(12) STANDARD PATENT (11) Application No. **AU 2018375695 B2**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Modified norovirus VP1 proteins and VLPS comprising modified norovirus VP1 proteins

(51) International Patent Classification(s)
C12N 15/40 (2006.01) ***C07K 16/10*** (2006.01)
A01H 5/00 (2018.01) ***C12N 5/10*** (2006.01)
A61K 39/12 (2006.01) ***C12N 7/01*** (2006.01)
A61P 31/14 (2006.01) ***C12N 15/82*** (2006.01)
A61P 37/04 (2006.01) ***C12P 21/02*** (2006.01)
C07K 14/08 (2006.01)

(21) Application No: **2018375695** (22) Date of Filing: **2018.11.30**

(87) WIPO No: **WO19/104439**

(30) Priority Data

(31) Number	(32) Date	(33) Country
62/712,744	**2018.07.31**	**US**
62/593,006	**2017.11.30**	**US**

(43) Publication Date: **2019.06.06**
(44) Accepted Journal Date: **2025.01.02**

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(56) Related Art
WO 2018/170603 A1
WO 2017/191264 A1
DATABASE Protein 4 February 2017 (2017-02-04), MA, C. ET AL.: "capsid protein, partial [Norovirus sp.]", XP055616759, retrieved from NCBI Database accession no. APY24054

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
06 June 2019 (06.06.2019)

WIPO | PCT

(10) International Publication Number
WO 2019/104439 A1

(51) International Patent Classification:
C12N 15/40 (2006.01) *C07K 16/10* (2006.01)
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A61K 39/12 (2006.01) *C12N 5/10* (2006.01)
A61P 31/14 (2006.01) *C12N 7/01* (2006.01)
A61P 37/04 (2006.01) *C12P 21/02* (2006.01)
C07K 14/08 (2006.01)

(21) International Application Number:
PCT/CA2018/051530

(22) International Filing Date:
30 November 2018 (30.11.2018)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
62/593,006 30 November 2017 (30.11.2017) US
62/712,744 31 July 2018 (31.07.2018) US

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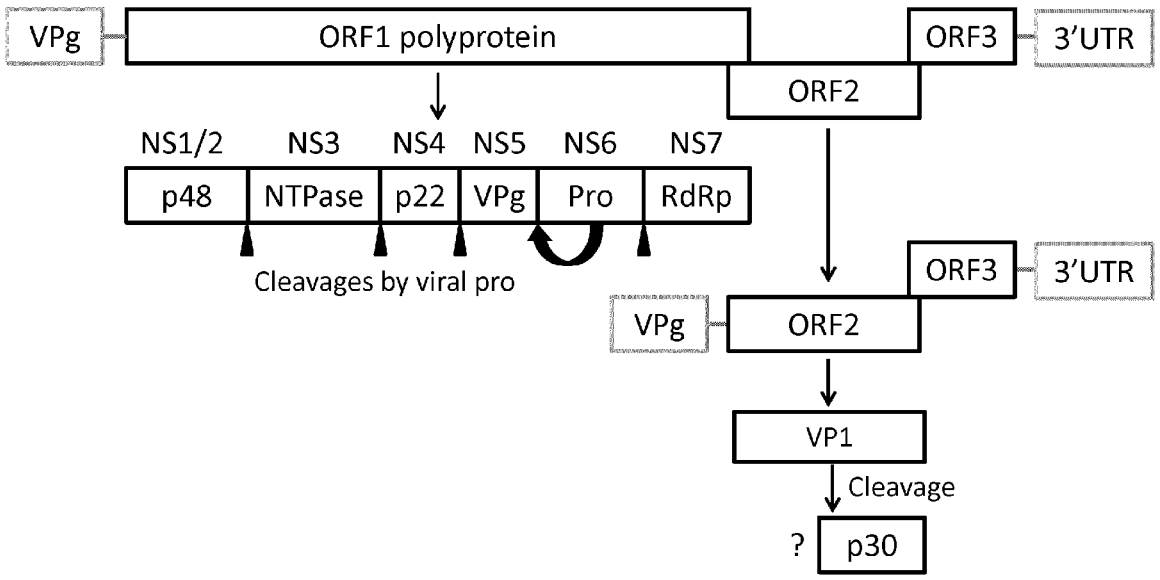
(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK,

(54) Title: MODIFIED NOROVIRUS VP1 PROTEINS AND VLPS COMPRISING MODIFIED NOROVIRUS VP1 PROTEINS

Figure 1A



(57) Abstract: Nucleic acids encoding modified norovirus VP1 proteins, and VLPs comprising one or more of the modified norovirus VP1 proteins are provided. Methods for modified norovirus VP1 protein, and norovirus VLP, production in plants, portions of the plant or a plant cell, are also described.

WO 2019/104439 A1

[Continued on next page]

EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

— *with international search report (Art. 21(3))*
— *with sequence listing part of description (Rule 5.2(a))*
— *in black and white; the international application as filed contained color or greyscale and is available for download from PATENTSCOPE*

Modified norovirus VP1 proteins and VLPs comprising modified norovirus VP1 proteins

FIELD OF INVENTION

[0001] The present invention relates to modified norovirus VP1 proteins, VLPs comprising modified norovirus VP1 proteins, and methods of producing the same.

BACKGROUND OF THE INVENTION

[0002] The global disease burden attributed to norovirus infection is high, being associated with an estimated 20% of all worldwide diarrheal cases and causing over 200,000 deaths annually. Noroviruses are the primary cause of foodborne disease outbreaks in North America and are the causative agent for the majority of healthcare-associated outbreaks amongst the elderly. Norovirus strains are also recognized as being the leading cause of pediatric gastrointestinal illness worldwide.

[0003] Noroviruses comprise one of a number of genera of the family *Caliciviridae*. The human norovirus genome is a single-stranded, positive-sense RNA molecule encoding three open reading frames (ORFs) and capped on its 5' end by a VPg protein. ORF1 encodes six non-structural viral proteins, including VPg, an RNA-dependent RNA polymerase, and a viral protease. ORF2 encodes the major structural capsid protein (VP1). ORF3 encodes a minor capsid protein (VP2).

[0004] VP1 is comprised of 2 domains: a shell (S) domain, and a protruding (P) domain. The S domain, for example of GI.1 strains, comprises the first 225 N-terminal amino acids and contains structural elements necessary for capsid assembly and the formation of the viral icosahedron. The P domain comprises the remainder of the VP1 protein and is further comprised of a P1 sub-domain and a P2 sub-domain. The P2 sub-domain is referred to as the hypervariable domain and is thought to play an important role in receptor binding and immune reactivity.

[0005] VP1 proteins form dimers via P domain-mediated protein interactions. Dimerization increases the stability of the virion capsid and results in formation of the protrusions extending from the base core of the norovirus particle formed by S

domains. When expressed, norovirus VP1 proteins can automatically assemble to form 2 virion structures: a 180-mer capsid structure with T=3 icosahedral symmetry having a 38-40 nm diameter; and a 60-mer capsid structure with T=1 icosahedral symmetry having a 23 nm diameter.

[0006] VP2, the minor structural protein, has a molecular weight (MW) of approximately 21-24 kDa. Studies suggest that VP2 is highly basic and located inside the capsid. The function of VP2 is not yet fully understood but it is generally believed to play a role in capsid stability by protecting the virions from disassembly and degradation (Bertolotti-Ciarlet A., Crawford S.E., Hutson A.M., Estes M.K. 2003, J. Virol. 77:11603-11615). VP2 may also have a function during RNA genome packaging. The amount of VP2 minor structural protein in virions is relatively low with 1.5 to 8 copies incorporated into the mature virion. Bertolotti-Ciarlet et. al. (2003) report that in insect and mammalian cells, VLPs composed of VP1/VP2 are more resistant to protease cleavage than those with only VP1, and that expression of VP2 in *cis*, results in an increase in VP1 protein production. In addition, the presence of the 3'UTR downstream of the ORF2 gene increases the steady-state levels of NV ORF2 mRNA. The greatest increase in VP1 expression was observed when ORF2 + ORF3 + 3'UTR, residing on the same construct and under regulation of one promoter, was expressed. Expression of VP2 in *trans* did not result in any increase in VP1 expression, indicating that the subgenomic organization of ORF2-ORF2-3'UTR was required for the observed increase in VP1 production.

[0007] Noroviruses are classified according to their phylogenetic clustering of the VP1 amino acid sequence. Seven genogroups have been classified to date (GI through GVII) with only genogroups GI, GII, and GIV known to infect humans. Of the 32 specific genotypes currently associated with human infections, GII.4 noroviruses have been responsible for the majority of recent norovirus outbreaks. New strains of GII.4 emerge every two to three years, evolving by a process driven by mutations in epitope determining regions of the hypervariable P2 domain of VP1. This process allows the norovirus to escape humoral immune responses acquired by previous exposure to earlier strains.

[0008] While faced with the difficulty of rapidly evolving and genetically diverse norovirus strains, the development of effective norovirus vaccines has been exacerbated by additional challenges. For instance, until recently, human norovirus could not be grown in cell culture and even now, robust cell culture systems for both VLPs and live attenuated noroviruses are lacking.

[0009] An additional challenge in vaccine development is that immunity to norovirus infection is strain and genotype specific with minimal cross-immunity conferred against other genogroups. Furthermore, immunity to a norovirus strain is not life-long and is estimated to persist from anywhere between six months and nine years.

[0010] Various approaches have been undertaken to develop a suitable vaccine against norovirus infection including the production of recombinant norovirus proteins in insect and plant expression systems.

[0011] Huo *et al.* (*Virus Research*, 2015, 204:1-5) demonstrated that an M27G mutant capsid protein, of norovirus VP1 VLPs produced in insect SF9 cells, resulted in the production of 38 nm and 21 nm VLPs, comprising proteins of 58 kDa and 55 kDa. The 55 kDa protein was a result of degradation or cleavage of the full-length P1 capsid protein as opposed to the translated product of an internal start codon. N-terminal deletion mutants comprising 26 or 38 deleted amino acid residues of the VP1 protein, resulted in the production of 21 nm VLPs. The 26 amino acid deletion mutants produced low numbers of 38 nm VLPs whereas 38 amino acid deletion mutants did not result in formation of 38 nm VLPs.

[0012] US 2013/0273105 teaches the production of norovirus formulations comprising antigenic peptides, proteins or VLPs derived from genogroup I (G1), genogroup II (GII), or consensus viral sequences. The norovirus antigens may include variants of the capsid proteins expressed in the VLPs.

[0013] US 2015/0023995 provides a vaccine formulation comprising VLPs produced in insect Sf9 cells, the VLPs comprising a composite amino acid sequence derived from at least two viral protein sequences. For Example, a composite GII.4 VP1 VLP, comprising a VP1 sequence from GII.4 Minerva 2006-a, and GII.4 Laurens 2006-b and GII.4 Houston 2002 norovirus strains, is described. Composite sequences derived

2018375695 29 Nov 2024

from GII.1, GII.2 Snow Mountain and GII.3, as well as GI composite sequences derived from Norwalk GI.1, Southampton GI.1, and Chiba GI.1 are also described.

[0014] Mason *et al.* (*Proc Natl Acad Sci U.S.A.*, 1996, 93(11):5335-40) teach the use of genetically engineered tobacco plants and potato tubers to express GI.1 norovirus VLPs from native VP1 protein. The plant produced norovirus VLPs are morphologically and physically similar to the 38 nm Norwalk VLPs produced in insect cells. Oral administration of purified tobacco-produced Norwalk VLPs from native capsid protein, or potato tubers expressing GI.1 capsid protein induced a humoral immune response in mice and humans (Tacket *et al.*, *J. Infect. Dis.*, 2000, 182(1):302-5).

[0015] Huang *et al.* (*Biotechnol. Bioeng.*, 2009, 103(4):706-14) describe a geminivirus-derived DNA replicon vector for production of GI.1 norovirus VLP in plants. Co-delivery of bean yellow dwarf virus-derived vector and Rep/RepA-supplying vector in *Nicotiana benthamiana* resulted in rapid and robust protein production.

[0015a] Any reference to or discussion of any document, act or item of knowledge in this specification is included solely for the purpose of providing a context for the present invention. It is not suggested or represented that any of these matters or any combination thereof formed at the priority date part of the common general knowledge, or was known to be relevant to an attempt to solve any problem with which this specification is concerned.

[0015b] For the avoidance of doubt, in this specification, the terms 'comprises', 'comprising', 'includes', 'including', or similar terms are intended to mean a non-exclusive inclusion, such that a method, system or apparatus that comprises a list of elements does not include those elements solely, but may well include other elements not listed.

SUMMARY OF THE INVENTION

[0016] The present invention relates to modified norovirus proteins, virus like particles (VLPs) comprising modified norovirus proteins, and methods of producing norovirus proteins, and virus like particles (VLPs) comprising modified norovirus proteins.

[0016a] In a first aspect, the invention relates to a modified norovirus VP1 protein comprising

one or more than one conserved amino acid substitution when compared to a corresponding wild type norovirus VP1 protein, wherein the one or more than one conserved amino acid substitution

are selected from a group consisting of amino acids in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), and wherein

the norovirus VP1 protein is not a GI.1 genotype.

[0016b] In a second aspect, the invention relates to a modified norovirus VP1 protein comprising one or more than one conserved amino acid substitution at a position in sequence alignment with amino acids 43, 57, 84 or 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), wherein:

the conserved amino acid substitution at the position in sequence alignment with amino acid 43 is to isoleucine, methionine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine;

the conserved amino acid substitution at the position in sequence alignment with amino acid 57 is to leucine, alanine, glycine, serine, asparagine, glutamine, or histidine;

the conserved amino acid substitution at the position in sequence alignment with amino acid 84 is to asparagine, cysteine, threonine, alanine, or lysine;

the conserved amino acid substitution at the position in sequence alignment with amino acid 94 is to leucine, isoleucine, methionine, valine, threonine, asparagine, lysine, or histidine; and

wherein the norovirus VP1 protein is not a GI.1 genotype.

[0016c] In a third aspect, the invention relates to a recombinant polynucleotide encoding the modified norovirus VP1 protein of the first or second aspect.

[0016d] In a fourth aspect, the invention relates to a virus-like particle (VLP) comprising the modified norovirus VP1 of the first or second aspect.

[0016e] In a fifth aspect, the invention relates to a method of producing a norovirus VP1 protein in a plant, portion of a plant or a plant cell, comprising:

introducing the recombinant polynucleotide of the third aspect; and

incubating the plant, portion of the plant or the plant cell under conditions that permit expression of the norovirus VP1 protein.

[0016f] In a sixth aspect, the invention relates to a norovirus VP1 protein produced by the method of the fifth aspect.

[0016g] In a seventh aspect, the invention relates to a method of producing a norovirus virus like particle (VLP) in a plant, portion of a plant or a plant cell, comprising:

introducing the recombinant polynucleotide of the third aspect; and

incubating the plant, portion of the plant or the plant cell under conditions that permit expression of the norovirus VLP.

[0016h] In an eighth aspect, the invention relates to a norovirus virus like particle (VLP) produced by the method of the seventh aspect.

[0016i] In a ninth aspect, the invention relates to a virus-like particle (VLP) comprising the norovirus VP1 protein and the norovirus VP2 protein produced by a method of the invention.

[0016j] In a tenth aspect, the invention relates to a method of producing an antibody or antibody fragment comprising, administering the norovirus VP1 protein of the first, second, or sixth aspect to a subject, or a host animal, thereby producing the antibody or the antibody fragment.

[0016k] In an eleventh aspect, the invention relates to a method of producing an antibody or an antibody fragment comprising, administering the VLP of the fourth, eighth, or ninth aspect to a subject, or a host animal, thereby producing the antibody or the antibody fragment.

[0016l] In a twelfth aspect, the invention relates to a plant, portion of the plant, or plant cell comprising the norovirus VP1 protein of the first, second, or sixth aspect.

[0016m] In a thirteenth aspect, the invention relates to a plant, portion of the plant, or plant cell comprising the VLP of the fourth, eighth, or ninth aspect .

[0016n] In a fourteenth aspect, the invention relates to a plant, portion of the plant, or plant cell comprising the recombinant polynucleotide of the third aspect.

[0016o] In a fifteenth aspect, the invention relates to a plant extract comprising the norovirus VP1 protein produced by the method of the fifth aspect.

[0016p] In a sixteenth aspect, the invention relates to a plant extract comprising the norovirus VLP produced by the method of the seventh aspect.

[0016q] In a seventeenth aspect, the invention relates to a composition comprising an effective dose of the norovirus VP1 protein of the first, second, or sixth aspect or an effective dose of the VLP of the fourth, eighth, or ninth aspect, and a pharmaceutically acceptable carrier, adjuvant, vehicle or excipient.

[0016r] In an eighteenth aspect, the invention relates to a vaccine comprising an effective dose of the norovirus VP1 protein of the first, second, or sixth aspect or an effective dose of the VLP of the fourth, eighth, or ninth aspect.

[0016s] In a nineteenth aspect, the invention relates to a method for inducing an immune response comprising administering to a subject in need thereof an effective dose of the composition of the seventeenth aspect or the vaccine of the eighteenth aspect.

[0016t] In a twentieth aspect, the invention relates to use of the composition of the seventeenth aspect or the vaccine of the eighteenth aspect in the manufacture of a medicament for inducing an immune response.

[0016u] In a twenty-first aspect, the invention relates to an antibody or antibody fragment prepared by administering the norovirus VP1 protein of the first, second, or sixth aspect to a subject, or host animal.

[0016v] In a twenty-second aspect, the invention relates to an antibody or antibody fragment prepared by administering the VLP of the fourth, eighth, or ninth aspect to a subject, or host animal.

[0016w] In a twenty-third aspect, the invention relates to a method for inducing immunity to a norovirus infection in a subject, the method comprising administering the VLP of the fourth, eighth, or ninth aspect to the subject.

[0016x] In a twenty-fourth aspect, the invention relates to a method of producing a modified norovirus VP1 protein, the method comprising:

(i) providing a norovirus VP1 protein, wherein the norovirus VP1 protein is not a GI.1 genotype;

(ii) making one or more than one conserved amino acid substitution in the amino acid sequence of the norovirus VP1 protein, selected from:

an amino acid substitution at a position in sequence alignment with amino acid 43 of reference sequence SEQ ID NO:1 to valine, isoleucine, leucine, methionine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine;

an amino acid substitution at a position in sequence alignment with amino acid 57 of reference sequence SEQ ID NO:1 to isoleucine, leucine, valine, alanine, glycine, serine, threonine, asparagine, glutamine, lysine, or histidine;

an amino acid substitution at a position in sequence alignment with amino acid 84 of reference sequence SEQ ID NO:1 to serine, asparagine, cysteine, threonine, alanine, lysine or histidine; and

an amino acid substitution at a position in sequence alignment with amino acid 94 of reference sequence SEQ ID NO:1 to leucine, isoleucine, methionine, valine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine.

[0017] In one aspect, the invention relates to producing modified norovirus proteins, VLPs comprising modified norovirus proteins, and to produce VLPs comprising modified norovirus proteins in plants.

[0018] As described herein, there is provided a recombinant polynucleotide comprising, a nucleotide sequence encoding a modified norovirus VP1 protein, wherein the modified norovirus VP1 protein comprises one or more than one substitution, modification or mutation at:

an amino acid selected from positions in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1,

a deletion of a peptide fragment in sequence alignment with amino acids 39-46 of norovirus VP1 genotype GI.1,

amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1, are mutated to the sequence SSTAVATA, or

a combination thereof, and

the nucleotide sequence is not derived from a genotype GI.1 norovirus VP1.

[0019] Also provided is the recombinant polynucleotide as described above, wherein the nucleotide sequence is derived from a norovirus VP1 selected from a group consisting of genotypes GI.2, GI.3. GI.5, GI.7, GII.2, GII.3, GII.4, GII.6, GII.12 and GII.17. For example, which is not to be considered limiting, the nucleotide sequence may be derived from the group comprising of G1.2/Leuven/2003/BEL GI.3/S29/2008/Lilla Edet/Sweden, GI.5/Siklos-HUN5407/2013/HUN, GI.7/USA/2014/GA5043, GII.2/CGMH47/2011/TW; GII.3/Jingzhou/2013402/CHN, GII.4/Sydney/NSW0514/2012/AU, GII.6/Ohio/490/2012/USA, GII.12/HS206/2010/USA, and GII.17_Kawa_2014_A0A077KVU6.

[0020] The recombinant polynucleotide described above may comprise specific substitutions, modifications or mutations, independently selected from the following:

a substitution, modification or mutation at the position in sequence alignment with amino acid 43 of VP1 genotype GI.1 to valine, isoleucine, leucine, methionine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine;

a substitution, modification or mutation at the position in sequence alignment with amino acid 57 of VP1 genotype GI.1 to isoleucine, leucine, valine, alanine, glycine, serine, threonine, asparagine, glutamine, lysine, or histidine;

a substitution, modification or mutation at the position in sequence alignment with amino acid 84 of VP1 genotype GI.1 to serine, asparagine, cysteine, threonine, alanine, lysine or histidine; and

a substitution, modification or mutation at the position in sequence alignment with amino acid 94 of VP1 genotype GI.1 to leucine, isoleucine, methionine, valine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine.

[0021] Any of the recombinant polynucleotides described above may also be optimized for human codon usage, increased GC content, or a combination thereof.

[0022] A modified norovirus VP1 protein encoded by any one of the recombinant polynucleotides described above is also described herein. Furthermore, a VLP comprising the modified norovirus VP1 protein encoded by any one of the recombinant polynucleotides described above, is also disclosed. The VLP comprising the norovirus VP1 protein encoded by any one of the recombinant polynucleotides described above, may further comprise a norovirus VP2 protein.

[0023] A method for producing a modified norovirus VP1 in a plant, portion of a plant or plant cell is also provided herein. The modified norovirus VP1 may be encoded by any one of the recombinant polynucleotides described above. The method comprises introducing one or more than one of the recombinant polynucleotide described above into the plant, the portion of the plant or the plant cell, and incubating the plant, the portion of the plant or the plant cell under conditions that permit expression of the one or more than one modified norovirus VP1 protein. The method provided herein may further comprise a step of harvesting the plant, portion of the plant, or the plant cell. Additionally, the method may comprise a step of extracting, purifying, or both extracting and purifying the one or more than one modofied norovirus VP1 protein from the plant, the portion of the plant or the plant cell. Furthermore, in the step of introducing, the method may further comprise introducing a second nucleic acid sequence encoding a norovirus VP2 protein into the plant, the portion of the plant, or the plant cell, and in the step of incubating, the conditions permit co-expression and co-production of both the one or more than one modified norovirus VP1 protein and the norovirus VP2 protein in the plant, portion of the plant or the plant cell.

[0024] Also described is a method for producing a norovirus virus like particle (VLP) in a plant, portion of a plant or plant cell, wherein the VLP comprises one or more than one of the modified norovirus VP1 proteins encoded by one or more of the recombinant polynucleotides described above. The method comprises introducing one or more than one of the recombinant polynucleotides described above into the plant, the portion of the plant or the plant cell, and incubating the plant, the portion of the plant or the plant cell under conditions that permit expression of the one or more than one modified norovirus VP1 protein, thereby producing the norovirus VLP. The method provided herein may further comprise a step of harvesting the plant, portion of the plant, or the plant cell. Additionally, the method may comprise a step of extracting, purifying, or both extracting and purifying the norovirus VLP from the plant, the portion of the plant or the plant cell. Furthermore, in the step of introducing, the method may further comprise introducing a second nucleic acid sequence encoding a norovirus VP2 protein into the plant, the portion of the plant, or the plant cell, and in the step of incubating, the conditions permit co-expression and co-production of both the modified norovirus VP1 protein and the norovirus VP2 protein in the plant, portion of the plant or the plant cell thereby producing the norovirus VLP. The norovirus VLP produced by the method described herein may have a diameter of about 15 nm to 50nm. Alternatively, the VLP may have a diameter of about 23 nm (for T=1 icosahedral symmetry) or about 38 nm (for T=3 icosahedral symmetry).

[0025] A method of producing an antibody or antibody fragment is provided herein, wherein the method comprises administering one or more than one of the modified norovirus VP1 proteins encoded by one or more than one of the recombinant polynucleotide described above, or the norovirus VLP comprising one or more than one of the modified norovirus VP1 protein, to a subject or a host animal, thereby producing the antibody or the antibody fragment.

[0026] Also provided herein is a plant, portion of the plant, or plant cell comprising the recombinant polynucleotide described above, the modified norovirus VP1 encoded by one or more than one of the recombinant polynucleotide, or the norovirus VLP comprising one or more than one the modified norovirus VP1 protein.

[0027] A composition for inducing an immune response is also described herein. The composition comprises, an effective dose of one or more than one of the modified norovirus VP1 protein encoded by one or more than one of the recombinant polynucleotide described above, or the norovirus VLP comprising one or more than one of the modified norovirus VP1 protein, and a pharmaceutically acceptable carrier, adjuvant, vehicle or excipient.

[0028] The present disclosure also provides a vaccine for inducing an immune response, wherein the vaccine comprises an effective dose of one or more than one of the modified norovirus VP1 proteins encoded by one or more than one of the recombinant polynucleotide described above, or the VLP comprising one or more than one of the modified norovirus VP1 protein.

[0029] Multiple strains of Norovirus have been characterized, and norovirus strains may evolve over time. Therefore, the present disclosure is also directed to VP1 and VP2 proteins from norovirus that exhibit from about 30-100% or any amount therebetween, amino acid sequence identity, to the VP1 protein, the VP2 protein, or both the VP1 and the VP2 proteins, of any of the norovirus strains listed in Figures 2A and 2B, provided that the VP1 protein can be expressed in a plant, and that the VP1 protein induces immunity to norovirus in a subject, when the VP1 protein is administered to the subject. For example, norovirus strains include strains having 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100%, or any amount therebetween, amino acid sequence identity (sequence similarity; percent identity; percent similarity) to the VP1 protein, the VP2 protein, or both the VP1 and the VP2 proteins, with any of the strains listed in Figures 2A and 2B, provided that the VP1 protein can be expressed in a plant, and the VP1 protein induces immunity to norovirus in a subject, when the VP1 protein is administered to the subject.

[0030] An antibody or antibody fragment is provided herein, wherein the antibody or antibody fragment is prepared by administering one or more than one of the modified norovirus VP1 encoded by one or more than one of the recombinant polynucleotide described above, or the norovirus VLP comprising one or more than one of the modified norovirus VP1, to a subject or host animal.

[0031] Also described herein is a method of inducing immunity to a norovirus infection in a subject, wherein the method comprises administering one or more than one of the modified norovirus VP1 protein encoded by one or more than one of the recombinant polynucleotide described above, or the norovirus VLP comprising one or more than one of the modified norovirus VP1 protein. The one or more than one of the modified norovirus VP1 protein, or the norovirus VLP may be administered to the subject orally, intranasally, intramuscularly, intraperitoneally, intravenously subcutaneously, rectally, or intravaginally.

[0032] This summary of the invention does not necessarily describe all features of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] These and other features of the invention will become more apparent from the following description in which reference is made to the appended drawings wherein:

[0034] **FIGURE 1A** shows a schematic representation of the linear structure of the norovirus genome and the polyprotein and proteins translated therefrom. **FIGURE 1B** shows a ribbon diagram representation of the 3-dimensional structure of the norovirus VP1 protein comprising a shell (S) domain, a P1 subdomain (P1), and a P2 subdomain (P2). **FIGURE 1C** shows a ribbon diagram representation of the 3-dimensional structure of a norovirus VP1 protein dimer comprising of two S domains (S), two P1 subdomains (P1), and two P2 subdomains (P2).

[0035] **FIGURE 2A** shows Uniprot and NCBI references for several norovirus VP1 (upper panel) and VP2 (lower panel) proteins. **FIGURE 2B** shows NCBI references for several norovirus VP1 (upper panel) and VP2 (lower panel) nucleic acid sequences. **FIGURE 2C** shows an alignment of several S domains of norovirus VP1 proteins. The norovirus GI.1 sequence (SEQ ID NO:1) is used as a reference sequence to which the other norovirus VP1 sequences (GI.2, SEQ ID NO:4; GI.3, SEQ ID NO:6; GI.5, SEQ ID NO:12; GI.7 SEQ ID NO:101; GII.1. SEQ ID NO:13; GII.2. SEQ ID NO:14; GII.3, SEQ ID NO:15; GII.4, SEQ ID NO:16; GII.5,SEQ ID NO:17; GII.6, SEQ ID NO:20; GII.7,SEQ ID NO:18; GII.12, SEQ ID NO:19; GII.13, SEQ ID NO:22; GII.14,SEQ ID NO:32; GII.17, SEQ ID NO:24; and GII.21, SEQ ID NO:26)

are aligned. The VP1 amino acid sequences for the "GII" family of VP1 proteins comprise a 3 amino acid deletion at amino acids 14-16, and a one amino acid deletion at position 26, this results in an alignment offset between the GII VP1 sequences and the GI VP1 sequences by 4 amino acids.

[0036] **FIGURE 3A** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *Nicotiana benthamiana* leaves, 9 days post infiltration (DPI) with left panel: wild type (wt) human codon-optimized (hCod) GI.1/United States/Norwalk/1968 VP1 (Construct #: 2724; SEQ ID NO:3 (nucleotide); SEQ ID NO: 1 (amino acid)) and hCod GI.5 VP1 (Construct #: 3980; SEQ ID NO:33 (nucleotide); SEQ ID NO:12 (amino acid); center panel: wild type GI.1 and wt hCod GII.12/United States/HS206/2010 VP1 (Construct #: 3995; SEQ ID NO:87 (nucleotide); SEQ ID NO:19 (amino acid)); and right panel: wild type GI.1 and wt hCod GII.4/Sydney/NSW0514/2012 VP1 (Construct #: 3760; SEQ ID NO:52 (nucleotide); SEQ ID NO:16 (amino acid)). Arrow: VP1 norovirus protein. First lane in each of the panels crude protein extracts prepared from mock infiltrated *N. benthamiana* leaves. **FIGURE 3B** upper panel shows norovirus protein expression and VLP assembly using Coomassie-stained SDS-PAGE analysis of fractions from an iodixanol density gradient separation of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod VP1 GI.1/United States/Norwalk/1968 VP1 (construct #2724), or wt hCod VP1 (construct #2724) and co-expressed with wt hCod VP2 (construct #2725). Lower panel shows electron micrographs of norovirus VLPs purified from 33% iodixanol gradient fractions of VP1 or co-expression of VP1 and VP2 proteins. An electron micrograph of native norovirus VLP is shown for comparison. **FIGURE 3C** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing left panel: wt hCod GI.5/Hungary/Siklos/HUN5407/2013 VP1 (Construct #: 3980; SEQ ID NO:33 (nucleotide); SEQ ID NO: 12 (amino acid)); right panel: GII.12/United States/HS206/2010 VP1 (Construct #: 3995; SEQ ID NO:87 (nucleotide); SEQ ID NO: 19 (amino acid). **FIGURE 3D** shows GI.1 VLP-specific total IgG titers measured in serum samples from animals after IM immunization with one dose (Day 21) and two doses (Day 42) of 1 μg or 10 μg of each formulation. Total IgG titers

were measured by ELISA using GI.1 VLP-coated plates (LOQ = 100). Total IgG titers per treatment group (n=8 animals/group) are represented by geometric mean titer (GMT) with a 95 % confidence interval. Same letter (A, B, C, D): no significant difference detected between treatment groups ($p > 0.05$).

[0037] **FIGURE 4A** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GI.2 VP1 (Construct #: 3300; SEQ ID NO:5 (nucleotide); SEQ ID NO:4 (amino acid)). **FIGURE 4B** shows electron micrographs of norovirus VLPs purified from 29-35% iodixanol gradient fractions of VP1.

[0038] **FIGURE 5A** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *N. benthamiana* leaves, 9 days post infiltration (DPI) with wt hCod GI.3/S29/2008/Lila Edet/Sweden VP1 (Construct #: 3979; SEQ ID NO:7 (nucleotide); SEQ ID NO:6 (amino acid)), mut hCod GI.3/S29/2008/Lila Edet/Sweden_S94L VP1 (Construct #: 4141; SEQ ID NO:9 (nucleotide); SEQ ID NO:8 (amino acid)), or mut hCod GI.3/S29/2008/Lila Edet/Sweden_Q84S+S94L VP1 (Construct #: 4142; SEQ ID NO:11 (nucleotide); SEQ ID NO:10 (amino acid)), with and without wt hCod GI.3/S29/2008/Lila Edet/Sweden VP2 (Construct #: 3303; SEQ ID NO:95 (nucleotide); SEQ ID NO:94 (amino acid)). First lane: crude protein extracts prepared from mock infiltrated *N. benthamiana* leaves. **FIGURE 5B** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GI.3/S29/2008/Lila Edet/Sweden VP1 (Construct #: 3979, left panel), mut hCod GI.3/S29/2008/Lila Edet/Sweden VP1_S94L (Construct #: 4141, middle panel), or mut hCod GI.3/S29/2008/Lila Edet/Sweden VP1_Q84S+S94L (Construct #:4142, right panel). **FIGURE 5C** shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GI.3/S29/2008/Lila Edet/Sweden VP1 (Construct #: 3979, left panel; fractions F2+F3, F6+F7 of Figure 5B), mut hCod GI.3/S29/2008/Lila Edet/Sweden VP1_S94L (Construct #: 4141, middle panel; fractions F2 - F6 of Figure 5B), or mut hCod GI.3/S29/2008/Lila Edet/Sweden VP1_Q84S+S94L (Construct #: 4142, right panel;

fractions F2 - F6 of Figure 5B). 15,000X magnification; scale bar = 500 nm. **FIGURE 5D** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *N. benthamiana* leaves, 9 days post infiltration (DPI) with mut hCod GI.3/S29/2008/Lila Edet/Sweden_M57I+S94L VP1 (Construct #:4180; SEQ ID NO:171 (nucleotide); SEQ ID NO:172 (amino acid)). **FIGURE 5E** shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing mut hCod GI.3/S29/2008/Lila Edet/Sweden_M57I+S94L VP1 (Construct #: 4180); 15,000X magnification; scale bar = 500 nm. **FIGURE 5F** shows the relative yield of VLPs comprising non-native VP1 GI.3 with substitutions at amino acid position 94, compared to the VLP yield of wild-type GI.3 (GI.3 S94; set as "Fold Change" of 1): C#: construct number.

[0039] **FIGURE 6A** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *N. benthamiana* leaves, 9 days post infiltration (DPI) with wt hCod GI.1/United States/Norwalk/1968 VP1 (Construct #:2724; SEQ ID NO:3 (nucleotide); SEQ ID NO:1 (amino acid)), wt hCod GI.5/Siklos/HUN5407/2013/HUN VP1 (Construct #: 3980; SEQ ID NO:33 (nucleotide); SEQ ID NO:12 (amino acid)), mut hCod GI.5/Siklos/HUN5407/2013/HUN_Q84S VP1 (Construct #: 4130; SEQ ID NO:35 (nucleotide); SEQ ID NO:34 (amino acid)), mut hCod GI.5/Siklos/HUN5407/2013/HUN_A94L VP1 (Construct #: 4131; SEQ ID NO:37 (nucleotide); SEQ ID NO:36 (amino acid)) or mut hCod GI.5/Siklos/HUN5407/2013/HUN_Q84S+A94L VP1 (Construct #: 4132; SEQ ID NO:39 (nucleotide); SEQ ID NO:38 (amino acid)). Arrow: VP1 norovirus protein; First lane = crude protein extracts prepared from mock infiltrated *N. benthamiana* leaves. **FIGURE 6B** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing, from left to right, wt hCod GI.5/Siklos/HUN5407/2013/HUN VP1 (Construct # 3980), mut hCod GI.5/Siklos/HUN5407/2013/HUN_Q84S VP1 (Construct #: 4130, left panel), mut hCod GI.5/Siklos/HUN5407/2013/HUN_A94L VP1 (Construct #: 4131, middle panel), or mut HCod GI.5/Siklos/HUN5407/2013/HUN_Q84S+A94L VP1 (Construct #: 4132, right panel).

FIGURE 6C shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing, from left to right, wt hCod GI.5/Siklos/HUN5407/2013/HUN VP1 (Construct # 3980), wt hCod GI.5/Siklos/HUN5407/2013/HUN_Q84S VP1 (Construct #:4130, left panel), mut hCod GI.5/Siklos/HUN5407/2013/HUN_A94L VP1 (Construct #: 4131, middle panel), or mut hCod GI.5/Siklos/HUN5407/2013/HUN_Q84S+A94L VP1 (Construct #: 4132, right panel). 15,000X magnification; scale bar = 200 nm. **FIGURE 6D** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing, from left to right, wt hCod GI.7/GA5043/USA/2014 VP1 (Construct # 4209; SEQ ID NO:101 (nucleotide); SEQ ID NO:204 (amino acid)), mut hCod GI.7/GA5043/USA/2014_R84S (Construct #4210; SEQ ID NO:176 (nucleotide); SEQ ID NO:177 (amino acid)), mut hCod GI.7/GA5043/USA/2014_M57I (Construct 4217; SEQ ID NO:178 (nucleotide); SEQ ID NO:179 (amino acid)), mut hCod GI.7/GA5043/USA/2014_M57I+R84S Construct # 4218; SEQ ID NO:180(nucleotide); SEQ ID NO:181 (amino acid)). * samples obtained for TEM analysis (see Figure 6E). **FIGURE 6E** shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing, Top left: wt hCod GI.7/GA5043/USA/2014 VP1 (Construct # 4209), Top right: mut hCod GI.7/GA5043/USA/2014_R84S (Construct #4210); Bottom left: mut hCod GI.7/GA5043/USA/2014_M57I (Construct 4217); Bottom Right mut hCod GI.7/GA5043/USA/2014_M57I+R84S Contract # 4218). 15,000X magnification; scale bar = 500 nm. **FIGURE 6F** shows the relative yield of VLPs comprising non-native VP1 GI.7 with substitutions at amino acid position 57, compared to the VLP yield of wild-type GI.7 (GI.7 M57; set as "Fold Change" of 1): C#: construct number.

[0040] **FIGURE 7A** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *N. benthamiana* leaves, 9 days post infiltration (DPI) with wt hCod GII.2/CGMH47/2011/TW VP1 (Construct #: 3982; SEQ ID NO:40 (nucleotide); SEQ ID NO:14 (amino acid)), mut hCod GII.2/CGMH47/2011/TW_E80S VP1 (Construct #: 4143; SEQ ID NO:86

(nucleotide); SEQ ID NO:85 (amino acid)), mut hCod GII.2/CGMH47/2011/TW _A90L VP1 (Construct #: 4144; SEQ ID NO:42 (nucleotide); SEQ ID NO:41 (amino acid)) or mut hCod GII.2/CGMH47/2011/TW _E80S+A90L VP1 (Construct #: 4145; SEQ ID NO:44 (nucleotide); SEQ ID NO:43 (amino acid)). Arrow: VP1 norovirus protein; First lane = crude protein extracts prepared from mock infiltrated N. benthamiana leaves. **FIGURE 7B** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing, from left to right, wt hCod GII.2/CGMH47/2011/TW VP1 (Construct # 3982), mut hCod GII.2/CGMH47/2011/TW_E80S VP1 (Construct #4143), mut hCod GII.2/CGMH47/2011/TW _A90L (Construct #: 4144), or mut hCod GII.2/CGMH47/2011/TW _E80S+A90L VP1 (Construct #: 4145). **FIGURE 7C** shows Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves (upper part of each panel), and transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 29-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves (lower part of each panel), expressing: Top Left Panel: wt hCod GII.2/CGMH47/2011/TW VP1 (Construct # 3982), Top Right panel mut hCod GII.2/CGMH47/2011/TW_E80S+A90L VP1 (Construct #4145); Bottom Left Panel: mut hCod GII.2/CGMH47/2011/TW_A39V+E80S+A90L VP1 (Construct # 4182; SEQ ID NO:183 (nucleotide); SEQ ID NO:182 (amino acid)); Bottom Right Panel: mut hCod GII.2/CGMH47/2011/TW_M53I+E80S+A90L VP1 (Construct # 4183 SEQ ID NO:185 (nucleotide); SEQ ID NO:184 (amino acid)); 15,000X magnification; scale bar = 500 nm.

[0041] **FIGURE 8A** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing, from left to right, wt hCod GII.3/Jingzhou/2013402/CHN VP1 (Construct #: 3983; SEQ ID NO:45 (nucleotide); SEQ ID NO: 15 (amino acid; first panel)), mut hCod GII.3/Jingzhou/2013402/CHN_E80S VP1 (Construct #: 4146, ; SEQ ID NO:47 (nucleotide); SEQ ID NO:46 (amino acid; second panel)), mut hCod GII.3/Jingzhou/2013402/CHN_A90L VP1 (Construct #: 4147, ; SEQ ID NO:49 (nucleotide); SEQ ID NO:48 (amino acid; third panel)), or mut hCod GII.3/Jingzhou/2013402/CHN_E80S+A90L VP1 (Construct #: 4148, SEQ ID NO:51

(nucleotide); SEQ ID NO:50 (amino acid; fourth panel)). **FIGURE 8B** shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.3/Jingzhou/2013402/CHN VP1 (Construct #3983, first panel), or mut hCod GII.3/Jingzhou/2013402/CHN_E80S VP1 (Construct #: 4146, second panel). 15,000X magnification; scale bar = 500 nm.

