCCCAATTTAATGTTGTGCGTGGTGATGCACAG	8793	AQFNVVRGDAQ	13382	FNVVRGD	0.167044	-0.1792
SyS2095	4205	GCCCAAATCGTCAGAGGCATGAACCAAGCACAG	8794	AQIVRGMNQAQ	13383	IVRGMNQ	0.166951	-0.18861
SyS2096	4206	GCCCAACAACACACCCCCACCCTCAACGCACAG	8795	AQQHTPTLNAQ	13384	QHTPTLN	0.166887	-0.19846
GS1222	4207	GCCCAAAGCCTCGGCAAAGAACCCCTCGCACAG	8796	AQSLGKEPLAQ	13385	SLGKEPL	0.166818	-0.16484
SyS2097	4208	GCCCAAAGCAGCGGCCACGGCCTCAACGCACAG	8797	AQSSGHGLNAQ	13386	SSGHGLN	0.166803	0.1418
GS1223	4209	GCCCAACGGATTAATAGTGATTCTACTGCACAG	8798	AQRINSDSTAQ	13387	RINSDST	0.16679	-0.12903
SyS2098	4210	GCCCAAAATCCGCATAATCATCCTGTTGCACAG	8799	AQNPHNHPVAQ	13388	NPHNHPV	0.166789	-0.19375
SyS2100	4211	GCCCAATCGCATAAGCCGTCGACGGTTGCACAG	8800	AQSHKPSTVAQ	13389	SHKPSTV	0.166718	-0.19739
SyS2101	4212	GCCCAAAGCAGCATGAGCACCACCTACGCACAG	8801	AQSSMSTTYAQ	13390	SSMSTTY	0.166718	-0.19739
SyS2102	4213	GCCCAAGGTGCTGCTGCTTCTAATCCTGCACAG	8802	AQGAAASNPAQ	13391	GAAASNP	0.166693	-0.11859
GS1224	4214	GCCCAAATGAACCAAAGAGAACAAAAAGCACAG	8803	AQMNQREQKAQ	13392	MNQREQK	0.166658	-0.16125
SyS2103	4215	GCCCAATCGTATCCTAGTAATCCGCGGGCACAG	8804	AQSYPSNPRAQ	13393	SYPSNPR	0.166484	-0.2083
SyS2104	4216	GCCCAACTGCGTGATTTTGTGACTGATGCACAG	8805	AQLRDFVTDAQ	13394	LRDFVTD	0.166484	-0.2083
GS1225	4217	GCCCAAAACAACACCGTCATGAGAAGCGCACAG	8806	AQNNTVMRSAQ	13395	NNTVMRS	0.166403	0.078355
SyS2105	4218	GCCCAACTCAGCCCCAGAAAATACATCGCACAG	8807	AQLSPRKYIAQ	13396	LSPRKYI	0.166309	-0.21557
SyS2106	4219	GCCCAACACATCAGACCCCCCCAGCCCCGCACAG	8808	AQHIRPPSPAQ	13397	HIRPPSP	0.166309	-0.21557
SyS2107	4220	GCCCAACCTTATGTGTCGACTACTGCGGCACAG	8809	AQPYVSTTAAQ	13398	PYVSTTA	0.166295	-0.20216
SyS2108	4221	GCCCAAGTCAACCACGGCAGCCCCACCGCACAG	8810	AQVNHGSPTAQ	13399	VNHGSPT	0.166263	-0.07616
SyS2109	4222	GCCCAAAGTGGTTATCTTAATGGTGCGGCACAG	8811	AQSGYLNGAAQ	13400	SGYLNGA	0.166181	-0.21202
SyS2110	4223	GCCCAAAGTCGGGAGAGGACGTCTGATGCACAG	8812	AQSRERTSDAQ	13401	SRERTSD	0.166115	-0.01918
GS1227	4224	GCCCAAACCCACAGCGTCACCAGAAGCGCACAG	8813	AQTHSVTRSAQ	13402	THSVTRS	0.166033	-0.10592
GS1228	4225	GCCCAACTTGTTGCGAATAAGAATGCGGCACAG	8814	AQLVANKNAAQ	13403	LVANKNA	0.16597	-0.12426
GS1229	4226	GCCCAAAATTTTACGGATCGTGCTACTGCACAG	8815	AQNFTDRATAQ	13404	NFTDRAT	0.165948	-0.16337
SyS2111	4227	GCCCAATATAGGACGAGTACTTTGGCGGCACAG	8816	AQYRTSTLAAQ	13405	YRTSTLA	0.165933	-0.09069
GS1230	4228	GCCCAACACGTCATGAACAAACAAGCCGCACAG	8817	AQHVMNKQAAQ	13406	HVMNKQA	0.165928	-0.14151
SyS2112	4229	GCCCAAGCCACCAACAACCCCGCCAGCGCACAG	8818	AQATNNPASAQ	13407	ATNNPAS	0.1659	-0.23012
SyS2113	4230	GCCCAAACCATCATGAAAGCCCAAACCGCACAG	8819	AQTIMKAQTAQ	13408	TIMKAQT	0.1659	0.100294
SyS2114	4231	GCCCAAGGCATGAGCACCATGACCCCCGCACAG	8820	AQGMSTMTPAQ	13409	GMSTMTP	0.165745	-0.07802
GS1231	4232	GCCCAAGGCACCCCCATCTACAAACAAGCACAG	8821	AQGTPIYKQAQ	13410	GTPIYKQ	0.165686	-0.18188
SyS2115	4233	GCCCAAAATGGTACGTTGGAGAAGGCGGCACAG	8822	AQNGTLEKAAQ	13411	NGTLEKA	0.165659	-0.05555

FIG. 33 (Continued)

SyS2116	4234	GCCCAAAGCAACGAAAGAACCATCCCCGCACAG	8823	AQSNERTIPAQ	13412	SNERTIP	0.165594	-0.1198
SyS2117	4235	GCCCAAATTCCGGTGTCTATTCAGGCTGCACAG	8824	AQIPVSIQAAQ	13413	IPVSIQA	0.165516	-0.17998
SyS2118	4236	GCCCAAAACCTCCAAAGAGAAGGCCCCGCACAG	8825	AQNLQREGPAQ	13414	NLQREGP	0.165401	-0.00546
GS1234	4237	GCCCAAGGGGAGGGTGGTAAGTCTAATGCACAG	8826	AQGEGGKSNAQ	13415	GEGGKSN	0.165262	-0.17672
SyS2119	4238	GCCCAATTGCAGGGTAATGGGAGGAATGCACAG	8827	AQLQGNGRNAQ	13416	LQGNGRN	0.165238	-0.13798
GS1236	4239	GCCCAACTCGTCAGCAGCACCAGCGAAGCACAG	8828	AQLVSSTSEAQ	13417	LVSSTSE	0.165149	-0.17863
SyS2120	4240	GCCCAAAGCCTCGCCGGCAACACCACCGCACAG	8829	AQSLAGNTTAQ	13418	SLAGNTT	0.165128	-0.11547
SyS2122	4241	GCCCAATTGACTGTTGGTAATAATGTGGCACAG	8830	AQLTVGNNVAQ	13419	LTVGNNV	0.164995	-0.1489
SyS2123	4242	GCCCAAAGCATCCTCACCAGAGACAGCGCACAG	8831	AQSILTRDSAQ	13420	SILTRDS	0.164909	-0.15253
SyS2124	4243	GCCCAAGTTCTTGTTGATTCGCGTGCGGCACAG	8832	AQVLVDSRAAQ	13421	VLVDSRA	0.164849	-0.20588
SyS2125	4244	GCCCAAGGCGTCGCCAGCACCACCACCGCACAG	8833	AQGVASTTTAQ	13422	GVASTTT	0.164819	-0.15617
SyS2126	4245	GCCCAACACGGCGCCAACCTCAGCGTCGCACAG	8834	AQHGANLSVAQ	13423	HGANLSV	0.164788	-0.05676
SyS2127	4246	GCCCAATCGTTTAATCAGCCGTCTGTTGCACAG	8835	AQSFNQPSVAQ	13424	SFNQPSV	0.164762	-0.04976
GS1238	4247	GCCCAACTCAACCAAAACCAAAGAGTCGCACAG	8836	AQLNQNQRVAQ	13425	LNQNQRV	0.164752	-0.15317
SyS2128	4248	GCCCAAAGAATCGACAGCCAAGACACCGCACAG	8837	AQRIDSQDTAQ	13426	RIDSQDT	0.164726	-0.20951
GS1239	4249	GCCCAAACCGTCCCCGGCAGACCCAGCGCACAG	8838	AQTVPGRPSAQ	13427	TVPGRPS	0.164623	-0.14779
SyS2130	4250	GCCCAACGTGAGCCGAATAATACGAGTGCACAG	8839	AQREPNNTSAQ	13428	REPNNTS	0.164588	-0.05033
SyS2131	4251	GCCCAAGAAAGAATGACCATGCACGCCGCACAG	8840	AQERMTMHAAQ	13429	ERMTMHA	0.164489	-0.12101
GS1240	4252	GCCCAAATTGCTATTCAGAATGATCGGGCACAG	8841	AQIAIQNDRAQ	13430	IAIQNDR	0.164441	-0.14603
SyS2132	4253	GCCCAACTTGGGGCTCAGTCTATTTCGGCACAG	8842	AQLGAQSISAQ	13431	LGAQSIS	0.164426	-0.17072
SS136	4254	GCCCAAGCGGGGGATAAGACGTATGTTGCACAG	8843	AQAGDKTYVAQ	13432	AGDKTYV	0.164227	-0.35249
SyS2135	4255	GCCCAAATGAATAGGACTGCGTATACTGCACAG	8844	AQMNRTAYTAQ	13433	MNRTAYT	0.164206	-0.17799
SyS2136	4256	GCCCAAGCGCTGCCTGGGGGTCTTATGGCACAG	8845	AQALPGGLMAQ	13434	ALPGGLM	0.164168	-0.22406
GS1241	4257	GCCCAACTCAAAAACCACGACACCACCGCACAG	8846	AQLKNHDTTAQ	13435	LKNHDTT	0.164164	-0.02897
SyS2138	4258	GCCCAACCCCTCAACTACGCCCTCGAAGCACAG	8847	AQPLNYALEAQ	13436	PLNYALE	0.164085	-0.2231
SyS2139	4259	GCCCAAAGCAAACAAATGCACACAACGACGCACAG	8848	AQSKQMHNDAQ	13437	SKQMHND	0.163943	-0.14283
SyS2140	4260	GCCCAAACGGCGCATACGACTCCTTTTGCACAG	8849	AQTAHTTPFAQ	13438	TAHTTPF	0.163842	-0.14647
SyS2141	4261	GCCCAACTCAAAACCGGCGACAGCCAAGCACAG	8850	AQLKTGDSQAQ	13439	LKTGDSQ	0.163842	-0.14647
SyS2142	4262	GCCCAATATTCTACGACGGCTGAGTATGCACAG	8851	AQYSTTAEYAQ	13440	YSTTAEY	0.163781	-0.19107
SyP66	4263	GCCCAACCGCTGGATCGGACGGGTGAGGCACAG	8852	AQPLDRTGEAQ	13441	PLDRTGE	0.163769	-0.04278
SyS2144	4264	GCCCAAGGCCCCGGCGAAGTCAAAATCGCACAG	8853	AQGPGEVKIAQ	13442	GPGEVKI	0.163669	-0.17505
GS1243	4265	GCCCAACTCAGAAACCTCGACCTCAACGCACAG	8854	AQLRNLDLNAQ	13443	LRNLDLN	0.163512	-0.09845

FIG. 33 (Continued)

SyS2145	4266	GCCCAACTGGGGTCTACTTTGACTAAGGCACAG	8855	AQLGSTLTKAQ	13444	LGSTLTK	0.163495	-0.14302
GS1244	4267	GCCCAATTGAGGCCTGTGAGTGAGCATGCACAG	8856	AQLRPVSEHAQ	13445	LRPVSEH	0.1634	-0.16842
GS1245	4268	GCCCAAAGTAGGAGTCTGACTGAGATGGCACAG	8857	AQSRSLTEMAQ	13446	SRSLTEM	0.163369	-0.17577
SyS2147	4269	GCCCAAAACGGCCTCAGCACCACCATGGCACAG	8858	AQNGLSTTMAQ	13447	NGLSTTM	0.163348	-0.16889
GS1247	4270	GCCCAACATGATAAGACGTATGCGATGGCACAG	8859	AQHDKTYAMAQ	13448	HDKTYAM	0.163317	-0.16304
SyS2148	4271	GCCCAAGTTCCGTCGGATAAGATGCGTGCACAG	8860	AQVPSDKMRAQ	13449	VPSDKMR	0.163313	-0.2268
SyS2149	4272	GCCCAAGGCGCCCACAACCTCCTCACCGCACAG	8861	AQGAHNLLTAQ	13450	GAHNLLT	0.163277	-0.20345
GS1248	4273	GCCCAAAGCACCAGCACCATGGTCATGGCACAG	8862	AQSTSTMVMAQ	13451	STSTMVM	0.163265	-0.11218
SS137	4274	GCCCAAAACATGGCCCACGAAAGCAAAGCACAG	8863	AQNMAHESKAQ	13452	NMAHESK	0.163246	-0.34932
SyS2151	4275	GCCCAATATCTTGGGGTGGGTGCTACTGCACAG	8864	AQYLGVGATAQ	13453	YLGVGAT	0.163021	-0.17193
SyS2152	4276	GCCCAAGCCAGCGAATACAACCAACACGCACAG	8865	AQASEYNQHAQ	13454	ASEYNQH	0.162953	-0.21072
SyS2153	4277	GCCCAAAGAGCCGAAGGCGACAAAATCGCACAG	8866	AQRAEGDKIAQ	13455	RAEGDKI	0.162815	-0.18861
SyS2154	4278	GCCCAATCTAGTGGTAGTAGTTTTCATGCACAG	8867	AQSSGSSFHAQ	13456	SSGSSFH	0.162597	-0.218
SyS2155	4279	GCCCAATGGGGCAAAGAATACACCGGCGCACAG	8868	AQWGKEYTGAQ	13457	WGKEYTG	0.162268	-0.12824
SyS2156	4280	GCCCAACCTGCTTCGGGGGCTATGCCTGCACAG	8869	AQPASGAMPAQ	13458	PASGAMP	0.16218	0.044005
SyS2158	4281	GCCCAAAGGGGGGCGGTTGTTGTGGCTGCACAG	8870	AQRGAVVVAAQ	13459	RGAVVVA	0.161915	-0.16587
GS1249	4282	GCCCAAGTGATGATGCAGAATCATGCTGCACAG	8871	AQVMMQNHAAQ	13460	VMMQNHA	0.161911	-0.12712
GS1250	4283	GCCCAACAAGACAGACTCCAAAGCAGAGCACAG	8872	AQQDRLQSRAQ	13461	QDRLQSR	0.161891	-0.14906
SyS2159	4284	GCCCAAGGTCATGCTGCTGTTTCTGTGGCACAG	8873	AQGHAAVSVAQ	13462	GHAAVSV	0.161865	0.031161
SyS2160	4285	GCCCAAGACAAAACCGACAGCACCCCCGCACAG	8874	AQDKTDSTPAQ	13463	DKTDSTP	0.161817	-0.20216
GP176	4286	GCCCAAGTGCCTCCGACTTCTTTTACTGCACAG	8875	AQVPPTSFTAQ	13464	VPPTSFT	0.161782	-0.06149
GS1251	4287	GCCCAAGTCGGCCCCAACGCCCAACACGCACAG	8876	AQVGPNAQHAQ	13465	VGPNAQH	0.16174	-0.06577
SyS2161	4288	GCCCAACATCATGGTCGGGCTGATACTGCACAG	8877	AQHHGRADTAQ	13466	HHGRADT	0.161642	-0.23419
GS1253	4289	GCCCAACATGTTAATATGGGTCCGGCGGCACAG	8878	AQHVNMGPAAQ	13467	HVNMGPA	0.161627	-0.1747
SyS2162	4290	GCCCAACACGCCACCAAGAAACCAGCGCACAG	8879	AQHATKETSAQ	13468	HATKETS	0.161604	-0.17998
SyS2163	4291	GCCCAATTGGCTACGGGTGTGAGTAATGCACAG	8880	AQLATGVSNAQ	13469	LATGVSN	0.161594	-0.07794
SyS2164	4292	GCCCAAAGCCTCGGCAGCTACCCCACCGCACAG	8881	AQSLGSYPTAQ	13470	SLGSYPT	0.1614	-0.11737
SyS2165	4293	GCCCAAGGCAGCAAAGCCTACGTCGGCGCACAG	8882	AQGSKAYVGAQ	13471	GSKAYVG	0.161272	-0.12101
SyS2167	4294	GCCCAACAAGACAGAATGAGCGTCAACGCACAG	8883	AQQDRMSVNAQ	13472	QDRMSVN	0.161186	-0.18954
SyS2168	4295	GCCCAATGGTCGGATTCTCTGAGGGATGCACAG	8884	AQWSDSLRDAQ	13473	WSDSLRD	0.161166	-0.21194
SyS2169	4296	GCCCAAACGAAGGTGCCTATGACTCAGGCACAG	8885	AQTKVPMTQAQ	13474	TKVPMTQ	0.161135	-0.08946
SyS2170	4297	GCCCAATCTCCGTTGTCTGATCGGTTGGCACAG	8886	AQSPLSDRLAQ	13475	SPLSDRL	0.161094	-0.18405

FIG. 33 (Continued)

SyS2171	4298	GCCCAACTGTATGGTAGTTCGGTTGTTGCACAG	8887	AQLYGSSVVAQ	13476	LYGSSVV	0.161094	-0.18405
SyS2172	4299	GCCCAACCGACGCAGACTGTTAGTTCGGCACAG	8888	AQPTQTVSSAQ	13477	PTQTVSS	0.161094	-0.18405
GP178	4300	GCCCAACTGAATAAGCTGCTTGGGGCGGCACAG	8889	AQLNKLLGAAQ	13478	LNKLLGA	0.160777	0.340925
SyS2173	4301	GCCCAACATTCTAATCAGGAGCCTCGGGCACAG	8890	AQHSNQEPRAQ	13479	HSNQEPR	0.160633	-0.17106
SyS2174	4302	GCCCAAAACGGCGCCAGCATCCACACAGCGCACAG	8891	AQNGASIHSAQ	13480	NGASIHS	0.16061	0.144677
SyS2175	4303	GCCCAACTCAGCCAACAAAGACTCCAAGCACAG	8892	AQLSQQRLQAQ	13481	LSQQRLQ	0.160413	-0.02302
GS1258	4304	GCCCAACTCCCCCACGGCACCATGAACGCACAG	8893	AQLPHGTMNAQ	13482	LPHGTMN	0.160361	-0.12536
SyS2176	4305	GCCCAAAGCAGCCCCCGACGCCAAATACGCACAG	8894	AQSSPDAKYAQ	13483	SSPDAKY	0.160306	-0.1986
GS1259	4306	GCCCAATTCCACACCCCCGCCGGCAACGCACAG	8895	AQFHTPAGNAQ	13484	FHTPAGN	0.160249	-0.13792
SyS2177	4307	GCCCAAAGAACCACCGCCAACAGCCTCGCACAG	8896	AQRTTANSLAQ	13485	RTTANSL	0.16022	-0.09434
SyS2178	4308	GCCCAATTGGATAAGACTATTCCTCAGGCACAG	8897	AQLDKTIPQAQ	13486	LDKTIPQ	0.160087	-0.20224
SyS2179	4309	GCCCAATGGCAAGGCAACAGACAAGCCGCACAG	8898	AQWQGNRQAAQ	13487	WQGNRQA	0.160025	-0.07373
SyS2181	4310	GCCCAAGGGTATGGTACGATTACGCCTGCACAG	8899	AQGYGTITPAQ	13488	GYGTITP	0.159821	-0.02887
GS1260	4311	GCCCAAATGAGAGAACACAAAACAAAGCCGCACAG	8900	AQMREQNKAAQ	13489	MREQNKA	0.15981	-0.17201
SyS2183	4312	GCCCAAAACCTCGCCGGCCTCACCGGCGCACAG	8901	AQNLAGLTGAQ	13490	NLAGLTG	0.159698	-0.16889
SyS2184	4313	GCCCAATGGTTTAAGGCTGGGAGTGCTGCACAG	8902	AQWFKAGSAAQ	13491	WFKAGSA	0.159617	-0.20951
SyS2185	4314	GCCCAAATCAACGTCGCCCCCTACAAAGCACAG	8903	AQINVAPYKAQ	13492	INVAPYK	0.159555	-0.16102
SyS2186	4315	GCCCAAGGGGGTGCATTCGAATGGTCAGGCACAG	8904	AQGVHSNGQAQ	13493	GVHSNGQ	0.159514	-0.10739
SyS2187	4316	GCCCAAATGAGCGCCAGCACCAACACCGCACAG	8905	AQMSASTNTAQ	13494	MSASTNT	0.15942	-0.1344
GS1263	4317	GCCCAAGGCAGCCACAACGCCCAAGGCGCACAG	8906	AQGSHNAQGAQ	13495	GSHNAQG	0.159285	-0.08901
SyS2189	4318	GCCCAAATCAGCGCCGTCCCCAAAAACGCACAG	8907	AQISAVPKNAQ	13496	ISAVPKN	0.159253	-0.17875
SyS2190	4319	GCCCAAGCCGGCGGCATGCAAAAACGCACAG	8908	AQAGGGMQNAQ	13497	AGGGMQN	0.159207	-0.1198
SyS2191	4320	GCCCAACTCCTCAACACCACCAGCACCGCACAG	8909	AQLLNTTSTAQ	13498	LLNTTST	0.159024	0.011774
SyS2192	4321	GCCCAAACTAATACTGTGAGTGCTAGTGCACAG	8910	AQTNTVSASAQ	13499	TNTVSAS	0.158935	0.332609
SyS2193	4322	GCCCAACAGTTGTCTCCGATTGCTATGGCACAG	8911	AQQLSPIAMAQ	13500	QLSPIAM	0.158902	-0.19618
GS1264	4323	GCCCAAGCGCCGCGGGGTGTTAATTTGGCACAG	8912	AQAPRGVNLAQ	13501	APRGVNL	0.158854	-0.18149
SyS2194	4324	GCCCAACTTACTCGTACGTCGGTGGATGCACAG	8913	AQLTRTSVDAQ	13502	LTRTSVD	0.158821	-0.01311
SyS2195	4325	GCCCAACTGGGGCAGAAGGCGCCTACTGCACAG	8914	AQLGQKAPTAQ	13503	LGQKAPT	0.158804	-0.1069
SyS2196	4326	GCCCAAAAGAATGCGCCGCCTCTGACGGCACAG	8915	AQKNAPPLTAQ	13504	KNAPPLT	0.158756	-0.21694
SyS2197	4327	GCCCAAGTCAGAAACGCCGTCCACGCCGCACAG	8916	AQVRNAVHAAQ	13505	VRNAVHA	0.158629	-0.12577
SyS2198	4328	GCCCAAATCAGACACATGGACGCCCCCCGCACAG	8917	AQIRHMDAPAQ	13506	IRHMDAP	0.158527	-0.1792
SyS2200	4329	GCCCAAGGTGCTCCTTTGGTTGCTACTGCACAG	8918	AQGAPLVATAQ	13507	GAPLVAT	0.15843	-0.17629

FIG. 33 (Continued)

SyS2201	4330	GCCCAATCTGATCATAATGCTCGTGGGGCACAG	8919	AQSDHNARGAQ	13508	SDHNARG	0.158426	-0.15859
SyS2202	4331	GCCCAAATCAGCGACACCCTCCACTACGCACAG	8920	AQISDTLHYAQ	13509	ISDTLHY	0.158424	-0.08821
GS1266	4332	GCCCAAAACAACAGAGGCAGCATCAGCGCACAG	8921	AQNNRGSISAQ	13510	NNRGSIS	0.158422	-0.05843
GS1267	4333	GCCCAACAAAGAGAAAGAGACGGCGTCGCACAG	8922	AQQRERDGVAQ	13511	QRERDGV	0.158316	-0.10804
SyS2203	4334	GCCCAAAGTAAGCAGGATGTGCGTGCTGCACAG	8923	AQSKQDVRAAQ	13512	SKQDVRA	0.158297	-0.18284
SyS2204	4335	GCCCAAAACAGCGGCAGACTCAACGTCGCACAG	8924	AQNSGRLNVAQ	13513	NSGRLNV	0.158284	-0.17013
SyS2205	4336	GCCCAAGGCCCCAGCGTCGAAAGCAACGCACAG	8925	AQGPSVESNAQ	13514	GPSVESN	0.158284	-0.23296
GS1268	4337	GCCCAATTGCTTTCTTCTTCGCCTTCTGCACAG	8926	AQLLSSSPSAQ	13515	LLSSSPS	0.158261	-0.16394
SyS2206	4338	GCCCAAAAAGTCCTCGTCAGCGGCAGCGCACAG	8927	AQKVLVSGSAQ	13516	KVLVSGS	0.158127	-0.20709
SyS2207	4339	GCCCAAGATGTGCGGAATACTATTGCTGCACAG	8928	AQDVRNTIAAQ	13517	DVRNTIA	0.158027	-0.07579
GS1270	4340	GCCCAACATAAGTTGGTGACGAAGGATGCACAG	8929	AQHKLVTKDAQ	13518	HKLVTKD	0.157915	-0.1747
GS1271	4341	GCCCAACCGTATGTTTCGGGTGTTCCTGCACAG	8930	AQPYVSGVPAQ	13519	PYVSGVP	0.157885	-0.11277
SyS2209	4342	GCCCAAACGACTAAGGCTTCGTTTACTGCACAG	8931	AQTTKASFTAQ	13520	TTKASFT	0.15776	-0.17998
GS1272	4343	GCCCAAACCCCCCCACGGCCCCGACGCCGCACAG	8932	AQTPHGPDAAQ	13521	TPHGPDA	0.157568	-0.18368
SyS2210	4344	GCCCAAGATTATCGTCAGACTGATCATGCACAG	8933	AQDYRQTDHAQ	13522	DYRQTDH	0.157547	-0.17314
SyS2211	4345	GCCCAACACAGCCCCCAAACCCGACCACGCACAG	8934	AQHSPKPDHAQ	13523	HSPKPDH	0.157547	-0.19375
SyS2212	4346	GCCCAAGCGTATGGTCAGGTGCCTCCTGCACAG	8935	AQAYGQVPPAQ	13524	AYGQVPP	0.157393	-0.07373
SyS2213	4347	GCCCAAAGCAACCAAGGCCTCGCCGGCGCACAG	8936	AQSNQGLAGAQ	13525	SNQGLAG	0.157367	-0.11495
SyS2214	4348	GCCCAAATCAACAGCCCCATCGGCAACGCACAG	8937	AQINSPIGNAQ	13526	INSPIGN	0.157315	-0.09779
SyS2215	4349	GCCCAACAAAACCAAATCATGAGCGGCGCACAG	8938	AQQNQIMSGAQ	13527	QNQIMSG	0.157275	-0.19739
SyS2216	4350	GCCCAAGTCTACCAAGGCAACCAAAACGCACAG	8939	AQVYQGNQNAQ	13528	VYQGNQN	0.157122	-0.05314
GS1273	4351	GCCCAAGGCAGCAACAGCCAACACACCGCACAG	8940	AQGSNSQHTAQ	13529	GSNSQHT	0.156944	-0.11091
SyS2217	4352	GCCCAAAAGCAGGAGCCGTCGGATAGGGCACAG	8941	AQKQEPSDRAQ	13530	KQEPSDR	0.156938	-0.14283
GS1274	4353	GCCCAACACAGAAGCAGCCCCGCCGCCGCACAG	8942	AQHRSSPAAAQ	13531	HRSSPAA	0.156784	-0.15945
SyS2219	4354	GCCCAAAATGAGGGGAATTCGATGAAGGCACAG	8943	AQNEGNSMKAQ	13532	NEGNSMK	0.156665	-0.08967
GS1277	4355	GCCCAAAGACCCGACAAAGGCCCCATGGCACAG	8944	AQRPDKGPMAQ	13533	RPDKGPM	0.156399	-0.15764
SyS2222	4356	GCCCAAGCGATTGTGTCTCATCCGCTGGCACAG	8945	AQAIVSHPLAQ	13534	AIVSHPL	0.156109	-0.19805
GS1279	4357	GCCCAAACCCAAGGCGAAAGACCCGTCGCACAG	8946	AQTQGERPVAQ	13535	TQGERPV	0.156022	-0.17386
SyS2225	4358	GCCCAATACGTCAACAGCGCCCCCCAAAGCACAG	8947	AQYVNSAPKAQ	13536	YVNSAPK	0.155853	-0.17799
GS1280	4359	GCCCAACCTTCGGGGACTTCGATTGTGGCACAG	8948	AQPSGTSIVAQ	13537	PSGTSIV	0.155836	-0.17919
SyS2226	4360	GCCCAAAGCGTCGGCGCCAACAGAAGCGCACAG	8949	AQSVGANRSAQ	13538	SVGANRS	0.155529	-0.18491
SyS2227	4361	GCCCAATCTGCGCATTTTAATCATTCGGCACAG	8950	AQSAHFNHSAQ	13539	SAHFNHS	0.155529	-0.18491

FIG. 33 (Continued)

GS1282	4362	GCCCAAAAAGTCAACAGCGCCCACCTCGCACAG	8951	AQKVNSAHLAQ	13540	KVNSAHL	0.155467	-0.17768
SyS2228	4363	GCCCAAGGTTTTGGGAATATGGGGGCTGCACAG	8952	AQGFGNMGAAQ	13541	GFGNMGA	0.155296	-0.15411
SS146	4364	GCCCAAAATCTTAAGCCTGAGACTGATGCACAG	8953	AQNLKPETDAQ	13542	NLKPETD	0.155264	-0.38304
SyS2230	4365	GCCCAACCGAATTCGAATACTGCGTTTGCACAG	8954	AQPNSNTAFAQ	13543	PNSNTAF	0.155257	-0.10441
SyS2231	4366	GCCCAACATGATACTCTGAGGACTCCTGCACAG	8955	AQHDTLRTPAQ	13544	HDTLRTP	0.155231	-0.15132
SyS2232	4367	GCCCAAAGGTTTCCGCAGGCGCCTCCGGCACAG	8956	AQRFPQAPPAQ	13545	RFPQAPP	0.155196	-0.11737
GS1283	4368	GCCCAATCGTCGGGTAATAAGTCGGATGCACAG	8957	AQSSGNKSDAQ	13546	SSGNKSD	0.155174	-0.17958
SyS2233	4369	GCCCAAATGTCGAAGATGGCGGATCGGGCACAG	8958	AQMSKMADRAQ	13547	MSKMADR	0.154977	-0.20588
SyS2234	4370	GCCCAAGAACACAGAGAAACCAGCATCGCACAG	8959	AQEHRETSIAQ	13548	EHRETSI	0.154977	-0.20588
SyS2235	4371	GCCCAAAGCACCGAATACCCCGTCCCCGCACAG	8960	AQSTEYPVPAQ	13549	STEYPVP	0.154868	-0.20709
SyS2236	4372	GCCCAAGACAAAAGCATGAACCCCAGCGCACAG	8961	AQDKSMNPSAQ	13550	DKSMNPS	0.154833	-0.20093
SyS2238	4373	GCCCAAGAATACCACAACAACCTCAAAGCACAG	8962	AQEYHNNLKAQ	13551	EYHNNLK	0.154533	-0.06931
SyS2240	4374	GCCCAAATTTTTACGAATACGGGTCATGCACAG	8963	AQIFTNTGHAQ	13552	IFTNTGH	0.154185	-0.1172
GS1286	4375	GCCCAAAAAAGCAACAGCCCCCTCGCCGCACAG	8964	AQKSNSPLAAQ	13553	KSNSPLA	0.154173	-0.02046
SyS2241	4376	GCCCAATACAGCAGCGGCTACAACGCCGCACAG	8965	AQYSSGYNAAQ	13554	YSSGYNA	0.154102	-0.11859
SyS2242	4377	GCCCAAGGTTCTAAGACGCAGGGGGATGCACAG	8966	AQGSKTQGDAQ	13555	GSKTQGD	0.154063	-0.07131
GS1287	4378	GCCCAAATTGTTTCTGGGTCGAGTCAGGCACAG	8967	AQIVSGSSQAQ	13556	IVSGSSQ	0.154011	-0.15192
SyS2243	4379	GCCCAAAGCCTCATCAACAGCACCTACGCACAG	8968	AQSLINSTYAQ	13557	SLINSTY	0.153985	-0.19981
SyS2244	4380	GCCCAAAACATGAAAATCCAACACGTCGCACAG	8969	AQNMKIQHVAQ	13558	NMKIQHV	0.153984	-0.21078
GS1288	4381	GCCCAAGATTCGACGAAGTTGGGTCATGCACAG	8970	AQDSTKLGHAQ	13559	DSTKLGH	0.153977	-0.10614
SyS2245	4382	GCCCAACAGTCGCATGGGACGTCTAGTGCACAG	8971	AQQSHGTSSAQ	13560	QSHGTSS	0.153941	-0.10525
GS1289	4383	GCCCAAAAAGACAACAACAGAAGCGCCGCACAG	8972	AQKDNNRSAAQ	13561	KDNNRSA	0.153885	-0.16432
GS1290	4384	GCCCAATTCCAACCCAGCTACGCCGCCGCACAG	8973	AQFQPSYAAAQ	13562	FQPSYAA	0.153844	-0.15586
SyS2247	4385	GCCCAACCCACCGTCCAAATGAAAGCCGCACAG	8974	AQPTVQMKAAQ	13563	PTVQMKA	0.153624	-0.20345
SyS2248	4386	GCCCAATCGCCGACGAGTAGTACTTTTGCACAG	8975	AQSPTSSTFAQ	13564	SPTSSTF	0.153496	-0.11204
GS1291	4387	GCCCAAGGCAGAGACGCCAACGTCCCCGCACAG	8976	AQGRDANVPAQ	13565	GRDANVP	0.153342	-0.08109
SyS2251	4388	GCCCAAACCCTCATGAGCACCAGCCCCGCACAG	8977	AQTLMSTSPAQ	13566	TLMSTSP	0.153097	-0.16344
GS1292	4389	GCCCAACTGCATGGGGCTACTACGACTGCACAG	8978	AQLHGATTTAQ	13567	LHGATTT	0.153076	-0.10916
GS1293	4390	GCCCAAAGGACTAATGAGGTTATGCGGGCACAG	8979	AQRTNEVMRAQ	13568	RTNEVMR	0.153076	-0.18054
SyS2253	4391	GCCCAAGATAATCTGAGGGTTACGGCGGCACAG	8980	AQDNLRVTAAQ	13569	DNLRVTA	0.153058	-0.21448
GS1294	4392	GCCCAAAGGCAGGCGGGGGATCAGCTTGCACAG	8981	AQRQAGDQLAQ	13570	RQAGDQL	0.152865	-0.13857
SyS2254	4393	GCCCAAGTCGGCCAACACCTCACCCACGCACAG	8982	AQVGQHLTHAQ	13571	VGQHLTH	0.152852	-0.13677

FIG. 33 (Continued)

SyS2255	4394	GCCCAACTCAGCGCCGCCAGCGGCATCGCACAG	8983	AQLSAASGIAQ	13572	LSAASGI	0.152829	-0.16497
SyS2256	4395	GCCCAAAGCAGCCACAACGGCTTCATCGCACAG	8984	AQSSHNGFIAQ	13573	SSHNGFI	0.152739	-0.14425
GS1296	4396	GCCCAAAACGCCACCAGACAATACAGCGCACAG	8985	AQNATRQYSAQ	13574	NATRQYS	0.152256	-0.06882
GS1297	4397	GCCCAAGTCAGCAGACAAAGCCTCGGCGCACAG	8986	AQVSRQSLGAQ	13575	VSRQSLG	0.152253	-0.15676
SyS2259	4398	GCCCAAGACGTCGTCAAACCCCACGGCGCACAG	8987	AQDVVKPHGAQ	13576	DVVKPHG	0.152101	-0.10404
SyS2260	4399	GCCCAAGGGATTGGGGGTATTAGTTCTGCACAG	8988	AQGIGGISSAQ	13577	GIGGISS	0.152077	-0.00277
SyS2262	4400	GCCCAAACTAATAATAGTCTGCGTGAGGCACAG	8989	AQTNNSLREAQ	13578	TNNSLRE	0.151972	-0.02172
SyS2263	4401	GCCCAAACGCGTACGGCTTCGGCGCTGGCACAG	8990	AQTRTASALAQ	13579	TRTASAL	0.15196	-0.08332
SyS2264	4402	GCCCAAACTACGACGGCTCCGAGTCCGGCACAG	8991	AQTTTAPSPAQ	13580	TTTAPSP	0.151942	0.097476
SyS2265	4403	GCCCAAAACGCCAGCATGAGCAGCATCGCACAG	8992	AQNASMSSIAQ	13581	NASMSSI	0.151936	0.127665
SyS2266	4404	GCCCAAACCCAACCCCACAGAGGCCTCGCACAG	8993	AQTQPHRGLAQ	13582	TQPHRGL	0.151921	-0.20466
SyS2267	4405	GCCCAAAGACTCGACCACCACAGCAGCGCACAG	8994	AQRLDHHSSAQ	13583	RLDHHSS	0.151906	-0.2305
SyS2268	4406	GCCCAAGAAAACACCACCAGAATCGCCGCACAG	8995	AQENTTRIAAQ	13584	ENTTRIA	0.151859	0.202781
GS1299	4407	GCCCAAAGCCTCAGAGGCAACGAAGCCGCACAG	8996	AQSLRGNEAAQ	13585	SLRGNEA	0.151754	-0.16718
GS1300	4408	GCCCAACCTAATGTTCCTTCGCATTCTGCACAG	8997	AQPNVPSHSAQ	13586	PNVPSHS	0.15171	-0.18278
SyS2269	4409	GCCCAAGGGATGCCTTTGATGAAGATGGCACAG	8998	AQGMPLMKMAQ	13587	GMPLMKM	0.151503	-0.2083
SyS2270	4410	GCCCAACAGAAGACTGAGCGGACGGTTGCACAG	8999	AQQKTERTVAQ	13588	QKTERTV	0.15144	-0.03374
SyS2271	4411	GCCCAAAACCACACCAACCACAGCAGCGCACAG	9000	AQNHTNHSSAQ	13589	NHTNHSS	0.151411	-0.16829
GS1302	4412	GCCCAAGGGCTGGGGAATAGGTCTGCTGCACAG	9001	AQGLGNRSAAQ	13590	GLGNRSA	0.15133	-0.17958
GS1303	4413	GCCCAAGACCTCGACAAAAGAGGCCTCGCACAG	9002	AQDLDKRGLAQ	13591	DLDKRGL	0.151278	-0.07669
SyS2273	4414	GCCCAACTCACCAACGCCCAACCCGACGCACAG	9003	AQLTNAQPDAQ	13592	LTNAQPD	0.151194	-0.21571
SyS2275	4415	GCCCAAACGAAGCCTGATTATCTGGTTGCACAG	9004	AQTKPDYLVAQ	13593	TKPDYLV	0.151065	-0.15859
SyS2276	4416	GCCCAAAAGTTGCAGTTGCATGAGGTTGCACAG	9005	AQKLQLHEVAQ	13594	KLQLHEV	0.150883	-0.08921
SyS2277	4417	GCCCAAACGTCTGTGACGATTTCGAGTGCACAG	9006	AQTSVTISSAQ	13595	TSVTISS	0.150853	-0.08154
SyS2278	4418	GCCCAAAATTCGAGTAATAGGGCTGAGGCACAG	9007	AQNSSNRAEAQ	13596	NSSNRAE	0.150815	-0.09555
GS1304	4419	GCCCAACTCGAACACGGCACCAGAATCGCACAG	9008	AQLEHGTRIAQ	13597	LEHGTRI	0.150746	-0.07792
GS1305	4420	GCCCAAACCCTCCAAATGAGAGAACACGCACAG	9009	AQTLQMREHAQ	13598	TLQMREH	0.150701	-0.13475
GS1306	4421	GCCCAAGGCAGCCCCACCGCCCAAACCGCACAG	9010	AQGSPTAQTAQ	13599	GSPTAQT	0.150489	-0.15945
SyS2280	4422	GCCCAAAATAAGGGGCAGACGCTTACTGCACAG	9011	AQNKGQTLTAQ	13600	NKGQTLT	0.150205	-0.20588
SyS2281	4423	GCCCAATCGGTGGGTCATCGGGATATGGCACAG	9012	AQSVGHRDMAQ	13601	SVGHRDM	0.150092	-0.15617
GS1308	4424	GCCCAAAGAGACAAAAGCAGCATGCACGCACAG	9013	AQRDKSSMHAQ	13602	RDKSSMH	0.149802	-0.13189
SyS2283	4425	GCCCAAGTCAGCGTCATCAACAACACCGCACAG	9014	AQVSVINNTAQ	13603	VSVINNT	0.14972	-0.11447

FIG. 33 (Continued)

SyS2284	4426	GCCCAACTTCCTAATTCTGCTTTTAGTGCACAG	9015	AQLPNSAFSAQ	13604	LPNSAFS	0.149676	-0.02892
GS1309	4427	GCCCAACGTACGGTGTCTACGGATGATGCACAG	9016	AQRTVSTDDAQ	13605	RTVSTDD	0.149671	-0.18368
GS1310	4428	GCCCAACTCATGGACAGAATGGCCAGCGCACAG	9017	AQLMDRMASAQ	13606	LMDRMAS	0.149549	-0.14121
SyS2285	4429	GCCCAACCGAGTGGGTTTAATACTTTGGCACAG	9018	AQPSGFNTLAQ	13607	PSGFNTL	0.149506	-0.21078
SyS2286	4430	GCCCAAAAAAGCGCCCAACCATGAGCGCACAG	9019	AQKSAQPMSAQ	13608	KSAQPMS	0.149458	-0.11374
SyS2287	4431	GCCCAAACCGGCCTCAGCGTCCAAAAAGCACAG	9020	AQTGLSVQKAQ	13609	TGLSVQK	0.149458	-0.23618
SyS2288	4432	GCCCAACACGGCTTCCCCGCCGGCCCCGCACAG	9021	AQHGFPAGPAQ	13610	HGFPAGP	0.149413	-0.19981
SyS2289	4433	GCCCAAAGCTACGAAGCCGTCGGCATCGCACAG	9022	AQSYEAVGIAQ	13611	SYEAVGI	0.149397	-0.13594
SyS2290	4434	GCCCAAACCGCCAAAGGCGTCCTCAGCGCACAG	9023	AQTAKGVLSAQ	13612	TAKGVLS	0.149081	-0.22649
SS153	4435	GCCCAAGGCGCCAGCACCCACAACGCCGCACAG	9024	AQGASTHNAAQ	13613	GASTHNA	0.149034	-0.40725
SyS2291	4436	GCCCAAATCATCAAAGAAATCCCCGCCGCACAG	9025	AQIIKEIPAAQ	13614	IIKEIPA	0.149013	-0.16708
GS1313	4437	GCCCAAAACCACGTCATCAGCAACGGCGCACAG	9026	AQNHVISNGAQ	13615	NHVISNG	0.148941	-0.12903
SyS2293	4438	GCCCAATACACCAACATGGCCGGCGTCGCACAG	9027	AQYTNMAGVAQ	13616	YTNMAGV	0.148928	-0.14405
SyS2294	4439	GCCCAATTCAACAGAATCGGCGCCGGCGCACAG	9028	AQFNRIGAGAQ	13617	FNRIGAG	0.14886	-0.12101
SyS2295	4440	GCCCAATGGAGCACCATGATGAAAAGCGCACAG	9029	AQWSTMMKSAQ	13618	WSTMMKS	0.148757	-0.21679
SyS2296	4441	GCCCAAACCGCCCCCGCCAACCACGTCGCACAG	9030	AQTAPANHVAQ	13619	TAPANHV	0.148692	0.040594
SyS2298	4442	GCCCAAATGCATGGGGGTTCGGAGCTGGCACAG	9031	AQMHGGSELAQ	13620	MHGGSEL	0.148583	-0.18737
GS1314	4443	GCCCAAATGAGTAGGATGGGGGTGGCGGCACAG	9032	AQMSRMGVAAQ	13621	MSRMGVA	0.148576	-0.1774
GS1315	4444	GCCCAAACTCGGATTAGTGAGGTTCTTGCACAG	9033	AQTRISEVLAQ	13622	TRISEVL	0.148534	-0.1313
SyS2299	4445	GCCCAAAGCGGCCCCGGCCTCAGAACCGCACAG	9034	AQSGPGLRTAQ	13623	SGPGLRT	0.148397	-0.13798
GS1316	4446	GCCCAAGATAAGCGTCATCATGCGGAGGCACAG	9035	AQDKRHHAEAQ	13624	DKRHHAE	0.148387	-0.10709
SyS2300	4447	GCCCAATTGACGCAGAATGATCGGCCTGCACAG	9036	AQLTQNDRPAQ	13625	LTQNDRP	0.148385	-0.19353
GS1317	4448	GCCCAAAGCGTCACCACCAGCCACGTCGCACAG	9037	AQSVTTSHVAQ	13626	SVTTSHV	0.148348	-0.17919
SyS2301	4449	GCCCAAATGCTCACCGGCGGCACCAACGCACAG	9038	AQMLTGGTNAQ	13627	MLTGGTN	0.148306	-0.17259
SyS2302	4450	GCCCAAGACAACGTCGCCAACGCCGGCGCACAG	9039	AQDNVANAGAQ	13628	DNVANAG	0.148252	-0.125
SyS2303	4451	GCCCAAATGACCACCAACAGCATCGCCGCACAG	9040	AQMTTNSIAAQ	13629	MTTNSIA	0.148226	-0.22042
SyS2304	4452	GCCCAAATGCGTACGCAGTCTCTGTCGGCACAG	9041	AQMRTQSLSAQ	13630	MRTQSLS	0.14815	0.030244
GS1318	4453	GCCCAATACGGCAGCTTCACCGGCCAAGCACAG	9042	AQYGSFTGQAQ	13631	YGSFTGQ	0.148082	-0.14334
GS1320	4454	GCCCAAGGCCCCATGCTCCTCAAAGCCGCACAG	9043	AQGPMLLKAAQ	13632	GPMLLKA	0.148051	-0.16753
SyS2305	4455	GCCCAAATGACCCAAAAAGCCCCCGTCGCACAG	9044	AQMTQKAPVAQ	13633	MTQKAPV	0.147926	-0.03714
GS1321	4456	GCCCAAAGCGCCAACGCCACCAAACTCGCACAG	9045	AQSANATKLAQ	13634	SANATKL	0.147918	-0.10232
SyS2306	4457	GCCCAATTCAACGGCAGCCTCGCCATGGCACAG	9046	AQFNGSLAMAQ	13635	FNGSLAM	0.147866	-0.14302

FIG. 33 (Continued)

SyS2308	4458	GCCCAAATTGTTAATGCTAAGCTTACTGCACAG	9047	AQIVNAKLTAQ	13636	IVNAKLT	0.147749	-0.20103
SyS2310	4459	GCCCAAATGTTCAGCGGCCTCCAAGCCGCACAG	9048	AQMFSGLQAAQ	13637	MFSGLQA	0.147689	-0.23296
GS1322	4460	GCCCAAGTGGATTATCGGGTGAATGGTGCACAG	9049	AQVDYRVNGAQ	13638	VDYRVNG	0.147677	-0.16241
SyS2311	4461	GCCCAACTGGCTTCGGCTGGTAATGGTGCACAG	9050	AQLASAGNGAQ	13639	LASAGNG	0.147593	-0.07841
GS1323	4462	GCCCAACGTGATCTTCATTCTAAGGATGCACAG	9051	AQRDLHSKDAQ	13640	RDLHSKD	0.147554	-0.17958
SyS2313	4463	GCCCAAAGCCACGTCAGCAGAACCGCCGCACAG	9052	AQSHVSRTAAQ	13641	SHVSRTA	0.147511	0.008708
SyS2314	4464	GCCCAAACCCCCGTCCAAAGCCTCAGCGCACAG	9053	AQTPVQSLSAQ	13642	TPVQSLS	0.147458	-0.1444
SyS2315	4465	GCCCAATACCTCAACGGCAGCGAACTCGCACAG	9054	AQYLNGSELAQ	13643	YLNGSEL	0.147331	-0.1489
SyS2316	4466	GCCCAACCTGCTTTGAAGACTCATGAGGCACAG	9055	AQPALKTHEAQ	13644	PALKTHE	0.14732	0.228732
GS1324	4467	GCCCAAAATAAGTCTCTGACTTCTGATGCACAG	9056	AQNKSLTSDAQ	13645	NKSLTSD	0.147304	-0.16432
GS1325	4468	GCCCAATATAATGCTACTAAGTCGAGTGCACAG	9057	AQYNATKSSAQ	13646	YNATKSS	0.147262	-0.13189
GS1326	4469	GCCCAAATGCGGGATAAGAGTCATGATGCACAG	9058	AQMRDKSHDAQ	13647	MRDKSHD	0.147262	-0.13189
SyS2318	4470	GCCCAACACAGAACCGAAGGCCAAAACGCACAG	9059	AQHRTEGQNAQ	13648	HRTEGQN	0.147163	-0.041
SyS2319	4471	GCCCAACTCCACACAAACCCGACGAATTCGCACAG	9060	AQLHKPDEFAQ	13649	LHKPDEF	0.147149	-0.14672
SyS2320	4472	GCCCAAATTGCTGCGAGGCCTCCTTCGGCACAG	9061	AQIAARPPSAQ	13650	IAARPPS	0.14708	-0.16223
SyS2321	4473	GCCCAAACGCCTACGCATTATTCTCATGCACAG	9062	AQTPTHYSHAQ	13651	TPTHYSH	0.14708	-0.19496
GP183	4474	GCCCAATCGACTTTTTCGGCTGATAGGGCACAG	9063	AQSTFSADRAQ	13652	STFSADR	0.147035	-0.07197
SyP68	4475	GCCCAACAGTCGGTGCAGGTGACGGCTGCACAG	9064	AQQSVQVTAAQ	13653	QSVQVTA	0.146995	-0.04053
SyS2322	4476	GCCCAACTCGACAGCAGCAGAAACAGAGCACAG	9065	AQLDSSRNRAQ	13654	LDSSRNR	0.146928	-0.18527
GS1327	4477	GCCCAAAGACAACCCCAAAGCACCGTCGCACAG	9066	AQRQPQSTVAQ	13655	RQPQSTV	0.146727	-0.01889
SyS2323	4478	GCCCAAAGAGTCGACGACGGCGTCAGAGCACAG	9067	AQRVDDGVRAQ	13656	RVDDGVR	0.146717	-0.07779
GS1328	4479	GCCCAAAAAATCACCAACACCTACAGCGCACAG	9068	AQKITNTYSAQ	13657	KITNTYS	0.146679	-0.1481
GS1329	4480	GCCCAACCTGGGAAGGCGACTCCTCCTGCACAG	9069	AQPGKATPPAQ	13658	PGKATPP	0.146646	-0.15317
GS1330	4481	GCCCAATTCAGCACCCACACCCCCCCCGCACAG	9070	AQFSTHTPPAQ	13659	FSTHTPP	0.146343	-0.13761
SyS2324	4482	GCCCAACTCGCCCCCAACATGAGACTCGCACAG	9071	AQLAPNMRLAQ	13660	LAPNMRL	0.146185	-0.21194
SS154	4483	GCCCAAAACCTCCCCAGAACCAACGTCGCACAG	9072	AQNLPRTNVAQ	13661	NLPRTNV	0.146169	-0.35701
GS1331	4484	GCCCAAGAGACGAGTAATGTGAATCGTGCACAG	9073	AQETSNVNRAQ	13662	ETSNVNR	0.14611	-0.18188
SyS2325	4485	GCCCAAGGCAGCACCGACCACAGACTCGCACAG	9074	AQGSTDHRLAQ	13663	GSTDHRL	0.145928	-0.13071
SS155	4486	GCCCAAGTCAACACCGCCATGCCCGCCGCACAG	9075	AQVNTAMPAAQ	13664	VNTAMPA	0.145614	-0.40725
GS1335	4487	GCCCAAATGGTTGCTCGGGATCAGAATGCACAG	9076	AQMVARDQNAQ	13665	MVARDQN	0.145535	-0.13881
SyS2328	4488	GCCCAAAAAAACAACCCCGTCCTCCACGCACAG	9077	AQKNNPVLHAQ	13666	KNNPVLH	0.145436	-0.18984
GS1337	4489	GCCCAAGATTCGACGACGGTTAGGCTTGCACAG	9078	AQDSTTVRLAQ	13667	DSTTVRL	0.145378	-0.10767

FIG. 33 (Continued)

SyS2329	4490	GCCCAAAAACTCAACGTCATGAACGACGCACAG	9079	AQKLNVMNDAQ	13668	KLNVMND	0.145256	-0.15738
GS1339	4491	GCCCAAAGCCTCAGAGACAAAAACGCCGCACAG	9080	AQSLRDKNAAQ	13669	SLRDKNA	0.145231	-0.18727
SyS2330	4492	GCCCAAGGTGTTGGTAATAGTCTGAGTGCACAG	9081	AQGVGNSLSAQ	13670	GVGNSLS	0.145202	-0.01482
SyS2332	4493	GCCCAATTCAGCAAAACCAACTTCAACGCACAG	9082	AQFSKTNFNAQ	13671	FSKTNFN	0.145119	-0.22557
GS1342	4494	GCCCAAGCTAATCGGCCTTCGCTGCCTGCACAG	9083	AQANRPSLPAQ	13672	ANRPSLP	0.144885	-0.0877
GS1343	4495	GCCCAAGACAGCCAAACCAACAGAGTCGCACAG	9084	AQDSQTNRVAQ	13673	DSQTNRV	0.144816	-0.09307
SyS2333	4496	GCCCAAATTTCGACGTCGTCTCCGGTTGCACAG	9085	AQISTSSPVAQ	13674	ISTSSPV	0.144754	-0.12222
SyS2334	4497	GCCCAAATCCTCAAAATCACCGAAGGCGCACAG	9086	AQILKITEGAQ	13675	ILKITEG	0.144609	-0.14918
GS1344	4498	GCCCAATTTCGTCCGGCGTCTGAGATTGCACAG	9087	AQFRPASEIAQ	13676	FRPASEI	0.144534	-0.13935
SyS2335	4499	GCCCAAAAAAAAGACAGCGAACCCCTCGCACAG	9088	AQKKDSEPLAQ	13677	KKDSEPL	0.144431	0.01409
SyS2336	4500	GCCCAAAACGCCAGACCCCTCACCGCCGCACAG	9089	AQNARPLTAAQ	13678	NARPLTA	0.144383	-0.05797
SyS2338	4501	GCCCAAAAGGCGGCTAGGATGGAGACTGCACAG	9090	AQKAARMETAQ	13679	KAARMET	0.144286	-0.10236
SyS2340	4502	GCCCAACACGCCCAACGTCAGCAGCAGAGCACAG	9091	AQHANVSSRAQ	13680	HANVSSR	0.144111	-0.14672
SyS2341	4503	GCCCAAACCAGCACCACCCAAACCAGCGCACAG	9092	AQTSTTQTSAQ	13681	TSTTQTS	0.144008	-0.21448
SyS2342	4504	GCCCAAAGTGCGTTGTCGCTGAGTCCGGCACAG	9093	AQSALSLSPAQ	13682	SALSLSP	0.143867	-0.11439
SyS2343	4505	GCCCAAGCTAATGTTCAGATTCAGTCGGCACAG	9094	AQANVQIQSAQ	13683	ANVQIQS	0.143839	-0.19739
GS1346	4506	GCCCAAACCCCCAGCAGCAACAGCCTCGCACAG	9095	AQTPSSNSLAQ	13684	TPSSNSL	0.143816	-0.14429
SyS2345	4507	GCCCAAACGATGACGGGGCCTGGTCATGCACAG	9096	AQTMTGPGHAQ	13685	TMTGPGH	0.143627	-0.14425
SyS2346	4508	GCCCAAATTACTGCTCAGATTACGAATGCACAG	9097	AQITAQITNAQ	13686	ITAQITN	0.143574	-0.22064
SyS2348	4509	GCCCAACTTCCTAATCCTTCGTCTCGGGCACAG	9098	AQLPNPSSRAQ	13687	LPNPSSR	0.143468	-0.19723
SyS2349	4510	GCCCAAAAGATGGGGACTATGACGCCTGCACAG	9099	AQKMGTMTPAQ	13688	KMGTMTP	0.143411	-0.08828
GS1347	4511	GCCCAATACACCAACGGCAGAATCAACGCACAG	9100	AQYTNGRINAQ	13689	YTNGRIN	0.143337	-0.13284
SyS2350	4512	GCCCAAGATGGGAGTAATGTGGTGAAGGCACAG	9101	AQDGSNVVKAQ	13690	DGSNVVK	0.143302	-0.21202
GS1348	4513	GCCCAACTCCCCCTCAGCATCCCCGCCGCACAG	9102	AQLPLSIPAAQ	13691	LPLSIPA	0.143269	-0.17481
GS1349	4514	GCCCAAGAAAGCAGACTCAGCAGCAGCGCACAG	9103	AQESRLSSSAQ	13692	ESRLSSS	0.143208	-0.16814
SyS2351	4515	GCCCAAATGAGTCCTTCTCGGGGTAATGCACAG	9104	AQMSPSRGNAQ	13693	MSPSRGN	0.143199	-0.13677
SyS2352	4516	GCCCAAAGCGTCCACGCCGCCAAACAAGCACAG	9105	AQSVHAAKQAQ	13694	SVHAAKQ	0.143145	-0.14647
SyS2353	4517	GCCCAAGCGTTTTCTAGTGGTACTTCGGCACAG	9106	AQAFSSGTSAQ	13695	AFSSGTS	0.143125	0.020339
GS1350	4518	GCCCAAACTGGGTGGTCTCCTTCGCCTGCACAG	9107	AQTGWSPSPAQ	13696	TGWSPSP	0.143107	-0.15478
SyS2354	4519	GCCCAAGCGTCGCATAGTGCGAGTGGTGCACAG	9108	AQASHSASGAQ	13697	ASHSASG	0.143021	-0.23012
GS1353	4520	GCCCAAGTCACCCCCAGAAGCCCCCTCGCACAG	9109	AQVTPRSPLAQ	13698	VTPRSPL	0.142958	-0.12807
GS1354	4521	GCCCAAACTGAGCGTGATACTAGTCGTGCACAG	9110	AQTERDTSRAQ	13699	TERDTSR	0.142958	-0.1159

FIG. 33 (Continued)

SyS2355	4522	GCCCAATACACCCTCACCGGCACCACCGCACAG	9111	AQYTLTGTTAQ	13700	YTLTGTT	0.142869	-0.18527
SyS2356	4523	GCCCAAGACCTCAGAGTCAGCAGAGACGCACAG	9112	AQDLRVSRDAQ	13701	DLRVSRD	0.142848	-0.13071
SyS2357	4524	GCCCAACTTATTGCGTCGCATACGGCGGCACAG	9113	AQLIASHTAAQ	13702	LIASHTA	0.142848	-0.13071
SyS2358	4525	GCCCAACAGCGTTCTGAGAATTCGCATGCACAG	9114	AQQRSENSHAQ	13703	QRSENSH	0.142835	-0.08424
GS1355	4526	GCCCAAAGTGCGAGTAATCAGACTTATGCACAG	9115	AQSASNQTYAQ	13704	SASNQTY	0.142747	-0.17005
SyS2360	4527	GCCCAATTGGAGAAGGTGCTGCAGCCGGCACAG	9116	AQLEKVLQPAQ	13705	LEKVLQP	0.142579	-0.23296
SyS2361	4528	GCCCAAAATAGTGGTCCGTTGGTGATTGCACAG	9117	AQNSGPLVIAQ	13706	NSGPLVI	0.142353	-0.17829
SyS2362	4529	GCCCAAGGCACCATCCACAGCCCCGTCGCACAG	9118	AQGTIHSPVAQ	13707	GTIHSPV	0.142285	-0.23376
SyS2363	4530	GCCCAAAACAAAAACGGCGAAGTCCTCGCACAG	9119	AQNKNGEVLAQ	13708	NKNGEVL	0.142243	-0.13686
SyS2364	4531	GCCCAACCCATGAACGAAAGAGAAAGAGCACAG	9120	AQPMNERERAQ	13709	PMNERER	0.1422	-0.1986
SyS2366	4532	GCCCAAGGCAGCAACAACCTCCACCCCGCACAG	9121	AQGSNNLHPAQ	13710	GSNNLHP	0.141901	-0.14768
SyS2367	4533	GCCCAAATGAGCCTCCACGCCAAAAGCGCACAG	9122	AQMSLHAKSAQ	13711	MSLHAKS	0.141901	-0.18284
SyS2368	4534	GCCCAACAAGAAAAAGCCCTCGCCAGAGCACAG	9123	AQQEKALARAQ	13712	QEKALAR	0.141841	-0.08342
SP45	4535	GCCCAAGATCGTAGTACGCATGCTAAGGCACAG	9124	AQDRSTHAKAQ	13713	DRSTHAK	0.141804	-0.05361
SyS2369	4536	GCCCAAATTGTGAGGGGTGATACGTCTGCACAG	9125	AQIVRGDTSAQ	13714	IVRGDTS	0.141804	-0.2305
GS1359	4537	GCCCAAAGCAGCGGCGGCATGAACGAAGCACAG	9126	AQSSGGMNEAQ	13715	SSGGMNE	0.141777	-0.17386
SyS2370	4538	GCCCAAAAGTTGCATGCTGTTGAGGCTGCACAG	9127	AQKLHAVEAAQ	13716	KLHAVEA	0.141757	-0.19254
SyS2371	4539	GCCCAAATGTTCGCCGAAGGCACCGTCGCACAG	9128	AQMFAEGTVAQ	13717	MFAEGTV	0.14166	-0.18984
GS1360	4540	GCCCAAACCCTCGGCAGAGTCCCCCAAGCACAG	9129	AQTLGRVPQAQ	13718	TLGRVPQ	0.141609	-0.12235
GS1361	4541	GCCCAACTCCTCGGCAACAAAGACAAAGCACAG	9130	AQLLGNKDKAQ	13719	LLGNKDK	0.141569	-0.13971
GS1362	4542	GCCCAAAGAGTCAACACCAGCACCGACGCACAG	9131	AQRVNTSTDAQ	13720	RVNTSTD	0.141559	0.158617
SyS2372	4543	GCCCAACCCCAAGGCGTCAGCCCCGCCGCACAG	9132	AQPQGVSPAAQ	13721	PQGVSPA	0.14153	-0.18121
SyS2373	4544	GCCCAAGGCGCCGTCCTCAGCAAAGCCGCACAG	9133	AQGAVLSKAAQ	13722	GAVLSKA	0.14147	-0.14056
SyS2374	4545	GCCCAACTCGGCCACGCCGCCACCAGCGCACAG	9134	AQLGHAATSAQ	13723	LGHAATS	0.141412	-0.21194
SyS2375	4546	GCCCAAAGCGGCTTCAGCAGCACCGCCGCACAG	9135	AQSGFSSTAAQ	13724	SGFSSTA	0.141288	-0.12331
SyS2376	4547	GCCCAATTGGTGAATCAGCCTCAGTCGGCACAG	9136	AQLVNQPQSAQ	13725	LVNQPQS	0.141288	-0.12331
GS1366	4548	GCCCAAGGTCGTGCGGAGGTGGGGATTGCACAG	9137	AQGRAEVGIAQ	13726	GRAEVGI	0.141255	-0.16932
GS1369	4549	GCCCAAGTCCTCGCCACCAAAAACAGCGCACAG	9138	AQVLATKNSAQ	13727	VLATKNS	0.140992	-0.15764
SyS2378	4550	GCCCAACAGGCTCATGCGTTTGCGGATGCACAG	9139	AQQAHAFADAQ	13728	QAHAFAD	0.140963	-0.20588
SyS2379	4551	GCCCAAAACCTCGACACCGTCAAAACCGCACAG	9140	AQNLDTVKTAQ	13729	NLDTVKT	0.140932	-0.21941
SyS2380	4552	GCCCAACGTCCGCAGACTCTGCCGAATGCACAG	9141	AQRPQTLPNAQ	13730	RPQTLPN	0.140903	-0.17013
SyS2381	4553	GCCCAAAACCCCAGAAACAGCCCCACCGCACAG	9142	AQNPRNSPTAQ	13731	NPRNSPT	0.140813	-0.1392

FIG. 33 (Continued)

SyS2382	4554	GCCCAACATGTGCAGATGGATGCGGATGCACAG	9143	AQHVQMDADAQ	13732	HVQMDAD	0.140761	-0.1071
GS1371	4555	GCCCAAACTTATCGGACTGAGCCGGTGGCACAG	9144	AQTYRTEPVAQ	13733	TYRTEPV	0.14075	-0.18099
SyS2383	4556	GCCCAACCCGGCCTCGTCAACATGAGCGCACAG	9145	AQPGLVNMSAQ	13734	PGLVNMS	0.140733	-0.21557
SyS2384	4557	GCCCAAAGCCTCAGCCAAGGCCCCGCCGCACAG	9146	AQSLSQGPAAQ	13735	SLSQGPA	0.14057	-0.10768
SyS2385	4558	GCCCAACTGGGTGCTTCTGGTTATACGGCACAG	9147	AQLGASGYTAQ	13736	LGASGYT	0.14047	-0.22527
SyS2386	4559	GCCCAAAGCGCCGTCACCACCATGCCCGCACAG	9148	AQSAVTTMPAQ	13737	SAVTTMP	0.14044	-0.23419
GP186	4560	GCCCAAAAGGTGAATGCTGAGCTTCTTGCACAG	9149	AQKVNAELLAQ	13738	KVNAELL	0.140309	-0.07287
SyS2387	4561	GCCCAACCGTTTACGCCTAAGTTGAGTGCACAG	9150	AQPFTPKLSAQ	13739	PFTPKLS	0.140302	-0.20951
GS1372	4562	GCCCAAATGAGAAGCACCAACGCCAGCGCACAG	9151	AQMRSTNASAQ	13740	MRSTNAS	0.140251	-0.14868
SyS2388	4563	GCCCAAGTGATGTATGCGCGTGGGGATGCACAG	9152	AQVMYARGDAQ	13741	VMYARGD	0.140081	-0.11698
GS1373	4564	GCCCAACGGGTTGGTAGTACGATGCAGGCACAG	9153	AQRVGSTMQAQ	13742	RVGSTMQ	0.140075	-0.16146
SP47	4565	GCCCAATTGACGGTGGCGGTTGAGACTGCACAG	9154	AQLTVAVETAQ	13743	LTVAVET	0.139972	-0.05361
SyS2390	4566	GCCCAATGGACTAATTCTGGTAGTTCTGCACAG	9155	AQWTNSGSSAQ	13744	WTNSGSS	0.139811	-0.18769
GS1374	4567	GCCCAACACGCCATGAGAGGCACCGGCGCACAG	9156	AQHAMRGTGAQ	13745	HAMRGTG	0.139811	-0.16842
SyS2391	4568	GCCCAACACCAAGACGTCAGAGGCAGCGCACAG	9157	AQHQDVRGSAQ	13746	HQDVRGS	0.139527	-0.18861
GS1375	4569	GCCCAAAGCTTCCAAAGAGAAATCCCCGCACAG	9158	AQSFQREIPAQ	13747	SFQREIP	0.13934	-0.09891
GS1377	4570	GCCCAACTCCAAAGAGCCGCCCTCAACGCACAG	9159	AQLQRAALNAQ	13748	LQRAALN	0.1391	-0.16528
SyS2392	4571	GCCCAAAGCGACGCCACCATCAGACCCGCACAG	9160	AQSDATIRPAQ	13749	SDATIRP	0.139008	0.01549
GS1378	4572	GCCCAACAAATGAGCACCGGCAGAGTCGCACAG	9161	AQQMSTGRVAQ	13750	QMSTGRV	0.13898	-0.10908
GS1379	4573	GCCCAAAGAAGCACCCAAGCCATCCCCGCACAG	9162	AQRSTQAIPAQ	13751	RSTQAIP	0.138749	-0.15766
SyS2395	4574	GCCCAACAAATCAGAGACGCCAACGCCGCACAG	9163	AQQIRDANAAQ	13752	QIRDANA	0.138593	-0.14056
GS1382	4575	GCCCAACTCCACACCAGCAACGCCTACGCACAG	9164	AQLHTSNAYAQ	13753	LHTSNAY	0.138339	-0.18368
SS160	4576	GCCCAATCTTCTGGGCTGGGGACGCCTGCACAG	9165	AQSSGLGTPAQ	13754	SSGLGTP	0.138099	-0.36216
SyS2396	4577	GCCCAAGACCACACAAACCCGTCAGAGACGCACAG	9166	AQDHKPVRDAQ	13755	DHKPVRD	0.138062	-0.16708
GS1383	4578	GCCCAAATGAAACTCGTCAGCGTCGGCGCACAG	9167	AQMKLVSVGAQ	13756	MKLVSVG	0.138012	-0.12152
SyS2397	4579	GCCCAAGGTGAGCAGAGTCTTAAGGCGGCACAG	9168	AQGEQSLKAAQ	13757	GEQSLKA	0.137822	-0.16102
GS1385	4580	GCCCAAATGACCAGCGGCACCAACGGCGCACAG	9169	AQMTSGTNGAQ	13758	MTSGTNG	0.137741	-0.16304
SyS2398	4581	GCCCAACATGCGGCTAAGGGTGTTGTTGCACAG	9170	AQHAAKGVVAQ	13759	HAAKGVV	0.137688	-0.1392
SyS2401	4582	GCCCAAAGCAGCAGACAAAACGAACCCGCACAG	9171	AQSSRQNEPAQ	13760	SSRQNEP	0.137659	-0.23012
SyS2402	4583	GCCCAAGCCCTCATCAACAGACCCAACGCACAG	9172	AQALINRPNAQ	13761	ALINRPN	0.137501	-0.08183
SyS2403	4584	GCCCAATTGAGGTCTTCTATGGCGTCTGCACAG	9173	AQLRSSMASAQ	13762	LRSSMAS	0.137488	-0.17072
SyS2404	4585	GCCCAAAATAATGAGTATTCGAAGCTGGCACAG	9174	AQNNEYSKLAQ	13763	NNEYSKL	0.137304	-0.13033

FIG. 33 (Continued)

GS1386	4586	GCCCAAACTGGGCGTTTGAATGGGGAGGCACAG	9175	AQTGRLNGEAQ	13764	TGRLNGE	0.137105	-0.15001
GS1387	4587	GCCCAAACCAACAGCCACGCCGTCAGAGCACAG	9176	AQTNSHAVRAQ	13765	TNSHAVR	0.137064	-0.10066
SyS2406	4588	GCCCAAATCGTCACCAACCACAGCCACGCACAG	9177	AQIVTNHSHAQ	13766	IVTNHSH	0.136985	0.018624
GS1388	4589	GCCCAAGCCCTCACCAGAGACATCACCGCACAG	9178	AQALTRDITAQ	13767	ALTRDIT	0.136966	-0.10929
SyS2407	4590	GCCCAAGGCATCGCCAACCAAGGCGTCGCACAG	9179	AQGIANQGVAQ	13768	GIANQGV	0.136871	-0.02727
GP188	4591	GCCCAAAATACTGTGCGTTCTCAGCAGGCACAG	9180	AQNTVRSQQAQ	13769	NTVRSQQ	0.136631	-0.07079
SyS2409	4592	GCCCAAATGGAGAATTCGAATAAGGCTGCACAG	9181	AQMENSNKAAQ	13770	MENSNKA	0.136602	-0.21078
SyS2410	4593	GCCCAAGGTACGGTTAGGGTGCAGGCTGCACAG	9182	AQGTVRVQAAQ	13771	GTVRVQA	0.136485	-0.00948
SyS2411	4594	GCCCAAACCACCAGCCACCTCATCGACGCACAG	9183	AQTTSHLIDAQ	13772	TTSHLID	0.136485	-0.16223
GS1389	4595	GCCCAAGGTACGCAGGCGCATCAGGGTGCACAG	9184	AQGTQAHQGAQ	13773	GTQAHQG	0.13647	-0.00419
GS1390	4596	GCCCAAAAAATGAGCGCCAGCAGCGTCGCACAG	9185	AQKMSASSVAQ	13774	KMSASSV	0.136227	-0.15586
SyS2414	4597	GCCCAAAGCCTCAAAGTCAACCCCGGCGCACAG	9186	AQSLKVNPGAQ	13775	SLKVNPG	0.136211	-0.22164
GP189	4598	GCCCAATCGACTGGGACGTCTACTCTTGCACAG	9187	AQSTGTSTLAQ	13776	STGTSTL	0.136041	0.207438
SyS2415	4599	GCCCAAGTTTTGACGAATCGTGAGCAGGCACAG	9188	AQVLTNREQAQ	13777	VLTNREQ	0.135897	-0.05665
SyS2416	4600	GCCCAACTCGACGTCAGCAGAACCCTCGCACAG	9189	AQLDVSRTLAQ	13778	LDVSRTL	0.135826	-0.18769
SyS2417	4601	GCCCAATCGTTTGGGACTGAGAGTCGTGCACAG	9190	AQSFGTESRAQ	13779	SFGTESR	0.135821	0.273431
SyS2418	4602	GCCCAACAGCTTGCGAAGGGGAATTATGCACAG	9191	AQQLAKGNYAQ	13780	QLAKGNY	0.135676	-0.22557
SyS2419	4603	GCCCAAGCCAAAAACGACCCCAGAGCCGCACAG	9192	AQAKNDPRAAQ	13781	AKNDPRA	0.135675	0.015165
SyS2420	4604	GCCCAACTCACCCAAGTCGGCGGCACCGCACAG	9193	AQLTQVGGTAQ	13782	LTQVGGT	0.135637	-0.18163
SyS2421	4605	GCCCAAAAGCAGAATACTACTTCTCTGGCACAG	9194	AQKQNTTSLAQ	13783	KQNTTSL	0.135601	-0.23133
SyS2423	4606	GCCCAACTTTCGACTAGGGCTGAGGATGCACAG	9195	AQLSTRAEDAQ	13784	LSTRAED	0.135448	-0.23419
GS1394	4607	GCCCAAACCGTCCCCAACATCCCCATGGCACAG	9196	AQTVPNIPMAQ	13785	TVPNIPM	0.135363	-0.15317
GS1395	4608	GCCCAAAATTCGTTGTCTAAGCTGTCGGCACAG	9197	AQNSLSKLSAQ	13786	NSLSKLS	0.13513	-0.00256
SyS2424	4609	GCCCAAATGAATGAGCATCAGATGAAGGCACAG	9198	AQMNEHQMKAQ	13787	MNEHQMK	0.135017	-0.20339
GS1396	4610	GCCCAAGACGTCAAAGGCCACCAAAGCGCACAG	9199	AQDVKGHQSAQ	13788	DVKGHQS	0.135013	-0.096
SyS2427	4611	GCCCAAGACGTCAGCCTCCAAAAAGACGCACAG	9200	AQDVSLQKDAQ	13789	DVSLQKD	0.134944	-0.11931
GS1397	4612	GCCCAAACCAGACCCAGCGGCACCTACGCACAG	9201	AQTRPSGTYAQ	13790	TRPSGTY	0.134868	-0.16932
SyS2429	4613	GCCCAAGTTAAGGGGCCGGATTCTCTTGCACAG	9202	AQVKGPDSLAQ	13791	VKGPDSL	0.134815	-0.1792
SyS2430	4614	GCCCAAAACCACAGCAGCTACGAACTCGCACAG	9203	AQNHSSYELAQ	13792	NHSSYEL	0.13473	-0.14526
SyS2431	4615	GCCCAAACCGTCAGAACCCCCCTCATCGCACAG	9204	AQTVRTPLIAQ	13793	TVRTPLI	0.134668	-0.23497
SyS2432	4616	GCCCAAGCCAGCATCGACAGCCAACACGCACAG	9205	AQASIDSQHAQ	13794	ASIDSQH	0.134524	-0.20093
GS1401	4617	GCCCAAGATCAGAAGAATTCTGGGCATGCACAG	9206	AQDQKNSGHAQ	13795	DQKNSGH	0.134505	-0.18054

FIG. 33 (Continued)

SyS2434	4618	GCCCAACTCGACACCAACAACAAAGCCGCACAG	9207	AQLDTNNKAAQ	13796	LDTNNKA	0.134292	0.171043
GP190	4619	GCCCAAGCGAGTGCTCATGCGCAGGTTGCACAG	9208	AQASAHAQVAQ	13797	ASAHAQV	0.134161	0.132411
GS1403	4620	GCCCAAGACAGCGGCAAACACAACGACGCACAG	9209	AQDSGKHNDAQ	13798	DSGKHND	0.134104	-0.17919
GS1404	4621	GCCCAACTTAATCGGAATAGTGGTATGGCACAG	9210	AQLNRNSGMAQ	13799	LNRNSGM	0.134006	-0.08579
SyS2436	4622	GCCCAACCCACCATGCTCCCCGACAAAGCACAG	9211	AQPTMLPDKAQ	13800	PTMLPDK	0.133981	-0.21818
GS1406	4623	GCCCAAAGCACCCAAGTCAGCAACTACGCACAG	9212	AQSTQVSNYAQ	13801	STQVSNY	0.133756	-0.10556
SyS2439	4624	GCCCAATCTAATCAGACGCTGATGAGTGCACAG	9213	AQSNQTLMSAQ	13802	SNQTLMS	0.133656	-0.2268
GS1407	4625	GCCCAAAGAAACCCCGGCAGCACCAGCGCACAG	9214	AQRNPGSTSAQ	13803	RNPGSTS	0.133603	-0.05879
GS1409	4626	GCCCAACGTATGGCTCAGGGTTATAGTGCACAG	9215	AQRMAQGYSAQ	13804	RMAQGYS	0.133569	-0.1747
SyS2441	4627	GCCCAACAGGTTATGCGTCAGAGTAGTGCACAG	9216	AQQVMRQSSAQ	13805	QVMRQSS	0.133377	-0.22649
SyS2442	4628	GCCCAAAAGAATACGACGGTTAGTGATGCACAG	9217	AQKNTTVSDAQ	13806	KNTTVSD	0.133377	-0.22649
SyS2443	4629	GCCCAAACCGGCAAAACCGCCAGAGACGCACAG	9218	AQTGKTARDAQ	13807	TGKTARD	0.133287	-0.17382
SyS2444	4630	GCCCAAATCCTCAGAACCCTCACCGAAGCACAG	9219	AQILRTLTEAQ	13808	ILRTLTE	0.133244	-0.12829
GS1411	4631	GCCCAAAGACTCGACAACGCCGGCATGGCACAG	9220	AQRLDNAGMAQ	13809	RLDNAGM	0.133189	-0.08971
SyS2445	4632	GCCCAAAGTGGTACTGGTAGGCAGCAGGCACAG	9221	AQSGTGRQQAQ	13810	SGTGRQQ	0.133033	-0.1101
SyS2447	4633	GCCCAACTCGGCAAAGACACCTTCAGCGCACAG	9222	AQLGKDTFSAQ	13811	LGKDTFS	0.132869	-0.1242
GS1413	4634	GCCCAACGGTATGATGGGTCTGTGGCTGCACAG	9223	AQRYDGSVAAQ	13812	RYDGSVA	0.132847	-0.13504
SyS2448	4635	GCCCAAGCCCACTACCCCGCCAGCACCGCACAG	9224	AQAHYPASTAQ	13813	AHYPAST	0.132836	-0.14405
SyS2449	4636	GCCCAAAAAAGCAACGGCAGCCCCCCTCGCACAG	9225	AQKSNGSPLAQ	13814	KSNGSPL	0.132749	-0.09137
SyS2450	4637	GCCCAAAGAGACCTCGTCCTCACCAAAGCACAG	9226	AQRDLVLTKAQ	13815	RDLVLTK	0.132711	-0.13986
SyS2451	4638	GCCCAAACCAGCAACCCCGGCAACATGGCACAG	9227	AQTSNPGNMAQ	13816	TSNPGNM	0.132642	-0.18405
GS1414	4639	GCCCAATTGCCGAGGCCGAGTAATACGGCACAG	9228	AQLPRPSNTAQ	13817	LPRPSNT	0.132631	-0.16573
SyS2452	4640	GCCCAAACCGGCGGCGGCAGCTTCAGCGCACAG	9229	AQTGGGSFSAQ	13818	TGGGSFS	0.132596	0.004539
SyS2454	4641	GCCCAATACCCCAACAAAGAACTCAGCGCACAG	9230	AQYPNKELSAQ	13819	YPNKELS	0.132195	-0.06134
SyS2456	4642	GCCCAAACGATGGTGCATCAGGAGTCTGCACAG	9231	AQTMVHQESAQ	13820	TMVHQES	0.132057	-0.01475
SyS2457	4643	GCCCAAGTTAATAGTAATAATTCGATGGCACAG	9232	AQVNSNNSMAQ	13821	VNSNNSM	0.132035	-0.11468
GS1416	4644	GCCCAAAACGGCGTCCACGTCACCCCCGCACAG	9233	AQNGVHVTPAQ	13822	NGVHVTP	0.132015	-0.04532
SyS2458	4645	GCCCAAGCCAAATACCTCAACAGCAACGCACAG	9234	AQAKYLNSNAQ	13823	AKYLNSN	0.131997	-0.13316
SyS2460	4646	GCCCAAGGTATGACGAAGAATGGTGGGGCACAG	9235	AQGMTKNGGAQ	13824	GMTKNGG	0.131765	0.019619
SyS2461	4647	GCCCAACGGGCGCGTGATGAGGGTATGGCACAG	9236	AQRARDEGMAQ	13825	RARDEGM	0.131684	-0.09036
GS1418	4648	GCCCAAGTCCCCAGCCCCGGCGCCACCGCACAG	9237	AQVPSPGATAQ	13826	VPSPGAT	0.131628	-0.18188
GS1419	4649	GCCCAAAAAACCCAACTCGGCCAAATGGCACAG	9238	AQKTQLGQMAQ	13827	KTQLGQM	0.131628	-0.18188

FIG. 33 (Continued)

SyS2462	4650	GCCCAATCTACTTCGACGATTCAGCCGGCACAG	9239	AQSTSTIQPAQ	13828	STSTIQP	0.131508	-0.12707
SyS2463	4651	GCCCAACGTAAGGAGAATGCTAGTTATGCACAG	9240	AQRKENASYAQ	13829	RKENASY	0.131186	-0.19739
SyS2464	4652	GCCCAACTGACGAATCATGGGAATGTTGCACAG	9241	AQLTNHGNVAQ	13830	LTNHGNV	0.131105	-0.11468
SyS2465	4653	GCCCAACTCGACAACGTCCACAGCCACGCACAG	9242	AQLDNVHSHAQ	13831	LDNVHSH	0.131105	-0.20339
SyS2466	4654	GCCCAACCCACCATGGCCGTCACCCCCGCACAG	9243	AQPTMAVTPAQ	13832	PTMAVTP	0.131105	-0.22557
SyS2467	4655	GCCCAAAAGCCTGAGCGTACTGAGGCGGCACAG	9244	AQKPERTEAAQ	13833	KPERTEA	0.131079	-0.17314
GS1420	4656	GCCCAAACCGGCGACAGAAAAAGCGGCGCACAG	9245	AQTGDRKSGAQ	13834	TGDRKSG	0.131063	-0.16623
GS1421	4657	GCCCAAGCTAAGCATACTTCGTTTCCTGCACAG	9246	AQAKHTSFPAQ	13835	AKHTSFP	0.131036	-0.171
GS1422	4658	GCCCAAGGGTTGGTTGCGTCGTTGGGGGCACAG	9247	AQGLVASLGAQ	13836	GLVASLG	0.131036	-0.171
SyS2468	4659	GCCCAATCTGTTCCTAGGTCGGAGTTGGCACAG	9248	AQSVPRSELAQ	13837	SVPRSEL	0.130804	-0.11824
GS1425	4660	GCCCAAGCTGAGAGGATTGGTATGGGTGCACAG	9249	AQAERIGMGAQ	13838	AERIGMG	0.130715	-0.04864
SyP69	4661	GCCCAATCTCTGGTTCGGCAGTCTGATGCACAG	9250	AQSLVRQSDAQ	13839	SLVRQSD	0.130711	-0.04411
SyS2470	4662	GCCCAACACGTCAAAGCCAACCCCATCGCACAG	9251	AQHVKANPIAQ	13840	HVKANPI	0.130681	-0.20093
SyS2473	4663	GCCCAAGTCGTCGACACCCTCAAAAACGCACAG	9252	AQVVDTLKNAQ	13841	VVDTLKN	0.130632	-0.11957
SyS2474	4664	GCCCAACAGATTCCTTATAATTCGTCGGCACAG	9253	AQQIPYNSSAQ	13842	QIPYNSS	0.130617	0.06558
SyS2475	4665	GCCCAAGCTGATCATTCTATGCATGTTGCACAG	9254	AQADHSMHVAQ	13843	ADHSMHV	0.130612	-0.2231
SyS2476	4666	GCCCAAAACCACGTCACCGCCCAAGCCGCACAG	9255	AQNHVTAQAAQ	13844	NHVTAQA	0.130454	-0.0399
GS1429	4667	GCCCAAACCAACTTCACCAAAAGCGGCGCACAG	9256	AQTNFTKSGAQ	13845	TNFTKSG	0.130388	0.51224
SyS2477	4668	GCCCAATATGGTCATTCGATGACTAATGCACAG	9257	AQYGHSMTNAQ	13846	YGHSMTN	0.130368	-0.17678
SyS2479	4669	GCCCAAATGAGACCCGACCTCAAAACCGCACAG	9258	AQMRPDLKTAQ	13847	MRPDLKT	0.130368	-0.23133
SyS2480	4670	GCCCAAGGCCCCGGCACCAGCTTCAAAGCACAG	9259	AQGPGTSFKAQ	13848	GPGTSFK	0.130368	-0.23133
SyS2481	4671	GCCCAAAGTTCTACGACTCCTGGGCTTGCACAG	9260	AQSSTTPGLAQ	13849	SSTTPGL	0.130295	-0.09714
SS170	4672	GCCCAATCGGTGAAGGCTAATCCTACTGCACAG	9261	AQSVKANPTAQ	13850	SVKANPT	0.130019	-0.37951
GS1430	4673	GCCCAAACCCCCACCGTCTTCACCCCCGCACAG	9262	AQTPTVFTPAQ	13851	TPTVFTP	0.129999	-0.15574
GP193	4674	GCCCAAATGCTGCCTAGTCCTGGGTCGGCACAG	9263	AQMLPSPGSAQ	13852	MLPSPGS	0.129923	-0.06982
GS1432	4675	GCCCAAAACTTCGACTACGCCAAACCCGCACAG	9264	AQNFDYAKPAQ	13853	NFDYAKP	0.129793	-0.15945
SyS2482	4676	GCCCAAACCCTCAACACCAGCCCCATGGCACAG	9265	AQTLNTSPMAQ	13854	TLNTSPM	0.129754	-0.11431
SyS2483	4677	GCCCAAACCAACAGCCCCAAAAGCACCGCACAG	9266	AQTNSPKSTAQ	13855	TNSPKST	0.129681	-0.17136
SyS2484	4678	GCCCAAGTCACCCCCGGCAGATACAGCGCACAG	9267	AQVTPGRYSAQ	13856	VTPGRYS	0.129681	-0.17136
SyS2485	4679	GCCCAAACCAGAGTCAGCAACCTCGACGCACAG	9268	AQTRVSNLDAQ	13857	TRVSNLD	0.129667	0.015982
GS1433	4680	GCCCAAAGTCATGGTCCTGATAGGACGGCACAG	9269	AQSHGPDRTAQ	13858	SHGPDRT	0.129608	-0.18278
SyS2488	4681	GCCCAAAATATTCATACGGCTACGACTGCACAG	9270	AQNIHTATTAQ	13859	NIHTATT	0.12948	-0.21072

FIG. 33 (Continued)

SyS2490	4682	GCCCAATTGCTTCCGCAGACTACGCTTGCACAG	9271	AQLLPQTTLAQ	13860	LLPQTTL	0.129383	-0.05215
SyS2491	4683	GCCCAACGTACTAATGATACTTCGGCGGCACAG	9272	AQRTNDTSAAQ	13861	RTNDTSA	0.12914	-0.15534
GS1435	4684	GCCCAAGAAAGAAACGGCAGCCACGAAGCACAG	9273	AQERNGSHEAQ	13862	ERNGSHE	0.129106	-0.14524
GS1436	4685	GCCCAAAACACCAGAGAAGCCTTCATCGCACAG	9274	AQNTREAFIAQ	13863	NTREAFI	0.129068	-0.15676
GS1437	4686	GCCCAAGTCGGCCAATACGCCAGCCCCGCACAG	9275	AQVGQYASPAQ	13864	VGQYASP	0.129006	0.012421
GS1438	4687	GCCCAAGTCGCCGAAACCGGCAGAACCGCACAG	9276	AQVAETGRTAQ	13865	VAETGRT	0.128986	-0.17672
GS1439	4688	GCCCAAATGAGCGCCGGCAGCAACAGCGCACAG	9277	AQMSAGSNSAQ	13866	MSAGSNS	0.128951	-0.17381
SyS2492	4689	GCCCAACTCAGCCCCAAAAACGCCCAAGCACAG	9278	AQLSPKNAQAQ	13867	LSPKNAQ	0.128916	-0.17799
SyS2497	4690	GCCCAAAGCGGCACCAGCCAACTCCCCGCACAG	9279	AQSGTSQLPAQ	13868	SGTSQLP	0.128594	-0.19969
SS171	4691	GCCCAAAGACTCCAAGACAAACCCCAAGCACAG	9280	AQRLQDKPQAQ	13869	RLQDKPQ	0.12854	-0.41153
SyS2498	4692	GCCCAAAACGTCCCCAGAAGCAGCGTCGCACAG	9281	AQNVPRSSVAQ	13870	NVPRSSV	0.128415	-0.15738
SyS2500	4693	GCCCAAGCCCTCGGCAGCCCCAGACCCGCACAG	9282	AQALGSPRPAQ	13871	ALGSPRP	0.128407	-0.13686
SyS2501	4694	GCCCAAGCGAAGGAGCCTATGAGTGCGGCACAG	9283	AQAKEPMSAAQ	13872	AKEPMSA	0.128223	-0.19723
GS1441	4695	GCCCAAGCCGTCAGCGGCGCCGCCCACGCACAG	9284	AQAVSGAAHAQ	13873	AVSGAAH	0.128127	-0.15781
SyS2502	4696	GCCCAATACAACACAAAAGCGCCGCCGCACAG	9285	AQYNNKSAAAQ	13874	YNNKSAA	0.12811	-0.15904
SyS2503	4697	GCCCAACAAGTCAGCGTCAGAAAACCTCGCACAG	9286	AQQVSVRNLAQ	13875	QVSVRNL	0.12807	-0.18769
SyS2504	4698	GCCCAAAAGGGTACTCATCCTCCGGCTGCACAG	9287	AQKGTHPPAAQ	13876	KGTHPPA	0.12807	-0.18769
GS1442	4699	GCCCAACAGTATCCTAATAGTAAGGTTGCACAG	9288	AQQYPNSKVAQ	13877	QYPNSKV	0.128026	-0.16623
SyS2505	4700	GCCCAACATAATGCTTCGAATTCTGGGGCACAG	9289	AQHNASNSGAQ	13878	HNASNSG	0.127942	-0.14283
SyS2507	4701	GCCCAAGAACTCAACCCCAAATTCATCGCACAG	9290	AQELNPKFIAQ	13879	ELNPKFI	0.127896	-0.19981
SyS2508	4702	GCCCAATCGCGTGAGACTCCTGGGACTGCACAG	9291	AQSRETPGTAQ	13880	SRETPGT	0.127851	0.095109
SyS2509	4703	GCCCAAAATTTTAAGCCGCAGAATGAGGCACAG	9292	AQNFKPQNEAQ	13881	NFKPQNE	0.127738	-0.18121
SyS2510	4704	GCCCAAGCTATGACTTCGGGGTCGGCGGCACAG	9293	AQAMTSGSAAQ	13882	AMTSGSA	0.127637	-0.16708
GS1443	4705	GCCCAAAAGGATCCGAGGAGTACGTTGGCACAG	9294	AQKDPRSTLAQ	13883	KDPRSTL	0.127399	-0.16842
GS1444	4706	GCCCAAGACAGAGGCACCAGAACCGTCGCACAG	9295	AQDRGTRTVAQ	13884	DRGTRTV	0.127399	-0.16842
GS1445	4707	GCCCAAAGCCTCGCCAGAAACAACGTCGCACAG	9296	AQSLARNNVAQ	13885	SLARNNV	0.127397	-0.15097
SyS2511	4708	GCCCAAGCCATCAGATTCAACGAACCCGCACAG	9297	AQAIRFNEPAQ	13886	AIRFNEP	0.127317	-0.23012
SyS2512	4709	GCCCAACACAACACCACATCGCCACCCCCGCACAG	9298	AQQHHIATPAQ	13887	QHHIATP	0.127284	0.014485
GS1447	4710	GCCCAACAGATTTTGAGGGAGCCGGTGGCACAG	9299	AQQILREPVAQ	13888	QILREPV	0.127158	-0.17291
GS1448	4711	GCCCAAACTGTTGTTAATAAGCTTAGTGCACAG	9300	AQTVVNKLSAQ	13889	TVVNKLS	0.127158	-0.17291
SyS2513	4712	GCCCAAAGAGACAACACCACCAAATTCGCACAG	9301	AQRDNTTKFAQ	13890	RDNTTKF	0.127154	0.054334
SyS2515	4713	GCCCAAAGCCTCCTCAGCACCCTCGGCGCACAG	9302	AQSLLSTLGAQ	13891	SLLSTLG	0.127046	-0.22803

FIG. 33 (Continued)

SyS2516	4714	GCCCAAGGCCAAGTCCCCGTCACCAGAGCACAG	9303	AQGQVPVTRAQ	13892	GQVPVTR	0.126817	-0.1319
SyS2517	4715	GCCCAAATCCAAAACAGCCTCATGCCCGCACAG	9304	AQIQNSLMPAQ	13893	IQNSLMP	0.126654	-0.0084
GP194	4716	GCCCAACAGCATAATACGCAGAATACTGCACAG	9305	AQQHNTQNTAQ	13894	QHNTQNT	0.126648	-0.07218
SyS2518	4717	GCCCAAGTCGGCCCCACCATGACCCACGCACAG	9306	AQVGPTMTHAQ	13895	VGPTMTH	0.126491	-0.15781
GS1450	4718	GCCCAAACCAACGTCACCATGGCCAGAGCACAG	9307	AQTNVTMARAQ	13896	TNVTMAR	0.126427	-0.17481
GS1451	4719	GCCCAAAGCGCCCACTTCACCGGCACCGCACAG	9308	AQSAHFTGTAQ	13897	SAHFTGT	0.126427	-0.17481
GS1453	4720	GCCCAAAGATACAGCGTCAACGACAAAGCACAG	9309	AQRYSVNDKAQ	13898	RYSVNDK	0.126337	-0.17201
SyS2519	4721	GCCCAAGTCTACAAAAGCGCCGACCCCCGCACAG	9310	AQVYKSADPAQ	13899	VYKSADP	0.126276	-0.13556
SyS2521	4722	GCCCAAGTCCACACCGCCCTCCCCATGGCACAG	9311	AQVHTALPMAQ	13900	VHTALPM	0.126124	-0.17435
SyS2522	4723	GCCCAAACTATTAGTAGTGCTGGTATTGCACAG	9312	AQTISSAGIAQ	13901	TISSAGI	0.126033	-0.07473
GS1455	4724	GCCCAAAGGTTGCCTTCGACTCAGGCGGCACAG	9313	AQRLPSTQAAQ	13902	RLPSTQA	0.126016	-0.12848
SyS2523	4725	GCCCAAAGCCAAGAAAGAGCCATGAGCGCACAG	9314	AQSQERAMSAQ	13903	SQERAMS	0.125872	-0.20709
GS1456	4726	GCCCAAATGAATCAGCTTGCGAATCCTGCACAG	9315	AQMNQLANPAQ	13904	MNQLANP	0.125837	-0.12712
SyS2524	4727	GCCCAATTTGGGGCGACTAGTGGGCAGGCACAG	9316	AQFGATSGQAQ	13905	FGATSGQ	0.12559	-0.11323
SyS2525	4728	GCCCAAACGCTTCTTCGTTCTCCTGCTGCACAG	9317	AQTLLRSPAAQ	13906	TLLRSPA	0.125488	-0.14526
GS1457	4729	GCCCAACTTAGGTCGAATGTGTCGAATGCACAG	9318	AQLRSNVSNAQ	13907	LRSNVSN	0.125352	-0.12087
GS1458	4730	GCCCAAATCGCCAACAGCCAAGCCGCCGCACAG	9319	AQIANSQAAAQ	13908	IANSQAA	0.125352	-0.10113
TS177	4731	GCCCAATCTAATCGTATTGTGCCTGTTGCACAG	9320	AQSNRIVPVAQ	13909	SNRIVPV	0.125315	-0.25713
GP197	4732	GCCCAATCTCCGAATCCTTCTAATGCGGCACAG	9321	AQSPNPSNAAQ	13910	SPNPSNA	0.125295	-0.0703
SyS2526	4733	GCCCAAAAATGGGACAGCGCCAACGAAGCACAG	9322	AQKWDSANEAQ	13911	KWDSANE	0.125284	-0.10361
SyS2527	4734	GCCCAAGCTTCTCGTCAGGGTGAGGCTGCACAG	9323	AQASRQGEAAQ	13912	ASRQGEA	0.125259	-0.10404
SyS2528	4735	GCCCAAGTTCCTGGGAATAGTCCTCATGCACAG	9324	AQVPGNSPHAQ	13913	VPGNSPH	0.125198	-0.15738
SyS2529	4736	GCCCAAAGCGCCACCACCAACAGCGTCGCACAG	9325	AQSATTNSVAQ	13914	SATTNSV	0.125189	0.067512
SyS2530	4737	GCCCAACACATCGGCGCCAGACAAGTCGCACAG	9326	AQHIGARQVAQ	13915	HIGARQV	0.125155	-0.15904
GS1462	4738	GCCCAACTTACGGATCGTTCTCCTATGGCACAG	9327	AQLTDRSPMAQ	13916	LTDRSPM	0.125019	-0.13728
SyS2531	4739	GCCCAAAATCCGACGCAGGCTGTTTTGGCACAG	9328	AQNPTQAVLAQ	13917	NPTQAVL	0.124871	-0.21679
GS1464	4740	GCCCAAACCAAAAACGAAACCGGCACCGCACAG	9329	AQTKNETGTAQ	13918	TKNETGT	0.124832	-0.05823
SyS2533	4741	GCCCAACTCACCGCCACCCTCACCAGCGCACAG	9330	AQLTATLTSAQ	13919	LTATLTS	0.124607	-0.2268
SyS2535	4742	GCCCAATATAAGGCTAGTTATGCTGCGGCACAG	9331	AQYKASYAAAQ	13920	YKASYAA	0.124548	-0.07814
SyS2536	4743	GCCCAAACTCTTCCTGATAAGGTGTCGGCACAG	9332	AQTLPDKVSAQ	13921	TLPDKVS	0.124499	-0.18163
SyS2537	4744	GCCCAAAATAATCATATTCCTTTGGCTGCACAG	9333	AQNNHIPLAAQ	13922	NNHIPLA	0.12448	-0.10087
SyS2538	4745	GCCCAATCTAATCTGACGTCTAATCCTGCACAG	9334	AQSNLTSNPAQ	13923	SNLTSNP	0.124443	0.020734

FIG. 33 (Continued)

SS177	4746	GCCCAACAACAAAACGACAGAAACGCCGCACAG	9335	AQQQNDRNAAQ	13924	QQNDRNA	0.124316	-0.33917
SyS2540	4747	GCCCAAATGCTCAGCACCAACAGAAGCGCACAG	9336	AQMLSTNRSAQ	13925	MLSTNRS	0.124294	-0.18769
SyS2541	4748	GCCCAAATCACCAGCGCCACCCTCAGCGCACAG	9337	AQITSATLSAQ	13926	ITSATLS	0.124242	-0.22434
GS1465	4749	GCCCAAGTCGACGCCATGCAAAGACCCGCACAG	9338	AQVDAMQRPAQ	13927	VDAMQRP	0.124217	-0.16051
GS1466	4750	GCCCAAAGAGAAGCCAACTACGCCAGCGCACAG	9339	AQREANYASAQ	13928	REANYAS	0.124095	-0.18368
GS1467	4751	GCCCAACGTAGTAATAATGCTGATCTGGCACAG	9340	AQRSNNADLAQ	13929	RSNNADL	0.12408	-0.18054
SyS2542	4752	GCCCAAGGCCTCGACAAAATGGGCAGCGCACAG	9341	AQGLDKMGSAQ	13930	GLDKMGS	0.124074	-0.00826
GS1468	4753	GCCCAATTCACCACCAGCCACGCCCCCGCACAG	9342	AQFTTSHAPAQ	13931	FTTSHAP	0.123988	-0.13761
GS1469	4754	GCCCAAGACAAAAGCGTCAAATTCGCCGCACAG	9343	AQDKSVKFAAQ	13932	DKSVKFA	0.123988	-0.13761
SyS2544	4755	GCCCAACACGCCAAAAAAGAACTCCAAGCACAG	9344	AQHAKKELQAQ	13933	HAKKELQ	0.123802	-0.22042
SyS2546	4756	GCCCAAGTCGAAAGCAAAGGCGCCAGCGCACAG	9345	AQVESKGASAQ	13934	VESKGAS	0.123704	0.11358
GS1470	4757	GCCCAAAAAACCGCCCCCAGCATGGGCGCACAG	9346	AQKTAPSMGAQ	13935	KTAPSMG	0.123698	-0.14537
GS1471	4758	GCCCAAGGCCTCAGAACCGACAACAGAGCACAG	9347	AQGLRTDNRAQ	13936	GLRTDNR	0.123641	-0.1476
SyS2548	4759	GCCCAACGTATTGCGGGGAATAATCCTGCACAG	9348	AQRIAGNNPAQ	13937	RIAGNNP	0.123582	-0.1295
GS1472	4760	GCCCAAAAAGACCCCCACCAAGTCGTCGCACAG	9349	AQKDPHQVVAQ	13938	KDPHQVV	0.123524	-0.16241
SyS2549	4761	GCCCAAGAGCAGACTCCGCATAATTCGGCACAG	9350	AQEQTPHNSAQ	13939	EQTPHNS	0.123505	-0.22649
SyS2550	4762	GCCCAAGGGCTGGATAAGGGGAATTGGGCACAG	9351	AQGLDKGNWAQ	13940	GLDKGNW	0.12349	-0.08183
SyS2551	4763	GCCCAACCTTCGAATGGGAATTATTCGGCACAG	9352	AQPSNGNYSAQ	13941	PSNGNYS	0.123474	-0.17072
SyS2552	4764	GCCCAAGGCAGACCCGGCATCGGCAGCGCACAG	9353	AQGRPGIGSAQ	13942	GRPGIGS	0.123474	-0.17072
SyS2553	4765	GCCCAAAGGACGTCTCCTGGGGTGTCGGCACAG	9354	AQRTSPGVSAQ	13943	RTSPGVS	0.123431	-0.18737
SyS2554	4766	GCCCAAGTCAACGCCAGCCTCATCAGCGCACAG	9355	AQVNASLISAQ	13944	VNASLIS	0.123431	-0.18737
SyS2555	4767	GCCCAAAAAACCAGCACCAACCTCCAAGCACAG	9356	AQKTSTNLQAQ	13945	KTSTNLQ	0.1234	-0.13556
SyS2556	4768	GCCCAAATGGATATGAAGCAGAATATGGCACAG	9357	AQMDMKQNMAQ	13946	MDMKQNM	0.123199	-0.09592
SyS2557	4769	GCCCAAGATCTTAATGGGATTAATGTTGCACAG	9358	AQDLNGINVAQ	13947	DLNGINV	0.12317	-0.17988
GS1475	4770	GCCCAACGTACGCCTCCGAGTTTTGAGGCACAG	9359	AQRTPPSFEAQ	13948	RTPPSFE	0.122987	-0.12067
SyS2559	4771	GCCCAAGACTTCCACGACAGAAAAGGCGCACAG	9360	AQDFHDRKGAQ	13949	DFHDRKG	0.122909	-0.13314
GS1476	4772	GCCCAACTCCACACCCAAACCCAAACCGCACAG	9361	AQLHTQTQTAQ	13950	LHTQTQT	0.122656	-0.17381
SyS2561	4773	GCCCAACTCGGCGCCAGCAACAACGCCGCACAG	9362	AQLGASNNAAQ	13951	LGASNNA	0.122644	-0.09068
SyS2562	4774	GCCCAAATCGCCAGCGTCCCCAGAGACGCACAG	9363	AQIASVPRDAQ	13952	IASVPRD	0.122568	-0.22803
SyS2563	4775	GCCCAAAAAGCCAAAGACGTCGGCGACGCACAG	9364	AQKAKDVGDAQ	13953	KAKDVGD	0.122492	-0.14548
SyS2564	4776	GCCCAAAGCGCCTTCGCCGCCAAACAAGCACAG	9365	AQSAFAAKQAQ	13954	SAFAAKQ	0.122374	-0.11616
SyS2565	4777	GCCCAAGTCTACCAAGGCCAACACCTCGCACAG	9366	AQVYQGQHLAQ	13955	VYQGQHL	0.12237	-0.19353