[0042] **FIGURE 9A** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *N. benthamiana* leaves, 9 days post infiltration (DPI) with wt GI.1/United States/Norwalk/1968 VP1 (Construct #: 2724; SEQ ID NO:3 (nucleotide); SEQ ID NO:1 (amino acid)), wt hCod GII.4/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760; SEQ ID NO:52 (nucleotide); SEQ ID NO:16 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU _A39V VP1 (Construct #: 4155; SEQ ID NO:54 (nucleotide); SEQ ID NO:53 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_V47P VP1 (Construct #: 4156; SEQ ID NO:56 (nucleotide); SEQ ID NO:55 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_R53I VP1 (Construct #: 4157; SEQ ID NO:58 (nucleotide); SEQ ID NO:57 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133; SEQ ID NO:60 (nucleotide); SEQ ID NO:59 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_S90L VP1 (Construct #: 4134; SEQ ID NO:62 (nucleotide); SEQ ID NO:61 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_Δ35-42 VP1 (Construct #: 4158; SEQ ID NO:64 (nucleotide); SEQ ID NO:63 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_SSTAVATA VP1 (Construct #: 4159; SEQ ID NO:66 (nucleotide); SEQ ID NO:65 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S+A39V(Construct #: 4165; SEQ ID NO:68 (nucleotide); SEQ ID NO:67 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S+V47P VP1 (Construct #: 4166; SEQ ID NO:70 (nucleotide); SEQ ID NO:69 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_ P80S+R53I VP1 (Construct #: 4167; SEQ ID NO:72 (nucleotide); SEQ ID NO:71 (amino acid)), mut hCod

GII.4/Sydney/NSW0514/2012/AU_P80S+S90L VP1 (Construct #: 4135; SEQ ID NO:74 (nucleotide); SEQ ID NO:73 (amino acid)), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S+Δ35-42 VP1 (Construct #: 4168; SEQ ID NO:76 (nucleotide); SEQ ID NO:75 (amino acid)), or mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S+SSTAVATA VP1 (Construct #: 4169; SEQ ID NO:78 (nucleotide); SEQ ID NO:77 (amino acid)). Arrow: VP1 norovirus protein; First lane = crude protein extracts prepared from mock infiltrated *N. benthamiana* leaves. **FIGURE 9B** shows a Coomassie-stained SDS-PAGE analysis (upper panel) and transmission electron micrographs (TEM; lower panel; 15,000X magnification; scale bar = 200 nm) of virus like particles (VLPs) purified from iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.4/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133), mut hCod GII.4/Sydney/NSW0514/2012/AU_S90L VP1 (Construct #: 4134), GII.4/Sydney/NSW0514/2012/AU_P80S+S90L VP1 (Construct #: 4135). **FIGURE 9C** shows a Coomassie-stained SDS-PAGE analysis (upper panel) and transmission electron micrographs (TEM; lower panel; 15,000X magnification; scale bar = 200 nm) of virus like particles (VLPs) purified from iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.4/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133), mut hCod GII.4/Sydney/NSW0514/2012/AU _A39V VP1 (Construct #: 4155), mut hCod GII.4/Sydney/NSW0514/2012/AU_ P80S+A39V (Construct #: 4165), mut hCod GII.4/Sydney/NSW0514/2012/AU_Δ35-42 VP1 (Construct #: 4158), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S+Δ35-42 VP1 (Construct #: 4168). **FIGURE 9D** shows a Coomassie-stained SDS-PAGE analysis (upper panel) and transmission electron micrographs (TEM; lower panel; 15,000X magnification; scale bar = 200 nm) of virus like particles (VLPs) purified from iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.4/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133), mut hCod GII.4/Sydney/NSW0514/2012/AU_R53I VP1 (Construct #: 4157), mut hCod GII.4/Sydney/NSW0514/2012/AU_R53I+P80S VP1 (Construct #: 4167). **FIGURE**

9E shows a Coomassie-stained SDS-PAGE analysis of virus like particles (VLPs) purified from iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.4/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133), mut hCod GII.4/Sydney/NSW0514/2012/AU_V47P VP1 (Construct #: 4156, mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S+V47P VP1 (Construct #: 4166). **FIGURE 9F** shows a Coomassie-stained SDS-PAGE analysis of virus like particles (VLPs) purified from iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.4/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760), mut hCod GII.4/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133), mut hCod GII.4/Sydney/NSW0514/2012/AU_SSTAVATA VP1 (Construct #: 4159), mut hCod GII.4/Sydney/NSW0514/2012/AU_SSTAVATA+P80S VP1 (Construct #: 4169). **FIGURE 9G** shows Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves (upper panel), and transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves (lower panel), expressing: Left Panel: mut hCod GII.4/Sydney/NSW0514/2012/AU_R53I+P80S VP1 (Construct # 4167); Right panel mut hCod GII.4/Sydney/NSW0514/2012/AU_A39V+R53I+ P80S VP1 (Construct #4186; SEQ ID NO:191 (nucleotide); SEQ ID NO:190 (amino acid)); 15,000X magnification; scale bar = 500 nm. **FIGURE 9H** shows the relative yield of VLPs comprising non-native VP1 GII.4/2012 with substitutions at amino acid position 80, compared to the VLP yield of wild-type (native) GII.4/2012 (GII.4/2012 P80 set as "Fold Change" of 1; C#: construct number. **FIGURE 9I** shows the relative yield of VLPs comprising VP1 GII.4/2012 (P80S) with an additional substitution at amino acid position 39, compared to the VLP yield of GII.4/2012 (P80S) comprising A39. GII.4/2012 (P80S) A39 set as "Fold Change" of 1; C#: construct number.

[0043] **FIGURE 10A** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.6/Ohio/490/2012/USA VP1 (Construct #: 3993; SEQ ID NO:21 (nucleotide); SEQ ID NO: 20 (amino acid)) and wt hCod

GII.6/HS245/2010/USA VP2 (Construct #: 3307; SEQ ID NO:97 (nucleotide); SEQ ID NO:96 (amino acid)), mut hCod GII.6/Ohio/490/2012/USA_E80S VP1 (Construct #: 4149; SEQ ID NO:80 (nucleotide); SEQ ID NO:79 (amino acid)) and wt hCod GII.6/HS245/2010/USA VP2 (Construct #: 3307), mut hCod GII.6/Ohio/490/2012/USA_S90L VP1 (Construct #: 4150; SEQ ID NO:82 (nucleotide); SEQ ID NO:81 (amino acid))) and wt hCod GII.6/HS245/2010/USA VP2 (Construct #3307), or mut hCod GII.6/Ohio/490/2012/USA_E80S+S90L VP1 (Construct #: 4151; SEQ ID NO:84 (nucleotide); SEQ ID NO:83 (amino acid)) and wt hCod GII.6/HS245/2010/USA VP2 (Construct #: 3307). **FIGURE 10B** shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt hCod GII.6/Ohio/490/2012/USA VP1 (Construct #: 3993) and wt hCod GII.6/HS245/2010/USA VP2 (Construct #: 3307), mut hCod GII.6/Ohio/490/2012/USA_S90L VP1 (Construct #: 4150) and wt hCod GII.6/HS245/2010/USA VP2 (Construct #: 3307). 15,000X magnification; scale bar = 200 nm.

[0044] **FIGURE 11A** shows a Coomassie-stained SDS-PAGE of crude protein extracts prepared from agroinfiltrated *N. benthamiana* leaves, 9 days post infiltration (DPI) with wt hCod GI.1/United States/Norwalk/1968 VP1 (Construct #: 2724; SEQ ID NO:3 (nucleotide); SEQ ID NO: 1 (amino acid)), wt hCod GII.12/HS206/2010/USA VP1 (Construct #: 3995; SEQ ID NO:87 (nucleotide); SEQ ID NO:19 (amino acid)), mut hCod GII.12/HS206/2010/USA_E80S VP1 (Construct #: 4136; SEQ ID NO:89 (nucleotide); SEQ ID NO:88 (amino acid)), mut hCod GII.12/HS206/2010/USA_A90L VP1 (Construct #: 4137; SEQ ID NO:91 (nucleotide); SEQ ID NO:90 (amino acid)), or mut hCod GII.12/HS206/2010/USA_E80S+A90L VP1 (Construct #: 4138; SEQ ID NO:93 (nucleotide); SEQ ID NO:92 (amino acid)). First lane = crude protein extracts prepared from mock infiltrated *N. benthamiana* leaves. **FIGURE 11B** shows a Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt GII.12/HS206/2010/USA VP1 (Construct #: 3995), GII.12/HS206/2010/USA_E80S VP1 (Construct #: 4136), GII.12/HS206/2010/USA_A90L VP1 (Construct #: 4137),

or GII.12/HS206/2010/USA_E80S+A90L VP1 (Construct #: 4138). **FIGURE 11C** shows transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves expressing wt GII.12/HS206/2010/USA VP1 (Construct #: 3995, first panel GII.12/HS206/2010/USA_P80S VP1 (Construct #: 4136, second panel), GII.12/HS206/2010/USA_S90L VP1 (Construct #: 4137, third panel), or GII.12/HS206/2010/USA_P80S+S90L VP1 (Construct #: 4138, fourth panel).15,000X magnification; scale bar = 500 nm. **FIGURE 11D** shows Coomassie-stained SDS-PAGE analysis of iodixanol density gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves (upper part of each panel), and transmission electron micrographs (TEM) of virus like particles (VLPs) purified from 31-35% iodixanol gradient fractions of crude protein extracts prepared from *N. benthamiana* leaves (lower part of each panel), expressing: Top Left Panel: wt hCod GII.17 Kawa 2014 A0A077KVU6VP1 (Construct # 3998; SEQ ID NO:25 (nucleotide); SEQ ID NO:24 (amino acid)), Top Right panel mut hCod GII.17 Kawa 2014 A0A077KVU6_A90L VP1 (Construct #4232; SEQ ID NO:197 (nucleotide); SEQ ID NO:196 (amino acid)); Bottom Left Panel: mut hCod GII.17 Kawa 2014 A0A077KVU6_A39V VP1 (Construct # 4234; SEQ ID NO:193 (nucleotide); SEQ ID NO:192 (amino acid)); Bottom Right Panel: mut hCod GII.17 Kawa 2014 A0A077KVU6_R53I VP1 (Construct # 4235; SEQ ID NO:195 (nucleotide); SEQ ID NO:194 (amino acid)); 15,000X magnification; scale bar = 500 nm.

[0045] **FIGURE 12A** shows the amino acid sequence of VP1 GI.1 United States Norwalk 1968 (SEQ ID NO:1); **FIGURE 12B** shows the nucleic acid sequence of wild type VP1 GI.1 United States Norwalk 1968 (SEQ ID NO:2); **FIGURE 12C** shows the nucleic acid sequence of hCod VP1 GI.1 United States Norwalk 1968 (SEQ ID NO:3).

[0046] **FIGURE 13A** shows the amino acid sequence of VP1 G1.2 Leuven 2003 D2DEL3 (SEQ ID NO:4); **FIGURE 13B** shows the nucleic acid sequence of hCod VP1 G1.2 Leuven 2003 D2DEL3 (SEQ ID NO:5).

[0047] **FIGURE 14A** shows the amino acid sequence of VP1 GI.3 LillaEdet 2008 H2DG70 (SEQ ID NO:6); **FIGURE 14B** shows the nucleic acid sequence of hCod GI.3 LillaEdet 2008 H2DG70 (SEQ ID NO:7).

[0048] **FIGURE 15A** shows the amino acid sequence of VP1 GI.5 Siklos HUN5407 2013 HUN AHW99832 (SEQ ID NO:12). **FIGURE 15B** shows the nucleic acid sequence of hCod VP1 GI.5 Siklos HUN5407 2013 HUN AHW99832 (SEQ ID NO:33).

[0049] **FIGURE 16A** shows the amino acid sequence of GI.7/GA5043/USA/2014 VP1 (SEQ ID NO:101). **FIGURE 16B** shows the nucleic acid sequence of GI.7/GA5043/USA/2014 VP1 (SEQ ID NO:175). **FIGURE 16C** shows the amino acid sequence of VP1 GII.1 Ascension208 2010 USA AFA55174 (SEQ ID NO:13).

[0050] **FIGURE 17A** shows the amino acid sequence of VP1 GII.2 CGMH47 2011 TW AGT39206 (SEQ ID NO:14). **FIGURE 17B** shows the nucleic acid sequence of hCod VP1 GII.2 CGMH47 2011 TW AGT39206 (SEQ ID NO:40).

[0051] **FIGURE 18A** shows the amino acid sequence of VP1 GII.3 Jingzhou 2013402 CHN AGX01095 (SEQ ID NO:15). **Figure 18B** shows the nucleic acid sequence of hCod VP1 GII.3 Jingzhou 2013402 CHN AGX01095 (SEQ ID NO:45).

[0052] **FIGURE 19A** shows the amino acid sequence of VP1 GII.4 Sydney NSW0514 2012 (SEQ ID NO:16). **FIGURE 19B** shows the nucleic acid sequence of hCod VP1 GII.4 Sydney NSW0514 2012 (SEQ ID NO: 52). **FIGURE 19C** shows the amino acid sequence of VP1 US96: GII.4 Dresden174 1997 DE AY741811 (SEQ ID NO:27). **FIGURE 19D** shows the amino acid sequence of VP1 FH02: GII.4 FarmingtonHills 2002 US AY502023 (SEQ ID NO:28). **FIGURE 19E** shows the amino acid sequence of VP1 Hnt04:GII.4 Hunter-NSW504D 2004 AU DQ078814 (SEQ ID NO:29). **FIGURE 19F** shows the amino acid sequence of VP1 2006b: GII.4 Shellharbour-NSW696T 2006 AU EF684915 (SEQ ID NO:30). **FIGURE 19G** shows the amino acid sequence of VP1NO09: GII.4 Orange-NSW001P 2008 AU GQ845367 (SEQ ID NO:31).

[0053] **FIGURE 20** shows the amino acid sequence of VP1 GII.5 Alberta 2013 CA ALT54485 (SEQ ID NO:17).

[0054] **FIGURE 21A** shows the amino acid sequence of VP1 GII.6 Ohio 2012 M9T020 (SEQ ID NO:20). **FIGURE 21B** shows the nucleic acid sequence of hCod-optimized VP1 GII.6 Ohio 2012 M9T020 (SEQ ID NO:21);

[0055] **FIGURE 22** shows the amino acid sequence of VP1 GII.7 Musa 2010 AII73774 (SEQ ID NO:18).

[0056] **FIGURE 23A** shows the amino acid sequence of VP1 GII.12_HS206_2010_USA_AEI29586 (SEQ ID NO:19); **FIGURE 23B** shows the nucleic acid sequence of hCod VP1 GII.12_HS206_2010_USA AEI29586 (SEQ ID NO:87).

[0057] **FIGURE 24A** shows the amino acid sequence of VP1 GII.13 VA173 2010 H9AWU4 (SEQ ID NO:22). **FIGURE 24B** shows the nucleic acid sequence of human codon-optimized VP1 GII.13 VA173 2010 H9AWU4 (SEQ ID NO:23).

[0058] **FIGURE 25** shows the amino acid sequence of VP1 GII.14 Saga 2008 JPN ADE28701 (SEQ ID NO:32).

[0059] **FIGURE 26A** shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6 (SEQ ID NO:24). **FIGURE 26B** shows the nucleic acid sequence of human codon-optimized VP1 GII.17 Kawa 2014 A0A077KVU6 (SEQ ID NO:25).

[0060] **FIGURE 27** shows the amino acid sequence of VP1 GII.21 Sali 2011 USA AFC89665 (SEQ ID NO:26).

[0061] **FIGURE 28A** shows the amino acid sequence of modified VP1 GI.3_Lil08_Q84S (SEQ ID NO:98). **FIGURE 28B** shows the nucleic acid sequence of VP1 GI.3_Lil08_Q84S (SEQ ID NO:167). **FIGURE 28C** shows the amino acid sequence of VP1 GI.3 Lil08_S94L (SEQ ID NO:8). **FIGURE 28D** shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_S94L (SEQ ID NO:9). **FIGURE 28E** shows the amino acid sequence of VP1 GI.3 Lil08_Q84S+S94L (SEQ ID NO:10). **FIGURE 28F** shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_Q84S+S94L (SEQ ID

NO:11). **FIGURE 28G** shows the amino acid sequence of VP1 GI.3 Lil08_A43V+S94L (SEQ ID NO:170). **FIGURE 28H** shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_A43V+S94L (SEQ ID NO:169). **FIGURE 28I** shows the amino acid sequence of VP1 GI.3 Lil08_M57I+S94L (SEQ ID NO:172). **FIGURE 28J** shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_M57I+S94L (SEQ ID NO:171). **FIGURE 28K** shows the amino acid sequence of VP1 GI.3 Lil08_A43V+M57I+S94L (SEQ ID NO:174). **FIGURE 28L** shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_A43V+M57I+S94L (SEQ ID NO:173). **FIGURE 28M** shows the amino acid sequence of VP1_GI.3_Lil08_S94X (SEQ ID NO:292); wherein **X** is selected from V, I M, T, E, D, N, Q, K, or H. **FIGURE 28N** shows the human codon optimized sequence of VP1_GI.3_Lil08_S94X (SEQ ID NO:293); wherein **X** is selected from a codon encoding V (e.g. **XXX**=GTG), I (e.g. **XXX**=ATC), M (e.g. **XXX**=ATG), T (e.g. **XXX**=ACC), E (e.g. **XXX**=GAG), D (e.g. **XXX**=GAC), N (e.g. **XXX**=AAC), Q (e.g. **XXX**=CAG), K (e.g. **XXX**=AAG), or H (e.g. **XXX**=CAC).

[0062] **FIGURE 29A** shows the amino acid sequence of modified VP1 GI.5 Siklos Q84S (SEQ ID NO:34). **FIGURE 29B** shows the nucleic acid sequence of modified VP1 GI.5 Siklos Q84S (SEQ ID NO:35). **FIGURE 29C** shows the amino acid sequence of VP1 GI.5 Siklos A94L (SEQ ID NO:36). **FIGURE 29D** shows the nucleic acid sequence of hCod VP1 GI.5 Siklos A94L (SEQ ID NO:37). **FIGURE 29E** shows the amino acid sequence of VP1 GI.5 Siklos Q84S+A94L (SEQ ID NO:38). **FIGURE 29F** shows the nucleic acid sequence of hCod VP1 GI.5 Siklos Q84S+A94L (SEQ ID NO:39). **FIGURE 29G** shows the amino acid sequence of modified VP1 GI.7/GA5043/USA/2014_R84S (SEQ ID NO:177). **FIGURE 29H** shows the nucleic acid sequence of modified VP1 hCod GI.7/GA5043/USA/2014_R84S (SEQ ID NO:176). **FIGURE 29I** shows the amino acid sequence of modified VP1 GI.7/GA5043/USA/2014_M57I (SEQ ID NO:179). **FIGURE 29J** shows the nucleic acid sequence of modified VP1 hCod GI.7/GA5043/USA/2014_M57I (SEQ ID NO:178). **FIGURE 29K** shows the amino acid sequence of modified VP1GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:181). **FIGURE 29L** shows the nucleic acid sequence of modified VP1 hCod GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:180). **FIGURE 29M** shows the

amino acid sequence of VP1_GI.7/GA5043/USA/2014_M57X (SEQ ID NO:290); wherein **X** is selected from L, G, S, T, N, Q, K or H. **FIGURE 29N** shows human codon optimized VP1_GI.7/GA5043/USA/2014_M57X (SEQ ID NO:291); wherein **X** is selected from a codon encoding L (e.g. **XXX**=CTG), G (e.g. **XXX**=GGC), S (e.g. **XXX**=AGC), T (e.g. **XXX**=ACC), N (e.g. **XXX**=AAC), Q (e.g. **XXX**=CAG), K (e.g. **XXX**=AAG), or H (e.g. **XXX**=CAC).

[0063] **FIGURE 30A** shows the amino acid sequence of VP1 GII.2 CGMH47 E80S (SEQ ID NO:85). **FIGURE 30B** shows the nucleic acid sequence of hCod VP1 GII.2 CGMH47 E80S (SEQ ID NO:86) . **FIGURE 30C** shows the amino acid sequence of VP1 GII.2 CGMH47 A90L (SEQ ID NO:41); **FIGURE 30D** shows the nucleic acid sequence of hCod VP1 GII.2 CGMH47 A90L (SEQ ID NO:42). **FIGURE 30E** shows the amino acid sequence of VP1_GII.2_CGMH47_E80S+A90L (SEQ ID NO:43). **FIGURE 30F** shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_E80S+A90L (SEQ ID NO:44). **FIGURE 30G** shows the amino acid sequence of VP1_GII.2_CGMH47_A39V+E80S+A90L (SEQ ID NO:182). **FIGURE 30H** shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_ A39V+E80S+A90L (SEQ ID NO:183). **FIGURE 30I** shows the amino acid sequence of VP1_GII.2_CGMH47_R53I+E80S+A90L (SEQ ID NO:184). **FIGURE 30J** shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_ R53I+E80S+A90L (SEQ ID NO:185). **FIGURE 30K** shows the amino acid sequence of VP1_GII.2_CGMH47_ A39V+R53I+E80S+A90L (SEQ ID NO:186). **FIGURE 30L** shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_ A39V+R53I+E80S+A90L (SEQ ID NO:187).

[0064] **FIGURE 31A** shows the amino acid sequence of VP1 GII.3_Jing_E80S (SEQ ID NO:46). **FIGURE 31B** shows the nucleic acid sequence of hCod VP1 GII.3_Jing_E80S (SEQ ID NO:47). **FIGURE 31C** the amino acid sequence of VP1 GII.3_Jing_A90L (SEQ ID NO:48). **FIGURE 31D** shows the nucleic acid sequence of hCod VP1 GII.3_Jing_A90L (SEQ ID NO:49). **FIGURE 31E** the amino acid sequence of VP1 GII.3_Jing_E80S+A90L (SEQ ID NO:50). **FIGURE 31F** shows the nucleic acid sequence of hCod VP1 GII.3_Jing_E80S+A90L (SEQ ID NO:51).

[0065] **FIGURE 32A** shows the amino acid sequence of VP1 GII.4 Syd12 A39V (SEQ ID NO:53). **FIGURE 32B** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_A39V (SEQ ID NO:54). **FIGURE 32C** shows the amino acid sequence of VP1 GII.4_Syd12_V47P (SEQ ID NO:55). **FIGURE 32D** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_V47P (SEQ ID NO:56). **FIGURE 32E** shows the amino acid sequence of VP1 GII.4_Syd12_R53I (SEQ ID NO:57). **FIGURE 32F** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_R53I (SEQ ID NO:58). **FIGURE 32G** shows the amino acid sequence of VP1; GII.4_Syd12_P80S (SEQ ID NO:59). **FIGURE 32H** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S (SEQ IDNO:60). **FIGURE 32I** shows the amino acid sequence of VP1 GII.4_Syd12_S90L (SEQ ID NO:61). **FIGURE 32J** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_S90L (SEQ IDNO:62). **FIGURE 32K** shows the amino acid sequence of VP1GII.4_Syd12_Δ35-42 (SEQ ID NO:63). **FIGURE 32L** shows the nucleic acid sequence of hCod VP1GII.4_Syd12_Δ35-42 (SEQ IDNO:64). **FIGURE 32M** shows the amino acid sequence of VP1 GII.4_Syd12_SSTAVATA (SEQ ID NO:65). **FIGURE 32N** shows the nucleic acid sequence of hCodVP1 GII.4_Syd12_SSTAVATA (SEQ ID NO:66). **FIGURE 32O** shows the amino acid sequence of VP1GII.4_Syd12_P80S+A39V (SEQ ID NO:67). **FIGURE 32P** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+A39V (SEQ ID NO:68). **FIGURE 32Q** shows the amino acid sequence of VP1 GII.4_Syd12_P80S+V47P (SEQ ID NO:69). **FIGURE 32R** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+V47P (SEQ ID NO:70). **FIGURE 32S** shows the amino acid sequence of VP1GII.4_Syd12_P80S+R53I (SEQ ID NO:71). **FIGURE 32T** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+R53I (SEQ ID NO:72). **FIGURE 32U** shows the amino acid sequence of VP1 GII.4_Syd12_P80S+S90L (SEQ ID NO:73). **FIGURE 32V** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+S90L (SEQ ID NO:74). **FIGURE 32W** shows the amino acid sequence of VP1 GII.4_Syd12_P80S+Δ35-42 (SEQ ID NO:75). **FIGURE 32X** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+Δ35-42 (SEQ ID NO:76). **FIGURE 32Y** shows the amino acid sequence of VP1 GII.4_Syd12_P80S+SSTAVATA (SEQ ID NO:77). **FIGURE 32Z** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+SSTAVATA

(SEQ ID NO:78). **FIGURE 32AA** shows the amino acid sequence of VP1 GII.4 Syd12 A39V+R53I (SEQ ID NO:188). **FIGURE 32BB** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_A39V+R53I (SEQ ID NO:189). **FIGURE 32CC** shows the amino acid sequence of VP1 GII.4 Syd12 A39V+R53I+P80S (SEQ ID NO:190). **FIGURE 32DD** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_A39V+R53I+P80S (SEQ ID NO:191). **FIGURE 32EE** shows the nucleic acid sequence of human codon optimized VP1 GII.4_Syd12_P80X (SEQ ID NO:287); wherein X is selected from a codon encoding A (e.g. **XXX**=GCC), N (e.g. **XXX**=AAC), K (e.g. **XXX**=AAG), or H (e.g. **XXX**=CAC). **FIGURE 32FF** shows the amino acid sequence of VP1_GII.4_Syd12_P80X (SEQ ID NO:286); wherein **X** is selected from A, N, K, or H. **FIGURE 32GG** shows the nucleic acid sequence of human codon optimize sequence of VP1 GII.4_Syd12_P80S+A39X (SEQ ID NO:289); wherein X is selected from a codon encoding I (e.g. **XXX**=ATC), M (e.g. **XXX**=ATG), G (e.g. **XXX**=GGC), S (e.g. **XXX**=AGC), E (e.g. **XXX**=GAG), D (e.g. **XXX**=GAC), N (e.g. **XXX**=AAC), Q (e.g. **XXX**=CAG), K (e.g. **XXX**=AAG), or H (e.g. **XXX**=CAC). **FIGURE 32HH** show the amino acid sequence of VP1_GII.4_Syd12_P80S+A39X (SEQ ID NO:288); wherein **X** is selected from I, M, G, S, E, D, N, Q, K, or H.

[0066] **FIGURE 33A** shows the amino acid sequence of VP1 GII.6_Ohio_E80S (SEQ ID NO:79). **FIGURE 33**B shows the nucleic acid sequence of hCod VP1 GII.6_Ohio_E80S (SEQ ID NO:80). **FIGURE 33C** shows the amino acid sequence of VP1 GII.6_Ohio_S90L (SEQ ID NO:81). **FIGURE 33D** shows the nucleic acid sequence of hCod VP1 GII.6_Ohio_S90L (SEQ ID NO:82). **FIGURE 33E** shows the amino acid sequence of VP1 GII.6_Ohio_E80S+S90L (SEQ ID NO:83). **FIGURE 33F** shows the nucleic acid sequence of hCod VP1 GII.6_Ohio_E80S+S90L (SEQ ID NO:84).

FIGURE 34A shows the amino acid sequence of VP1 GII.12_HS10_E80S (SEQ ID NO:88). **FIGURE 34B** shows the nucleic acid sequence of hCod VP1 GII.12_HS10_E80S (SEQ ID NO:89). **FIGURE 34C** shows the amino acid sequence of VP1 GII.12_HS10_A90L (SEQ ID NO:90). **FIGURE 34D** shows the nucleic acid sequence of hCod VP1 GII.12_HS10_A90L (SEQ ID NO:91). **FIGURE 34E** shows

the amino acid sequence of VP1 GII.12_HS10_E80S+A90L (SEQ ID NO:92); **FIGURE 34F** shows the nucleic acid sequence of hCod VP1 GII.12_HS10_E80S+A90L (SEQ ID NO:93). **FIGURE 34G** shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_A39V (SEQ ID NO:192). **FIGURE 34H** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V (SEQ ID NO:193). **FIGURE 34I** shows the amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:194). **FIGURE 34J** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:195). **FIGURE 34K** shows the amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_A90L (SEQ ID NO:196). **FIGURE 34L** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A90L (SEQ ID NO:197). **FIGURE 34M** shows the amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_A39V+M53I (SEQ ID NO:198). **FIGURE 34N** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V+M53I (SEQ ID NO:199). **FIGURE 34O** shows the amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_E80S+A90L (SEQ ID NO:200). **FIGURE 34P** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_E80S+A90L (SEQ ID NO:201);

[0067] **FIGURE 35A** shows the amino acid sequence of VP2_GI.1_Norwalk (SEQ ID NO:99). **FIGURE 35B** shows the nucleic acid sequence of human codon optimized VP.2_GI1_Norwalk (SEQ ID NO:100).

[0068] **FIGURE 36A** shows the amino acid sequence of VP2_GI.3_Lil08 (SEQ ID NO:94). **FIGURE 36B** shows the nucleic acid sequence of human codon optimized VP2_GI.3_Lil08 (SEQ ID NO:95).

[0069] **FIGURE 37A** shows the amino acid sequence of VP2_GII.6_HS10 (SEQ ID NO:96). **FIGURE 37B** shows the nucleic acid sequence of human codon optimized VP2_GII6_HS10 (SEQ ID NO:97).

[0070] **FIGURE 38A** shows the cloning vector 1190 from left to right T-DNA (SEQ ID NO:162). **FIGURE 38B** shows the construct 2724 from 2X35S promoter to NOS terminator (SEQ ID NO:163). **FIGURE 38C** shows the cloning vector 3677

from left to right T-DNA (SEQ ID NO:164). **FIGURE 38D** shows the construct 4133 from 2X35S promoter to NOS terminator (SEQ ID NO:165). **FIGURE 38E** shows the construct 4135 from 2X35S promoter to NOS terminator (SEQ ID NO:166).

[0071] **FIGURE 39A** shows a schematic representation of construct 2724 (VP1 Wt GI.1 hCod). **FIGURE 39B** shows a schematic representation of construct 3300 (VP1 Wt GI.2 hCod). **FIGURE 39C** shows a schematic representation of construct 3979 (VP1 Wt GI.3 hCod).

[0072] **FIGURE 40A** shows a schematic representation of construct 4140 (VP1 GI.3_Q84S hCod). **FIGURE 40B** shows a schematic representation of construct 4141 (VP1 GI.3_S94L hCod). **FIGURE 40C** shows a schematic representation of construct 4142 (VP1 GI.3_P84S+S94L hCod). **FIGURE 40D** shows a schematic representation of construct 4179 (VP1 GI.3_A43V+S94L hCod). **FIGURE 40E** shows a schematic representation of construct 4180 (VP1 GI.3_M57I+S94L hCod). **FIGURE 40F** shows a schematic representation of construct 4181 (VP1 GI.3_A43V+M57I+S94L hCod).

[0073] **FIGURE 41A** shows a schematic representation of construct 3980 (VP1 Wt GI.5 hCod (Wt GI.5 hCod). **FIGURE 41B** shows a schematic representation of construct 4130 (VP1 GI.5_Q84S). **FIGURE 41C** shows a schematic representation of construct 4131 (VP1 GI.5_A94L hCod). **FIGURE 41D** shows a schematic representation of construct 4132 (VP1 GI.5_Q84S+A94L hCod). **FIGURE 41E** shows a schematic representation of construct 4210 (VP1 GI.7_R84S hCod). **FIGURE 41F** shows a schematic representation of construct 4217 (VP1 GI.7_M57I hCod). **FIGURE 41G** shows a schematic representation of construct 4218 (VP1 GI.7_M57I+R84S hCod).

[0074] **FIGURE 42A** shows a schematic representation of construct 3982 (Wt VP1 GII.2 hCod). **FIGURE 42B** shows a schematic representation of construct 4143 (VP1 GII.2_E80S). **FIGURE 42C** shows a schematic representation of construct 4144 (VP1 GII.2_A90L hCod). **FIGURE 42D** shows a schematic representation of construct 4145 (VP1 GII.2_E80S+A90L hCod). **FIGURE 42E** shows a schematic representation of construct 4182 (VP1 GII.2_A39V+E80S+A90L hCod). **FIGURE**

42F shows a schematic representation of construct 4183 (VP1 GII.2_R53I+E80S+A90L hCod). **FIGURE 42G** shows a schematic representation of construct 4184 (VP1 GII.2_A39V+R53I+E80S+A90L hCod).

[0075] **FIGURE 43A** shows a schematic representation of construct 3983 (Wt VP1 GII.3 hCod). **FIGURE 43B** shows a schematic representation of construct 4146 (VP1 GII.3_E80S hCod). **FIGURE 43C** shows a schematic representation of construct 4147 (VP1 GII.3_A90L hCod). **FIGURE 43D** shows a schematic representation of construct 4148 (VP1 GII.3_E80S+A90L).

[0076] **FIGURE 44A** shows a schematic representation of construct 3760 (Wt VP1 GII.4 hCod). **FIGURE 44B** shows a schematic representation of construct 4155 (VP1 GII.4_A39V hCod). **FIGURE 44C** shows a schematic representation of construct 4156 (VP1 GII.4_V47P hCod). **FIGURE 44D** shows a schematic representation of construct 4157 (VP1 GII.4_R53I hCod). **FIGURE 44E** shows a schematic representation of construct 4133 (VP1 GII.4_P80S hCod). **FIGURE 44F** shows a schematic representation of construct 4134 (VP1 GII.4_S90L hCod). **FIGURE 44G** shows a schematic representation of construct 4158 (VP1 GII.4_ Δ35-42 hCod). **FIGURE 44H** shows a schematic representation of construct 4159 (VP1 GII.4_SSTAVATA hCod). **FIGURE 44I** shows a schematic representation of construct 4165 (VP1 GII.4_A39V+P80S hCod). **FIGURE 44J** shows a schematic representation of construct 4166 (VP1 GII.4_V47P+P80S hCod). **FIGURE 44K** shows a schematic representation of construct 4167 (VP1 GII.4_R53I+P80S hCod). **FIGURE 44L** shows a schematic representation of construct 4135 (VP1 GII.4_P80S+S90L hCod). **FIGURE 44M** shows a schematic representation of construct 4168 (GII.4_ P80S+Δ35-42 hCod). **FIGURE 44N** shows a schematic representation of construct 4169 (VP1 GII.4_P80S+SSTAVATA hCod). **FIGURE 44O** shows a schematic representation of construct 4185 (VP1 GII.4_A39V+R53I hCod). **FIGURE 44P** shows a schematic representation of construct 4186 (VP1 GII.4_A39V+R53I+P80S hCod).

[0077] **FIGURE 45A** shows a schematic representation of construct 3993 (Wt VP1 GII.6 hCod). **FIGURE 45B** shows a schematic representation of construct 4149 (VP1 GII.6_E80S hCod). **FIGURE 45C** shows a schematic representation of

construct 4150 (VP1 GII.6_S90L hCod). **FIGURE 45D** shows a schematic representation of construct 4151 (VP1 GII.6_E80S+S90L).

[0078] **FIGURE 46A** shows a schematic representation of construct 3995 (Wt VP1 GII.12 hCod). **FIGURE 46B** shows a schematic representation of construct 4136 (VP1 GII.12_E80S hCod. **FIGURE 46C** shows a schematic representation of construct 4137 (VP1 GII.12_A90L hCod). **FIGURE 46D** shows a schematic representation of construct 4138 (VP1 GII.12_E80S+A90L). **FIGURE 46E** shows a schematic representation of construct 4234 (VP1 GII.17_A39V). **FIGURE 46F** shows a schematic representation of construct 4235 (VP1 GII.17_R53I). **FIGURE 46G** shows a schematic representation of construct 4232 (VP1 GII.17_ A90L). **FIGURE 46H** shows a schematic representation of construct 4236 (VP1 GII.17_A39V+R53I). **FIGURE 46I** shows a schematic representation of construct 4233 (VP1 GII.17_E80S+A90L).

[0079] **FIGURE 47A** shows a schematic representation of construct 2725 (Wt VP2 GI.1). **FIGURE 47B** shows a schematic representation of construct 3303 (Wt VP2 GI.3 hCod). **FIGURE 47C** shows a schematic representation of construct 3307 (Wt VP2 GII.6).

[0080] **FIGURE 48** shows a schematic representation of construct 1190 (Cloning vector 1190).

[0081] **FIGURE 49** shows a schematic representation of construct 3677 (Cloning vector 3677).

[0082] **FIGURE 50A** shows a schematic representation of GII.4 P80X constructs (cloning vectors), wherein X is selected from: A (construct 4281); N (construct 4285); K (construct 4286); or H (construct 4287). **FIGURE 50B** shows a schematic representation of GII.4 P80s+A39X constructs (cloning vectors), wherein X is selected from I (construct 4256); M (construct 4257); G (construct 4258); S (construct 4259); E (construct 4260); D (construct 4261); N (construct 4262); Q (construct 4263); construct K (4264); or H (construct 4265).

[0083] **FIGURE 51** shows a schematic representation of GI.7 M57X constructs (cloning vectors), wherein X is selected from: L (construct 4266); G (construct 4268); S (construct 4269); T (construct 4270; N (construct 4273); Q (construct 4274); K (construct 4275); or H (construct 4276).

[0084] **FIGURE 52** shows a schematic representation of GI.3 S94X constructs (cloning vectors), wherein X is selected from: V (construct 4288); I (construct 4289); M (construct 4290); T (construct 4292); E (construct 4293); D (construct 4294); N (construct 4295); Q (construct 4296); K (construct 4297); or H (construct 4298).

[0085] DETAILED DESCRIPTION

[0086] The following description is of a preferred embodiment.

[0087] As used herein, the terms "comprising," "having," "including" and "containing," and grammatical variations thereof, are inclusive or open-ended and do not exclude additional, un-recited elements and/or method steps. The term "consisting essentially of" when used herein in connection with a use or method, denotes that additional elements and/or method steps may be present, but that these additions do not materially affect the manner in which the recited method or use functions. The term "consisting of" when used herein in connection with a use or method, excludes the presence of additional elements and/or method steps. A use or method described herein as comprising certain elements and/or steps may also, in certain embodiments, consist essentially of those elements and/or steps, and in other embodiments consist of those elements and/or steps, whether or not these embodiments are specifically referred to. In addition, the use of the singular includes the plural, and "or" means "and/or" unless otherwise stated. The term "plurality" as used herein means more than one, for example, two or more, three or more, four or more, and the like. Unless otherwise defined herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art. As used herein, the term "about" refers to an approximately +/-10% variation from a given value. It is to be understood that such a variation is always included in any given value provided herein, whether or not it is specifically referred to. The use of the word "a" or "an" when used herein in conjunction with the term

"comprising" may mean "one," but it is also consistent with the meaning of "one or more," "at least one" and "one or more than one."

[0088] The term "plant", "portion of a plant", "plant portion", "plant matter", "plant biomass", "plant material", plant extract", or "plant leaves", as used herein, may comprise an entire plant, tissue, cells, or any fraction thereof, intracellular plant components, extracellular plant components, liquid or solid extracts of plants, or a combination thereof, that are capable of providing the transcriptional, translational, and post-translational machinery for expression of one or more than one nucleic acids described herein, and/or from which an expressed protein or VLP may be extracted and purified. Plants may include, but are not limited to, agricultural crops including for example canola, Brassica spp., maize, Nicotiana spp., (tobacco) for example, *Nicotiana benthamiana, Nicotiana rustica, Nicotiana, tabacum, Nicotiana alata, Arabidopsis thaliana*, alfalfa, potato, sweet potato (*Ipomoea batatus*), ginseng, pea, oat, rice, soybean, wheat, barley, sunflower, cotton, corn, rye (*Secale cereale*), sorghum (*Sorghum bicolor, Sorghum vulgare*), safflower (*Carthamus tinctorius*).

[0089] The term "plant portion", as used herein, refers to any part of the plant including but not limited to leaves, stem, root, flowers, fruits, a plant cell obtained from leaves, stem, root, flowers, fruits, a plant extract obtained from leaves, stem, root, flowers, fruits, or a combination thereof. The term "plant extract", as used herein, refers to a plant-derived product that is obtained following treating a plant, a portion of a plant, a plant cell, or a combination thereof, physically (for example by freezing followed by extraction in a suitable buffer), mechanically (for example by grinding or homogenizing the plant or portion of the plant followed by extraction in a suitable buffer), enzymatically (for example using cell wall degrading enzymes), chemically (for example using one or more chelators or buffers), or a combination thereof. A plant extract may be further processed to remove undesired plant components for example cell wall debris. A plant extract may be obtained to assist in the recovery of one or more components from the plant, portion of the plant or plant cell, for example a protein (including protein complexes, protein surprastructures and/or VLPs), a nucleic acid, a lipid, a carbohydrate, or a combination thereof from the plant, portion of the plant, or plant cell. If the plant extract comprises proteins, then it may be referred to as a protein extract. A protein extract may be a crude plant

extract, a partially purified plant or protein extract, or a purified product, that comprises one or more proteins, protein complexes, protein suprastructures, and/or VLPs, from the plant tissue. If desired a protein extract, or a plant extract, may be partially purified using techniques known to one of skill in the art, for example, the extract may be subjected to salt or pH precipitation, centrifugation, gradient density centrifugation, filtration, chromatography, for example, size exclusion chromatography, ion exchange chromatography, affinity chromatography, or a combination thereof. A protein extract may also be purified, using techniques that are known to one of skill in the art.

[0090] The term "nucleic acid segment" as used herein refers to a sequence of nucleic acids that encodes a protein of interest. In addition to the sequence of nucleic acids, the nucleic acid segment comprises a regulatory region and a terminator that are operatively linked to the sequence of nucleic acids. The regulatory region may for example comprise a promoter, and optionally, an enhancer element operatively linked to the promoter.

[0091] The term "nucleic acid complex" as used herein refers to a combination of two or more than two nucleic acid segments. The two or more than two nucleic acid segments may be present in a single nucleic acid, so that the nucleic acid complex comprises two, or more than two nucleic acid segments, with each nucleic acid segment under the control of a regulatory region and a terminator. Alternatively, the nucleic acid complex may comprise two or more separate nucleic acids, each of the nucleic acids comprising one or more than one nucleic acid segment, where each nucleic acid segment is under the control of a regulatory region and a terminator. For example a nucleic acid complex may comprise one nucleic acid that comprises two nucleic acid segments, a nucleic acid complex may comprise two nucleic acids, each nucleic acid comprising one nucleic acid segment, or a nucleic acid complex may comprise two or more than two nucleic acids, with each nucleic acid comprising one or more than one nucleic acid segment.

[0092] The term "vector" or "expression vector", as used herein, refers to a recombinant nucleic acid for transferring exogenous nucleic acid sequences into host cells (e.g. plant cells) and directing expression of the exogenous nucleic acid

sequences in the host cells. "Expression cassette" refers to a nucleotide sequence comprising a nucleic acid of interest under the control of, and operably (or operatively) linked to, an appropriate promoter or other regulatory elements for transcription of the nucleic acid of interest in a host cell. As one of skill in the art would appreciate, the expression cassette may comprise a termination (terminator) sequence that is any sequence that is active in the plant host. For example the termination sequence may be derived from the RNA-2 genome segment of a bipartite RNA virus, e.g. a comovirus, the termination sequence may be a NOS terminator, or terminator sequence may be obtained from the 3'UTR of the alfalfa plastocyanin gene.

[0093] The constructs of the present disclosure may further comprise a 3' untranslated region (UTR). A 3' untranslated region contains a polyadenylation signal and any other regulatory signals capable of effecting mRNA processing or gene expression. The polyadenylation signal is usually characterized by effecting the addition of polyadenylic acid tracks to the 3' end of the mRNA precursor. Polyadenylation signals are commonly recognized by the presence of homology to the canonical form 5' AATAAA-3' although variations are not uncommon. Non-limiting examples of suitable 3'untranslated regions are the 3' transcribed non-translated regions containing a polyadenylation signal of *Agrobacterium* tumor inducing (Ti) plasmid genes, such as the nopaline synthase (Nos gene) and plant genes such as the soybean storage protein genes, the small subunit of the ribulose-1, 5-bisphosphate carboxylase gene (ssRUBISCO; US 4,962,028; which is incorporated herein by reference), the promoter used in regulating plastocyanin expression.