FIG. 33 (Continued)

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SyS2567	4778	GCCCAATACCTCCCCGCCGCCAGCAGCGCACAG	9367	AQYLPAASSAQ	13956	YLPAASS	0.122028	-0.15738
SyS2568	4779	GCCCAAAGCCCCCAGCACCGTCATCAGCGCACAG	9368	AQSPSTVISAQ	13957	SPSTVIS	0.121889	-0.22164
SyS2569	4780	GCCCAAGGCACCAACAAACCCCCCCGACGCACAG	9369	AQGTNKPPDAQ	13958	GTNKPPD	0.121621	-0.22064
SyS2570	4781	GCCCAAGAAAGCACCGGCGCCATCAGAGCACAG	9370	AQESTGAIRAQ	13959	ESTGAIR	0.121621	-0.22064
SS180	4782	GCCCAACTCATGAACACCACCATCGCCGCACAG	9371	AQLMNTTIAAQ	13960	LMNTTIA	0.121608	-0.32745
GS1478	4783	GCCCAAATGGCGGGTGTTGCTCAGCCTGCACAG	9372	AQMAGVAQPAQ	13961	MAGVAQP	0.121335	-0.18637
SyS2573	4784	GCCCAACGGCCGGAGCTTAAGCGTGAGGCACAG	9373	AQRPELKREAQ	13962	RPELKRE	0.121162	-0.20466
SyS2574	4785	GCCCAAAAAGCCCAAGACACCCCCACCGCACAG	9374	AQKAQDTPTAQ	13963	KAQDTPT	0.121141	-0.07163
GS1480	4786	GCCCAAAGCACCAACCACAGCACCAGCGCACAG	9375	AQSTNHSTSAQ	13964	STNHSTS	0.120864	-0.17291
GS1481	4787	GCCCAATTCCCCAGAACCACCACCGACGCACAG	9376	AQFPRTTTDAQ	13965	FPRTTTD	0.120827	-0.11818
SyS2576	4788	GCCCAATCGCGTGCTCATAATTTGGATGCACAG	9377	AQSRAHNLDAQ	13966	SRAHNLD	0.120812	-0.23173
SyS2577	4789	GCCCAACGTACTATTCAGGAGGGGATTGCACAG	9378	AQRTIQEGIAQ	13967	RTIQEGI	0.120812	-0.23173
GS1482	4790	GCCCAAGGCGGCAAAAGCTTCGCCCAAGCACAG	9379	AQGGKSFAQAQ	13968	GGKSFAQ	0.120713	-0.18054
SyS2578	4791	GCCCAAGGCAGACCCAGCAGCACCCAAGCACAG	9380	AQGRPSSTQAQ	13969	GRPSSTQ	0.120696	-0.01043
SyS2579	4792	GCCCAAAACCCCCCTCAACACCAGCACCGCACAG	9381	AQNPLNTSTAQ	13970	NPLNTST	0.120592	-0.13772
GS1483	4793	GCCCAAGAAAACCTCAGCAACGGCAGAGCACAG	9382	AQENLSNGRAQ	13971	ENLSNGR	0.120537	-0.0855
GP199	4794	GCCCAAGAGAATACTATTCGGATGAGTGCACAG	9383	AQENTIRMSAQ	13972	ENTIRMS	0.12044	-0.07273
SyS2582	4795	GCCCAACCCCCCAGAAGCATGCCCATGGCACAG	9384	AQPPRSMPMAQ	13973	PPRSMPM	0.120421	-0.16466
SyS2583	4796	GCCCAACTCCTCAGCAGCAACCTCCCCGCACAG	9385	AQLLSSNLPAQ	13974	LLSSNLP	0.120362	-0.09427
SyS2586	4797	GCCCAAAGAGTCCAAAGCCTCAACGAAGCACAG	9386	AQRVQSLNEAQ	13975	RVQSLNE	0.120212	-0.06599
SyS2588	4798	GCCCAACCGAGGAGGGCGCAGGATGATGCACAG	9387	AQPRRAQDDAQ	13976	PRRAQDD	0.119774	-0.17678
SyS2589	4799	GCCCAACAAGGCAACGTCAACGTCGGCGCACAG	9388	AQQGNVNVGAQ	13977	QGNVNVG	0.11977	-0.05616
GS1484	4800	GCCCAAAGCGGCGAAACCCTCAGAGGCGCACAG	9389	AQSGETLRGAQ	13978	SGETLRG	0.119683	-0.05248
SyS2590	4801	GCCCAACACGTCAGCCACAACACCGACGCACAG	9390	AQHVSHNTDAQ	13979	HVSHNTD	0.119543	-0.20093
SyS2592	4802	GCCCAATTTGGTGGGGGGTCGCTGGTTGCACAG	9391	AQFGGGSLVAQ	13980	FGGGSLV	0.119216	-0.10883
SyS2593	4803	GCCCAACCCAGCCTCAGAAGCGAAGGCGCACAG	9392	AQPSLRSEGAQ	13981	PSLRSEG	0.119011	-0.00524
SS186	4804	GCCCAAGTGCGTAGTGAGAATGGTGTGGCACAG	9393	AQVRSENGVAQ	13982	VRSENGV	0.118723	-0.33991
SyS2594	4805	GCCCAAACCCTCAAAGTCACCGGCGACGCACAG	9394	AQTLKVTGDAQ	13983	TLKVTGD	0.118628	-0.14041
SyS2595	4806	GCCCAAGTCCCCAAAGTCTACCTCGACGCACAG	9395	AQVPKVYLDAQ	13984	VPKVYLD	0.118518	-0.16766
SyS2597	4807	GCCCAAACTAGTATGCGGAATACGGAGGCACAG	9396	AQTSMRNTEAQ	13985	TSMRNTE	0.118368	-0.09192
GS1486	4808	GCCCAAGGCTACAGCCACGGCAGCATGGCACAG	9397	AQGYSHGSMAQ	13986	GYSHGSM	0.118333	-0.05276
SyS2598	4809	GCCCAAGCCACCTTCCCCGAAAAACAAGCACAG	9398	AQATFPEKQAQ	13987	ATFPEKQ	0.118306	-0.18614

FIG. 33 (Continued)

SyS2599	4810	GCCCAAACCGGCCCCACCCACGGCACCGCACAG	9399	AQTGPTHGTAQ	13988	TGPTHGT	0.118306	-0.18614
GS1490	4811	GCCCAAACCAACGACACGCCCCCCGCACAG	9400	AQTNDRHAPAQ	13989	TNDRHAP	0.118185	-0.1451
SyS2600	4812	GCCCAAAGACACCTCGCCAGCGTCGACGCACAG	9401	AQRHLASVDAQ	13990	RHLASVD	0.118181	-0.22803
SyS2601	4813	GCCCAAAATATGATTCAGCCTAGTAATGCACAG	9402	AQNMIQPSNAQ	13991	NMIQPSN	0.118011	-0.22406
GS1492	4814	GCCCAAAACCTCAGCGGCAGCCCCCGCCGCACAG	9403	AQNLSGSPAAQ	13992	NLSGSPA	0.117908	-0.11652
SyS2602	4815	GCCCAACAAACCGTCGGCCCCCTCCCCGCACAG	9404	AQQTVGPLPAQ	13993	QTVGPLP	0.117854	-0.21557
SyS2604	4816	GCCCAAGTCGGCCACCTCAGCAGAGACGCACAG	9405	AQVGHLSRDAQ	13994	VGHLSRD	0.117641	-0.03829
SyS2605	4817	GCCCAACAAAACTTCAACGCCGGCCACCGCACAG	9406	AQQNFNAGHAQ	13995	QNFNAGH	0.117535	-0.0709
GS1493	4818	GCCCAACTCACCGGCGCCGCCAGAGTCGCACAG	9407	AQLTGAARVAQ	13996	LTGAARV	0.117519	-0.17919
GS1494	4819	GCCCAAGGGACTCGTCCGACTGCGACGGCACAG	9408	AQGTRPTATAQ	13997	GTRPTAT	0.117449	-0.15669
SyS2607	4820	GCCCAAATGCCCCCTCAGCGTCGCCCCCGCACAG	9409	AQMPLSVAPAQ	13998	MPLSVAP	0.116992	-0.1392
GS1495	4821	GCCCAAGACAGAGTCCAACAATTCAGCGCACAG	9410	AQDRVQQFSAQ	13999	DRVQQFS	0.11689	-0.16146
SyS2610	4822	GCCCAAAACAACGACACCAGCACCAAAGCACAG	9411	AQNNDTSTKAQ	14000	NNDTSTK	0.116554	-0.23419
SyS2611	4823	GCCCAACCTTCGAAGAATACTCATATTGCACAG	9412	AQPSKNTHIAQ	14001	PSKNTHI	0.116554	-0.23419
SyS2612	4824	GCCCAACCTTTTAAGGCTGATGTTACGGCACAG	9413	AQPFKADVTAQ	14002	PFKADVT	0.116512	-0.20224
SyS2613	4825	GCCCAACCTAAGACTCCTACTTATGTGGCACAG	9414	AQPKTPTYVAQ	14003	PKTPTYV	0.116298	-0.20586
SyS2614	4826	GCCCAACTCACCAACATGACCACCCCCGCACAG	9415	AQLTNMTTPAQ	14004	LTNMTTP	0.116179	0.069335
SyS2615	4827	GCCCAAGGTAGTAAGGTGCATCTTTCTGCACAG	9416	AQGSKVHLSAQ	14005	GSKVHLS	0.116046	-0.22527
SyS2616	4828	GCCCAATCTATTCCGGGTTATAATAATGCACAG	9417	AQSIPGYNNAQ	14006	SIPGYNN	0.116006	-0.21679
GS1497	4829	GCCCAAATGAAAACCGCCGAAAGCTACGCACAG	9418	AQMKTAESYAQ	14007	MKTAESY	0.115832	-0.1756
SyS2618	4830	GCCCAAAACGGCGACAGACTCCTCAACGCACAG	9419	AQNGDRLLNAQ	14008	NGDRLLN	0.115647	0.03466
SS189	4831	GCCCAAGGCACCACCCACACCAGCCTCGCACAG	9420	AQGTTHTSLAQ	14009	GTTHTSL	0.11558	-0.38281
GS1499	4832	GCCCAACTCGGCCCCAGCACCCAAAGCGCACAG	9421	AQLGPSTQSAQ	14010	LGPSTQS	0.115388	-0.14619
SyS2619	4833	GCCCAAATGAACGCCCTCACCGACACAAAGCACAG	9422	AQMNALTDKAQ	14011	MNALTDK	0.115181	-0.16027
SyS2620	4834	GCCCAAAGCAGCAAAGAAATCAGCCTCGCACAG	9423	AQSSKEISLAQ	14012	SSKEISL	0.114992	-0.07231
SyS2621	4835	GCCCAACTCGACAACGGCACCACCAGAGGCACAG	9424	AQLDNGTTRAQ	14013	LDNGTTR	0.114827	-0.15288
SyS2622	4836	GCCCAACGTGTGAATTTTAATTCGGATGCACAG	9425	AQRVNFNSDAQ	14014	RVNFNSD	0.114822	-0.20345
SyS2623	4837	GCCCAAAACATGCAAGCCATCAGCAACGCACAG	9426	AQNMQAISNAQ	14015	NMQAISN	0.114811	-0.08155
SyS2624	4838	GCCCAAAACACCAACCCCAGAAGCATCGCACAG	9427	AQNTNPRSIAQ	14016	NTNPRSI	0.114545	0.005791
SyS2625	4839	GCCCAAAAAATCAACAGCAACAGCCCCCGCACAG	9428	AQKINSNSPAQ	14017	KINSNSP	0.114472	-0.07131
GS1501	4840	GCCCAAGTCCCCCTCGGCAAAGCCAGCGCACAG	9429	AQVPLGKASAQ	14018	VPLGKAS	0.114441	-0.18637
SyS2628	4841	GCCCAACGGCTGAATCATAATTCGCCTGCACAG	9430	AQRLNHNSPAQ	14019	RLNHNSP	0.11425	-0.20216

FIG. 33 (Continued)

GS1502	4842	GCCCAACAACTCAACACCGTCCTCCCCGCACAG	9431	AQQLNTVLPAQ	14020	QLNTVLP	0.114132	-0.18054
SyS2630	4843	GCCCAAGACAGCTTCGGCAAAAGCCTCGCACAG	9432	AQDSFGKSLAQ	14021	DSFGKSL	0.114045	-0.16643
SyS2631	4844	GCCCAAAAGCCGCCTAAGTTGGTTGATGCACAG	9433	AQKPPKLVDAQ	14022	KPPKLVD	0.113972	-0.17314
GS1504	4845	GCCCAACAAATCACCGTCGGCAAACCCGCACAG	9434	AQQITVGKPAQ	14023	QITVGKP	0.113906	-0.15574
GS1505	4846	GCCCAACAACACCCCCACGGCCAACAAGCACAG	9435	AQQHPHGQQAQ	14024	QHPHGQQ	0.113842	-0.16214
SyS2633	4847	GCCCAAACTTCGACTAATATGGCGGCTGCACAG	9436	AQTSTNMAAAQ	14025	TSTNMAA	0.113622	-0.04892
SyS2634	4848	GCCCAACAAGGCGGCCTCGCCGTCGTCGCACAG	9437	AQQGGLAVVAQ	14026	QGGLAVV	0.113622	-0.15657
GS1507	4849	GCCCAAGGGAGGGGTAGTCTTCCGTTTGCACAG	9438	AQGRGSLPFAQ	14027	GRGSLPF	0.113603	-0.18816
SyS2637	4850	GCCCAAAGCGGCAAACCCGCCAGCGAAGCACAG	9439	AQSGKPASEAQ	14028	SGKPASE	0.113257	-0.18245
GS1508	4851	GCCCAACGGTCTCGTTAGTGTGAATTCTGCACAG	9440	AQRSVSVNSAQ	14029	RSVSVNS	0.11314	-0.18245
SyS2638	4852	GCCCAAGACAGAGGCGGCGTCGTCGCCGCACAG	9441	AQDRGGVVAAQ	14030	DRGGVVA	0.113119	-0.20466
SyS2639	4853	GCCCAAGGTCGTGAGACTGGTTTTTCGGCACAG	9442	AQGRETGFSAQ	14031	GRETGFS	0.112987	-0.21315
SyS2640	4854	GCCCAACAGATTGTTCCGTCGAATCCGGCACAG	9443	AQQIVPSNPAQ	14032	QIVPSNP	0.112987	-0.21315
SyP73	4855	GCCCAAACGACGTTGGGTCATAGTTATTCACAG	9444	AQTTLGHSYSQ	14033	TTLGHSY	0.11285	-0.03826
SyS2642	4856	GCCCAAAGCAGAGAATTCCAACTCGCCGCACAG	9445	AQSREFQLAAQ	14034	SREFQLA	0.112786	-0.15738
GS1510	4857	GCCCAAGGCAGAGACCACAACATCGGCGCACAG	9446	AQGRDHNIGAQ	14035	GRDHNIG	0.112781	-0.17386
TS179	4858	GCCCAATCGAATAATTCTCGGCCGAATGCACAG	9447	AQSNNSRPNAQ	14036	SNNSRPN	0.112766	-0.14993
SyS2643	4859	GCCCAAAAAAACCAAAGCAGCGACCTCGCACAG	9448	AQKNQSSDLAQ	14037	KNQSSDL	0.11276	0.0834
SyS2644	4860	GCCCAACCCAACGACAGAGCCCACGGCGCACAG	9449	AQPNDRAHGAQ	14038	PNDRAHG	0.112742	-0.19375
SyS2645	4861	GCCCAAGCTCTGACTAGGACTCAGTCTGCACAG	9450	AQALTRTQSAQ	14039	ALTRTQS	0.11269	-0.10041
SyS2647	4862	GCCCAAATGAGACCCCCCAGCGACAAAGCACAG	9451	AQMRPPSDKAQ	14040	MRPPSDK	0.112599	-0.20224
TS180	4863	GCCCAAACGAATTCGACTACGAAGTCGGCACAG	9452	AQTNSTTKSAQ	14041	TNSTTKS	0.112569	-0.20873
SyS2648	4864	GCCCAAGGCAGACACGGCATGACCGCCGCACAG	9453	AQGRHGMTAAQ	14042	GRHGMTA	0.112548	-0.08222
GS1511	4865	GCCCAAGTCAGCCACATCAGCCCCGCCGCACAG	9454	AQVSHISPAAQ	14043	VSHISPA	0.112496	-0.13761
GS1512	4866	GCCCAAAAGGTTACTAGTAATAGTTCGGCACAG	9455	AQKVTSNSSAQ	14044	KVTSNSS	0.112386	-0.16241
SyS2649	4867	GCCCAAATGTACGGCCCCGGCGCCAGCGCACAG	9456	AQMYGPGASAQ	14045	MYGPGAS	0.112262	-0.19133
GS1514	4868	GCCCAAGTCCTCAGAAGCAACACCCCCGCACAG	9457	AQVLRSNTPAQ	14046	VLRSNTP	0.112217	-0.12617
SyS2650	4869	GCCCAAAATAGTAGTTCTAGTAATAAGGCACAG	9458	AQNSSSSNKAQ	14047	NSSSSNK	0.112213	-0.20989
SyS2652	4870	GCCCAAAGCACCGAAAAAAGCACCAGCGCACAG	9459	AQSTEKSTSAQ	14048	STEKSTS	0.11211	-0.0765
GS1516	4871	GCCCAAAACACCAACGGCAACAAAGGCGCACAG	9460	AQNTNGNKGAQ	14049	NTNGNKG	0.112014	-0.18149
GP205	4872	GCCCAAATTACGACTAATCTGGGGGCGGCACAG	9461	AQITTNLGAAQ	14050	ITTNLGA	0.111979	-0.07377
GS1517	4873	GCCCAAATCCAAAAACCCCAAAGCAGCGCACAG	9462	AQIQKPQSSAQ	14051	IQKPQSS	0.111935	-0.18457

FIG. 33 (Continued)

SyS2654	4874	GCCCAAGTGAGGGATGCGGCTTATACGGCACAG	9463	AQVRDAAYTAQ	14052	VRDAAYT	0.111823	-0.18614
GS1519	4875	GCCCAAGCCAGAAGCAGCACCGGCGCCGCACAG	9464	AQARSSTGAAQ	14053	ARSSTGA	0.111751	-0.17291
GP206	4876	GCCCAAACGTCTGTTCATAATAAGGTTGCACAG	9465	AQTSVHNKVAQ	14054	TSVHNKV	0.11171	-0.06996
SyS2655	4877	GCCCAAACTATTTCGACTCATGGTACTGCACAG	9466	AQTISTHGTAQ	14055	TISTHGT	0.111706	-0.16951
SyS2657	4878	GCCCAAACCGTCACCAACATCAACTTCGCACAG	9467	AQTVTNINFAQ	14056	TVTNINF	0.111589	-0.22434
SyS2658	4879	GCCCAAAGCATCAACAGCAACCACATCGCACAG	9468	AQSINSNHIAQ	14057	SINSNHI	0.111382	-0.1198
SyS2659	4880	GCCCAACAAAAAGCCGGCTACAGCAACGCACAG	9469	AQQKAGYSNAQ	14058	QKAGYSN	0.111146	0.158487
SyS2660	4881	GCCCAAGCCAGAGACACCGTCAGAACCGCACAG	9470	AQARDTVRTAQ	14059	ARDTVRT	0.111115	-0.17557
SyS2661	4882	GCCCAATATAAGGATCAGACGAAGGTTGCACAG	9471	AQYKDQTKVAQ	14060	YKDQTKV	0.11098	-0.20955
SyS2662	4883	GCCCAAAACATCGGCCTCAACCCCATGGCACAG	9472	AQNIGLNPMAQ	14061	NIGLNPM	0.11098	-0.20955
SyS2663	4884	GCCCAAGGCAGCACCAACATGATCTACGCACAG	9473	AQGSTNMIYAQ	14062	GSTNMIY	0.110958	-0.1207
GS1521	4885	GCCCAAATCGACGCCCAAAGGCCTCAAAGCACAG	9474	AQIDAKGLKAQ	14063	IDAKGLK	0.110926	-0.10224
SyS2664	4886	GCCCAAGTCGTCAGCCACAACCTCACCGCACAG	9475	AQVVSHNLTAQ	14064	VVSHNLT	0.110909	-0.18405
GS1522	4887	GCCCAAACTGTGTCTCTGAAGACTGCGGCACAG	9476	AQTVSLKTAAQ	14065	TVSLKTA	0.110728	-0.18368
GS1523	4888	GCCCAATACAGCGGCAGCAACTACCACGCACAG	9477	AQYSGSNYHAQ	14066	YSGSNYH	0.110728	-0.18368
SyS2665	4889	GCCCAACCGAGTGATGCTACGATGGGGGCACAG	9478	AQPSDATMGAQ	14067	PSDATMG	0.110688	-0.14003
SyS2666	4890	GCCCAATGGGGGGAGACTACGAATGGTGCACAG	9479	AQWGETTNGAQ	14068	WGETTNG	0.110488	-0.15497
GP207	4891	GCCCAAAATTATCATAAGACGATGCCGGCACAG	9480	AQNYHKTMPAQ	14069	NYHKTMP	0.110443	-0.07301
SyS2667	4892	GCCCAAGCCAGACACGAACTCCCCGTCGCACAG	9481	AQARHELPVAQ	14070	ARHELPV	0.110199	-0.18491
SyS2668	4893	GCCCAACACAACCTCACCAGAAACCTCGCACAG	9482	AQHNLTRNLAQ	14071	HNLTRNL	0.110124	0.296664
GS1526	4894	GCCCAAGGTCCGCAGATTGGTACGGTGGCACAG	9483	AQGPQIGTVAQ	14072	GPQIGTV	0.109435	-0.13719
SyS2670	4895	GCCCAAATGAGAGCCGACAGCAACGTCGCACAG	9484	AQMRADSNVAQ	14073	MRADSNV	0.108975	0.017461
SyS2671	4896	GCCCAAGTCGCCAACGGCCCCACCACCGCACAG	9485	AQVANGPTTAQ	14074	VANGPTT	0.108861	-0.11592
GS1528	4897	GCCCAAACCAAAAAACCTCAACACCTACGCACAG	9486	AQTKNLNTYAQ	14075	TKNLNTY	0.108797	-0.17291
GS1529	4898	GCCCAAGACAGACTCGGCGCCAGAAGCGCACAG	9487	AQDRLGARSAQ	14076	DRLGARS	0.108797	-0.16432
SyS2672	4899	GCCCAAAACATCGGCAGCGGCCAAAAAGCACAG	9488	AQNIGSGQKAQ	14077	NIGSGQK	0.108746	-0.19107
GP208	4900	GCCCAAGGTAGGGAGATGACGAATCCGGCACAG	9489	AQGREMTNPAQ	14078	GREMTNP	0.108745	-0.07363
SyS2674	4901	GCCCAAATTATGGCTGCTGCGCATTCGGCACAG	9490	AQIMAAAHSAQ	14079	IMAAAHS	0.108479	-0.15859
SyS2675	4902	GCCCAAAGCGACCAAAGAATCCACCCCGCACAG	9491	AQSDQRIHPAQ	14080	SDQRIHP	0.108479	-0.15859
SyS2676	4903	GCCCAAGTTTCTGGTCAGACGAATATGGCACAG	9492	AQVSGQTNMAQ	14081	VSGQTNM	0.108381	-0.21072
SyS2677	4904	GCCCAATACAGCCTCGGCAGCGAACCCGCACAG	9493	AQYSLGSEPAQ	14082	YSLGSEP	0.10832	-0.19981
SyS2678	4905	GCCCAATCTACGCTGAAGGCTCTGACGGCACAG	9494	AQSTLKALTAQ	14083	STLKALT	0.108295	-0.16397

FIG. 33 (Continued)

SyS2679	4906	GCCCAAAGCGCCCTCATCCCCAGCCCCGCACAG	9495	AQSALIPSPAQ	14084	SALIPSP	0.108266	-0.1889
GS1530	4907	GCCCAAACCAGCCAAGCCGGCAACCAAGCACAG	9496	AQTSQAGNQAQ	14085	TSQAGNQ	0.108221	-0.05787
GS1531	4908	GCCCAAAAACACGCCAGCCTCCCCATCGCACAG	9497	AQKHASLPIAQ	14086	KHASLPI	0.108122	-0.15676
GS1532	4909	GCCCAACTCGACCAACTCACCAAAAACGCACAG	9498	AQLDQLTKNAQ	14087	LDQLTKN	0.108122	-0.15676
SyS2680	4910	GCCCAAATGGCCAGAAGCACCGACAGAGCACAG	9499	AQMARSTDRAQ	14088	MARSTDR	0.108107	-0.14526
SyS2681	4911	GCCCAAAGTTATAATCATATTGAGAAGGCACAG	9500	AQSYNHIEKAQ	14089	SYNHIEK	0.108002	-0.23012
SS193	4912	GCCCAAGTCAACCACATCCAACCCATGGCACAG	9501	AQVNHIQPMAQ	14090	VNHIQPM	0.107975	-0.33355
GS1533	4913	GCCCAAAGCAGAGCCGAACCCAAACTCGCACAG	9502	AQSRAEPKLAQ	14091	SRAEPKL	0.10781	-0.16394
GS1534	4914	GCCCAAGCCAGCCACATCGGCAACAGCGCACAG	9503	AQASHIGNSAQ	14092	ASHIGNS	0.107759	-0.18637
SyS2682	4915	GCCCAACATCAGGGTTTTGCGAGTGCTGCACAG	9504	AQHQGFASAAQ	14093	HQGFASA	0.107489	0.012345
SyS2684	4916	GCCCAAGAGGGTAAGTCTATTATGCCGGCACAG	9505	AQEGKSIMPAQ	14094	EGKSIMP	0.107301	-0.20709
SyS2685	4917	GCCCAACTCACCGGCATGCACAGCACCGCACAG	9506	AQLTGMHSTAQ	14095	LTGMHST	0.107301	-0.20709
SyS2686	4918	GCCCAAAGTAATCCTAGTACTATTCATGCACAG	9507	AQSNPSTIHAQ	14096	SNPSTIH	0.107232	-0.12873
SyS2688	4919	GCCCAAAGCAGAGACCAACCCACCAGCGCACAG	9508	AQSRDQPTSAQ	14097	SRDQPTS	0.107118	-0.18163
SyS2689	4920	GCCCAAAAAACCGCCGAACCCTACACCGCACAG	9509	AQKTAEPYTAQ	14098	KTAEPYT	0.107074	-0.18491
SyS2690	4921	GCCCAAATTGGTTCTAATCCTGATAAGGCACAG	9510	AQIGSNPDKAQ	14099	IGSNPDK	0.107034	-0.21436
SyS2691	4922	GCCCAACTCGCCAGCACCTTCAGCCCCGCACAG	9511	AQLASTFSPAQ	14100	LASTFSP	0.107031	-0.17998
SyS2692	4923	GCCCAACTTGTTAGGCTTAATACTTCTGCACAG	9512	AQLVRLNTSAQ	14101	LVRLNTS	0.106997	-0.22527
SyP76	4924	GCCCAATTTCAGGATCTGCGTGCGCAAGCACAG	9513	AQFQDLRAQAQ	14102	FQDLRAQ	0.10698	-0.03979
GS1537	4925	GCCCAAATCAGCCACAGCCCCCAAACCGCACAG	9514	AQISHSPQTAQ	14103	ISHSPQT	0.106884	-0.171
SyS2693	4926	GCCCAATTCCAAGACGGCCAAAGAGAAGCACAG	9515	AQFQDGQREAQ	14104	FQDGQRE	0.106797	-0.11297
SyS2694	4927	GCCCAAGACACCAGAGAAGCCTTCAGAGCACAG	9516	AQDTREAFRAQ	14105	DTREAFR	0.106757	-0.1792
SyS2695	4928	GCCCAATTGGTTGCTGATGCGCGTCCTGCACAG	9517	AQLVADARPAQ	14106	LVADARP	0.106656	-0.20103
GS1540	4929	GCCCAAAGCTTCAGCAGCGGCGCCGGCGCACAG	9518	AQSFSSGAGAQ	14107	SFSSGAG	0.10653	-0.08043
SyS2696	4930	GCCCAAGATGTGTTGACTGGGAAGAGTGCACAG	9519	AQDVLTGKSAQ	14108	DVLTGKS	0.106522	-0.15496
SyS2697	4931	GCCCAAAAGATGGTGTTGAATAATGCTGCACAG	9520	AQKMVLNNAAQ	14109	KMVLNNA	0.106481	-0.17225
SyS2698	4932	GCCCAACGGAAGATTGATACGATGTCTGCACAG	9521	AQRKIDTMSAQ	14110	RKIDTMS	0.106265	-0.13872
GS1541	4933	GCCCAAATGTCTCAGGTGATTACTGGGGCACAG	9522	AQMSQVITGAQ	14111	MSQVITG	0.106232	-0.1439
GP212	4934	GCCCAAACGTATGATACGCGGAATACTGCACAG	9523	AQTYDTRNTAQ	14112	TYDTRNT	0.106211	-0.06295
SyS2699	4935	GCCCAATATAGGGATGGTTCGGGTAGTGCACAG	9524	AQYRDGSGSAQ	14113	YRDGSGS	0.105987	0.014681
GS1542	4936	GCCCAAGGGAATATTAGTCCTGCGGGGGGCACAG	9525	AQGNISPAGAQ	14114	GNISPAG	0.105627	-0.18149
SyS2700	4937	GCCCAAAAAGCCGGCCTCGGCCTCAGCGCACAG	9526	AQKAGLGLSAQ	14115	KAGLGLS	0.105529	-0.21571

FIG. 33 (Continued)

GP214	4938	GCCCAACGTCATGTGGAGAAGGATACTGCACAG	9527	AQRHVEKDTAQ	14116	RHVEKDT	0.105492	-0.07433
GS1543	4939	GCCCAAAAAGAAGTCAGAGCCAACGCCGCACAG	9528	AQKEVRANAAQ	14117	KEVRANA	0.105404	-0.15764
SyS2701	4940	GCCCAAGAGAGTAAGCCTCTTCCTGCGGCACAG	9529	AQESKPLPAAQ	14118	ESKPLPA	0.105201	-0.21557
SyS2702	4941	GCCCAAACGTTGAGTCATAATAGTATGGCACAG	9530	AQTLSHNSMAQ	14119	TLSHNSM	0.105046	0.006619
SyS2703	4942	GCCCAAGTCGGCAGCTACACCGTCAGCGCACAG	9531	AQVGSYTVSAQ	14120	VGSYTVS	0.105013	-0.22649
SyS2704	4943	GCCCAACAAAGCGCCACCAGCCTCACCGCACAG	9532	AQQSATSLTAQ	14121	QSATSLT	0.104841	-0.06501
GS1546	4944	GCCCAACACGCCAACGGCCTCAGAGACGCACAG	9533	AQHANGLRDAQ	14122	HANGLRD	0.104497	-0.15955
GS1547	4945	GCCCAAAGAATGAGCCACGACAGCCCCGCACAG	9534	AQRMSHDSPAQ	14123	RMSHDSP	0.104494	-0.18637
SyS2705	4946	GCCCAAAAGCATAGTGGTCTTGAGTCTGCACAG	9535	AQKHSGLESAQ	14124	KHSGLES	0.104319	-0.17314
SyS2707	4947	GCCCAAAAACTCAGCACCGCCATCGAAGCACAG	9536	AQKLSTAIEAQ	14125	KLSTAIE	0.103851	-0.06923
SyS2708	4948	GCCCAAAACAGCAAACAACTCCTCCTCGCACAG	9537	AQNSKQLLLAQ	14126	NSKQLLL	0.10377	-0.20709
SyS2709	4949	GCCCAATCGCTTCATAATAATCGTGTGGCACAG	9538	AQSLHNNRVAQ	14127	SLHNNRV	0.103655	-0.12587
SyS2710	4950	GCCCAAAGCGCCGACAGAAGCATCACCGCACAG	9539	AQSADRSITAQ	14128	SADRSIT	0.103582	-0.14162
SyS2711	4951	GCCCAACCCACCGGCAGACCCCAAGAAGCACAG	9540	AQPTGRPQEAQ	14129	PTGRPQE	0.103492	-0.1792
SyS2712	4952	GCCCAAAAGACTGTTCAGGAGCCTTTGGCACAG	9541	AQKTVQEPLAQ	14130	KTVQEPL	0.10347	-0.22926
SyS2715	4953	GCCCAAAGCACCAAAGCCCTCAGCAACGCACAG	9542	AQSTKALSNAQ	14131	STKALSN	0.103085	-0.13677
GS1551	4954	GCCCAAAGCAACCAAAGCACCAGAAGCGCACAG	9543	AQSNQSTRSAQ	14132	SNQSTRS	0.103015	-0.15138
SyS2716	4955	GCCCAAGGTGTTGAGGGGAGTTCGCGGGCACAG	9544	AQGVEGSSRAQ	14133	GVEGSSR	0.102975	-0.21436
SyS2717	4956	GCCCAACTCCACCAAGGCCCCAGCAGCGCACAG	9545	AQLHQGPSSAQ	14134	LHQGPSS	0.102855	-0.099
GS1552	4957	GCCCAAGTCGACAGCAGAAACGTCGTCGCACAG	9546	AQVDSRNVVAQ	14135	VDSRNVV	0.102836	-0.118
SyS2718	4958	GCCCAACTTGGGAAGCAGACGGCTTTGGCACAG	9547	AQLGKQTALAQ	14136	LGKQTAL	0.102831	-0.1615
SyS2719	4959	GCCCAAAGCGGCAACAGAACCAACATGGCACAG	9548	AQSGNRTNMAQ	14137	SGNRTNM	0.102775	0.06214
GS1553	4960	GCCCAAGTCAAAGGCTACGCCAGCACCGCACAG	9549	AQVKGYASTAQ	14138	VKGYAST	0.102753	-0.16051
SyS2720	4961	GCCCAAGCTTCTGTTAGTTCGTCGAGTGCACAG	9550	AQASVSSSSAQ	14139	ASVSSSS	0.102658	0.00519
SyS2722	4962	GCCCAACTCCAACTCAAAAGCGGCATGGCACAG	9551	AQLQLKSGMAQ	14140	LQLKSGM	0.102481	-0.07053
SyS2723	4963	GCCCAAGATATGCGTGCGTCTGGGAGTGCACAG	9552	AQDMRASGSAQ	14141	DMRASGS	0.102358	-0.19107
GP216	4964	GCCCAATTGACTGCTACGCTGCCTTATGCACAG	9553	AQLTATLPYAQ	14142	LTATLPY	0.102226	-0.0676
GS1555	4965	GCCCAAAGTAATGCTCCTAATTCGTATGCACAG	9554	AQSNAPNSYAQ	14143	SNAPNSY	0.102094	-0.10049
SyS2726	4966	GCCCAAAAAGTCGAAAGCAGCAGAGCCGCACAG	9555	AQKVESSRAAQ	14144	KVESSRA	0.102054	-0.20586
GS1556	4967	GCCCAATGGAGCAACAGCACCACCGTCGCACAG	9556	AQWSNSTTVAQ	14145	WSNSTTV	0.10196	-0.17381
GP217	4968	GCCCAATCTCTTATTCATACGCGTCCTGCACAG	9557	AQSLIHTRPAQ	14146	SLIHTRP	0.101865	-0.0719
SyS2727	4969	GCCCAAACGCTTTCTAGTCCTCATAATGCACAG	9558	AQTLSSPHNAQ	14147	TLSSPHN	0.101849	-0.22042

FIG. 33 (Continued)

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SyS2728	4970	GCCCAAGTGCCTAGGTTTAATGGTAATGCACAG	9559	AQVPRFNGNAQ	14148	VPRFNGN	0.101797	-0.16466
GS1557	4971	GCCCAATTCAACCACAGCGGCAGCGGCGCACAG	9560	AQFNHSGSGAQ	14149	FNHSGSG	0.101435	-0.14048
SyS2731	4972	GCCCAATGGGTCGACACCAACAGCAAAGCACAG	9561	AQWVDTNSKAQ	14150	WVDTNSK	0.101312	-0.23296
SyS2732	4973	GCCCAACATTCGGATGGTTCTAGGCTTGCACAG	9562	AQHSDGSRLAQ	14151	HSDGSRL	0.101267	-0.20224
SyS2734	4974	GCCCAAAGGCAGGCGGTTCAGACTTCTGCACAG	9563	AQRQAVQTSAQ	14152	RQAVQTS	0.101257	-0.17259
GS1558	4975	GCCCAAATGCACAGCGGCATCCCCACCGCACAG	9564	AQMHSGIPTAQ	14153	MHSGIPT	0.101243	-0.171
SyS2735	4976	GCCCAAGTGAAGGATCAGGGGCGTTCTGCACAG	9565	AQVKDQGRSAQ	14154	VKDQGRS	0.101228	-0.11222
GS1559	4977	GCCCAAAGACCCACCCTCAGCAACCAAGCACAG	9566	AQRPTLSNQAQ	14155	RPTLSNQ	0.101216	-0.18368
SyS2736	4978	GCCCAAGTCAGCAAAAGCGCCGCCCTCGCACAG	9567	AQVSKSAALAQ	14156	VSKSAAL	0.101086	0.020684
GS1560	4979	GCCCAAAAGGATAGTCATCTGTCGTCGGCACAG	9568	AQKDSHLSSAQ	14157	KDSHLSS	0.101076	-0.10167
GS1561	4980	GCCCAAGTCGGCGTCAGAATGACCGGCGCGCACAG	9569	AQVGVRMTGAQ	14158	VGVRMTG	0.101055	-0.1756
SyS2737	4981	GCCCAAGCTGATCGGCTTTTGAATTCGGCACAG	9570	AQADRLLNSAQ	14159	ADRLLNS	0.100992	-0.22891
GS1563	4982	GCCCAAGGCAGCGAACTCAGAACCGGCGCGCACAG	9571	AQGSELRTGAQ	14160	GSELRTG	0.100602	-0.16718
SyS2741	4983	GCCCAAATGAAACTCAGCACCAGCAGCGCACAG	9572	AQMKLSTSSAQ	14161	MKLSTSS	0.100379	-0.20462
SyS2742	4984	GCCCAACAAGCCTACAACATCGTCCCCGCACAG	9573	AQQAYNIVPAQ	14162	QAYNIVP	0.100369	-0.19496
GS1564	4985	GCCCAAGTCGGCGGCAACATCAGAACCGCACAG	9574	AQVGGNIRTAQ	14163	VGGNIRT	0.100363	-0.18245
SyS2744	4986	GCCCAAAGTTATCAGCAGACGTTGGGGGCACAG	9575	AQSYQQTLGAQ	14164	SYQQTLG	0.100031	-0.21448
SyS2745	4987	GCCCAAATGAGACCCACCCCCACCGACGCACAG	9576	AQMRPTPTDAQ	14165	MRPTPTD	0.099936	-0.22164
GS1565	4988	GCCCAAAGGAAGGCGAATGATCTGAATGCACAG	9577	AQRKANDLNAQ	14166	RKANDLN	0.099903	-0.14779
SyS2746	4989	GCCCAAATCAGCGGCACCGCCAGCACCGCACAG	9578	AQISGTASTAQ	14167	ISGTAST	0.099888	-0.17136
GS1566	4990	GCCCAATACGTCCAACTCAACAACGCCGCACAG	9579	AQYVQLNNAAQ	14168	YVQLNNA	0.099805	-0.09965
SyS2747	4991	GCCCAAACCGAAAAAGGCTGGGGCCCCGCACAG	9580	AQTEKGWGPAQ	14169	TEKGWGP	0.099789	-0.0324
GP219	4992	GCCCAATCTCCGCAGAGGCATAATAGTGCACAG	9581	AQSPQRHNSAQ	14170	SPQRHNS	0.099622	-0.07162
SyS2748	4993	GCCCAATACACCCACATGACCGAAAGAGCACAG	9582	AQYTHMTERAQ	14171	YTHMTER	0.099615	-0.13451
SyS2749	4994	GCCCAAGATCGGTCTATGCAGCAGGCTGCACAG	9583	AQDRSMQQAAQ	14172	DRSMQQA	0.099482	-0.12465
GS1568	4995	GCCCAAGACACCATGAACGCCATGAGAGCACAG	9584	AQDTMNAMRAQ	14173	DTMNAMR	0.099158	-0.18188
SyS2750	4996	GCCCAACTCAAACCCGGCCACATGGTCGCACAG	9585	AQLKPGHMVAQ	14174	LKPGHMV	0.099141	-0.19353
GS1570	4997	GCCCAACAATTCAACAGCAAAGACACCGCACAG	9586	AQQFNSKDTAQ	14175	QFNSKDT	0.098945	-0.04968
GS1571	4998	GCCCAATGGACCAACAGCAGACCCATGGCACAG	9587	AQWTNSRPMAQ	14176	WTNSRPM	0.098784	-0.15843
GS1572	4999	GCCCAATTGCTGACGACTTCTTCTGAGGCACAG	9588	AQLLTTSSEAQ	14177	LLTTSSE	0.098761	-0.13998
SyS2752	5000	GCCCAACAGCGTGCTTCTTCTGGTTCTGCACAG	9589	AQQRASSGSAQ	14178	QRASSGS	0.098675	-0.14647
SyS2753	5001	GCCCAACCCAAAGAAAGCAACAACATGGCACAG	9590	AQPKESNNMAQ	14179	PKESNNM	0.098625	-0.2277

FIG. 33 (Continued)

SyS2754	5002	GCCCAAGCCAAACACGTCGCCACCGAAGCACAG	9591	AQAKHVATEAQ	14180	AKHVATE	0.098546	-0.17013
GS1573	5003	GCCCAAACTCAGTCGAGTACGTATTCGGCACAG	9592	AQTQSSTYSAQ	14181	TQSSTYS	0.098504	-0.18054
SyS2755	5004	GCCCAACCCAGAACCAGCACCAACATCGCACAG	9593	AQPRTSTNIAQ	14182	PRTSTNI	0.098455	-0.17259
GS1574	5005	GCCCAAAGACTCGCCAGCAACAGCGACGCACAG	9594	AQRLASNSDAQ	14183	RLASNSD	0.098382	-0.11377
SyS2759	5006	GCCCAAGGCCCCCTCCAAACCAACGCCGCACAG	9595	AQGPLQTNAAQ	14184	GPLQTNA	0.098167	-0.21571
SyS2760	5007	GCCCAAAAAGTCAGCGCCATGAGCGACGCACAG	9596	AQKVSAMSDAQ	14185	KVSAMSD	0.098115	-0.17314
SyS2763	5008	GCCCAAGCTGGGAAGTATGTTAATTCTGCACAG	9597	AQAGKYVNSAQ	14186	AGKYVNS	0.09743	-0.218
GS1578	5009	GCCCAACCCAAAAGCGGCAGCCCCAGCGCACAG	9598	AQPKSGSPSAQ	14187	PKSGSPS	0.097428	-0.16663
SyS2764	5010	GCCCAATTTATTTCTAATGGGAGTTCGGCACAG	9599	AQFISNGSSAQ	14188	FISNGSS	0.097369	-0.19981
SyS2766	5011	GCCCAAAATCTGAATGCGATGCATAAGGCACAG	9600	AQNLNAMHKAQ	14189	NLNAMHK	0.097204	-0.1336
SyS2767	5012	GCCCAAGAGTCGCATGCGCGGGAGGGGGCACAG	9601	AQESHAREGAQ	14190	ESHAREG	0.097196	-0.23376
GS1579	5013	GCCCAAACTGTGGTTGGGGTTAGGGGTGCACAG	9602	AQTVVGVRGAQ	14191	TVVGVRG	0.097193	-0.18009
SyS2768	5014	GCCCAAGCCAAAGCCACCGTCCCCAGCGCACAG	9603	AQAKATVPSAQ	14192	AKATVPS	0.097158	-0.21557
GS1580	5015	GCCCAAACCAAAACCGTCAACATGACCGCACAG	9604	AQTKTVNMTAQ	14193	TKTVNMT	0.097046	-0.10651
SyS2770	5016	GCCCAACAAAGCAGCCTCAAACTCACCGCACAG	9605	AQQSSLKLTAQ	14194	QSSLKLT	0.096895	-0.14041
GS1583	5017	GCCCAAAACGCCCAAAGAACCGGCCCCGCACAG	9606	AQNAQRTGPAQ	14195	NAQRTGP	0.096888	-0.10782
GS1584	5018	GCCCAAAACAGAAGAGACGCCACCCCCGCACAG	9607	AQNRRDATPAQ	14196	NRRDATP	0.096778	-0.01327
SyS2771	5019	GCCCAAGGCAACCAAAACACCCTCCTCGCACAG	9608	AQGNQNTLLAQ	14197	GNQNTLL	0.096736	-0.20955
SyS2772	5020	GCCCAAACCAGAGTCAGCGGCAGCGCCGCACAG	9609	AQTRVSGSAAQ	14198	TRVSGSA	0.096732	-0.16516
GS1585	5021	GCCCAAGTTACGACGGCGATGATGTCGGCACAG	9610	AQVTTAMMSAQ	14199	VTTAMMS	0.09673	-0.17863
SyS2773	5022	GCCCAAGACAGAACCCCCATCGCCCACGCACAG	9611	AQDRTPIAHAQ	14200	DRTPIAH	0.096605	-0.22891
SyS2774	5023	GCCCAACTCCCCCCTCAACAGCAGACCCGCACAG	9612	AQLPLNSRPAQ	14201	LPLNSRP	0.096472	-0.00342
GS1586	5024	GCCCAACCGCAGGCTTCGCAGGCTAATGCACAG	9613	AQPQASQANAQ	14202	PQASQAN	0.096411	-0.15209
GS1587	5025	GCCCAAACGGCGAGGAATGTTCCTAATGCACAG	9614	AQTARNVPNAQ	14203	TARNVPN	0.09629	-0.1101
SyS2777	5026	GCCCAACTCAACGGCATCCTCAGCCAAGCACAG	9615	AQLNGILSQAQ	14204	LNGILSQ	0.096081	0.102848
SyS2778	5027	GCCCAACTGCAGGATAAGACTCTTAATGCACAG	9616	AQLQDKTLNAQ	14205	LQDKTLN	0.096058	-0.22406
GS1588	5028	GCCCAATATCGGGGTGAGAATAATCCTGCACAG	9617	AQYRGENNPAQ	14206	YRGENNP	0.095988	-0.18727
SyS2779	5029	GCCCAAGTCAACAAACAACTCAACAGCGCACAG	9618	AQVNKQLNSAQ	14207	VNKQLNS	0.095982	-0.13932
SyS2780	5030	GCCCAAGTCCTCAAAGACGACGGCCACGCACAG	9619	AQVLKDDGHAQ	14208	VLKDDGH	0.095976	-0.09007
SyS2781	5031	GCCCAAACTCGGGGGGAGGTTTCGCTGGCACAG	9620	AQTRGEVSLAQ	14209	TRGEVSL	0.095937	-0.16766
SyS2782	5032	GCCCAAGAGTTTCAGAGGATGCATCCGGCACAG	9621	AQEFQRMHPAQ	14210	EFQRMHP	0.095928	-0.20345
SyS2783	5033	GCCCAAATCAGCCCCATGAGCACCAGCGCACAG	9622	AQISPMSTSAQ	14211	ISPMSTS	0.095846	-0.14405

FIG. 33 (Continued)

SyS2784	5034	GCCCAACTCGGCCACGACCACGCCACCGCACAG	9623	AQLGHDHATAQ	14212	LGHDHAT	0.0958	-0.22164
GS1590	5035	GCCCAACTCAGCCCCCGGCCCCCAACAAGCACAG	9624	AQLSPGPQQAQ	14213	LSPGPQQ	0.095745	-0.171
GP221	5036	GCCCAAAAGTTTAGGGGGGAGGAGCCTGCACAG	9625	AQKFRGEEPAQ	14214	KFRGEEP	0.095692	-0.06711
GS1591	5037	GCCCAACAGGGTTCTCGTCTGGCTTCGGCACAG	9626	AQQGSRLASAQ	14215	QGSRLAS	0.095684	-0.16753
SyS2786	5038	GCCCAATGGGAGCGTTCTCAGTTGTCTGCACAG	9627	AQWERSQLSAQ	14216	WERSQLS	0.095581	-0.20093
SyS2787	5039	GCCCAACAGCAGAAGGCGGCTAATGGGGCACAG	9628	AQQQKAANGAQ	14217	QQKAANG	0.095548	-0.01243
SyS2788	5040	GCCCAATATACGCTGAGTCTGAGTAGTGCACAG	9629	AQYTLSLSSAQ	14218	YTLSLSS	0.095427	-0.20339
SyS2789	5041	GCCCAAGGCCTCATCCCCAACAACAGCGCACAG	9630	AQGLIPNNSAQ	14219	GLIPNNS	0.095235	-0.23173
SyS2790	5042	GCCCAAAGCGTCCCCGTCAGCAGAACCGCACAG	9631	AQSVPVSRTAQ	14220	SVPVSRT	0.095224	-0.08979
SP51	5043	GCCCAAAATAAGCAGCAGTCTCAGACGGCACAG	9632	AQNKQQSQTAQ	14221	NKQQSQT	0.095031	-0.04883
SyS2792	5044	GCCCAAAGCAAACACAGCGTCCAAGTCGCACAG	9633	AQSKHSVQVAQ	14222	SKHSVQV	0.095008	-0.01372
GS1592	5045	GCCCAAAATCGTCCTTCTCAGCAGGGGGGCACAG	9634	AQNRPSQQGAQ	14223	NRPSQQG	0.094956	-0.08958
SyS2793	5046	GCCCAACAAGAATACAGAAACACCCTCGCACAG	9635	AQQEYRNTLAQ	14224	QEYRNTL	0.094903	-0.17072
SyS2794	5047	GCCCAATTCGAAAGAGACAGAATGGGCGCACAG	9636	AQFERDRMGAQ	14225	FERDRMG	0.094881	-0.19133
SyS2795	5048	GCCCAAAGCACCAGCAGCAACCTCAGCGCACAG	9637	AQSTSSNLSAQ	14226	STSSNLS	0.094566	-0.23012
SyS2796	5049	GCCCAAAGAAGCCTCGAAGGCATCGTCGCACAG	9638	AQRSLEGIVAQ	14227	RSLEGIV	0.094566	-0.23012
SyS2797	5050	GCCCAAGGCAACAGCAGACTCGACCCCGCACAG	9639	AQGNSRLDPAQ	14228	GNSRLDP	0.094522	-0.12222
GS1594	5051	GCCCAAATCGACACCATCGGCAAAGCCGCACAG	9640	AQIDTIGKAAQ	14229	IDTIGKA	0.094385	-0.15766
SyS2799	5052	GCCCAACTGGATCATACGAGTCGTGCGGCACAG	9641	AQLDHTSRAAQ	14230	LDHTSRA	0.094325	-0.18405
SyS2800	5053	GCCCAATGGGGCCAAACCAACAGCAGCGCACAG	9642	AQWGQTNSSAQ	14231	WGQTNSS	0.094236	-0.10601
GS1596	5054	GCCCAAGCGCGGGGTAATCTGTCGAGTGCACAG	9643	AQARGNLSSAQ	14232	ARGNLSS	0.094135	-0.14906
SyS2801	5055	GCCCAAGACAACATGAAACTCCACGTCGCACAG	9644	AQDNMKLHVAQ	14233	DNMKLHV	0.094093	-0.22527
SyS2802	5056	GCCCAAGAAAAAAACCCAACAAAGCTACGCACAG	9645	AQEKTQQSYAQ	14234	EKTQQSY	0.094009	-0.08103
GS1597	5057	GCCCAATCGAATGGTTTGGCGCGGAATGCACAG	9646	AQSNGLARNAQ	14235	SNGLARN	0.093844	-0.16118
GS1598	5058	GCCCAAGTCGTCAGCCACAGACCCGCCGCACAG	9647	AQVVSHRPAAQ	14236	VVSHRPA	0.093796	-0.17112
SyS2803	5059	GCCCAAAGTTTGGGTGTTAGTCGGAATGCACAG	9648	AQSLGVSRNAQ	14237	SLGVSRN	0.093666	-0.06472
SyS2804	5060	GCCCAAGACCACAGCCACGGCAGAGACGCACAG	9649	AQDHSHGRDAQ	14238	DHSHGRD	0.093446	-0.218
SyP78	5061	GCCCAATCGACTCATCAGGTGGCGAATGCACAG	9650	AQSTHQVANAQ	14239	STHQVAN	0.093182	-0.0423
SyS2806	5062	GCCCAAAATCAGAGTGCGAGTAGTCGGGCACAG	9651	AQNQSASSRAQ	14240	NQSASSR	0.09291	-0.16223
SyS2807	5063	GCCCAAGTCACCGTCGGCAGCCACATGGCACAG	9652	AQVTVGSHMAQ	14241	VTVGSHM	0.092881	-0.13936
SyS2808	5064	GCCCAAAGCAGCAACATCGCCCCAAAACGCACAG	9653	AQSSNIAQNAQ	14242	SSNIAQN	0.092827	-0.11131
GP222	5065	GCCCAATTGAATGAGATGGCTACTCCTGCACAG	9654	AQLNEMATPAQ	14243	LNEMATP	0.092632	-0.071

FIG. 33 (Continued)

GS1600	5066	GCCCAAAGCACCAAAATCGAAAGAGACGCACAG	9655	AQSTKIERDAQ	14244	STKIERD	0.092384	-0.16337
SyS2811	5067	GCCCAAAACCTCGTCGACGCCAGAATCGCACAG	9656	AQNLVDARIAQ	14245	NLVDARI	0.092338	-0.20345
GS1601	5068	GCCCAATACAGCACCGGCAAAGACGCCGCACAG	9657	AQYSTGKDAAQ	14246	YSTGKDA	0.092318	-0.16663
SyS2812	5069	GCCCAAACCCAAGGCATCGTCACCAGCGCACAG	9658	AQTQGIVTSAQ	14247	TQGIVTS	0.092249	-0.22187
SyS2813	5070	GCCCAATCTTTTGGGGCTACGAGTTTGGCACAG	9659	AQSFGATSLAQ	14248	SFGATSL	0.092013	-0.22434
SyP79	5071	GCCCAAACTGCGGGGATGTCTTCGCGGGCACAG	9660	AQTAGMSSRAQ	14249	TAGMSSR	0.091732	-0.03931
SyS2815	5072	GCCCAAAGAGACAACAGCCTCATCCCCGCACAG	9661	AQRDNSLIPAQ	14250	RDNSLIP	0.091477	-0.06762
SyS2816	5073	GCCCAAAAGACTAATGCTGATTATGGGGCACAG	9662	AQKTNADYGAQ	14251	KTNADYG	0.09146	-0.13314
GS1602	5074	GCCCAAGTCAACCCCCACAGAACCATGGCACAG	9663	AQVNPHRTMAQ	14252	VNPHRTM	0.091294	-0.14811
GS1603	5075	GCCCAAGATATTCGTGGGAGGCCTACTGCACAG	9664	AQDIRGRPTAQ	14253	DIRGRPT	0.091275	-0.16528
SyS2818	5076	GCCCAACGTGAGGTTTCGAGTACTTCTGCACAG	9665	AQREVSSTSAQ	14254	REVSSTS	0.091098	-0.0482
SyS2819	5077	GCCCAAGTCAGCCAAGGCACCAGAGTCGCACAG	9666	AQVSQGTRVAQ	14255	VSQGTRV	0.091058	-0.12344
SyS2820	5078	GCCCAAAAGACGCCTATTATGCATGCGGCACAG	9667	AQKTPIMHAAQ	14256	KTPIMHA	0.090778	-0.14647
GP224	5079	GCCCAACTGGAGTCGCGGGATACGGTTGCACAG	9668	AQLESRDTVAQ	14257	LESRDTV	0.090555	-0.07426
SyS2822	5080	GCCCAAGTCCTCAACAGCAGCATGACCGCACAG	9669	AQVLNSSMTAQ	14258	VLNSSMT	0.090547	-0.22064
GS1605	5081	GCCCAATTTCGGACTGTGACGCAGGCGGCACAG	9670	AQFRTVTQAAQ	14259	FRTVTQA	0.090305	-0.15001
SyS2823	5082	GCCCAAACCGGCGCCATGAACATGACCGCACAG	9671	AQTGAMNMTAQ	14260	TGAMNMT	0.09021	0.113384
GS1606	5083	GCCCAATTGAAGACTCAGAATTATTCTGCACAG	9672	AQLKTQNYSAQ	14261	LKTQNYS	0.090046	-0.18457
GS1607	5084	GCCCAACAGAAGACGATGTTGACTGCTGCACAG	9673	AQQKTMLTAAQ	14262	QKTMLTA	0.089785	-0.10968
SyS2824	5085	GCCCAAAGTAATATTATTGGTTCGGATGCACAG	9674	AQSNIIGSDAQ	14263	SNIIGSD	0.089711	-0.20562
SyS2825	5086	GCCCAATCGGTGTCGGTTTCGAAGATGGCACAG	9675	AQSVSVSKMAQ	14264	SVSVSKM	0.089669	-0.22042
SyS2826	5087	GCCCAAGCGGCGCAGGTTTCGCATGCTGCACAG	9676	AQAAQVSHAAQ	14265	AAQVSHA	0.089533	-0.18284
SyS2827	5088	GCCCAAATTAATGTGGTTGAGAAGGCTGCACAG	9677	AQINVVEKAAQ	14266	INVVEKA	0.089471	-0.14819
SyS2829	5089	GCCCAAATGCTCAGAGGCGACCTCCCCGCACAG	9678	AQMLRGDLPAQ	14267	MLRGDLP	0.089436	-0.18245
SyS2830	5090	GCCCAAAACCTCCCCACCATGCAACCCGCACAG	9679	AQNLPTMQPAQ	14268	NLPTMQP	0.089402	-0.21557
SyS2831	5091	GCCCAATTCCAAGACAAAATCAACAGAGCACAG	9680	AQFQDKINRAQ	14269	FQDKINR	0.089402	-0.21557
GS1609	5092	GCCCAAAGCAGACAAACCATCGAAACCGCACAG	9681	AQSRQTIETAQ	14270	SRQTIET	0.089312	-0.12392
SyS2833	5093	GCCCAACTCCACAGCAAACTCAACGGCGCACAG	9682	AQLHSKLNGAQ	14271	LHSKLNG	0.089225	-0.17557
SyS2834	5094	GCCCAAACCCCCAGCGCCAGCAACATGGCACAG	9683	AQTPSASNMAQ	14272	TPSASNM	0.089132	-0.23296
GS1611	5095	GCCCAAGCTAATACGGCTATTAGGACTGCACAG	9684	AQANTAIRTAQ	14273	ANTAIRT	0.088865	-0.18637
GS1612	5096	GCCCAAAGCCCCCTACAACCAAAACAACGCACAG	9685	AQSPYNQNNAQ	14274	SPYNQNN	0.088563	-0.18009
SyS2835	5097	GCCCAATCGGGGAAGCAGCAGACGACTGCACAG	9686	AQSGKQQTTAQ	14275	SGKQQTT	0.088368	-0.06888

FIG. 33 (Continued)

SyS2837	5098	GCCCAAAATCTTCCGGTGCAGGGGAGTGCACAG	9687	AQNLPVQGSAQ	14276	NLPVQGS	0.088146	-0.00262
SyS2838	5099	GCCCAACCCAACCTCACCACCGAAAGAGCACAG	9688	AQPNLTTERAQ	14277	PNLTTER	0.088109	-0.05808
GP227	5100	GCCCAAGCTAGTCTTGTTAATACTGCTGCACAG	9689	AQASLVNTAAQ	14278	ASLVNTA	0.088065	-0.06829
SyS2839	5101	GCCCAATCTACTGCGGGGGATACTCGGGCACAG	9690	AQSTAGDTRAQ	14279	STAGDTR	0.088063	-0.14531
GS1613	5102	GCCCAACTCAGAGACACCAGAACCGACGCACAG	9691	AQLRDTRTDAQ	14280	LRDTRTD	0.087948	-0.1433
GS1614	5103	GCCCAACTCCAACAAGCCCAACCCCAAGCACAG	9692	AQLQQAQPQAQ	14281	LQQAQPQ	0.087727	-0.17919
SyS2841	5104	GCCCAATATTCTCCTCATGTTACGCCTGCACAG	9693	AQYSPHVTPAQ	14282	YSPHVTP	0.087653	-0.07979
GS1615	5105	GCCCAACTCCAAATCAAAACCAGCCCCCGCACAG	9694	AQLQIKTSPAQ	14283	LQIKTSP	0.087649	-0.11568
GP228	5106	GCCCAAAGGGTGCCTCCGAATCTGCAGGCACAG	9695	AQRVPPNLQAQ	14284	RVPPNLQ	0.087556	-0.0685
SyS2842	5107	GCCCAACTTGCTGAGCATCCGAAGACGGCACAG	9696	AQLAEHPKTAQ	14285	LAEHPKT	0.087554	-0.21679
SyS2843	5108	GCCCAAATTGCGGCGCGTAGTCCGTTGGCACAG	9697	AQIAARSPLAQ	14286	IAARSPL	0.087495	-0.06327
SyS2844	5109	GCCCAAAGTGGTAAGCAGCATGAGGATGCACAG	9698	AQSGKQHEDAQ	14287	SGKQHED	0.087338	-0.23173
SyS2846	5110	GCCCAAATTGGGAATCTGCAGGCGACGGCACAG	9699	AQIGNLQATAQ	14288	IGNLQAT	0.087023	-0.15011
SyS2847	5111	GCCCAACCTGATGCTTCTCAGCGGGTTGCACAG	9700	AQPDASQRVAQ	14289	PDASQRV	0.087004	-0.16283
SyS2849	5112	GCCCAAGCTGTGGATAGGATGACGCCTGCACAG	9701	AQAVDRMTPAQ	14290	AVDRMTP	0.086492	-0.04762
GP229	5113	GCCCAATTTGGGCGTGAGAAGCCGGCTGCACAG	9702	AQFGREKPAAQ	14291	FGREKPA	0.086492	-0.0728
GS1619	5114	GCCCAACTTAATAATAGGCCGCAGTTGGCACAG	9703	AQLNNRPQLAQ	14292	LNNRPQL	0.086134	-0.08574
SyS2853	5115	GCCCAAAATTTTCATGGTCGGACTGATGCACAG	9704	AQNFHGRTDAQ	14293	NFHGRTD	0.085757	-0.22042
SyS2854	5116	GCCCAAGGCGTCAGACTCAGCAGCACCGCACAG	9705	AQGVRLSSTAQ	14294	GVRLSST	0.085645	-0.17875
SyS2856	5117	GCCCAAACCGTCAACAGCCACAGACAAGCACAG	9706	AQTVNSHRQAQ	14295	TVNSHRQ	0.085229	-0.1986
SyP82	5118	GCCCAAAATAGTAATCATACGCCTAGGGCACAG	9707	AQNSNHTPRAQ	14296	NSNHTPR	0.085172	-0.04369
SyS2857	5119	GCCCAAGCCAACACCATCACCGTCGTCGCACAG	9708	AQANTITVVAQ	14297	ANTITVV	0.085083	-0.19133
GS1623	5120	GCCCAAGACGTCACCCAAAGCAAACCCGCACAG	9709	AQDVTQSKPAQ	14298	DVTQSKP	0.084872	-0.16663
TS181	5121	GCCCAAGGTAATCATGCGCGTAATCTGGCACAG	9710	AQGNHARNLAQ	14299	GNHARNL	0.084694	-0.26297
SyS2859	5122	GCCCAACACACACAGAGACACCAGCATGGCACAG	9711	AQQHRDTSMAQ	14300	QHRDTSM	0.084679	-0.16708
SyS2860	5123	GCCCAACTGCAGGGTAGGCTGACGTCGGCACAG	9712	AQLQGRLTSAQ	14301	LQGRLTS	0.084645	-0.16466
SyS2861	5124	GCCCAAATTTCTATGAGGGAGCAGTCGGCACAG	9713	AQISMREQSAQ	14302	ISMREQS	0.084611	-0.16223
GS1624	5125	GCCCAAACCAGAAACTTCGACCACACACCGCACAG	9714	AQTRNFDHTAQ	14303	TRNFDHT	0.084554	-0.1756
SyS2862	5126	GCCCAAGCTAGTCATCGGGCGCAGATTGCACAG	9715	AQASHRAQIAQ	14304	ASHRAQI	0.084508	-0.06218
GP232	5127	GCCCAAAATCAGCAGAGTCCTCATAAGGCACAG	9716	AQNQQSPHKAQ	14305	NQQSPHK	0.084412	-0.06961
SyS2863	5128	GCCCAAAGGCCGGGGGAGTCGAATCCTGCACAG	9717	AQRPGESNPAQ	14306	RPGESNP	0.084402	-0.08538
SyS2864	5129	GCCCAAGCGCGTGATAGTAGTATTATGGCACAG	9718	AQARDSSIMAQ	14307	ARDSSIM	0.084397	-0.09353

FIG. 33 (Continued)

GS1625	5130	GCCCAAACCGGCATGAGCACCCAAGTCGCACAG	9719	AQTGMSTQVAQ	14308	TGMSTQV	0.084373	-0.1586
SyS2865	5131	GCCCAAATGGGTGTGAAGGCGGATATTGCACAG	9720	AQMGVKADIAQ	14309	MGVKADI	0.084327	0.025771
SyS2866	5132	GCCCAACAATTCAAAGGCATCACCCAAGCACAG	9721	AQQFKGITQAQ	14310	QFKGITQ	0.084326	-0.01044
SyS2867	5133	GCCCAACACAACAACAGCCCCACCCACGCACAG	9722	AQHNNSPTHAQ	14311	HNNSPTH	0.084074	-0.23618
SyS2868	5134	GCCCAAGACAGCAACTTCACCAGCGCCGCACAG	9723	AQDSNFTSAAQ	14312	DSNFTSA	0.083991	-0.23133
SyP83	5135	GCCCAAGCGGTTCCGCATATGGGTACGGCACAG	9724	AQAVPHMGTAQ	14313	AVPHMGT	0.083983	-0.04282
SyS2869	5136	GCCCAAGTCGTCAGCCCCAACCTCATGGCACAG	9725	AQVVSPNLMAQ	14314	VVSPNLM	0.083952	-0.22891
SyS2870	5137	GCCCAACCCTTCCCCAAAACCCTCGACGCACAG	9726	AQPFPKTLDAQ	14315	PFPKTLD	0.08395	-0.19353
GP233	5138	GCCCAACAGAGTGCGGGTCTTGCGGAGGCACAG	9727	AQQSAGLAEAQ	14316	QSAGLAE	0.083906	-0.07245
GS1627	5139	GCCCAAGGCAAAGCCCACGACCTCGCCGCACAG	9728	AQGKAHDLAAQ	14317	GKAHDLA	0.083898	-0.17672
GS1629	5140	GCCCAACAAAGAATCAGCACCAACGCCGCACAG	9729	AQQRISTNAAQ	14318	QRISTNA	0.083603	-0.08402
SyS2872	5141	GCCCAATGGCTCACCACCGGCAGCAGCGCACAG	9730	AQWLTTGSSAQ	14319	WLTTGSS	0.083427	-0.22064
SyS2873	5142	GCCCAATACAGAGCCCAAGGCCCCCTCGCACAG	9731	AQYRAQGPLAQ	14320	YRAQGPL	0.083416	-0.18284
SyS2874	5143	GCCCAAGTGATGAAGAGGTATGATGAGGCACAG	9732	AQVMKRYDEAQ	14321	VMKRYDE	0.083375	-0.17799
GS1631	5144	GCCCAACTCGAATACAGCCAAAGAGACGCACAG	9733	AQLEYSQRDAQ	14322	LEYSQRD	0.083359	-0.18368
SyS2876	5145	GCCCAACTCCAAAAAGTCCACCTCGGCGCACAG	9734	AQLQKVHLGAQ	14323	LQKVHLG	0.083283	-0.16587
GP234	5146	GCCCAACGTTCTCATTCGCATCCTTCGGCACAG	9735	AQRSHSHPSAQ	14324	RSHSHPS	0.083166	-0.07405
SyS2878	5147	GCCCAACACACCTTCACCAGCACCGGCGCACAG	9736	AQHTFTSTGAQ	14325	HTFTSTG	0.082801	-0.06161
GS1632	5148	GCCCAATCTGTTGGTAGTGGTCCTGGTGCACAG	9737	AQSVGSGPGAQ	14326	SVGSGPG	0.082658	-0.1765
SyS2880	5149	GCCCAACAAAGCTTCAACGGCAGCAACGCACAG	9738	AQQSFNGSNAQ	14327	QSFNGSN	0.08265	-0.22557
SyS2881	5150	GCCCAAGTCACCGCCATCAGAGGCGCCGCACAG	9739	AQVTAIRGAAQ	14328	VTAIRGA	0.082407	-0.14105
GS1634	5151	GCCCAATTGGGGAAGACGTCTTATAGTGCACAG	9740	AQLGKTSYSAQ	14329	LGKTSYS	0.082225	-0.12353
GS1636	5152	GCCCAAAGTACGATGGCGATGGCTTCTGCACAG	9741	AQSTMAMASAQ	14330	STMAMAS	0.082049	-0.13139
SyS2882	5153	GCCCAAGCTTCTGGTAGGTCTTCTGCTGCACAG	9742	AQASGRSSAAQ	14331	ASGRSSA	0.081913	-0.13556
SyS2883	5154	GCCCAAGGCAGAACCCCCGCCGTCGAAGCACAG	9743	AQGRTPAVEAQ	14332	GRTPAVE	0.081913	-0.14283
SyS2884	5155	GCCCAAGGCAGAATCGACGTCAGCAGCGCACAG	9744	AQGRIDVSSAQ	14333	GRIDVSS	0.081913	-0.16223
SyS2886	5156	GCCCAAACCCCCAAAGTCAACAGCAGCGCACAG	9745	AQTPKVNSSAQ	14334	TPKVNSS	0.081913	-0.18648
SyS2887	5157	GCCCAAAGTGTTCGGAATTCGACTACTGCACAG	9746	AQSVRNSTTAQ	14335	SVRNSTT	0.081913	-0.1986
SyS2888	5158	GCCCAAGTTAATGGTGCTCAGCAGATTGCACAG	9747	AQVNGAQQIAQ	14336	VNGAQQI	0.081913	-0.20588
SyS2889	5159	GCCCAAAACAGAGCCGAAAGCTTCAGAGCACAG	9748	AQNRAESFRAQ	14337	NRAESFR	0.081913	-0.22042
SyS2891	5160	GCCCAACACGACAGAGCCAGCGTCAGAGCACAG	9749	AQHDRASVRAQ	14338	HDRASVR	0.081913	-0.22285
GS1637	5161	GCCCAAGACAGCCCCAGCAGAGGCAGAGCACAG	9750	AQDSPSRGRAQ	14339	DSPSRGR	0.081895	-0.13812

FIG. 33 (Continued)

GS1638	5162	GCCCAAAGCAACAACATCCACAGCAAAGCACAG	9751	AQSNNIHSKAQ	14340	SNNIHSK	0.081895	-0.13812
GS1639	5163	GCCCAAATCAACAACATCGTCATCCCCGCACAG	9752	AQINNIVIPAQ	14341	INNIVIP	0.081806	-0.18149
GS1640	5164	GCCCAAATTCGGAGTTCTGATGAGACGGCACAG	9753	AQIRSSDETAQ	14342	IRSSDET	0.081637	-0.17201
SyS2893	5165	GCCCAAAACATGCCCAGCCTCGTCGCCGCACAG	9754	AQNMPSLVAAQ	14343	NMPSLVA	0.081507	-0.07591
GP235	5166	GCCCAAAATAGGACGCTGGAGTCTATTGCACAG	9755	AQNRTLESIAQ	14344	NRTLESI	0.081383	-0.06975
SyS2894	5167	GCCCAACCCCAACACAACAACCCGCACAG	9756	AQPQHNNQPAQ	14345	PQHNNQP	0.081218	-0.05341
GS1643	5168	GCCCAACTCGGCTACAACGCCCACCCCGCACAG	9757	AQLGYNAHPAQ	14346	LGYNAHP	0.080886	-0.12719
SyS2897	5169	GCCCAACTCAAACACCAATACGACGGCGCACAG	9758	AQLKHQYDGAQ	14347	LKHQYDG	0.080743	-0.13435
GS1644	5170	GCCCAACACTACAGCCCCACCAGAGAAGCACAG	9759	AQHYSPTREAQ	14348	HYSPTRE	0.08058	-0.13312
GS1646	5171	GCCCAAAGCTACAGAAGCACCAGCGACGCACAG	9760	AQSYRSTSDAQ	14349	SYRSTSD	0.080284	-0.106
SyS2898	5172	GCCCAAGTTACGCCTACTGCGGCTCTTGCACAG	9761	AQVTPTAALAQ	14350	VTPTAAL	0.080182	-0.22926
SyS2899	5173	GCCCAATTGGAGCAGCGGTATAGTTCTGCACAG	9762	AQLEQRYSSAQ	14351	LEQRYSS	0.080126	-0.21194
SyS2900	5174	GCCCAAATGAATAATATTAGGCAGTCTGCACAG	9763	AQMNNIRQSAQ	14352	MNNIRQS	0.080126	-0.21194
GS1647	5175	GCCCAAAGTAGTCGTAATGATGCTTCTGCACAG	9764	AQSSRNDASAQ	14353	SSRNDAS	0.079783	-0.10036
SyS2902	5176	GCCCAAGGCACCGACAGAAAACCCTTCGCACAG	9765	AQGTDRKPFAQ	14354	GTDRKPF	0.07975	-0.21202
SyS2903	5177	GCCCAAAGAGTCAACAAAGAAGACAGAGCACAG	9766	AQRVNKEDRAQ	14355	RVNKEDR	0.079514	-0.2231
SyS2904	5178	GCCCAAACCGGCAGAAGCCTCGCCACCGCACAG	9767	AQTGRSLATAQ	14356	TGRSLAT	0.079216	-0.16466
SyS2905	5179	GCCCAAATGAAGTCTTCGACGTCGAATGCACAG	9768	AQMKSSTSNAQ	14357	MKSSTSN	0.07906	-0.22557
GS1651	5180	GCCCAAAGACACGACCTCGCCAGCAACGCACAG	9769	AQRHDLASNAQ	14358	RHDLASN	0.078859	-0.16909
SyS2906	5181	GCCCAATTGATGGCGGTGTCTACTCCGGCACAG	9770	AQLMAVSTPAQ	14359	LMAVSTP	0.078782	-0.09648
SyS2907	5182	GCCCAAAGAGAAGGCATCTACACCCTCGCACAG	9771	AQREGIYTLAQ	14360	REGIYTL	0.078638	-0.1783
SyS2910	5183	GCCCAAGACAACAAAGGCAGCCTCAGCGCACAG	9772	AQDNKGSLSAQ	14361	DNKGSLS	0.078127	-0.14438
SyS2914	5184	GCCCAAAAAGGCCAAGTCACCCACGGCGCACAG	9773	AQKGQVTHGAQ	14362	KGQVTHG	0.077531	-0.22434
SyS2915	5185	GCCCAAAGTAAGACTCTGAATAATCTTGCACAG	9774	AQSKTLNNLAQ	14363	SKTLNNL	0.077419	-0.06551
SyS2916	5186	GCCCAAAGGAATCCGCAGGTTCCTACTGCACAG	9775	AQRNPQVPTAQ	14364	RNPQVPT	0.076921	-0.20224
SS210	5187	GCCCAAAGTGCGAATGCGTCTAATACTGCACAG	9776	AQSANASNTAQ	14365	SANASNT	0.076865	-0.34975
GS1654	5188	GCCCAAGGCTACATGAAACCCGCCATCGCACAG	9777	AQGYMKPAIAQ	14366	GYMKPAI	0.076811	-0.13236
SyS2917	5189	GCCCAAAGCAGCCACGGCCCCACCCCCGCACAG	9778	AQSSHGPTPAQ	14367	SSHGPTP	0.076743	-0.15738
GS1655	5190	GCCCAAAGCACCAGAAACCCCCCCCAAGCACAG	9779	AQSTRNPPQAQ	14368	STRNPPQ	0.076738	-0.17386
GS1656	5191	GCCCAACTCAACAGAATCAACGAACAAGCACAG	9780	AQLNRINEQAQ	14369	LNRINEQ	0.076662	-0.15138
SyS2918	5192	GCCCAAGGCGCCGCCAAAAGCCAAAACGCACAG	9781	AQGAAKSQNAQ	14370	GAAKSQN	0.076533	-0.22064
SyS2919	5193	GCCCAACTCCCCACCCTCCACGGCCCCGCACAG	9782	AQLPTLHGPAQ	14371	LPTLHGP	0.076416	-0.16951

FIG. 33 (Continued)

SyS2920	5194	GCCCAAGTCCCCAGCACCATCAAAGGCGCACAG	9783	AQVPSTIKGAQ	14372	VPSTIKG	0.076072	-0.06158
GS1658	5195	GCCCAAACGTCGTCTATGCGGGAGTCGGCACAG	9784	AQTSSMRESAQ	14373	TSSMRES	0.076046	-0.15574
SyS2921	5196	GCCCAACTCATGAGCAGCAACAACGCCGCACAG	9785	AQLMSSNNAAQ	14374	LMSSNNA	0.076028	0.036405
SyS2922	5197	GCCCAAGCCAAAACCCAAAGCGCCACCGCACAG	9786	AQAKTQSATAQ	14375	AKTQSAT	0.076006	-0.23173
SyS2923	5198	GCCCAAAAGGAGGGGCAGTCTAGGTATGCACAG	9787	AQKEGQSRYAQ	14376	KEGQSRY	0.076006	-0.23173
SyS2924	5199	GCCCAAAAAGTCAACAGCAGCGCCACCGCACAG	9788	AQKVNSSATAQ	14377	KVNSSAT	0.075872	-0.15657
GS1659	5200	GCCCAAAGAACCACCAGCCTCGTCGCCGCACAG	9789	AQRTTSLVAAQ	14378	RTTSLVA	0.075859	-0.16814
GS1660	5201	GCCCAAATGACTAATCAGAGTGCGCATGCACAG	9790	AQMTNQSAHAQ	14379	MTNQSAH	0.075702	-0.09086
GS1661	5202	GCCCAACCCCACATCAGAGGCGAAAACGCACAG	9791	AQPHIRGENAQ	14380	PHIRGEN	0.075512	-0.1774
SyS2925	5203	GCCCAAAGAACCCAAAGCAGCATCAGCGCACAG	9792	AQRTQSSISAQ	14381	RTQSSIS	0.075407	-0.11999
SyS2927	5204	GCCCAAATGTTTACGACGACGGGTGCGGCACAG	9793	AQMFTTTGAAQ	14382	MFTTTGA	0.075331	0.191298
GS1662	5205	GCCCAAAGCAACATCAAACTCATGGCCGCACAG	9794	AQSNIKLMAAQ	14383	SNIKLMA	0.075323	-0.15001
GS1663	5206	GCCCAATCGACTCAGGGTACTCGGGATGCACAG	9795	AQSTQGTRDAQ	14384	STQGTRD	0.075323	-0.17577
SyS2929	5207	GCCCAAATTTTGTCGGGGCGTAATGGTGCACAG	9796	AQILSGRNGAQ	14385	ILSGRNG	0.07519	-0.16587
GP238	5208	GCCCAAGGGCTGAAGGTGTCTGGGTCTGCACAG	9797	AQGLKVSGSAQ	14386	GLKVSGS	0.075124	-0.0719
GS1666	5209	GCCCAAACCGGCGCCAACCTCCCCAACGCACAG	9798	AQTGANLPNAQ	14387	TGANLPN	0.074952	-0.18368
SyS2933	5210	GCCCAATACAGCCTCAGCATGCCCAACGCACAG	9799	AQYSLSMPNAQ	14388	YSLSMPN	0.074455	-0.19846
SyS2934	5211	GCCCAAACTTTTGAGAGGAAGGCTGCGGCACAG	9800	AQTFERKAAAQ	14389	TFERKAA	0.07445	-0.18527
GS1667	5212	GCCCAACTCGGCAGAGCCAGCAGCGTCGCACAG	9801	AQLGRASSVAQ	14390	LGRASSV	0.074286	-0.18637
SyS2936	5213	GCCCAAAGAACCAAAACCAGCGACGGCGCACAG	9802	AQRTKTSDGAQ	14391	RTKTSDG	0.074203	-0.15738
SyS2937	5214	GCCCAACTCAACCCCCACCTCGGCCCCCGCACAG	9803	AQLNPHLGPAQ	14392	LNPHLGP	0.074203	-0.15738
SyS2938	5215	GCCCAAATCATGCCCAACAACACCATGGCACAG	9804	AQIMPNNTMAQ	14393	IMPNNTM	0.074133	-0.1923
SyS2940	5216	GCCCAACATAAGAGTGATAGTGGTTATGCACAG	9805	AQHKSDSGYAQ	14394	HKSDSGY	0.073819	-0.10745
GS1670	5217	GCCCAAGATCGGCTGAATAAGAATAGTGCACAG	9806	AQDRLNKNSAQ	14395	DRLNKNS	0.07374	-0.03379
GS1671	5218	GCCCAAATGAGCGGCGGCAGCAGCAAAGCACAG	9807	AQMSGGSSKAQ	14396	MSGGSSK	0.073582	-0.18547
GS1673	5219	GCCCAACAGCGTGAGCAGGGGAATGCTGCACAG	9808	AQQREQGNAAQ	14397	QREQGNA	0.073506	-0.07984
SyS2941	5220	GCCCAAGGTGGTGGTAATGTGACGTCGGCACAG	9809	AQGGGNVTSAQ	14398	GGGNVTS	0.073363	-0.11899
GP239	5221	GCCCAAAATCTGAAGAATGCGTATGTTGCACAG	9810	AQNLKNAYVAQ	14399	NLKNAYV	0.073205	-0.06961
SyS2942	5222	GCCCAAAGCAAAAACGACAGACCCGGCGCACAG	9811	AQSKNDRPGAQ	14400	SKNDRPG	0.073138	-0.12344
SyS2943	5223	GCCCAAAGAGGCAGCGGCCAAGACATCGCACAG	9812	AQRGSGQDIAQ	14401	RGSGQDI	0.0731	-0.15374
SyS2944	5224	GCCCAAGTCGGCAGCAACACCAGCTACGCACAG	9813	AQVGSNTSYAQ	14402	VGSNTSY	0.073063	-0.03729
SyS2946	5225	GCCCAAAGCCCCAGAATCGGCAGCACCGCACAG	9814	AQSPRIGSTAQ	14403	SPRIGST	0.072976	-0.21436

FIG. 33 (Continued)

SyS2947	5226	GCCCAAGGTACTTTGAAGGAGACTAGTGCACAG	9815	AQGTLKETSAQ	14404	GTLKETS	0.072976	-0.21436
SyS2948	5227	GCCCAAAGCATCCAAAGAACCGTCGCCGCACAG	9816	AQSIQRTVAAQ	14405	SIQRTVA	0.072957	-0.12829
SyS2950	5228	GCCCAAAGAGGCGAAAGCAACGGCACCGCACAG	9817	AQRGESNGTAQ	14406	RGESNGT	0.072864	-0.13071
SyS2951	5229	GCCCAAGAACCCAGCAACGCCAGAGTCGCACAG	9818	AQEPSNARVAQ	14407	EPSNARV	0.072852	-0.21448
GS1674	5230	GCCCAAAGCCAAGCCACCATGAACAAAGCACAG	9819	AQSQATMNKAQ	14408	SQATMNK	0.072824	-0.03657
SyS2952	5231	GCCCAAGCCCAAGGCACCAGCACCACCGCACAG	9820	AQAQGTSTTAQ	14409	AQGTSTT	0.072774	0.021058
SyS2953	5232	GCCCAATACATGAGCAAAAACAACCTCGCACAG	9821	AQYMSKNNLAQ	14410	YMSKNNL	0.072703	-0.08453
GP241	5233	GCCCAAAATACGACGAATATGTCGAAGGCACAG	9822	AQNTTNMSKAQ	14411	NTTNMSK	0.072684	-0.06642
GS1675	5234	GCCCAATCGAAGGCTTCTAAGACTGAGGCACAG	9823	AQSKASKTEAQ	14412	SKASKTE	0.072653	-0.15764
SyS2955	5235	GCCCAAATGGCTGGTTCTATTGTTACTGCACAG	9824	AQMAGSIVTAQ	14413	MAGSIVT	0.072511	-0.22164
SyS2956	5236	GCCCAAGTGAATTCGAGTCAGACTCCTGCACAG	9825	AQVNSSQTPAQ	14414	VNSSQTP	0.07248	-0.17875
SyP88	5237	GCCCAAACTCGTAGTGCTCTTCTTGATGCACAG	9826	AQTRSALLDAQ	14415	TRSALLD	0.07245	-0.03959
SyS2958	5238	GCCCAAGGGATTAGTTATTCGCCTTCTGCACAG	9827	AQGISYSPSAQ	14416	GISYSPS	0.072408	-0.17433
SyS2959	5239	GCCCAACATGGGAGGGAGGTTCCGCAGGCACAG	9828	AQHGREVPQAQ	14417	HGREVPQ	0.07239	0.073051
GS1677	5240	GCCCAAACCAGAAGCGCCGACAACAGAGCACAG	9829	AQTRSADNRAQ	14418	TRSADNR	0.072342	-0.09862
SyS2962	5241	GCCCAATCTGGGAATTCGTCGCGTGGTGCACAG	9830	AQSGNSSRGAQ	14419	SGNSSRG	0.0723	-0.20216
SyS2963	5242	GCCCAAACGACGAAGGGGAATCCTTCGGCACAG	9831	AQTTKGNPSAQ	14420	TTKGNPS	0.071966	-0.20345
GS1679	5243	GCCCAAGACATGAGAAGCACCAGAGACGCACAG	9832	AQDMRSTRDAQ	14421	DMRSTRD	0.071824	-0.16842
SyS2964	5244	GCCCAACTGGGTAATTCGTTGCCGGCTGCACAG	9833	AQLGNSLPAAQ	14422	LGNSLPA	0.071809	-0.02082
GS1680	5245	GCCCAATTGACTAGTATGTCGATTCCTGCACAG	9834	AQLTSMSIPAQ	14423	LTSMSIP	0.071702	-0.1756
SyS2967	5246	GCCCAAGGCACCCACATCAAACAAGCCGCACAG	9835	AQGTHIKQAAQ	14424	GTHIKQA	0.071536	-0.18527
GS1681	5247	GCCCAAACTCAGGGTCGTATTGTTAGTGCACAG	9836	AQTQGRIVSAQ	14425	TQGRIVS	0.071228	-0.1296
SyS2970	5248	GCCCAACTCGGCGGCAACAACACCCTCGCACAG	9837	AQLGGNNTLAQ	14426	LGGNNTL	0.071141	-0.11838
SyS2971	5249	GCCCAAATGTCTGCGAATAATGGTCGTGCACAG	9838	AQMSANNGRAQ	14427	MSANNGR	0.071102	-0.0887
GP242	5250	GCCCAAGTTACTAATCCGATGAGTGCGGCACAG	9839	AQVTNPMSAAQ	14428	VTNPMSA	0.070957	-0.07086
SyS2972	5251	GCCCAAGAGGCTTATAAGTCTACGTCGGCACAG	9840	AQEAYKSTSAQ	14429	EAYKSTS	0.070916	-0.17193
SyS2975	5252	GCCCAAAGACCCAACAACCAAGGCCAAGCACAG	9841	AQRPNNQGQAQ	14430	RPNNQGQ	0.070759	-0.15288
SyS2976	5253	GCCCAAATGAATTTTGCGGGTAGTGGTGCACAG	9842	AQMNFAGSGAQ	14431	MNFAGSG	0.07066	-0.13071
GP243	5254	GCCCAAAAGACTAATCATAGTTCGTCTGCACAG	9843	AQKTNHSSSAQ	14432	KTNHSSS	0.070635	-0.06975
SyS2977	5255	GCCCAAAATGGGTATGGGTCGCAGACGGCACAG	9844	AQNGYGSQTAQ	14433	NGYGSQT	0.070529	-0.0094
SyS2978	5256	GCCCAAAAAACCGGCCACCAATTCACCGCACAG	9845	AQKTGHQFTAQ	14434	KTGHQFT	0.070429	-0.21818
SyS2979	5257	GCCCAAACCGCCAGAACCCTCCAACTCGCACAG	9846	AQTARTLQLAQ	14435	TARTLQL	0.070336	-0.1247

FIG. 33 (Continued)

SS213	5258	GCCCAACAAGCCAGCACCACCCAAATCGCACAG	9847	AQQASTTQIAQ	14436	QASTTQI	0.070288	-0.3987
SyS2980	5259	GCCCAAACTGCTTTTGATACGCGTGGTGCACAG	9848	AQTAFDTRGAQ	14437	TAFDTRG	0.070216	-0.0582
SyS2981	5260	GCCCAAGTCAACAGCCACGTCGCCAGAGCACAG	9849	AQVNSHVARAQ	14438	VNSHVAR	0.070107	0.01137
SyS2983	5261	GCCCAAAGTCCGCTTCATTCTAATACGGCACAG	9850	AQSPLHSNTAQ	14439	SPLHSNT	0.069894	-0.20951
SyS2984	5262	GCCCAACTCAGCAGAGTCACCATCAACGCACAG	9851	AQLSRVTINAQ	14440	LSRVTIN	0.069886	-0.1307
SyS2987	5263	GCCCAAACTCAGCATAATGTGGATTCGGCACAG	9852	AQTQHNVDSAQ	14441	TQHNVDS	0.069682	-0.21448
SyS2988	5264	GCCCAAACCTTCCAAACCAGCAACAGCGCACAG	9853	AQTFQTSNSAQ	14442	TFQTSNS	0.069368	0.003859
SyS2989	5265	GCCCAAAGTAATCATGTTAGTGTTAATGCACAG	9854	AQSNHVSVNAQ	14443	SNHVSVN	0.069358	-0.15496
SyS2990	5266	GCCCAAATGCTCCACAGCAGCATCACCGCACAG	9855	AQMLHSSITAQ	14444	MLHSSIT	0.069253	-0.2231
GS1685	5267	GCCCAACTGAAGGCTACTGATGGGTCGGCACAG	9856	AQLKATDGSAQ	14445	LKATDGS	0.068961	-0.16753
GS1686	5268	GCCCAACTCGGCAACATGCACACAACATGGCACAG	9857	AQLGNMHNMAQ	14446	LGNMHNM	0.068637	-0.10508
SyS2993	5269	GCCCAAATCAACAGACTCATCAGCGGCGCACAG	9858	AQINRLISGAQ	14447	INRLISG	0.068598	0.031034
SyS2994	5270	GCCCAAACCAGAAGCAACCTCGCCAGCGCACAG	9859	AQTRSNLASAQ	14448	TRSNLAS	0.068554	-0.15288
SyS2995	5271	GCCCAACATTCGAATGGTGTTAGGGGGGCACAG	9860	AQHSNGVRGAQ	14449	HSNGVRG	0.06839	-0.09686
SyS2997	5272	GCCCAAGCCGGCAACCCCAGAGAAAAAGCACAG	9861	AQAGNPREKAQ	14450	AGNPREK	0.068322	-0.12337
SyS2999	5273	GCCCAAAGAGCCAGAGACGTCGACGAAGCACAG	9862	AQRARDVDEAQ	14451	RARDVDE	0.067899	-0.17678
SS217	5274	GCCCAAGTCAGCAACGGCCCCAGCCTCGCACAG	9863	AQVSNGPSLAQ	14452	VSNGPSL	0.067877	-0.37204
GS1687	5275	GCCCAAGCGAATCAGAGGGGTGTTGGGGCACAG	9864	AQANQRGVGAQ	14453	ANQRGVG	0.067791	-0.14599
GS1688	5276	GCCCAAATGAGAAGCGAAACCCTCAACGCACAG	9865	AQMRSETLNAQ	14454	MRSETLN	0.06777	-0.171
GS1689	5277	GCCCAAAAACCCAGCAGCCAACTCCTCGCACAG	9866	AQKPSSQLLAQ	14455	KPSSQLL	0.067749	-0.10538
SyS3000	5278	GCCCAAAGCCTCAGACCCCACGACAGAGCACAG	9867	AQSLRPHDRAQ	14456	SLRPHDR	0.067635	-0.23376
GS1690	5279	GCCCAAGGTTCGAATGCTTCGAAGTATGCACAG	9868	AQGSNASKYAQ	14457	GSNASKY	0.067496	-0.09073
SyS3002	5280	GCCCAAACCAACAGAGACCTCGGCCCCGCACAG	9869	AQTNRDLGPAQ	14458	TNRDLGP	0.067362	-0.23618
SyS3004	5281	GCCCAATGGGGGTCTACTGCGGGTGCTGCACAG	9870	AQWGSTAGAAQ	14459	WGSTAGA	0.067211	-0.14795
SyS3005	5282	GCCCAAATCAGCGGCGCCGACAGAACCGCACAG	9871	AQISGADRTAQ	14460	ISGADRT	0.067202	-0.06067
SyS3007	5283	GCCCAAAGCGCCGTCAGAAGCCCCATCGCACAG	9872	AQSAVRSPIAQ	14461	SAVRSPI	0.067136	-0.18648
GS1693	5284	GCCCAAAGAGTCAGCCACACCGAAACCGCACAG	9873	AQRVSHTETAQ	14462	RVSHTET	0.066771	-0.12188
SyS3008	5285	GCCCAAAAAGCCAACAGCCAAATCACCGCACAG	9874	AQKANSQITAQ	14463	KANSQIT	0.066615	-0.2268
SyS3009	5286	GCCCAACCGAGTGTGTATCGTGAGCCTGCACAG	9875	AQPSVYREPAQ	14464	PSVYREP	0.066506	-0.19375
SyS3010	5287	GCCCAAACCACACCAACTTCGTCACCAGCGCACAG	9876	AQTTNFVTSAQ	14465	TTNFVTS	0.066487	-0.196
SyS3011	5288	GCCCAAAACCTCATGCCCACCGACAGAGCACAG	9877	AQNLMPTDRAQ	14466	NLMPTDR	0.066443	-0.0508
GS1695	5289	GCCCAAACCAACCACACCGGCAGCCAAGCACAG	9878	AQTNHTGSQAQ	14467	TNHTGSQ	0.066407	-0.16304

FIG. 33 (Continued)

GS1696	5290	GCCCAACACTGGAACGGCACCAACCCCGCACAG	9879	AQHWNGTNPAQ	14468	HWNGTNP	0.066366	-0.10986
GS1697	5291	GCCCAACATAAGTCTATTGGTCAGGAGGCACAG	9880	AQHKSIGQEAQ	14469	HKSIGQE	0.066155	-0.17768
SyS3012	5292	GCCCAAACTCGGCCGATTCCGATTAGTGCACAG	9881	AQTRPIPISAQ	14470	TRPIPIS	0.065601	-0.18769
SyS3013	5293	GCCCAAAACCCCGGCATGAGCAGAATGGCACAG	9882	AQNPGMSRMAQ	14471	NPGMSRM	0.065579	-0.20345
SyS3015	5294	GCCCAAATTGCTAATCGGGTGTCGCCTGCACAG	9883	AQIANRVSPAQ	14472	IANRVSP	0.065325	-0.21325
GP244	5295	GCCCAAACGGCGTTGGCGAATCAGAAGGCACAG	9884	AQTALANQKAQ	14473	TALANQK	0.065317	0.093523
SyS3016	5296	GCCCAAACTTCGCTTTCTTCTTCTGCTGCACAG	9885	AQTSLSSSAAQ	14474	TSLSSSA	0.06508	-0.17118
GS1700	5297	GCCCAAGCTTTGACTGGTAATATGTCGGCACAG	9886	AQALTGNMSAQ	14475	ALTGNMS	0.064735	-0.13712
GS1701	5298	GCCCAAATGCAGACGAAGAATGTGCCGGCACAG	9887	AQMQTKNVPAQ	14476	MQTKNVP	0.064729	-0.16432
GP246	5299	GCCCAACAGGCGACTAAGACTAATGTTGCACAG	9888	AQQATKTNVAQ	14477	QATKTNV	0.064527	-0.07329
GS1702	5300	GCCCAACTCCACACCACCAGCGTCGCACAG	9889	AQLHTTSSVAQ	14478	LHTTSSV	0.064309	-0.06184
GS1703	5301	GCCCAATACGTCCAAAGCAGCAGCAACGCACAG	9890	AQYVQSSSNAQ	14479	YVQSSSN	0.064226	-0.18368
SyS3017	5302	GCCCAAACGATGAAGATTCGTACTGAGGCACAG	9891	AQTMKIRTEAQ	14480	TMKIRTE	0.063807	-0.19133
SyS3019	5303	GCCCAAAAGAGTCATTCGCCTGGGTCGGCACAG	9892	AQKSHSPGSAQ	14481	KSHSPGS	0.063552	-0.19375
GP248	5304	GCCCAAAAGGCGGTGGATCCTCCGAATGCACAG	9893	AQKAVDPPNAQ	14482	KAVDPPN	0.06345	-0.07301
SyS3021	5305	GCCCAAAATGCTCCTCCTATGAGTCCTGCACAG	9894	AQNAPPMSPAQ	14483	NAPPMSP	0.063019	-0.21194
SyS3022	5306	GCCCAAATCAACAAAATGTTCACCCCCGCACAG	9895	AQINKMFTPAQ	14484	INKMFTP	0.062922	-0.18245
GS1704	5307	GCCCAATATGCTAAGGCGACTTTGGGTGCACAG	9896	AQYAKATLGAQ	14485	YAKATLG	0.062788	-0.15955
GS1705	5308	GCCCAACATCTTGCGCGTCCGTCTGAGGCACAG	9897	AQHLARPSEAQ	14486	HLARPSE	0.062657	-0.14328
SyS3024	5309	GCCCAACAACTCAACAGCGACAGAAACGCACAG	9898	AQQLNSDRNAQ	14487	QLNSDRN	0.062537	-0.17678
SyS3026	5310	GCCCAAATGAGGCCTGATACTAGTTATGCACAG	9899	AQMRPDTSYAQ	14488	MRPDTSY	0.061794	-0.07565
SyS3027	5311	GCCCAAGGCGTCGCCATGAGCAGCGGCGCACAG	9900	AQGVAMSSGAQ	14489	GVAMSSG	0.061421	-0.22187
SyS3028	5312	GCCCAAGGTCATTCTAGGCCTGATCGGGCACAG	9901	AQGHSRPDRAQ	14490	GHSRPDR	0.061217	-0.21315
SyS3029	5313	GCCCAAGTCTTCCAAGCCACCAGAACCGCACAG	9902	AQVFQATRTAQ	14491	VFQATRT	0.06105	-0.14842
SyP91	5314	GCCCAAACTTCGTTGACGTCGTATACTGCACAG	9903	AQTSLTSYTAQ	14492	TSLTSYT	0.06097	-0.04186
SyS3032	5315	GCCCAAAAACTCAACACCGGCGACATCGCACAG	9904	AQKLNTGDIAQ	14493	KLNTGDI	0.06088	-0.09377
GS1708	5316	GCCCAAAGAACCAACGAAACCATCGTCGCACAG	9905	AQRTNETIVAQ	14494	RTNETIV	0.060773	-0.10144
SyS3033	5317	GCCCAAAGACTCCAAAACAGCACCCCCGCACAG	9906	AQRLQNSTPAQ	14495	RLQNSTP	0.060769	-0.14526
SyS3036	5318	GCCCAAACGTCGCGGCTTACTAGTGGGGCACAG	9907	AQTSRLTSGAQ	14496	TSRLTSG	0.060537	-0.18284
SyS3037	5319	GCCCAAAGCAACACCACCTTCAGCGCCGCACAG	9908	AQSNTTFSAAQ	14497	SNTTFSA	0.060537	-0.218
SyS3038	5320	GCCCAAGACCAAAGAAGCAGCCCCGCCGCACAG	9909	AQDQRSSPAAQ	14498	DQRSSPA	0.060474	0.074204
GS1709	5321	GCCCAAGTTGGGAGTGGTGGGTCTCGTGCACAG	9910	AQVGSGGSRAQ	14499	VGSGGSR	0.060342	-0.18149

FIG. 33 (Continued)

SyS3039	5322	GCCCAAAGAAGCACCAACGCCCCCAACGCACAG	9911	AQRSTNAPNAQ	14500	RSTNAPN	0.060253	-0.18527
GP249	5323	GCCCAAATGGCGGGTCAGCAGCGGTTGGCACAG	9912	AQMAGQQRLAQ	14501	MAGQQRL	0.060214	-0.07405
GS1710	5324	GCCCAAATTAGGAATTCTGCTCCTCCTGCACAG	9913	AQIRNSAPPAQ	14502	IRNSAPP	0.060006	-0.16753
SyS3040	5325	GCCCAACTGTCGACTAAGAGTTTTAATGCACAG	9914	AQLSTKSFNAQ	14503	LSTKSFN	0.059895	-0.0596
GS1711	5326	GCCCAATGGCCGGGGTCGATTACTGCGGCACAG	9915	AQWPGSITAAQ	14504	WPGSITA	0.059836	-0.1026
SS224	5327	GCCCAAACCGGCGGCGTCCACGCCCAAGCACAG	9916	AQTGGVHAQAQ	14505	TGGVHAQ	0.059719	-0.36534
GS1713	5328	GCCCAATCTGAGAGGTCGTCTATGGCTGCACAG	9917	AQSERSSMAAQ	14506	SERSSMA	0.059554	-0.17386
SyS3042	5329	GCCCAATTTCAGAATGGTCGGAATAATGCACAG	9918	AQFQNGRNNAQ	14507	FQNGRNN	0.05943	-0.22527
SyS3045	5330	GCCCAAGGCGGCAGCAGACTCCCCCCAAGCACAG	9919	AQGGSRLPQAQ	14508	GGSRLPQ	0.059246	0.005703
SyS3047	5331	GCCCAAGGCGGCAACAGCCTCAGCGTCGCACAG	9920	AQGGNSLSVAQ	14509	GGNSLSV	0.058708	-0.19739
SyS3048	5332	GCCCAATCGAAGAAGATTGATCATGGTGCACAG	9921	AQSKKIDHGAQ	14510	SKKIDHG	0.058708	-0.19739
SyS3049	5333	GCCCAATATCGTGATACGTTGGCGGCTGCACAG	9922	AQYRDTLAAAQ	14511	YRDTLAA	0.05864	-0.10104
GS1715	5334	GCCCAACTCCACAGCGGCGAAAGAAACGCACAG	9923	AQLHSGERNAQ	14512	LHSGERN	0.058356	-0.13213
SyS3050	5335	GCCCAAATTATGCCTCATGGTTCGCCTGCACAG	9924	AQIMPHGSPAQ	14513	IMPHGSP	0.05825	-0.17629
SyS3051	5336	GCCCAAACCGCCCAGAACCCTCAACATGGCACAG	9925	AQTARTLNMAQ	14514	TARTLNM	0.05825	-0.12147
SyP93	5337	GCCCAAGCTAGTGTTCAGGGGCATAGTGCACAG	9926	AQASVQGHSAQ	14515	ASVQGHS	0.058222	-0.04362
SyS3054	5338	GCCCAATTGAATAATGCTGGGAGGGCGGCACAG	9927	AQLNNAGRAAQ	14516	LNNAGRA	0.058102	-0.20216
SyS3056	5339	GCCCAAGGCCTCAGAGGCAGCCACGCCGCACAG	9928	AQGLRGSHAAQ	14517	GLRGSHA	0.058027	-0.15011
SyS3057	5340	GCCCAATTTGTGCGTGATTCTTATTCGGCACAG	9929	AQFVRDSYSAQ	14518	FVRDSYS	0.057988	-0.1214
GS1716	5341	GCCCAAGGCAGATTCACCGGCACCGAAGCACAG	9930	AQGRFTGTEAQ	14519	GRFTGTE	0.057942	-0.17577
SP53	5342	GCCCAACGTCAGAATCCGATTGAGCTTGCACAG	9931	AQRQNPIELAQ	14520	RQNPIEL	0.057876	-0.05124
SyS3058	5343	GCCCAAGTCAGAGACAAATTCGGCACCGCACAG	9932	AQVRDKFGTAQ	14521	VRDKFGT	0.057761	-0.15253
GS1717	5344	GCCCAACTCCCCAGCAACAGCAAGAGCACAG	9933	AQLPSNSNRAQ	14522	LPSNSNR	0.057489	-0.18547
SyS3061	5345	GCCCAAGTCAGACAAGAACACACCAGCGCACAG	9934	AQVRQEHTSAQ	14523	VRQEHTS	0.057485	-0.13639
SyS3062	5346	GCCCAAATCAGACAAGGCCCCACCAACGCACAG	9935	AQIRQGPTNAQ	14524	IRQGPTN	0.057472	-0.22434
SyS3063	5347	GCCCAAGACTACAGCAAAAGCAACACCGCACAG	9936	AQDYSKSNTAQ	14525	DYSKSNT	0.057421	-0.11995
SyS3064	5348	GCCCAAATGTCGAATGTTAATGTTTCGGCACAG	9937	AQMSNVNVSAQ	14526	MSNVNVS	0.057014	-0.22891
SyS3066	5349	GCCCAAATGAGCAGCGGCAGAAGCCTCGCACAG	9938	AQMSSGRSLAQ	14527	MSSGRSL	0.056536	-0.21194
SyS3067	5350	GCCCAAGGCCTCAGAGACATCAGAGCCGCACAG	9939	AQGLRDIRAAQ	14528	GLRDIRA	0.056134	-0.21436
SyS3068	5351	GCCCAACTGATTTCTGCTCATAAGGGTGCACAG	9940	AQLISAHKGAQ	14529	LISAHKG	0.056125	-0.18984
SyS3069	5352	GCCCAACCCATCAACACCCACGCCGCCACAG	9941	AQPINTHAAAQ	14530	PINTHAA	0.055919	-0.03722
SyS3070	5353	GCCCAAATGCCTCATGTGGGGAATGCTGCACAG	9942	AQMPHVGNAAQ	14531	MPHVGNA	0.055761	-0.196