[0094] By "regulatory region" "regulatory element" or "promoter" it is meant a portion of nucleic acid typically, but not always, upstream of the protein coding region of a gene, which may be comprised of either DNA or RNA, or both DNA and RNA. When a regulatory region is active, and in operative association, or operatively linked, with a nucleotide sequence of interest, this may result in expression of the nucleotide sequence of interest. A regulatory element may be capable of mediating organ specificity, or controlling developmental or temporal gene activation. A "regulatory region" includes promoter elements, core promoter elements exhibiting a basal promoter activity, elements that are inducible in response to an external stimulus, elements that mediate promoter activity such as negative regulatory elements or

transcriptional enhancers. "Regulatory region", as used herein, also includes elements that are active following transcription, for example, regulatory elements that modulate gene expression such as translational and transcriptional enhancers, translational and transcriptional repressors, upstream activating sequences, and mRNA instability determinants. Several of these latter elements may be located proximal to the coding region.

[0095] In the context of this disclosure, the term "regulatory element" or "regulatory region" typically refers to a sequence of DNA, usually, but not always, upstream (5') to the coding sequence of a structural gene, which controls the expression of the coding region by providing the recognition for RNA polymerase and/or other factors required for transcription to start at a particular site. However, it is to be understood that other nucleotide sequences, located within introns, or 3' of the sequence may also contribute to the regulation of expression of a coding region of interest. An example of a regulatory element that provides for the recognition for RNA polymerase or other transcriptional factors to ensure initiation at a particular site is a promoter element. Most, but not all, eukaryotic promoter elements contain a TATA box, a conserved nucleic acid sequence comprised of adenosine and thymidine nucleotide base pairs usually situated approximately 25 base pairs upstream of a transcriptional start site. A promoter element may comprise a basal promoter element, responsible for the initiation of transcription, as well as other regulatory elements that modify gene expression.

[0096] There are several types of regulatory regions, including those that are developmentally regulated, inducible or constitutive. A regulatory region that is developmentally regulated, or controls the differential expression of a gene under its control, is activated within certain organs or tissues of an organ at specific times during the development of that organ or tissue. However, some regulatory regions that are developmentally regulated may preferentially be active within certain organs or tissues at specific developmental stages, they may also be active in a developmentally regulated manner, or at a basal level in other organs or tissues within the plant as well. Examples of tissue-specific regulatory regions, for example see-specific a regulatory region, include the napin promoter, and the cruciferin promoter (Rask et al., 1998, J. Plant Physiol. 152: 595-599; Bilodeau et al., 1994, Plant Cell 14:

125-130). An example of a leaf-specific promoter includes the plastocyanin promoter (see US 7,125,978, which is incorporated herein by reference).

[0097] An inducible regulatory region is one that is capable of directly or indirectly activating transcription of one or more DNA sequences or genes in response to an inducer. In the absence of an inducer the DNA sequences or genes will not be transcribed. Typically the protein factor that binds specifically to an inducible regulatory region to activate transcription may be present in an inactive form, which is then directly or indirectly converted to the active form by the inducer. However, the protein factor may also be absent. The inducer can be a chemical agent such as a protein, metabolite, growth regulator, herbicide or phenolic compound or a physiological stress imposed directly by heat, cold, salt, or toxic elements or indirectly through the action of a pathogen or disease agent such as a virus. A plant cell containing an inducible regulatory region may be exposed to an inducer by externally applying the inducer to the cell or plant such as by spraying, watering, heating or similar methods. Inducible regulatory elements may be derived from either plant or non-plant genes (e.g. Gatz, C. and Lenk, I.R.P., 1998, Trends Plant Sci. 3, 352-358). Examples, of potential inducible promoters include, but not limited to, tetracycline-inducible promoter (Gatz, C.,1997, Ann. Rev. Plant Physiol. Plant Mol. Biol. 48, 89-108), steroid inducible promoter (Aoyama, T. and Chua, N.H.,1997, Plant J. 2, 397-404) and ethanol-inducible promoter (Salter, M.G., et al, 1998, Plant Journal 16, 127-132; Caddick, M.X., et al,1998, Nature Biotech. 16, 177-180) cytokinin inducible IB6 and CKI1 genes (Brandstatter, I. and Kieber, J.J.,1998, Plant Cell 10, 1009-1019; Kakimoto, T., 1996, Science 274, 982-985) and the auxin inducible element, DR5 (Ulmasov, T., et al., 1997, Plant Cell 9, 1963-1971).

[0098] A constitutive regulatory region directs the expression of a gene throughout the various parts of a plant and continuously throughout plant development. Examples of known constitutive regulatory elements include promoters associated with the CaMV 35S transcript. (p35S; Odell et al., 1985, Nature, 313: 810-812; which is incorporated herein by reference), the rice actin 1 (Zhang et al, 1991, Plant Cell, 3: 1155-1165), actin 2 (An *et al.*, 1996, *Plant J.*, 10: 107-121), or tms 2 (U.S. 5,428,147), and triosephosphate isomerase 1 (Xu et. al., 1994, Plant Physiol. 106: 459-467) genes, the maize ubiquitin 1 gene (Cornejo et al, 1993, Plant Mol. Biol. 29:

637-646), the *Arabidopsis* ubiquitin 1 and 6 genes (Holtorf et al, 1995, Plant Mol. Biol. 29: 637-646), the tobacco translational initiation factor 4A gene (Mandel et al, 1995 Plant Mol. Biol. 29: 995-1004); the Cassava Vein Mosaic Virus promoter, pCAS, (Verdaguer et al., 1996); the promoter of the small subunit of ribulose biphosphate carboxylase, pRbcS: (Outchkourov et al., 2003), the pUbi (for monocots and dicots).

[0099] The term "constitutive" as used herein does not necessarily indicate that a nucleotide sequence under control of the constitutive regulatory region is expressed at the same level in all cell types, but that the sequence is expressed in a wide range of cell types even though variation in abundance is often observed.

[00100] The expression constructs as described above may be present in a vector. The vector may comprise border sequences which permit the transfer and integration of the expression cassette into the genome of the organism or host. The construct may be a plant binary vector, for example a binary transformation vector based on pPZP (Hajdukiewicz, et al. 1994). Other example constructs include pBin19 (see Frisch, D. A., L. W. Harris-Haller, et al. 1995, *Plant Molecular Biology* 27: 405-409).

[00101] The term “native”, “native protein” or “native domain”, as used herein, refers to a protein or domain having a primary amino acid sequence identical to wildtype. Native proteins or domains may be encoded by nucleotide sequences having 100% sequence similarity to the wildtype sequence. A native amino acid sequence may also be encoded by a human codon (hCod) optimized nucleotide sequence or a nucleotide sequence comprising an increased GC content when compared to the wild type nucleotide sequence provided that the amino acid sequence encoded by the hCod-nucleotide sequence exhibits 100% sequence identity with the native amino acid sequence.

[00102] By a nucleotide sequence that is “human codon optimized” or a “hCod” nucleotide sequence, it is meant the selection of appropriate DNA nucleotides for the synthesis of an oligonucleotide sequence or fragment thereof that approaches the codon usage generally found within an oligonucleotide sequence of a human nucleotide sequence. By “increased GC content” it is meant the selection of

appropriate DNA nucleotides for the synthesis of an oligonucleotide sequence or fragment thereof in order to approach codon usage that, when compared to the corresponding native oligonucleotide sequence, comprises an increase of GC content, for example, from about 1 to about 30%, or any amount therebetween, over the length of the coding portion of the oligonucleotide sequence. For example, from about 1, 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30%, or any amount therebetween, over the length of the coding portion of the oligonucleotide sequence. As described below, a human codon optimized nucleotide sequence, or a nucleotide sequence comprising an increased GC content (when compared to the wild type nucleotide sequence) exhibits increased expression within a plant, portion of a plant, or a plant cell, when compared to expression of the non-human optimized (or lower GC content) nucleotide sequence.

[00103] Norovirus VP1 mutant proteins (also termed modified VP1 protein, or modified norovirus VP1 protein) and methods of producing norovirus VP1 mutant proteins in plants are described herein. Several of the modified norovirus VP1 proteins comprise specific substitutions, modifications or mutations in the S domain of non-GI.1 VP1s, to the corresponding amino acids that are found in GI.1 S domains. It has been observed that in certain norovirus genotypes, mutating specific amino acids to the corresponding amino acids found in GI.1 VP1s, results in similar or improved VP1 and/or VLP characteristics as compared to the wildtype (non-GI.1) VP1 and/or VLP. Examples of improved characteristics of the VP1and/or VLP include:

- increased VP1 protein yield when expressed in plant cells as compared to the yield of wildtype VP1 of the same genotype that does not comprise the substitution(s), modification(s) or mutation(s);

- increased density of VLPs comprised of the modified VP1 proteins (for example as determined using density gradient separation, and optionally SDS-PAGE and/or Western analysis) as compared to the density of VLPs comprising wildtype VP1 of the same genotype that does not comprise the substitution(s), modification(s) or mutation(s);

- improved integrity, stability, or both integrity and stability, of VLPs that are comprised of the modified VP1 proteins as compared to the integrity, stability or both of VLPs comprising wildtype VP1 of the same genotype that does not comprise the substitution(s), modification(s) or mutation(s);

- increased VLP yield when expressed in plant cells as compared to the wildtype level of VLP production of the same genotype that does not comprise the substitution(s), modification(s) or mutation(s);

- improved accumulation of VLPs that are comprised of the modified VP1 proteins as compared to the accumulation of VLPs comprising wildtype VP1 of the same genotype that does not comprise the substitution(s), modification(s) or mutation(s);

- a greater proportion of VLPs that assemble into 38 nm VLPs as opposed to 23 nm VLPs as compared to the wildtype VP1 of the same genotype that does not comprise the substitution(s), modification(s) or mutation(s); and

- a combination thereof.

[00104] For example, the modified norovirus VP1 protein, and methods of producing the modified norovirus VP1 protein, may include a nucleotide sequence encoding a VP1 protein comprising an S domain substitution, mutation, or modification, at any one or more amino acids in sequence alignment with positions 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1; see Figure 2C), or a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), or a combination thereof. The sequence encoding the norovirus VP1 mutant protein may be optimized for human codon usage, for increased GC content, or a combination thereof.

[00105] With reference to the sequences shown in Figure 2C, the norovirus GI.1 sequence (SEQ ID NO:1) is used as a reference sequence against which the other norovirus VP1 sequences may be aligned. The VP1 amino acid sequences for the "GII" family of VP1 proteins comprise a 4 amino acid deletion relative to the GI.1 sequence, comprising a 3 amino acid deletion at positions 14-16, and a one amino acid

deletion at position 26. As a result, the alignments between the GII VP1 sequences and the GI VP1 sequences are offset by 3 amino acids after amino acid 13, and 4 amino acids after position 26. For example, amino acid 84 of GI.1, aligns with amino acid 80 of GII.4 (see Figure 2C). Reference to a substitution, modification or mutation at position 84 (GI.1) and 80 (GII.4) therefore refer to the same aligned amino acids:

Strain	amino acid alignment				
GI:	39-46	43	57	84	94
GII:	35-42	39	53	80	90

[00106] Also provided herein are methods of increasing production of VLPs comprising modified norovirus VP1 proteins, in plants. For example, a method may involve introducing a nucleic acid encoding a norovirus VP1 mutant protein, as described herein, into the plant, portion of the plant, or plant cell. One or more than one norovirus mutant protein may be expressed in a plant, portion of the plant, or plant cell, in order to produce a VLP comprising one or more than one modified norovirus protein. Alternatively, the method may comprise providing a plant, portion of the plant, or plant cell that comprises the nucleic acid encoding the modified norovirus VP1 protein as described herein, and expressing the nucleic acid encoding the modified norovirus VP1 protein in order to produce a VLP comprising the one or more than one modified norovirus protein.

[00107] The methods of producing a VLP comprising a VP1 mutant protein may also comprise a step of co-expressing a nucleic acid sequence encoding a VP2 protein in the plant, portion of the plant, or plant cell.

[00108] The term “single construct” or “single constructs”, as used herein, refers to nucleic acid vectors comprising a single nucleic acid sequence. The term “dual construct” or “dual constructs”, as used herein, refers to a nucleic acid vector comprising two nucleic acid sequences.

[00109] By co-expression it is meant the introduction and expression of two or more nucleotide sequences, each of the two or more nucleotide sequences encoding a

protein of interest, or a fragment of a protein of interest within a plant, portion of a plant or a plant cell. The two or more nucleotide sequences may be introduced into the plant, portion of the plant or the plant cell within one vector, so that each of the two or more nucleotide sequences is under the control of a separate regulatory region (e.g. comprising a dual construct). Alternatively, the two or more nucleotide sequences may be introduced into the plant, portion of the plant or the plant cell within separate vectors (e.g. comprising single constructs), and each vector comprising appropriate regulatory regions for the expression of the corresponding nucleic acid. For example, two nucleotide sequences, each on a separate vector and introduced into separate *Agrobacterium tumefaciens* hosts, may be co-expressed by mixing suspensions of each *A. tumefaciens* host in a desired volume (for example, an equal volume, or the ratios of each *A. tumefaciens* host may be altered) before vacuum infiltration. In this manner, co-infiltration of multiple *A. tumifaciens* suspensions permits co-expression of multiple transgenes.

[00110] The nucleic acid comprising encoding a norovirus VP1 mutant protein as described herein may further comprise sequences that enhance expression of the norovirus VP1 mutant protein in the plant, portion of the plant, or plant cell. Sequences that enhance expression may include, a CPMV enhancer element, or a plant-derived expression enhancer, in operative association with the nucleic acid encoding the norovirus VP1 mutant protein. The sequence encoding the VP1 mutant protein may also be optimized for human codon usage, increased GC content, or a combination thereof. Furthermore, a nucleic acid encoding VP2 may be co-expressed along with the sequence encoding the VP1 mutant protein. The co-expression of a nucleic acid encoding VP2 may lead to an increased yield, increased density, increased integrity, or combination thereof, of VLPs that comprise the one or more than one type of VP1 mutant protein.

[00111] The term "CPMV enhancer element", as used herein, refers to a nucleotide sequence encoding the 5'UTR regulating the Cowpea Mosaic Virus (CPMV) RNA2 polypeptide or a modified CPMV sequence as is known in the art. For example, a CPMV enhancer element or a CPMV expression enhancer, includes a nucleotide sequence as described in WO2015/14367; WO2015/103704; WO2007/135480; WO2009/087391; Sainsbury F., and Lomonossoff G.P., (2008, Plant Physiol. 148: pp.

1212-1218), each of which is incorporated herein by reference. A CPMV enhancer sequence can enhance expression of a downstream heterologous open reading frame (ORF) to which they are attached. The CPMV expression enhancer may include CPMV HT, CPMVX (where X=160, 155, 150, 114), for example CPMV 160, CPMVX+ (where X=160, 155, 150, 114), for example CPMV 160+, CPMV-HT+, CPMV HT+[WT115], or CPMV HT+ [511] (WO2015/143567; WO2015/103704 which are incorporated herein by reference). The CPMV expression enhancer may be used within a plant expression system comprising a regulatory region that is operatively linked with the CPMV expression enhancer sequence and a nucleotide sequence of interest. The term "5'UTR" or "5' untranslated region" or "5' leader sequence" refers to regions of an mRNA that are not translated. The 5'UTR typically begins at the transcription start site and ends just before the translation initiation site or start codon of the coding region. The 5' UTR may modulate the stability and/or translation of an mRNA transcript.

[00112] The term "plant-derived expression enhancer", as used herein, refers to a nucleotide sequence obtained from a plant, the nucleotide sequence encoding a 5'UTR. Examples of a plant derived expression enhancer are described in US Provisional Patent Application No.62/643,053 (Filed March 14, 2018; which is incorporated herein by reference) or in Diamos A.G. et. al. (2016, Front Plt Sci. 7:1-15; which is incorporated herein by reference). The plant-derived expression enhancer may be selected from nbMT78, nbATL75, nbDJ46, nbCHP79, nbEN42, atHSP69, atGRP62, atPK65, atRP46, nb30S72, nbGT61, nbPV55, nbPPI43, nbPM64 (SEQ ID NO:14), and nbH2A86 as described in US 62/643,053). The plant derived expression enhancer may be used within a plant expression system comprising a regulatory region that is operatively linked with the plant-derived expression enhancer sequence and a nucleotide sequence of interest.

[00113] The term "5'UTR" or "5' untranslated region" or "5' leader sequence" refers to regions of an mRNA that are not translated. The 5'UTR typically begins at the transcription start site and ends just before the translation initiation site or start codon of the coding region. The 5' UTR may modulate the stability and/or translation of an mRNA transcript.

[00114] By "operatively linked" it is meant that the particular sequences interact either directly or indirectly to carry out an intended function, such as mediation or modulation of expression of a nucleic acid sequence. The interaction of operatively linked sequences may, for example, be mediated by proteins that interact with the operatively linked sequences.

[00115] When one or more than one type of the modified norovirus VP1 protein is expressed in the plant, portion of the plant or the plant cell, the one or more than one modified VP1 proteins auto-assemble into VLPs. The plant or portion of the plant may be harvested under suitable extraction and purification conditions to maintain the integrity of the VLP, and the VLP comprising the one or more than one type of VP1 mutant (modified) protein may be purified. The one or more than one VP1 mutant protein may also be co-expressed with nucleotide sequence encoding VP2, so that the VLP may comprise both modified VP1 protein and VP2 protein. The present disclosure also provides for the production of one or more than one type of VP1 mutant protein as described herein within a plant, portion of a plant, or plant cell, and the extraction and purification of the one or more than one type of VP1 mutant protein from the plant, the portion of the plant, or the plant cell to produce plant matter, a plant extract, or a protein extract, comprising the modified (mutant) VP1 protein.

[00116] Plant matter, a plant extract, or a protein extract comprising the norovirus VP1 mutant protein as described herein is also provided. The plant matter, plant extract, or protein extract may be used to induce immunity to norovirus infection in a subject. Alternatively, the VP1 mutant protein, or the VLP comprising the VP1 mutant protein (and optionally VP2), may be purified or partially purified, and the purified or partially purified preparation may be used to induce immunity to a norovirus infection in a subject.

[00117] The present disclosure also provides a composition comprising an effective dose of one or more than one type of modified norovirus VP1 protein, or VLPs comprising one or more than one modified norovirus VP1 protein, and optionally VP2, for inducing an immune response, and a pharmaceutically acceptable carrier, adjuvant, vehicle, or excipient.

[00118] Also provided herein are methods of inducing immunity to a norovirus infection in a subject comprising of administering one or more than one type of mutant (modified) norovirus VP1 protein or VLPs comprising one or more than one types of norovirus VP1 mutant proteins to a subject orally, intranasally, intramuscularly, intraperitoneally, intravenously, subcutaneously, rectally, or intravaginally.

[00119] The term "norovirus", as used herein, refers to a non-enveloped viral strain of the genus *norovirus* of the family *Caliciviridae* that is characterized as having a single-stranded, positive-sense RNA. The norovirus genome is 7,654 nucleotides in length. The ORF1 encodes a nonstructural polyprotein that is cleaved by viral 3C-like protease into 6 proteins, including an RNA-dependent RNA polymerase. ORF2 and ORF3 encode a major (VP1) and a minor (VP2) capsid protein, respectively (see Figure 1A).

[00120] Norovirus strains as disclosed herein include any known norovirus strain, but also modifications to known norovirus strains that are known to develop on a regular basis over time. For example, norovirus strains may include (as described by their amino acids sequences), but are not limited to Hu/GI.1/United States/Norwalk/1968 (GI.1; SEQ ID NO:1; Figure 12A), Hu/GI.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; Figure 13A), Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; Figure 14A), Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; Figure 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; Figure 16A), Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; Figure 16B), Hu/GII.2/CGMH47/2011/TW (GII.2; SEQ ID NO: 14; Figure 17A), Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO: 15; Figure 18A), Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO: 16; Figure 19A), US96/GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27; Figure 19C), FH02/GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28; Figure 19D), Hnt04:GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29; Figure 19E), 2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30; Figure 19F), NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31; Figure 19G), Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; Figure 20), Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; Figure 21A),

GII.7/Musa/2010/All73774 (GII.7; SEQ ID NO:18; Figure 22), Hu/GII.12/HS206/2010/USA (GII.12; SEQ ID NO: 19; Figure 23A), GII.13/VA173/2010/H9AWU4 (GII.13; SEQ ID NO:22; Figure 24A), GII.14_Saga_2008_JPN_ADE28701 native VP1 (GII.14; SEQ ID NO: 32; Figure 25), Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO: 24; Figure 26A), and Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; Figure 27). Norovirus strains are known to readily mutate from year-to-year. Therefore, Norovirus strains also include strains having from about 30-100% or any amount therebetween, amino acid sequence identity, to the VP1 protein, the VP2 protein, or both the VP1 and the VP2 proteins, with any of the above norovirus strains of the strains listed above and in Figures 2A and 2B, provided that the VP1 protein can be expressed (i.e. produced) in a plant and that the VP1 protein induces immunity to norovirus in a subject, when the VP1 protein is administered to the subject. For example, norovirus strains also include strains having 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100%, or any amount therebetween, amino acid sequence identity (sequence similarity; percent identity; percent similarity) to the VP1 protein, the VP2 protein, or both the VP1 and the VP2 proteins, with any of the above norovirus strains of the strains listed above and in Figures 2A and 2B, provided that the that the VP1 protein can be expressed in a plant and that the VP1 protein induces immunity to norovirus in a subject, when the VP1 protein is administered to the subject. An amino acid sequence identity comparison between the S domain of VP1 proteins of several norovirus strains, which are not to be considered limiting, is shown in Figure 2C.

[00121] The terms “percent similarity”, “sequence similarity”, “percent identity”, or “sequence identity”, when referring to a particular sequence, are used for example as set forth in the University of Wisconsin GCG software program, or by manual alignment and visual inspection (see, e.g., Current Protocols in Molecular Biology, Ausubel et al., eds. 1995 supplement). Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, using for example the algorithm of Smith & Waterman, (1981, Adv. Appl. Math. 2:482), by the alignment algorithm of Needleman & Wunsch, (1970, J. Mol. Biol. 48:443), by the search for similarity method of Pearson

& Lipman, (1988, Proc. Natl. Acad. Sci. USA 85:2444), by computerized implementations of these algorithms (for example: GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, Wis.).

[00122] An example of an algorithm suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., (1977, Nuc. Acids Res. 25:3389-3402) and Altschul et al., (1990, J. Mol. Biol. 215:403-410), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. For example the BLASTN program (for nucleotide sequences) may use as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program may use as defaults a word length of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, 1989, Proc. Natl. Acad. Sci. USA 89:10915) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (see URL: ncbi.nlm.nih.gov/).

[00123] The term "VP1", as used herein, refers to the norovirus major capsid protein or polypeptide comprising an amino acid sequence similar to the protein or polypeptide encoded by ORF2 of one or more strains of norovirus as described herein. The major capsid protein folds into two principal domains, a shell (S) domain and a protruding (P) domain (see Figure 1B). The VP1 protein forms a dimer (Figure 1C) when incorporated into a virus like particle, or a VLP. The first portion of the N-terminal of VP1 comprise the S domain, with the remainder of the VP1 polypeptide comprising the P domain. For example, in GI.1, the first 225 amino acids of the N-terminal VP1 protein comprise the S domain. When folded, the VP1 assumes a conformation as depicted in FIGURE 1B, comprising of a globular S domain (bottom of ribbon structure) and a P domain (top of ribbon structure).

[00124] As shown in Figure 1C, the VP1 protein dimerizes via P-domain interactions. These interactions stabilize the spontaneous assembly of norovirus capsid molecules.

[00125] Methods to produce norovirus VP1 proteins and modified norovirus VP1 proteins in a plant, portion of a plant or a plant cell are described herein that involve introducing the recombinant polynucleotide encoding the norovirus VP1 protein or modified VP1 protein, and incubating the plant, portion of the plant or the plant cell under conditions that permit expression of the norovirus VP1 protein or modified norovirus protein. However, it is also to be understood that norovirus VP1 proteins may be obtained from norovirus VLPs that comprise the VP1 protein, as described in Ausar et al. (Ausar S.F., Foubert T.R, Hudson M.H., Vedvick T.S., Middaugh C.R., 2006, J. Biol. Chem. 281:19478-19488). For example norovirus VLPs comprising norovirus proteins or modified norovirus proteins may dissociate at pH 8 and above, or at temperatures above 55°C, into their VP1 protein constituents, thereby yielding VP1 protein.

[00126] The term "virus like particle", "VLP", "virus like particles", or "VLPs", as used herein, refers to a norovirus virus like particle(s) that comprise one or more than one type of norovirus VP1 protein, one or more than one type of VP1 mutant protein, or a combination thereof, and that self-assemble into non-replicating, non-enveloped, non-infectious viral capsid structures lacking all parts of the norovirus genome. For example, the VLP may comprise one type of a modified VP1 protein as described herein, or the VLP may comprise two or more different modified VP1 proteins described herein. Furthermore the VLP may comprise a VP2 protein. VLPs comprising VP1 protein, VP1+VP2 protein, modified VP1 protein, or modified VP1 protein +VP2 protein are of the size from about 15nm to 50nm or any amount therebetween, for example 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50nm, or any amount therebetween. For example, for T=1 icosahedral symmetry, VLPs may be about 23 nm, or for T=3 icosahedral symmetry, VLPs may be from about 38 to about 40 nm.

[00127] As shown in the electron micrographs of Figures 3B, 4B, 5C, 5E, 6C, 6E, 7C, 8B, 9B, 9C, 9D, 9G, 10B, 11C and 11D, plant produced VP1 proteins and modified VP1 proteins derived from several norovirus strains self-assemble into VLPs.

Norovirus VP1 Protein Production in Plants

[00128] The VP1 protein includes any VP1 protein comprising an amino acid sequence having from about 30 to about 100%, from about 40 to about 100%, from about 50 to about 100%, from about 60 to about 100%, from about 70 to about 100%, from about 80 to about 100%, from about 85 to about 100% from about 90 to about 100%, or from about 95 to about 100% from about 98 to about 100%, or any amount therebetween, sequence identity (which may be also termed sequence similarity) with a VP1 amino acid sequence from a norovirus GI.1 (SEQ ID NO:1; Figure 12A), GI.2 (SEQ ID NO:4; Figure 13A), GI.3 (SEQ ID NO:6; Figure 14A), GI.5 (SEQ ID NO:12; Figure 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; Figure 16A), GII.1 (SEQ ID NO:13; Figure 16B), GII.2 (SEQ ID NO:14; Figure 17A), GII.3 (SEQ ID NO:15; Figure 18A), GII.4/Sydney (SEQ ID NO:16; Figure 19A), GII.4/Dresden (SEQ ID NO:27; Figure 19C), GII.4/FarmingtonHills (SEQ ID NO:28; Figure 19D), GII.4/Hunter (SEQ ID NO:29; Figure 19E), GII.4/Shellharbour (SEQ ID NO:30; Figure 19F), GII.4/Orange (SEQ ID NO:31; Figure 19G), GII.5 (SEQ ID No:17; Figure 20), GII.6 (SEQ ID NO:20; Figure 21A), GII. 7 (SEQ ID NO:18; Figure 22), GII.12 (SEQ ID NO:19; Figure 23A), GII.13 (SEQ ID NO:22; Figure 24A), GII.14/Saga (SEQ ID NO:32; Figure 25), GII.17 (SEQ ID NO:24; Figure 26A), GII.21 (SEQ ID NO:26; Figure 27), provided that the VP1 protein is expressed in a plant and it induces immunity to norovirus when administered to a subject.

[00129] The VP1 protein as described herein is modified and comprises an S domain substitution, modification or mutation, at any one or more amino acids in sequence alignment with positions 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1; see Figure 2C), or a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), or a combination thereof. The nucleotide sequence encoding the modified norovirus VP1 protein may be optimized for human codon usage, for increased GC content, or a

combination thereof. The modified VP1 protein may be expressed in a plant, portion of a plant, or plant cell.

[00130] As shown in Figure 2C, relative to the hypervariable P domain, the primary amino acid sequence of the norovirus VP1 S domain is well conserved. For example, the VP1 S domain sequences of the norovirus strains shown in Figure 2C, have sequences ranging from 55.2 - 98.9% identity to the S domain of GI.1 VP1. For example, nucleic acid sequences described herein may exhibit from about 55 to about 99%, or any amount therebetween sequence identity to the S domain of GI.1 VP1, For example, nucleic acid sequences described herein may exhibit from about 55, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or any amount therebetween, sequence identity to the S domain of GI.1 VP1.

[00131] As previously shown in US provisional application 62/475,660 (filed March 23, 2017; which is incorporated herein by reference) and PCT/CA2018/050352 (filed March 23, 2018, which is incorporated herein by reference), wild type (also termed native) norovirus VP1 protein may be produced in plants and VLPs comprising the VP1 protein produced. Vacuum infiltration of leaves (from *N. benthamiana*) with *Agrobacterium tumefaciens* comprising expression vectors encoding GI.1 VP1 as a single nucleic acid construct, GI.1 VP2 as a single nucleic acid construct, both GI.1 VP1 and VP2, with VP1 and VP2 nucleic acid sequences introduced in separate vectors ("VP1+VP2"; dual constructs), or on the same vector ("VP1/VP2" or "VP1/VP2/3'UTR"; single nucleic acid constructs) to permit co-expression of the VP1 and/or VP2 sequences and the leaves examined for VP1 and VP2 production. After 6 or 9 days post infiltration (6 DPI and 9 DPI, respectively), total crude protein extracts were prepared from leaf homogenates, separated by SDS-PAGE, and stained with Coomassie Brilliant Blue dye. Leaves infiltrated with expression vectors comprising nucleotide sequences that correspond to wildtype GI.1 ORF2, encoding the VP1 protein, produced low or non-detectable levels of GI.1 VP1 as determined using Coomassie stained gels. In contrast, leaves infiltrated with expression vectors comprising GI.1 VP1 nucleotide sequences that were codon optimized for human expression (hCod), or enriched for GC content when compared to the GC content of the wildtype VP1 nucleic acid sequence, produced increased amounts of GI.1 VP1

protein in Coomassie stained gels. Demonstrating that hCod GI.1 VP1 may be produced in plants when VP1 is expressed on its own.

[00132] Furthermore, as described in US provisional application 62/475,660 and PCT/CA2018/050352 (filed March 23, 2017; and March 23, 2018, respectively, both of which are incorporated herein by reference), leaves infiltrated with vectors comprising either wildtype GI.1 VP1 and VP2 or human codon optimized GI.1 VP1 and VP2 produced low levels of GI.1 VP1 protein in Coomassie stained gels, suggesting that expression of VP1 is not enhanced by the presence of VP2 when co-expressed in *cis* on the same vector, using the same organization as found in the viral genome (using one promoter to control expression). However, when VP1 or human codon optimized VP1 was co-expressed in *trans* (on a separate construct) along with VP2 or hCod VP2 (hCod VP1+VP2), respectively, an increase in VP1 protein was observed. Each of the VP1 and VP2 nucleic acid segments comprised a regulatory region and a terminator, and the constructs were introduced into the plants as a nucleic acid complex, and this resulted in a corresponding increase in VP1 protein yield.

[00133] This observation is in contrast to that observed in insect and mammalian cells (Bertolotti-Ciarlet A., Crawford S.E., Hutson A.M., Estes M.K. 2003, J. Virol. 77:11603-11615), who reported that an increase in VP1 expression was only observed when VP1 and VP2 (or VP1+VP2+3'UTR) resided in *cis*, and were co-expressed using the same organization as that found in the viral genome, under the control of one promoter and terminator. No increase in VP1 expression was observed by Bertolotti-Ciarlet (2003) in insect or mammalian cells, when VP1 and VP2 were co-expressed in *trans*.

[00134] As described in more detail below, when the modified VP1 proteins, as described herein, are expressed in plants, it is preferred that the ORF3 sequence encoding VP2 is obtained from the same norovirus genotype and strain as that used to obtain the modified VP1 sequence. In the examples provided herein, and unless otherwise stated, the modified VP1 protein and the VP2 protein are obtained from the same norovirus genotype and strain , and the nucleotide sequences encoding the modified VP1 protein and the VP2 protein are co-expressed in the plant using separate expression systems, for example, on separate plasmids, or VP1 and VP2 may be

expressed on the same vector but each of the sequences encoding VP1 and VP2 should be under the control of separate promoter and terminator sequences, so that they have a separate expression system.

[00135] The yield, or amount of extracted, norovirus VP1 protein and the production of VLPs comprising norovirus VP1 proteins in a plant, differs depending on the genotype of the norovirus VP1 being expressed. For example, as shown in Figure 3A, the expression of wild type GI.1 VP1, GI.5 VP1, and GII.12 VP1 was robust with good protein yields (determined using SDS PAGE). Furthermore, high density wild type GI.1 VLPs, having well-formed capsids that are predominantly 38 nm in diameter were also produced (Figure 3B), and high density VLPs were produced from plants expressing wild type GI.5 VLPs, GII.12 VLPs (Figure 3C) and GI.2 VLPs, (Figure 4A). In contrast, wild type GII.4 VP1 was poorly expressed in plants (Figures 3A right hand panel), and low yields of VP1 protein, or non-detectable amounts of VP1 protein (using SDS-PAGE) were observed following expression other wild type VP1 proteins in plants, for example, GII.2 VP1, GII.3 VP1 and GII.6 VP1 (Table 5, Example 3).

[00136] Furthermore, expression of native VP1 proteins in plants may result in VLPs characterized as comprising a higher proportion of 23 nm VLPs rather than 38nm VLPs. For example, expression of wild type GI.3 VP1 results in the production of a significant number of 23nm VLPs (see Figure 5C, left hand panel). A greater proportion of 23nm VLPs also results in the VLPs characterized as being less dense following density gradient centrifugation (see Figure 5B left hand panel).

[00137] The present disclosure provides nucleic acid sequences encoding modified norovirus VP1 proteins, wherein the modified norovirus VP1 comprises one or more than one substitution, modification or mutation at an amino acid selected from a group consisting of amino acids in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) or a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus genotype VP1 GI.1 (SEQ ID NO:1), or a combination thereof. Plant expressing nucleic acid sequences encoding the modified norovirus VP1 protein, and comprising one or more than one substitution, modification or mutation at an amino acid selected from a group

consisting of amino acids in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 or a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus genotype VP1 GI.1, or a combination thereof, exhibit similar or improved VP1, and/or VLP characteristics as compared to the wildtype VP1 and/or VLP that does not comprise the one or more than one substitution, modification or mutation.

[00138] Examples of improved characteristics of the modified VP1 and/or VLP include,

- increased modified VP1 protein yield (determined for example using Coomassie stained SDS-PAGE and Western analysis) when expressed in plant cells as compared to the wildtype VP1 that does not comprise the one or more than one substitution, modification or mutation. For example, increased yields of modified VP1 protein may range from 1.5 to 50 fold, or any amount there between, over that of the corresponding wild type VP1 yield;

- increased density of VLPs comprising the modified VP1 proteins, for example as determined using iodixanol density gradient separation of protein extracts as compared to density gradient separation of the wildtype VP1 that does not comprise the one or more than one substitution, modification or mutation. For example, VLPs comprising modified VP1 protein may be observed in the same or more dense fractions following density gradient centrifugation;

- improved integrity of VLPs that are comprised of the modified VP1 proteins compared to the wildtype VP1 that does not comprise the one or more than one substitution, modification or mutation. For example, the number of disrupted, or partially assembled, VLPs may be determined using TEM;

- increased VLP yield when expressed in plant cells as compared to the wildtype level of VLP production of the same genotype that does not comprise the substitution(s), modification(s) or mutation (s). VLP yield may be determined in washed samples obtained from VLP containing fractions following density gradient centrifugation using TEM. For example, increased yields of VLPs comprising

modified VP1 protein may range from 1.5 to 20 fold, or any amount there between, over that of the corresponding yield of VLPs comprising wild type VP1 protein;

- improved accumulation of VLPs that are comprised of the modified VP1 proteins as compared to the accumulation of VLPs comprising wildtype VP1 of the same genotype that does not comprise the substitution(s), modification(s) or mutation (s);

- a greater proportion of VLPs that assemble into 38 nm VLPs as opposed to 23 nm VLPs, compared to VLPs comprising the wildtype VP1 that does not comprise the one or more than one substitution, modification or mutation (determined using TEM); and

- a combination of these improved characteristics.

[00139] Without wishing to be bound by theory, VLPs that are observed in higher density fractions following density gradient centrifugation, as compared to wildtype norovirus VLPs, indicates that the assembly of the VLPs comprising native VP1 may be less stable when expressed in, and extracted from, plants, than VLPs comprising the modified VP1 protein. The native VLP may therefore be more susceptible to malformed capsid particles and the generation of fragmentation products. As a result, the VLPs comprising modified VP1 protein that are characterized as having increased density may also exhibit greater structural integrity than VLPs produced using the corresponding wildtype VP1.

[00140] The nucleic acid sequences described herein may exhibit from about 50% to about 99% sequence similarity with any of the nucleic acid sequences encoding VP1 as identified above and as listed in Figures 2A-C, excluding GI. For example, nucleic acid sequences described herein may exhibit from about 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or any amount therebetween, sequence identity with any of the nucleic acid sequences encoding a norovirus VP1, for example from, Hu/GI.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; Figure 12A), Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; Figure 14A), Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; Figure 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; Figure 16A),

Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; Figure 16B), Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14; Figure 17A), Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO: 15; Figure 18A),Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO: 16; Figure 19A), US96/GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27; Figure 19C), FH02/GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28; Figure 19D), Hnt04:GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29; Figure 19E), 2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30; Figure 19F), NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31; Figure 19G), Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; Figure 20), Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; Figure 21A), G11.7/Musa/2010/All73774 (GII7; SEQ ID NO:18; Figure 22), Hu/GII.12/HS206/2010/USA (GII.12; SEQ ID NO: 19; Figure 23A), GII.13/VA173/2010/H9AWU4 (SEQ ID NO:22; Figure 24A), GII.14_Saga_2008_JPN_ADE28701 native VP1 (SEQ ID NO: 32; Figure 25), Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO: 24; Figure 26A), Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; Figure 27), provided that the VP1 protein induces immunity to norovirus in a subject, when the VP1 protein is administered to the subject.

[00141] Similarly, the present invention includes amino acid sequences that exhibit from about 30% to about 99% or any amount therebetween, sequence similarity with any of the VP1 sequences for example, Hu/GI.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; Figure 12A), Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; Figure 14A), Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; Figure 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; Figure 16A), Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; Figure 16B), Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14; Figure 17A), Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO: 15; Figure 18A),Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO: 16; Figure 19A), US96/GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27; Figure 19C), FH02/GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28; Figure 19D), Hnt04:GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29; Figure 19E),

2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30; Figure 19F), NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31; Figure 19G), Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; Figure 20), Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; Figure 21A), G11.7/Musa/2010/All73774 (GII7; SEQ ID NO:18; Figure 22), Hu/GII.12/HS206/2010/USA (GII.12; SEQ ID NO: 19; Figure 23A), GII.13/VA173/2010/H9AWU4 (SEQ ID NO:22; Figure 24A), GII.14_Saga_2008_JPN_ADE28701 native VP1 (SEQ ID NO: 32; Figure 25), Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO: 24; Figure 26A), Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; Figure 27), provided that the VP1 protein induces immunity to norovirus when administered to a subject. For example, the amino acid sequences described herein may have from about 30, 32, 34, 36, 38. 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or any amount therebetween, sequence similarity with any of the VP1 amino acid sequences defined above, provided that the VP1 protein induces immunity to norovirus when administered to a subject.

[00142] By "VP1 mutant protein", "mutant VP1 protein", "modified VP1 protein", "modified norovirus VP1 protein" and the like, it is meant, a norovirus VP1 protein comprising one or more than one substitution, mutation, or modification, at positions or amino acids in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1; see Table 1 below), or a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), or a combination thereof. The terms "residue", "residue amino acid" and "amino acid" are used interchangeably, and typically refer to an amino acid at a specified position (location) within an amino acid sequence.

2018375695 29 Nov 2024

[00143]

Table 1: Listing of Norovirus genotypes (strains) and equivalent amino acid locations of GI and GII strains.

Position (GI.1 numbering)	43	57	84	94
Genotype	AA in equivalent position			
GI.1	V43	I57	S84	L94
GI.2	V43	V57	Q84	S94
GI.3	A43	M57	Q84	S94
GI.5	L43	F57	Q84	A94
GI.7	V43	M57	R84	L94
GII.1	A39	R53	E80	A90
GII.2	A39	R53	E80	A90
GII.3	A39	M53	E80	A90
GII.4	A39	R53	P80	S90
GII.5	A39	R53	E80	A90
GII.6	A39	R53	E80	S90
GII.7	T39	R53	E80	A90
GII.12	A39	R53	E80	A90
GII.13	A39	R53	E80	A90
GII.14	A39	R53	E80	A90
GII.17	A39	R53	E80	A90
GII.21	A39	R53	E80	A90

[00144] As used herein, the term "conserved substitution" or "conservative substitution" refers to the presence of an amino acid residue in the sequence of the GII.4 VP1 protein that is different from, but it is in the same class of amino acid as the described substitution. For example, a nonpolar amino acid may be used to replace a nonpolar amino acid, an aromatic amino acid to replace an aromatic amino acid, a polar-uncharged amino acid to replace a polar-uncharged amino acid, and/or a charged amino acid to replace a charged amino acid). In addition, conservative substitutions can encompass an amino acid having an interfacial hydropathy value of the same sign and generally of similar magnitude as the amino acid that is replacing the corresponding wild type amino acid.

[00145] As used herein, the term "nonpolar amino acid" refers to glycine (G, Gly), alanine (A, Ala), valine (V, Val), leucine (L, Leu), isoleucine (I, Ile), and proline (P, Pro); the term "aromatic residue"(or aromatic amino acid) refers to phenylalanine (F, Phe), tyrosine (Y, Tyr), and tryptophan (W, Trp); the term "polar uncharged amino acid" refers to serine (S, Ser), threonine (T, Thr), cysteine (C, Cys), methionine (M, Met), asparagine (N, Asn) and glutamine (Q, Gln); the term "charged amino acid" refers to the negatively charged amino acids aspartic acid (D, Asp) and glutamic acid (E, Glu), as well as the positively charged amino acids lysine (K, Lys), arginine (R, Arg), and histidine (H, His). Other classification of amino acids may be as follows: amino acids with hydrophobic side chain (aliphatic): Alanine (A, Ala), Isoleucine (I, Ile), Leucine (L, Leu), Methionine (M, Met) and Valine (V, Val);amino acids with hydrophobic side chain (aromatic): Phenylalanine (F, Phe), Tryptophan (W, Trp), Tyrosine (Y, Tyr); amino acids with polar neutral side chain: Asparagine (N, Asn), Cysteine (C, Cys), Glutamine (Q, Gln), Serine (S, Ser) and Threonine (T, Thr); amino acids with electrically charged side chains (acidic): Aspartic acid (D, Asp), Glutamic acid (E, Glu);amino acids with electrically charged side chains (basic): Arginine (R, Arg); Histidine (H, His); Lysine (K, Lys), Glycine G, Gly) and Proline (P, Pro).

[00146] Conservative amino acid substitutions are likely to have a similar effect on the activity of the resultant modified GII.4 VP1 protein as the original substitution or modification. Further information about conservative substitutions can be found, for example, in Ben Bassat et al. (J. Bacteriol, 169:751-757, 1987), O'Regan et al. (Gene, 77:237-251, 1989), Sahin-Toth et al. (Protein ScL, 3:240-247, 1994), Hochuli et al (Bio/Technology, 6:1321-1325, 1988).