FIG. 33 (Continued)

SyS3071	5354	GCCCAATATGGTTCTTCTGCGATTAATGCACAG	9943	AQYGSSAINAQ	14532	YGSSAIN	0.055471	-0.22557
SyS3073	5355	GCCCAACATGCTTCTATGCCTAGTTCTGCACAG	9944	AQHASMPSSAQ	14533	HASMPSS	0.055168	-0.08783
SyS3074	5356	GCCCAATTTGGGGAGAATGCTCGTTTTGCACAG	9945	AQFGENARFAQ	14534	FGENARF	0.055162	-0.131
SyS3076	5357	GCCCAATCTAGGCATGATTTGCCTTCTGCACAG	9946	AQSRHDLPSAQ	14535	SRHDLPS	0.055032	-0.20224
SyS3077	5358	GCCCAACGGTCGCAGGGTGCGAATATGGCACAG	9947	AQRSQGANMAQ	14536	RSQGANM	0.054873	-0.14214
SyS3078	5359	GCCCAAGCCAACAGCAACAGCCACAGCGCACAG	9948	AQANSNSHSAQ	14537	ANSNSHS	0.054709	0.06627
GP255	5360	GCCCAACAGGCTAGGCAGAATCAGGGTGCACAG	9949	AQQARQNQGAQ	14538	QARQNQG	0.054577	-0.06905
GS1723	5361	GCCCAAGGTGTGGCTAGTAATACGACGGCACAG	9950	AQGVASNTTAQ	14539	GVASNTT	0.054331	-0.12484
GS1724	5362	GCCCAAAAGTATAGTTCTTCTCAGAGTGCACAG	9951	AQKYSSSQSAQ	14540	KYSSSQS	0.054225	-0.16528
SyS3081	5363	GCCCAAAGCGCCAAAACCCTCAACACCGCACAG	9952	AQSAKTLNTAQ	14541	SAKTLNT	0.054008	-0.06036
SyS3082	5364	GCCCAAGGCATCAGAACCACCAACGCCGCACAG	9953	AQGIRTTNAAQ	14542	GIRTTNA	0.053754	-0.12222
GP257	5365	GCCCAAATGAATACGACGATTAATAGGGCACAG	9954	AQMNTTINRAQ	14543	MNTTINR	0.053729	-0.06843
SyS3083	5366	GCCCAACTCAAAAACACCAGCCTCCCCGCACAG	9955	AQLKNTSLPAQ	14544	LKNTSLP	0.053711	-0.19254
GS1725	5367	GCCCAAACTAATCGTGCTGCTACGATGGCACAG	9956	AQTNRAATMAQ	14545	TNRAATM	0.053552	-0.07849
SyS3084	5368	GCCCAACACGGCTACCCCAACGTCCCCGCACAG	9957	AQHGYPNVPAQ	14546	HGYPNVP	0.053161	-0.20955
SyS3085	5369	GCCCAATGGGGCTACAGAGGCGCCGAAGCACAG	9958	AQWGYRGAEAQ	14547	WGYRGAE	0.053019	-0.20683
SyS3086	5370	GCCCAACTCCTCGTCACCAACACCAGCGCACAG	9959	AQLLVTNTSAQ	14548	LLVTNTS	0.052911	-0.20586
SP54	5371	GCCCAAAAGAATCGTCTTCCTCCTGATGCACAG	9960	AQKNRLPPDAQ	14549	KNRLPPD	0.052816	-0.05331
GP259	5372	GCCCAATATCGTTCGCAGGAGCATCCGGCACAG	9961	AQYRSQEHPAQ	14550	YRSQEHP	0.052745	-0.07356
GS1728	5373	GCCCAACACGGCGGCAGAGTCAGCCCCGCACAG	9962	AQHGGRVSPAQ	14551	HGGRVSP	0.052674	-0.08274
SP55	5374	GCCCAAGGGCAGAATAGGCTTGCTTCGGCACAG	9963	AQGQNRLASAQ	14552	GQNRLAS	0.052585	-0.05282
GS1729	5375	GCCCAACAGTCGGTTTCTGCTACGAGGGCACAG	9964	AQQSVSATRAQ	14553	QSVSATR	0.052569	-0.11912
GS1730	5376	GCCCAACAAAGACCCATCCCCCAAGCCGCACAG	9965	AQQRPIPQAAQ	14554	QRPIPQA	0.052511	-0.09282
GP260	5377	GCCCAACAGAGGGCGATTGGTATTGAGGCACAG	9966	AQQRAIGIEAQ	14555	QRAIGIE	0.052081	-0.06454
GS1731	5378	GCCCAATTTGGGCATGTGGGTATTAATGCACAG	9967	AQFGHVGINAQ	14556	FGHVGIN	0.052078	-0.15412
SyS3088	5379	GCCCAATTTGAGCATGTTCGTTCGGAGGCACAG	9968	AQFEHVRSEAQ	14557	FEHVRSE	0.051845	-0.23618
SyS3089	5380	GCCCAAAAAAGCGTCACCAGCAACACCGCACAG	9969	AQKSVTSNTAQ	14558	KSVTSNT	0.051777	-0.061
SyS3090	5381	GCCCAACTCACCGGCAACGTCACCGCCGCACAG	9970	AQLTGNVTAAQ	14559	LTGNVTA	0.051576	-0.21448
GS1732	5382	GCCCAAAATCATGCGTATCCGTCGGCGGCACAG	9971	AQNHAYPSAAQ	14560	NHAYPSA	0.051489	-0.16034
SyS3091	5383	GCCCAAATGCCGCAGGGTAAGAGTGTTGCACAG	9972	AQMPQGKSVAQ	14561	MPQGKSV	0.051435	-0.18163
SyS3092	5384	GCCCAACTCAGAACCGCCGCCACCAGCGCACAG	9973	AQLRTAATSAQ	14562	LRTAATS	0.051386	-0.23012
SyS3095	5385	GCCCAAGATTCTCAGCATCGGGTTTCTGCACAG	9974	AQDSQHRVSAQ	14563	DSQHRVS	0.05101	-0.15253

FIG. 33 (Continued)

SyS3096	5386	GCCCAATTCCTCAACGAACACACCGTCGCACAG	9975	AQFLNEHTVAQ	14564	FLNEHTV	0.050937	-0.10186
SyS3098	5387	GCCCAAAACAGCACCGGCACCAGCATGGCACAG	9976	AQNSTGTSMAQ	14565	NSTGTSM	0.050651	-0.03019
SyP98	5388	GCCCAACATAGTCCTCCTATGTCGGCGGCACAG	9977	AQHSPPMSAAQ	14566	HSPPMSA	0.05057	-0.0435
SyS3099	5389	GCCCAATTGATGTCGCAGCGTCCTACGGCACAG	9978	AQLMSQRPTAQ	14567	LMSQRPT	0.050441	-0.22649
SyS3100	5390	GCCCAAAACACCAACGTCAACCCCCCCCGCACAG	9979	AQNTNVNPPAQ	14568	NTNVNPP	0.050347	-0.18042
SyS3104	5391	GCCCAATGGGGTGGTTATTCTTCGGCTGCACAG	9980	AQWGGYSSAAQ	14569	WGGYSSA	0.050081	-0.2231
GS1733	5392	GCCCAATACAGCCTCAACCCCAGCGGCGCACAG	9981	AQYSLNPSGAQ	14570	YSLNPSG	0.050057	-0.05463
GS1734	5393	GCCCAAAAAGAAAGCAAAGACAGAGTCGCACAG	9982	AQKESKDRVAQ	14571	KESKDRV	0.050049	-0.18054
SyS3105	5394	GCCCAAAAGCTGGTGTCGAGTCCTGATGCACAG	9983	AQKLVSSPDAQ	14572	KLVSSPD	0.049827	-0.16829
SyS3106	5395	GCCCAAAACACCGCCAGCCACAACGCCGCACAG	9984	AQNTASHNAAQ	14573	NTASHNA	0.049827	-0.16829
SyS3107	5396	GCCCAAGACATGAGCAACAAAACCTACGCACAG	9985	AQDMSNKTYAQ	14574	DMSNKTY	0.049793	-0.19133
SyS3108	5397	GCCCAACTCGTCCACAAAGACTTCCCCGCACAG	9986	AQLVHKDFPAQ	14575	LVHKDFP	0.049712	-0.21571
SyS3109	5398	GCCCAAAAACCCGCCCTCGCCCAAAACGCACAG	9987	AQKPALAQNAQ	14576	KPALAQN	0.049542	-0.23296
GS1735	5399	GCCCAAGGCAACGCCCAACCAGCAAAGCACAG	9988	AQGNAQPSKAQ	14577	GNAQPSK	0.049521	-0.09141
SyS3110	5400	GCCCAAAGAGTCGCCCACACCGAAAACGCACAG	9989	AQRVAHTENAQ	14578	RVAHTEN	0.049496	-0.10715
SyS3111	5401	GCCCAAGTTTCTGCGTCTTTTATGGCGGCACAG	9990	AQVSASFMAAQ	14579	VSASFMA	0.049437	-0.02125
SyS3112	5402	GCCCAACGGGTGCTGACGGCTGATGCTGCACAG	9991	AQRVLTADAAQ	14580	RVLTADA	0.049329	-0.08038
GS1737	5403	GCCCAAACCGTCGTCGGCACCAAACAAGCACAG	9992	AQTVVGTKQAQ	14581	TVVGTKQ	0.049239	-0.16241
SyS3113	5404	GCCCAACTTGCGAGGACGCAGCCTTCTCACAG	9993	AQLARTQPSAQ	14582	LARTQPS	0.049237	-0.21679
GS1738	5405	GCCCAAATGTCGAGTAGTCATTCTGCTGCACAG	9994	AQMSSSHSAAQ	14583	MSSSHSA	0.049163	-0.17768
GP261	5406	GCCCAACCGTCTTCGAAGTCTCCGTCGGCACAG	9995	AQPSSKSPSAQ	14584	PSSKSPS	0.049142	-0.0728
GP262	5407	GCCCAATATTCTGGTGCGATGTCGGTGGCACAG	9996	AQYSGAMSVAQ	14585	YSGAMSV	0.049076	-0.06114
SyS3114	5408	GCCCAACCGCCGCCTACGAAGTCGTATGCACAG	9997	AQPPPTKSYAQ	14586	PPPTKSY	0.048985	-0.00892
SyP100	5409	GCCCAATCTGCGCCGCATGCTACGACGGCACAG	9998	AQSAPHATTAQ	14587	SAPHATT	0.048581	-0.04347
SyS3116	5410	GCCCAAGCTTCTAAGCCTATGGTTGCTGCACAG	9999	AQASKPMVAAQ	14588	ASKPMVA	0.04844	-0.2277
SyS3117	5411	GCCCAAACCCTCACCTACGGCGACAGAGCACAG	10000	AQTLTYGDRAQ	14589	TLTYGDR	0.048421	-0.20709
SyS3118	5412	GCCCAAGCCAGAAGCGACAGCAAAGACGCACAG	10001	AQARSDSKDAQ	14590	ARSDSKD	0.048221	-0.17505
SyS3119	5413	GCCCAAATGAGCAAAGCCGCCAGCCTCGCACAG	10002	AQMSKAASLAQ	14591	MSKAASL	0.047752	-0.19496
SyS3121	5414	GCCCAAAGCACCCACACCAGCGCCGTCGCACAG	10003	AQSTHTSAVAQ	14592	STHTSAV	0.047188	-0.1233
GS1742	5415	GCCCAAACTGCTCGTCTTCAGGATGGTGCACAG	10004	AQTARLQDGAQ	14593	TARLQDG	0.047164	-0.13739
SyS3122	5416	GCCCAAAGACCCGTCCTCGGCCAACCCGCACAG	10005	AQRPVLGQPAQ	14594	RPVLGQP	0.047021	-0.22649
SyS3123	5417	GCCCAAGCCAGCTTCAAAACCGAAGTCGCACAG	10006	AQASFKTEVAQ	14595	ASFKTEV	0.046975	-0.08471

FIG. 33 (Continued)

GS1743	5418	GCCCAAGTCACCAGAACCGTCAACGCCGCACAG	10007	AQVTRTVNAAQ	14596	VTRTVNA	0.046915	-0.16663
SyS3125	5419	GCCCAAGACCACGCCAGAAGCGGCGGCGCACAG	10008	AQDHARSGGAQ	14597	DHARSGG	0.046836	-0.21571
GS1744	5420	GCCCAAACGACGCATTTGACGGTGAGTGCACAG	10009	AQTTHLTVSAQ	14598	TTHLTVS	0.046543	-0.10586
SyS3126	5421	GCCCAAGTCCCCAAAAGCAACGGCACCGCACAG	10010	AQVPKSNGTAQ	14599	VPKSNGT	0.046485	-0.16708
SyS3127	5422	GCCCAAAGACTCGGCGTCGGCCCCGAAGCACAG	10011	AQRLGVGPEAQ	14600	RLGVGPE	0.046192	-0.17557
SyS3128	5423	GCCCAAAACAACAGACAAACCAGCGACGCACAG	10012	AQNNRQTSDAQ	14601	NNRQTSD	0.046184	-0.14302
SyS3129	5424	GCCCAAAGATTCACCAACAACGAAGCCGCACAG	10013	AQRFTNNEAAQ	14602	RFTNNEA	0.045922	0.054373
SyS3131	5425	GCCCAAAGTTCGCATCAGATGCGGGGGGGCACAG	10014	AQSSHQMRGAQ	14603	SSHQMRG	0.045403	-0.18648
GS1745	5426	GCCCAAACTACGATGGGGACGATGTTGGCACAG	10015	AQTTMGTMLAQ	14604	TTMGTML	0.044961	-0.14435
SyS3133	5427	GCCCAAACCAACGGCGGCGTCCCCATCGCACAG	10016	AQTNGGVPIAQ	14605	TNGGVPI	0.04489	-0.09496
SyS3135	5428	GCCCAAAAAAGCAACGAAGGCAACGGCGCGCACAG	10017	AQKSNEGNGAQ	14606	KSNEGNG	0.044718	-0.06873
SyS3137	5429	GCCCAAAACGTCGCCATGACCACCCTCGCACAG	10018	AQNVAMTTLAQ	14607	NVAMTTL	0.044662	0.069739
SyS3138	5430	GCCCAATACAGCGGCCACACCCCCATGGCACAG	10019	AQYSGHTPMAQ	14608	YSGHTPM	0.044417	0.00379
GP266	5431	GCCCAAGGTACTCCGAATCGGGCGCTGGCACAG	10020	AQGTPNRALAQ	14609	GTPNRAL	0.0441	-0.06683
SyS3141	5432	GCCCAAAGAAGCGGCCCCACCCAACCCGCACAG	10021	AQRSGPTQPAQ	14610	RSGPTQP	0.043925	-0.19375
SyS3142	5433	GCCCAAATCTTCAACCTCAAACAAGACGCACAG	10022	AQIFNLKQDAQ	14611	IFNLKQD	0.043579	-0.0447
SyS3143	5434	GCCCAACACGCCATGAGCCTCAGCCCCGCACAG	10023	AQHAMSLSPAQ	14612	HAMSLSP	0.04335	-0.14871
SyS3144	5435	GCCCAAAGCGAAAGCATGCTCAGAGAAGCACAG	10024	AQSESMLREAQ	14613	SESMLRE	0.043343	0.006658
SyS3146	5436	GCCCAACTCCCCAGACCCCCCCCAAGCCGCACAG	10025	AQLPRPPQAAQ	14614	LPRPPQA	0.043059	-0.22187
GP268	5437	GCCCAACTTGGTCTTGGGGCTTTGTCTGCACAG	10026	AQLGLGALSAQ	14615	LGLGALS	0.042709	-0.07245
SyS3148	5438	GCCCAAATTCCTAAGTCGGCGGATATTGCACAG	10027	AQIPKSADIAQ	14616	IPKSADI	0.042447	-0.09151
SyS3150	5439	GCCCAAGCTCAGTCGTTGCGTACTATGGCACAG	10028	AQAQSLRTMAQ	14617	AQSLRTM	0.042077	-0.19113
SyP103	5440	GCCCAAATGCTTACTAGTTCGTTGGATGCACAG	10029	AQMLTSSLDAQ	14618	MLTSSLD	0.041856	-0.03909
SyS3151	5441	GCCCAAATCTACAGAGACAACGAAAGAGCACAG	10030	AQIYRDNERAQ	14619	IYRDNER	0.041758	-0.20345
SyS3155	5442	GCCCAAAGCCCCCCCACCATGCCCGCCGCACAG	10031	AQSPPTMPAAQ	14620	SPPTMPA	0.041298	-0.18769
SyS3156	5443	GCCCAACCTATGAGGAGTGGTACGCCTGCACAG	10032	AQPMRSGTPAQ	14621	PMRSGTP	0.041276	-0.10941
GS1750	5444	GCCCAACTCCTCAGCAAAAGCAGCGAAGCACAG	10033	AQLLSKSSEAQ	14622	LLSKSSE	0.041269	0.009441
SyS3157	5445	GCCCAAACCGCCAACTTCCAAGAAAGAGCACAG	10034	AQTANFQERAQ	14623	TANFQER	0.041022	-0.22406
GS1751	5446	GCCCAAAGCGGCAACAGACCCGTCACCGCACAG	10035	AQSGNRPVTAQ	14624	SGNRPVT	0.040905	-0.17381
SyS3158	5447	GCCCAACTGAATCAGGTTGATAGTCGTGCACAG	10036	AQLNQVDSRAQ	14625	LNQVDSR	0.040817	-0.14836
SyS3159	5448	GCCCAAATTACGCCGAGTTCTAGTAAGGCACAG	10037	AQITPSSSKAQ	14626	ITPSSSK	0.040646	-0.20224
SyS3160	5449	GCCCAAGATGTTTCGCTTACTAAGGCGGCACAG	10038	AQDVSLTKAAQ	14627	DVSLTKA	0.040618	-0.17351

FIG. 33 (Continued)

SyS3161	5450	GCCCAAATCAACATGAGAACCGCCGTCGCACAG	10039	AQINMRTAVAQ	14628	INMRTAV	0.040605	-0.196
SyS3165	5451	GCCCAATCTAAGAATACTGGTAGTGCTGCACAG	10040	AQSKNTGSAAQ	14629	SKNTGSA	0.039045	-0.19353
SyS3166	5452	GCCCAAGGCAGCGCCCACCAAGAACCCGCACAG	10041	AQGSAHQEPAQ	14630	GSAHQEP	0.038738	-0.15431
SyS3167	5453	GCCCAATCGAAGAATGCTCTGAATCATGCACAG	10042	AQSKNALNHAQ	14631	SKNALNH	0.038724	-0.15493
SyS3169	5454	GCCCAAGGTAAGGCTGTTTCTGTGAGTGCACAG	10043	AQGKAVSVSAQ	14632	GKAVSVS	0.038307	-0.21941
SyS3170	5455	GCCCAATATTCGGGGACTGGTACGGTTGCACAG	10044	AQYSGTGTVAQ	14633	YSGTGTV	0.038212	-0.05651
SyS3171	5456	GCCCAAAGTATTCCTGATCGTCGTGGTGCACAG	10045	AQSIPDRRGAQ	14634	SIPDRRG	0.038196	-0.19011
SyS3172	5457	GCCCAAAACATCGCCAACCTCAACGCCGCACAG	10046	AQNIANLNAAQ	14635	NIANLNA	0.038109	-0.08121
GP271	5458	GCCCAATCTGGTGCGCGTGAGTTGAATGCACAG	10047	AQSGARELNAQ	14636	SGARELN	0.037867	-0.0669
GS1758	5459	GCCCAAGGCCACACAGCTACACCAAAGAAGCACAG	10048	AQGHSYTKEAQ	14637	GHSYTKE	0.037813	-0.17022
GS1759	5460	GCCCAAACCCTCAACAGCATCAGAGCCGCACAG	10049	AQTLNSIRAAQ	14638	TLNSIRA	0.037735	-0.18547
GS1760	5461	GCCCAATTGTCTCTTTCTTCGATTGCTGCACAG	10050	AQLSLSSIAAQ	14639	LSLSSIA	0.037722	-0.11989
SyS3176	5462	GCCCAAAATGTTAGTCGGGTGACGAATGCACAG	10051	AQNVSRVTNAQ	14640	NVSRVTN	0.037619	-0.19254
GP272	5463	GCCCAATATGATACGACGGCGAATCGGGCACAG	10052	AQYDTTANRAQ	14641	YDTTANR	0.037535	-0.07377
SS235	5464	GCCCAAATCGACAGACTCAACAGCAGCGCACAG	10053	AQIDRLNSSAQ	14642	IDRLNSS	0.037392	-0.32512
SyS3179	5465	GCCCAAACCACCACCAACAGAATCAGCGCACAG	10054	AQTTTNRISAQ	14643	TTTNRIS	0.037156	-0.20216
GP273	5466	GCCCAATTTAATACGGTTAGGGATAGGGCACAG	10055	AQFNTVRDRAQ	14644	FNTVRDR	0.037001	-0.07086
SyP104	5467	GCCCAACGTACGTTGGCGGATGAGCTTGCACAG	10056	AQRTLADELAQ	14645	RTLADEL	0.036972	-0.04415
SyS3181	5468	GCCCAAAGGCATACTATTGAGCAGGCGGCGCACAG	10057	AQRHTIEQAAQ	14646	RHTIEQA	0.036633	-0.07978
SyS3183	5469	GCCCAACAAACCATGGGCAGCAGCGTCGCACAG	10058	AQQTMGSSVAQ	14647	QTMGSSV	0.036028	-0.19375
SyS3184	5470	GCCCAACTTAATAGGCCGCAGCATAGTGCACAG	10059	AQLNRPQHSAQ	14648	LNRPQHS	0.035803	-0.23173
SyS3185	5471	GCCCAAATGAGCGTCGCCCTCAGAGGCGCACAG	10060	AQMSVALRGAQ	14649	MSVALRG	0.035678	-0.21557
GS1761	5472	GCCCAAGACAACCTCGCCAGAATGGGCGCACAG	10061	AQDNLARMGAQ	14650	DNLARMG	0.035588	-0.10134
SyS3187	5473	GCCCAAACGGCGCATAATGCTTTGCTGGCACAG	10062	AQTAHNALLAQ	14651	TAHNALL	0.035533	-0.17102
SyS3189	5474	GCCCAACATACGGATCGGTCTGGGCTTGCACAG	10063	AQHTDRSGLAQ	14652	HTDRSGL	0.03511	-0.06215
SyS3190	5475	GCCCAATACGTCGGCGGCATCGTCCCCGCACAG	10064	AQYVGGIVPAQ	14653	YVGGIVP	0.03509	-0.2268
SyS3191	5476	GCCCAAAAGCCGAATCAGACTCCGAATGCACAG	10065	AQKPNQTPNAQ	14654	KPNQTPN	0.034864	-0.19846
SyS3193	5477	GCCCAAGCCGGCAGCAGCCTCCTCCCCGCACAG	10066	AQAGSSLLPAQ	14655	AGSSLLP	0.034195	-0.22557
SyS3194	5478	GCCCAAAGTAATGTTCATGATAGGTCGGCACAG	10067	AQSNVHDRSAQ	14656	SNVHDRS	0.034117	-0.04524
SyS3196	5479	GCCCAAGTCACCAAACTCGGCAGCCCCGCACAG	10068	AQVTKLGSPAQ	14657	VTKLGSP	0.033726	-0.17629
GS1763	5480	GCCCAAAGAGGCGTCGAAAGAAGCAGCGCACAG	10069	AQRGVERSSAQ	14658	RGVERSS	0.033626	-0.14503
SyS3197	5481	GCCCAAACGAGTCTTAGTGGTTCGAATGCACAG	10070	AQTSLSGSNAQ	14659	TSLSGSN	0.033051	-0.22803

FIG. 33 (Continued)

SyS3198	5482	GCCCAACTCAGCCTCAGCACCAACAACGCACAG	10071	AQLSLSTNNAQ	14660	LSLSTNN	0.03277	-0.20588
GS1766	5483	GCCCAACTCGGCCAAATCACCAGACCCGCACAG	10072	AQLGQITRPAQ	14661	LGQITRP	0.032735	-0.13666
SyS3199	5484	GCCCAAAATGCGTCTCCTGGGAGTAGTGCACAG	10073	AQNASPGSSAQ	14662	NASPGSS	0.032455	-0.15335
SyS3200	5485	GCCCAAATGAAGGCGAATAGTCTTTCGGCACAG	10074	AQMKANSLSAQ	14663	MKANSLS	0.032347	-0.16951
SyS3201	5486	GCCCAACATAAGGGGATGGCGAATTCGGCACAG	10075	AQHKGMANSAQ	14664	HKGMANS	0.032108	-0.14425
GS1769	5487	GCCCAAGGCAGAAACAACTACCCCGACGCACAG	10076	AQGRNNYPDAQ	14665	GRNNYPD	0.031842	-0.09188
SyS3204	5488	GCCCAACTCCCCGACCAAAAATGGCAAGCACAG	10077	AQLPDQKWQAQ	14666	LPDQKWQ	0.031415	-0.21325
SyS3206	5489	GCCCAAGGCGTCAACAACAGAGGCAGCGCACAG	10078	AQGVNNRGSAQ	14667	GVNNRGS	0.0313	0.063353
GS1771	5490	GCCCAAAACAGAATCGGCATGCAACCCGCACAG	10079	AQNRIGMQPAQ	14668	NRIGMQP	0.031094	-0.07541
SyS3208	5491	GCCCAAGAGAAGGTGCCGAGTCTGAATGCACAG	10080	AQEKVPSLNAQ	14669	EKVPSLN	0.031014	-0.23012
GS1772	5492	GCCCAAGGCAGAGACAGCAGCAACCCCGCACAG	10081	AQGRDSSNPAQ	14670	GRDSSNP	0.030896	-0.10468
SyS3209	5493	GCCCAAACCGGCAGACCCAACCTCATGGCACAG	10082	AQTGRPNLMAQ	14671	TGRPNLM	0.030687	-0.22649
SyS3212	5494	GCCCAAGTCGCCGGCAGAAGCCCCATGGCACAG	10083	AQVAGRSPMAQ	14672	VAGRSPM	0.030511	-0.16344
SyS3213	5495	GCCCAACTCCCCCACGTCAGCGTCCCCGCACAG	10084	AQLPHVSVPAQ	14673	LPHVSVP	0.030241	-0.19618
SyS3214	5496	GCCCAACTCAGAACCGGCAGCTTCGCCGCACAG	10085	AQLRTGSFAAQ	14674	LRTGSFA	0.029936	-0.16587
SyS3216	5497	GCCCAAGCGGGTGTTTCTAGTGGGAGTGCACAG	10086	AQAGVSSGSAQ	14675	AGVSSGS	0.029244	-0.14892
GS1773	5498	GCCCAATGGAGAGACAGCGGCCACGGCGCACAG	10087	AQWRDSGHGAQ	14676	WRDSGHG	0.029219	-0.16663
SyS3217	5499	GCCCAAAGCTTCGGCAACAGACCCGTCGCACAG	10088	AQSFGNRPVAQ	14677	SFGNRPV	0.029098	-0.20093
SyS3218	5500	GCCCAAAAAGTCAGCCACACAACGGCGACGCACAG	10089	AQKVSHNGDAQ	14678	KVSHNGD	0.029043	-0.13435
SyS3220	5501	GCCCAAAACACCCCCCCCTACGTCCAAGCACAG	10090	AQNTPPYVQAQ	14679	NTPPYVQ	0.028913	-0.09322
SyS3222	5502	GCCCAAAAGAAGGATAATAATCAGCCGGCACAG	10091	AQKKDNNQPAQ	14680	KKDNNQP	0.028636	-0.07058
GS1774	5503	GCCCAAACTATTAAGTCTTTGCCTGTGGCACAG	10092	AQTIKSLPVAQ	14681	TIKSLPV	0.028464	-0.08628
GS1775	5504	GCCCAAATTAATGCGATGCGGTCGCAGGCACAG	10093	AQINAMRSQAQ	14682	INAMRSQ	0.028288	-0.12055
SyS3223	5505	GCCCAAGGCAACAGCATCGCCAAAGGCGCACAG	10094	AQGNSIAKGAQ	14683	GNSIAKG	0.028156	-0.14283
GP279	5506	GCCCAAGTTACTACTCCTAAGGCTTTTGCACAG	10095	AQVTTPKAFAQ	14684	VTTPKAF	0.028102	-0.07259
SyS3224	5507	GCCCAAGGCAGCGTCGCCGGCAGCAGAGCACAG	10096	AQGSVAGSRAQ	14685	GSVAGSR	0.028078	-0.18614
GS1777	5508	GCCCAAAGTGCTAATAATGCTCCTAAGGCACAG	10097	AQSANNAPKAQ	14686	SANNAPK	0.027939	-0.14408
GS1778	5509	GCCCAAGACAGACTCAACCCCCTCCCCGCACAG	10098	AQDRLNPLPAQ	14687	DRLNPLP	0.027045	-0.07977
GS1779	5510	GCCCAAAGAAACCAACCCACCGACGTCGCACAG	10099	AQRNQPTDVAQ	14688	RNQPTDV	0.026888	-0.09709
SyS3227	5511	GCCCAAACCCAAGTCGGCAGCGGCCCCGCACAG	10100	AQTQVGSGPAQ	14689	TQVGSGP	0.026786	0.288018
GS1780	5512	GCCCAACTGAGTCAGGTTTCGAGGCCGGCACAG	10101	AQLSQVSRPAQ	14690	LSQVSRP	0.02663	-0.1747
SyS3228	5513	GCCCAAAACGGCGCCAACCTCCAAATGGCACAG	10102	AQNGANLQMAQ	14691	NGANLQM	0.026629	-0.03438

FIG. 33 (Continued)

SyS3229	5514	GCCCAAATGTTGACGACGAATTCTGTGGCACAG	10103	AQMLTTNSVAQ	14692	MLTTNSV	0.026559	-0.21818
SyS3230	5515	GCCCAAACTTCTACGCGTCCTTCTCCGGCACAG	10104	AQTSTRPSPAQ	14693	TSTRPSP	0.026559	-0.21818
GS1781	5516	GCCCAAAAATACATCGGCAGCGGCGAAGCACAG	10105	AQKYIGSGEAQ	14694	KYIGSGE	0.026538	-0.12177
TS186	5517	GCCCAAAAATAATCTTACGAGAGGGTTACGGCACAG	10106	AQNNLTRVTAQ	14695	NNLTRVT	0.026508	-0.34346
SyS3231	5518	GCCCAAAAAATCGAAACCATGATGCCCGCACAG	10107	AQKIETMMPAQ	14696	KIETMMP	0.025789	-0.09946
SyS3233	5519	GCCCAACTCAGCCACCACACCAGAGACGCACAG	10108	AQLSHHTRDAQ	14697	LSHHTRD	0.025678	-0.16587
GS1782	5520	GCCCAAACTCGGACGAATCCTACTGAGGCACAG	10109	AQTRTNPTEAQ	14698	TRTNPTE	0.025594	-0.16753
GS1783	5521	GCCCAAAGCACCAGAAACGTCGTCGGCGCACAG	10110	AQSTRNVVGAQ	14699	STRNVVG	0.025529	-0.05289
SyS3234	5522	GCCCAAAGCGTCGACCTCAGAAAAGACGCACAG	10111	AQSVDLRKDAQ	14700	SVDLRKD	0.025464	-0.20345
SyS3235	5523	GCCCAAAACGCCGCCGCCCCCGCCAGAGCACAG	10112	AQNAAAPARAQ	14701	NAAAPAR	0.025463	-0.1406
SyS3236	5524	GCCCAAACCCAAATCGCCATCAGCCCCCGCACAG	10113	AQTQIAISPAQ	14702	TQIAISP	0.025204	-0.07054
GS1785	5525	GCCCAACACAAAAAAACCTCAGCCAAAGCGCACAG	10114	AQQKNLSQSAQ	14703	QKNLSQS	0.024848	-0.17672
SyP106	5526	GCCCAAACTTCTATGGGTGGTGAGCCTGCACAG	10115	AQTSMGGEPAQ	14704	TSMGGEP	0.024606	-0.04136
GS1786	5527	GCCCAATCTACGTCGCATCAGAATACGGCACAG	10116	AQSTSHQNTAQ	14705	STSHQNT	0.024595	-0.17005
GS1787	5528	GCCCAACTCAGAGGCAGCATGCAAAGCGCACAG	10117	AQLRGSMQSAQ	14706	LRGSMQS	0.024509	-0.17381
SyS3240	5529	GCCCAAGTCACCCACCAAATCCACACAACGCACAG	10118	AQVTHQIHNAQ	14707	VTHQIHN	0.024364	-0.1133
SyS3241	5530	GCCCAAAACGTCAGAAACGCCCCCGGCGCACAG	10119	AQNVRNAPGAQ	14708	NVRNAPG	0.024296	-0.1392
GP283	5531	GCCCAACAGTCGAGGAGTGCTGCTGCGGCACAG	10120	AQQSRSAAAAQ	14709	QSRSAAA	0.023847	-0.07363
GS1789	5532	GCCCAACATAATCAGGCGCCTTCGGGTGCACAG	10121	AQHNQAPSGAQ	14710	HNQAPSG	0.023511	-0.11187
GS1791	5533	GCCCAAATTGGTTCGATGCATCATACTGCACAG	10122	AQIGSMHHTAQ	14711	IGSMHHT	0.022872	-0.12394
SyS3245	5534	GCCCAAACCAACCCCGGCCCCCTCGCCGCACAG	10123	AQTNPGPLAAQ	14712	TNPGPLA	0.022868	-0.11515
GS1792	5535	GCCCAAAACACCCCCCACAACGCCAGCGCACAG	10124	AQNTPHNASAQ	14713	NTPHNAS	0.022732	-0.11479
GS1793	5536	GCCCAAAGAGTCATCGGCAACAGCAGCGCACAG	10125	AQRVIGNSSAQ	14714	RVIGNSS	0.022466	-0.11769
SyS3247	5537	GCCCAATCGACTGGGAATCGGTCGGTTGCACAG	10126	AQSTGNRSVAQ	14715	STGNRSV	0.02232	-0.22042
SS243	5538	GCCCAAATGAATTCTGAGGTGACTCGGGCACAG	10127	AQMNSEVTRAQ	14716	MNSEVTR	0.022135	-0.39527
SyS3248	5539	GCCCAACAGCAGGCTAAGGGTTCGACTGCACAG	10128	AQQQAKGSTAQ	14717	QQAKGST	0.022131	0.090546
SyS3249	5540	GCCCAACTTGGTATTCAGCGTGGGGGGTGCACAG	10129	AQLGIQRGGAQ	14718	LGIQRGG	0.022113	-0.16397
SyS3250	5541	GCCCAACATGTGGGTGCGGCTACTTCGGCACAG	10130	AQHVGAATSAQ	14719	HVGAATS	0.022058	-0.06734
SyS3251	5542	GCCCAAAAGTGGAATTCTACGATGGAGGCACAG	10131	AQKWNSTMEAQ	14720	KWNSTME	0.021626	-0.17678
SyS3252	5543	GCCCAAAGCAGAGTCCCCGAAAGCAACGCACAG	10132	AQSRVPESNAQ	14721	SRVPESN	0.021378	0.016613
SyS3254	5544	GCCCAACTCATGGCCAAAAGCATGAGCGCACAG	10133	AQLMAKSMSAQ	14722	LMAKSMS	0.020763	-0.136
GP287	5545	GCCCAACGGCCTATGGAGCCTTCGATTGCACAG	10134	AQRPMEPSIAQ	14723	RPMEPSI	0.020678	-0.07287

FIG. 33 (Continued)

GS1796	5546	GCCCAACAAGTCACCAGCAGCAGACCCGCACAG	10135	AQQVTSSRPAQ	14724	QVTSSRP	0.020514	-0.17291
SyS3255	5547	GCCCAAAGAGACGCCAACATGAGCAGCGCACAG	10136	AQRDANMSSAQ	14725	RDANMSS	0.020461	-0.22891
SyP107	5548	GCCCAAGGTTTGCTGAGTCAGGATGGGGCACAG	10137	AQGLLSQDGAQ	14726	GLLSQDG	0.020461	-0.03624
SyS3256	5549	GCCCAAACCATCAACGCCCACAGCATCGCACAG	10138	AQTINAHSIAQ	14727	TINAHSI	0.020285	-0.2305
GS1798	5550	GCCCAACTTACGGGTAATAAGCCGCAGGCACAG	10139	AQLTGNKPQAQ	14728	LTGNKPQ	0.020189	-0.06129
SyS3258	5551	GCCCAAACCTTCGACACCAACAAAACCGCACAG	10140	AQTFDTNKTAQ	14729	TFDTNKT	0.020006	0.0216
GP288	5552	GCCCAAACTCTGCAGACGACGCGTCTTGCACAG	10141	AQTLQTTRLAQ	14730	TLQTTRL	0.019833	-0.06975
SyS3260	5553	GCCCAAACCAGCCAAATGAGAAGCCCCCGCACAG	10142	AQTSQMRSPAQ	14731	TSQMRSP	0.019503	-0.18121
SyS3263	5554	GCCCAAGTTAGTCCTTCTAATAAGGCTGCACAG	10143	AQVSPSNKAAQ	14732	VSPSNKA	0.01927	-0.04747
SyS3264	5555	GCCCAACTTAATCGGACGTATCCTCCTGCACAG	10144	AQLNRTYPPAQ	14733	LNRTYPP	0.019243	-0.05825
SyS3265	5556	GCCCAAAATGCGGAGCTGGCTGTGAGGGCACAG	10145	AQNAELAVRAQ	14734	NAELAVR	0.019069	0.012759
GS1799	5557	GCCCAAAGGCCGAATACGACGACTGATGCACAG	10146	AQRPNTTTDAQ	14735	RPNTTTD	0.019007	-0.16051
TS188	5558	GCCCAAACCAACAGAACCCAACTCTACGCACAG	10147	AQTNRTQLYAQ	14736	TNRTQLY	0.018992	-0.36487
GS1800	5559	GCCCAACCCAAAAGCAGCGGCATCAACGCACAG	10148	AQPKSSGINAQ	14737	PKSSGIN	0.018919	-0.16623
SyS3266	5560	GCCCAAAACAACAGCAACACCAGACAAGCACAG	10149	AQNNSNTRQAQ	14738	NNSNTRQ	0.01874	-0.17193
SyS3267	5561	GCCCAACGTGTGACGGATGCTGGGTCGGCACAG	10150	AQRVTDAGSAQ	14739	RVTDAGS	0.018655	-0.01219
SyS3269	5562	GCCCAAGACACCCCCACCACCAGAACCGCACAG	10151	AQDTPTTRTAQ	14740	DTPTTRT	0.018548	-0.21194
SyS3270	5563	GCCCAAAACCTCAACCTCAGCATGAGCGCACAG	10152	AQNLNLSMSAQ	14741	NLNLSMS	0.018456	-0.13777
SyS3271	5564	GCCCAACCTAATCGGACTGCTAATAATGCACAG	10153	AQPNRTANNAQ	14742	PNRTANN	0.018422	-0.23012
SyS3272	5565	GCCCAATGGAATCGGACGAGTACGGCTGCACAG	10154	AQWNRTSTAAQ	14743	WNRTSTA	0.018254	-0.13798
SyS3273	5566	GCCCAACAAAGCAACCCCGTCATCCCCGCACAG	10155	AQQSNPVIPAQ	14744	QSNPVIP	0.018084	-0.12294
SyS3274	5567	GCCCAAATCAGAAACGTCACCAGCGACGCACAG	10156	AQIRNVTSDAQ	14745	IRNVTSD	0.017976	-0.17752
GS1801	5568	GCCCAAGAAGTCACCGACACCACCAGAGCACAG	10157	AQEVTDTTRAQ	14746	EVTDTTR	0.017963	-0.13433
GS1802	5569	GCCCAAGCCCAAAACAAAAGCGGCCCCGCACAG	10158	AQAQNKSGPAQ	14747	AQNKSGP	0.017856	-0.04694
GS1803	5570	GCCCAATATATTAATCAGACTGAGTCTGCACAG	10159	AQYINQTESAQ	14748	YINQTES	0.017623	-0.14919
GS1804	5571	GCCCAAAGAGTCCCCGTCAGCGAAAACGCACAG	10160	AQRVPVSENAQ	14749	RVPVSEN	0.017595	-0.18727
SyS3276	5572	GCCCAACAAAACGGCACCAAACTCCAAGCACAG	10161	AQQNGTKLQAQ	14750	QNGTKLQ	0.017587	-0.03676
SyS3278	5573	GCCCAAGGGTATTCTAATAATACGGCTGCACAG	10162	AQGYSNNTAAQ	14751	GYSNNTA	0.017267	-0.1097
SyS3279	5574	GCCCAAAACAGAGGCATGGGCAACGTCGCACAG	10163	AQNRGMGNVAQ	14752	NRGMGNV	0.017194	-0.18405
GS1805	5575	GCCCAATATATGAGGGATCCGTCGACTGCACAG	10164	AQYMRDPSTAQ	14753	YMRDPST	0.016919	-0.14227
SyS3281	5576	GCCCAAAGCATCCCCAGCAGAGACGTCGCACAG	10165	AQSIPSRDVAQ	14754	SIPSRDV	0.016767	-0.23419
SyS3282	5577	GCCCAAGGTCCTGTTTCTATGAATTCTGCACAG	10166	AQGPVSMNSAQ	14755	GPVSMNS	0.016767	-0.23419

FIG. 33 (Continued)

SyP109	5578	GCCCAATCTGAGGGGGTGACTCGTCTTGCACAG	10167	AQSEGVTRLAQ	14756	SEGVTRL	0.016584	-0.04225
SyS3285	5579	GCCCAAAGCGTCAACGCCGGCGCCATGGCACAG	10168	AQSVNAGAMAQ	14757	SVNAGAM	0.0165	-0.19431
SyS3286	5580	GCCCAAGAGATGACGAAGACGATTCCTGCACAG	10169	AQEMTKTIPAQ	14758	EMTKTIP	0.016449	-0.2277
SyS3287	5581	GCCCAACACGCCAGCGTCAAAATGCCCGCACAG	10170	AQHASVKMPAQ	14759	HASVKMP	0.016342	-0.19011
SS247	5582	GCCCAAAACAACGGCCTCAAACTCAGCGCACAG	10171	AQNNGLKLSAQ	14760	NNGLKLS	0.015858	-0.37779
GP293	5583	GCCCAACCTGTTTCTCATAATGCTGGTGCACAG	10172	AQPVSHNAGAQ	14761	PVSHNAG	0.015689	-0.06496
SyS3290	5584	GCCCAAAAAGTCGCCGCCGCCGCCGCCGCACAG	10173	AQKVAAAAAAQ	14762	KVAAAAA	0.015496	-0.22649
SyS3291	5585	GCCCAAATGGCGAATGCGATTAGGAGTGCACAG	10174	AQMANAIRSAQ	14763	MANAIRS	0.015463	-0.2268
SS248	5586	GCCCAATTCGGCCAAAGCACCAGCGGCGCACAG	10175	AQFGQSTSGAQ	14764	FGQSTSG	0.015166	-0.30325
GP294	5587	GCCCAAACGTCGAGTACGATTCTTAGGGCACAG	10176	AQTSSTILRAQ	14765	TSSTILR	0.015153	-0.07218
SyS3294	5588	GCCCAAAACGTCAGCAGAGCCGAACACGCACAG	10177	AQNVSRAEHAQ	14766	NVSRAEH	0.014814	-0.218
SyS3295	5589	GCCCAAAGAACCGCCCCCAGCACCGAAGCACAG	10178	AQRTAPSTEAQ	14767	RTAPSTE	0.014569	0.032334
SyS3297	5590	GCCCAACTCGCCAGAAGCGAACACCTCGCACAG	10179	AQLARSEHLAQ	14768	LARSEHL	0.014209	-0.11809
SyS3298	5591	GCCCAAAGCACCGGCCACCCCAGCCAAGCACAG	10180	AQSTGHPSQAQ	14769	STGHPSQ	0.014148	-0.08
GS1811	5592	GCCCAATCGCGTCCGGATAAGAATCTGGCACAG	10181	AQSRPDKNLAQ	14770	SRPDKNL	0.014135	-0.10291
SyS3299	5593	GCCCAAAAAAAAAGCGACAGCCCCCAACGCACAG	10182	AQKKSDSPNAQ	14771	KKSDSPN	0.014026	-0.13578
SS250	5594	GCCCAAGTCAACAGCAGAATCTACGCCGCACAG	10183	AQVNSRIYAAQ	14772	VNSRIYA	0.013946	-0.36314
GS1814	5595	GCCCAACTGCGGCAGATGGCTAATGGGGCACAG	10184	AQLRQMANGAQ	14773	LRQMANG	0.013231	-0.18637
SyS3301	5596	GCCCAAGAAAGACTCAAAGGCAGCAGCGCACAG	10185	AQERLKGSSAQ	14774	ERLKGSS	0.012774	0.017944
GP297	5597	GCCCAAATGTCGTATATGCGGGTGGATGCACAG	10186	AQMSYMRVDAQ	14775	MSYMRVD	0.012568	-0.06801
GP298	5598	GCCCAATTTAATTCTAAGCTTCAGCTTGCACAG	10187	AQFNSKLQLAQ	14776	FNSKLQL	0.012457	-0.07356
SyS3302	5599	GCCCAAAGAGAACACGTCAACGACAGCGCACAG	10188	AQREHVNDSAQ	14777	REHVNDS	0.012246	-0.16819
SyS3303	5600	GCCCAAGGCAGCCCCCAGCCAAAACACCGCACAG	10189	AQGSPSQNTAQ	14778	GSPSQNT	0.012182	-0.12853
SyS3304	5601	GCCCAACATACTGCTGAGAAGGCTCCGGCACAG	10190	AQHTAEKAPAQ	14779	HTAEKAP	0.011841	-0.13024
SyS3305	5602	GCCCAAAGCATGAGCGGCAAACTCGACGCACAG	10191	AQSMSGKLDAQ	14780	SMSGKLD	0.011656	-0.14283
SyS3306	5603	GCCCAAACCAGCCAAAGCAGAACCAGCGCACAG	10192	AQTSQSRTSAQ	14781	TSQSRTS	0.011418	-0.17013
SyS3307	5604	GCCCAATGGCCGACGCAGAGTGGTAGTGCACAG	10193	AQWPTQSGSAQ	14782	WPTQSGS	0.01135	-0.07352
TS190	5605	GCCCAAGACAACACCACCAGACTCAAAGCACAG	10194	AQDNTTRLKAQ	14783	DNTTRLK	0.011299	-0.32818
SyP110	5606	GCCCAATCGTCTGCTGGGAAGTGGGCACAG	10195	AQSSAAGKWAQ	14784	SSAAGKW	0.011192	-0.0418
SyS3311	5607	GCCCAATCGAAGTTTGCTCATGTGGCTGCACAG	10196	AQSKFAHVAAQ	14785	SKFAHVA	0.010513	-0.19981
GS1820	5608	GCCCAACAAACCTACCAAGGCAGCACCGCACAG	10197	AQQTYQGSTAQ	14786	QTYQGST	0.010458	-0.18054
SyS3312	5609	GCCCAAACCGTCAACCTCAACAGAGCCGCACAG	10198	AQTVNLNRAAQ	14787	TVNLNRA	0.010308	-0.19969

FIG. 33 (Continued)

SyS3313	5610	GCCCAAAGATACGGCAGCAGCCTCCCCGCACAG	10199	AQRYGSSLPAQ	14788	RYGSSLP	0.009869	-0.21072
GS1822	5611	GCCCAAAGAAGCAACAGCAGCAACCTCGCACAG	10200	AQRSNSSNLAQ	14789	RSNSSNL	0.009735	-0.09744
GS1823	5612	GCCCAACAAGGCCCCAGCATCAGAGACGCACAG	10201	AQQGPSIRDAQ	14790	QGPSIRD	0.00931	-0.17112
GS1824	5613	GCCCAATGGAGAGACCTCGCCCCCGTCGCACAG	10202	AQWRDLAPVAQ	14791	WRDLAPV	0.009233	-0.1186
SyS3316	5614	GCCCAACACAGCGACATCCAAAGACCCGCACAG	10203	AQHSDIQRPAQ	14792	HSDIQRP	0.009085	-0.01571
GS1825	5615	GCCCAATTGGCGGCGATGACGAATGCTGCACAG	10204	AQLAAMTNAAQ	14793	LAAMTNA	0.008985	-0.10156
SyS3317	5616	GCCCAAAGCGCCAACCACACCCACACCGCACAG	10205	AQSANHTHTAQ	14794	SANHTHT	0.008908	-0.08086
SyS3318	5617	GCCCAAGGGAAGCTGTCGGTGGAGAATGCACAG	10206	AQGKLSVENAQ	14795	GKLSVEN	0.008617	-0.07767
SyS3319	5618	GCCCAAAAACCCGGCGCCAACCCCCCCCGCACAG	10207	AQKPGANPPAQ	14796	KPGANPP	0.008265	-0.07573
GP301	5619	GCCCAACTTACTGAGGGTCGTCATGATGCACAG	10208	AQLTEGRHDAQ	14797	LTEGRHD	0.008187	-0.07148
SyP112	5620	GCCCAACTTGGGTCGAATATTTATCCGGCACAG	10209	AQLGSNIYPAQ	14798	LGSNIYP	0.00806	-0.03861
SyS3321	5621	GCCCAAAACGGCGCCCACAGCAGCGAAGCACAG	10210	AQNGAHSSEAQ	14799	NGAHSSE	0.007822	-0.08193
GS1826	5622	GCCCAAAATACGATGGGTGGTGCGGCGGCACAG	10211	AQNTMGGAAAQ	14800	NTMGGAA	0.007814	-0.14962
SyS3322	5623	GCCCAAAGAACCCCCATCGGCCAACCCGCACAG	10212	AQRTPIGQPAQ	14801	RTPIGQP	0.007542	-0.18648
SyS3323	5624	GCCCAATATAGTGTGGCTCAGCAGCCGGCACAG	10213	AQYSVAQQPAQ	14802	YSVAQQP	0.007381	-0.22064
GP303	5625	GCCCAACCTCATTCTAAGGGGATGCTTGCACAG	10214	AQPHSKGMLAQ	14803	PHSKGML	0.007181	-0.0685
GS1827	5626	GCCCAAGTTCCGGCGCATGGGATGGGTGCACAG	10215	AQVPAHGMGAQ	14804	VPAHGMG	0.007168	-0.12619
SyS3324	5627	GCCCAAATTGGTGGGGTTCCTCAGCGTGCACAG	10216	AQIGGVPQRAQ	14805	IGGVPQR	0.007145	-0.12889
SyS3325	5628	GCCCAAGTGCAGGGGACGGTTTCGAGGGCACAG	10217	AQVQGTVSRAQ	14806	VQGTVSR	0.007118	-0.15153
SyS3326	5629	GCCCAAAGTGGTGGGAGTGGTGCTCCTGCACAG	10218	AQSGGSGAPAQ	14807	SGGSGAP	0.006964	-0.05146
SyS3327	5630	GCCCAAAAAGTCCCCACCCAAACCGAAGCACAG	10219	AQKVPTQTEAQ	14808	KVPTQTE	0.006686	-0.09626
SyS3328	5631	GCCCAAATTTCGACGATGAAGCCTAGTGCACAG	10220	AQISTMKPSAQ	14809	ISTMKPS	0.006591	-0.15981
SyS3329	5632	GCCCAAAGCAGAGTCGTCGAACAAGCCGCACAG	10221	AQSRVVEQAAQ	14810	SRVVEQA	0.006345	-0.21818
SyS3331	5633	GCCCAAGTCCTCAGCAGACAAAGCACCGCACAG	10222	AQVLSRQSTAQ	14811	VLSRQST	0.006155	-0.23376
SyS3332	5634	GCCCAAGTCGTCACCACCAGCAGCATGGCACAG	10223	AQVVTTSSMAQ	14812	VVTTSSM	0.006155	-0.23376
SyP114	5635	GCCCAAAGTACGGGTTCTTCGGGTTTGGCACAG	10224	AQSTGSSGLAQ	14813	STGSSGL	0.006086	-0.04068
TS192	5636	GCCCAACCCAACAGAGCCGCCAACAACGCACAG	10225	AQPNRAANNAQ	14814	PNRAANN	0.005926	-0.37804
SyS3333	5637	GCCCAATATCCTGTTAATAGTCAGCCTGCACAG	10226	AQYPVNSQPAQ	14815	YPVNSQP	0.005608	-0.22042
SyS3334	5638	GCCCAAAAAAGCGCCAGCCCCTACGACGCACAG	10227	AQKSASPYDAQ	14816	KSASPYD	0.005437	-0.08849
GS1830	5639	GCCCAAAGCAAAAGCTGGGGCGCCGCCGCACAG	10228	AQSKSWGAAAQ	14817	SKSWGAA	0.005259	-0.13947
SyS3335	5640	GCCCAATCTGCGATGCTGAAGGTTGATGCACAG	10229	AQSAMLKVDAQ	14818	SAMLKVD	0.005199	-0.20339
SP62	5641	GCCCAACGGAGTCAGACGATTCAGGCTGCACAG	10230	AQRSQTIQAAQ	14819	RSQTIQA	0.004569	-0.05254

FIG. 33 (Continued)

SyS3336	5642	GCCCAACCCAGCAGCAGACTCGGCGACGCACAG	10231	AQPSSRLGDAQ	14820	PSSRLGD	0.004505	0.004214
GS1831	5643	GCCCAAATCGGCCCCAGAGGCACCCAAGCACAG	10232	AQIGPRGTQAQ	14821	IGPRGTQ	0.004293	-0.15764
SyS3337	5644	GCCCAAGCCAGCAAAGGCCAATACCTCGCACAG	10233	AQASKGQYLAQ	14822	ASKGQYL	0.004037	-0.23497
GP306	5645	GCCCAAGTTAGGACTCTTACTGTTGATGCACAG	10234	AQVRTLTVDAQ	14823	VRTLTVD	0.003991	-0.06489
SyS3339	5646	GCCCAACGTGGGAATGCTGCGAATGAGGCACAG	10235	AQRGNAANEAQ	14824	RGNAANE	0.003862	-0.12561
SyS3340	5647	GCCCAATTCGGCAGCCACCCCAGCGTCGCACAG	10236	AQFGSHPSVAQ	14825	FGSHPSV	0.003469	-0.2231
GP309	5648	GCCCAAGGTCATCCGACTCCTGTTAATGCACAG	10237	AQGHPTPVNAQ	14826	GHPTPVN	0.003421	-0.06822
GS1833	5649	GCCCAAAGCCTCAACCCCGTCAGAATGGCACAG	10238	AQSLNPVRMAQ	14827	SLNPVRM	0.002868	-0.1138
GP312	5650	GCCCAAAGTATTCGGGGTCAGCCTTTTGCACAG	10239	AQSIRGQPFAQ	14828	SIRGQPF	0.002583	-0.07405
GS1835	5651	GCCCAAACCGCCCAAATTCAACCAAGGCGCACAG	10240	AQTAKFNQGAQ	14829	TAKFNQG	0.002515	-0.11596
SyS3342	5652	GCCCAATTGATTTCGACGCATGATATGGCACAG	10241	AQLISTHDMAQ	14830	LISTHDM	0.002485	-0.14369
SyS3345	5653	GCCCAACAAAGCAGAGACAACATCAGAGCACAG	10242	AQQSRDNIRAQ	14831	QSRDNIR	0.002214	-0.11916
SyS3346	5654	GCCCAAAACAACGGCAACAAAGGCTTCGCACAG	10243	AQNNGNKGFAQ	14832	NNGNKGF	0.002093	-0.21325
GP315	5655	GCCCAAAATGTGAATTATGATGGGCGGGCACAG	10244	AQNVNYDGRAQ	14833	NVNYDGR	0.001863	-0.07225
GS1841	5656	GCCCAATTCATGAAAGGCGCCAGCGCCGCACAG	10245	AQFMKGASAAQ	14834	FMKGASA	0.001531	-0.15945
SyS3349	5657	GCCCAACTCGCCACCAGCACCCAAATGGCACAG	10246	AQLATSTQMAQ	14835	LATSTQM	0.001488	-0.218
SyS3350	5658	GCCCAAGTTCATGGTGGGTATTCGGCTGCACAG	10247	AQVHGGYSAAQ	14836	VHGGYSA	0.001485	-0.22434
SS254	5659	GCCCAAAGAGGCAGCGAACCCATGCAAGCACAG	10248	AQRGSEPMQAQ	14837	RGSEPMQ	0.001241	-0.3679
GP317	5660	GCCCAAGGTCTGCGTACGAGTGGGACGGCACAG	10249	AQGLRTSGTAQ	14838	GLRTSGT	0.001025	-0.06413
SyS3351	5661	GCCCAACTCTACAAAGGCGGCGTCAGCGCACAG	10250	AQLYKGGVSAQ	14839	LYKGGVS	0.000806	-0.23012
SyS3353	5662	GCCCAAATGAAAACCCACAGCCCCCCCGCACAG	10251	AQMKTHSPPAQ	14840	MKTHSPP	0.000291	-0.09473

FIG. 33 (Continued)

SUBSTITUTE SHEET (RULE 26)

Enrich_ rank (within libraries)	SEQ ID NO:	Sequence	SEQ ID NO:	11 mer Amino Acid	SEQ ID NO:	7 mer Amino acid	Brain-mean-enrichment score (log10)	Brain-mean-standardized-read count (RC)
TS32	14841	GCCCAAAGCAACAGCATCAGACTCGTCGCACAG	14881	AQSNSIRLVAQ	14921	SNSIRLV	0.763114	1.058208
TS70	14842	GCCCAACCCAACACCATCAGAAACGTCGCACAG	14882	AQPNTIRNVAQ	14922	PNTIRNV	0.660528	0.629407
SyS52	14843	GCCCAAACCAGCCTCGGCTACAGCAGCGCACAG	14883	AQTSLGYSSAQ	14923	TSLGYSS	0.727167	0.736367
SyS140	14844	GCCCAAATGGGCGCCGACCACAGAACCGCACAG	14884	AQMGADHRTAQ	14924	MGADHRT	0.548749	0.159265
SyS58	14845	GCCCAAGGTGATAATAGTCTGACTAGGGCACAG	14885	AQGDNSLTRAQ	14925	GDNSLTR	0.717624	0.075033
SyS201	14846	GCCCAAACCCCCCAAAGCCAAGAAATGGCACAG	14886	AQTPQSQEMAQ	14926	TPQSQEM	0.494147	0.127468
SyS61	14847	GCCCAAAGCGGCGTCAGCACCACCGACGCACAG	14887	AQSGVSTTDAQ	14927	SGVSTTD	0.711249	-0.01534
SyS97	14848	GCCCAAGAAGGCCTCGGCAACGCCGCCGCACAG	14888	AQEGLGNAAAQ	14928	EGLGNAA	0.59339	-0.02116
SyS176	14849	GCCCAAATTGCTGAGAATCTGAGTGCTGCACAG	14889	AQIAENLSAAQ	14929	IAENLSA	0.517935	-0.10864
SyS154	14850	GCCCAACTCGGCGACATCACCGGCTTCGCACAG	14890	AQLGDITGFAQ	14930	LGDITGF	0.537047	-0.10198
SyS101	14851	GCCCAAAGTCAGCTGCATAGGTTGCAGGCACAG	14891	AQSQLHRLQAQ	14931	SQLHRLQ	0.588997	-0.13052
SyS45	14852	GCCCAACCTATTATTACTATGCCTGCTGCACAG	14892	AQPIITMPAAQ	14932	PIITMPA	0.767318	-0.10299
SyS205	14853	GCCCAATGGAGCCACAGCGAAAACAGCGCACAG	14893	AQWSHSENSAQ	14933	WSHSENS	0.492196	-0.02126
SyS30	14854	GCCCAATTGACTCAGCAGACGGATGTTGCACAG	14894	AQLTQQTDVAQ	14934	LTQQTDV	0.936974	0.055201
SyS136	14855	GCCCAAGGTATGAGTGGGGTTGCTCAGGCACAG	14895	AQGMSGVAQAQ	14935	GMSGVAQ	0.552736	-0.0578
SyS128	14856	GCCCAACCGACTAATATTATGCTTGATGCACAG	14896	AQPTNIMLDAQ	14936	PTNIMLD	0.560313	-0.07894
SyS71	14857	GCCCAAAACCCCACCCTCATCACCCTCGCACAG	14897	AQNPTLITLAQ	14937	NPTLITL	0.655924	0.146275
SyS100	14858	GCCCAACCGGGTGGGGGTTTGACTCCGGCACAG	14898	AQPGGGLTPAQ	14938	PGGGLTP	0.591748	-0.07925
SyS134	14859	GCCCAAGATCGTGATTCTGTGCAGAATGCACAG	14899	AQDRDSVQNAQ	14939	DRDSVQN	0.55654	-0.05483
SyS152	14860	GCCCAACTTAATGGGTTGAATGTGTCTGCACAG	14900	AQLNGLNVSAQ	14940	LNGLNVS	0.537505	-0.02999
SyS68	14861	GCCCAAGCCCAAACCAGCAACGACCCCGCACAG	14901	AQAQTSNDPAQ	14941	AQTSNDP	0.669325	0.289379
SyS137	14862	GCCCAATCTGCGCCTAATGTGACTATTGCACAG	14902	AQSAPNVTIAQ	14942	SAPNVTI	0.551278	0.041441
SyS129	14863	GCCCAACCCAACATGAGCGCCATGATCGCACAG	14903	AQPNMSAMIAQ	14943	PNMSAMI	0.559451	0.270198
GS64	14864	GCCCAATACAGCGCCGACAAAACCACCGCACAG	14904	AQYSADKTTAQ	14944	YSADKTT	0.583168	0.057165

FIG. 34

SyS48	14865	GCCCAACGTGTGGATGCGGTTTTGAGTGCACAG	14905	AQRVDAVLSAQ	14945	RVDAVLS	0.750458	0.650222
SyS138	14866	GCCCAAGGCACCGCCGTCTTCACCGCCGCACAG	14906	AQGTAVFTAAQ	14946	GTAVFTA	0.549912	0.15966
SyS83	14867	GCCCAAACCCTCAGCGGCGCCCTCACCGCACAG	14907	AQTLSGALTAQ	14947	TLSGALT	0.628275	0.306806
SyS59	14868	GCCCAACACGCCGACAACAGACTCAAAGCACAG	14908	AQHADNRLKAQ	14948	HADNRLK	0.714815	-0.04579
SyS173	14869	GCCCAAACTCAGGGTCCGGGTCCGAAGGCACAG	14909	AQTQGPGPKAQ	14949	TQGPGPK	0.522239	0.297383
SyS148	14870	GCCCAAGTCGACGCCCTCAGCCACATGGCACAG	14910	AQVDALSHMAQ	14950	VDALSHM	0.539694	0.216373
SyS162	14871	GCCCAACGGAATGATGCGATTCTGAATGCACAG	14911	AQRNDAILNAQ	14951	RNDAILN	0.53456	0.251531
SP47	14872	GCCCAATTGACGGTGGCGGTTGAGACTGCACAG	14912	AQLTVAVETAQ	14952	LTVAVET	0.139972	-0.05361
SS33	14873	GCCCAAAGCCAAGCCATCGCCCCCAAAGCACAG	14913	AQSQAIAPKAQ	14953	SQAIAPK	0.51343	-0.30374
GS29	14874	GCCCAAGTCCTCAGCGTCAACCACCTCGCACAG	14914	AQVLSVNHLAQ	14954	VLSVNHL	0.765014	0.050802
SyS84	14875	GCCCAAAGCATCTACTACCACACCGAAGCACAG	14915	AQSIYYHTEAQ	14955	SIYYHTE	0.618441	-0.07907
GS45	14876	GCCCAAATGAACATCCTCAGAGAAGTCGCACAG	14916	AQMNILREVAQ	14956	MNILREV	0.654097	-0.09985
GS84	14877	GCCCAAAATATGCTTAAGCAGAGTGAGGCACAG	14917	AQNMLKQSEAQ	14957	NMLKQSE	0.537354	-0.06179
GS113	14878	GCCCAATTCATGCCCATCAGCAGCGCCGCACAG	14918	AQFMPISSAAQ	14958	FMPISSA	0.50124	-0.12446
GS27	14879	GCCCAAAAGAATGCTCCGATGCCTGATGCACAG	14919	AQKNAPMPDAQ	14959	KNAPMPD	0.772397	0.130152
GS117	14880	GCCCAAACCAACTACGACCTCAGAGCCGCACAG	14920	AQTNYDLRAAQ	14960	TNYDLRA	0.494623	-0.03099

FIG. 34 (Continued)

Enrich_ rank (within libraries)	SEQ ID NO:	Sequence (for 11 mer AA)	SEQ ID NO:	11 mer Amino Acid	Liver-mean-enrichment score (log10)
TS1	14961	GCCCAAAAAGCCTACAGCGTCCAAGTCGCACAG	15054	AQKAYSVQVAQ	1.15776
TS2	14962	GCCCAAAGAACCGCCAACGCCCTCGGCGCACAG	15055	AQRTANALGAQ	0.802247
TS3	14963	GCCCAAGTGACGGGGGTTCGGATTGGGGCACAG	15056	AQVTGVRIGAQ	0.75699
TS4	14964	GCCCAACCGCGGCCGGTGTCGAATGGGGCACAG	15057	AQPRPVSNGAQ	0.7305
TS5	14965	GCCCAATTCAGCGTCACCAGACAAGCCGCACAG	15058	AQFSVTRQAAQ	0.718621
TS6	14966	GCCCAATACCCCCACATGACCCACGACGCACAG	15059	AQYPHMTHDAQ	0.655794
TS7	14967	GCCCAAAGCAGCAGACTCAGCGTCGGCGCACAG	15060	AQSSRLSVGAQ	0.637971
TS8	14968	GCCCAACCGTTGAGTGGGGGTGTTCGTGCACAG	15061	AQPLSGGVRAQ	0.598554
TS9	14969	GCCCAAGGGCTGAAGGTGTCTGGGTCTGCACAG	15062	AQGLKVSGSAQ	0.569576
TS10	14970	GCCCAAAGCACCAGAAACGTCGTCGGCGCACAG	15063	AQSTRNVVGAQ	0.532567
TS11	14971	GCCCAAAGCGGCGGCACCAGAGAAGGCGCACAG	15064	AQSGGTREGAQ	0.501512
SyS1	14972	GCCCAAGGGCTGAAGGTGTCTGGGTCTGCACAG	15065	AQGLKVSGSAQ	0.777335
SyS2	14973	GCCCAAAACAACAACCAAAAAGTCTACGCACAG	15066	AQNNNQKVYAQ	0.610002
SyS3	14974	GCCCAAAGGCTTGATAGGACTGGTTTGGCACAG	15067	AQRLDRTGLAQ	0.588542
SyS4	14975	GCCCAAGTGGCGGGTCTGACTGTTCAGGCACAG	15068	AQVAGLTVQAQ	0.581695
SyS5	14976	GCCCAACATTCTGCGAAGACTATTGCGGCACAG	15069	AQHSAKTIAAQ	0.579949
SyS6	14977	GCCCAAAGCATCAGAGCCCCCGTCAGCGCACAG	15070	AQSIRAPVSAQ	0.572426
SyS7	14978	GCCCAACCCCGTCGGCACCAGAACCAGCGCACAG	15071	AQPVGTRTSAQ	0.560759
SyS8	14979	GCCCAAATCAACACCGCCAGCTACAAAGCACAG	15072	AQINTASYKAQ	0.542125
SyS9	14980	GCCCAAGGGAGGACGGTGCAGGATAGGGCACAG	15073	AQGRTVQDRAQ	0.528631
SyS10	14981	GCCCAAAGACTCACCAACAGCAACCAAGCACAG	15074	AQRLTNSNQAQ	0.516161
SyS11	14982	GCCCAAATGATCAGAGGCACCAGCAGCGCACAG	15075	AQMIRGTSSAQ	0.512891

FIG. 35

SyS12	14983	GCCCAATTTTCTGGTAGTGCTAGGGTTGCACAG	15076	AQFSGSARVAQ	0.509852
SyS13	14984	GCCCAACGTCAGCATCAGCTTCCTATGGCACAG	15077	AQRQHQLPMAQ	0.505918
SyS14	14985	GCCCAACCCCTCAGAAACATCAGCGCCGCACAG	15078	AQPLRNISAAQ	0.50497
SS1	14986	GCCCAACCGTATAGTGGGCAGCGGACTGCACAG	15079	AQPYSGQRTAQ	0.84953
SS2	14987	GCCCAACCTTCTGGTTCTGCGCGGAGTGCACAG	15080	AQPSGSARSAQ	0.82811
SS3	14988	GCCCAACCGCGTCATGCGACTCAGTCGGCACAG	15081	AQPRHATQSAQ	0.711312
SS4	14989	GCCCAATCGAAGGTTACGCCTCCTCTGGCACAG	15082	AQSKVTPPLAQ	0.687491
SS5	14990	GCCCAAAATACTTCTGGTGTGCCTAAGGCACAG	15083	AQNTSGVPKAQ	0.684638
SS6	14991	GCCCAAACCAGAAGCGAAGTCATGAAAGCACAG	15084	AQTRSEVMKAQ	0.683884
SS7	14992	GCCCAACGGACGGATGTGCGGACGAATGCACAG	15085	AQRTDVRTNAQ	0.682169
SS8	14993	GCCCAAATGCTCAGCGGCCAAGCCAGAGCACAG	15086	AQMLSGQARAQ	0.668364
SS9	14994	GCCCAATCTATGCTTACGAGTATATTGTTGCACAG	15087	AQSMLTSIVAQ	0.665818
SS10	14995	GCCCAACTTAGGGGTTCTGCTCAGGTGGCACAG	15088	AQLRGSAQVAQ	0.648123
SS11	14996	GCCCAAAAGCCATCAGCACCGCCAACCGCACAG	15089	AQKAISTANAQ	0.616958
SS12	14997	GCCCAAATCAGCGGCGTCCAAACCAGAGCACAG	15090	AQISGVQTRAQ	0.615015
SS13	14998	GCCCAAAAGCGGGCGCCTGCTGATTCTGCACAG	15091	AQKRAPADSAQ	0.611303
SS14	14999	GCCCAAGCTAATGCGATGGGTGATCATGCACAG	15092	AQANAMGDHAQ	0.611245
SS15	15000	GCCCAAAACACCCTCATCAACGTCAGCGCACAG	15093	AQNTLINVSAQ	0.607212
SS16	15001	GCCCAATGGTCTGATCCTAGTGATCTGGCACAG	15094	AQWSDPSDLAQ	0.59828
SS17	15002	GCCCAAAGAATCAGCACCCTCGGCCTCGCACAG	15095	AQRISTLGLAQ	0.595844
SS18	15003	GCCCAATTTAAGGTTAGTATTCAGCAGGCACAG	15096	AQFKVSIQQAQ	0.591275
SS19	15004	GCCCAACTTTCTACTGCGTTGACTGTGGCACAG	15097	AQLSTALTVAQ	0.591029
SS20	15005	GCCCAAGCCGAATACAACACCGGCGTCGCACAG	15098	AQAEYNTGVAQ	0.585999
SS21	15006	GCCCAAATTTCGGCTTCTCATTCTCGTGCACAG	15099	AQISASHSRAQ	0.574424
SS22	15007	GCCCAAGTCAACAGCCACGAAAGAGCCGCACAG	15100	AQVNSHERAAQ	0.573043
SS23	15008	GCCCAAGGTCTTCAGTCGCCGAGGTCTCTGCACAG	15101	AQGLQSPRSAQ	0.572095
SS24	15009	GCCCAAGGGGCTGCTGGTAAGAGTTTGGCACAG	15102	AQGAAGKSLAQ	0.571307
SS25	15010	GCCCAACTCAGCAACAGCGCCAGCCAAGCACAG	15103	AQLSNSASQAQ	0.569105
SS26	15011	GCCCAAAAACTCAGCACCCTCCACCAAGCACAG	15104	AQKLSTLHQAQ	0.568791
SS27	15012	GCCCAAATGAGAGGCCAAGGCGTCCACGCACAG	15105	AQMRGQGVHAQ	0.567657

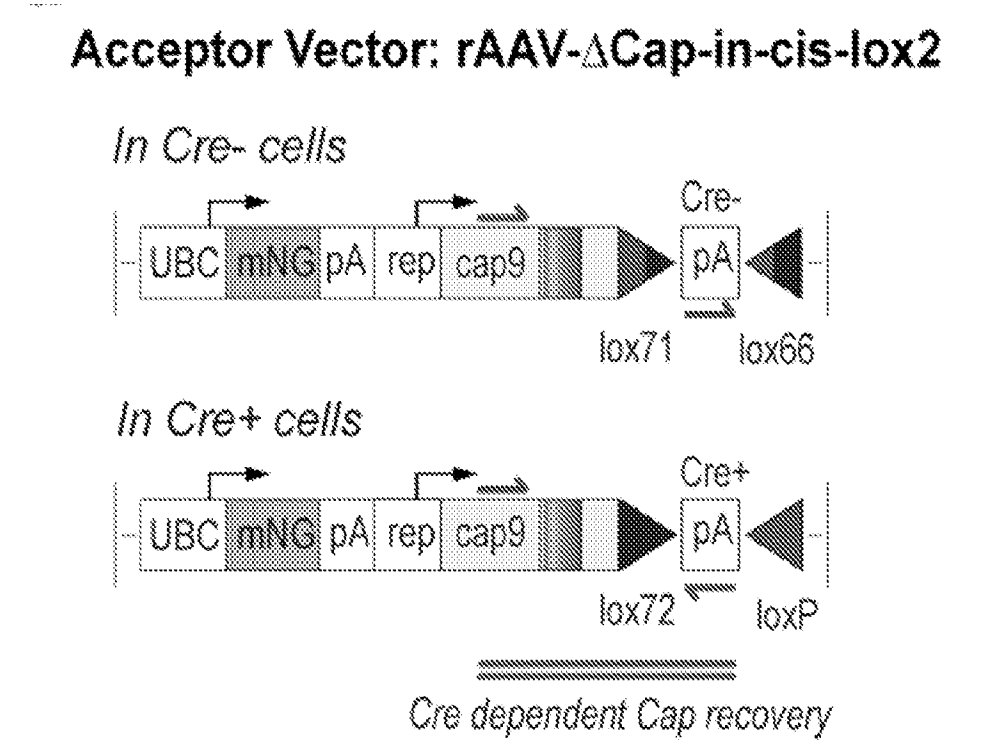
FIG. 35 (Continued)

SS28	15013	GCCCAACTTCCGGGTGGTGCGAGGTTGGCACAG	15106	AQLPGGARLAQ	0.564086
SS29	15014	GCCCAACTTGGTTCTGCGCTTACGAGGGGCACAG	15107	AQLGSALTRAQ	0.563314
SS30	15015	GCCCAAGGCACCACCAGAAGCCCCACCGCACAG	15108	AQGTTRSPTAQ	0.560705
SS31	15016	GCCCAAGGTCATATTTCGGCGCTTGCGGCACAG	15109	AQGHISALAAQ	0.552655
SS32	15017	GCCCAATCGATTTCTCCTCCTCGTACGGCACAG	15110	AQSISPPRTAQ	0.550578
SS33	15018	GCCCAATTTCAGCAGGATACTTATCTGGCACAG	15111	AQFQQDTYLAQ	0.548808
SS34	15019	GCCCAACTTCTTGCGACTGGGCTTAAGGCACAG	15112	AQLLATGLKAQ	0.545453
SS35	15020	GCCCAACTTAAGGTTGCGTCTGGTTTGGCACAG	15113	AQLKVASGLAQ	0.540598
SS36	15021	GCCCAATTCGACAACCCCAACAACGTCGCACAG	15114	AQFDNPNNVAQ	0.539231
SS37	15022	GCCCAATACCTCACCAGCGGCGGCTACGCACAG	15115	AQYLTSGGYAQ	0.538789
SS38	15023	GCCCAAAGAGACACCGTCAGCAGATACGGCACAG	15116	AQRDTVSRYAQ	0.535765
SS39	15024	GCCCAAATCAACACAAAGACAACAACCAAGCACAG	15117	AQINKDNNQAQ	0.531458
SS40	15025	GCCCAAATGGCCAACACCAGAAGCGCCGCACAG	15118	AQMANTRSAAQ	0.525721
SS41	15026	GCCCAAGAAAGCATCCAACAACTCAGCGCACAG	15119	AQESIQQLSAQ	0.525712
SS42	15027	GCCCAACTCACCAGAGTCGGCACCGTCGCACAG	15120	AQLTRVGTVAQ	0.520831
SS43	15028	GCCCAAGTCCAAGTCGCCATGAGAGCCGCACAG	15121	AQVQVAMRAAQ	0.520831
SS44	15029	GCCCAAACGGCTGCGCATGTTAGTTATGCACAG	15122	AQTAAHVSYAQ	0.520336
SS45	15030	GCCCAACCCAGCCACGCCAGAGCCAGCGCACAG	15123	AQPSHARASAQ	0.520336
SS46	15031	GCCCAAAATGTGCCGACTTCGCCGCGGGCACAG	15124	AQNVPTSPRAQ	0.520245
SS47	15032	GCCCAAAAAACCCAACTCGGCCAAATGGCACAG	15125	AQKTQLGQMAQ	0.519843
SS48	15033	GCCCAAAAAGCCAACAGCCAAATCACCGCACAG	15126	AQKANSQITAQ	0.519425
SS49	15034	GCCCAAAACAACAGCGGCCACATCAGCGCACAG	15127	AQNNSGHISAQ	0.518228
SS50	15035	GCCCAATTTCTTCTTACTTCGGATCCGGCACAG	15128	AQFLLTSDPAQ	0.515975
SS51	15036	GCCCAAGTTAAGACTGATCGGGTTCTGGCACAG	15129	AQVKTDRVLAQ	0.51183
SS52	15037	GCCCAAGTCAGCATCAGCGTCATGGGCGCACAG	15130	AQVSISVMGAQ	0.510987
SS53	15038	GCCCAAGCCGGCCTCGCCCACGCCACCGCACAG	15131	AQAGLAHATAQ	0.510068
SS54	15039	GCCCAACGGACTACGGCTAATTCGCTTGCACAG	15132	AQRTTANSLAQ	0.509233
SS55	15040	GCCCAATCGGTTCCTCCGAATAGGAATGCACAG	15133	AQSVPPNRNAQ	0.508166
SS56	15041	GCCCAACACAGCGGCCCCACCAGCAGCGCACAG	15134	AQHSGPTSSAQ	0.505295
SS57	15042	GCCCAAAAAACCAACACACCGTCCTCGCACAG	15135	AQKTNNTVLAQ	0.504377

FIG. 35 (Continued)

SS58	15043	GCCCAACCCGCCAGAATCCCCGGCAGCGCACAG	15136	AQPARIPGSAQ	0.50309
SS59	15044	GCCCAATTGTCTGCTCAGCTTCCGCGGGCACAG	15137	AQLSAQLPRAQ	0.503052
SS60	15045	GCCCAAGTTGGTTCTAGTAATACGTATGCACAG	15138	AQVGSSNTYAQ	0.502229
SS61	15046	GCCCAACTCATCAGCACCACCCACAGAGCACAG	15139	AQLISTTHRAQ	0.502083
GS1	15047	GCCCAATATGTTAATAGTGCTCCGAAGGCACAG	15140	AQYVNSAPKAQ	0.551681
GS2	15048	GCCCAAAACAACAACCAAAAAGTCTACGCACAG	15141	AQNNNQKVYAQ	0.532399
Gs3	15049	GCCCAAGGCACCAAAACCCACAGCCTCGCACAG	15142	AQGTKTHSLAQ	0.518459
GS4	15050	GCCCAACCCATCAGCGCCAACAGACTCGCACAG	15143	AQPISANRLAQ	0.512571
GS5	15051	GCCCAACACCCCAGCCTCAGACAAAGCGCACAG	15144	AQHPSLRQSAQ	0.508478
GS6	15052	GCCCAACCCAACAGAGCCGCCAACAACGCACAG	15145	AQPNRAANNAQ	0.508143
GS7	15053	GCCCAACCCAGCCACGCCAGAGCCAGCGCACAG	15146	AQPSHARASAQ	0.504054

FIG. 35 (Continued)


Acceptor Vector: rAAV-ΔCap-in-cis-lox2
In Cre- cells
UBC
mNG
pA
rep
cap9
Cre-
pA
lox71
lox66
In Cre+ cells
Cre+
lox72
loxP
Cre dependent Cap recovery

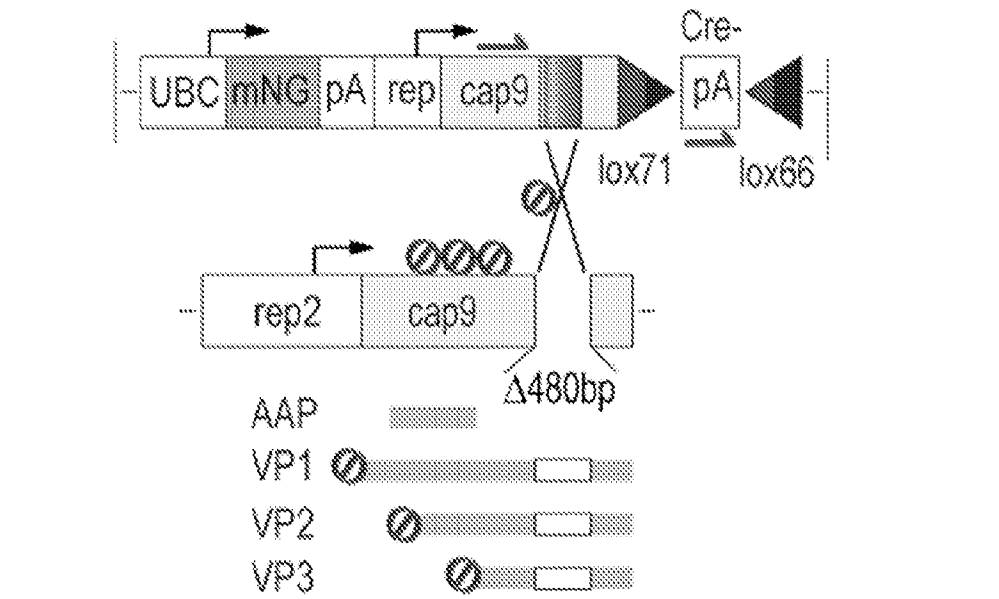

Rep-AAPΔCap Vector: Rep-AAP-ΔCap-in-trans
UBC
mNG
pA
rep
cap9
Cre-
pA
lox71
lox66
rep2
cap9
Δ480bp
AAP
VP1
VP2
VP3

FIG. 36

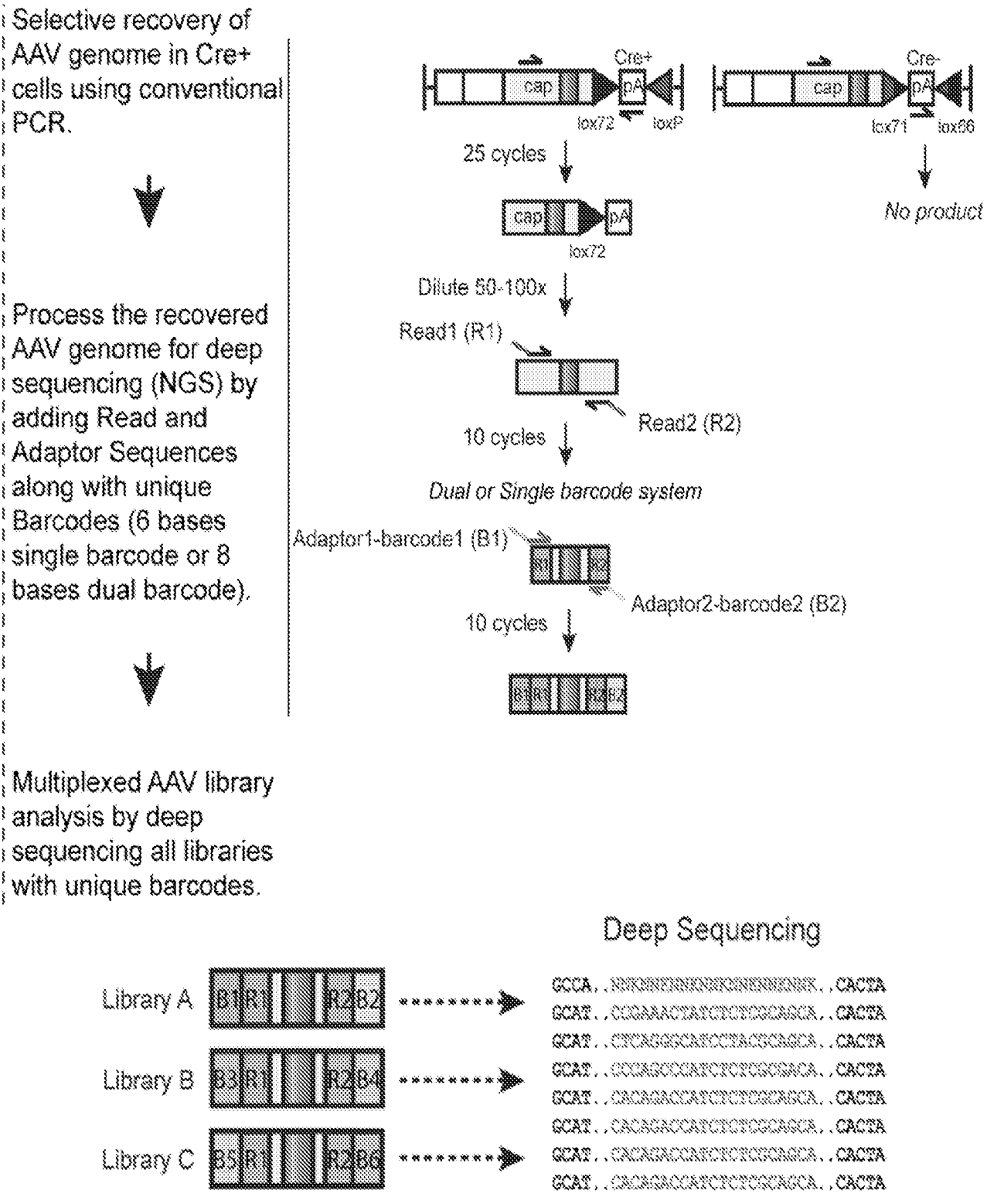

Selective recovery of AAV genome in Cre+ cells using conventional PCR.
Process the recovered AAV genome for deep sequencing (NGS) by adding Read and Adaptor Sequences along with unique Barcodes (6 bases single barcode or 8 bases dual barcode).
Multiplexed AAV library analysis by deep sequencing all libraries with unique barcodes.
Cre+
cap
pA
lox72
loxP
Cre-
lox71
lox66
No product
25 cycles
Dilute 50-100x
Read1 (R1)
Read2 (R2)
10 cycles
Dual or Single barcode system
Adaptor1-barcode1 (B1)
Adaptor2-barcode2 (B2)
10 cycles
Deep Sequencing
Library A
Library B
Library C
B1
R1
R2
B2
B3
B4
B5
B6
GCCA..CACTA
GCAT..CACTA

FIG. 37

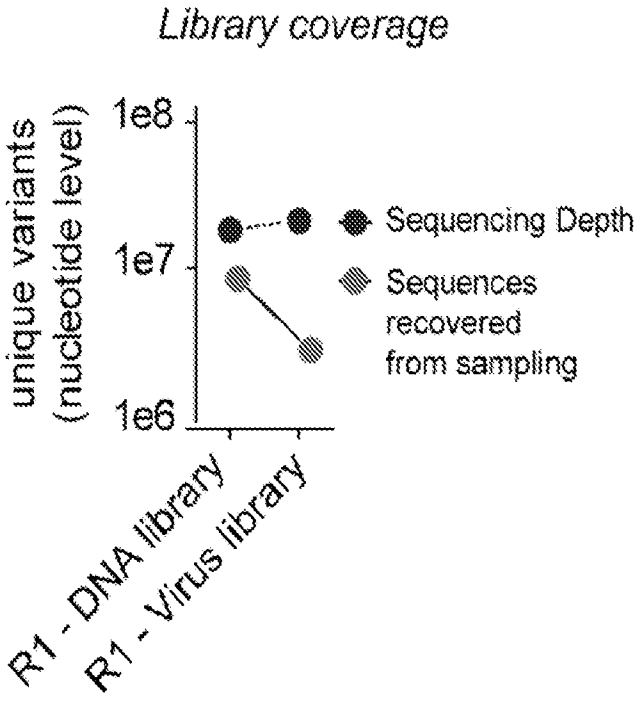

Library coverage
unique variants (nucleotide level)
1e8
1e7
1e6
Sequencing Depth
Sequences recovered from sampling
R1 - DNA library
R1 - Virus library

FIG. 38

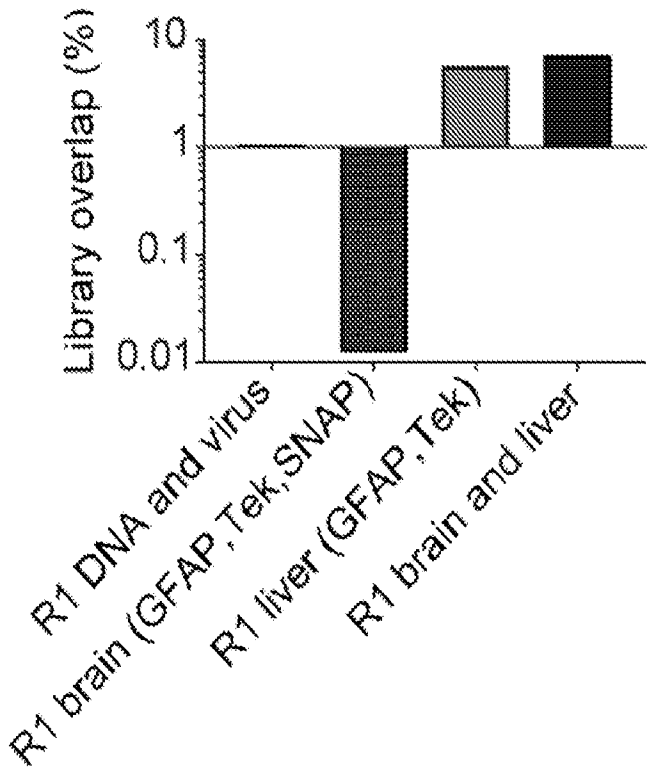

Library overlap (%)
10
1
0.1
0.01
R1 DNA and virus
R1 brain (GFAP,Tek,SNAP)
R1 liver (GFAP,Tek)
R1 brain and liver

FIG. 39

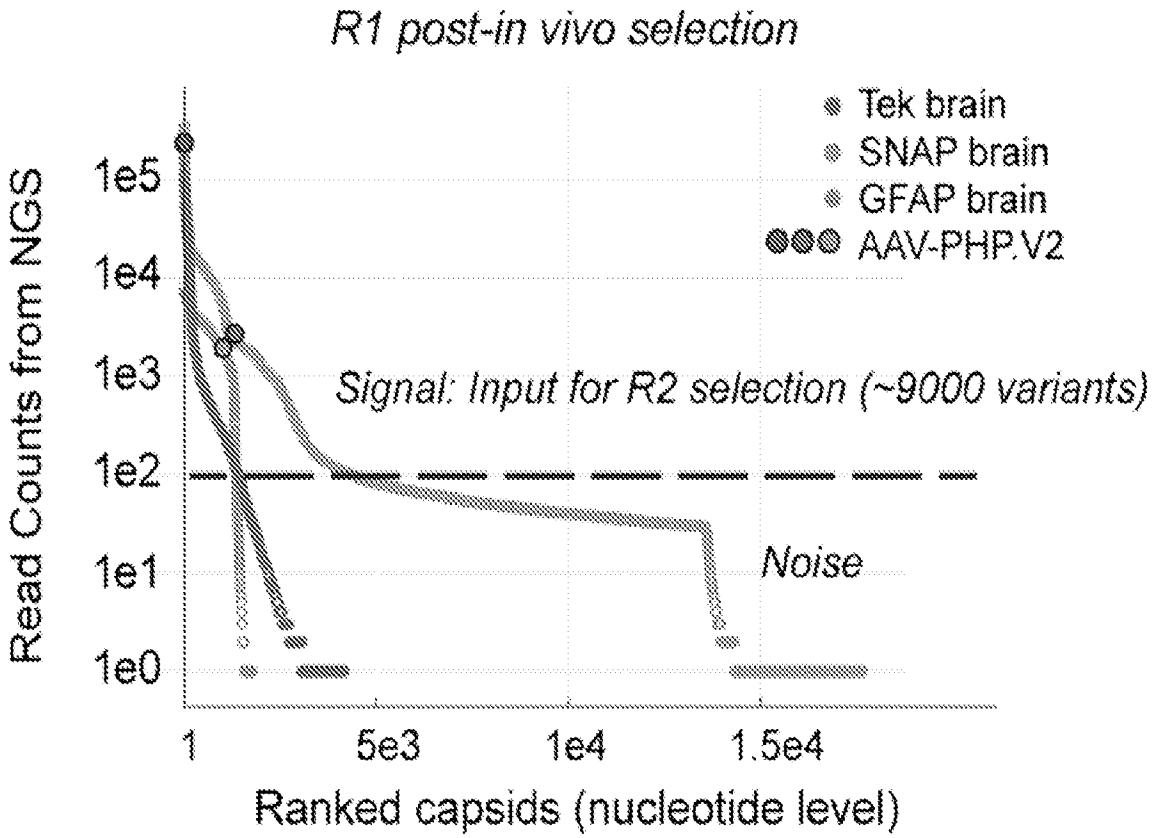


FIG. 40

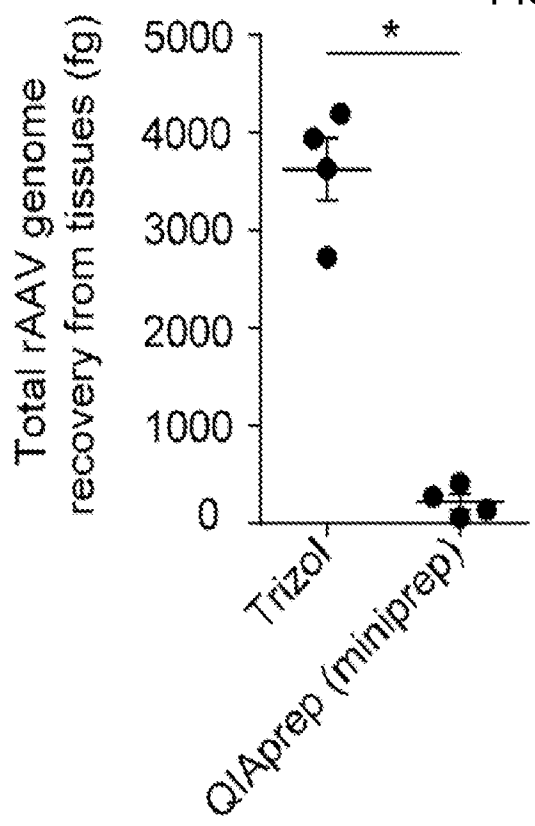


FIG. 41

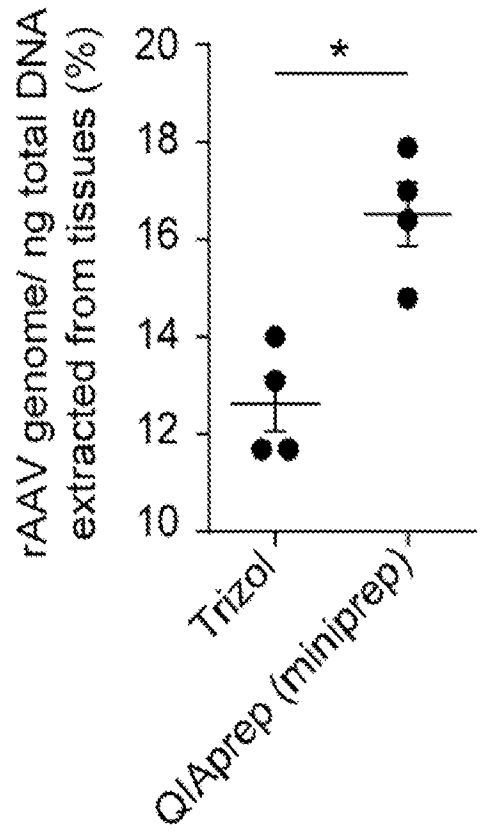


FIG. 42

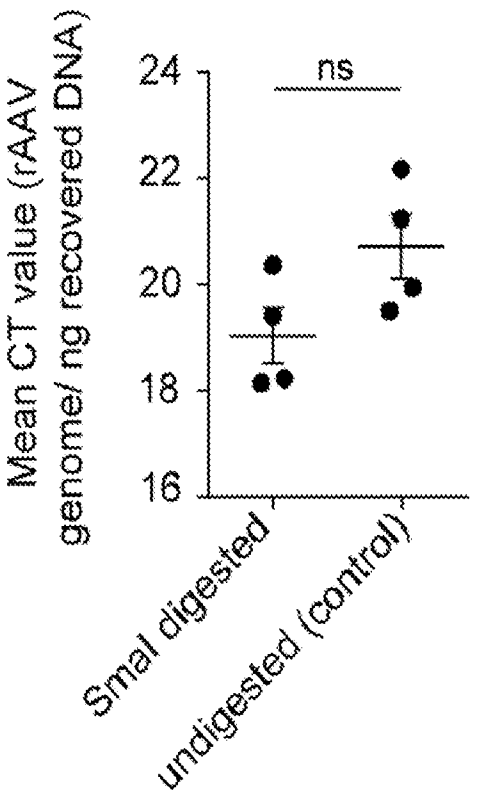


FIG. 43

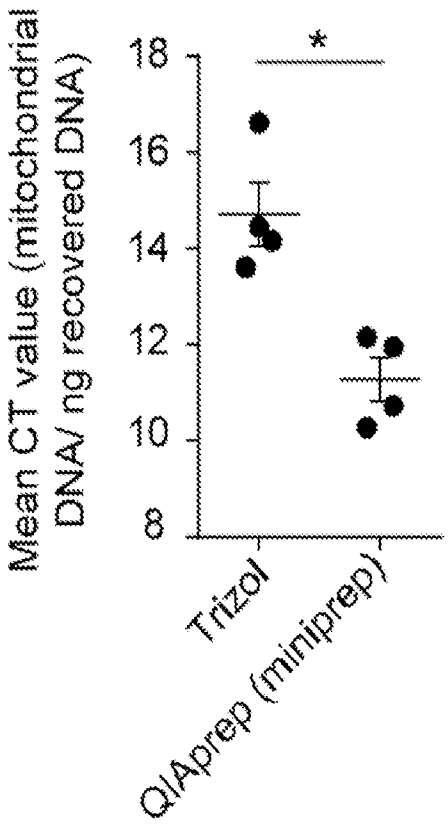


FIG. 44

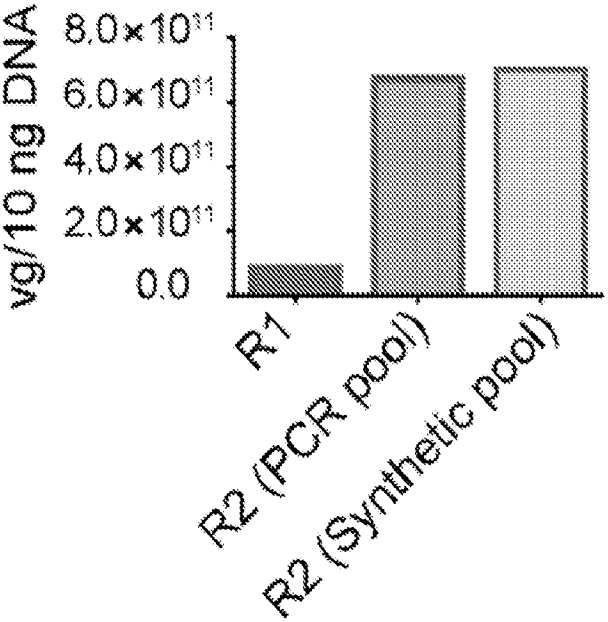


FIG. 45

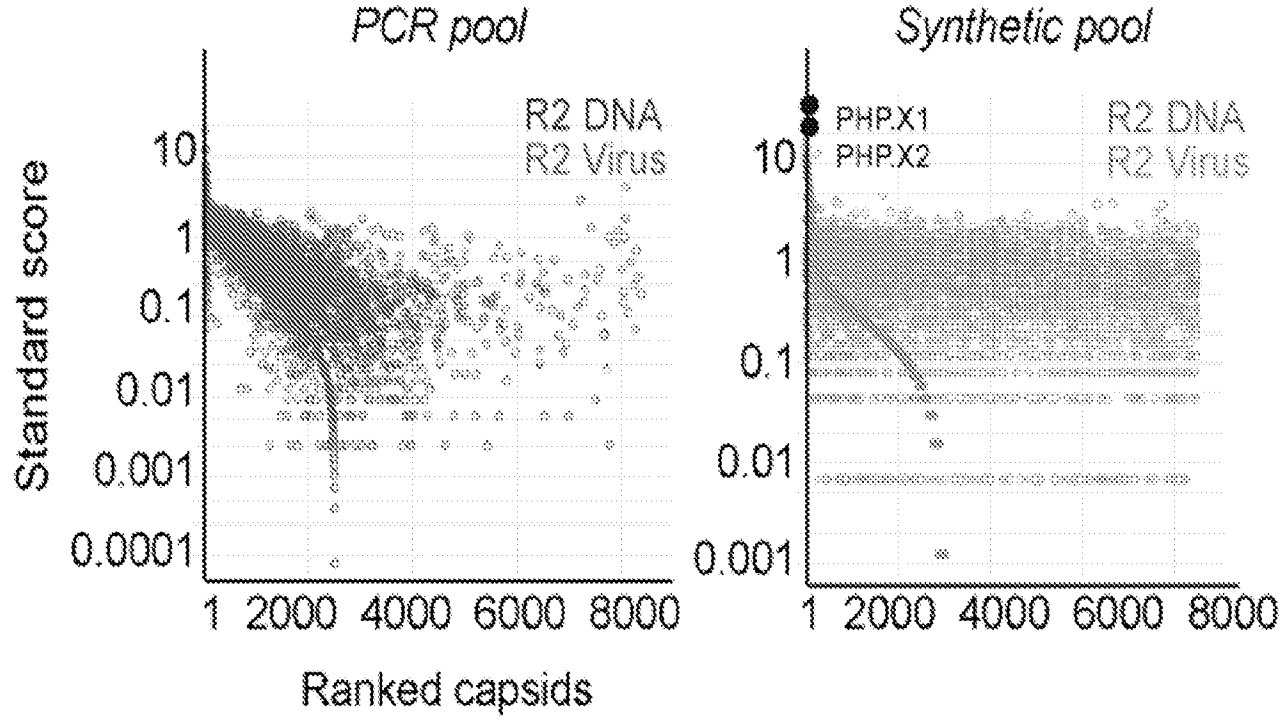

PCR pool
Synthetic pool
R2 DNA
R2 Virus
PHP.X1
PHP.X2
Standard score
10
1
0.1
0.01
0.001
0.0001
1 2000 4000 6000 8000
Ranked capsids

FIG. 46

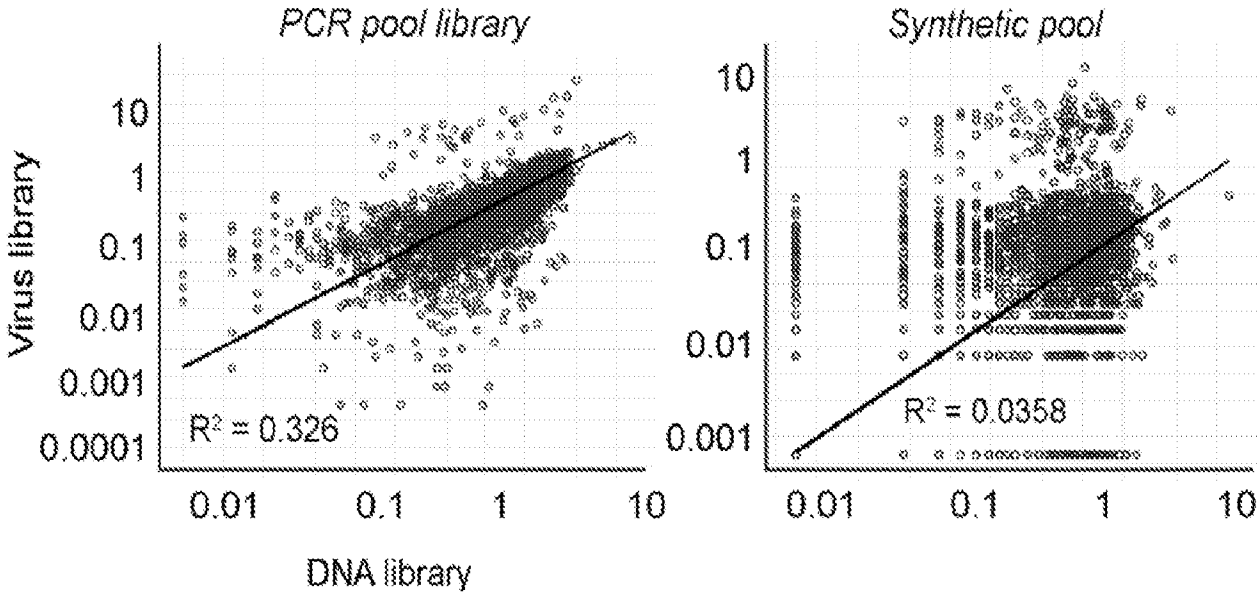

PCR pool library
Synthetic pool
Virus library
DNA library
R² = 0.326
R² = 0.0358
10
1
0.1
0.01
0.001
0.0001