[00147] The Blosum matrices are commonly used for determining the relatedness of polypeptide sequences (Henikoff et al., Proc. Natl. Acad. Sci. USA, 89:10915-10919, 1992). A threshold of 90% identity was used for the highly conserved target frequencies of the BLOSUM90 matrix. A threshold of 65% identity was used for the BLOSUM65 matrix. Scores of zero and above in the Blosum matrices are considered "conservative substitutions" at the percentage identity selected. The following table shows examples of conservative amino acid substitutions: Table 2.

[00148] **Table 2. Exemplary conservative amino acid substitutions.**

Original Residue	Very Highly - Conserved Substitutions	Highly Conserved Substitutions (from the Blosum90 Matrix)	Conserved Substitutions (from the Blosum65 Matrix)
Ala	Ser	Gly, Ser, Thr	Cys, Gly, Ser, Thr, Val
Arg	Lys	Gln, His, Lys	Asn, Gln, Glu, His, Lys
Asn	Gln; His	Asp, Gln, His, Lys, Ser, Thr	Arg, Asp, Gln, Glu, His, Lys, Ser, Thr
Asp	Glu	Asn, Glu	Asn, Gln, Glu, Ser
Cys	Ser	None	Ala
Gln	Asn	Arg, Asn, Glu, His, Lys, Met	Arg, Asn, Asp, Glu, His, Lys, Met, Ser
Glu	Asp	Asp, Gln, Lys	Arg, Asn, Asp, Gln, His, Lys, Ser
Gly	Pro	Ala	Ala, Ser
His	Asn; Gln	Arg, Asn, Gln, Tyr	Arg, Asn, Gln, Glu, Tyr
Ile	Leu; Val	Leu, Met, Val	Leu, Met, Phe, Val
Leu	Ile; Val	Ile, Met, Phe, Val	Ile, Met, Phe, Val
Lys	Arg; Gln; Glu	Arg, Asn, Gln, Glu	Arg, Asn, Gln, Glu, Ser,
Met	Leu; Ile	Gln, Ile, Leu, Val	Gln, Ile, Leu, Phe, Val
Phe	Met; Leu; Tyr	Leu, Trp, Tyr	Ile, Leu, Met, Trp, Tyr
Ser	Thr	Ala, Asn, Thr	Ala, Asn, Asp, Gln, Glu, Gly, Lys, Thr
Thr	Ser	Ala, Asn, Ser	Ala, Asn, Ser, Val
Trp	Tyr	Phe, Tyr	Phe, Tyr
Tyr	Trp; Phe	His, Phe, Trp	His, Phe, Trp
Val	Ile; Leu	Ile, Leu, Met	Ala, Ile, Leu, Met, Thr

[00149] For the modifications described herein, the amino acids may be substituted using very high conserved substitutions, highly conserved substitutions or conserved substitutions as outlined in Table 2, as well as aromatic, polar, polar uncharged, polar neutral, or non-polar, negatively charged, positively charged, hydrophobic amino acids as described above.

[00150] As described herein, modified VP1 proteins comprising one or more than one substitutions of amino acids at amino acids 43, 57, 84 and 94 (in GI strains, equivalent to amino acids 39, 53, 80 and 90 in GII strains), resulted in an improved characteristic of the modified VP1 protein, or VLP produced using the modified VP1 protein. It is to be understood that the improved characteristic is not limited to substituting the specific amino acid at the specified sites, as one of skill in the art would understand that amino acids with similar properties may be substituted for the amino acids at the identified positions. For example, the modification Q84S, comprises substituting glutamine at position 84 with serine, an amino acid characterized as having a polar neutral side chain. The glutamine at this position may

also be substituted with an alternate amino acid characterized as having a polar neutral side chain, for example either asparagine, cysteine, or threonine, i.e. Q84X, where X=S, N, C or T. Similarly, E80S, comprising a substitution of glutamate at position 80 with serine, or P80S (a proline to serine substitution), in addition to substituting the native amino acid with serine, the amino acid at this position may also be substituted with an amino acid having a polar neutral side chain, for example asparagine, cysteine, or threonine, i.e. P80X, where X=S, N, C or T. Furthermore, as described herein additional P80X variants may be used to produce VP1, where X is selected from S, A, N, K or H. In the modifications S94L, S90L, A94L, or A90L, that comprise substituting serine or alanine with leucine (an amino acid characterized as having a hydrophobic side chain), the native amino acid may be substituted using an amino acid characterized as having a hydrophobic side chain, for example either isoleucine, methionine, valine, or in the case of S94X or S90X, an alanine, i.e. S94X (S90X), where X=L, I, M, V or A, or A94X (A90X), where X=L, I, M or V. Furthermore, as described herein additional S94X variants may be used to produce VP1, where X is selected from V, I, M, T, E, D, N, Q, K, or H. The modification A39V that comprises substituting an alanine with valine (an amino acid characterized as having a hydrophobic side chain) at position 39, in addition to valine, native amino acid may also be substituted with an amino acid characterized as having a hydrophobic side chain, for example, isoleucine, leucine, or methionine i.e. A39X, where X=V, I, L or M. Furthermore, as described herein additional A39X variants may be used to produce VP1, where X is selected from I, M, G, S, E, D, N, Q, K, or H. The modification V47P comprising a substitution of valine with proline, may also comprise a substitution of valine with a glycine, i.e. V47X, where X=P or G. The modification R53I that comprises substituting an arginine with isoleucine (an amino acid characterized as having a hydrophobic side chain) at position 53, in addition to isoleucine, arginine may also be substituted with an amino acid characterized as having a hydrophobic side chain, for example, leucine, valine, alanine or methionine i.e. R53X, where X=I, L, V, A or M. The modification M57I that comprises substituting a methionine with isoleucine (an amino acid characterized as having a hydrophobic side chain) at position 57, in addition to isoleucine, methionine may also be substituted with an amino acid characterized as having a hydrophobic side chain, for example, leucine, valine, or alanine i.e. M57X, where X=I, L, V or A.

Furthermore, as described herein additional M57X variants may be used to produce VP1, where X is selected from L, G, S, T, N, Q, K, or H.

[00151] Examples of VP1 mutant proteins (modified VP1 proteins) include, but are not limited to, the following.

- GI.3_Q84S VP1 (GI.3_ Q84X, where X=S, N, C or T VP1): wherein the glutamine corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GI.3_Q84S; SEQ ID NO:98, Figure 28A), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_Q84S VP1 protein. For example, the GI.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_Q84S VP1 protein (SEQ ID NO:98, Figure 28A), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the GI.3 Q84X VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.3 VP1 may be obtained from any GI.3 strain, for example, but not limited to GI.3/S29/2008/Lilla Edet/Sweden (SEQ ID NO:6 amino acid; SEQ ID NO:7, nucleotide; Figures 14A, 14B).

- GI.3_S94X VP1, where X=L, I, A, V, M, T, E, D, N, Q, K, or H, wherein the serine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GI.3_S94L; SEQ ID NO:8, Figure 28C), valine, isoleucine, methionine, threonine, aspartic acid, glutamic acid, glutamine lysine or histidine (GI.3_S94X, where X=V, I, M, T, E, D, N, Q, K, or H; SEQ ID NO:292, Figure 28M), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_S94X VP1 protein, where X=L, V, I, M, T, E, D, N, Q, K, or H. For example, the GI.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_S94X VP1 protein, where X=L, V, I, M, T, E, D, N, Q, K, or H VP1 protein (SEQ ID NO:8, Figure 28C, SEQ ID

NO:292; Figure 28M), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, V, I, M, T, E, D, N, Q, K, or H, for example leucine, valine, isoleucine, methionine, threonine, aspartic acid, glutamic acid, glutamine lysine or histidine, and provided that the GI.3 S94X VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.3 VP1 may be obtained from any GI.3 strain, for example, but not limited to GI.3/S29/2008/Lilla Edet/Sweden (SEQ ID NO:6 amino acid; SEQ ID NO:7, nucleotide; Figures 14A, 14B).

- GI.3_ A43X+S94x VP1, where X= V, L, I or M, and x= L, I, A, V, M, T, E, D, N, Q, K, or H, wherein the alanine and serine corresponding to amino acids 43 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been substituted or mutated, for example but not limited to, to valine and leucine, respectively (GI.3_A43V+S94L; SEQ ID NO:170, Figure 28G), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_ A43V+S94L VP1 protein. For example, the GI.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_A43V+S94L VP1 protein (SEQ ID NO:170, Figure 28G), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43 and 94 of norovirus VP1 genotype GI.1 remain a V, L, I or M, for example valine, and an L, I, A, V, M, T, E, D, N, Q, K, or H, for example leucine, respectively, and provided that the GI.3_A43X +S94x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.3 VP1 may be obtained from any GI.3 strain, for example, but not limited to GI.3/S29/2008/Lilla Edet/Sweden (SEQ ID NO:6, amino acid; SEQ ID NO:7, nucleotide; Figures 14A, 14B).

- GI.3_ M57X+S94x VP1, where X= I, V, A, L, G, S, T, N, Q, K, or H and x= L, I, A, V, M, T, E, D, N, Q, K, wherein the methionine and serine corresponding to amino acids 57 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to isoleucine and leucine, respectively (GI.3_M57I+S94L; SEQ ID NO:172, Figure 28I), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid

sequence of the GI.3_M57I+S94L VP1 protein. For example, the GI.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_M57I+S94L VP1 protein (SEQ ID NO:172, Figure 28I), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 57 and 94 of norovirus VP1 genotype GI.1 remain an I, V, A, L, G, S, T, N, Q, K, or H, for example isoleucine, and an L, I, A, V, M, T, E, D, N, Q, K, for example leucine, respectively, and provided that the GI.3_M57X+S94x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.3 VP1 may be obtained from any GI.3 strain, for example, but not limited to GI.3/S29/2008/Lilla Edet/Sweden (SEQ ID NO:6, amino acid; SEQ ID NO:7, nucleotide; Figures 14A, 14B).

- GI.3_Q84X+S94x, VP1, where X=S, N, C or T, and x= L, I, A, V, M, T, E, D, N, Q, K, or H, wherein the glutamine and serine corresponding to amino acids 84 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GI.3_Q84S+S94L; SEQ ID NO:10, Figure 28E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_ Q84S+S94L VP1 protein. For example, the GI.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_ Q84S+S94L VP1 protein (SEQ ID NO:10, Figure 28E), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine, and an L, I, A, V, M, T, E, D, N, Q, K, or H, for example leucine, respectively, and provided that the GI.3_Q84X+S94x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.3 VP1 may be obtained from any GI.3 strain, for example, but not limited to GI.3/S29/2008/Lilla Edet/Sweden (SEQ ID NO:6, amino acid; SEQ ID NO:7, nucleotide; Figures 14A, 14B).

- GI.3_ A43X+M57z+S94x VP1, where X= V, L, I or M, z= I, V, A, L, G, S, T, N, Q, K, or H, and x= L, I, A, V, M, T, E, D, N, Q, K, or H, wherein the alanine,

methionine and serine corresponding to amino acids 43, 57 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to valine, isoleucine and leucine, respectively (GI.3_A43V+M57I+S94L; SEQ ID NO:174, Figure 28K), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_ A43V+M57I+S94L VP1 protein. For example, the GI.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.3_A43V+M57I+S94L VP1 protein (SEQ ID NO:174, Figure 28K), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43, 57 and 94 of norovirus VP1 genotype GI.1 remain a V, L, I or M, for example valine, a I, V, A, L, G, S, T, N, Q, K, or H, for example isoleucine, and L, I, A, V, M, T, E, D, N, Q, K, or H, for example leucine, respectively, and provided that the GI.3_A43X+M57z+S94x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.3 VP1 may be obtained from any GI.3 strain, for example, but not limited to GI.3/S29/2008/Lilla Edet/Sweden (SEQ ID NO:6, amino acid; SEQ ID NO:7, nucleotide; Figures 14A, 14B).

- GI.5_Q84S VP1 (GI.5_ Q84X, where X=S, N, C or T, VP1): wherein the glutamine corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GI.5_Q84S; SEQ ID NO:34, Figure 29A), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.5_Q84S VP1 protein. For example, the GI.5 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.5_Q84S VP1 protein (SEQ ID NO:34, Figure 29A), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.5 VP1 may be obtained from any GI.5 strain, for example, but not limited to GI.5/Siklos/HUN5407/2013/HUN (SEQ ID NO:12, amino acid; Figure 15A).

- GI.5_A94L VP1 (GI.5_ A94X, where X=L, I, M or V, VP1): wherein the alanine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GI.5_A94L; SEQ ID NO:36, Figure 29C), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.5_A94L VP1 protein. For example, the GI.5 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.5_A94L VP1 protein (SEQ ID NO:36, Figure 29C), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M or V, for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.5 VP1 may be obtained from any GI.5 strain, for example, but not limited to GI.5/Siklos/HUN5407/2013/HUN (SEQ ID NO:12, amino acid; Figure 15A).

- GI.5_Q84S+A94L VP1 (GI.5_Q84X, where X=S, N, C or T + A94X, where X=L, I, M or V, VP1): wherein the glutamine and alanine corresponding to amino acids 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GI.5_Q84S+A94L; SEQ ID NO:38, Figure 29E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.5_Q84S+A94L VP1 protein. For example, the GI.5 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.5_Q84S+A94L VP1 protein (SEQ ID NO:38, Figure 29E), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.5 VP1 may be obtained from any GI.5 strain, for example, but not limited to GI.5/Siklos/HUN5407/2013/HUN (SEQ ID NO:12, amino acid; Figure 15A).

- GI.7_M57X VP1, where X=I, V, A, L, G, S, T, N, Q, K, or H, wherein the methionine corresponding to amino acid 57 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to isoleucine (GI.7_M57I; SEQ ID NO:179, Figure 29I), valine, alanine, leucine, glycine, serine, threonine, asparagine, glutamine, lysine or histidine (GI.7_M57X VP1, where X=I, V, A, L, G, S, T, N, Q, K, or H; SEQ ID NO: 290; Figure 29M), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.7_M57X VP1 protein, where X=I, V, A, L, G, S, T, N, Q, K, or H. For example, the GI.7 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.7_M57X VP1 protein, where X=I, V, A, L, G, S, T, N, Q, K, or H; (SEQ ID NO:179, Figure 29I; SEQ ID NO:290; Figure 29M), provided that the substitution, modification or mutation at the position corresponding to amino acid 57 of norovirus VP1 genotype GI.1 remains an I, V, A, L, G, S, T, N, Q, K, or H, for example isoleucine, valine, alanine, leucine, glycine, serine, threonine, asparagine, glutamine, lysine or histidine, and provided that the GI.7_M57X VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.7 VP1 may be obtained from any GI.7 strain, for example, but not limited to GI.7/GA5043/USA/2014 (SEQ ID NO:101, amino acid; Figure 16A).

- GI.7_R84S VP1 (GI.7_R84X, where X=S, N, C, or T, VP1): wherein the arginine corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GI.7_R84S; SEQ ID NO:177, Figure 29G), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.7_R84S VP1 protein. For example, the GI.7 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.7_R84S VP1 protein (SEQ ID NO:177, Figure 29G), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.7 VP1

may be obtained from any GI.7 strain, for example, but not limited to GI.7/GA5043/USA/2014 (SEQ ID NO:101, amino acid; Figure 16A).

- GI.7_M57X+R84x VP1, where X= L, I, A, V, M, T, E, D, N, Q, K, or H, and x=S, N, C, or T, wherein the methionine and arginine, corresponding to amino acids 57 and 84, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to isoleucine and serine, respectively (GI.7_M57I+R84S; SEQ ID NO:181, Figure 29K), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.7_M57I+R84S VP1 protein. For example, the GI.7 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GI.7_M57I+R84S VP1 protein (SEQ ID NO:181, Figure 29K), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 57 and 84 of norovirus VP1 genotype GI.1 remain an L, I, A, V, M, T, E, D, N, Q, K, or H, for example isoleucine, and an S, N, C or T, for example serine, respectively, and provided that the GI.7_M57X+R84x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GI.7 VP1 may be obtained from any GI.7 strain, for example, but not limited to GI.7/GA5043/USA/2014 (SEQ ID NO:101, amino acid; Figure 16A).

- GII.2_E80S VP1 (GII.2_ E80X, where X=S, N, C or T, VP1): wherein the glutamic acid corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GII.2_E80S; SEQ ID NO:85, Figure 30A), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_E80S VP1 protein. For example, the GII.2 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_E80S VP1 protein (SEQ ID NO:85, Figure 30A), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.2 VP1 may be obtained from any GII.2 strain, for example,

but not limited to Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14, amino acid; Figure 17A).

-GII.2_A90L VP1 (GII.2_A90X, where X=L, I, M or V, VP1): wherein alanine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GII.2_A90L; SEQ ID NO:41, Figure 30C), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the mut GII.2_A90L VP1 protein. For example, the GII.2 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_A90L VP1 protein (SEQ ID NO:41, Figure 30C), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M or V for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.2 VP1 may be obtained from any GII.2 strain, for example, but not limited to Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14, amino acid; Figure 17A).

-GII.2_E80S+A90L VP1 (GII.2_E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the glutamic acid and alanine corresponding to amino acids 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GII.2_E80S+A90L; SEQ ID NO:43, Figure 30E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the mut GII.2_E80S+A90L VP1 protein. For example, the GII.2 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_E80S+A90L VP1 protein (SEQ ID NO:43, Figure 30E), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine, and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.2 VP1 may be obtained from any GII.2

strain, for example, but not limited to Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14, amino acid; Figure 17A).

-GII.2_A39V+E80S+A90L VP1 (GII.2_A39X, where X=V, L. I or M + E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the alanine, glutamic acid and alanine corresponding to amino acids 43, 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to valine, serine and leucine, respectively (GII.2_A39V+E80S+A90L; SEQ ID NO:182, Figure 30G), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_A39V+E80S+A90L VP1 protein. For example, the GII.2 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_A39V+E80S+A90L VP1 protein (SEQ ID NO:182, Figure 30G), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43, 84 and 94 of norovirus VP1 genotype GI.1 remain a V, I, L or M, for example valine, an S, N, C or T, for example serine, and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.2 VP1 may be obtained from any GII.2 strain, for example, but not limited to Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14, amino acid; Figure 17A).

-GII.2 R53I+E80S+A90L VP1 (GII.2_R53X, where X=I, L, M, V or A + E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the arginine, glutamic acid and alanine corresponding to amino acids 57, 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to isoleucine, serine and leucine, respectively (GII.2_M53I+E80S+A90L; SEQ ID NO:184, Figure 30I), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_M53I+E80S+A90L VP1 protein. For example, the GII.2 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_M53I+E80S+A90L VP1 protein (SEQ ID NO:184, Figure 30I), provided that the substitutions, modifications or mutations at the positions corresponding to

amino acids 57, 84 and 94 of norovirus VP1 genotype GI.1 remain an I, L, M or A, for example isoleucine, an S, N, C or T, for example serine, and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.2 VP1 may be obtained from any GII.2 strain, for example, but not limited to Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14, amino acid; Figure 17A).

-GII.2 A39V+R53I+E80S+A90L VP1 (GII.2_A39X, where X=V, I, L or, M + R53X, where X=I, L, M, A or V + E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the glutamic acid and alanine corresponding to amino acids 43, 57, 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to valine, isoleucine, serine and leucine, respectively (GII.2_ A39V+R53I+E80S+A90L; SEQ ID NO:186, Figure 30K), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_ A39V+R53I+E80S+A90L VP1 protein. For example, the GII.2 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.2_A39V+R53I+E80S+ A90L VP1 protein (SEQ ID NO:186, Figure 30K), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 remain an V, I, L or M, for example valine, an I, L, M, A or V, for example isoleucine, an S, N, C or T, for example serine, and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.2 VP1 may be obtained from any GII.2 strain, for example, but not limited to Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14, amino acid; Figure 17A).

- GII.3_E80S VP1 (GII.3_E80X, where X=S, N, C or T, VP1): wherein the glutamic acid corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GII.3_E80S; SEQ ID NO:46, Figure 31A), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the mut GII.3_E80S VP1 protein. For example, the GII.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or

any amount therebetween, sequence similarity with the amino acid sequence of the GII.3_E80S VP1 protein (SEQ ID NO:46, Figure 31A), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.3 VP1 may be obtained from any GII.3 strain, for example, but not limited to GII.3/Jingzhou/2013402/CHN (SEQ ID NO:15, amino acid; Figure 18A).

- GII.3_A90L VP1 (GII.3_A90X, where X=L, I, M or V, VP1): wherein the alanine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GII.3_A90L; SEQ ID NO:48, Figure 31C), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.3_A90L VP1 protein. For example, the GII.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.3_A90L VP1 protein (SEQ ID NO:48, Figure 31C), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M or V, for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.3 VP1 may be obtained from any GII.3 strain, for example, but not limited to GII.3/Jingzhou/2013402/CHN (SEQ ID NO:15, amino acid; Figure 18A).

- GII.3_E80S+A90L VP1 (GII.3_E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the glutamic acid and alanine corresponding to amino acids 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GII.3_E80S+A90L; SEQ ID NO:50, Figure 31E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.3_ E80S+A90L VP1 protein. For example, the GII.3 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino

acid sequence of the GII.3_ E80S+A90L VP1 protein (SEQ ID NO:50, Figure 31E), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine, and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.3 VP1 may be obtained from any GII.3 strain, for example, but not limited to GII.3/Jingzhou/2013402/CHN (SEQ ID NO:15, amino acid; Figure 18A).

- GII.4_A39X VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, wherein the alanine corresponding to amino acid 43 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to valine (GII.4_A39V; SEQ ID NO:53, Figure 32A), isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, histidine, or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_A39X VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, VP1 protein. For example which is not to be considered limiting, the GII.4 VP1 protein may have from about 0, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_A39V VP1 protein (SEQ ID NO:53, Figure 32A), provided that the substitution, modification or mutation at the position corresponding to amino acid 43 of norovirus VP1 genotype GI.1 remains a V, I, L, M, G, S, E, D, N, Q, K, or H, for example valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine, and provided that the GII.4_A39X VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_V47P VP1 (GII.4_V47X, where X=P or G, VP1): wherein the valine corresponding to amino acid 51 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to proline (GII.4_V47P; SEQ ID NO:55, Figure 32C), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_V47P VP1 protein.

For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_V47P VP1 protein (SEQ ID NO:55, Figure 32C), provided that the substitution, modification or mutation at the position corresponding to amino acid 51 of norovirus VP1 genotype GI.1 remains a P or G, for example proline, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_R53I VP1 (GII.4_R53I, where X=I, L, V, A or M, VP1): wherein the arginine corresponding to amino acid 57 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to isoleucine (GII.4_R53I; SEQ ID NO:57, Figure 32E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_R53I VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_R53I VP1 protein (SEQ ID NO:57, Figure 32E), provided that the substitution, modification or mutation at the position corresponding to amino acid 57 of norovirus VP1 genotype GI.1 remains an I, L, V, A or M, for example isoleucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_P80X VP1, where X=S, N, C, T, A, K, or H, wherein the proline corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GII.4_P80S; SEQ ID NO:59, Figure 32G), asparagine, cysteine, threonine, alanine, lysine, histidine, or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_P80S VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96,

97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_P80S VP1 protein (SEQ ID NO:59, Figure 32G), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, and provided that the GII.4_P80X VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_S90L VP1 (GII.4_S90X, where X=L, I, M, A or V, VP1): wherein the serine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GII.4_S90L; SEQ ID NO:61, Figure 32I), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_S90L VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_S90L VP1 protein (SEQ ID NO:61, Figure 32I), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M, A or V, for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_Δ35-42 VP1: wherein the amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been deleted (GII.4_Δ35-42; SEQ ID NO:63, Figure 32K), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ Δ35-42 VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the

GII.4_ Δ35-42 VP1 protein (SEQ ID NO:63, Figure 32K), provided that the amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) remain deleted, and that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_SSTAVATA VP1: wherein the amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated to the peptide sequence SSTAVATA (SEQ ID NO:168; GII.4_SSTAVATA; SEQ ID NO:65, Figure 32M), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the mut GII.4_ SSTAVATA VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ SSTAVATA VP1 protein (SEQ ID NO:65, Figure 32M), provided that the positions corresponding to amino acids 39-46 of norovirus VP1 genotype GI.1 remain the peptide sequence SSTAVATA, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_A39X+R53x VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, and x=I, L, M, A or V, wherein the alanine and arginine corresponding to amino acids 43 and 57, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine or histidine and isoleucine, respectively (e.g. GII.4_A39V+R53I; SEQ ID NO:188, Figure 32AA), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_A39V+R53I VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence

similarity with the amino acid sequence of the GII.4_A39V+R53I VP1 protein (SEQ ID NO:188, Figure 32AA), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43 and 57 of norovirus VP1 genotype GI.1 remain a V, I, L, M, G, S, E, D, N, Q, K, or H, for example valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine or histidine, and an I, L, M, V or A, for example isoleucine, respectively, and provided that the GII.4_A39X+R53x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_A39X+P80x VP1, where X= V, I, L, M, G, S, E, D, N, Q, K, or H, and x= S, N, C, T, A, K, or H, VP1): wherein the alanine and proline corresponding to amino acids 43 and 84, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been substituted or mutated, for example but not limited to, to valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine, and serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively (e.g. GII.4_A39V+P80S; SEQ ID NO:67, Figure 32O), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_A39X+P80x VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ A39V+P80S VP1 protein (SEQ ID NO:67, Figure 32O), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43 and 84 of norovirus VP1 genotype GI.1 remain a V, I, L, M, G, S, E, D, N, Q, K, or H, for example valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine, and an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively, and provided that the GII.4_A39X+P80x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to

GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_V47P+P80S VP1 (GII.4_V47X, where X=P or G + P80x, where x= S, N, C, T, A, K, or H VP1): wherein the valine and proline corresponding to amino acids 51 and 84, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been substituted or mutated, for example, to proline and serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively (e.g. GII.4_V47P+P80S; SEQ ID NO:69, Figure 32Q), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_V47P+P80S VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_V47P+P80S VP1 protein (SEQ ID NO:69, Figure 32Q), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 51 and 84 of norovirus VP1 genotype GI.1 remain a P or G, for example proline, and an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively, and provided that the GII.4_V47X+P80x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/(SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_R53I+P80S VP1 (GII.4_R53X, where X=I, L, V, A or M + P80x, where x= S, N, C, T, A, K, or H, VP1): wherein the arginine and proline corresponding to amino acids 57 and 84, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to an isoleucine and a serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively (e.g. GII.4_R53I+P80S; SEQ ID NO:71, Figure 32S), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_R53I+P80S VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_R53I+P80S VP1 protein (SEQ ID NO:71, Figure 32S), provided that the

substitution, modification or mutation at the position corresponding to amino acids 57 and 84 of norovirus VP1 genotype GI.1 remain an I, L, V, A or M, for example isoleucine, and an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, histidine, respectively, and provided that the GII.4_R53X+P80x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_P80S+S90L VP1 (GII.4_P80X, where X= S, N, C, T, A, K, or H + S90x, where x=L, I, M, A or V, VP1): wherein the proline and serine corresponding to amino acids 84 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, and leucine, respectively (e.g. GII.4_P80S+S90L; SEQ ID NO:73, Figure 32U), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ P80S+S90L VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ P80S+S90L VP1 protein (SEQ ID NO:73, Figure 32U), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, or histidine and an L, I, M, A or V, for example leucine, respectively, and provided that the GII.4_P80X+S90x VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_A39X+R53x+P80z VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, where x=I, L, M, A or V, and z= S, N, C, T, A, K, or H, wherein the alanine and arginine corresponding to amino acids 43, 57 and 84, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been substituted or mutated, for example, at position 39, to valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid,

glutamic acid, asparagine, glutamine, lysine, or histidine, at portion 53 to isoleucine, and at position 80 to serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively (e.g. GII.4_A39V+R53I+P80S; SEQ ID NO:190, Figure 32CC), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ A39V+R53I+P80S VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ A39V+R53I+P80S VP1 protein (SEQ ID NO:190, Figure 32CC), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 43, 57 and 84 of norovirus VP1 genotype GI.1 remain a V, I, L, M, G, S, E, D, N, Q, K, or H, for example valine, isoleucine, leucine, methionine, glycine, serine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine, an I, L, M, V or A, for example isoleucine, and an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, respectively, and provided that the GII.4_A39X+R53x+P80z VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/ AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_P80S+Δ35-42 VP1 (GII.4_P80X, where X= S, N, C, T, A, K, or H, +Δ35-42, VP1): wherein the proline corresponding to position 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, and the amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1 have been deleted (GII.4_P80S+Δ35-42; SEQ ID NO:75, Figure 32W), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_P80S+Δ35-42 VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_P80S+Δ35-42 VP1 protein (SEQ ID NO:75, Figure 32W), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus genotype GI.1 remains an S, N, C, T, A, K, or H, for example serine,

asparagine, cysteine, threonine, alanine, lysine, or histidine, and the amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1 remain deleted, and that the GII.4_P80X+Δ35-42 VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.4_P80S+SSTAVATA VP1 (GII.4_P80X, where X= S, N, C, T, A, K, or H + SSTAVATA, VP1): wherein the proline corresponding to position 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, and the amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1 have been mutated to the peptide sequence SSTAVATA (SEQ ID NO:168; GII.4_P80S+SSTAVATA; SEQ ID NO:77, Figure 32Y), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the mut GII.4_ P80S+SSTAVATA VP1 protein. For example, the GII.4 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.4_ P80S+SSTAVATA VP1 protein (SEQ ID NO:77, Figure 32Y), provided that the position corresponding to amino acid 84 or norovirus VP1 genotype GI.1 remains an S, N, C, T, A, K, or H, for example serine, asparagine, cysteine, threonine, alanine, lysine, or histidine, and the positions corresponding to amino acids 39-46 of norovirus VP1 genotype GI.1 remain the peptide sequence SSTAVATA, and that the GII.4_P80X+SSTAVATA VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.4 VP1 may be obtained from any GII.4 strain, for example, but not limited to GII.4/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; Figures 19A and 19B).

- GII.6_E80S VP1 (GII.6_E80X, where X=S, N, C or T, VP1): wherein the glutamic acid corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GII.6_E80S; SEQ ID NO:79, Figure 33A), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.6_E80S

VP1 protein. For example, the GII.6 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.6_E80S VP1 protein (SEQ ID NO:79, Figure 33A), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.6 VP1 may be obtained from any GII.6 strain, for example, but not limited to GII.6/Ohio/490/2012/USA (SEQ ID NO:20, amino acid; SEQ ID NO:21, nucleotide; Figures 21A and 21B).

- GII.6_S90L VP1 (GII.6_S90X, where X=L, I, M, A or V, VP1): wherein the serine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GII.6_S90L; SEQ ID NO:81, Figure 33C), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.6_S90L VP1 protein. For example, the GII.6 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.6_S90L VP1 protein (SEQ ID NO:81, Figure 33C), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M or V, for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.6 VP1 may be obtained from any GII.6 strain, for example, but not limited to GII.6/Ohio/490/2012/USA (SEQ ID NO:20, amino acid; SEQ ID NO:21, nucleotide; Figures 21A and 21B).

- GII.6_E80S+S90L VP1 (GII.6_E80X, where X=S, N, C or T + S90X, where X=L, I, M, A or V, VP1): wherein the glutamic acid and serine corresponding to amino acids 84 and 94, respectively of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GII.6_E80S+S90L; SEQ ID NO:83, Figure 33E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.6_ E80S+S90L VP1 protein. For example, the GII.6 VP1 protein

may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.6_ E80S+S90L VP1 protein (SEQ ID NO:83, Figure 33E), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine, and an L, I, M, A or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.6 VP1 may be obtained from any GII.6 strain, for example, but not limited to GII.6/Ohio/490/2012/USA (SEQ ID NO:20, amino acid; SEQ ID NO:21, nucleotide; Figures 21A and 21B).

- GII.12_E80S VP1 (GII.12_E80X, where X=S, N, C or T, VP1): wherein the glutamic acid corresponding to amino acid 84 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to serine (GII.12_E80S; SEQ ID NO:88, Figure 34A), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.12_E80S VP1 protein. For example, the GII.12 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.12_E80S VP1 protein (SEQ ID NO:88, Figure 34A), provided that the substitution, modification or mutation at the position corresponding to amino acid 84 of norovirus VP1 genotype GI.1 remains an S, N, C or T, for example serine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.12 VP1 may be obtained from any GII.12 strain, for example, but not limited to GII.12/HS206/2010/USA (SEQ ID NO:19, amino acid; Figures 23A).

- GII.12_A90L VP1 (GII.12_A90X, where X=L, I, M or V, VP1): wherein the alanine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GII.12_A90L; SEQ ID NO:90, Figure 34C), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.12_A90L VP1 protein. For example, the GII.12 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount

therebetween, sequence similarity with the amino acid sequence of the GII.12_A90L VP1 protein (SEQ ID NO:90, Figure 34C), provided that the substitution, modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M or V, for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.12 VP1 may be obtained from any GII.12 strain, for example, but not limited to GII.12/HS206/2010/USA (SEQ ID NO:19, amino acid; Figures 23A).

- GII.12_E80S+A90L VP1 (GII.12_E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the glutamic acid and alanine corresponding to amino acids 84 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GII.12_E80S+A90L; SEQ ID NO:92, Figure 34E), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.12_ E80S+A90L VP1 protein. For example, the GII.12 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.12_ E80S+A90L VP1 protein (SEQ ID NO:92, Figure 34E), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine, and an L, I. M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.12 VP1 may be obtained from any GII.12 strain, for example, but not limited to GII.12/HS206/2010/USA (SEQ ID NO:19, amino acid; Figures 23A).

- GII.17_A39V VP1 (GII.17_A39X, where X=V, I, L or M, VP1): wherein the alanine corresponding to amino acid 43 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to valine (GII.17_A39V; SEQ ID NO:192, Figure 34G), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_A39V VP1 protein. For example, the GII.17 VP1 protein may have from about 0, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount

therebetween, sequence similarity with the amino acid sequence of the GII.17_A39V VP1 protein (SEQ ID NO:192, Figure 34G), provided that the substitution, modification or mutation at the position corresponding to amino acid 43 of norovirus VP1 genotype GI.1 remains a V, I, L or M, for example valine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.17 VP1 may be obtained from any GII.17 strain, for example, but not limited to Hu/GII.17/Kawasaki323/2014/JP (SEQ ID NO:24, amino acid; SEQ ID NO:25, nucleotide; Figures 26A and 26B).

- GII.17 R53I VP1 (GII.17_R53I, where X=I, L, V, A or M, VP1): wherein the arginine corresponding to amino acid 57 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to isoleucine (GII.17_R53I; SEQ ID NO:194, Figure 34I), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_R53I VP1 protein. For example, the GII.17 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_R53I VP1 protein (SEQ ID NO:194, Figure 34I), provided that the substitution, modification or mutation at the position corresponding to amino acid 57 of norovirus VP1 genotype GI.1 remains an I, L, V, A or M, for example isoleucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.17 VP1 may be obtained from any GII.17 strain, for example, but not limited to Hu/GII.17/Kawasaki323/2014/JP (SEQ ID NO:24, amino acid; SEQ ID NO:25, nucleotide; Figures 26A and 26B).

- GII.17_A90L VP1 (GII.4_A90X, where X=L, I, M or V, VP1): wherein the serine corresponding to amino acid 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1) has been mutated, for example, to leucine (GII.17_A90L; SEQ ID NO:196, Figure 34K), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_A90L VP1 protein. For example, the GII.17 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_A90L VP1 protein (SEQ ID NO:196, Figure 34K), provided that the substitution,

modification or mutation at the position corresponding to amino acid 94 of norovirus VP1 genotype GI.1 remains an L, I, M or V, for example leucine, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.17 VP1 may be obtained from any GII.17 strain, for example, but not limited to Hu/GII.17/Kawasaki323/2014/JP (SEQ ID NO:24, amino acid; SEQ ID NO:25, nucleotide; Figures 26A and 26B).

- GII.17_A39V+R53I VP1 (GII.17_A39X, where X=V, I, L or M + R53X, where X=I, L, M, A or V, VP1): wherein the alanine and arginine corresponding to amino acids 43 and 57, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to valine and isoleucine, respectively (GII.17_A39V+R53I; SEQ ID NO:198, Figure 34M), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_A39V+R53I VP1 protein. For example, the GII.17 VP1 protein may have from about 0, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_A39V+R53I VP1 protein (SEQ ID NO:198, Figure 34M), provided that the substitutions, modifications or mutations at the positions corresponding to amino acid 43 and 57 of norovirus VP1 genotype GI.1 remain a V, I, L or M, for example valine, and an I, L, M, V or A, for example isoleucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.17 VP1 may be obtained from any GII.17 strain, for example, but not limited to Hu/GII.17/Kawasaki323/2014/JP (SEQ ID NO:24, amino acid; SEQ ID NO:25, nucleotide; Figures 26A and 26B).

- GII.17_E80S+A90L VP1 (GII.4_E80X, where X=S, N, C or T + A90X, where X=L, I, M or V, VP1): wherein the glutamic acid and alanine corresponding to amino acids 84 and 94, respectively, of norovirus VP1 genotype GI.1 (SEQ ID NO:1) have been mutated, for example, to serine and leucine, respectively (GII.17_E80S+A90L; SEQ ID NO:200, Figure 34O), or a sequence that exhibits from about 80-100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_ E80S+A90L VP1 protein. For example, the GII.17 VP1 protein may have from about 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94,

95, 96, 97, 98, 99, 100% or any amount therebetween, sequence similarity with the amino acid sequence of the GII.17_ E80S+A90L VP1 protein (SEQ ID NO:200, Figure 34O), provided that the substitutions, modifications or mutations at the positions corresponding to amino acids 84 and 94 of norovirus VP1 genotype GI.1 remain an S, N, C or T, for example serine, and an L, I, M or V, for example leucine, respectively, and provided that the VP1 protein induces immunity to norovirus when administered to a subject. The sequence encoding the GII.17 VP1 may be obtained from any GII.17 strain, for example, but not limited to Hu/GII.17/Kawasaki323/2014/JP (SEQ ID NO:24, amino acid; SEQ ID NO:25, nucleotide; Figures 26A and 26B).

VLP yield

[00152] An example of an improved characteristic of VP1 may be observed comparing the yields of VLPs comprising GI.3 VP1 protein is shown with reference to Figure 5B (see Example 3). Expression of modified norovirus VP1 proteins GI.3_S94X, where X=L, V, I, M, T, E, D, N, Q, K, or H (see Figure 5F), GI.3_M57I+S94L (see Figure 5D), and GI.3_Q84S+S94L (see Figure 5B) in plants resulted in similar or higher VLPs yields as compared to the yield of wildtype GI.3 VP1. Furthermore, expression of modified norovirus VP1 proteins GI.7_M57X, where X=I, L, G, S, T, N, Q, K, or H (see Figure 6F) in plants resulted in similar or higher VLPs yields as compared to the yield of wildtype GI.7 VP1.

[00153] An analogous improved characteristic of increased VLP yield is shown with reference to Figures 9A-9E, and 9H. VLPs comprising norovirus modified VP1 proteins GII.4_R53I (Figure 9D), GII.4_P80X, where X=S, A, N, K, or H (Figures 9B and 9H), GII.4_ P80S +R53I (Figure 9D), GII.4_ P80S +A39X, where X=V, I, M, T, E, D, N, Q, K, or H (Figures 9C and 9I), GII.4_P80S+S90L (Figure 9B), GII.4_P80S+Δ35-42 (Figure 9C), GII.4_ P80S +SSTAVATA (Figure 9F), and GII.4_A39V+R53I_P80S (Figure 9G), exhibited enhanced VLP yield in plants, while GII.4_ A39V and GII.4_ V47P exhibited a slight increase in protein yield, as compared to VLPs comprising wildtype GII.4 VP1.

[00154] Increased VLP yield, compared to wild type was also observed in plant extracts expressing GII.6_S90L VP1 (Figures 10A and 10B).

[00155] VLPs comprising modified VP1 protein with a substitution of an amino acid at position 84 (GI strains) or position 80 (GII strains, corresponding to, or in alignment with, position 84 of GI.1 VP1) exhibited the same (GI.3_Q84S; GI.5_Q84S, also see Figure 6B; GII.3_E80S, also see Figure 8A), or an increased (GI.7_R84S; GI.7_M57I+R84S; also see Figure 6D; GII.4_P80S also see Figures 9B-9F; GII.12_E80S) VLP yield when compared to the yield of VLPs comprising the corresponding wild type (native) VP1 protein.

[00156] VLPs comprising modified VP1 protein with a substitution of an amino acid at position 94(GI strains) or at position 90 (GII strains, corresponding to, or in alignment with, position 94 of GI.1 VP1) exhibited the same or an increase in VLP yield when compared to the yield of VLPs comprising the corresponding wild type, or native, VP1 protein, for all modified VP1 proteins that were examined (GI.3_S94X, where X=L, V, I, M, T, E, D, N, Q, K, or H (Figures 5B and 5F); GI.5_A94L (see Figure 6B); GII.2_A90L (see Figure 7B); GII.4_S90L (see Figure 9B); GII.6_S90L (see Figure 10A); GII.12_A90L (see Figure 11B); and GII.17_A90L (see Figure11D).

[00157] Similarly, VLPs comprising modified VP1 protein with a substitution of an amino acid at positions 84 and 94 (GI strains) or positions 80 and 90 (GII strains, corresponding to, or in alignment with, position 84 and 94 of GI.1 VP1) exhibited an increase in VLP yield when compared to the yield of VLPs comprising the corresponding wild type, or native, VP1 protein, for all modified VP1 proteins that were examined (GI.3_Q84S+S94L, also see Figure 5B; GI.5_Q84S+A94L, also see Figure 6B; GII.2_E80S+A90L, also see Figures 7B and 7C; GII.4_P80S+S90L, also see Figure 9B; and GII.12_E80S+A90L, also see Figure; 11B).

[00158] Additional modifications were also observed to increase VLP yield. These modifications include GI.3_M57I+S94L (Figure 5D), GI.7_M57I (Figure 6D), GI.7_M57I+R84S (Figure 6D), GII.2_A39V+E80S+A90L (Figure 7C), GII.2_R53I+E80S+A90L (Figure 7C), GII.4_R53I (Figure 9D), GII.4_A39V +P80X, where X=S, A, N, K, or H (Figures 9C and 9I); GII.4_R53I+ P80S (Figure 9D);

GII.4_V47P+ P80S (Figure 9E); GII.4_Δ35-42+ P80S (Figure 9C), and GII.4_A39V+R53I+P80S (Figure 9G).