FIG. 47

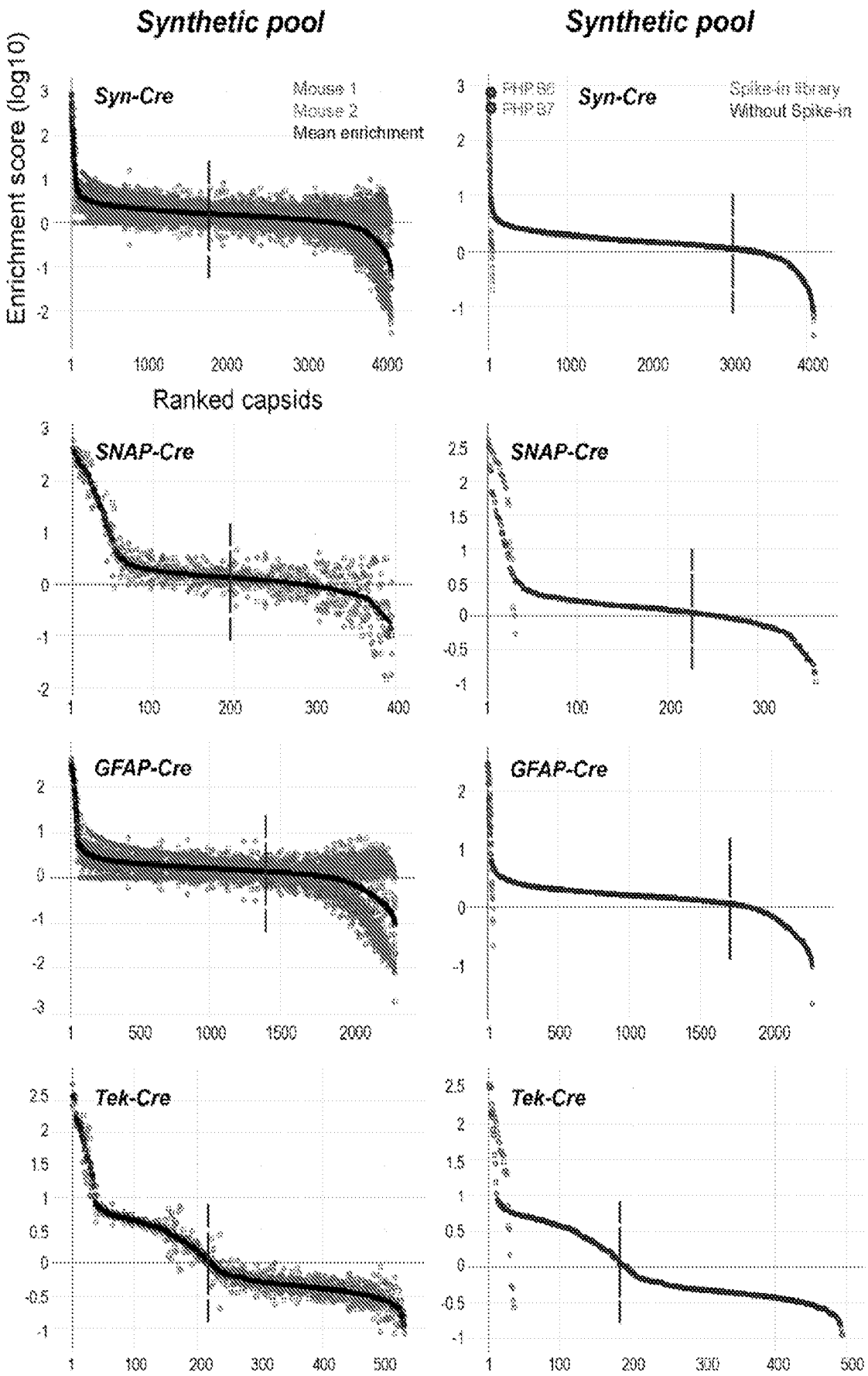

Synthetic pool
Synthetic pool
Enrichment score (log10)
Syn-Cre
Mouse 1
Mouse 2
Mean enrichment
PHP.B6
PHP.B7
Syn-Cre
Spike-in library
Without Spike-in
Ranked capsids
SNAP-Cre
SNAP-Cre
GFAP-Cre
GFAP-Cre
Tek-Cre
Tek-Cre

FIG. 48

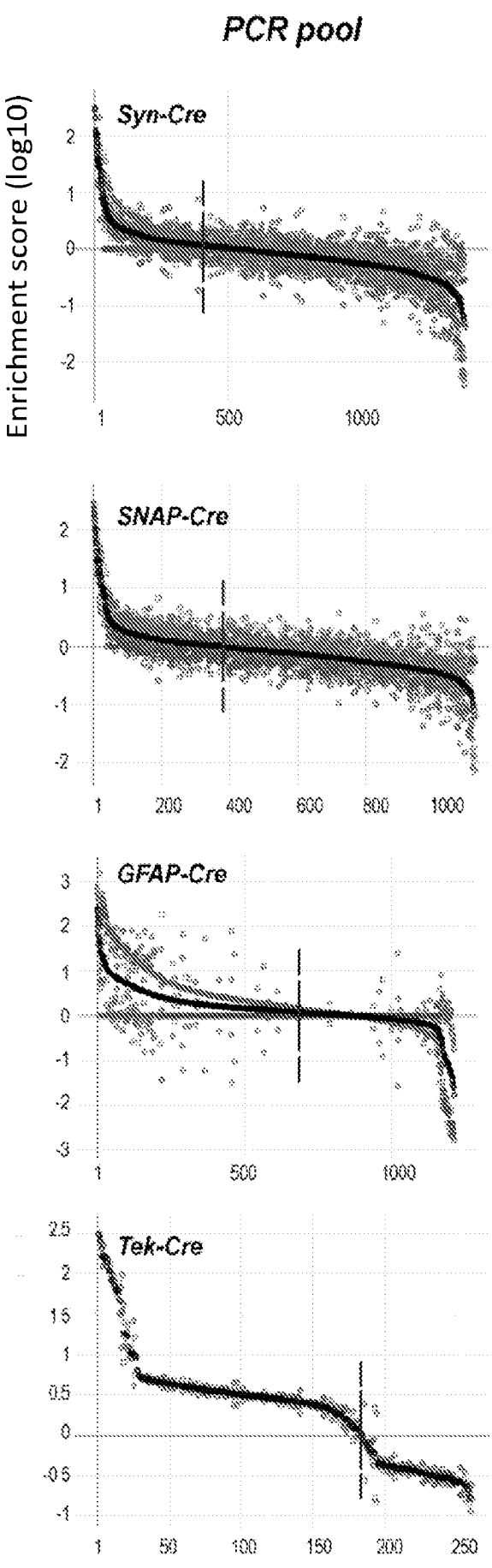


FIG. 48 (Continued)

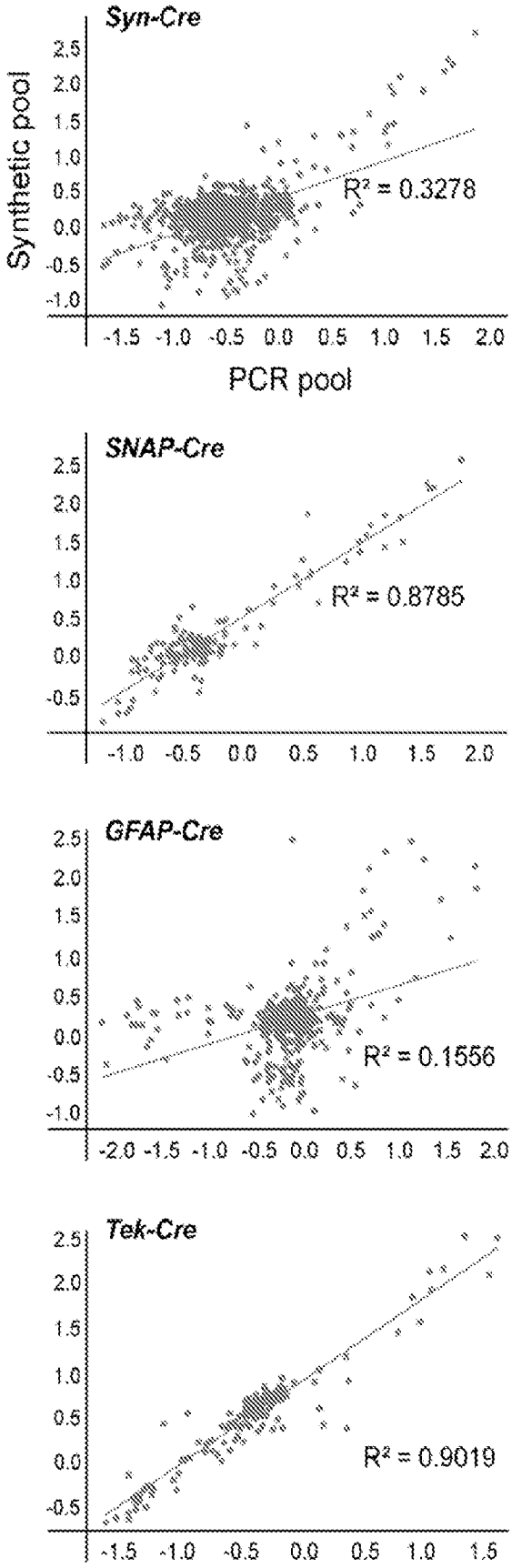

Syn-Cre
Synthetic pool
PCR pool
R² = 0.3278
SNAP-Cre
R² = 0.8785
GFAP-Cre
R² = 0.1556
Tek-Cre
R² = 0.9019

FIG. 49

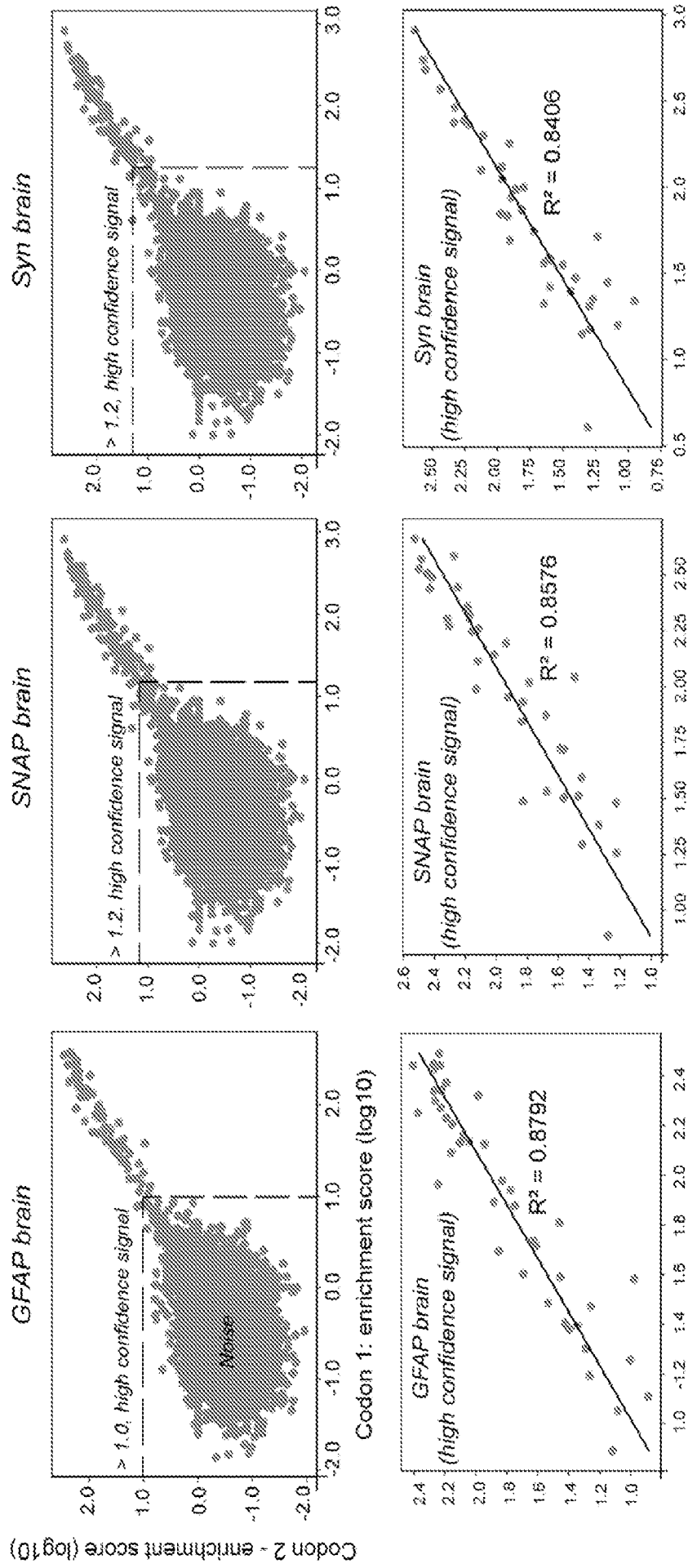

GFAP brain
SNAP brain
Syn brain
> 1.0, high confidence signal
> 1.2, high confidence signal
Mouse
(high confidence signal)
R² = 0.8792
R² = 0.8576
R² = 0.8406
Codon 2 - enrichment score (log10)
Codon 1: enrichment score (log10)

FIG. 50

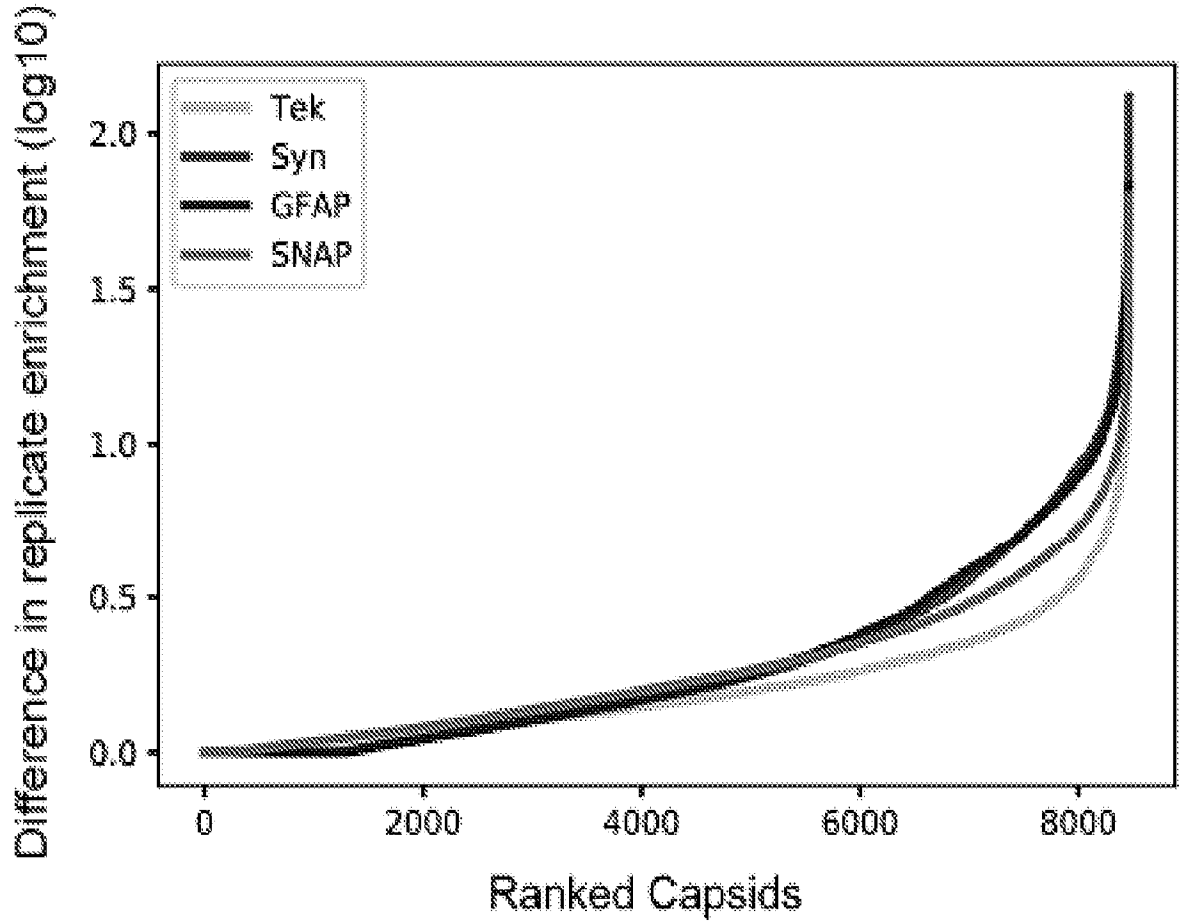

Tek
Syn
GFAP
SNAP
Difference in replicate enrichment (log10)
2.0
1.5
1.0
0.5
0.0
0
2000
4000
6000
8000
Ranked Capsids

FIG. 51

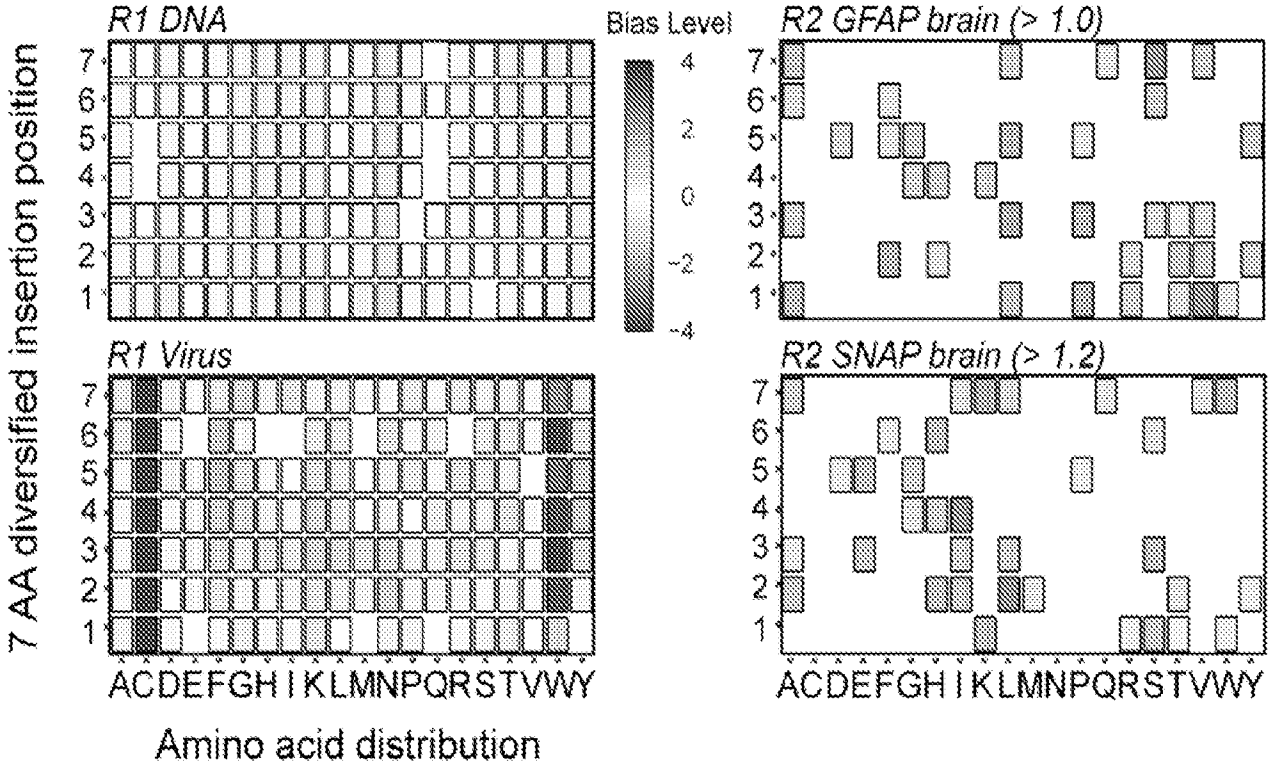

R1 DNA
R1 Virus
R2 GFAP brain (> 1.0)
R2 SNAP brain (> 1.2)
Bias Level
4
2
0
-2
-4
7 AA diversified insertion position
7
6
5
4
3
2
1
A C D E F G H I K L M N P Q R S T V W Y
Amino acid distribution

FIG. 52

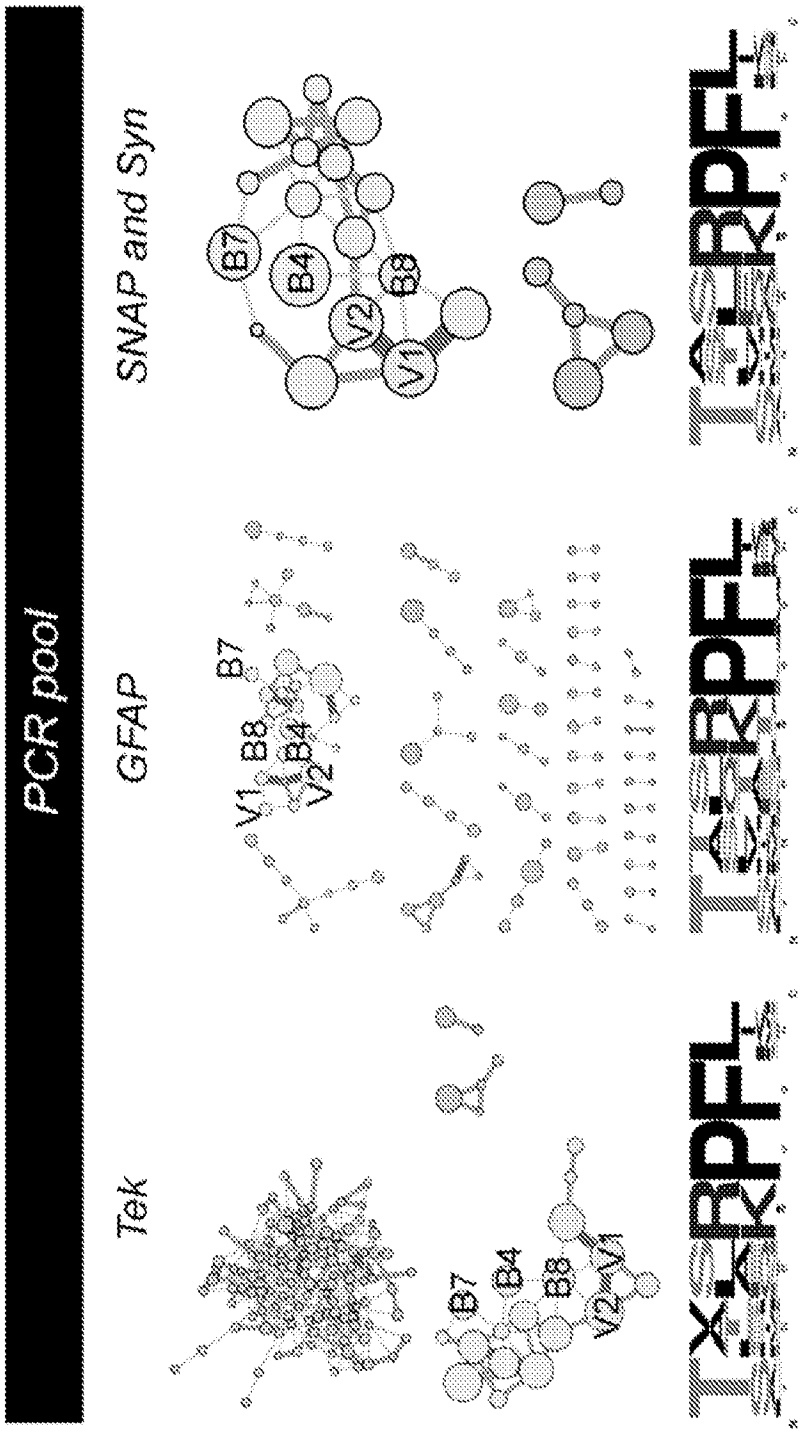

PCR pool
Tek
GFAP
SNAP and Syn
B7
B4
B8
V2
V1
TX-RPFL
TX-RPFL
TX-RPFL

FIG. 53

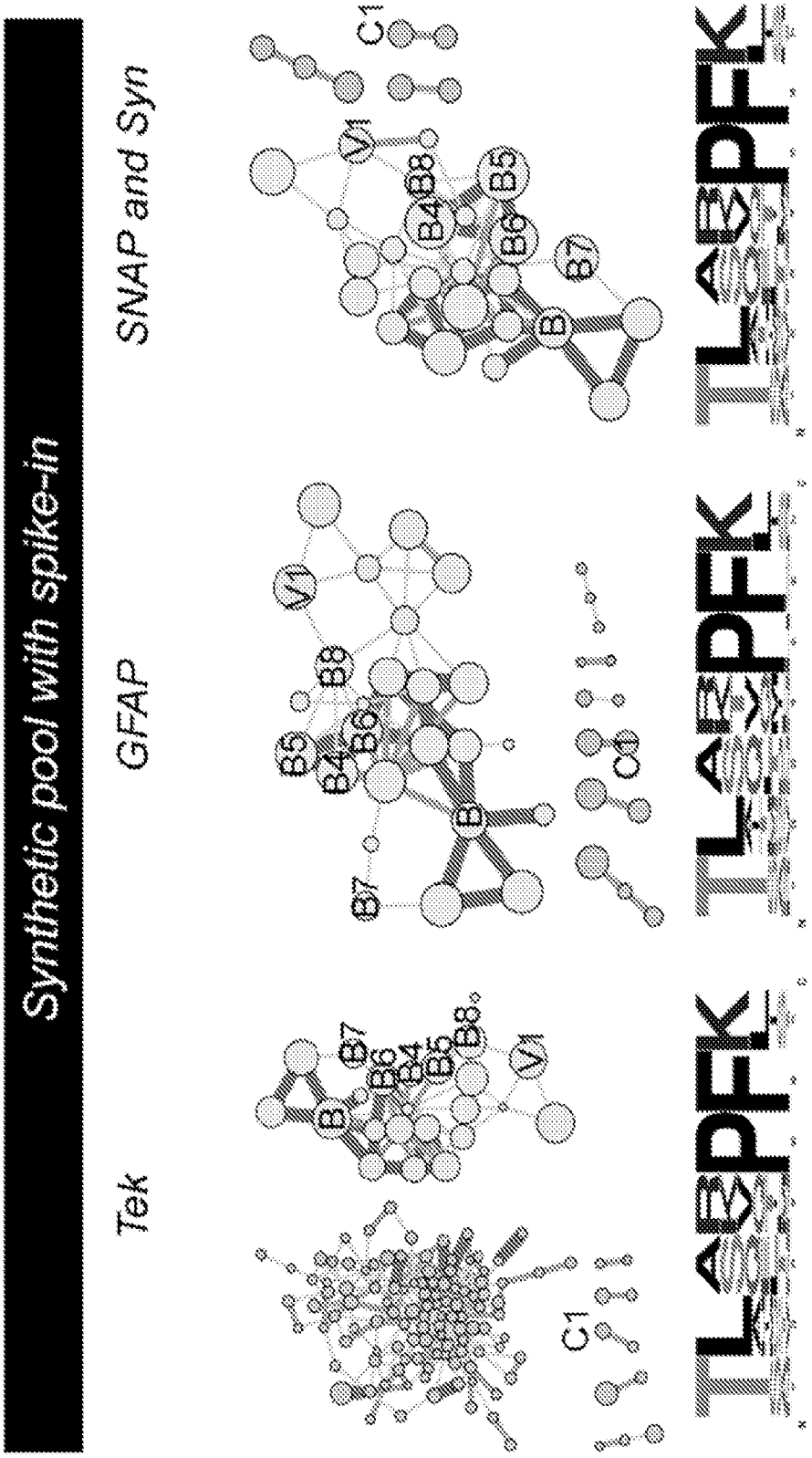


FIG. 53 (Continued)

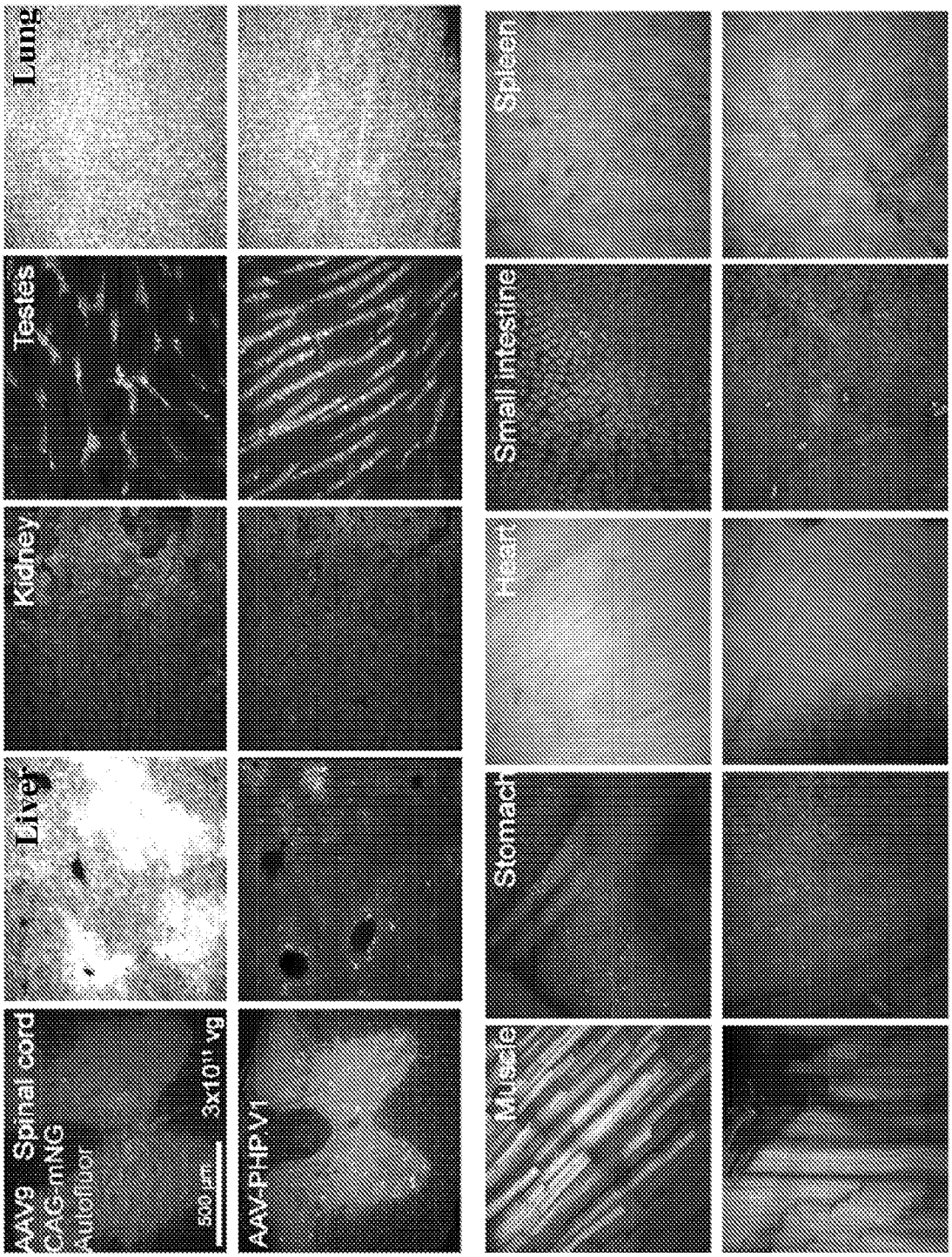

AAV9
CAG-mNG
Autofluor
3x10^11 vg
500 µm
Spinal cord
Liver
Kidney
Testes
Lung
AAV-PHP.V1
Muscle
Stomach
Heart
Small intestine
Spleen

FIG. 54

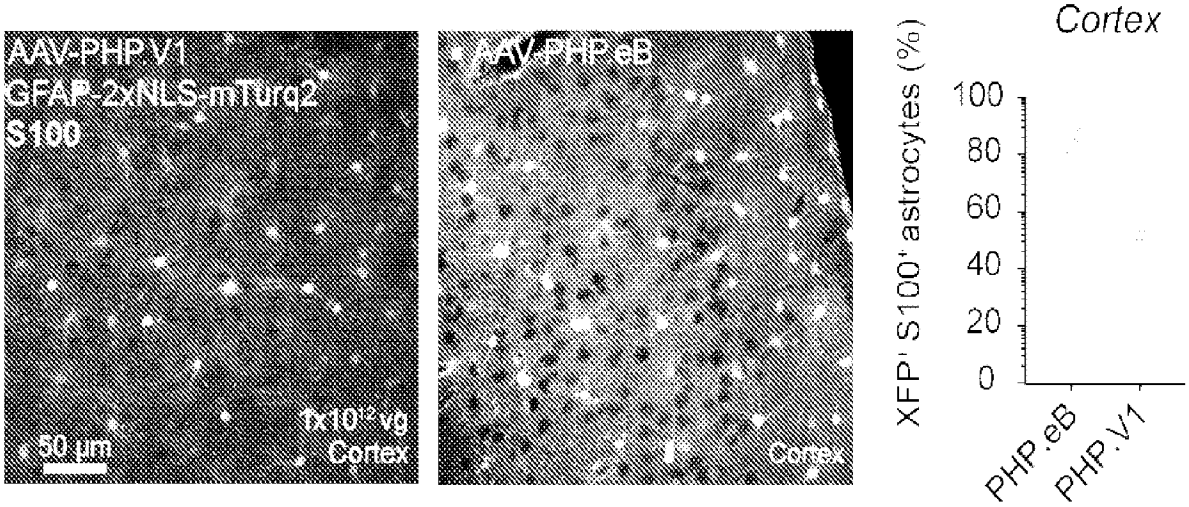


FIG. 55

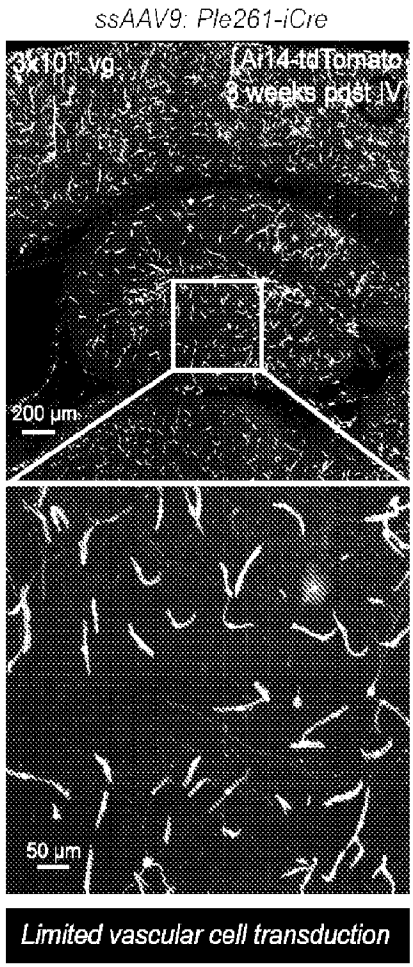


FIG. 56

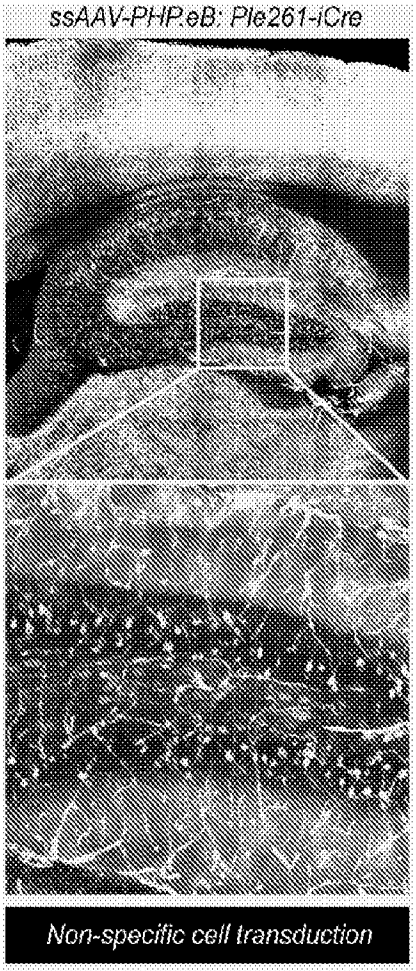


FIG. 57

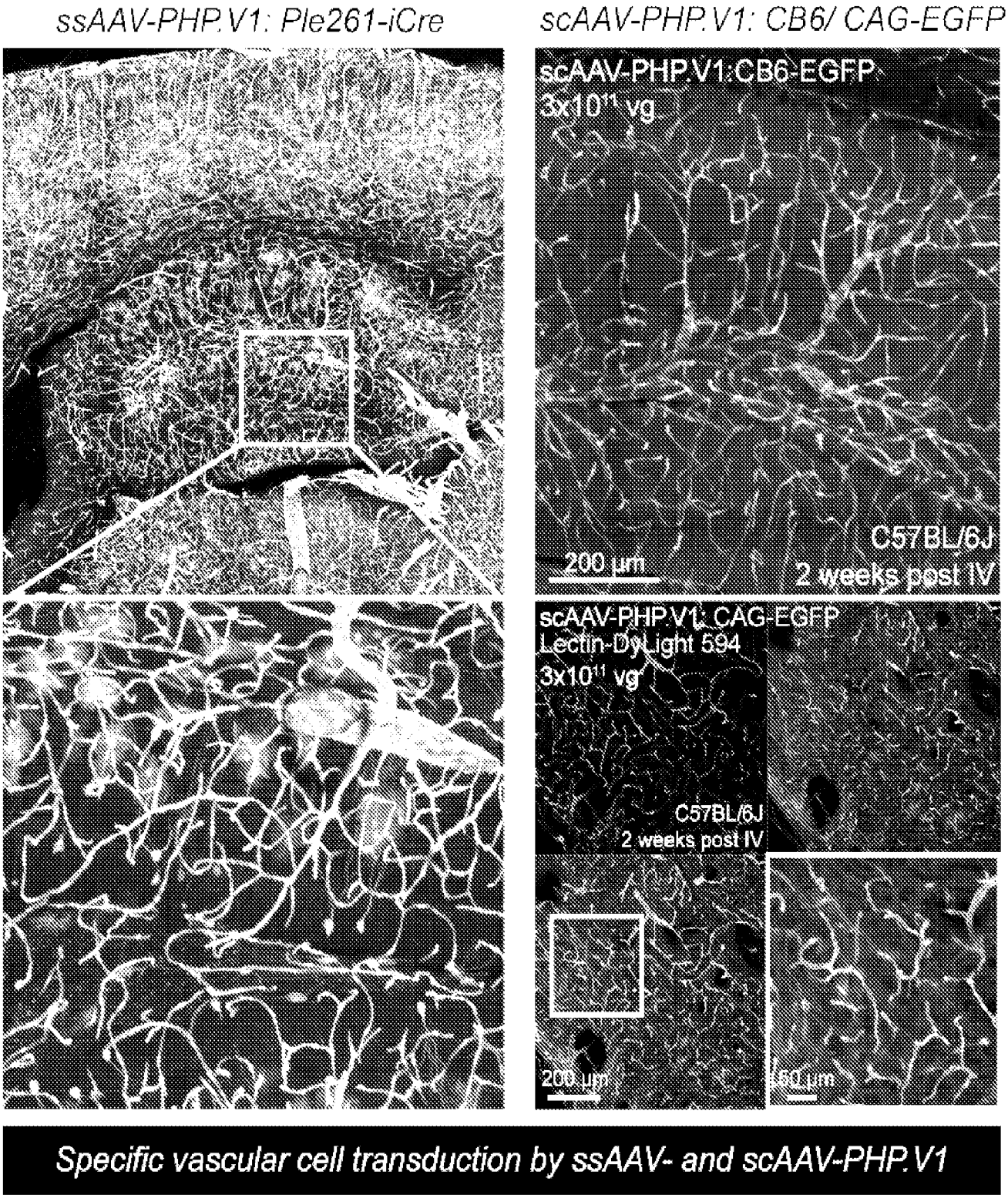

ssAAV-PHP.V1: Ple261-iCre
scAAV-PHP.V1: CB6/ CAG-EGFP
scAAV-PHP.V1:CB6-EGFP
3x10^11 vg
200 µm
C57BL/6J
2 weeks post IV
scAAV-PHP.V1: CAG-EGFP
Lectin-DyLight 594
3x10^11 vg
C57BL/6J
2 weeks post IV
200 µm
50 µm
Specific vascular cell transduction by ssAAV- and scAAV-PHP.V1

FIG. 58

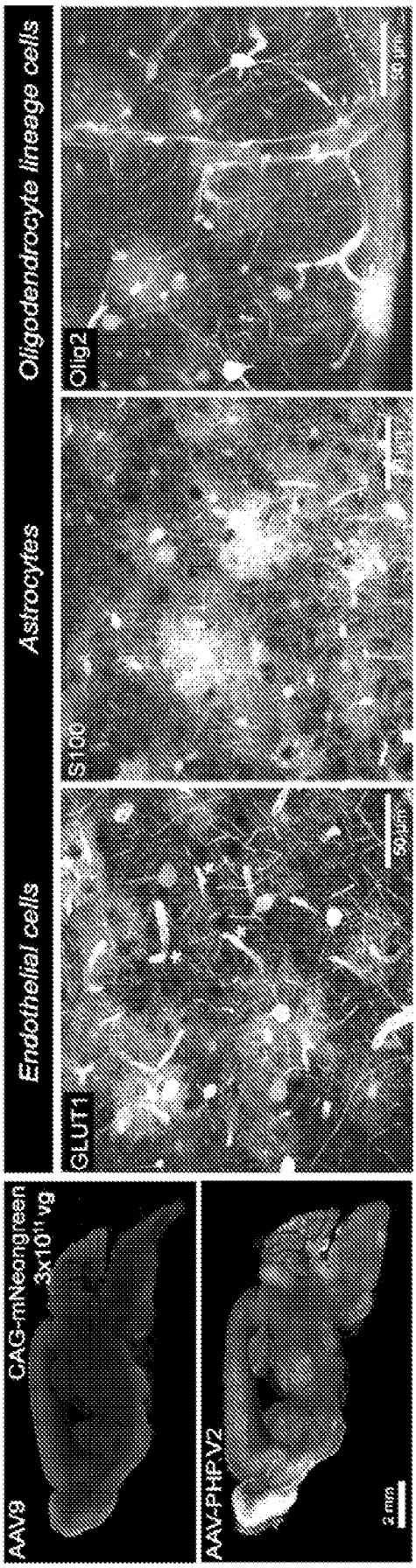

AAV9
CAG-mNeongreen
3x10^11 vg
AAV-PHP.V2
2 mm
Endothelial cells
Astrocytes
Oligodendrocyte lineage cells
GLUT1
S100
Olig2
50 μm

FIG. 59

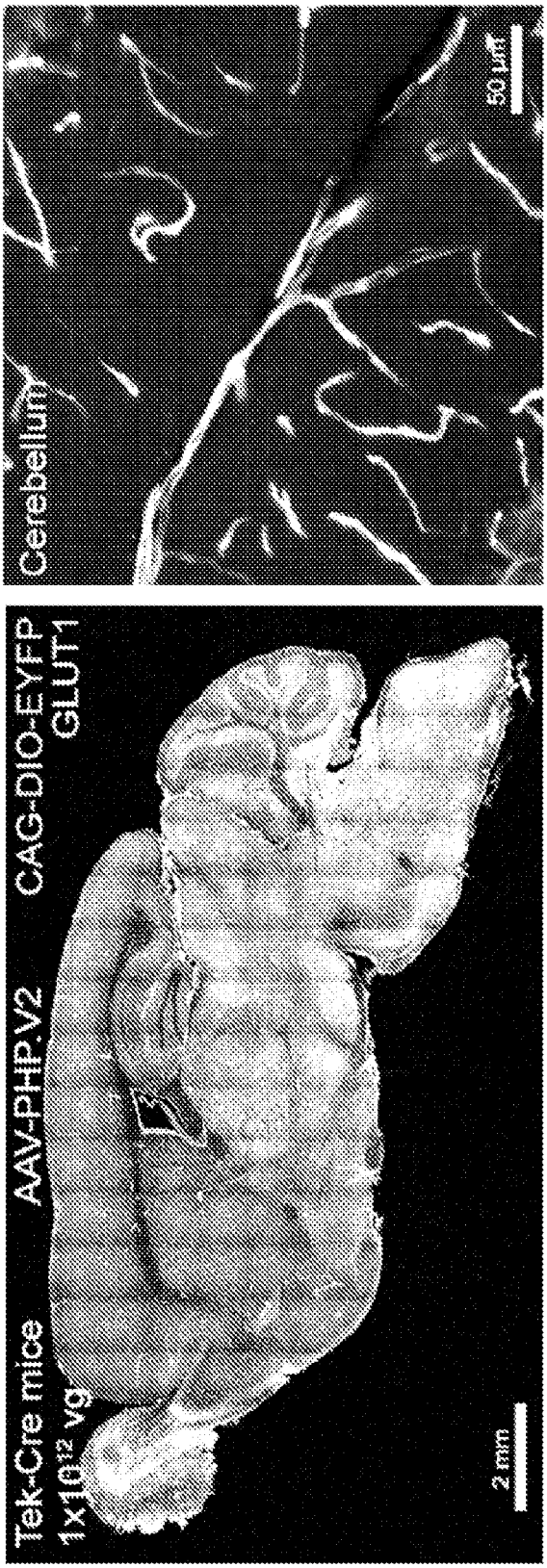
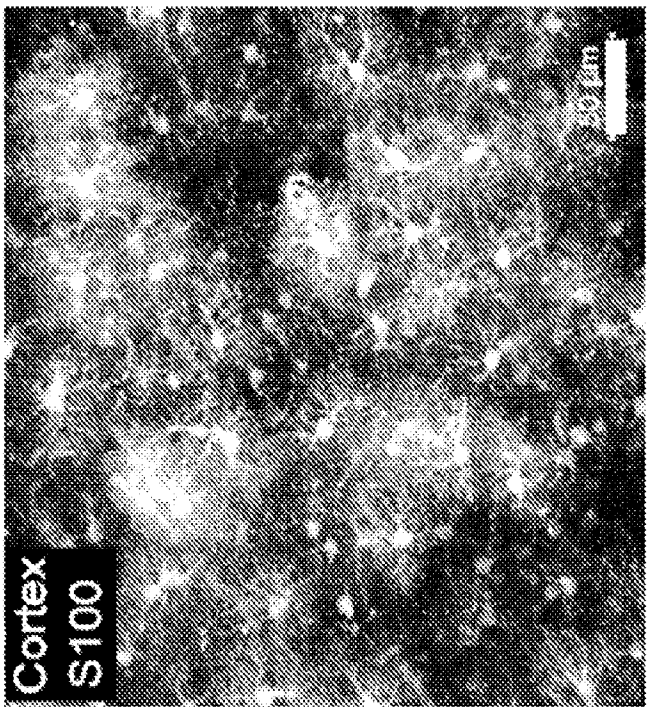

Tek-Cre mice
1x10^12 vg
AAV-PHP.V2
CAG-DIO-EYFP
GLUT1
2 mm
Cerebellum
50 µm
Striatum
Ventral midbrain
Cerebellum
Cortex
0
20
40
60
80
100
XFP+ GLUT1+ vasculature (%)

FIG. 60


Cortex
S100
50 µm

GFAP-Cre mice
1x10^12 vg
AAV-PHP.V2
CAG-DIO-EYFP
2 mm

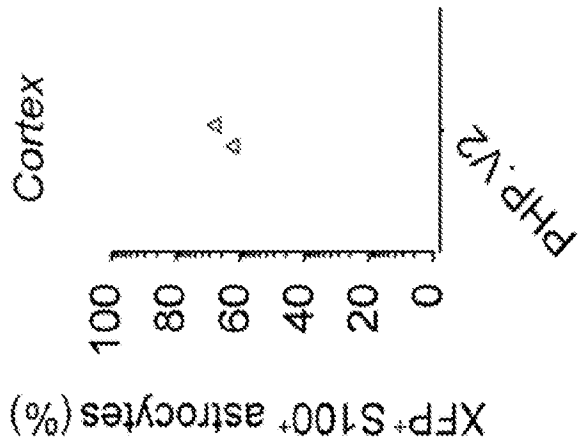

Cortex
100
80
60
40
20
0
XFP+ S100+ astrocytes (%)
PHP.V2

FIG. 61

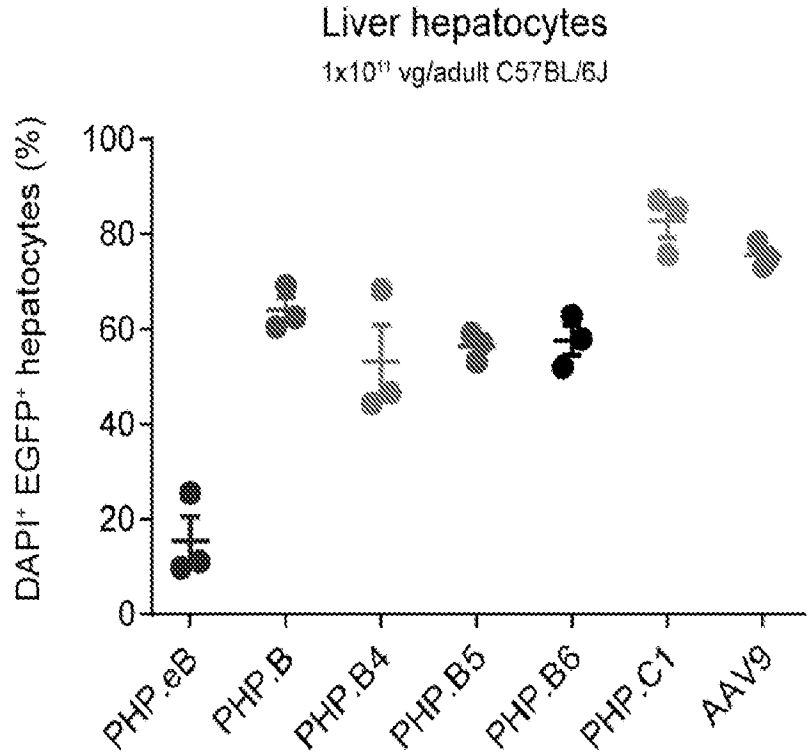

Liver hepatocytes
1x10^11 vg/adult C57BL/6J
DAPI+ EGFP+ hepatocytes (%)
100
80
60
40
20
0
PHP.eB
PHP.B
PHP.B4
PHP.B5
PHP.B6
PHP.C1
AAV9

FIG. 62

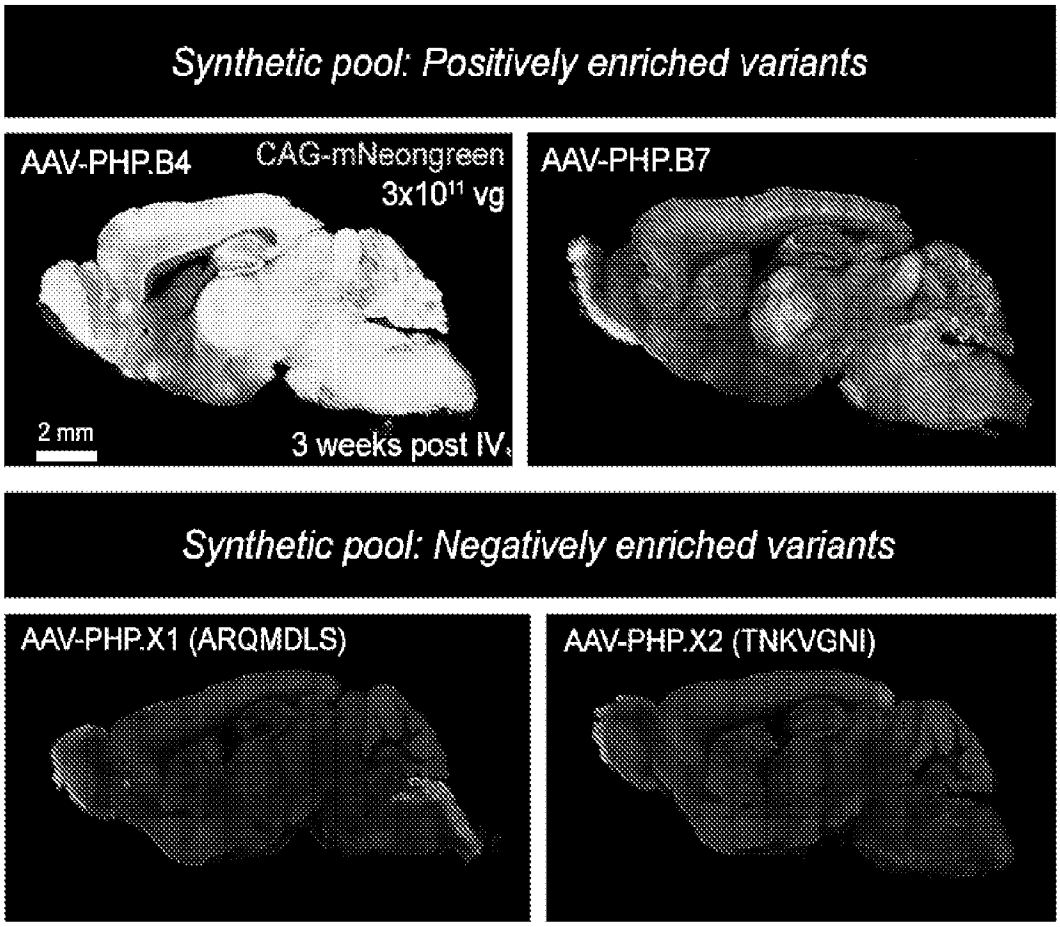
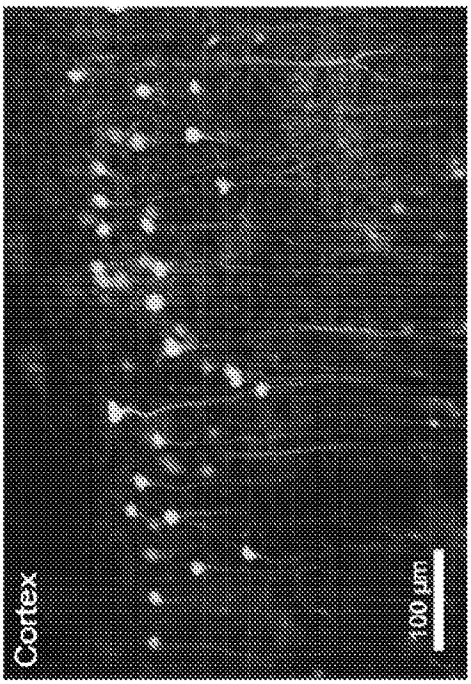

Synthetic pool: Positively enriched variants
AAV-PHP.B4
CAG-mNeongreen
3x10^11 vg
2 mm
3 weeks post IV
AAV-PHP.B7
Synthetic pool: Negatively enriched variants
AAV-PHP.X1 (ARQMDLS)
AAV-PHP.X2 (TNKVGNI)

FIG. 63


Cortex
100 µm

AAV-PHP.B8
CAG-mRuby2
3x10¹¹ vg
3 weeks post IV
2 mm

Hippocampus
100 µm

FIG. 64

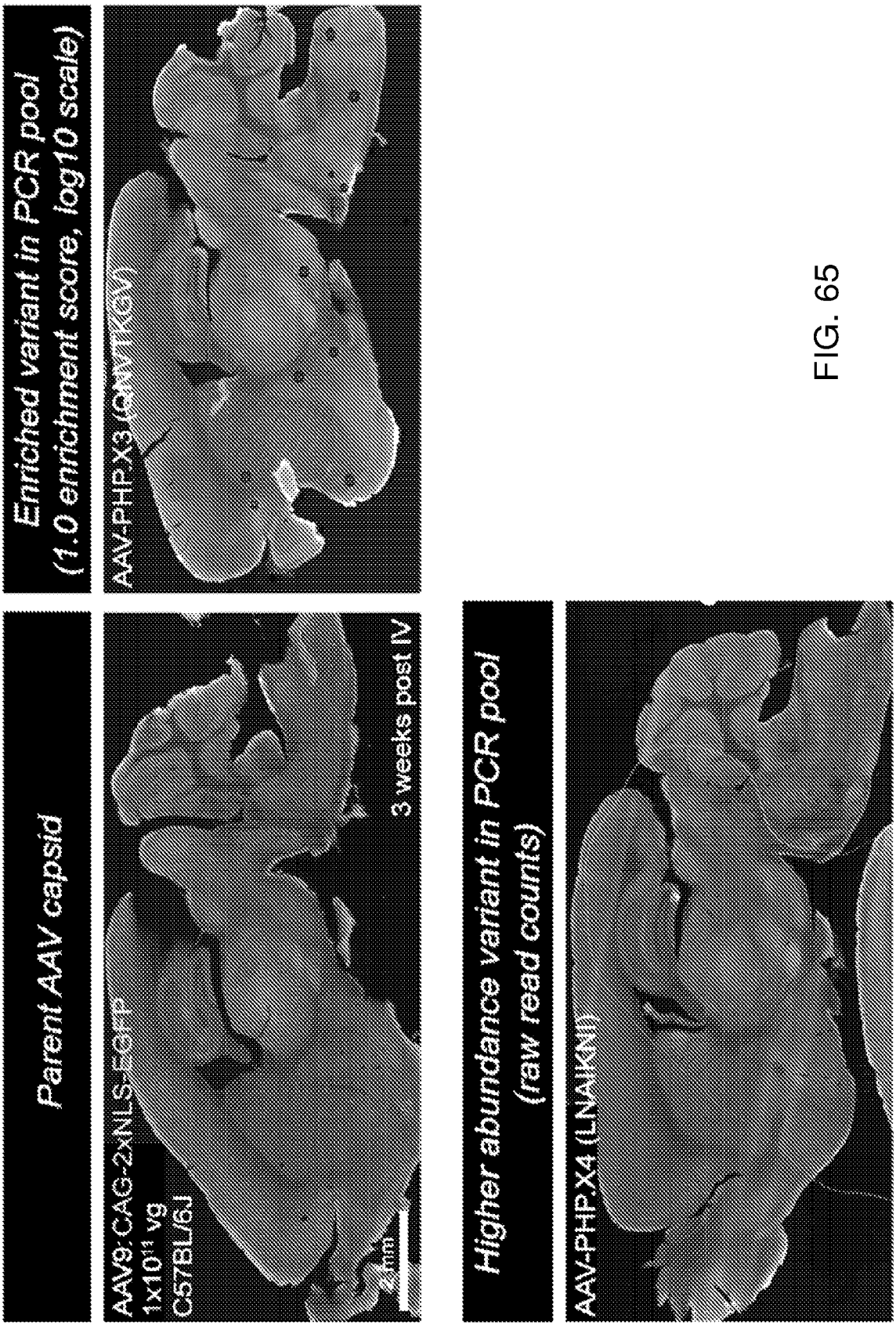

Parent AAV capsid
AAV9:CAG-2xNLS-EGFP
1x10^11 vg
C57BL/6J
3 weeks post IV
2 mm
Enriched variant in PCR pool
(1.0 enrichment score, log10 scale)
AAV-PHP.X3 (QNVTKQV)
Higher abundance variant in PCR pool
(raw read counts)
AAV-PHP.X4 (LNAIKNT)

FIG. 65

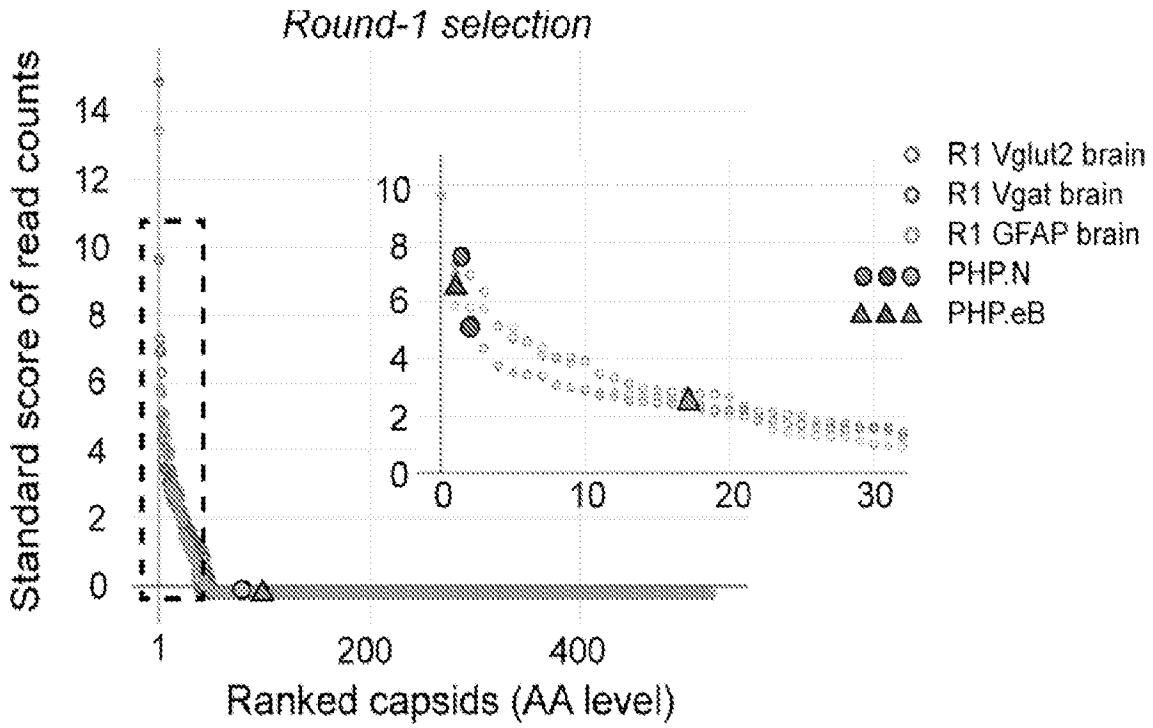

Round-1 selection
Standard score of read counts
14
12
10
8
6
4
2
0
10
8
6
4
2
0
0
10
20
30
1
200
400
Ranked capsids (AA level)
R1 Vglut2 brain
R1 Vgat brain
R1 GFAP brain
PHP.N
PHP.eB

FIG. 66

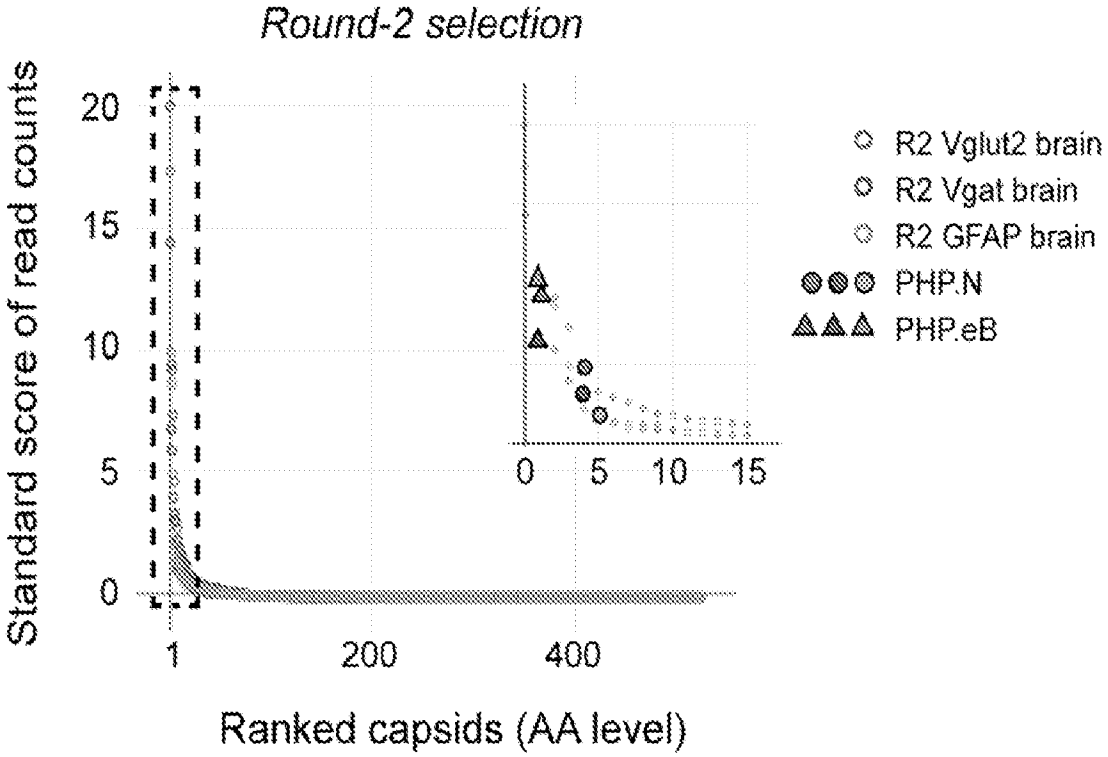

Round-2 selection
Standard score of read counts
20
15
10
5
0
0
5
10
15
1
200
400
Ranked capsids (AA level)
R2 Vglut2 brain
R2 Vgat brain
R2 GFAP brain
PHP.N
PHP.eB

FIG. 67

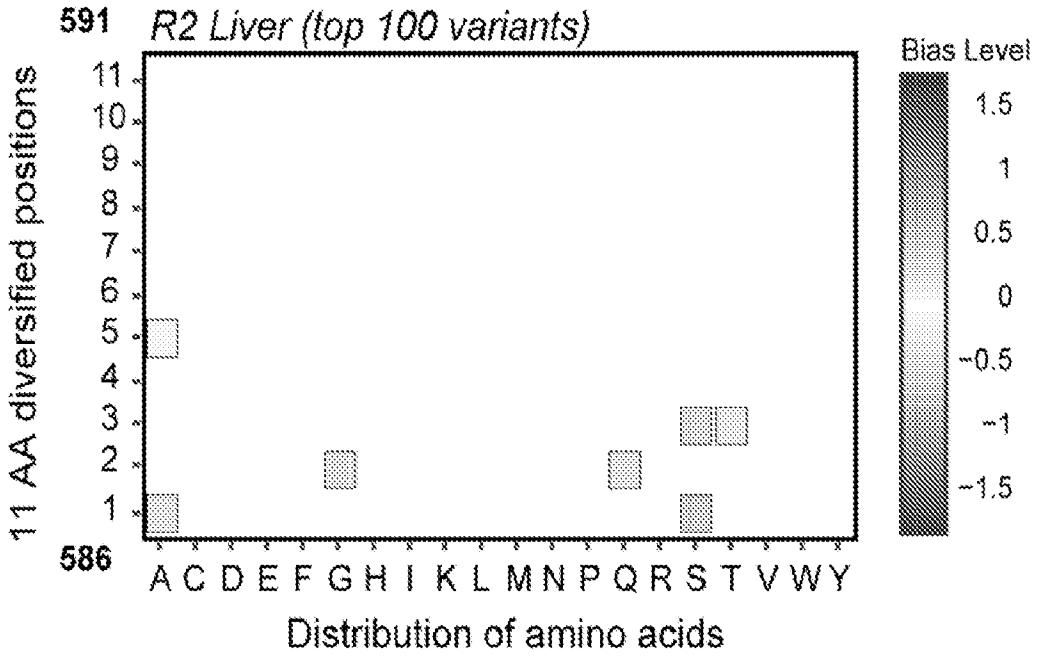

591
R2 Liver (top 100 variants)
11 AA diversified positions
11
10
9
8
7
6
5
4
3
2
1
586
A C D E F G H I K L M N P Q R S T V W Y
Distribution of amino acids
Bias Level
1.5
1
0.5
0
-0.5
-1
-1.5

FIG. 68

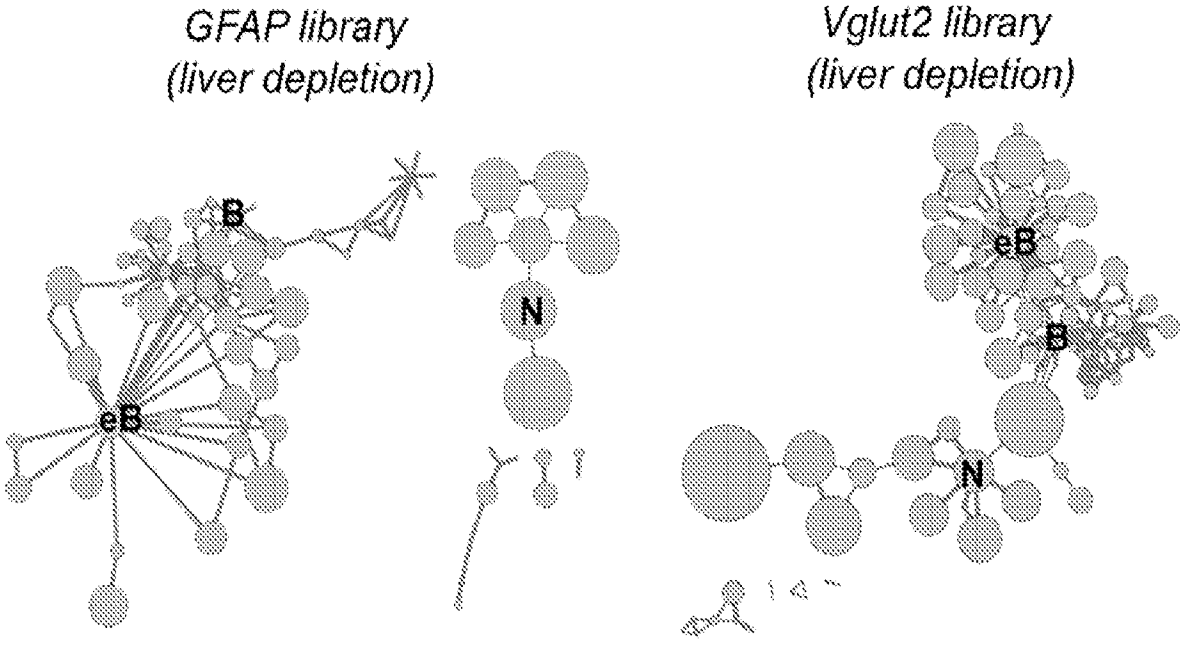

GFAP library
(liver depletion)
B
eB
N
Vglut2 library
(liver depletion)
eB
B
N

FIG. 69

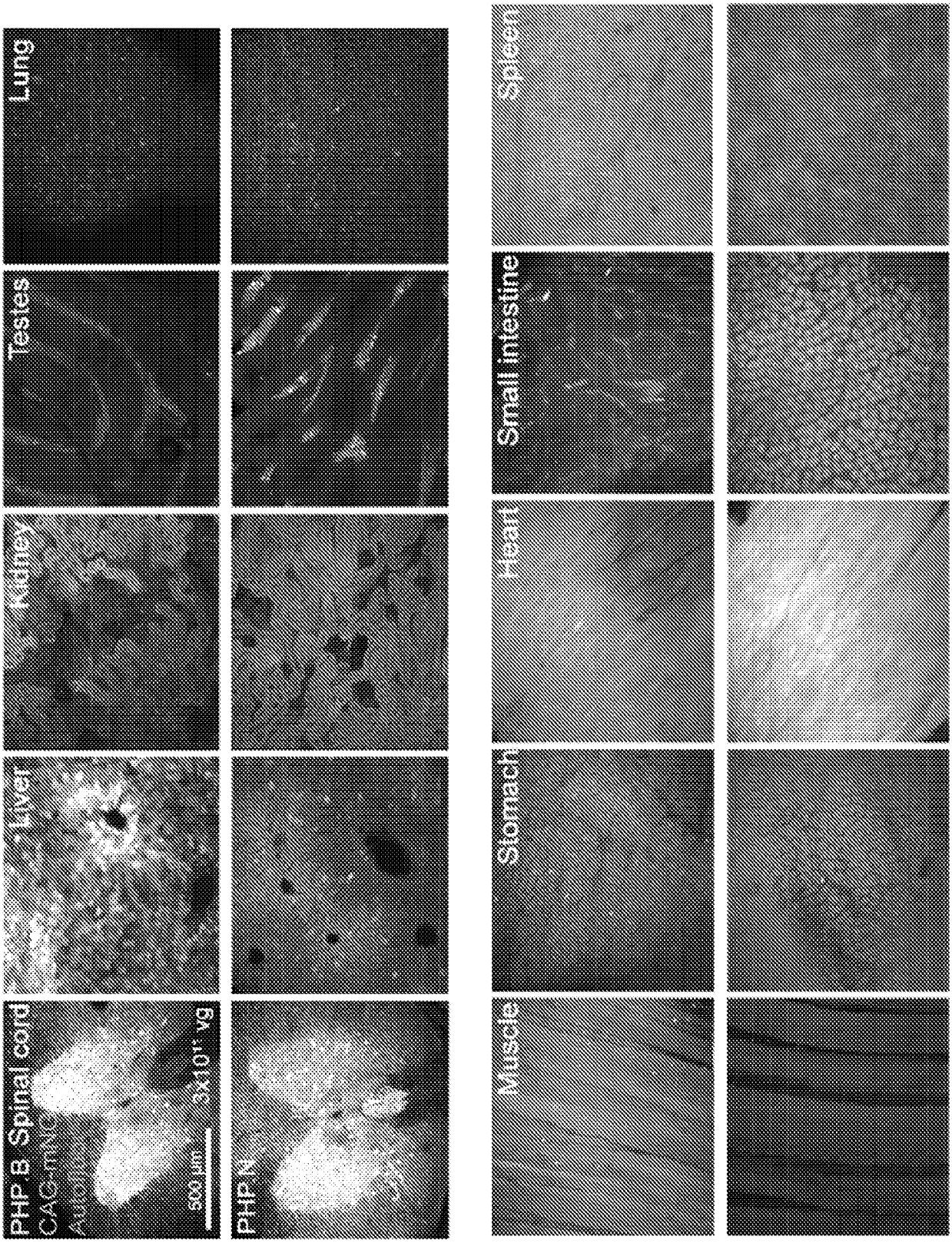

PHP.B
CAG-mNG
500 µm
3x10^11 vg
PHP.N
Spinal cord
Liver
Kidney
Testes
Lung
Muscle
Stomach
Heart
Small Intestine
Spleen

FIG. 70

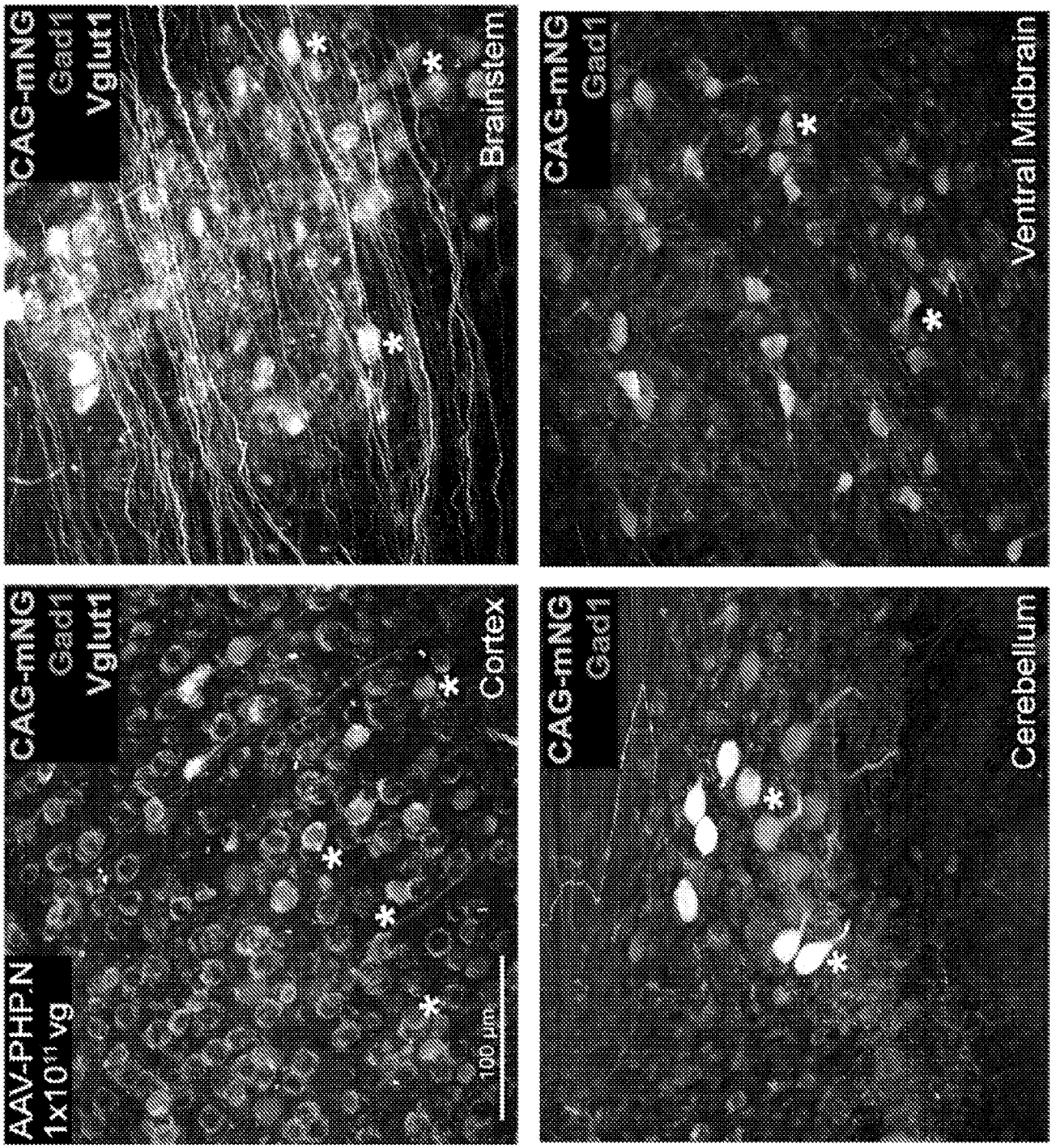
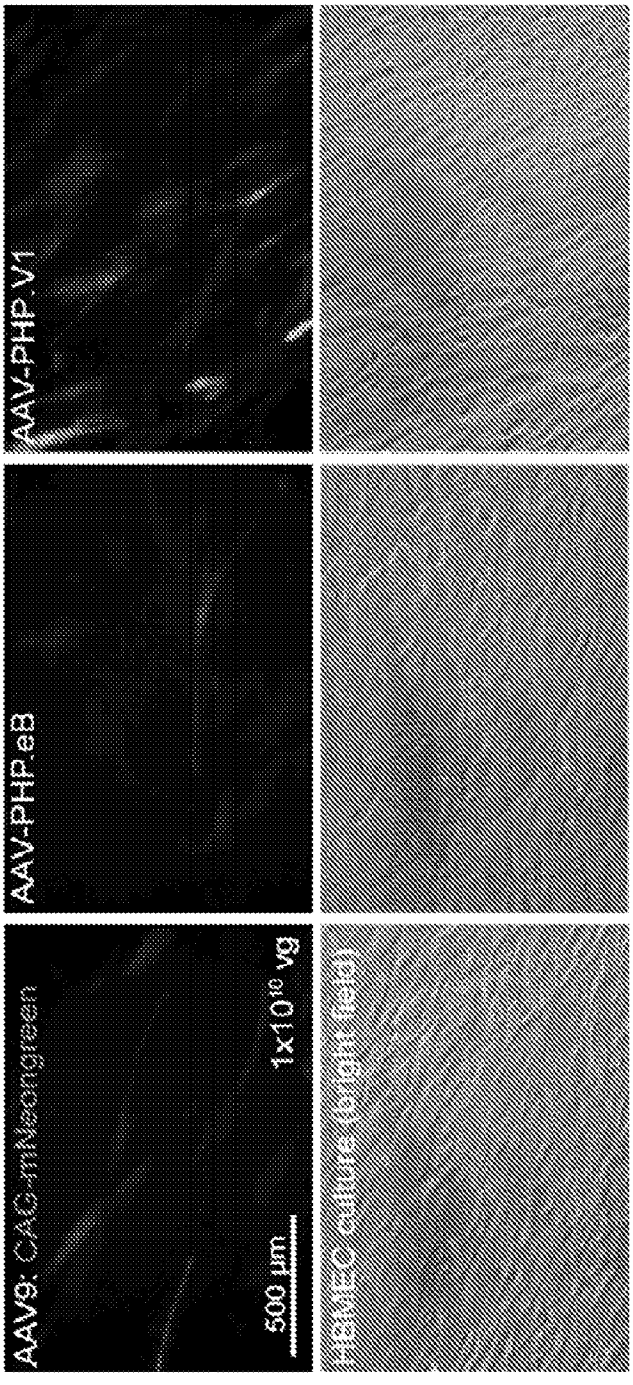

AAV-PHP.N
1x10^11 vg
CAG-mNG
Gad1
Vglut1
Cortex
100 µm
Brainstem
Ventral Midbrain
Cerebellum

FIG. 71


AAV9: CAG-mNeongreen
1x10^10 vg
500 µm
AAV-PHP.eB
AAV-PHP.V1
HEMEC cultures (bright field)

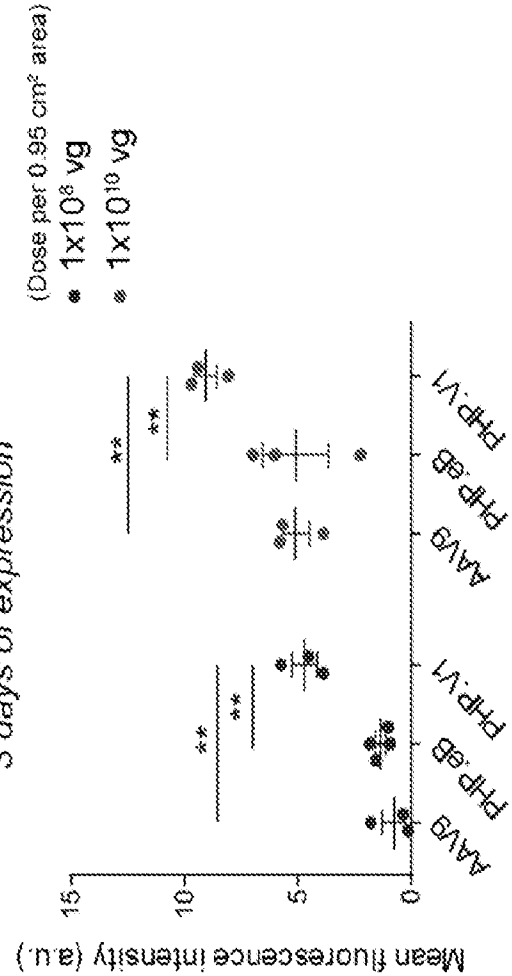

3 days of expression
(Dose per 0.95 cm² area)
1x10^8 vg
1x10^10 vg
Mean fluorescence intensity (a.u.)
0
5
10
15
**
**
**
**
AAV9
PHP.eB
PHP.V1
AAV9
PHP.eB
PHP.V1

FIG. 72

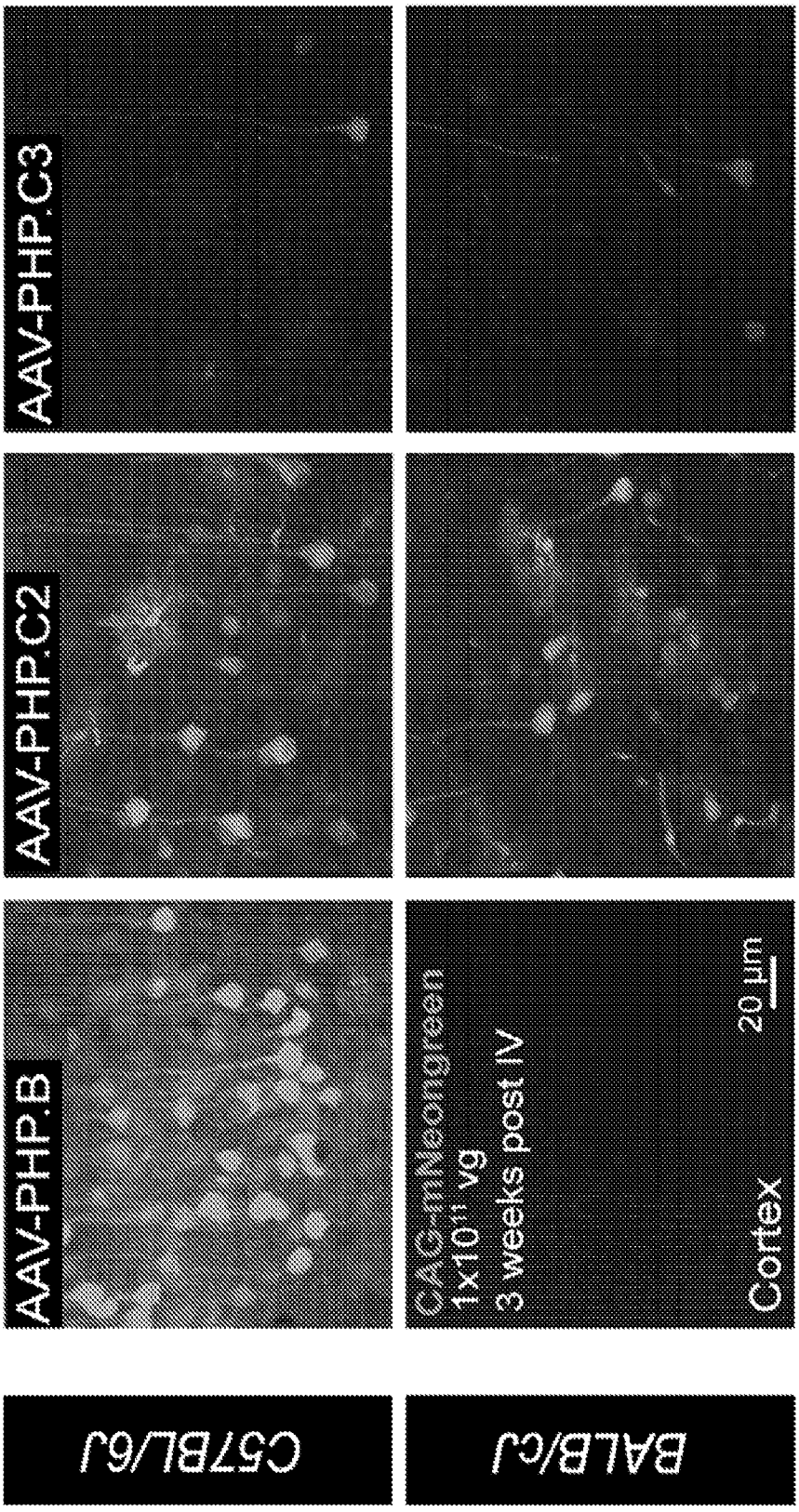

AAV-PHP.B
AAV-PHP.C2
AAV-PHP.C3
CAG-nNaongreen
1x10^11 vg
3 weeks post IV
Cortex
20 µm
C57BL/6J
BALB/cJ

FIG. 73

7-11 mer Peptide	Source (Selection study that first identified this peptide)	Mutation of variants identified from R1 selection in 7-mer-i-library from this study.	Predicted enrichment in brain (prior 7-mer-I synthetic pool selection)	SEQ ID NO:	Enrichment in brain as validated by M-CREATE (matched prediction
AQTLAVPFKAQ	7-mer-I AAV9 library (PHP.B) (Deverman et al, 2016)		High (validated in vivo) (Deverman et al, 2016)		High (Tek, Syn, SNAP, GFAP)
AQYTLSQGWAQ	7-mer-I AAV9 library (PHP.A) (Deverman et al, 2016)		High but poor virus production (validated in vivo) (Deverman et al, 2016)	15147	variant unrecovered in brain tissue
AQSVSKPFLAQ	7-mer-I AAV9 library (PHP.B2) (Deverman et al, 2016)		High (validated in vivo) (Deverman et al, 2016)	15148	High (Tek, Syn, SNAP, GFAP)
AQFTLTTPKAQ	7-mer-I AAV9 library (PHP.B3) (Deverman et al, 2016)		High (validated in vivo) (Deverman et al, 2016)	15149	High (Tek, Syn, SNAP, GFAP)
DGTLAVPFKAQ	3-mer-s PHP.B library (PHP.eB) (Chan et al, 2017)		High (validated in vivo) (Chan et al, 2017)		High (Tek, Syn, SNAP, GFAP)
AQQAVRTSLAQ	7-mer-I AAV9 library (PHP.S) (Chan et al, 2017)		Low (validated in vivo) (Chan et al, 2017)		Low (Tek, Syn)
AQTLAVPFSNP	3-mer-s PHP.B library (PHP.N)		High (validated in vivo in this study)		High (Tek, Syn, SNAP, GFAP)
AQTLQLPFKAQ	3-mer-s PHP.B library (PHP.B6)		(High (based on NGS/E. coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
AQTLQQPFKAQ	3-mer-s PHP.B library (PHP.B7)		(High (based on NGS/E. coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)

FIG. 74

DGTTLKPFLAQ	Current study	"AQ" on PHP.V2 substituted with "DG"	Unknown		variant unrecovered in brain tissue
DGTALKPFLAQ	Current study	"AQ" on PHP.V1 substituted with "DG"	Unknown		High (Syn, GFAP)
DGTTLKPFSNP	Current study	"AQ" on PHP.V2 substituted with "DG" and "LAQ" substituted with "SNP"	Unknown		Low (Syn)
AQTTLKPFSNP	Current study	"LAQ" on PHP.V2 substituted with "SNP"	Unknown		High (Tek, Syn, SNAP, GFAP)
ESTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15150	High (Tek, Syn, SNAP, GFAP)
GGTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15151	High (Tek, Syn, SNAP, GFAP)
AQTLATPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15152	High (Syn, SNAP, GFAP)
ATTLATPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15153	High (Tek, Syn, SNAP, GFAP)
DGTLATPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15154	High (Tek, Syn, SNAP, GFAP)
GGTLATPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15155	High (Tek, Syn, SNAP, GFAP)

FIG. 74 (Continued)

SGSLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15156	High (Tek, Syn, SNAP, GFAP)
AQTLAQPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15157	High (Tek, Syn, SNAP, GFAP)
AQTLSNPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15158	High (Tek, Syn, SNAP, GFAP)
AQTLSQPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15159	High (Tek, Syn, SNAP, GFAP)
EGTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15160	High (Tek, Syn, SNAP, GFAP)
DSTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15161	High (Tek, Syn, SNAP, GFAP)
NQTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15162	High (Tek, Syn, SNAP, GFAP)
SGNLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15163	High (Tek, Syn, SNAP, GFAP)
ATTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15164	High (Tek, Syn, SNAP, GFAP)
AQTLTMPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15165	High (Syn, SNAP, GFAP)
AQTLSTPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15166	High (Syn, SNAP, GFAP)

FIG. 74 (Continued)

QGTLAVPFKAQ	3-mer-s PHP.B library		(High (based on NGS/E. coli transformants from prior CREATE selection)	15167	High (Tek, Syn, SNAP, GFAP)

FIG. 74 (Continued)

SEQ ID	7-11 mer Peptide	Source (Selection study that first identified this peptide)	Mutation of variants identified from R1 selection in 7-mer-i library from this study.	Predicted enrichment in brain (prior 7-mer-i synthetic pool selection)	Enrichment in brain as validated by M-CREATE (against prediction)	Enrichment in brain as validated by M-CREATE (matched prediction)
	AQTLAVPFKAQ	7-mer-i AAV9 library (PHP.B) (Deverman et al, 2016)		High (validated in vivo) (Deverman et al, 2016)		High (Tek, Syn, SNAP, GFAP)
	AQYTLSQGWAQ	7-mer-i AAV9 library (PHP.A) (Deverman et al, 2016)		High but poor virus production (validated in vivo) (Deverman et al, 2016)		variant unrecovered in brain tissue
	AQSVSKPFLAQ	7-mer-i AAV9 library (PHP.B2) (Deverman et al, 2016)		High (validated in vivo) (Deverman et al, 2016)		High (Tek, Syn, SNAP, GFAP)
	AQFTLTTPKAQ	7-mer-i AAV9 library (PHP.B3) (Deverman et al, 2016)		High (validated in vivo) (Deverman et al, 2016)		High (Tek, Syn, SNAP, GFAP)
	DGTLAVPFKAQ	3-mer-s PHP.B library (PHP.eB) (Chan et al, 2017)		High (validated in vivo) (Chan et al, 2017)		High (Tek, Syn, SNAP, GFAP)
	AQQAVRTSLAQ	7-mer-i AAV9 library (PHP.S) (Chan et al, 2017)		Low (validated in vivo) (Chan et al, 2017)		Low (Tek, Syn)
	AQTLAVPFSNP	3-mer-s PHP.B library (PHP.N)		High (validated in vivo in this study)		High (Tek, Syn, SNAP, GFAP)

FIG. 75

	AQTLQLPFKAQ	3-mer-s PHP.B library (PHP.B6)		High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	AQTLQQPFKAQ	3-mer-s PHP.B library (PHP.B7)		High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	DGTTLKPFLAQ	Current study (*New design inspired from previously identified peptides*)	"AQ" on PHP.V2 substituted with "DG"	Unknown		variant unrecovered in brain tissue
	DGTALKPFLAQ	Current study (*New design inspired from previously identified peptides*)	"AQ" on PHP.V1 substituted with "DG"	Unknown		High (Syn, GFAP)
	DGTTLKPFSNP	Current study (*New design inspired from previously identified peptides*)	"AQ" on PHP.V2 substituted with "DG" and "LAQ" substituted with "SNP"	Unknown		Low (Syn)
	AQTTLKPFSNP	*design inspired from*	PHP.V2	Unknown		SNAP, GFAP)
	ESTLAVPFKAQ	3-mer-s PHP.B library		High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	GGTLAVPFKAQ	3-mer-s PHP.B library		High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)

FIG. 75 (Continued)

	AQTLATPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Syn, SNAP, GFAP)
	ATTLATPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	DGTLATPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	GGTLATPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	SGSLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	AQTLAQPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	AQTLSNPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	AQTLSQPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	EGTLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	DSTLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)

FIG. 75 (Continued)

	NQTLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	SGNLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	ATTLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
	AQTLTMPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Syn, SNAP, GFAP)
	AQTLSTPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Syn, SNAP, GFAP)
	QGTLAVPFKAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
15168	DGTLAVPFSNP	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek, Syn, SNAP, GFAP)
15169	DGTLAVPFRAQ	3-mer-s PHP.B library	High (based on NGS/E.coli transformants from prior CREATE selection)	variant unrecovered in brain tissue	
15170	AQNSREVNIAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)	High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low (Syn, SNAP)
15171	AQTREVNVIAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)	High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)

FIG. 75 (Continued)

SUBSTITUTE SHEET (RULE 26)

15172	AQIGMGHTLAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15173	AQTAETKFLAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15174	AQKATPPTEAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low (Syn)
15175	AQAETSRSVAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15176	AQTNRTIQTAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek), Low (Syn, SNAP, GFAP)
15177	AQYALTNDRAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	variant unrecovered in brain tissue	
15178	AQSVTNKMLAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn, Tek)
15179	AQSVQIVRGAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	

FIG. 75 (Continued)

15180	AQYPNTSQVAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low (Syn, Tek)
15181	AQYTLSQGTAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15182	AQWGLNRGTAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	variant unrecovered in brain tissue	
15183	AQTPKNVPDAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	variant unrecovered in brain tissue	
15184	AQYDPRGTDAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	variant unrecovered in brain tissue	
15185	AQVDTRPIQAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	
15186	AQTKSSYGVAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn, Tek)
15187	AQMNSTKNVAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		High (Tek), Low (Syn, SNAP, GFAP)

FIG. 75 (Continued)

SUBSTITUTE SHEET (RULE 26)

15188	AQSLHHGSSAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15189	AQSSPGAMHAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	variant unrecovered in brain tissue	
15190	AQSSYNDHPAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low (Syn)
15191	AQGAPRSSIAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Tek, Syn)
15192	AQQGSLYTSAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15193	AQHNAPGSLAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low (Syn)
15194	AQSLSPTINAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Syn)
15195	AQNNVTLLSAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low(Syn)

FIG. 75 (Continued)

15196	AQENRVKSAAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)	Low (GFAP)	Low (Tek, SNAP, Syn, SNAP)
15197	AQALNSVQPAQ	7-mer-i AAV9 library (prior selection study in GFAP-cre)		High in GFAP (based on NGS/E.coli transformants from prior CREATE selection)		Low (Tek, Syn)
	AAV9 capsid	parent serotype		low (validated in vivo)		low (Tek, Syn, SNAP, GFAP)

FIG. 75 (Continued)

7-11 mer Peptide	SNAP-Cre brain mean enrichment score (log10 scale)
AQTLQLPFKAQ	2.635622315
QGTLAVPFKAQ	2.560366902
AQTLSNPFKAQ	2.502118769
EGTLAVPFKAQ	2.482752751
DGTLAVPFKAQ	2.463683642
AQTLQQPFKAQ	2.419778506
AQTLATPFKAQ	2.413504952
SGSLAVPFKAQ	2.332201386
AQTLSTPFKAQ	2.299687253
DGTLATPFKAQ	2.291973997
GGTLAVPFKAQ	2.29043988
AQSVSKPFLAQ	2.284711601
AQTLAVPFKAQ	2.278601473
AQTLTMPFKAQ	2.221290966
ESTLAVPFKAQ	2.117205819
SGNLAVPFKAQ	2.105494998
AQTLSQPFKAQ	2.0935429
NQTLAVPFKAQ	2.016639766
AQTLAQPFKAQ	1.995025038
ATTLATPFKAQ	1.92915754
DSTLAVPFKAQ	1.905246666
AQTLAVPFSNP	1.738130019
GGTLATPFKAQ	1.695996385
ATTLAVPFKAQ	1.647772357
AQFTLTTPKAQ	1.10964487
DGTLAVPFSNP	0.989170037
AQTTLKPFSNP	0.848064508
AQMNSTKNVAQ	**0.133837545**
AQTNRTIQTAQ	**0.070636377**
AQNSREVNIAQ	**0.010923571**
AQENRVKSAAQ	**-0.270391873**
AAV9 parent	*-0.717369399*

FIG. 76

7-11 mer Peptide	GFAP-Cre brain mean enrichment score (log10 scale)
AQSVSKPFLAQ	2.432111357
AQTLQLPFKAQ	2.426669581
AQTLAVPFKAQ	2.424167734
SGSLAVPFKAQ	2.413393158
GGTLAVPFKAQ	2.397707224
SGNLAVPFKAQ	2.35782662
AQTLTMPFKAQ	2.35516667
AQTLQQPFKAQ	2.327525492
QGTLAVPFKAQ	2.306177613
DGTLAVPFKAQ	2.284953655
EGTLAVPFKAQ	2.254372157
AQTLSNPFKAQ	2.214426568
AQTLATPFKAQ	2.189159997
DGTLATPFKAQ	2.142993798
AQTLSQPFKAQ	2.114492139
ATTLATPFKAQ	2.109425827
AQTLSTPFKAQ	1.960573055
AQTLAQPFKAQ	1.922063594
ESTLAVPFKAQ	1.876988733
NQTLAVPFKAQ	1.793802999
ATTLAVPFKAQ	1.700418599
AQTLAVPFSNP	1.613667889
GGTLATPFKAQ	1.566031662
DSTLAVPFKAQ	1.378544566
AQTTLKPFSNP	1.101507461
AQFTLTTPKAQ	1.066406048
DGTLAVPFSNP	0.635613469
DGTALKPFLAQ	0.42534062
AQTNRTIQTAQ	**0.394388797**
AQMNSTKNVAQ	**0.358805861**
AQSSYNDHPAQ	**0.295857683**
AQSVQIVRGAQ	**0.183522142**
AQYPNTSQVAQ	**0.180040989**
AQVDTRPIQAQ	**0.178271526**
AQHNAPGSLAQ	**0.141306671**
AQKATPPTEAQ	**0.13263146**
AQENRVKSAAQ	**-0.025808641**
AQQAVRTSLAQ	**-0.219734424**
AQNSREVNIAQ	**-0.272580586**
AAV9 parent	*-0.463061913*
AQNNVTLLSAQ	**-0.666668537**

7-11 mer Peptide	SNAP-Cre brain mean enrichment score (log10 scale)
AQTLQLPFKAQ	2.635622315
QGTLAVPFKAQ	2.560366902
AQTLSNPFKAQ	2.502118769
EGTLAVPFKAQ	2.482752751
DGTLAVPFKAQ	2.463683642
AQTLQQPFKAQ	2.419778506
AQTLATPFKAQ	2.413504952
SGSLAVPFKAQ	2.332201386
AQTLSTPFKAQ	2.299687253
DGTLATPFKAQ	2.291973997
GGTLAVPFKAQ	2.29043988
AQSVSKPFLAQ	2.284711601
AQTLAVPFKAQ	2.278601473
AQTLTMPFKAQ	2.221290966
ESTLAVPFKAQ	2.117205819
SGNLAVPFKAQ	2.105494998
AQTLSQPFKAQ	2.0935429
NQTLAVPFKAQ	2.016639766
AQTLAQPFKAQ	1.995025038
ATTLATPFKAQ	1.92915754
DSTLAVPFKAQ	1.905246666
AQTLAVPFSNP	1.738130019
GGTLATPFKAQ	1.695996385
ATTLAVPFKAQ	1.647772357
AQFTLTTPKAQ	1.10964487
DGTLAVPFSNP	0.989170037
AQTTLKPFSNP	0.848064508
AQMNSTKNVAQ	**0.133837545**
AQTNRTIQTAQ	**0.070636377**
AQNSREVNIAQ	**0.010923571**
AQENRVKSAAQ	**-0.270391873**
AAV9 parent	*-0.717369399*

FIG. 76 (Continued)

7-11 mer Peptide	GFAP-Cre brain mean enrichment score (log10 scale)
AQSVSKPFLAQ	2.432111357
AQTLQLPFKAQ	2.426669581
AQTLAVPFKAQ	2.424167734
SGSLAVPFKAQ	2.413393158
GGTLAVPFKAQ	2.397707224
SGNLAVPFKAQ	2.35782662
AQTLTMPFKAQ	2.35516667
AQTLQQPFKAQ	2.327525492
QGTLAVPFKAQ	2.306177613
DGTLAVPFKAQ	2.284953655
EGTLAVPFKAQ	2.254372157
AQTLSNPFKAQ	2.214426568
AQTLATPFKAQ	2.189159997
DGTLATPFKAQ	2.142993798
AQTLSQPFKAQ	2.114492139
ATTLATPFKAQ	2.109425827
AQTLSTPFKAQ	1.960573055
AQTLAQPFKAQ	1.922063594
ESTLAVPFKAQ	1.876988733
NQTLAVPFKAQ	1.793802999
ATTLAVPFKAQ	1.700418599
AQTLAVPFSNP	1.613667889
GGTLATPFKAQ	1.566031662
DSTLAVPFKAQ	1.378544566
AQTTLKPFSNP	1.101507461
AQFTLTTPKAQ	1.066406048
DGTLAVPFSNP	0.635613469
DGTALKPFLAQ	0.42534062
AQTNRTIQTAQ	**0.394388797**
AQMNSTKNVAQ	**0.358805861**
AQSSYNDHPAQ	**0.295857683**
AQSVQIVRGAQ	**0.183522142**
AQYPNTSQVAQ	**0.180040989**
AQVDTRPIQAQ	**0.178271526**
AQHNAPGSLAQ	**0.141306671**
AQKATPPTEAQ	**0.13263146**
AQENRVKSAAQ	**-0.025808641**
AQQAVRTSLAQ	**-0.219734424**
AQNSREVNIAQ	**-0.272580586**
AAV9 parent	*-0.463061913*
AQNNVTLLSAQ	**-0.666668537**

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 20/27708

A. CLASSIFICATION OF SUBJECT MATTER

IPC - C07K 14/015, C07K 7/06, C12N 15/86, C12N 7/00 (2020.01)

CPC - A61K 48/0075, C07K 14/005, C12N 15/86, C12N 2750/14122

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See Search History document

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See Search History document

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
See Search History document

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2015/0079038 A1 (CALIFORNIA INSTITUTE OF TECHNOLOGY) 19 March 2015 (19.03.2015) para [0010]; para [0012]-[0013]; para [0024]; para [0027]; para [0033]; para [0045]; para [0191]; para [0201]; para [0218]-[0219]; Fig 24H; Fig. 24I	48-50
A	WO 2019/046069 A1 (THE REGENTS OF THE UNIVERSITY OF CALIFORNIA) 07 March 2019 (07.03.2019) whole document	48-50

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
"D" document cited by the applicant in the international application
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
23 June 2020	29 JUL 2020
Name and mailing address of the ISA/US Mail Stop PCT, Attn: ISA/US, Commissioner for Patents P.O. Box 1450, Alexandria, Virginia 22313-1450 Facsimile No. 571-273-8300	Authorized officer Lee Young Telephone No. PCT Helpdesk: 571-272-4300

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 20/27708

Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 1-47
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
Claims 1-47 are held unsearchable because these claims are to a SEQ ID NO, and the case has no searchable sequence listing.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying additional fees, this Authority did not invite payment of additional fees.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.

☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.

☐ No protest accompanied the payment of additional search fees.