Size, density, stability and quality of VLPs

[00159] As shown in Figure 5B, mutant norovirus VP1 proteins GI.3_S94L and GI.3_Q84S+S94L, exhibited the improved characteristic of VLPs having greater densities (determined by Coomassie stained SDS PAGE of iodixanol density gradient fractions of protein extracts), so that the VLPs are observed in fraction 1 (F1) and peaking in fractions F2-F6 as compared to wildtype norovirus GI.3 VP1. These results indicate that the assembly of native GI.3 VLPs may be less stable than GI.3_S94L VLPs and the native GI.3 VLP may be more susceptible to malformed capsid particles and the generation of fragmentation products. As a result, the VLPs comprising GI.3_S94L VP1, GI.3_M57I+S94L and GI.3_Q84S+S94L VP1 exhibit greater structural integrity than wildtype GI.3 VP1. It is also observed that VLPs comprising GI.3_S94L VP1, GI.3_M57I+S94L and GI.3_Q84S+S94L VP1 comprise a greater relative proportion of 38 nm diameter VLPs vs. 23nm diameter VLPs than wildtype (Figures 5C and 5E) as determined using transmission electron micrography (TEM).

[00160] VLPs comprising of GI.5_Q84S VP1, GI.5_A94L VP1, or GI.5_Q84S+A94L VP1 proteins exhibited an increase in yield, and GI.5_Q84S+A94L VP1 also exhibited greater density, stability and structural integrity (in a manner similar to that described above for VLPs produced using modified GI.3 VP1), as compared to wildtype norovirus GI.5 VP1 (Figure 6B). As shown in Figure 6C, the resulting VLPs had fewer damaged VLP particles, and a greater relative proportion of 38 nm diameter particles vs 23 nm diameter VLPs, as compared to wildtype.

[00161] VLPs comprising of GI.7_R84S, GI.7_M57I, GI.7_M57I+R84S VP1 proteins were also observed to exhibit the same or greater density as compared to wildtype norovirus GI.7 VP1 (Figure 6D). As shown in Figure 6E, the modified VLPs had fewer damaged VLP particles, and a greater relative proportion of 38 nm diameter particles vs 23 nm diameter VLPs, as compared to wildtype.

[00162] VLPs comprising of GII.2_E80S+A90L, GII.2_A39V+E80S+A90L VP1 proteins exhibited greater density, stability and structural integrity (in a manner similar to that described above) as compared to wildtype norovirus GII.2 VP1 (Figure 7C). As shown in Figure 7C, the modified VLPs had fewer damaged VLP particles, and a greater relative proportion of 38 nm diameter particles vs 23 nm diameter VLPs, as compared to wildtype.

[00163] Expression of GII.3_E80S in plants, resulted in VLPs of 38 nm diameter particles (Figure 8B). However, yields of VP1 protein (determined via SDS-PAGE) remained low.

[00164] As shown in Figures 9B, 9C, 9D and 9G, modified VP1 proteins, GII.4_A39V, GII.4_V47P, GII.4_R53I, GII.4_P80S, GII.4_S90L, GII.4_A39V+P80S, GII.4_R53I+P80S, GII.4_P80S+S90L, GII.4_P80S+Δ35-42 and GII.4_A39V+R53I+P80S all exhibited VLPs having greater densities, stability, and structural integrity than VLPs comprising wildtype GII.4 VP1 protein. Further, the VLPs comprising GII.4_A39V+P80S, GII.4_R53I+P80S, GII.4_P80S+S90L, GII.4_P80S+Δ35-42, and GII.4_A39V+R53I+P80S all had improved viral capsid integrity and fewer damaged particles as seen by TEM (Figures 9B, 9C, 9D and 9E). VLPs comprising GII.4_A39V+P80S and GII.4_P80S+Δ35-42 were also observed to have a greater proportion of 38 nm diameter particles vs 23 nm diameter particles as compared to wildtype GII.4 VLPs (Figures 9B and 9C). VLPs were also produced from GII.4_V47P; GII.4_V47P+P80S, GII.4_SSTAVATA; GII.4_P80S+SSTAVATA (Figures 9E and 9F).

[00165] As shown in Figures 10A and 10B, expression of modified norovirus VP1 protein GII.6_S90L produced 38 nm diameter VLPs, determined using transmission electron micrography (TEM).

[00166] VLPs comprising GII.12_E80S, GII.12_A90L and GII.12_E80S+A90L, also exhibited the improved characteristic of having a greater density of 38 nm diameter VLPs than VLPs comprising wildtype GII.12 VP1 (Figure 11C) as determined using transmission electron micrography (TEM).

[00167] VLPs comprising GII.17_A39V, GII.17_A90L, and GII.17_R53I, also exhibited the improved characteristic of having a greater density of 38 nm diameter VLPs than VLPs comprising wildtype GII.17 VP1 (Figure 11D) as determined using transmission electron micrography (TEM).

Induction of Immunity Against Norovirus Infection

[00168] An "immune response" generally refers to a response of the adaptive immune system of a subject. The adaptive immune system generally comprises a humoral response, and a cell-mediated response. The humoral response is the aspect of immunity that is mediated by secreted antibodies, produced in the cells of the B lymphocyte lineage (B cell). Secreted antibodies bind to antigens on the surfaces of invading microbes (such as viruses or bacteria), which flags them for destruction. Humoral immunity is used generally to refer to antibody production and the processes that accompany it, as well as the effector functions of antibodies, including Th2 cell activation and cytokine production, memory cell generation, opsonin promotion of phagocytosis, pathogen elimination and the like. The terms "modulate" or "modulation" or the like refer to an increase or decrease in a particular response or parameter, as determined by any of several assays generally known or used, some of which are exemplified herein.

[00169] A cell-mediated response is an immune response that does not involve antibodies but rather involves the activation of macrophages, natural killer cells (NK), antigen-specific cytotoxic T-lymphocytes, and the release of various cytokines in response to an antigen. Cell-mediated immunity is used generally to refer to some Th cell activation, Tc cell activation and T-cell mediated responses. Cell mediated immunity may be of particular importance in responding to viral infections.

[00170] For example, the induction of antigen specific CD8 positive T lymphocytes may be measured using an ELISPOT assay; stimulation of CD4 positive T-lymphocytes may be measured using a proliferation assay. Anti-norovirus antibody titres may be quantified using an ELISA assay; isotypes of antigen-specific or cross reactive antibodies may also be measured using anti-isotype antibodies (e.g. anti -IgG,

IgA, IgE or IgM). Methods and techniques for performing such assays are well-known in the art.

[00171] Cytokine presence or levels may also be quantified. For example a T-helper cell response (Th1/Th2) will be characterized by the measurement of IFN-γ and IL-4 secreting cells using by ELISA (e.g. BD Biosciences OptEIA kits). Peripheral blood mononuclear cells (PBMC) or splenocytes obtained from a subject may be cultured, and the supernatant analyzed. T lymphocytes may also be quantified by fluorescence-activated cell sorting (FACS), using marker specific fluorescent labels and methods as are known in the art.

[00172] A microneutralization assay may also be conducted to characterize an immune response in a subject, see for example the methods of Rowe *et al.*, 1973. Virus neutralization titers may be quantified in a number of ways, including: enumeration of lysis plaques (plaque assay) following crystal violent fixation/coloration of cells; microscopic observation of cell lysis in *in vitro* culture; and 2) ELISA and spectrophotometric detection of norovirus.

[00173] The term "epitope" or "epitopes", as used herein, refers to a structural part of an antigen to which an antibody specifically binds.

[00174] Immune response to plant produced wild type Norovirus native GI.1 (SEQ ID NO:1) VLP administration were performed using BALB/c mice (Example 4). Plant-produced modified VP1 proteins, or VLPs comprising modified VP1 proteins, for example, produced using GI.3_Q84S (construct 4140; SEQ ID NO:167), GI.3_S94L (construct 4141; SEQ ID NO:9), GI.3_A43V+S94L (construct 4179; SEQID NO:169), GI.3_M57I+S94L (construct 4180; SEQ ID NO:171), GI.3_P84S+S94L (construct 4142; SEQ ID NO:11), GI.3_A43V+M57I+S94L (construct 4181; SEQ ID NO:173), GI.5_Q84S (construct 4130; SEQ ID NO:35), GI.5_ A94L (construct 4131; SEQ ID NO:37), GI.5_Q84S+A94L (construct 4132; SEQ ID NO:39), GI.7_R84S (construct 4210; SEQ ID NO:176), GI.7_M57I (construct 4217; SEQ ID NO:178), GI.7_M57I+R84S (construct 4218; SEQ ID NO:180), GII.2_E80S (construct 4143; SEQ ID NO:86), GII.2_A90L (construct 4144; SEQ ID NO:42), GII.2_Q80S+A90L (construct 4145; SEQ ID NO:44),

GII.2_A39V+Q80S+A90L (construct 4182; SEQ ID NO:183), GII.2_R53I+Q80S+A90L (construct 4183; SEQ ID NO:185), GII.2_A39V+R53I+Q80S+A90L (construct 4184; SEQ ID NO:187), GII.3_E80S (construct 4146; SEQ ID NO:47), GII.3_A90L (construct 4147; SEQ ID NO:49), GII.3_E80S+A90L (construct 4148; SEQ ID NO:51), GII.4_A39V (construct 4155; SEQ ID NO:54), GII.4_V47P (construct 4156; SEQ ID NO:56), GII.4_R53I (construct 4157; SEQ ID NO:58), GII.4_P80S (construct 4133; SEQ ID NO:60), GII.4_S90L (construct 4134; SEQ ID NO:62), GII.4_ Δ35-42 (construct 4158; SEQ ID NO:64), GII.4_SSTAVATA (construct 4159; SEQ ID NO:66). GII.4_A39V+R53I (construct 4185; SEQ ID NO:189), GII.4_A39V+P80S (construct 4165; SEQ ID NO:68), GII.4_V47P+P80S (construct 4166; SEQ ID NO:70), GII.4_R53I+P80S (construct 4167; SEQ ID NO:72), GII.4_P80S+S90L (construct 4135; SEQ ID NO:74), GII.4_ Δ35-42+ P80S (construct 4168; SEQ ID NO:76), GII.4_P80S+SSTAVATA (construct 4169; SEQ ID NO:78), GII.4_A39V+R53I+P80S (construct 4186; SEQ ID NO:191), GII.6_E80S (construct 4149; SEQ ID NO:80), GII.6_S90L (construct 4150; SEQ ID NO:82), GII.6_E80S+S90L (construct 4151; SEQ ID NO:84), GII.12_E80S (construct 4136; SEQ ID NO:89), GII.12_A90L (construct 4137; SEQ ID NO:91), GII.12_E80S+A90L (construct 4138; SEQ ID NO:93), GII.17_A39V (construct 4234; SEQ ID NO:193), GII.17_R53I (construct 4235; SEQ ID NO:195), GII.17_A90L (construct 4232; SEQ ID NO:197), GII.17_A39V+R53I (construct 4236; SEQ ID NO:199), GII.17_E80S+A90L (construct 4233; SEQ ID NO:201), or a combination thereof, may also administered to mice. Serum samples from blood collected from animals were analyzed by ELISA for GI.1 VLP-specific total IgG and IgA antibodies using GI.1 VLP-coated plates. With reference to Figure 3D, mice immunized with plant norovirus native VP1 VLPs from GI.1 genotype exhibit GI.1 VLP-specific IgG antibody titers in sera for each treatment group. The IgG titer levels induced by each treatment were statistically higher than the titers quantified for the placebo group ($p < 0.05$). IgG titer level increased in a dose-dependent manner (significant difference detected between the 1 μg and 10 μg treatments formulated with or without Alhydrogel; $p < 0.05$). A significant increase of IgG titer level was also detected for each treatment group between Days 21 and 42 ($p < 0.05$). These results collectively

demonstrate the ability of plant produced Norovirus native VP1 VLPs to elicit a robust immune response in mice.

[00175] Therefore, there is provided herein a method of producing an antibody or antibody fragment comprising, administering a modified norovirus VP1 protein, or a norovirus VLP comprising one or more than one modified VP1 protein to a subject, or a host animal, thereby producing the antibody or the antibody fragment. The modified norovirus VP1 protein (either a GI VP1 protein or GII VP1 protein), comprising one or more than one substitution, modification or mutation at: an amino acid residue selected from positions in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1); a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1); amino acids corresponding to amino acid residues 39-46 of norovirus VP1 genotype GI.1 are mutated to the sequence SSTAVATA, or a combination thereof, and the nucleotide sequence is not derived from a genotype GI.1 norovirus VP1. The VLP may further comprise a norovirus VP2 protein.

[00176] There is also provided a composition for inducing an immune response comprising, an effective dose of the VLP comprising the modified norovirus VP1 protein, and a pharmaceutically acceptable carrier, adjuvant, vehicle or excipient.

Plant expression

[00177] The constructs of the present invention can be introduced into plant cells using Ti plasmids, Ri plasmids, plant virus vectors, direct DNA transformation, micro-injection, electroporation, etc. For reviews of such techniques see for example Weissbach and Weissbach, *Methods for Plant Molecular Biology*, Academy Press, New York VIII, pp. 421-463 (1988); Geierson and Corey, *Plant Molecular Biology*, 2d Ed. (1988); and Miki and Iyer, Fundamentals of Gene Transfer in Plants. In *Plant Metabolism*, 2d Ed. DT. Dennis, DH Turpin, DD Lefebrvre, DB Layzell (eds), Addison Wesly, Langmans Ltd. London, pp. 561-579 (1997). Other methods include direct DNA uptake, the use of liposomes, electroporation, for example using protoplasts, micro-injection, microprojectiles or whiskers, and vacuum infiltration. See, for example, Bilang, et al. (1991, *Gene* 100: 247-250), Scheid et al. (1991, *Mol.*

Gen. Genet. 228: 104-112), Guerche et al. (1987, *Plant Science* 52: 111-116), Neuhause et al. (1987, *Theor. Appl Genet.* 75: 30-36), Klein et al. (2987, *Nature* 327: 70-73); Freeman et al. (1984, *Plant Cell Physiol.* 29: 1353), Howell et al. (1980, *Science* 208: 1265), Horsch et al. (1985, *Science* 227: 1229-1231), DeBlock et al. (1989, *Plant Physiology* 91: 694-701), Methods for Plant Molecular Biology (Weissbach and Weissbach, eds., Academic Press Inc., 1988), Methods in Plant Molecular Biology (Schuler and Zielinski, eds., Academic Press Inc., 1989), WO 92/09696, WO 94/00583, EP 331083, EP 175966, Liu and Lomonossoff (2002, *J Virol Meth*, 105:343-348), EP 290395; WO 8706614; U.S. Pat. Nos. 4,945,050; 5,036,006; and 5,100,792, U.S. patent application Ser. Nos. 08/438,666, filed May 10, 1995, and 07/951,715, filed Sep. 25, 1992, (all of which are hereby incorporated by reference).

[00178] Transient expression methods may be used to express the constructs of the present invention (see D'Aoust et al., 2009, *Methods in molecular biology*, Vol 483, pages 41-50; Liu and Lomonossoff, 2002, *Journal of Virological Methods*, 105:343-348; which is incorporated herein by reference). Alternatively, a vacuum-based transient expression method, as described by Kapila et al. (1997, *Plant Sci.* 122, 101-108; which is incorporated herein by reference), or WO 00/063400, WO 00/037663 (which are incorporated herein by reference) may be used. These methods may include, for example, but are not limited to, a method of Agro-inoculation or Agro-infiltration, syringe infiltration, however, other transient methods may also be used as noted above. With Agro-inoculation, Agro-infiltration, or syringe infiltration, a mixture of *Agrobacteria* comprising the desired nucleic acid enter the intercellular spaces of a tissue, for example the leaves, aerial portion of the plant (including stem, leaves and flower), other portion of the plant (stem, root, flower), or the whole plant. After crossing the epidermis the *Agrobacteria* infect and transfer t-DNA copies into the cells. The t-DNA is episomally transcribed and the mRNA translated, leading to the production of the protein of interest in infected cells, however, the passage of t-DNA inside the nucleus is transient.

[00179] Also considered part of this invention are transgenic plants, plant cells or seeds containing the gene construct of the present invention that may be used as a platform plant suitable for transient protein expression described herein. Methods of

regenerating whole plants from plant cells are also known in the art (for example see Guerineau and Mullineaux (1993, Plant transformation and expression vectors. In: Plant Molecular Biology Labfax (Croy RRD ed) Oxford, BIOS Scientific Publishers, pp 121-148). In general, transformed plant cells are cultured in an appropriate medium, which may contain selective agents such as antibiotics, where selectable markers are used to facilitate identification of transformed plant cells. Once callus forms, shoot formation can be encouraged by employing the appropriate plant hormones in accordance with known methods and the shoots transferred to rooting medium for regeneration of plants. The plants may then be used to establish repetitive generations, either from seeds or using vegetative propagation techniques. Transgenic plants can also be generated without using tissue culture. Methods for stable transformation, and regeneration of these organisms are established in the art and known to one of skill in the art. Available techniques are reviewed in Vasil et al. (Cell Culture and Somatic Cell Genetics of Plants, VoI I, Il and III, Laboratory Procedures and Their Applications, Academic Press, 1984), and Weissbach and Weissbach (Methods for Plant Molecular Biology, Academic Press, 1989). The method of obtaining transformed and regenerated plants is not critical to the present invention.

[00180] If plants, plant portions or plant cells are to be transformed or co-transformed by two or more nucleic acid constructs, the nucleic acid construct may be introduced into the *Agrobacterium* in a single transfection event so that the nucleic acids are pooled, and the bacterial cells transfected. Alternatively, the constructs may be introduced serially. In this case, a first construct is introduced into the *Agrobacterium* as described, the cells are grown under selective conditions (e.g. in the presence of an antibiotic) where only the singly transformed bacteria can grow. Following this first selection step, a second nucleic acid construct is introduced into the *Agrobacterium* as described, and the cells are grown under doubly-selective conditions, where only the doubly-transformed bacteria can grow. The doubly-transformed bacteria may then be used to transform a plant, plant portion or plant cell as described herein, or may be subjected to a further transformation step to accommodate a third nucleic acid construct.

[00181] Alternatively, if plants, plant portions, or plant cells are to be transformed or co-transformed by two or more nucleic acid constructs, the nucleic acid construct may be introduced into the plant by co-infiltrating a mixture of *Agrobacterium* cells with the plant, plant portion, or plant cell, each *Agrobacterium* cell may comprise one or more constructs to be introduced within the plant. In order to vary the relative expression levels within the plant, plant portion or plant cell, of a nucleotide sequence of interest within a construct, during the step of infiltration, the concentration of the various *Agrobacteria* populations comprising the desired constructs may be varied.

[00182] Therefore, there is provided herein, a plant, a portion of a plant, a plant cell, or a plant extract, comprising, one or more than one modified norovirus VP1 protein, or a norovirus VLP comprising one or more than one modified VP1 protein. The one or more than one modified norovirus VP1 protein comprising one or more than one substitution, modification or mutation at a position selected from amino acid residues in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1); a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1); or a combination thereof, and the nucleotide sequence is not derived from a genotype GI.1 norovirus VP1. The VLP may further comprise a norovirus VP2 protein.

[00183] Also provided herein is a plant, portion of a plant, a plant cell, or a plant extract comprising, a polynucleotide sequence encoding one or more than one modified norovirus VP1 protein. The one or more than one modified norovirus VP1 protein comprising one or more than one substitution, modification or mutation at a position selected from amino acid residues in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1); a deletion of a peptide fragment in sequence alignment with amino acids 39 to 46 of norovirus VP1 genotype GI.1 (SEQ ID NO:1); or a combination thereof, and the nucleotide sequence is not derived from a genotype GI.1 norovirus VP1.

[00184] A list of the Norovirus strains and constructs is provided in Table 3.

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Table 3: Norovirus strains and constructs.

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
VP1 GI.1					
Wt GI.1 (aa)	Hu/GI.1/United States/Norwalk/1968	1	12A	--	
Wt GI.1 (na)	Hu/GI.1/United States/Norwalk/1968	2	12B	--	
Wt GI.1 hCod (na)	Hu/GI.1/United States/Norwalk/1968	3	12C	2724	39A
VP1 GI.2					
Wt GI.2 (aa)	Hu/G1.2/Leuven/2003/BEL	4	13A	--	
Wt GI.2 hCod (na)	Hu/G1.2/Leuven/2003/BEL	5	13B	3300	39B
VP1 GI.3					
Wt GI.3 (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	6	14A	--	
Wt GI.3 hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	7	14B	3979	39C
Mut GI.3_Q84S (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	98	28A		
Mut GI.3_Q84S hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	167	28B	4140	40A
Mut GI.3_S94L (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	8	28C	--	
Mut GI.3_S94L hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	9	28D	4141	40B
Mut GI.3_S94V (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94V hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4288	52
Mut GI.3_S94I (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94I hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4289	52
Mut GI.3_S94M (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94M hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4290	52
Mut GI.3_S94T (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94T hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4292	52
Mut GI.3_S94E (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94E hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4293	52
Mut GI.3_S94D (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94D hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4294	52
Mut GI.3_S94N (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94N hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4295	52
Mut GI.3_S94Q (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
Mut GI.3_S94Q hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4296	52
Mut GI.3_S94K (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94K hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4297	52
Mut GI.3_S94H (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	292	28M	--	
Mut GI.3_S94H hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	293	28N	4298	52
Mut GI.3_A43V+S94L (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	169	28H	4179	40D
Mut GI.3_A43V+S94L (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	170	28G	--	
Mut GI.3_M57I+S94L (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	171	28J	4180	40E
Mut GI.3_M57I+S94L (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	172	28I	--	
Mut GI.3_A43V+M57I+S94L (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	173	28L	4181	40F
Mut GI.3_A43V+M57I+S94L (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	174	28K	--	
Mut GI.3_Q84S+S94L (aa)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	10	28E	--	
Mut GI.3_Q84S+S94L hCod (na)	Hu/GI.3/S29/2008/Lilla Edet/Sweden	11	28F	4142	40C
VP1 GI.5					
Wt GI.5 (aa)	Hu/GI.5/Siklos/HUN5407/2013/HUN	12	15A	--	
Wt GI.5 hCod (na)	Hu/GI.5/Siklos/HUN5407/2013/HUN	33	15B	3980	41A
Mut GI.5_ Q84S (aa)	Hu/GI.5/Siklos/HUN5407/2013/HUN	34	29A	--	
Mut GI.5_Q84S (na)	Hu/GI.5/Siklos/HUN5407/2013/HUN	35	29B	4130	41B
Mut GI.5_ A94L (aa)	Hu/GI.5/Siklos/HUN5407/2013/HUN	36	29C	--	
Mut GI.5_A94L hCod (na)	Hu/GI.5/Siklos/HUN5407/2013/HUN	37	29D	4131	41C
Mut GI.5_Q84S+A94L (aa)	Hu/GI.5/Siklos/HUN5407/2013/HUN	38	29E	--	
Mut GI.5_Q84S+A94L hCod (na)	Hu/GI.5/Siklos/HUN5407/2013/HUN	39	29F	4132	41D
VP1 GI.7					
Wt GI.7 (na)	Hu/GI.7/USA/2014/GA5043	175	16B	--	
Wt GI.7 (aa)	Hu/GI.7/USA/2014/GA5043	101	16A	--	
Mut GI.7_R84S (na)	Hu/GI.7/USA/2014/GA5043	176	29H	4210	41E
Mut GI.7_R84S (aa)	Hu/GI.7/USA/2014/GA5043	177	29G	--	
Mut GI.7_M57I (na)	Hu/GI.7/USA/2014/GA5043	178	29J	4217	41F
Mut GI.7_M57I (aa)	Hu/GI.7/USA/2014/GA5043	179	29I	--	-
Mut GI.7_M57L (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4266	51
Mut GI.7_M57L (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
Mut GI.7_M57G (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4268	51
Mut GI.7_M57G (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57S (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4269	51
Mut GI.7_M57S (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57T (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4270	51
Mut GI.7_M57T (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57N (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4273	51
Mut GI.7_M57N (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57Q (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4274	51
Mut GI.7_M57Q (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57K (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4275	51
Mut GI.7_M57K (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57H (na)	Hu/GI.7/USA/2014/GA5043	291	29N	4276	51
Mut GI.7_M57H (aa)	Hu/GI.7/USA/2014/GA5043	290	29M	--	
Mut GI.7_M57I+R84S (na)	Hu/GI.7/USA/2014/GA5043	180	29L	4218	41G
Mut GI.7_M57I+R84S (aa)	Hu/GI.7/USA/2014/GA5043	181	29K		
VP1 GII.1					
Wt GII.1 (aa)	GII.1_Ascension208/2010/USA_AFA55174	13	16C	--	
VP1 GII.2					
Wt GII.2 (aa)	Hu/GII.2/CGMH47/2011/TW	14	17A	--	
Wt GII.2 hCod (na)	Hu/GII.2/CGMH47/2011/TW	40	17B	3982	42A
Mut GII.2_E80S (aa)	Hu/GII.2/CGMH47/2011/TW	85	30A	--	
Mut GII.2_E80S (aa)	Hu/GII.2/CGMH47/2011/TW	86	30B	4143	42B
Mut GII.2_A90L (aa)	Hu/GII.2/CGMH47/2011/TW	41	30C	--	
Mut GII.2_A90L hCod (na)	Hu/GII.2/CGMH47/2011/TW	42	30D	4144	42C
Mut GII.2_E80S+A90L (aa)	Hu/GII.2/CGMH47/2011/TW	43	30E	--	
Mut GII.2_E80S+A90L hCod (na)	Hu/GII.2/CGMH47/2011/TW	44	30F	4145	42D
Mut GII.2_A39V+E80S+A90L (aa)	Hu/GII.2/CGMH47/2011/TW	182	30G	--	
Mut GII.2_A39V+E80S+A90L hCod (na)	Hu/GII.2/CGMH47/2011/TW	183	30H	4182	42E
Mut GII.2_R53I+E80S+A90L (aa)	Hu/GII.2/CGMH47/2011/TW	184	30I	--	
Mut GII.2_R53I+E80S+A90L hCod (na)	Hu/GII.2/CGMH47/2011/TW	185	30J	4183	42F

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
Mut GII.2_A39V+R53I+E80S+A90L (aa)	Hu/GII.2/CGMH47/2011/TW	186	30K	--	
Mut GII.2_A39V+R53I+E80S+A90L hCod (na)	Hu/GII.2/CGMH47/2011/TW	187	30L	4184	42G
VP1 GII.3					
Wt GII.3 (aa)	Hu/GII.3/Jingzhou/2013402/CHN	15	18A	--	
Wt GII.3 hCod (na)	Hu/GII.3/Jingzhou/2013402/CHN	45	18B	3983	43A
Mut GII.3_E80S (aa)	Hu/GII.3/Jingzhou/2013402/CHN	46	31A	--	
Mut GII.3_E80S hCod (na)	Hu/GII.3/Jingzhou/2013402/CHN	47	31B	4146	43B
Mut GII.3_A90L (aa)	Hu/GII.3/Jingzhou/2013402/CHN	48	31C	--	
Mut GII.3_A90L hCod (na)	Hu/GII.3/Jingzhou/2013402/CHN	49	31D	4147	43C
Mut GII.3_E80S+A90L (aa)	Hu/GII.3/Jingzhou/2013402/CHN	50	31E	--	
Mut GII.3_E80S+A90L hCod (na)	Hu/GII.3/Jingzhou/2013402/CHN	51	31F	4148	43D
VP1 GII.4					
Wt GII.4 (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	16	19A	--	
Wt GII.4 hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	52	19B	3760	44A
Mut GII.4_A39V (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	53	32A	--	
Mut GII.4_A39V hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	54	32B	4155	44B
Mut GII.4_V47P (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	55	32C	--	
Mut GII.4_V47P hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	56	32D	4156	44C
Mut GII.4_R53I (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	57	32E	--	
Mut GII.4_R53I hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	58	32F	4157	44D
Mut GII.4_P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	59	32G	--	
Mut GII.4_P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	60	32H	4133	44E
Mut GII.4_P80A (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	287	32FF	--	
Mut GII.4_P80A hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	286	32EE	4281	50A
Mut GII.4_P80N (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	287	32FF	--	
Mut GII.4_P80N hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	286	32EE	4285	50A
Mut GII.4_P80K (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	287	32FF	--	
Mut GII.4_P80K hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	286	32EE	4286	50A
Mut GII.4_P80H (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	287	32FF	--	
Mut GII.4_P80H hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	286	32EE	4287	50A
Mut GII.4_S90L (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	61	32I	--	

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
Mut GII.4_S90L hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	62	32J	4134	44F
Mut GII.4_Δ35-42 (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	63	32K	--	
Mut GII.4_ Δ35-42 hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	64	32L	4158	44G
Mut GII.4_SSTAVATA (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	65	32M	--	
Mut GII.4_SSTAVATA hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	66	32N	4159	44H
Mut GII.4_A39V+R53I (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	188	32AA	--	
Mut GII.4_A39V+R53I hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	189	32BB	4185	44O
Mut GII.4_A39V+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	67	32O	--	
Mut GII.4_A39V+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	68	32P	4165	44I
Mut GII.4_A39I+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39I+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4256	50B
Mut GII.4_A39M+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39M+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4257	50B
Mut GII.4_A39G+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39G+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4258	50B
Mut GII.4_A39S+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39S+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4259	50B
Mut GII.4_A39E+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39E+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4260	50B
Mut GII.4_A39D+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39D+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4261	50B
Mut GII.4_A39N+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39N+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4262	50B
Mut GII.4_A39Q+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39Q+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4263	50B
Mut GII.4_A39K+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39K+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4264	50B
Mut GII.4_A39H+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	288	32HH	--	
Mut GII.4_A39H+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	289	32GG	4265	50B
Mut GII.4_V47P+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	69	32Q	--	
Mut GII.4_V47P+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	70	32R	4166	44J

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
Mut GII.4_R53I+P80S (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	71	32S	--	
Mut GII.4_R53I+P80S hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	72	32T	4167	44K
Mut GII.4_P80S+S90L (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	73	32U	--	
Mut GII.4_P80S+S90L hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	74	32V	4135	44L
Mut GII.4_P80S+Δ35-42 (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	75	32W	--	
Mut GII.4_ P80S+Δ35-42 hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	76	32X	4168	44M
Mut GII.4_P80S+SSTAVATA (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	77	32Y	--	
Mut GII.4_P80S+SSTAVATA hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	78	32Z	4169	44N
Mut GII.4_A39V+R53I+P80S(aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	190	32CC	--	
Mut GII.4_A39V+R53I+P80ShCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	191	32DD	4186	44P
Wt GII.4 (aa)	US96/GII.4/Dresden174/1997/DE_AY741811	27	19C	--	
Wt GII.4 (aa)	FHO2/GII.4/FarmingtonHills/2002/US_AY502023	28	19D	--	
Wt GII.4 (aa)	Hnt04:GII.4/Hunter-NSW504D/2004/AU_DQ078814	29	19E	--	
Wt GII.4 (aa)	2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915	30	19F	--	
Wt GII.4 (aa)	NO09/GII.4/Orange-NSW001P/2008/AU_GQ845367	31	19G	--	
VP1 GII.5					
Wt GII.5 (aa)	GII.5_Alberta/2013/CA_ALT54485	17	20	--	
VP1 GII.6					
Wt GII.6 (aa)	Hu/GII.6/Ohio/490/2012/USA	20	21A	--	
Wt GII.6 hCod (na)	Hu/GII.6/Ohio/490/2012/USA	21	21B	3993	45A
Mut GII.6_E80S (aa)	Hu/GII.6/Ohio/490/2012/USA	79	33A	--	
Mut GII.6_E80S hCod (na)	Hu/GII.6/Ohio/490/2012/USA	80	33B	4149	45B
Mut GII.6_S90L (aa)	Hu/GII.6/Ohio/490/2012/USA	81	33C	--	
Mut GII.6_S90L hCod (na)	Hu/GII.6/Ohio/490/2012/USA	82	33D	4150	45C
Mut GII.6_E80S+S90L (aa)	Hu/GII.6/Ohio/490/2012/USA	83	33E	--	
Mut GII.6_E80S+S90L hCod (na)	Hu/GII.6/Ohio/490/2012/USA	84	33F	4151	45D
VP1 GII.7					
Wt GII.7 (aa)	GII.7_Musa_2010_AII73774	18	22	--	

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
VP1 GII.12					
Wt GII.12 (aa)	GII.12_HS206_2010_USA_AEI29586	19	23A	--	
Wt GII.12 hCod (na)	GII.12_HS206_2010_USA_AEI29586	87	23B	3995	46A
Mut GII.12_E80S (aa)	GII.12_HS206_2010_USA_AEI29586	88	34A	--	
Mut GII.12_E80S hCod (na)	GII.12_HS206_2010_USA_AEI29586	89	34B	4136	46B
Mut GII.12_A90L (aa)	GII.12_HS206_2010_USA_AEI29586	90	34C	--	
Mut GII.12_A90L hCod (na)	GII.12_HS206_2010_USA_AEI29586	91	34D	4137	46C
Mut GII.12_E80S+A90L (aa)	GII.12_HS206_2010_USA_AEI29586	92	34E	--	
Mut GII.12_E80S+A90L hCod (na)	GII.12_HS206_2010_USA_AEI29586	93	34F	4138	46D
VP1 GII.13					
Wt GII.13 (aa)	GII.13_VA173_2010_H9AWU4	22	24A	--	
Wt GII.13 hCod (na)	GII.13_VA173_2010_H9AWU4	23	24B	--	
VP1 GII.14					
Wt GII.14 (aa)	GII.14_Saga/2008/JPN/_ADE28701	32	25	--	
VP1 GII.17					
Wt GII.17 (aa)	GII.17_Kawa_2014_A0A077KVU6	24	26A	--	
Wt GII.17 hCod (na)	GII.17_Kawa_2014_A0A077KVU6	25	26B	--	
Mut GII.17_A39V (aa)	GII.17_Kawa_2014_A0A077KVU6	192	34G	--	
Mut GII.17_A39V hCod (na)	GII.17_Kawa_2014_A0A077KVU6	193	34H	4234	46E
Mut GII.17_R53I (aa)	GII.17_Kawa_2014_A0A077KVU6	194	34I	--	
Mut GII.17_R53I hCod (na)	GII.17_Kawa_2014_A0A077KVU6	195	34J	4235	46F
Mut GII.17_A90L (aa)	GII.17_Kawa_2014_A0A077KVU6	196	34K	--	
Mut GII.17_A90L hCod (na)	GII.17_Kawa_2014_A0A077KVU6	197	34L	4232	46G
Mut GII.17_A39V+R53I (aa)	GII.17_Kawa_2014_A0A077KVU6	198	34M	--	
Mut GII.17_A39V+R53I hCod (na)	GII.17_Kawa_2014_A0A077KVU6	199	34N	4236	46H
Mut GII.17_E80S+A90L (aa)	GII.17_Kawa_2014_A0A077KVU6	200	34O	--	
Mut GII.17_ E80S+A90L hCod (na)	GII.17_Kawa_2014_A0A077KVU6	201	34P	4233	46I
VP1 GII.21					
Wt GII.21 (aa)	GII.21_Sali_2011_USA_AFC89665	26	27	--	

Trivial Name	Norovirus Strain	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
VP2					
Wt GI.1 (aa)	Hu/GI.1/United States/Norwalk/1968	99	35A	--	
Wt GI.1 hCod (na)	Hu/GI.1/United States/Norwalk/1968	100	35B	2725	47A
Wt GI.3 (aa)	GI.3/S29/2008/Lila Edet/Sweden	94	36A	--	
Wt GI.3 hCod (na)	GI.3/S29/2008/Lila Edet/Sweden	95	36B	3303	47B
Wt GII.6 (aa)	GII.6 HS245/2010/USA	96	37A	--	
Wt GII.6 hCod (na)	GII.6 HS245/2010/USA	97	37B	3307	47C

Construct	SEQ ID NO:	SEQ Fig #	Const #	Const.Fig #
Cloning vector 1190 from left to right T-DNA	162	38A	1190	48
Construct 2724 from 2X35S promoter to NOS terminator	163	38B	2724	
Cloning vector 3677 from left to right T-DNA	164	38C	3677	49
Construct 4133 from 2X35S promoter to NOS terminator	165	38D	4133	
Construct 4135 from 2X35S promoter to NOS terminator	166	38E	4135	

[00185] The present invention will be further illustrated in the following examples.

Example 1: Norovirus VP1 Constructs

[00186] The candidate sequences for VP1 and VP2 are available in Genbank (see Figures 2A and 2B). Non-limiting examples of these sequences are:

[00187] Hu/GI.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; Figure 13A);

[00188] Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; Figure 14A);

[00189] Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; Figure 15A);

[00190] Hu/GI.7/USA/2014/GA5043 (GI.7, SEQ ID NO:101, Figure 16A)

[00191] Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; Figure 16C);

[00192] Hu/GII.2/CGMH47/2011/TW (GII.2; SEQ ID NO:14; Figure 17A);

[00193] Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO:15; Figure 18A);

[00194] Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO:16; Figure 19A);

[00195] US96/GII.4/Dresden174/1997/DE_AY741811 (GII.4; SEQ ID NO:27; Figure 19C);

[00196] FH02/GII.4/FarmingtonHills/2002/US_AY502023 (GII.4; SEQ ID NO:28; Figure 19D);

[00197] Hnt04:GII.4/Hunter-NSW504D/2004/AU_DQ078814 (GII.4; SEQ ID NO:29; Figure 19E);

[00198] 2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915 (GII.4; SEQ ID NO:30; Figure 19F);

[00199] NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (GII.4; SEQ ID NO:31; Figure 19G);

[00200] GII.14_Saga_2008_JPN_ADE28701 native VP1 (GII.14; SEQ ID NO:32; Figure 25);

[00201] Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; Figure 20);

[00202] Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; Figure 21A);

[00203] G11.7/Musa/2010/All73774 (GII.7; SEQ ID NO:18; Figure 22);

[00204] Hu/GII.12/HS206/2010/USA (GII.12; SEQ ID NO:19; Figure 23A);

[00205] GII.13/VA173/2010/H9AWU4 (GII.13; SEQ ID NO:22; Figure 24A);

[00206] Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO:24; Figure 26A);

[00207] Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; Figure 27).

[00208] The primers listed in Table 4 were used to prepare the constructs described below.

Table 4 primers used to prepare constructs defined herein.

Primer	Sequence	SEQ ID NO
IF-NoV(US68)VP1(ORF1)(hCod).c	TCGTGCTTCGGCACCAGTACAATGATGATGGCTAGTAAAGATGCGACCT	102
IF-NoV(US68)VP1(ORF1)(hCod).r	ACTAAAGAAAATAGGCCTTTATCTCCGCAGACCGAGGCGTCCGCGGGCAGAA	103
IF-GI3Lil08VP1.c	TCGTGCTTCGGCACCAGTACAATGATGATGGCTTCCAAGGATGCTCCCA	104
IF-GI3Lil08VP1.r	ACTAAAGAAAATAGGCCTCTAGCTCCGTCTGATCCCGAGCCTCCGAACT	105
VP1_GI.3Lil08(S94L).r	CTGAGCCAAGTGGAGCAGAAACGGATTCAAGTGTGGTCCTAGCTGCAGGTCAAACAAGA	106
VP1_GI.3Lil08(S94L).c	AGGACCACACTTGAATCCGTTTCTGCTCCACTTGGCTCAGATGTATAATGGATGGG	107
VP1_GI.3Lil08(Q84S).r	GTGTGGTCCTAGGCTCAGGTCAAACAAGATGTCACCCGGGGTGTTGTTTGGGCTTAT	108
VP1_GI.3Lil08(Q84S).c	GGTGACATCTTGTTTGACCTGAGCCTAGGACCACACTTGAATCCGTTT	109
IF-GI3Lil08VP2.c	TCGTGCTTCGGCACCAGTACAATGGCTCAGGCAATCTTCGGCGCAATC	110
IF-GI3Lil08VP2.r	ACTAAAGAAAATAGGCCTTCACTTCCTCATGTTTGCGAACAGGGGAAGC	111
IF-(160)GI.5_Sikl13_VP1.c	TCGTGCTTCGGCACCAGTACAATGATGATGGCCTCCAAAGACGCTCCT	112
IF-GI.5_Sikl13_VP1.r	ACTAAAGAAAATAGGCCTTCAGCGCCGCACGCCAAGGCGCCCCCGGGCAGATG	113
GI.5(hCod)(Q84S).r	GATGAGGGCCTAAGCTCAGGTCGAACAGAATATCCCCTGGTGTGTTGTTAG	114
GI.5(hCod)(Q84S).c	TATTCTGTTCGACCTGAGCTTAGGCCCTCATCTCAACCCCTTCTTGGCCCA	115
GI.5(hCod)(A94L).r	ATCTGGCTCAGGTGGAGCAAGAAGGGGTTGAGATGAGGGCCTAACTGCAG	116
GI.5(hCod)(A94L).c	TCTCAACCCCTTCTTGCTCCACCTGAGCCAGATGTACAATGGCTGGGTGGG	117
IF-(160)GII.2_CGMH11_VP1.c	TCGTGCTTCGGCACCAGTACAATGAAGATGGCATCCAACGACGCCGCACCCAGC	118
IF-GII.2_CGMH11_VP1.r	ACTAAAGAAAATAGGCCTTTACTGGATCCGTCGGCGACCGTTCCCTGTGCCCA	119
VP1_GII.2CGMH11(E80S).r	TTCTGGTCCCAGGCTGAGATTGAGGAGCACTTCCCCAGGGCTATTTCTAGGGCTGACCG	120
VP1_GII.2CGMH11(E80S).c	GGAAGTGCTCCTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCT	121
VP1_GII.2CGMH11(A90L).r	TCCGGGCCAGGTGGAGCAGGTACGGATTAAGTTCTGGTCCCAGCTCGAGATTGAGGAGC	122
VP1_GII.2CGMH11(A90L).c	GGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAG	123
IF-(160)GII.3_Jing13_VP1.c	TCGTGCTTCGGCACCAGTACAATGAAAATGGCTTCCAACGATGCAGCACCCT	124
IF-GII.3_Jing13_VP1.r	ACTAAAGAAAATAGGCCTTTACTGGATCCGCCGTCTGCCATTGCCTGTAC	125
VP1_GII.3Jing13(E80S).r	ATTTCAGGGCCCAGGCTCAAATTCAAGAGAACCTCCCCGGGGGAGTTTCGAGGAGAGAC	126
VP1_GII.3Jing13(E80S).c	GGAGGTTCTCTTGAATTTGAGCCTGGGCCCTGAAATTAATCCTTATCT	127

Primer	Sequence	SEQ ID NO
VP1_GII.3Jing13(A90L).r	ATTCGGGCTAGATGGAGCAGATAAGGATTAATTTCAGGGCCCAGTTCCAAATTCAAGAG	128
VP1_GII.3Jing13(A90L).c	GGGCCCTGAAATTAATCCTTATCTGCTCCATCTAGCCCGAATGTACAACGGCTACG	129
IF-GII.4Syd12VP1.c	TCGTGCTTCGGCACCAGTACAATGAAAATGGCCTCGAGTGACGCTAACC	130
IF-GII.4Syd12VP1.r	ACTAAAGAAAATAGGCCTTCAGACAGCCCTGCGTCTGCCAGTCCCATT	131
VP1_GII.4Syd12(A39V).r	GACCGGCCACGGGGACTGCTATGGCTGCGCCCACCACAGGCTCCAGGGCCATCA	132
VP1_GII.4Syd12(A39V).c	GGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTG	133
VP1_GII.4Syd12(V47P).r	CGTATCCACGGGTCAATGGGATTCTGCTGACCGGCCACGGGCGCTGCTATG	134
VP1_GII.4Syd12(V47P).c	GGCCGGTCAGCAGAATCCCATTGACCCGTGGATACGCAACAATTTTGTCCAAG	135
VP1_GII.4Syd12(R53I).r	TGGACAAAATTGTTGATTATCCACGGGTCAATCACATTCTGCTGACCG	136
VP1_GII.4Syd12(R53I).c	GATTGACCCGTGGATAATCAACAATTTTGTCCAAGCCCCTGGTGGGGAGT	137
GII.4(P80S).r	GATCGGGTCCCAAGCTGGCCGACCACAGGATTTCTCCTGGCGCATTTCTC	138
GII.4(P80S).c	AATCCTGTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCAC	139
GII.4(S90L).r	ATCCGAGCGAGATGCAGCAAATAGGGGTTCAGATCGGGTCCCAATGGGGCCGACCA	140
GII.4(S90L).c	TCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGC	141
VP1_GII.4Syd12(Del(35-42)).r	CACATTCTGCTGACCGCCCACCACAGGCTCCAGGGCCATCACCTCATTAT	142
VP1_GII.4Syd12(Del(35-42)).c	GGAGCCTGTGGTGGGCGGTCAGCAGAATGTGATTGACCCGTGGATACG	143
VP1_GII.4Syd12(SSTAVATA).r	CTGACCGGCTGTAGCGACGGCGGTGGAGCTGCCCACCACAGGCTCCAGGGCCATCACCTC	144
VP1_GII.4Syd12(SSTAVATA).c	TGTGGTGGGCAGCTCCACCGCCGTCGCTACAGCCGGTCAGCAGAATGTGATTGACCCGTG	145
IF-GII.6Ohi12VP1.c	TCGTGCTTCGGCACCAGTACAATGAAGATGGCAAGCAACGACGCAGCTC	146
IF-GII.6Ohi12VP1.r	ACTAAAGAAAATAGGCCTTCACTGATCCCGGCGTCGCCCCTGGCCTGTCCCCAT	147
IF-GII.6HS10VP2.c	TCGTGCTTCGGCACCAGTACAATGGCCTCCGCATTTCTAGCTGGATTGGCC	148
IF-GII.6HS10VP2.r	ACTAAAGAAAATAGGCCTCTAAACTTGTGATTCTCCCCGTCGCCTGGGGTGTG	149
VP1_GII.6Ohi12(E80S).r	AGTTCAGGGCCGAGGCTCAGATTGAGCAGCATCTCGCCCGGGGAGTTCCGGGGGGAGAC	150
VP1_GII.6Ohi12(E80S).c	CGAGATGCTGCTCAATCTGAGCCTCGGCCCTGAACTAAACCCTTATCT	151
VP1_GII.6Ohi12(S90L).r	ATCCGTGAAAGGTGGAGCAGATAAGGGTTTAGTTCAGGGCCGAGTTCCAGATTGAGCAG	152
VP1_GII.6Ohi12(S90L).c	CCCTGAACTAAACCCTTATCTGCTCCACCTTTCACGGATGTACAATGGCTACGCAGGAG	153
IF-(160)GII.12_HS10_VP1.c	TCGTGCTTCGGCACCAGTACAATGAAGATGGCGTCTAATGATGCTGCTCCTT	154

Primer	Sequence	SEQ ID NO
IF-GII.12_HS10_VP1.r	ACTAAAGAAAATAGGCCTTTACTGCACACGCCTCCTCCCATTTCCTGTTCCCAT	155
GII.12(E80S).r	AGTTCTGGTCCTAAGCTCAAATTCAATAACACTTCGCCGGGGGAGTTT	156
GII.12(E80S).c	AGTGTTATTGAATTTGAGCTTAGGACCAGAACTCAACCCCTATCTGGCA	157
GII.12(A90L).r	ATCCGAGACAGATGGAGCAGATAGGGGTTGAGTTCTGGTCCTAATTCCAA	158
GII.12(A90L).c	ACTCAACCCCTATCTGCTCCATCTGTCTCGGATGTACAACGGCTATGCGGGCGGAGT	159
IF-NoV(US68)VP2(ORF3)(hCod).c	TCGTGCTTCGGCACCAGTACAATGGCTCAGGCCATTATTGGCGCCAT	160
IF-NoV(US68)VP2(ORF3)(hCod).r	ACTAAAGAAAATAGGCCTTCAGCGGCGGTTGTTAGCGAACAGAGGAAGTC	161
GI.3Lil08(M57I).r	CTGAACGTAATTTGAGATGATCCAGGGGTCGATCATGTTTACCTGTCCTGCGGTGGCGG	202
GI.3Lil08(M57I).c	GTAAACATGATCGACCCCTGGATCATCTCAAATTACGTTCAGGCTCCACAGGGGGAGTT	203
IF-(GI.7USA14)VP1.c	TCGTGCTTCGGCACCAGTACAATGATGATGGCCAGCAAGGACGCTCCGAGTA	204
IF-(GI.7USA14)VP1.r	ACTAAAGAAAATAGGCCTTCACACCCGCCTCACGCCGAGTCGTCGCACG	205
GI.7USA14_VP1(R84S).r	AGTGGGGTCCTAAGCTGAGGTCAAACAGAATATCCCCTGGGGTGTTAT	206
GI.7USA14_VP1(R84S).c	TATTCTGTTTGACCTCAGCTTAGGACCCCACTTGAACCCCTTTCTGCTTC	207
GI.7USA14_VP1(M57I).r	AACGAAATTGTTGATTATCCACGGGTCGATCATATTGACTTGGCCTGCAGT	208
GI.7USA14_VP1(M57I).c	GATCGACCCGTGGATAATCAACAATTTCGTTCAGGCACCAGAAGGAGA	209
GII.2CGMH11(A39V).r	TTTGTCTGCCCGGTCACAGGCACTGCGAGGGCAGCCCCTGCAACAGGCTCCAAGGCCATCAC	210
GII.2CGMH11(A39V).c	GTTGCAGGGGCTGCCCTCGCAGTGCCTGTGACCGGGCAGACAAATATCATCGATCCTTG	211
GII.2CGMH11(R53I).r	CACGAAATTAGCGATAATCCAAGGATCGATGATATTTGTCTGCCCGGTCACAGGAGCTG	212
GII.2CGMH11(R53I).c	GGCAGACAAATATCATCGATCCTTGGATTATCGCTAATTTCGTGCAAGCCCCAAATGGG	213
IF-GII17Kaw14VP1.c	TCGTGCTTCGGCACCAGTACAATGAAAATGGCATCTAACGACGCAGCCCCCTC	214
IF-GII17Kaw14VP1.r	ACTAAAGAAAATAGGCCTCTACTGAGCCCGGCGTCTGCCGTTACCGGTGCCCATTG	215
GII.17Kaw14(A90L).r	GCGGCTCAGATGCAGCAGATATGGATTGAGGTCAGGGCCGAGCTCAAGATTCAGGAGTA	216
GII.17Kaw14(A90L).c	CCTGACCTCAATCCATATCTGCTGCATCTGAGCCGCATGTACAATGGTTAC	217
GII.17Kaw14(A39V).r	ATTCTGCCCTGTCACTGGCACAGCTATAGCGGCGCCTGCAACCGGCTCTAGTGGAAGTG	218
GII.17Kaw14(A39V).c	AGGCGCCGCTATAGCTGTGCCAGTGACAGGGCAGAATAATATTATAGACCCTTGGATT	219
GII.17Kaw14(R53I).r	ACGAAGTTTGTGATAATCCAAGGGTCTATAATATTATTCTGCCCTGTCACTGGGGCAGC	220
GII.17Kaw14(R53I).c	GGCAGAATAATATTATAGACCCTTGGATTATCACAAACTTCGTGCAGGCACCCAACGGC	221

Primer	Sequence	SEQ ID NO
GII.4Syd12(P80A).r	ATCGGGTCCCAAGGCGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	222
GII.4Syd12(P80A).c	AATCCTGTGGTCGGCCGCCTTGGGACCCGATCTGAA CCCCTATTTGTCAC	223
GII.4Syd12(P80N).r	ATCGGGTCCCAAGTTGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	224
GII.4Syd12(P80N).c	AATCCTGTGGTCGGCCAACTTGGGACCCGATCTGAA CCCCTATTTGTCAC	225
GII.4Syd12(P80K).r	ATCGGGTCCCAACTTGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	226
GII.4Syd12(P80K).c	AATCCTGTGGTCGGCCAAGTTGGGACCCGATCTGAA CCCCTATTTGTCAC	227
GII.4Syd12(P80H).r	ATCGGGTCCCAAGTGGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	228
GII.4Syd12(P80H).c	AATCCTGTGGTCGGCCCACTTGGGACCCGATCTGAA CCCCTATTTGTCAC	229
GII.4Syd12(A39I).r	GACCGGCCACGGGGATTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	230
GII.4Syd12(A39I).c	GGGCGCAGCCATAGCAATCCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	231
GII.4Syd12(A39M).r	GACCGGCCACGGGCATTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	232
GII.4Syd12(A39M).c	GGGCGCAGCCATAGCAATGCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	233
GII.4Syd12(A39G).r	GACCGGCCACGGGGCCTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	234
GII.4Syd12(A39G).c	GGGCGCAGCCATAGCAGGCCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	235
GII.4Syd12(A39S).r	GACCGGCCACGGGGCTTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	236
GII.4Syd12(A39S).c	GGGCGCAGCCATAGCAAGCCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	237
GII.4Syd12(A39E).r	GACCGGCCACGGGCTCTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	238
GII.4Syd12(A39E).c	GGGCGCAGCCATAGCAGAGCCCGTGGCCGGTCAGCA GAATGTGATTGAC	239
GII.4Syd12(A39D).r	GACCGGCCACGGGGTCTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	240
GII.4Syd12(A39D).c	GGGCGCAGCCATAGCAGACCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	241
GII.4Syd12(A39N).r	ACCGGCCACGGGGTTTGCTATGGCTGCGCCCACCAC AGGCTCCAGGGCCATCAC	242
GII.4Syd12(A39N).c	GGGCGCAGCCATAGCAAACCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	243
GII.4Syd12(A39Q).r	GACCGGCCACGGGCTGTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	244
GII.4Syd12(A39Q).c	GGGCGCAGCCATAGCACAGCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	245
GII.4Syd12(A39K).r	GACCGGCCACGGGCTTTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCATCA	246
GII.4Syd12(A39K).c	GGGCGCAGCCATAGCAAAGCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	247
GII.4Syd12(A39H).r	GACCGGCCACGGGGTGTGCTATGGCTGCGCCCACCA CAGGCTCCAGGGCCA	248

GII.4Syd12(A39H).c	GGGCGCAGCCATAGCACACCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	249
GI.7USA14(M57L).r	GAACGAAATTGTTCAGTATCCACGGGTCGATCATAT TGACTTGGCCTGCA	250
GI.7USA14(M57L).c	GATCGACCCGTGGATACTGAACAATTTCGTTCAGGC ACCAGAAGGAGA	251
GI.7USA14(M57G).r	GAACGAAATTGTTGCCTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	252
GI.7USA14(M57G).c	GATCGACCCGTGGATAGGCAACAATTTCGTTCAGGC ACCAGAAGGAGA	253
GI.7USA14(M57S).r	GAACGAAATTGTTGCTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	254
GI.7USA14(M57S).c	GATCGACCCGTGGATAAGCAACAATTTCGTTCAGGC ACCAGAAGGAGA	255
GI.7USA14(M57T).r	GAACGAAATTGTTGGTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	256
GI.7USA14(M57T).c	GATCGACCCGTGGATAACCAACAATTTCGTTCAGGC ACCAGAAGGAGA	257
GI.7USA14(M57N).r	GAACGAAATTGTTGTTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	258
GI.7USA14(M57N).c	GATCGACCCGTGGATAAACAACAATTTCGTTCAGGC ACCAGAAGGAGA	259
GI.7USA14(M57Q).r	GAACGAAATTGTTCTGTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	260
GI.7USA14(M57Q).c	GATCGACCCGTGGATACAGAACAATTTCGTTCAGGC ACCAGAAGGAGA	261
GI.7USA14(M57K).r	GAACGAAATTGTTCTTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	262
GI.7USA14(M57K).c	GATCGACCCGTGGATAAAGAACAATTTCGTTCAGGC ACCAGAAGGAGA	263
GI.7USA14(M57H).r	GAACGAAATTGTTGTGTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	264
GI.7USA14(M57H).c	GATCGACCCGTGGATACACAACAATTTCGTTCAGGC ACCAGAAGGAGA	265
GI.3Lil08(S94V).r	TCTGAGCCAAGTGCACCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	266
GI.3Lil08(S94V).c	CTTGAATCCGTTTCTGGTGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	267
GI.3Lil08(S94I).r	TCTGAGCCAAGTGGATCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	268
GI.3Lil08(S94I).c	CTTGAATCCGTTTCTGATCCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	269
GI.3Lil08(S94M).r	TCTGAGCCAAGTGCATCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	270
GI.3Lil08(S94M).c	CTTGAATCCGTTTCTGATGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	271
GI.3Lil08(S94T).r	TCTGAGCCAAGTGGGTCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	272
GI.3Lil08(S94T).c	CTTGAATCCGTTTCTGACCCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	273
GI.3Lil08(S94E).r	TCTGAGCCAAGTGCTCCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	274
GI.3Lil08(S94E).c	CTTGAATCCGTTTCTGGAGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	275
GI.3Lil08(S94D).r	TCTGAGCCAAGTGGTCCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	276

GI.3LilO8(S94D).c	CTTGAATCCGTTTCTGGACCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	277
GI.3LilO8(S94N).r	TCTGAGCCAAGTGGTTCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	278
GI.3LilO8(S94N).c	CTTGAATCCGTTTCTGAACCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	279
GI.3LilO8(S94Q).r	TCTGAGCCAAGTGCTGCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	280
GI.3LilO8(S94Q).c	CTTGAATCCGTTTCTGCAGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	281
GI.3LilO8(S94K).r	TCTGAGCCAAGTGCTTCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	282
GI.3LilO8(S94K).c	CTTGAATCCGTTTCTGAAGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	283
GI.3LilO8(S94H).r	TCTGAGCCAAGTGGTGCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	284
GI.3LilO8(S94H).c	CTTGAATCCGTTTCTGCACCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	285

WT GI.1 Norovirus VP1: A2X35S/CPMV 160/ wt VP1 GI.1/ NOS (Construct number 2724)

[00209] A human codon-optimized sequence encoding VP1 from Norovirus strain GI.1/Norwalk/1968/US was cloned into 2X35S/CPMV 160/NOS expression system using the following PCR-based method. A fragment containing the GI.1 VP1 coding sequence was amplified using primers IF-NoV(US68)VP1(ORF2)(hCod).c (SEQ ID NO:102) and IF-NoV(US68)VP1(ORF2)(hCod).r (SEQ ID NO:103), using human codon-optimized GI.1 VP1 gene sequence (SEQ ID NO:3) as template. For sequence optimization, GI.1/Norwalk/1968/US VP1 protein sequence (Genbank accession number NP_056821) was backtranslated and optimized for human codon usage, GC content and mRNA structure. The PCR product was cloned in 2X35S/CPMV 160/NOS expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 1190 (SEQ ID NO:162; Figures 38A and 48) was digested with SacII and StuI restriction enzyme and the linearized plasmid was used for the In-Fusion assembly reaction. Construct number 1190 is an acceptor plasmid intended for “In Fusion” cloning of genes of interest in a 2X35S/CPMV 160/NOS-based expression cassette. It also incorporates a gene construct for the co-expression of the TBSV P19 suppressor of silencing under the alfalfa Plastocyanin gene promoter and terminator. The backbone is a pCAMBIA binary plasmid and the sequence from left to right t-DNA borders is presented in SEQ ID NO:162. The resulting construct

was given number 2724 (Figure 38B; SEQ ID NO: 163). The amino acid sequence of native VP1 from Norovirus strain GI.1/Norwalk/1968/US is presented in SEQ ID NO: 1. A representation of plasmid 2724 is presented in Figure 39A.

2X35S/CPMV 160/ GII.4_P80S (hCod)/ NOS + MAR (Construct number 4133)

[00210] A human codon-optimized sequence encoding VP1 from GII.4/Sydney/NSW0514/2012/AU comprising the P80S substitution in the S domain was cloned into 2X35S/CPMV 160/NOS+MAR expression system using the following PCR-based method. In a first round of PCR, a fragment containing the S domain with the mutated P80S amino acid was amplified using primers IF-GII.4Syd12VP1.c (SEQ ID NO:130) and GII.4(P80S).r (SEQ ID NO:138), using human codon-optimized GII.4 VP1 gene sequence (SEQ ID NO:52) as template. A second fragment containing the P80S substitution with the remaining of the S and P domain was amplified using GII.4(P80S).c (SEQ ID NO:139) and IF-GII.4Syd12VP1.r (SEQ ID NO:131), using human codon-optimized GII.4 VP1 gene sequence (SEQ ID NO:52) as template. For sequence optimization, GII.4/Sydney/NSW0514/2012/AU VP1 protein sequence (Genbank accession number AFV08795) was backtranslated and optimized for human codon usage, GC content and mRNA structure. The PCR products from both amplifications were then mixed and used as template for a second round of amplification using IF-GII.4Syd12VP1.c (SEQ ID NO:130) and IF-GII.4Syd12VP1.r (SEQ ID NO:131) as primers. The final PCR product was cloned in 2X35S/CPMV 160/NOS+MAR expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 3677 (SEQ ID NO:164; Figures 38C and 49) was digested with SacII and StuI restriction enzyme and the linearized plasmid was used for the In-Fusion assembly reaction. Construct number 3677 is an acceptor plasmid intended for "In Fusion" cloning of genes of interest in a 2X35S/CPMV 160/NOS+MAR-based expression cassette. It also incorporates a gene construct for the co-expression of the TBSV P19 suppressor of silencing under the alfalfa Plastocyanin gene promoter and terminator. The backbone is a pCAMBIA binary plasmid and the sequence from left to right t-DNA borders is presented in SEQ ID NO:164. The resulting construct was given number 4133 (Figure 38D; SEQ ID NO:165). The amino acid sequence of mutated

GII.4_P80S is presented in SEQ ID NO:59. A representation of plasmid 4133 is presented in Figure 44E.

2X35S/CPMV 160/ GII.4_P80S+S90L (hCod)/ NOS + MAR (Construct number 4135)

[00211] A human codon-optimized sequence encoding VP1 from GII.4/Sydney/NSW0514/2012/AU comprising the P80S and the S90L substitutions in the S domain was cloned into 2X35S/CPMV 160/NOS+MAR expression system using the following PCR-based method. In a first round of PCR, a fragment containing the S domain with the mutated P80S and S90L amino acids was amplified using primers IF-GII.4Syd12VP1.c (SEQ ID NO:130) and GII.4(S90L).r (SEQ ID NO:140), using human codon-optimized GII.4_P80S VP1 gene sequence (SEQ ID NO:60) as template. A second fragment containing the S90L substitution with the remaining of the S and P domain was amplified using GII.4(S90L).c (SEQ ID NO:141) and IF-GII.4Syd12VP1.r (SEQ ID NO:131), using human codon-optimized GII.4_P80S VP1 gene sequence (SEQ ID NO:60) as template. For sequence optimization, GII.4/Sydney/NSW0514/2012/AU VP1 protein sequence (Genbank accession number AFV08795) was backtranslated and optimized for human codon usage, GC content and mRNA structure. The PCR products from both amplifications were then mixed and used as template for a second round of amplification using IF-GII.4Syd12VP1.c (SEQ ID NO:130) and IF-GII.4Syd12VP1.r (SEQ ID NO:131) as primers. The final PCR product was cloned in 2X35S/CPMV 160/NOS+MAR expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 3677 (SEQ ID NO:164; Figures 38C and 49) was digested with SacII and StuI restriction enzyme and the linearized plasmid was used for the In-Fusion assembly reaction. Construct number 3677 is an acceptor plasmid intended for "In Fusion" cloning of genes of interest in a 2X35S/CPMV 160/NOS+MAR-based expression cassette. It also incorporates a gene construct for the co-expression of the TBSV P19 suppressor of silencing under the alfalfa Plastocyanin gene promoter and terminator. The backbone is a pCAMBIA binary plasmid and the sequence from left to right t-DNA borders is presented in SEQ ID NO:164. The resulting construct was given number 4135 (SEQ ID NO:166). The amino acid sequence of mutated

GII.4_P80S+S90L is presented in SEQ ID NO:73. A representation of plasmid 4135 is presented in Figure 44L.

[00212] A summary of the wildtype and mutated VP1 and VP2 proteins, primers, templates and products is provided in Tables 3 and 4. The VP1 proteins with single, double, triple, and quadruple modifications, substitutions, or mutations were constructed using the same methods as described above, with reference to construct # 4133 for single modification and # 4135 for the double, triple, and quadruple modifications. VP2 proteins are assembled using essentially the same method as that described for construct #2724.

Example 2: Methods

Agrobacterium tumefaciens Transfection

[00213] *Agrobacterium tumefaciens* strain AGL1 was transfected by electroporation with the native norovirus VP1, native norovirus VP2, or norovirus VP1 mutant protein expression vectors using the methods described by D'Aoust *et al.*, 2008 (*Plant Biotech. J.* 6:930-40). Transfected *Agrobacterium* were grown in YEB medium supplemented with 10 mM 2-(N-morpholino)ethanesulfonic acid (MES), 20 μM acetosyringone, 50 μg/ml kanamycin and 25 μg/ml of carbenicillin pH5.6 to an OD_{600} between 0.6 and 1.6. *Agrobacterium* suspensions were centrifuged before use and resuspended in infiltration medium (10 mM $MgCl_2$ and 10 mM MES pH 5.6).

Preparation of Plant Biomass, Inoculum and Agroinfiltration

[00214] *N. benthamiana* plants were grown from seeds in flats filled with a commercial peat moss substrate. The plants were allowed to grow in the greenhouse under a 16/8 photoperiod and a temperature regime of 25° C. day/20° C. night. Three weeks after seeding, individual plantlets were picked out, transplanted in pots and left to grow in the greenhouse for three additional weeks under the same environmental conditions

[00215] Agrobacteria transfected with each native norovirus VP1, native norovirus VP2, or norovirus VP1 mutant expression vector were grown in a YEB medium supplemented with 10 mM 2-(N-morpholino)ethanesulfonic acid (MES), 20 μM

acetosyringone, 50 µg/ml kanamycin and 25 µg/ml of carbenicillin pH5.6 until they reached an OD_{600} between 0.6 and 1.6. *Agrobacterium* suspensions were centrifuged before use and resuspended in infiltration medium (10 mM $MgCl_2$ and 10 mM MES pH 5.6) and stored overnight at 4° C. On the day of infiltration, culture batches were diluted in 2.5 culture volumes and allowed to warm before use. Whole plants of *N. benthamiana* were placed upside down in the bacterial suspension in an air-tight stainless steel tank under a vacuum of 20-40 Torr for 2-min. Plants were returned to the greenhouse for a 6 or 9 day incubation period until harvest.

Leaf Harvest and Total Protein Extraction

[00216] Following incubation, the aerial part of plants was harvested, frozen at −80° C. and crushed into pieces. Total soluble proteins were extracted by homogenizing (Polytron) each sample of frozen-crushed plant material in 2 volumes of cold 100 mM phosphate buffer pH 7.2 + 150 mM NaCl, 0.4 µg/ml Metabisulfite and 1 mM phenylmethanesulfonyl fluoride. After homogenization, the slurries were centrifuged at 10,000 g for 10 min at 4° C. and these clarified crude extracts (supernatant) kept for analyses.

[00217] The total protein content of clarified crude extracts was determined by the Bradford assay (Bio-Rad, Hercules, California) using bovine serum albumin as the reference standard. Proteins were separated by SDS-PAGE under reducing conditions using Criterion™ TGX Stain-Free™ precast gels (Bio-Rad Laboratories, Hercules, CA). Proteins were visualized by staining the gels with Coomassie Brilliant Blue. Alternatively, proteins were visualized with Gel Doc™ EZ imaging system (Bio-Rad Laboratories, Hercules, CA) and electrotransferred onto polyvinylene difluoride (PVDF) membranes (Roche Diagnostics Corporation, Indianapolis, Indiana) for immunodetection. Prior to immunoblotting, the membranes were blocked with 5% skim milk and 0.1% Tween-20 in Tris-buffered saline (TBS-T) for 16-18 h at 4° C.

Protein Analysis and Immunoblotting

[00218] Immunoblotting was performed with a first incubation with a primary mAb 242P antibody specific to VP1 from GI and GII genotypes, diluted 1/500 in 2% skim milk in TBS-Tween 20 0.1%. Peroxydase-conjugated goat anti-mouse (Jackson

Immunoresearch, cat #115-035-146) diluted 1/10000 was used as secondary antibody for chemiluminescence detection, diluted in 2% skim milk in TBS-Tween 20 0.1% Immunoreactive complexes were detected by chemiluminescence using luminol as the substrate (Roche Diagnostics Corporation). Horseradish peroxidase-enzyme conjugation of human IgG antibody was carried out by using the EZ-Link Plus® Activated Peroxidase conjugation kit (Pierce, Rockford, Ill.).

Analysis of VLP Formation/Iodixanol Gradients

[00219] Proteins were extracted from frozen biomass by mechanical extraction in a blender with 2 volumes of extraction buffer (100 mM phosphate buffer pH 7.2 + 150 mM NaCl). The slurry was filtered through a large pore nylon filter to remove large debris and centrifuged 5000 g for 5 min at 4°C. The supernatant was collected and centrifuged again at 5000 g for 30 min (4°C) to remove additional debris. The supernatant is then loaded on a discontinuous iodixanol density gradient. Analytical density gradient centrifugation was performed as follows: 38 ml tubes containing discontinuous iodixanol density gradient in acetate buffer (1 ml at 45%, 2 ml at 35%, 2 ml at 33%, 2 ml at 31%, 2 ml at 29% and 5 ml at 25% of iodixanol) were prepared and overlaid with 25 ml of the extracts containing the virus-like particles. The gradients were centrifuged at 175 000 g for 4 hours (4°C). After centrifugation, 1 ml fractions were collected from the bottom to the top and fractions were analyzed by SDS-PAGE combined with protein staining or Western blot.

Electron microscopy

[00220] Following centrifugation of partially clarified plant extracts on discontinuous iodixanol density gradients, as described above, fractions (1 ml/fraction) containing the samples are pooled, mixed with 100 mM PBS pH 7.2 + 150 mM NaCl buffer to completely fill the tube and centrifuged 120 minutes at 100000g. The pellets were re-suspended in 300-1000 µl of buffer depending of the VP1 quantity.

[00221] Carbon-coated copper grids with a 200 nm mesh size are made hydrophilic by placing the carbon side face up on a Whatman paper in a petri dish and incubated overnight at 4^{0}C. 20 µl of pooled fractions from density gradient centrifugation to be

observed by transmission electron microscopy (TEM) are deposited on a Parafilm and grids were floated with the carbon side facing down and incubated at room temperature for 5 minutes. Grids are then washed 4 times on 20 µl water droplet and the excess water from the last wash is drained by touching a Whatman paper with the side of the grid. Grids are then incubated 1 minute on a 20 µl droplet of 2% uranyl acetate in water. Grids are allowed to dry 5 minutes on a Whatman paper. Observation was performed under transmission electron microscopy at magnifications ranging from 10,000X to 150,000X.

Example 3: VP1 protein and VLP production in plants

[00222] *N. benthamiana* leaves were, vacuum infiltrated, as described in Example 2, with *Agrobacterium tumefaciens* comprising expression vectors encoding wildtype norovirus VP1s or mutant norovirus VP1 constructs to permit expression of the VP1 sequences, and the leaves examined for VP1 protein and/or VLP production. After 9 days post infiltration (DPI), total crude protein extracts were prepared from leaf homogenates were separated by SDS-PAGE, and stained with Coomassie (VP1 production), or separated using discontinuous iodixanol density gradients as described in Example 2, above (VLP production). Fractions from the density gradients were examined using Coomassie-stained SDS-PAGE. Norovirus VP1 proteins appear at an approximate 55-60kDa band. The occurrence of the VP1 protein within a fraction of the density gradients is indicative of the fraction(s) to which the VLPs equilibrate during density gradient centrifugation. The yield of VLPs obtained from peak fractions after density gradient centrifugation was also determined.

[00223] The yield, or amount of extracted, wild type norovirus VP1 protein from plants differs depending on the genotype of the norovirus VP1 being expressed. Wild type GI.1 VP1, GI.5 VP1, and GII.12 VP1 exhibit readily detectable protein yields as determined using SDS PAGE (Figure 3A). In contrast, wild type GII.4 VP1 was poorly expressed in plants (Figures 3A right hand panel), and low yields of VP1 protein, or non- detectable amounts of VP1 protein (using SDS-PAGE) were also observed following expression, for example, wild type GII.2 VP1, GII.3 VP1 and GII.6 VP1(Table 5).

Table 5: VP1 yields (determined in crude extracts) of several wildtype (native) norovirus strains produced in plants.

Genotype	Strain	Native
		Max yields
GI.1	GI.1/US/68	+++++
GI.3	S29/2008/Lilla Edet/Sweeden	+++
GII.2	CGMH47/2011/TW	++
GII.3	Jingzhou/2013402/CHN	-
GII.6	Ohio/490/2012/USA	+/-

GI.3 VLPs and VLPs comprising modified GI.3 VP1 proteins

[00224] Norovirus GI.3 VP1 constructs having a glutamine to serine substitution at position 84 (Q84S) resulted in similar yield than the wildtype GI.3 VP1, while norovirus GI.3 VP1 constructs having a serine to leucine substitution at position 94 (S94L), or combination of substitutions including the S94L substitution, exhibited a greater yield of VLP comprising the VP1 protein, of a 1.9 to 3.8 fold increase (S94L), a 4.2 fold increase (A43V+S94L), a 1.8 fold increase (Q84S+S94L), and a 10.2 fold increase (A34V+M57I+Q84S+S94L) as compared to VLPs comprising wild type GI.3 VP1. Furthermore, constructs having a serine to leucine, valine, isoleucine, methionine, threonine, glutamic acid, aspartic acid, asparagine, glutamine, lysine, or histidine substitution at position 94 (GI.3_S94X, where X= L, V, I, M, T, E, D, N, Q, K, or H), exhibited a greater yield, from about 1.2 to about 2.75 fold, compared to VLPs comprising the wild type GI.3 VP1 protein (Figure 5F).

[00225] As shown in Figures 5B and 5D, expression of norovirus GI.3 constructs having, a serine to leucine substitution at position 94 (S94L), or a combination including a glutamine to serine substitution at position 84 (Q84S) and a serine to leucine substitution at position 94 (Q84S+S94L), or methionine to isoleucine substitution at position 57 (M57I+S94L), resulted in a shift of VLPs into higher density fractions (F2-F6; 31-35% iodixanol), as compared to VLPs comprising

wildtype GI.3 VP1, which predominantly separated into lower density fractions (F8-F11; 25-29% iodixanol).

[00226] VLPs comprised of modified GI.3 VP1 proteins having a S94L substitution, a combination of Q84S+S94L, or a combination of M57I+S94L, had fewer damaged viral particles and a greater proportion of 38 nm particles, over 23 nm particles, when compared to wildtype GI.3 VLPs (Figures 5C and 5E).

GI.5 VLPs and VLPs comprising modified GI.5 VP1 proteins

[00227] Norovirus GI.5 VP1 constructs having a serine to proline substitution at position 84 (Q84S), an alanine to leucine substitution at position 94 (A94L), or a combination of these substitutions (Q84S+A94L), exhibited a similar yield of VP1 protein in plant extracts when compared to the yield of wild type GI.5 VP1 protein expressed in plants (Figure 6A). After gradient purification, centrifugation and resuspension, Norovirus GI.5 construct having an alanine to leucine substitution at position 94 (A94L) exhibited a greater yield, 1.5 fold increase, when compared to the wildtype GI.5 VP1.

[00228] As shown in Figure 6B, a GI.5 VP1 construct having a glutamine to serine substitution at position 84 in combination with an alanine to leucine substitution at position 94 (Q84S+A94L), resulted in VP1 proteins that exhibited a shift to higher density iodixianol fractions (29-31%) as compared to wildtype GI.5 VP1 (predominantly found in 25-29% iodixanol fractions). The VLP preparations also comprised fewer damaged viral particles when compared to wildtype GI.5 VLPs (Figure 6C).

GI.7 VLPs and VLPs comprising modified GI.7 VP1 proteins

[00229] Norovirus GI.7 VP1 constructs having an arginine to serine substitution at position 84 (R84S), a methionine to isoleucine substitution at position 57 (M57I), or a combination of these substitutions (M57I+ R84S), exhibited an increased yield of VP1 protein after gradient purification, centrifugation and resuspension, when compared to the wildtype GI.7 VP1. Furthermore, GI.7 constructs having a methionine to isoleucine, leucine, glycine, serine, threonine, asparagine, glutamine, lysine, or

histidine substitution at position 57 (GI.7_M57X, where X=I, L, G, S, T, N, Q, K, or H), exhibited a greater yield, from about 1.1 to about 1.95 fold, VLPs comprising the wild type GI.7 VP1 protein (Figure 6F).

[00230] As shown in Figure 6D, a GI.7 VP1 construct having the M57I, R84S or M57I+R84S substitutions resulted in VP1 proteins that exhibited a shift to higher density iodixianol fractions (31-35%) as compared to wildtype GI.7 VP1. The GI.7 VLP preparations having the M57I, R84S or M57I+R84S substitutions also comprised the same or fewer damaged viral particles when compared to wildtype GI.7 VLPs (Figure 6E).

GII.2 VLPs and VLPs comprising modified GII.2 VP1 proteins

[00231] Expression of modified norovirus VP1 proteins GII.2_A90L and GII.2_E80S+A90L in plants resulted in higher VP1 protein yield as compared to the yield of wildtype GII.2 VP1 (see Figure 7A).

[00232] Norovirus GII.2 VP1 constructs having a glutamate to serine substitution at position 84 and an alanine to leucine substitution at position 90 (E84S+A90L), an alanine to valine substitution at position 39, a glutamate to serine substitution at position 84, and an alanine to leucine substitution at position 90 (A39S+E84S+A90L), an arginine to isoleucine substitution at position 53, a glutamate to serine substitution at position 84, and an alanine to leucine substitution at position 90 (R53I+E84S+A90L), an alanine to valine substitution at position 39, an arginine to isoleucine substitution at position 53, a glutamate to serine substitution at position 84, and an alanine to leucine substitution at position 90 (A39V+R53I+E84S+A90L), all exhibited an increased yield of VP1 protein after gradient purification, centrifugation and resuspension, when compared to the wildtype GII.2 VP1.

[00233] Expression of a GII.2 VP1 constructs having a glutamic acid to serine substitution at position 80 (E80S), an alanine to leucine substitution at position 90 (A90L), or a glutamic acid to serine substitution at position 80 and an alanine to leucine substitution at positions 80 and 90 (E80S+A90L) resulted in similar production of VLPs as that of the wildtype GII.2 (Figure 7B). The GII.2 VLP preparations having the E80S+A90L, or A39V+ E80S+A90L substitution s also

comprised the same or fewer damaged viral particles when compared to wildtype GII.2 VLPs (Figure 7C).

GII.3 VLPs and VLPs comprising modified GII.3 VP1 proteins

[00234] Norovirus GII.3 VP1 constructs having a replacement of glutamic acid with serine at position 80 (E80S) exhibited a similar yield of VP1 protein in plant extracts, when compared to the yield of wild type GII.3 VP1 protein expressed in plants. The yields of VLPs comprising either wild type of modified VP1 protein were generally low.

[00235] Expression of a GII.3 VP1 constructs having a glutamic acid to serine substitution at position 80 (E80S) resulted in similar production of VLPs that resided in similar density iodixanol fractions (35%) as that of the wildtype GII.3 (Figure 8B).

GII.4 VLPs and VLPs comprising modified GII.4 VP1 proteins

[00236] With reference to Figures 9A, 9H and 9I, norovirus GII.4 VP1 constructs having: an arginine to isoleucine substitution at position 53 (R53I); a proline to serine , alanine, asparagine, lysine, or histidine substitution at position 80 (P80X, where X=S, A, N, K, or H); a serine to leucine substitution at position 90 (S90L); an alanine to valine, isoleucine, methionine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine substitution at position 39 (A39X, where X=V, I, M, T, E, D, N, Q, K, or H) in combination with a proline to serine substitution at position 80 (A39V+P80S); an arginine to isoleucine substitution at position 53 in combination with a proline to serine substitution at position 80 (R53I+P80S); a serine to leucine substitution at position 90 in combination with a proline to serine substitution at position 80 (P80S+S90L); and a deletion of positions 35 to 42 (Δ35-42) in combination with a proline to serine substitution at position 80 (Δ35-42+P80S), resulted in higher VP1 protein yields following extraction for plants, as compared to VP1 yields using wildtype GI.4.

[00237] For each of the tested modified GII.4 VP1 proteins, the VLP yield, comprising the various modified GII.4 VP1 proteins, was greater than that of VLPs comprising wild type GII.4 VP1 protein. A ten-fold increase in VLP yield was

2018375695 29 Nov 2024

observed in VLPs comprising GII.4_A39V VP1; from about a 1.4 to about a 2.7 fold increase in VLP yield was observed in VLPs comprising GII.4_P80X, where X=S, A, N, K, H, an over 8-fold increase in VLP yield was observed in VLPs comprising either GII.4_S90L VP1, or GII.4_Δ35-42+P80S VP1; a 14-fold fold increase in VLP yield was observed in VLPs comprising GII.4_P80S+P90L VP1; from about 1.3 to about 3.4 fold increase in VLP yield was observed in VLPs comprising GII.4_A39X+P80S VP1, where X=V, I, M, G, S, E, D, N, Q, K, or H, GII.4_R53I+P80S (21 fold increase), or GII.4_A39V+P80S+A90L VP1 (38.5 fold increase); a five-fold increase in VLP yield was observed in VLPs comprising GII.4_A39V+R53I VP1; a four-fold increase in VLP yield was observed in VLPs comprising GII.4_V47P+P80S VP1; and a 1.5- fold increase in VLP yield was observed in VLPs comprising GII.4_R53I VP1.

[00238] Results of VLPs comprising modified GII.4 proteins are shown in Figures 9B-9D and 9G. Constructs comprising GII.4 VP1 having: a proline to serine substitution at position 80 (P80S; Figure 9B, 9C, 9D); a serine to leucine substitution at position 90 (S90L; Figure 9B); an alanine to valine substitution at position 39 in combination with a proline to serine substitution at position 80 (A39V+P80S; Figure 9C); an arginine to isoleucine substitution at position 53 in combination with a proline to serine substitution at position 80 (R53I+P80S; Figure 9D); a proline to serine substitution at position 80 in combination with a serine to leucine substitution at position 90 (P80S+S90L; Figure 9B); a proline to serine substitution at position 80 in combination with a deletion of positions 35-42 (P80S+Δ35-42; Figure 9C), and an alanine to valine substitution at position 39, in combination with a proline to serine substitution at position 80 and a serine to leucine substitution at position 90 (GII.4_A39V+P80S+A90L; Figure 9G), resulted in the production of VLPs that reside in higher density iodixanol fractions (29-33%).

[00239] VLPs comprising GII.4 VP1 proteins having: a P80S substitution in combination with an S90L substitution (P80S+S90L; Figure 9B); an A39V substitution in combination with a P80S substitution
25 (A39V+P80S; Figure 9C); a P80S substitution in combination with a deletion of positions 35-42 (Δ35-42+P80S; Figure 9C); an R53I substitution in combination with a P80S substitution (R53I+P80S; Figure 9D); and an alanine to valine substitution at position 39, in

combination with a proline to serine substitution at position 80 and a serine to leucine substitution at position 90 (GII.4_A39V+P80S+A90L; Figure 9G), had fewer damaged viral particles and/or a greater ratio of 38 nm particles:23 nm particles, as compared to wildtype GII.4 VLPs.

GII.6 VLPs and VLPs comprising modified GII.6 VP1 proteins

[00240] Increased VLP yield of over 2.2 fold, compared to wild type, (determined following gradient purification, centrifugation and resuspension) was also observed in plant extracts expressing GII.6_S90L VP1.

GII.12 VLPs and VLPs comprising modified GII.12 VP1 proteins

[00241] The yield of modified GII.12, for example, GII.12 comprising a glutamic to serine substitution at position 80 (E80S), an arginine to leucine substitution at position 90 (A90L), or a combination of these substitutions (E80S+A90L) resulted in an increase of about 1.2 – 1.4 fold compared to wild type, (determined following gradient purification, centrifugation and resuspension; Figure 11A).

[00242] GII.12 constructs having: a glutamic acid to serine substitution at position 80 (E80S); an alanine to leucine substitution at position 90 (A90L); and a combination thereof (E80S+A90L), resulted in the expression of GII.12 VP1 protein that resided in higher density iodixanol fractions (33-35%) as compared to wildtype GII.12 VP1 (31-33%).

GII.17 VLPs and VLPs comprising modified GII.17 VP1 proteins

[00243] The yield of modified GII.17, for example, GII.17 comprising an alanine to valine substitution at position 39 (A39V), a arginine to isoleucine substitution at position 53 (R53I), or an alanine to leucine substitution at position 90 (A90L) resulted in an increase of about 1.1 – 3.4 fold compared to wild type, (determined following gradient purification, centrifugation and resuspension).

[00244] GII.17 constructs having: an alanine to valine substitution at position 39 (A39V), a arginine to isoleucine substitution at position 53 (R53I), or an alanine to leucine substitution at position 90 (A90L), resulted in the expression of GII.17 VP1

protein that resided in higher density iodixanol fractions (33-35%) as compared to wildtype GII.12 VP1 (31-33%).

[00245] Collectively, the above described results demonstrate that protein components from the high density iodixanol gradient fractions demonstrate that Norovirus VP1 proteins, and modified Norovirus VP1 proteins, were found to self-assemble into VLPs in plants. The isolated VLPs comprised of mutant VP1 proteins exhibited a structural conformation similar to that of wildtype norovirus virion particles.

Example 4: Immune response using VP1

[00246] Studies on the immune response to Norovirus native GI.1 (SEQ ID NO:1) VLP administration were performed with 6-8 week old female BALB/c mice (Charles River Laboratories). Thirty seven mice were randomly divided into four groups of eight animals for Norovirus VLP vaccine and a group of five animals for placebo. All groups were injected using intramuscular immunization. All groups were immunized in a two-dose regimen, the boost immunization being administered 3 weeks following the first immunization.

[00247] For intramuscular administration in hind legs, two groups (eight animals) of unanaesthetized mice were immunized with the plant-made VLP native VP1 from Norovirus GI.1 genotype vaccine (1 or 10 μg). Placebo group (five animals) was immunized using the same route and regimen as the candidate vaccine using vaccine buffer (PBS at pH 6.0).

[00248] To measure the potential benefit of adjuvant, two groups of animals (8 animals) were immunized by intramuscular administration in hind legs on unanaesthetized mice with 1 or 10 μg plant-made VLP Norovirus vaccine plus one volume Alhydrogel 2% (alum, Cedarlane Laboratories Ltd., Burlington, Ontario, Canada). All groups were immunized according to a prime-boost regimen with the boost immunization performed 3 weeks following the first immunization.

[00249] Mice were evaluated through clinical observations during the in-life period as followed: daily monitoring for mortality and clinical signs, weekly detailed

examinations, injection site observations and body weight measurements. All animals were under observation and sacrificed on Day 42 for gross examination. Blood was collected from all animals prior to dosing on Day 0, on Days 21 and 42 (21 days after each immunization). Samples were processed to isolate the serum for specific antibody response analyses.

[00250] Serum samples from blood collected on Days 21 and 42 from all animals were analyzed individually by ELISA for GI.1 VLP-specific total IgG and IgA antibodies using GI.1 VLP-coated plates. Pre-immune serum samples (Day 0 – prior dosing) collected from all animals were pooled by treatment group and each pool was analyzed to insure that they were negative (or below the cut-off value of the analytical test).

[00251] Descriptive statistics were performed using GraphPad Prism software (Version 6.05; GraphPad Software, La Jolla, CA, USA). Antibody titers measured for each group were reported as geometric mean titer (GMT) with 95 % confidence intervals (CI). Half of the value of the limit of detection was attributed to antibody titers below the limit of detection of the method specific to the tested antibodies. Therefore, in this study, an animal was considered to be a positive responder if its GMT value for a determined condition was equal or above the limit of detection of the method (LOQ = 100). Statistical comparisons between IgG titers of treatment groups were performed using one-way ANOVA followed by a Tukey's test on log10-transformed data. A comparison between the placebo group and each treatment group was also performed using oneway ANOVA followed by a post hoc Dunnett's test on log10-transformed data.

[00252] The GI.1 VLP-specific total IgG titers that were measured in serum samples from all animals after IM immunization with one dose (Day 21) and two doses (Day 42) of 1 μg or 10 μg of each formulation. Total IgG titers were measured by ELISA using GI.1 VLP-coated plates (LOQ = 100). The results are present in Figure 3D. Total IgG titers per treatment group (n=8 animals/group) are represented by geometric mean titer (GMT) with a 95 % confidence interval. Statistical comparisons between IgG titers of treatment groups were performed using one-way ANOVA followed by a Tukey's test on log10-transformed data. A comparison between the placebo group

and each treatment group was also performed using one-way ANOVA followed by a post-hoc Dunnett's test on log10-transformed data. Significant differences were annotated as letters in Figure 3D (the same letter indicates that no significant difference was detected between treatment groups; $p > 0.05$).

[00253] In a similar manner plant-produced modified VP1 proteins, as described herein, including for example: produced using GI.3_Q84S (construct 4140; SEQ ID NO:167), GI.3_S94L (construct 4141; SEQ ID NO:9), GI.3_A43V+S94L (construct 4179; SEQ ID NO:169), GI.3_M57I+S94L (construct 4180; SEQ ID NO:171), GI.3_P84S+S94L (construct 4142; SEQ ID NO:11), GI.3_A43V+M57I+S94L (construct 4181; SEQ ID NO:173), GI.5_Q84S (construct 4130; SEQ ID NO:35), GI.5_ A94L (construct 4131; SEQ ID NO:37), GI.5_Q84S+A94L (construct 4132; SEQ ID NO:39), GI.7_R84S (construct 4210; SEQ ID NO:176), GI.7_M57I (construct 4217; SEQ ID NO:178), GI.7_M57I+R84S (construct 4218; SEQ ID NO:180), GII.2_E80S (construct 4143; SEQ ID NO:86), GII.2_A90L (construct 4144; SEQ ID NO:42), GII.2_E80S+A90L (construct 4145; SEQ ID NO:44), GII.2_A39V+E80S+A90L (construct 4182; SEQ ID NO:183), GII.2_R53I+E80S+A90L (construct 4183; SEQ ID NO:185), GII.2_A39V+R53I+E80S+A90L (construct 4184; SEQ ID NO:187), GII.3_E80S (construct 4146; SEQ ID NO:47), GII.3_A90L (construct 4147; SEQ ID NO:49), GII.3_E80S+A90L (construct 4148; SEQ ID NO:51), GII.4_A39V (construct 4155; SEQ ID NO:54), GII.4_V47P (construct 4156; SEQ ID NO:56), GII.4_R53I (construct 4157; SEQ ID NO:58), GII.4_P80S (construct 4133; SEQ ID NO:60), GII.4_S90L (construct 4134; SEQ ID NO:62), GII.4_ Δ35-42 (construct 4158; SEQ ID NO:64), GII.4_SSTAVATA (construct 4159; SEQ ID NO:66). GII.4_A39V+R53I (construct 4185; SEQ ID NO:189), GII.4_A39V+P80S (construct 4165; SEQ ID NO:68), GII.4_V47P+P80S (construct 4166; SEQ ID NO:70), GII.4_R53I+P80S (construct 4167; SEQ ID NO:72), GII.4_P80S+S90L (construct 4135; SEQ ID NO:74), GII.4_ Δ35-42+ P80S (construct 4168; SEQ ID NO:76), GII.4_P80S+SSTAVATA (construct 4169; SEQ ID NO:78), GII.4_A39V+R53I+P80S (construct 4186; SEQ ID NO:191), GII.6_E80S (construct 4149; SEQ ID NO:80), GII.6_S90L (construct 4150; SEQ ID NO:82), GII.6_E80S+S90L (construct 4151; SEQ ID NO:84), GII.12_E80S (construct 4136;

SEQ ID NO:89), GII.12_A90L (construct 4137; SEQ ID NO:91), GII.12_E80S+A90L (construct 4138; SEQ ID NO:93), GII.17_A39V (construct 4234; SEQ ID NO:193), GII.17_R53I (construct 4235; SEQ ID NO:195), GII.17_A90L (construct 4232; SEQ ID NO:197), GII.17_A39V+R53I (construct 4236; SEQ ID NO:199), GII.17_E80S+A90L (construct 4233; SEQ ID NO:201), or a combination thereof, may be administered to mice following the same protocol as described in this example.

[00254] Mouse immune response to Norovirus native VP1 VLPs

[00255] As demonstrated in Figure 3D, mice immunized with plant-made Norovirus native VP1 VLPs from GI.1 genotype had shown GI.1 VLP-specific IgG antibody titers in sera and were detected for each treatment group on Days 21 and 42. IgG titer levels that were induced by each treatment on Days 21 and 42 were statistically higher than the titers quantified for the placebo group ($p < 0.05$). On each day, IgG titer level increased in a dose-dependent manner as demonstrated by the significant differences detected between the 1 µg and 10 µg treatments formulated with Alhydrogel or not ($p < 0.05$) and the addition of Alhydrogel to the NoV VLP vaccine enhanced significantly the induced immune response at doses of 1 µg and 10 µg ($p < 0.05$). A significant increase of IgG titer level was also detected for each treatment group between Days 21 and 42 ($p < 0.05$). These results collectively demonstrate the ability of plant produced Norovirus native VP1 VLPs to elicit a robust immune response in mice.

[00256] Similar results may also be observed with the administration of VLPs comprising modified VP1 proteins, including for example: produced using GI.3_Q84S (construct 4140; SEQ ID NO:167), GI.3_S94L (construct 4141; SEQ ID NO:9), GI.3_A43V+S94L (construct 4179; SEQ ID NO:169), GI.3_M57I+S94L (construct 4180; SEQ ID NO:171), GI.3_P84S+S94L (construct 4142; SEQ ID NO:11), GI.3_A43V+M57I+S94L (construct 4181; SEQ ID NO:173), GI.5_Q84S (construct 4130; SEQ ID NO:35), GI.5_ A94L (construct 4131; SEQ ID NO:37), GI.5_Q84S+A94L (construct 4132; SEQ ID NO:39), GI.7_R84S (construct 4210; SEQ ID NO:176), GI.7_M57I (construct 4217; SEQ ID NO:178), GI.7_M57I+R84S (construct 4218; SEQ ID NO:180), GII.2_E80S (construct 4143; SEQ ID NO:86),

GII.2_A90L (construct 4144; SEQ ID NO:42), GII.2_E80S+A90L (construct 4145; SEQ ID NO:44), GII.2_A39V+E80S+A90L (construct 4182; SEQ ID NO:183), GII.2_R53I+E80S+A90L (construct 4183; SEQ ID NO:185), GII.2_A39V+R53I+E80S+A90L (construct 4184; SEQ ID NO:187), GII.3_E80S (construct 4146; SEQ ID NO:47), GII.3_A90L (construct 4147; SEQ ID NO:49), GII.3_E80S+A90L (construct 4148; SEQ ID NO:51), GII.4_A39V (construct 4155; SEQ ID NO:54), GII.4_V47P (construct 4156; SEQ ID NO:56), GII.4_R53I (construct 4157; SEQ ID NO:58), GII.4_P80S (construct 4133; SEQ ID NO:60), GII.4_S90L (construct 4134; SEQ ID NO:62), GII.4_ Δ35-42 (construct 4158; SEQ ID NO:64), GII.4_SSTAVATA (construct 4159; SEQ ID NO:66). GII.4_A39V+R53I (construct 4185; SEQ ID NO:189), GII.4_A39V+P80S (construct 4165; SEQ ID NO:68), GII.4_V47P+P80S (construct 4166; SEQ ID NO:70), GII.4_R53I+P80S (construct 4167; SEQ ID NO:72), GII.4_P80S+S90L (construct 4135; SEQ ID NO:74), GII.4_ Δ35-42+ P80S (construct 4168; SEQ ID NO:76), GII.4_P80S+SSTAVATA (construct 4169; SEQ ID NO:78), GII.4_A39V+R53I+P80S (construct 4186; SEQ ID NO:191), GII.6_E80S (construct 4149; SEQ ID NO:80), GII.6_S90L (construct 4150; SEQ ID NO:82), GII.6_E80S+S90L (construct 4151; SEQ ID NO:84), GII.12_E80S (construct 4136; SEQ ID NO:89), GII.12_A90L (construct 4137; SEQ ID NO:91), GII.12_E80S+A90L (construct 4138; SEQ ID NO:93), GII.17_A39V (construct 4234; SEQ ID NO:193), GII.17_R53I (construct 4235; SEQ ID NO:195), GII.17_A90L (construct 4232; SEQ ID NO:197), GII.17_A39V+R53I (construct 4236; SEQ ID NO:199), GII.17_E80S+A90L (construct 4233; SEQ ID NO:201), or a combination thereof, following the same protocol as described in this example.

[00257] All citations are hereby incorporated by reference.

[00258] The present invention has been described with regard to one or more embodiments. However, it will be apparent to persons skilled in the art that a number of variations and modifications can be made to the described subject matter. The scope of the claims should not be limited by the preferred embodiments set forth in the examples, but should be given the broadest interpretation consistent with the description as a whole

2018375695 29 Nov 2024

Claims

1. A modified norovirus VP1 protein comprising

one or more than one conserved amino acid substitution when compared to a corresponding wild type norovirus VP1 protein, wherein the one or more than one conserved amino acid substitution are selected from a group consisting of amino acids in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), and wherein

the norovirus VP1 protein is not a GI.1 genotype.

2. A modified norovirus VP1 protein comprising one or more than one conserved amino acid substitution at a position in sequence alignment with amino acids 43, 57, 84 or 94 of norovirus VP1 genotype GI.1 (SEQ ID NO:1), wherein:

the conserved amino acid substitution at the position in sequence alignment with amino acid 43 is to isoleucine, methionine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine;

the conserved amino acid substitution at the position in sequence alignment with amino acid 57 is to leucine, alanine, glycine, serine, asparagine, glutamine, or histidine;

the conserved amino acid substitution at the position in sequence alignment with amino acid 84 is to asparagine, cysteine, threonine, alanine, or lysine;

the conserved amino acid substitution at the position in sequence alignment with amino acid 94 is to leucine, isoleucine, methionine, valine, threonine, asparagine, lysine, or histidine; and

wherein the norovirus VP1 protein is not a GI.1 genotype.

3. The modified norovirus VP1 protein of claim 1 or 2, wherein the wild type norovirus VP1 is selected from a group consisting of genotypes GI.3. GI.5, GI.7, GII.2, GII.3, GII.4, GII.6, GII.12 and GII.17.

4. The modified norovirus VP1 protein of claim 1,

2018375695 29 Nov 2024

wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 43 is to valine, isoleucine, leucine, methionine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine.

5. The modified norovirus VP1 protein of claim 1, wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 57 is to isoleucine, leucine, valine, alanine, glycine, serine, threonine, asparagine, glutamine, lysine, or histidine.

6. The modified norovirus VP1 protein of claim 1, wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 84 is to serine, asparagine, cysteine, threonine, alanine, lysine or histidine.

7. The modified norovirus VP1 protein of claim 1, wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 94 is to leucine, isoleucine, methionine, valine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, histidine.

8. The modified norovirus VP1 protein of claim 1 or 2,

wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 43 is to valine;

wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 57 is to isoleucine;

wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 84 is to serine; or

wherein the one or more than one conserved substitution at the position in sequence alignment with amino acid 94 is to leucine.

9. A recombinant polynucleotide encoding the modified norovirus VP1 protein of any one of claims 1 to 8.

10. The recombinant polynucleotide of claim 9, wherein the codon usage of the nucleotide sequence is optimized to human codon usage, increased GC content, or a combination thereof.

11. The recombinant polynucleotide of claim 9, wherein the polynucleotide comprises a vector.

2018375695 29 Nov 2024

12. A virus-like particle (VLP) comprising the modified norovirus VP1 of any one of claims 1 to 8.

13. The VLP of claim 12, further comprising a norovirus VP2 protein.

14. A method of producing a norovirus VP1 protein in a plant, portion of a plant or a plant cell, comprising:

introducing the recombinant polynucleotide of any one of claims 9 to 11; and

incubating the plant, portion of the plant or the plant cell under conditions that permit expression of the norovirus VP1 protein.

15. The method of claim 14, wherein the method further comprises a step of harvesting the plant, portion of the plant, or the plant cell.

16. The method of claim 15, wherein the method further comprises a step of extracting, purifying, or both extracting and purifying the norovirus VP1 protein from the plant, the portion of the plant or the plant cell.

17. A norovirus VP1 protein produced by the method of any one of claims 14 to 16.

18. The method of claim 14, wherein in the step of introducing, a second polynucleotide encoding a norovirus VP2 protein is introduced into the plant, the portion of the plant or the plant cell, and in the step of incubating, the conditions permit co-expression and co-production of both the norovirus VP1 protein and the norovirus VP2 protein in the plant, portion of the plant, or the plant cell.

19. The method of claim 18, wherein the method further comprises a step of harvesting the plant, the portion of the plant or the plant cell.

20. The method of claim 19, wherein the method further comprises a step of extracting, purifying, or both extracting and purifying the norovirus VP1 protein and norovirus VP2 protein.

21. A method of producing a norovirus virus like particle (VLP) in a plant, portion of a plant or a plant cell, comprising:

introducing the recombinant polynucleotide of any one of claims 9 to 11; and

2018375695 29 Nov 2024

incubating the plant, portion of the plant or the plant cell under conditions that permit expression of the norovirus VLP.

22. The method of claim 21, wherein the method further comprises a step of harvesting the plant, portion of the plant, or the plant cell.

23. The method of claim 22, wherein the method further comprises a step of extracting, purifying, or both extracting and purifying the norovirus VLP from the plant, the portion of the plant or the plant cell.

24. A norovirus virus like particle (VLP) produced by the method of any one of claims 21 to 23.

25. The method of claim 21, wherein in the step of introducing, a second polynucleotide encoding a norovirus VP2 protein is introduced into the plant, the portion of the plant or the plant cell, and in the step of incubating, the conditions permit co-expression and co-production of both the norovirus VP1 protein and the norovirus VP2 protein in the plant, portion of the plant, or the plant cell.

26. The method of claim 25, wherein the method further comprises a step of harvesting the plant, the portion of the plant or the plant cell.

27. The method of claim 26, wherein the method further comprises a step of extracting, purifying or both extracting and purifying a virus-like particle (VLP) from the plant, the portion of the plant or the plant cell, wherein the VLP comprises the norovirus VP1 protein and the norovirus VP2 protein.

28. A virus-like particle (VLP) comprising the norovirus VP1 protein and the norovirus VP2 protein produced by the method of claim 27.

29. A method of producing an antibody or antibody fragment comprising, administering the norovirus VP1 protein of any one of claims 1 to 8 or 17 to a subject, or a host animal, thereby producing the antibody or the antibody fragment.

30. A method of producing an antibody or an antibody fragment comprising, administering the VLP of any one of claims 12, 13, 24 or 28 to a subject, or a host animal, thereby producing the antibody or the antibody fragment.

31. A plant, portion of the plant, or plant cell comprising the norovirus VP1 protein of any one of claims 1 to 8 or 17.

2018375695 29 Nov 2024

32. A plant, portion of the plant, or plant cell comprising the VLP of any one of claims 12, 13, 24 or 28.

33. A plant, portion of the plant, or plant cell comprising the recombinant polynucleotide of claim 9 to 11.

34. A plant extract comprising the norovirus VP1 protein produced by the method of any one of claims 14 to 16 or 18 to 20.

35. A plant extract comprising the norovirus VLP produced by the method of any one of claims 21 to 23 or 25 to 27.

36. A composition comprising an effective dose of the norovirus VP1 protein of any one of claims 1 to 8 or 17 or an effective dose of the VLP of any one of claims 12, 13, 24 or 28, and a pharmaceutically acceptable carrier, adjuvant, vehicle or excipient.

37. A vaccine comprising an effective dose of the norovirus VP1 protein of any one of claims 1 to 8 or 17 or an effective dose of the VLP of any one of claims 12, 13, 24 or 28.

38 A method for inducing an immune response comprising administering to a subject in need thereof an effective dose of the composition of claim 36 or the vaccine of claim 37.

39. Use of the composition of claim 36 or the vaccine of claim 37 in the manufacture of a medicament for inducing an immune response.

40. An antibody or antibody fragment prepared by administering the norovirus VP1 protein of any one of claims 1 to 8 or 17 to a subject, or host animal.

41. An antibody or antibody fragment prepared by administering the VLP of any one of claims 12, 13, 24 or 28 to a subject, or host animal.

42. A method for inducing immunity to a norovirus infection in a subject, the method comprising administering the VLP of any one of claims 12, 13, 24 or 28 to the subject.

43. The method of claim 42, wherein the VLP is administered to the subject orally intranasally, intramuscularly, intraperitoneally, intravenously, subcutaneously, rectally, or intravaginally.

2018375695 29 Nov 2024

44. A method of producing a modified norovirus VP1 protein, the method comprising:

(i) providing a norovirus VP1 protein, wherein the norovirus VP1 protein is not a GI.1 genotype;

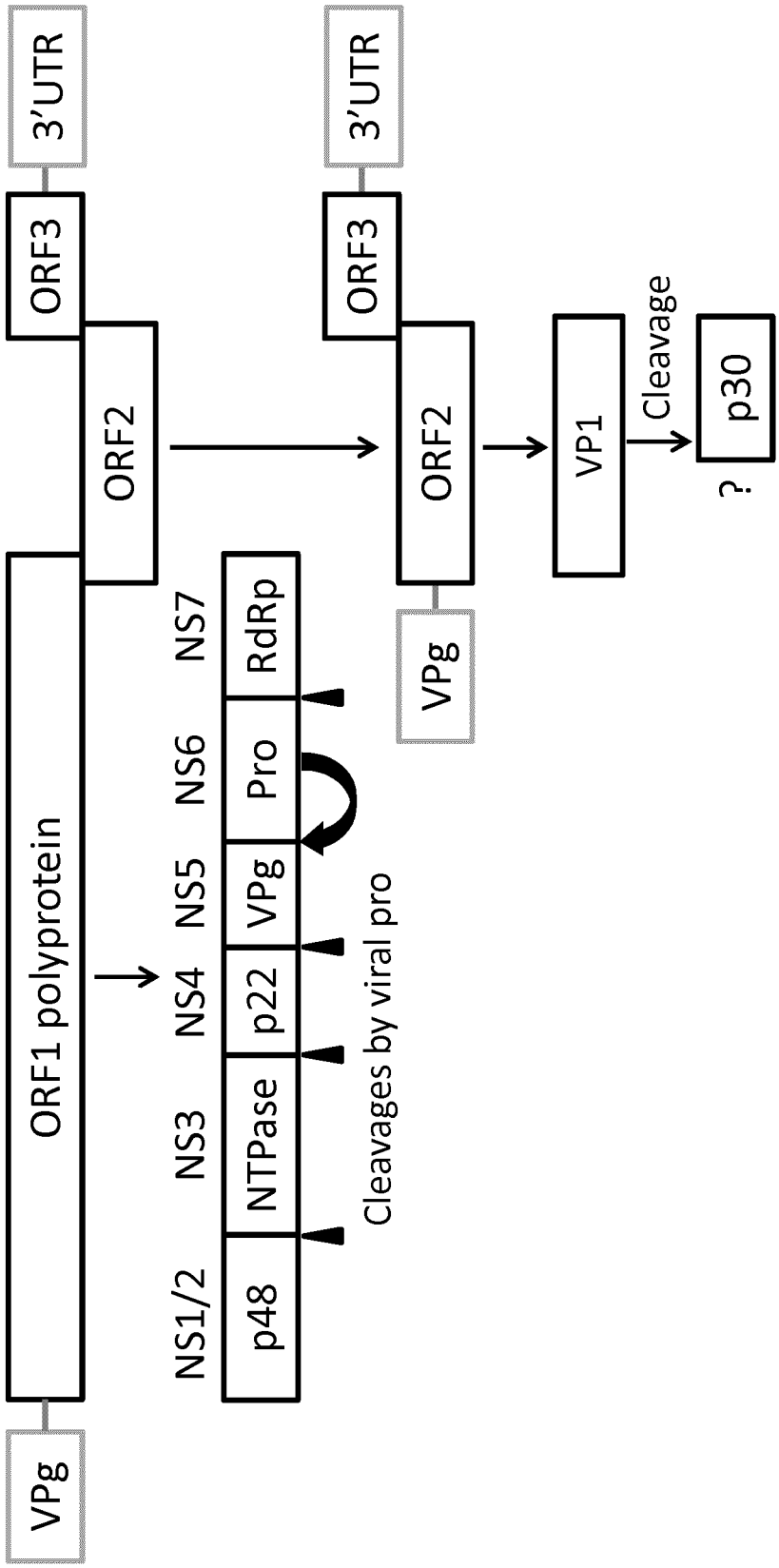
(ii) making one or more than one conserved amino acid substitution in the amino acid sequence of the norovirus VP1 protein, selected from:

an amino acid substitution at a position in sequence alignment with amino acid 43 of reference sequence SEQ ID NO:1 to valine, isoleucine, leucine, methionine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine;

an amino acid substitution at a position in sequence alignment with amino acid 57 of reference sequence SEQ ID NO:1 to isoleucine, leucine, valine, alanine, glycine, serine, threonine, asparagine, glutamine, lysine, or histidine;

an amino acid substitution at a position in sequence alignment with amino acid 84 of reference sequence SEQ ID NO:1 to serine, asparagine, cysteine, threonine, alanine, lysine or histidine; and

an amino acid substitution at a position in sequence alignment with amino acid 94 of reference sequence SEQ ID NO:1 to leucine, isoleucine, methionine, valine, threonine, aspartic acid, glutamic acid, asparagine, glutamine, lysine, or histidine.


3'UTR
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ORF2
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VPg
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VPg
Pro
RdRp
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VPg
VP1
Cleavage
p30
?

Figure 1A

Figure 1C

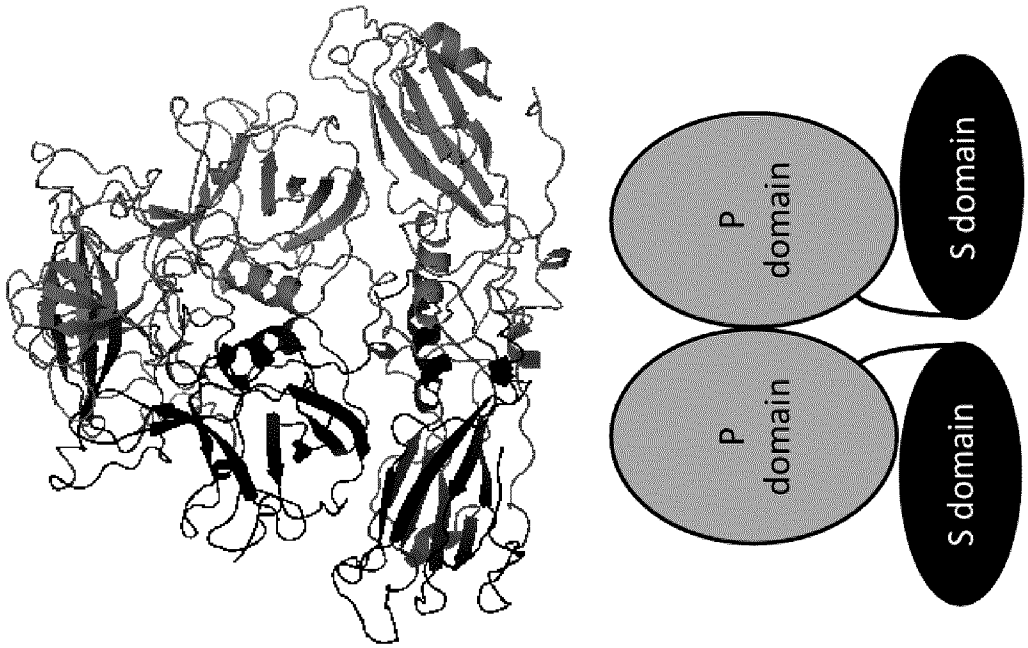


Figure 1B

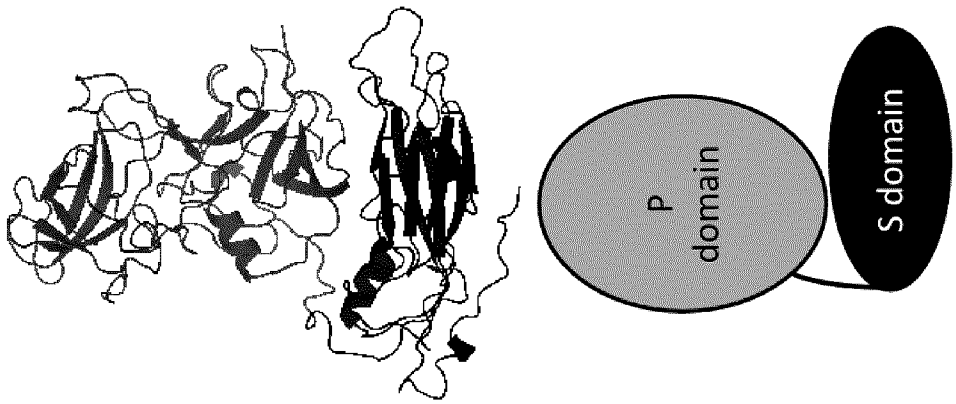


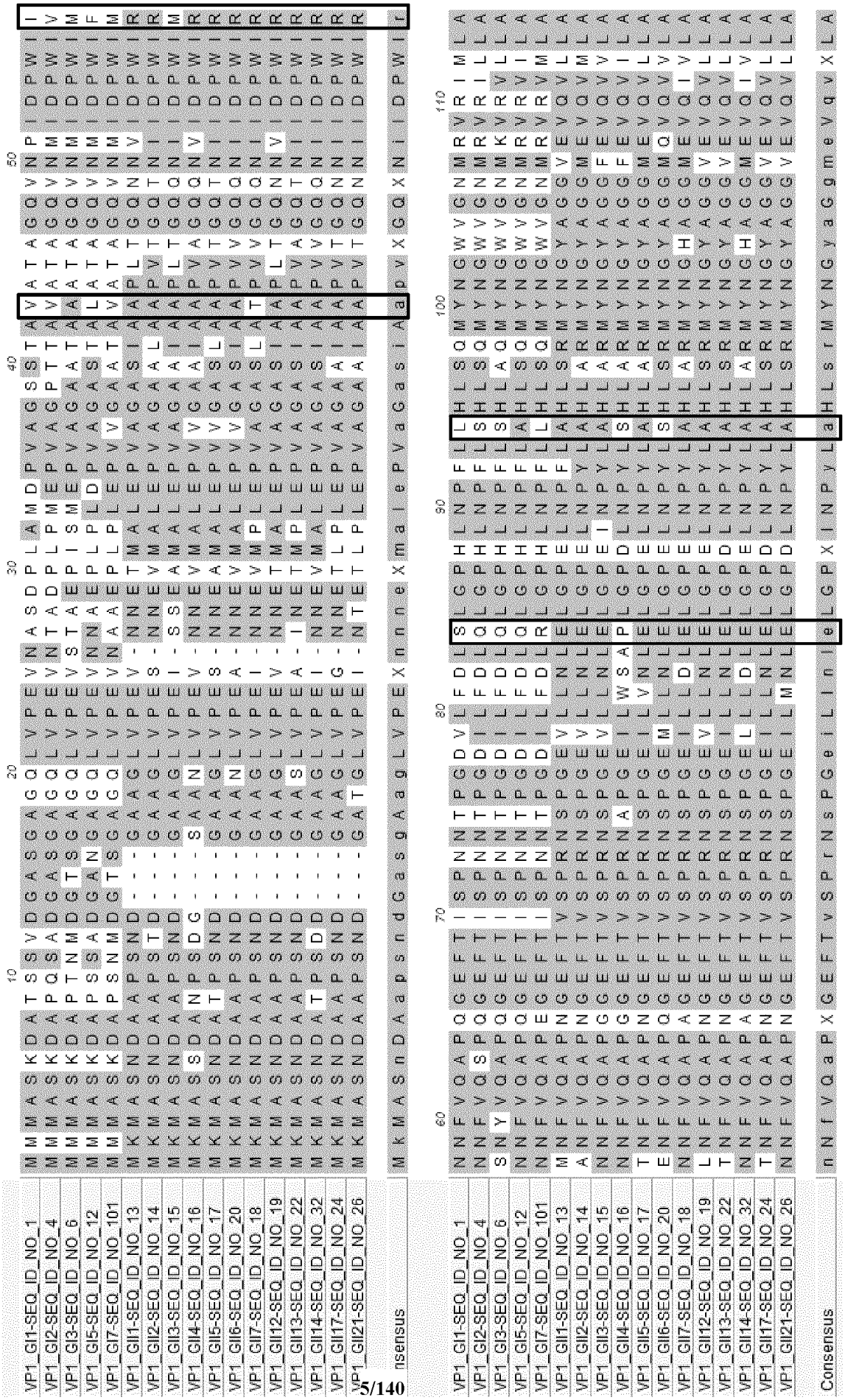
Figure 2A

Norovirus VP1 Major Capsid Amino Acid Sequences	
Access (Uniprot)	**Access (NCBI)**	**Strain Name**
Q83884	NP_056821	Hu/GI.1/United States/Norwalk/1968
D2DEL3	ACU56258	Hu/GI.2/Leuven/2003/BEL
H2DG70	AEY77318	Hu/GI.3/S29/2008/Lilla Edet/Sweden
A0A023NFH0	AHW99832	Hu/GI.5/Siklos/HUN5407/2013/HUN
A0A1I9WIM4	APA31979	Hu/GI.7/GA5043/USA/2014
H6V703	AFA55174	Hu/GII.1/Ascension208/2010/USA
S5ZGB5	AGT39206	Hu/GII.2/CGMH47/2011/TW
U3RI89	AGX01095	Hu/GII.3/Jingzhou/2013402/CHN
K4LM89	AFV08795	Hu/GII.4/Sydney/NSW0514/2012/AU
A0A1I9WIL4	APA31970	Hu/USA/2015/GII.P16_GII.4_Sydney/CA3477
A0A0U3E729	ALT54485	Hu/GII.5/AlbertaEI390/2013/CA
M9T020	AGI96397	Hu/GII.6/Ohio/490/2012/USA
F8SRB4	AEI29586	Hu/GII.12/HS206/2010/USA
H9AWU4	AFC89656	Hu/GII.17/Kawasaki323/2014/JP
H9AWV4	AFC89665	Hu/GII.21/Salisbury150/2011/USA
Norovirus VP2 Minor Capsid Amino Acid Sequence		
Access (Uniprot)	**Access (NCBI)**	**Strain Name**
W6APL0	AHI59155	Hu/GII.6/HS245/2010/USA

Figure 2B

Norovirus VP1 Major Capsid Nucleotide Sequences	
Genome Access (NCBI)	**Strain Name**
M87661	Hu/GI.1/United States/Norwalk/1968
FJ515294	Hu/GI.2/Leuven/2003/BEL
JN603244	Hu/GI.3/S29/2008/Lilla Edet/Sweden
KJ402295	Hu/GI.5/Siklos/HUN5407/2013/HUN
KX907730	Hu/GI.7/GA5043/USA/2014
JN797508	Hu/GII.1/Ascension208/2010/USA
KC464505	Hu/GII.2/CGMH47/2011/TW
KF306213	Hu/GII.3/Jingzhou/2013402/CHN
JX459908	Hu/GII.4/Sydney/NSW0514/2012/AU
KU311160	Hu/GII.5/AlbertaEI390/2013/CA
KC464321	Hu/GII.6/Ohio/490/2012/USA
HQ664990	Hu/GII.12/HS206/2010/USA
JN899242	Hu/GII.17/Kawasaki323/2014/JP
JN899245	Hu/GII.21/Salisbury150/2011/USA
Norovirus VP2 Minor Capsid Nucleotide Sequence	
Access (NCBI)	**Strain Name**
KJ407072	Hu/GII.6/HS245/2010/USA

Figure 2C-1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VP1_GII2-SEQ_ID_NO_14
VP1_GII3-SEQ_ID_NO_15
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VP1_GII5-SEQ_ID_NO_17
VP1_GII6-SEQ_ID_NO_20
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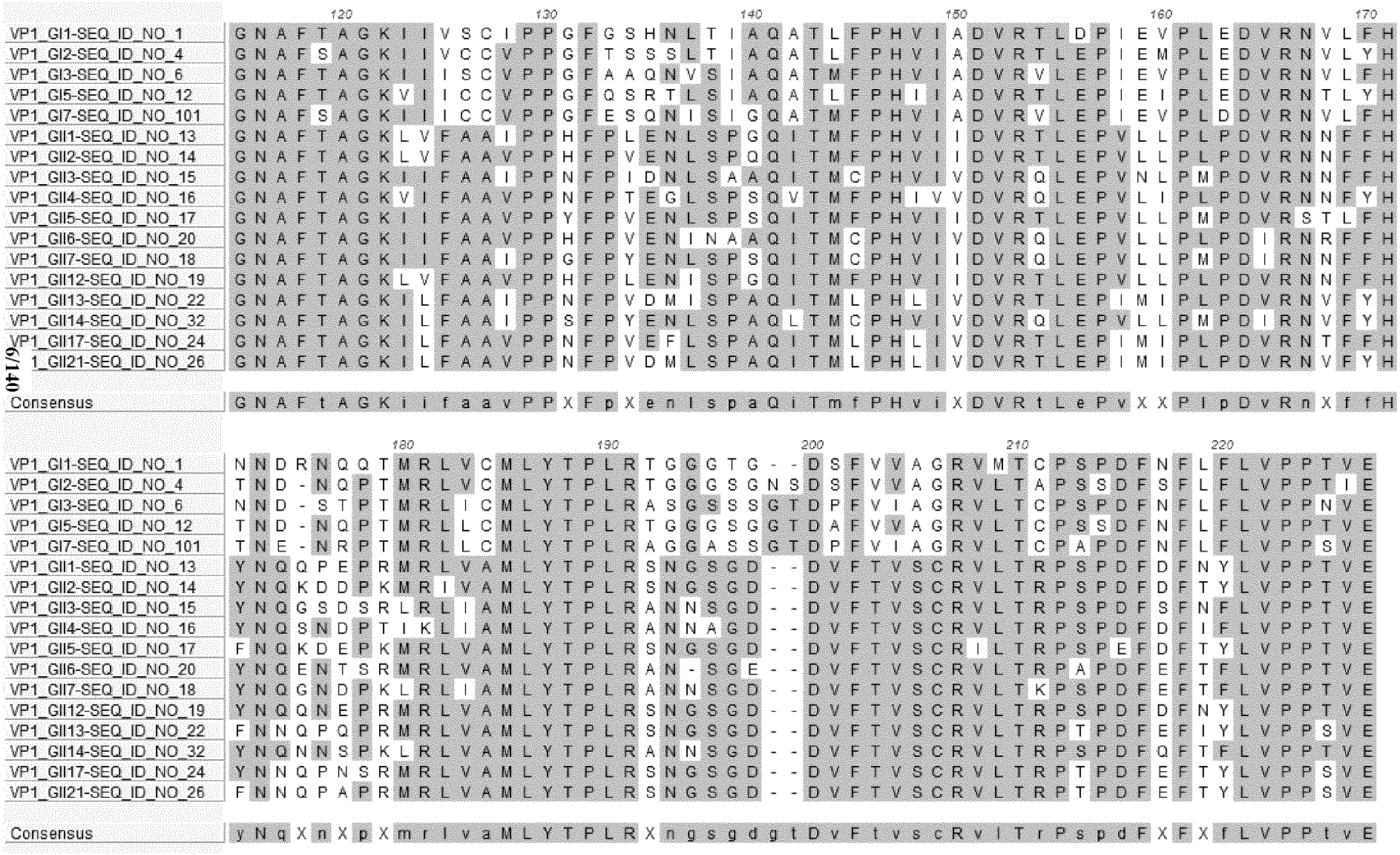
nsensus
Consensus

Figure 2C-2


120 130 140 150 160 170
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VP1_GI2-SEQ_ID_NO_4 GNAFSAGKIIVCCVPPGFTSSSLTIAQATLFPHVIADVRTLEPIEMPLEDVRNVLYH
VP1_GI3-SEQ_ID_NO_6 GNAFTAGKIIISCVPPGFAAQNVSIAQATMFPHVIADVRVLEPIEVPLEDVRNVLFH
VP1_GI5-SEQ_ID_NO_12 GNAFTAGKVIICCVPPGFQSRTLSIAQATLFPHIIADVRTLEPIEIPLEDVRNTLYH
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VP1_GII1-SEQ_ID_NO_13 GNAFTAGKLVFAAIPPHFPLENLSPGQITMFPHVIIDVRTLEPVLLPLPDVRNNFFH
VP1_GII2-SEQ_ID_NO_14 GNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLLPLPDVRNNFFH
VP1_GII3-SEQ_ID_NO_15 GNAFTAGKIIFAAIPPNFPIDNLSAAQITMCPHVIVDVRQLEPVNLPMPDVRNNFFH
VP1_GII4-SEQ_ID_NO_16 GNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLIPLPDVRNNFYH
VP1_GII5-SEQ_ID_NO_17 GNAFTAGKIIFAAVPPYFPVENLSPSQITMFPHVIIDVRTLEPVLLPMPDVRSTLFH
VP1_GII6-SEQ_ID_NO_20 GNAFTAGKIIFAAVPPHFPVENINAAQITMCPHVIVDVRQLEPVLLPLPDIRNRFFH
VP1_GII7-SEQ_ID_NO_18 GNAFTAGKIIFAAIPPGFPYENLSPSQITMCPHVIIDVRQLEPVLLPMPDIRNNFFH
VP1_GII12-SEQ_ID_NO_19 GNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVIIDVRTLEPVLLPLPDVRNNFFH
VP1_GII13-SEQ_ID_NO_22 GNAFTAGKILFAAIPPNFPVDMISPAQITMLPHLIVDVRTLEPIMIPLPDVRNVFYH
VP1_GII14-SEQ_ID_NO_32 GNAFTAGKILFAAIPPSFPYENLSPAQLTMCPHVIVDVRQLEPVLLPMPDIRNVFYH
VP1_GII17-SEQ_ID_NO_24 GNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLIVDVRTLEPIMIPLPDVRNTFFH
VP1_GII21-SEQ_ID_NO_26 GNAFTAGKILFAAVPPNFPVDMLSPAQITMLPHLIVDVRTLEPIMIPLPDVRNVFYH
Consensus GNAFtAGKiifaavPPXFpXenlspaQiTmfPHvixDVRtLePvXXPIpDvRnXfFH
180 190 200 210 220
VP1_GI1-SEQ_ID_NO_1 NNDRNQQTMRLVCMLYTPLRTGGGTG--DSFVVAGRVMTCPSPDFNFLFLVPPTVE
VP1_GI2-SEQ_ID_NO_4 TND-NQPTMRLVCMLYTPLRTGGGSGNSDSFVVAGRVLTAPSSDFSFLFLVPPTIE
VP1_GI3-SEQ_ID_NO_6 NND-STPTMRLICMLYTPLRASGGSSSGTDPFVIAGRVLTCPSPDFNFLFLVPPNVE
VP1_GI5-SEQ_ID_NO_12 TND-NQPTMRLLCMLYTPLRTGGGSGGTDAFVVAGRVLTCPSSDFNFLFLVPPTVE
VP1_GI7-SEQ_ID_NO_101 TNE-NRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPDFNFLFLVPPSVE
VP1_GII1-SEQ_ID_NO_13 YNQQPEPRMRLVAMLYTPLRSNGSGD--DVFTVSCRVLTRPSPDFDFNYLVPPTVE
VP1_GII2-SEQ_ID_NO_14 YNQKDDPKMRIVAMLYTPLRSNGSGD--DVFTVSCRVLTRPSPDFDFTYLVPPTVE
VP1_GII3-SEQ_ID_NO_15 YNQGSDSRLRLIAMLYTPLRANNSGD--DVFTVSCRVLTRPSPDFSFNFLVPPTVE
VP1_GII4-SEQ_ID_NO_16 YNQSNDPTIKLIAMLYTPLRANNAGD--DVFTVSCRVLTRPSPDFDFIFLVPPTVE
VP1_GII5-SEQ_ID_NO_17 FNQKDEPKMRLVAMLYTPLRSNGSGD--DVFTVSCRILTRPSPEFDFTYLVPPTVE
VP1_GII6-SEQ_ID_NO_20 YNQENTSRMRLVAMLYTPLRAN-SGE--DVFTVSCRVLTRPAPDFEFTFLVPPTVE
VP1_GII7-SEQ_ID_NO_18 YNQGNDPKLRLIAMLYTPLRANNSGD--DVFTVSCRVLTKPSPDFEFTFLVPPTVE
VP1_GII12-SEQ_ID_NO_19 YNQQNEPRMRLVAMLYTPLRSNGSGD--DVFTVSCRVLTRPSPDFDFNYLVPPTVE
VP1_GII13-SEQ_ID_NO_22 FNNQPQPRMRLVAMLYTPLRSNGSGD--DVFTVSCRVLTRPTPDFEFIYLVPPSVE
VP1_GII14-SEQ_ID_NO_32 YNQNNSPKLRLVAMLYTPLRANNSGD--DVFTVSCRVLTRPSPDFQFTFLVPPTVE
VP1_GII17-SEQ_ID_NO_24 YNNQPNSRMRLVAMLYTPLRSNGSGD--DVFTVSCRVLTRPTPDFEFTYLVPPSVE
VP1_GII21-SEQ_ID_NO_26 FNNQPAPRMRLVAMLYTPLRSNGSGD--DVFTVSCRVLTRPTPDFEFTYLVPPSVE
Consensus yNqXnXpXmrlvaMLYTPLRXngsgdgtDvFtvscRvlTrPspdFXFXfLVPPtvE

Figure 3A

GII.4
GI.1
225.0
150.0
100.0
75.0
50.0
35.0
25.0
15.0
GII.12
GI.1
225.0
150.0
100.0
75.0
50.0
35.0
25.0
15.0
GI.5
GI.1
225.0
150.0
100.0
75.0
50.0
35.0
25.0
15.0

FIGURE 3B

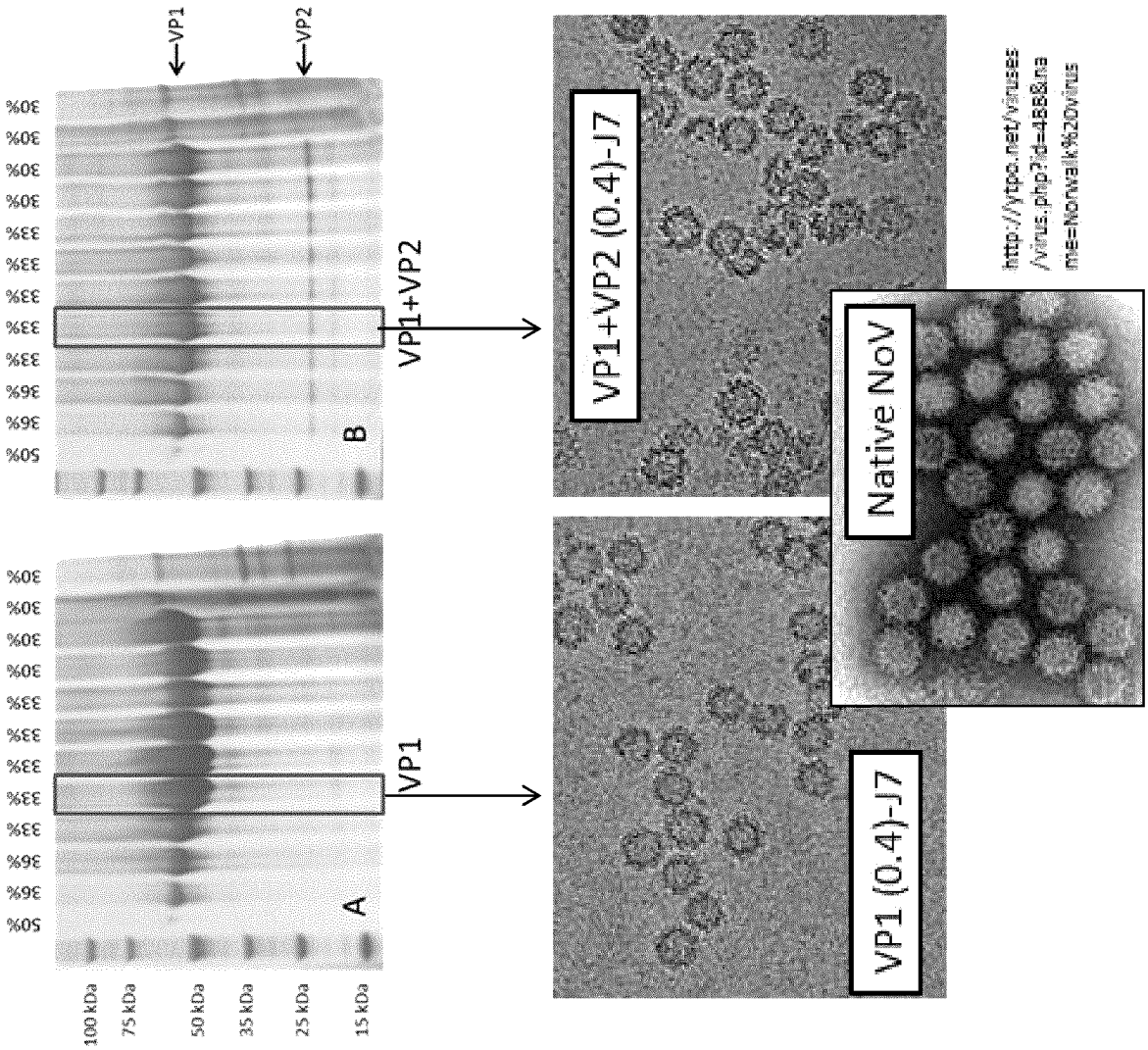

VP1
VP2
B
A
VP1+VP2
VP1
100 kDa
75 kDa
50 kDa
35 kDa
25 kDa
15 kDa
VP1+VP2 (0.4)-J7
VP1 (0.4)-J7
Native NoV
http://ytpo.net/viruses/virus.php?id=458&name=Norwalk%20virus

Figure 3C

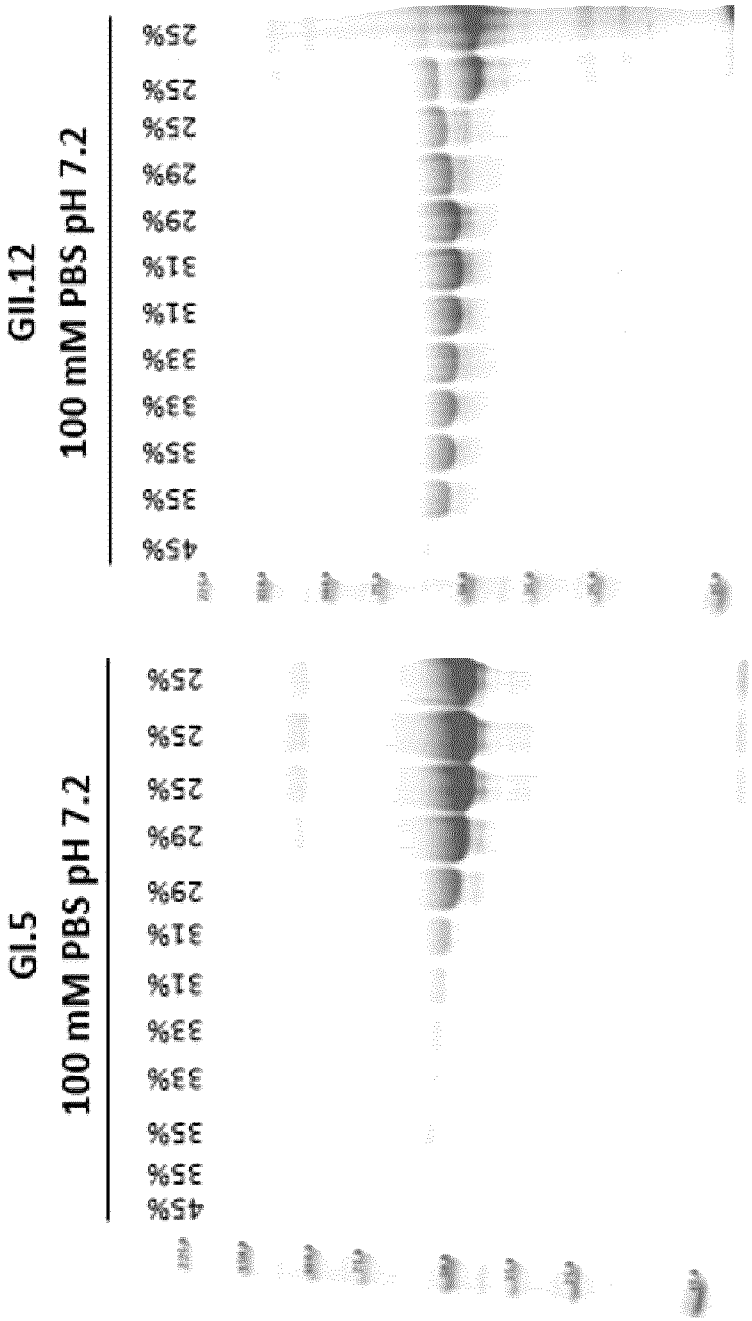

GII.12
100 mM PBS pH 7.2
25%
25%
25%
29%
29%
31%
31%
33%
33%
35%
35%
45%
GI.5
100 mM PBS pH 7.2
25%
25%
25%
29%
29%
31%
31%
33%
33%
35%
35%
45%

FIGURE 3D

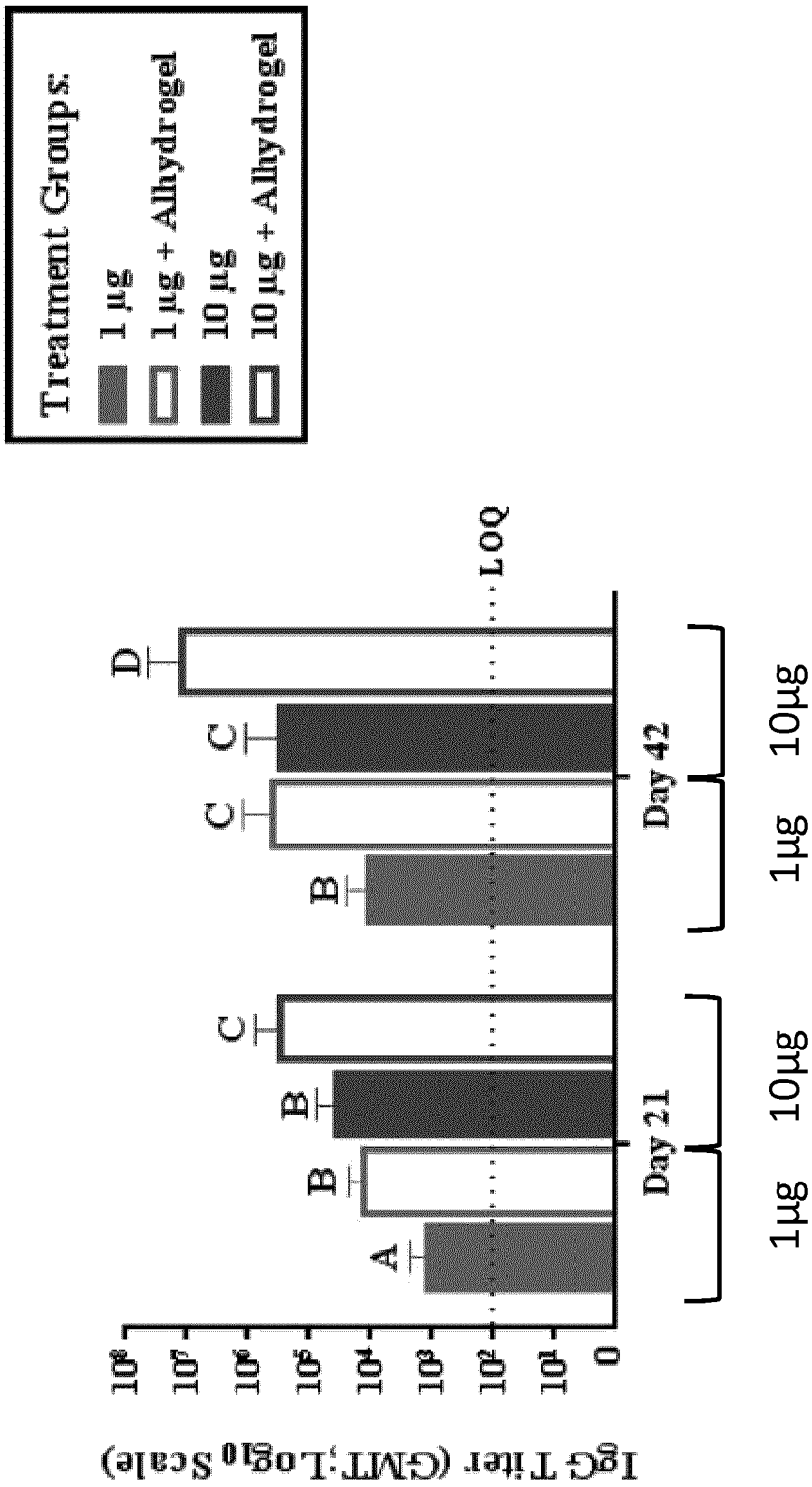

Treatment Groups:
1 µg
1 µg + Alhydrogel
10 µg
10 µg + Alhydrogel
IgG Titer (GMT; Log10 Scale)
10⁸
10⁷
10⁶
10⁵
10⁴
10³
10²
10¹
0
LOQ
A
B
B
B
C
C
C
D
Day 21
Day 42
1µg
10µg
1µg
10µg

Figure 4B

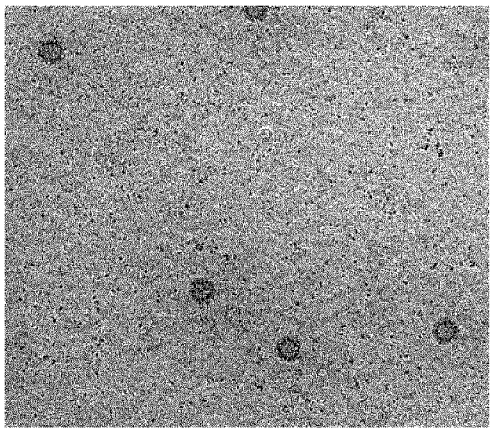
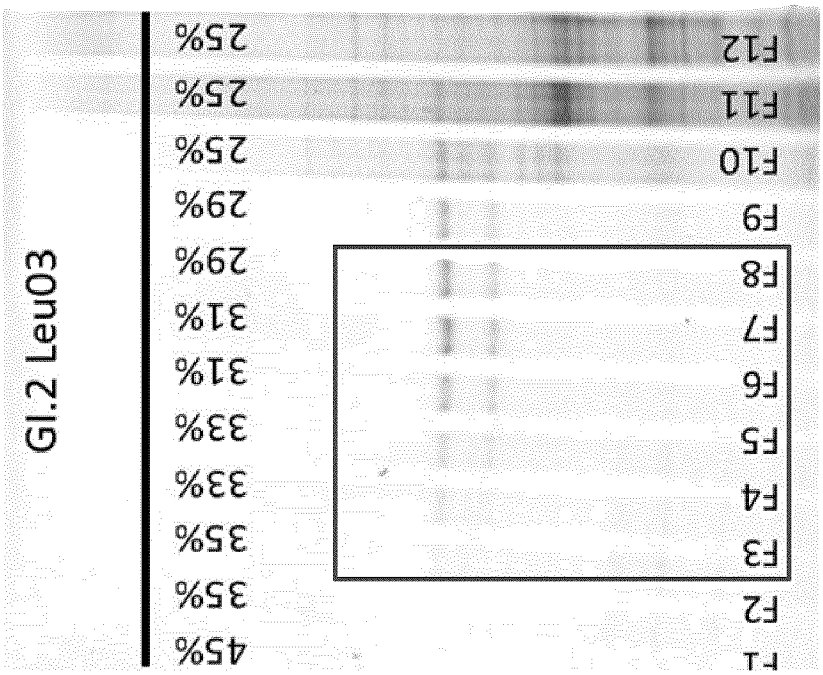
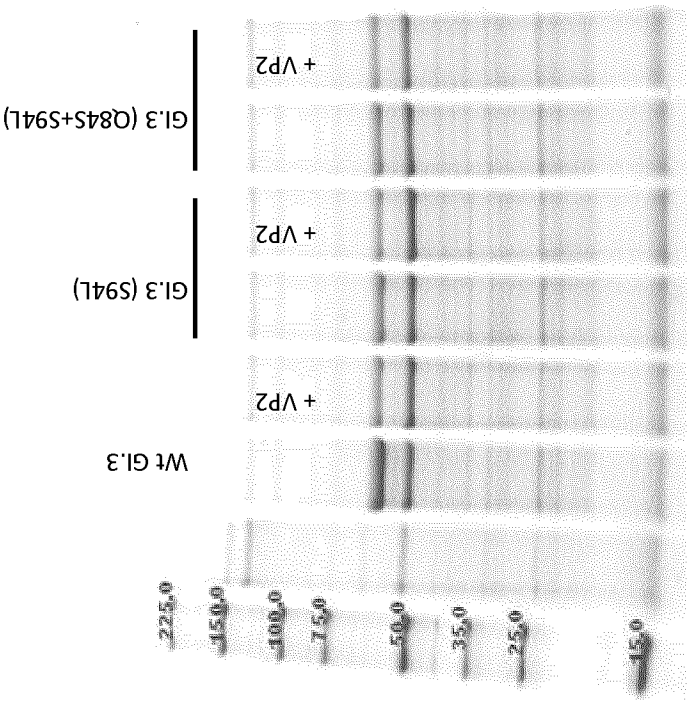


Figure 4A



GI.3/S29/2008/Lila Edet/Sweden

Figure 5A



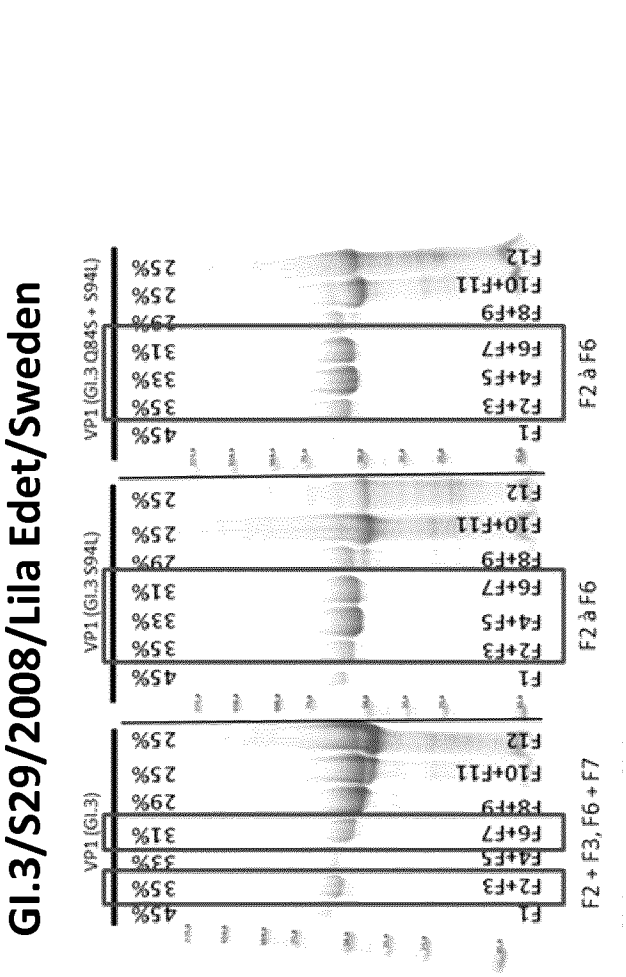


Figure 5B

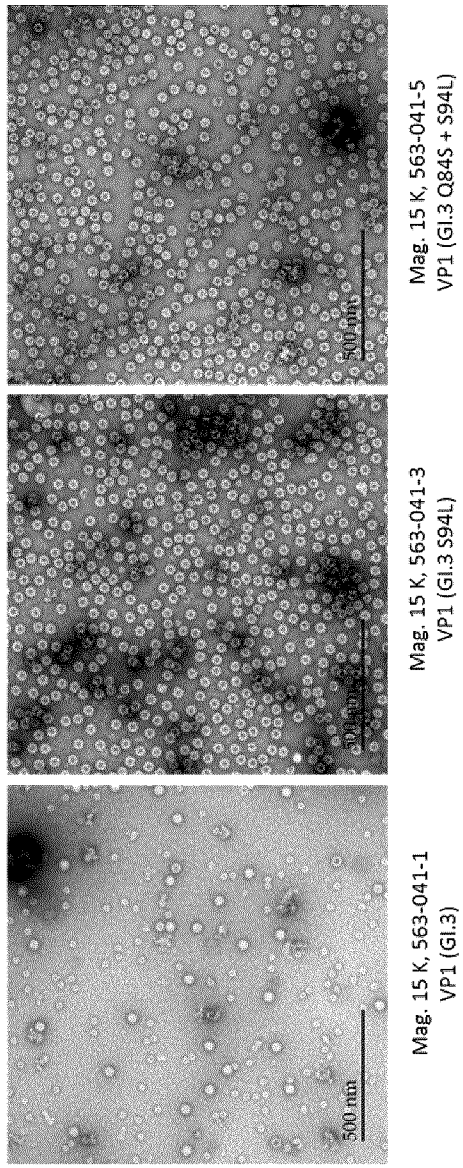


Figure 5C

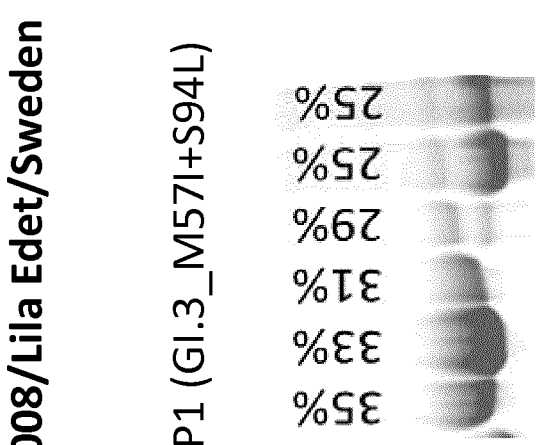


Figure 5D

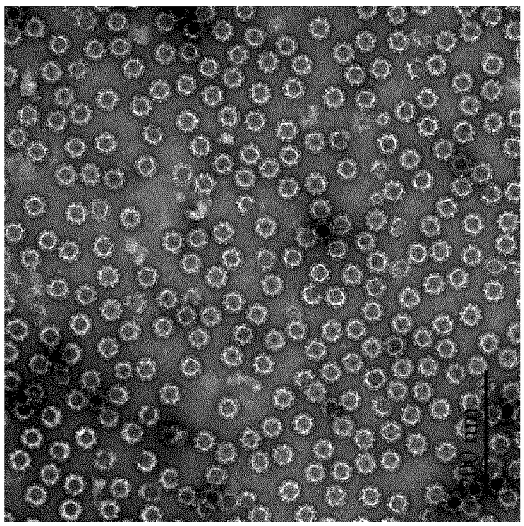
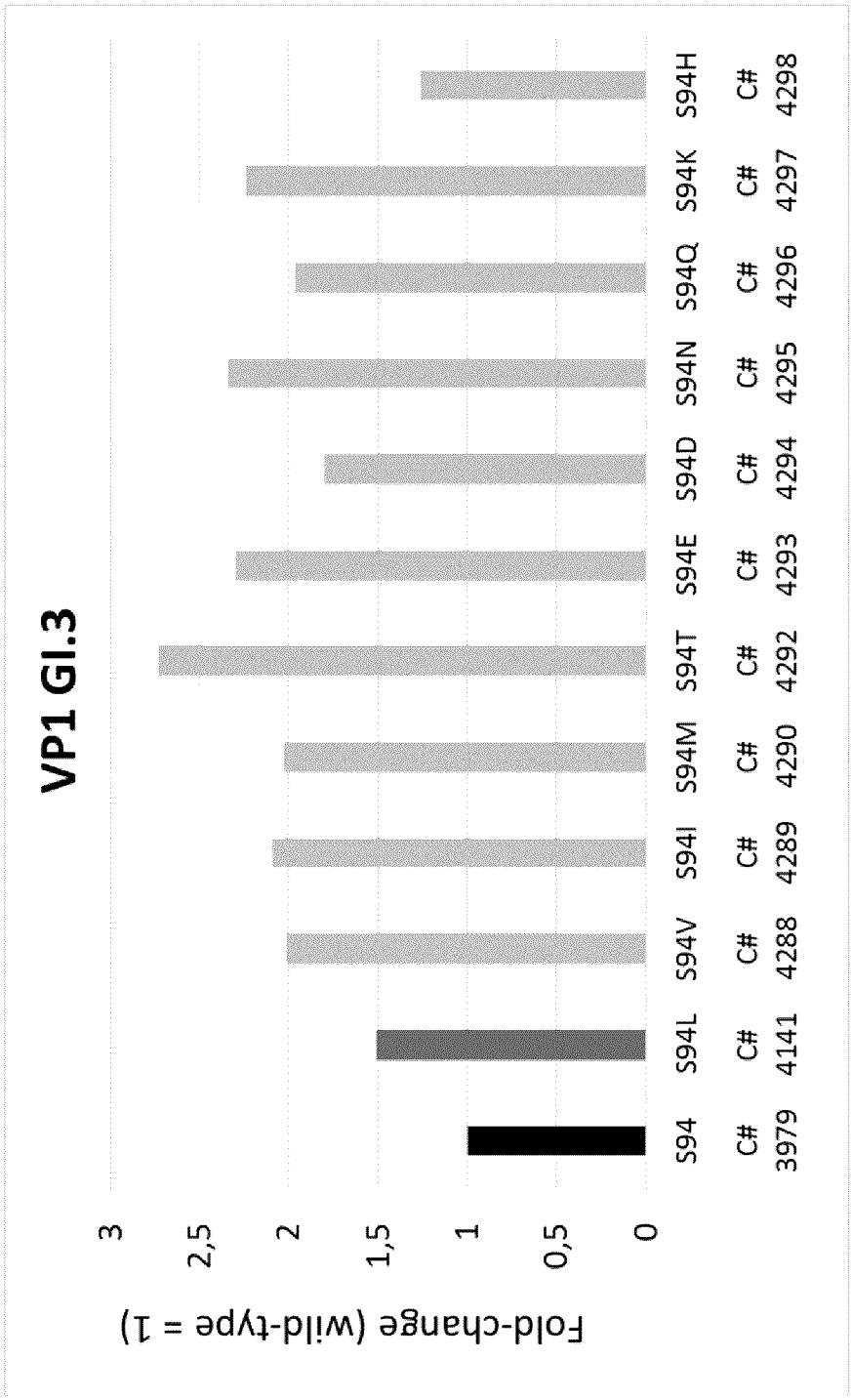


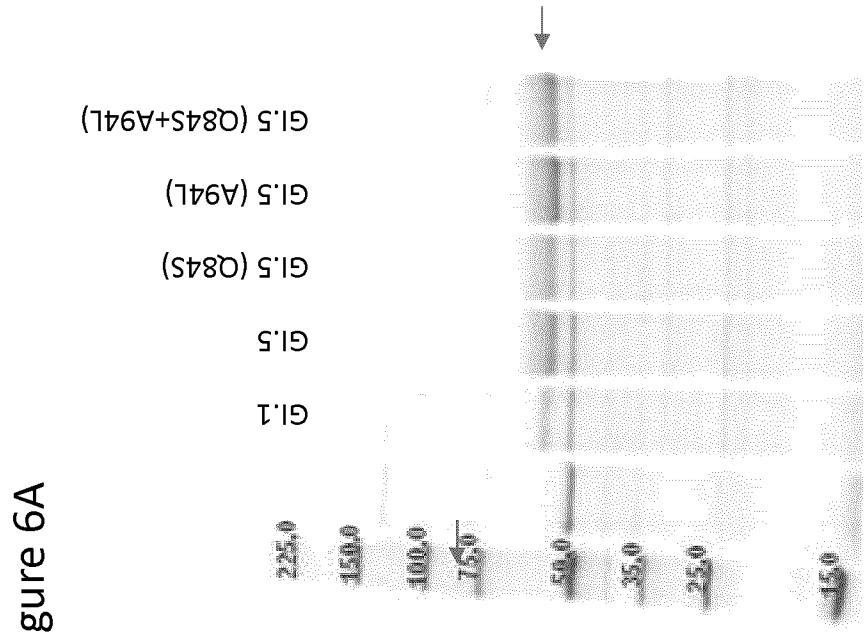
Figure 5E

Figure 5F


VP1 GI.3
Fold-change (wild-type = 1)
3
2,5
2
1,5
1
0,5
0
S94
C# 3979
S94L
C# 4141
S94V
C# 4288
S94I
C# 4289
S94M
C# 4290
S94T
C# 4292
S94E
C# 4293
S94D
C# 4294
S94N
C# 4295
S94Q
C# 4296
S94K
C# 4297
S94H
C# 4298

GI.5/Siklos/HUN54107/2013/HUN

Figure 6A



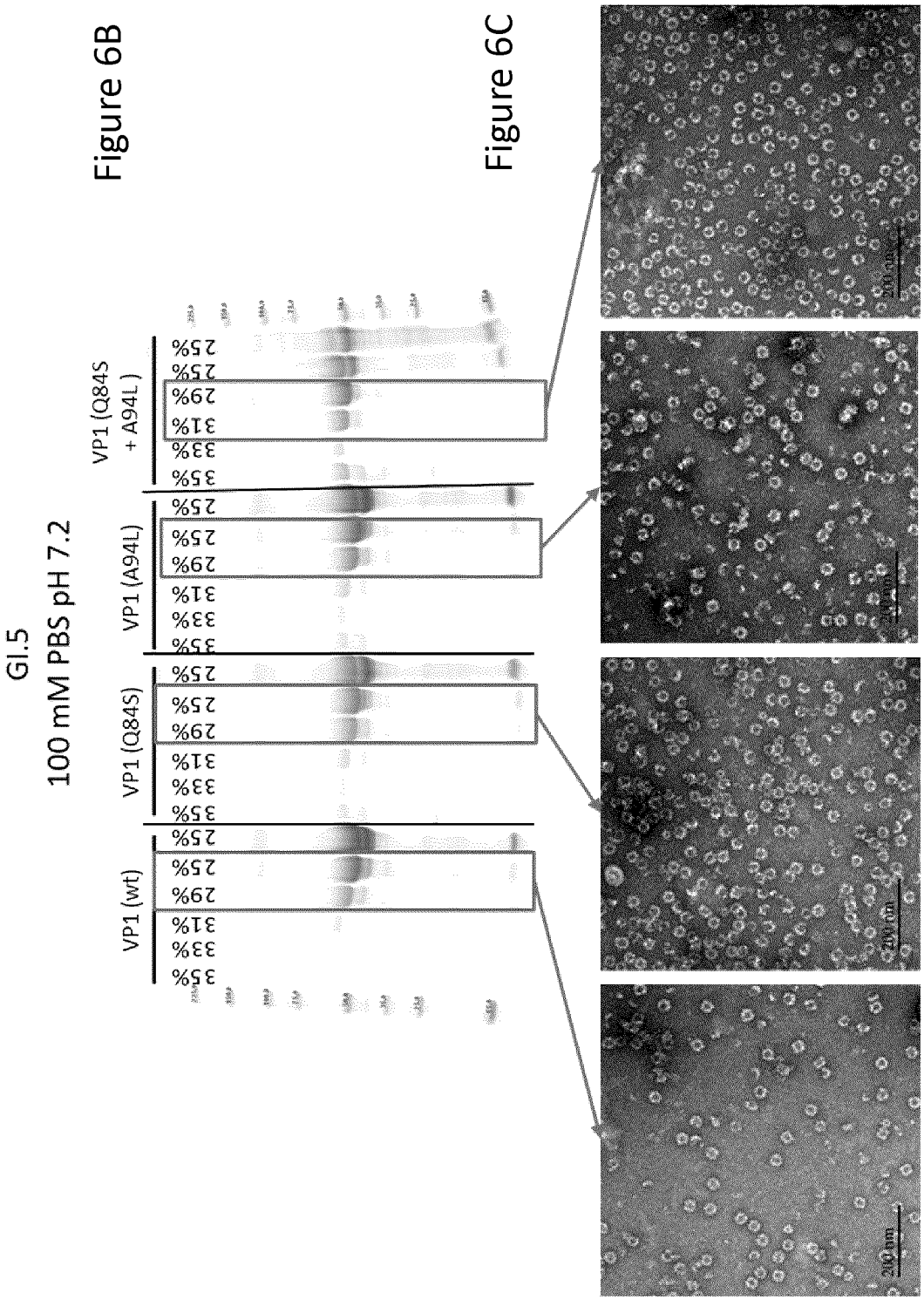
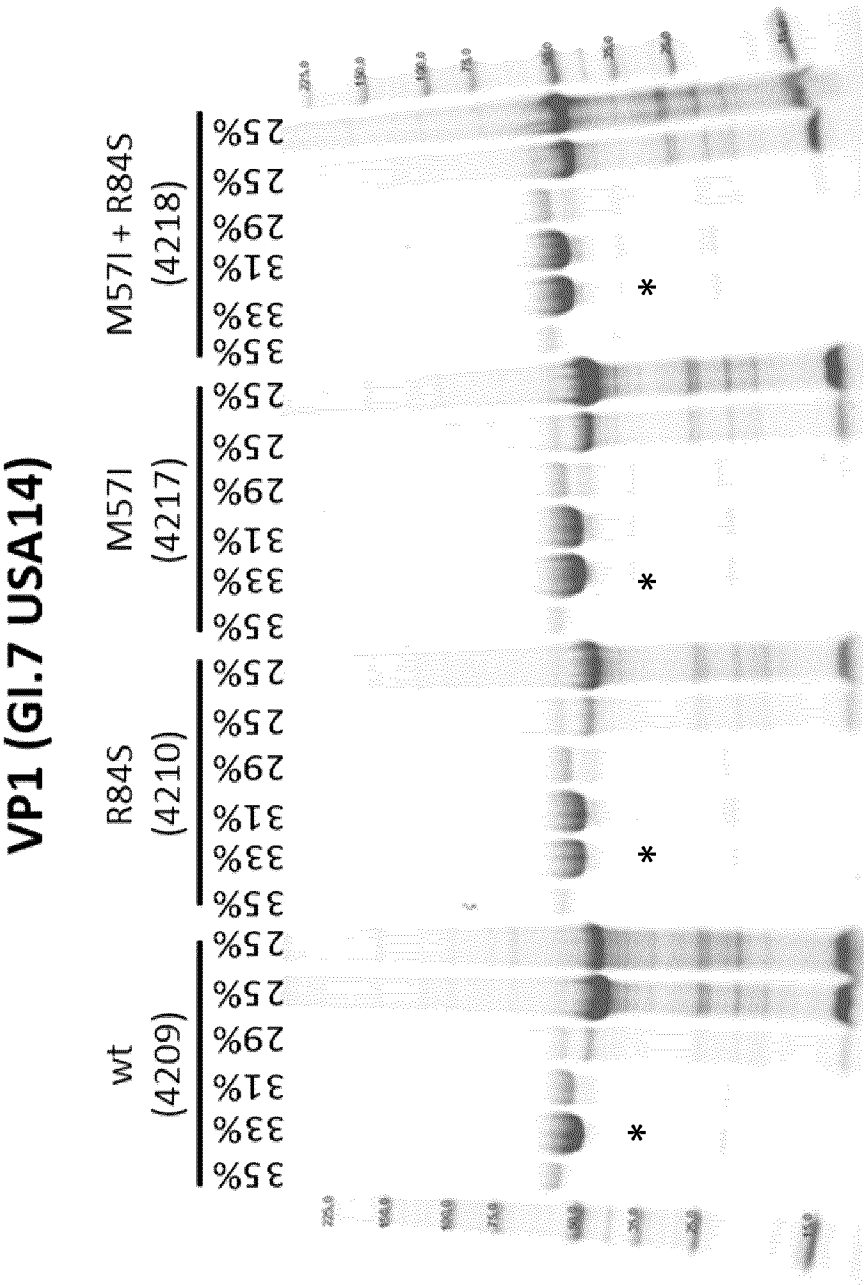


Figure 6B
Figure 6C
GI.5
100 mM PBS pH 7.2
VP1 (Q84S + A94L)
VP1 (A94L)
VP1 (Q84S)
VP1 (wt)
25%
25%
29%
31%
33%
35%
200 nm

Figure 6D


VP1 (GI.7 USA14)
wt (4209)
R84S (4210)
M571 (4217)
M571 + R84S (4218)
25%
25%
29%
31%
33%
35%
*

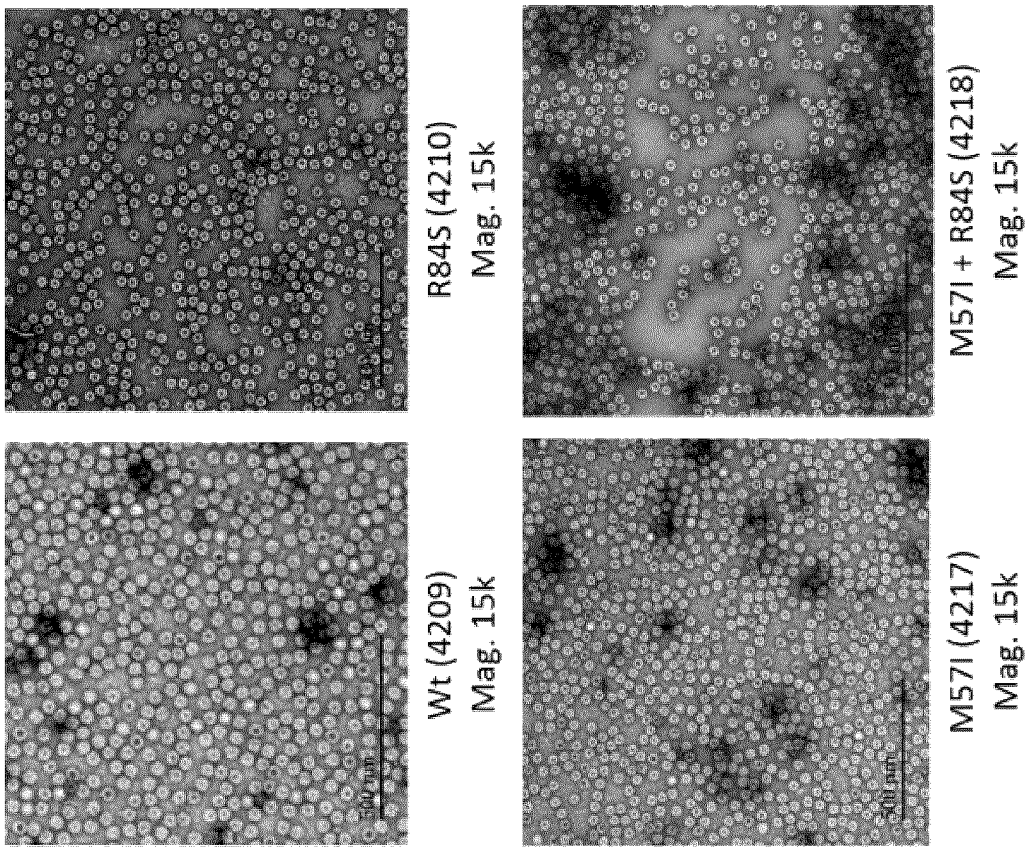

VP1 GI.7/GA5043/USA/2014
Wt (4209)
Mag. 15k
R84S (4210)
Mag. 15k
M57I (4217)
Mag. 15k
M57I + R84S (4218)
Mag. 15k

Figure 6E

Figure 6F

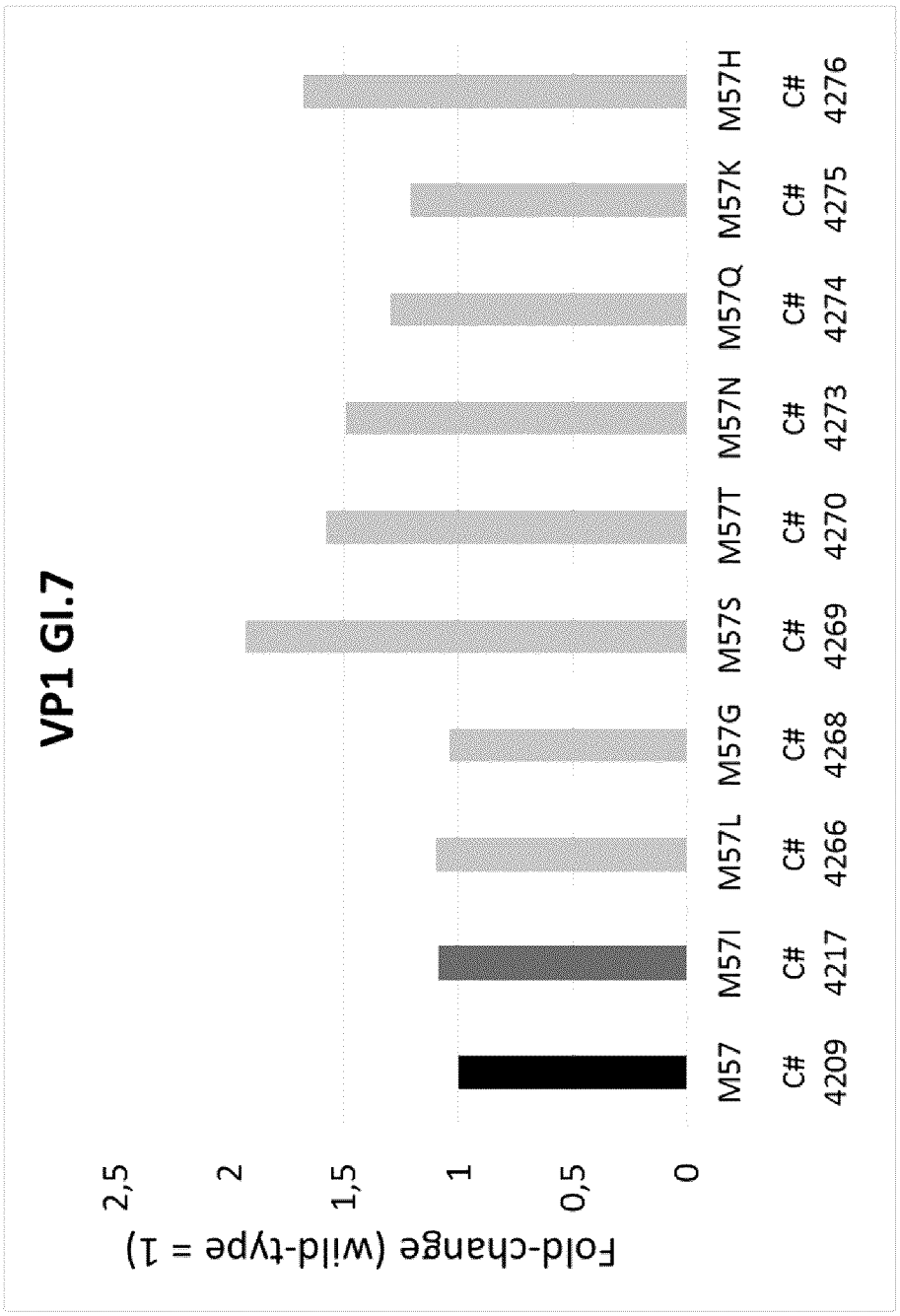

VP1 GI.7
Fold-change (wild-type = 1)
2,5
2
1,5
1
0,5
0
M57
C# 4209
M57I
C# 4217
M57L
C# 4266
M57G
C# 4268
M57S
C# 4269
M57T
C# 4270
M57N
C# 4273
M57Q
C# 4274
M57K
C# 4275
M57H
C# 4276

Figure 7A

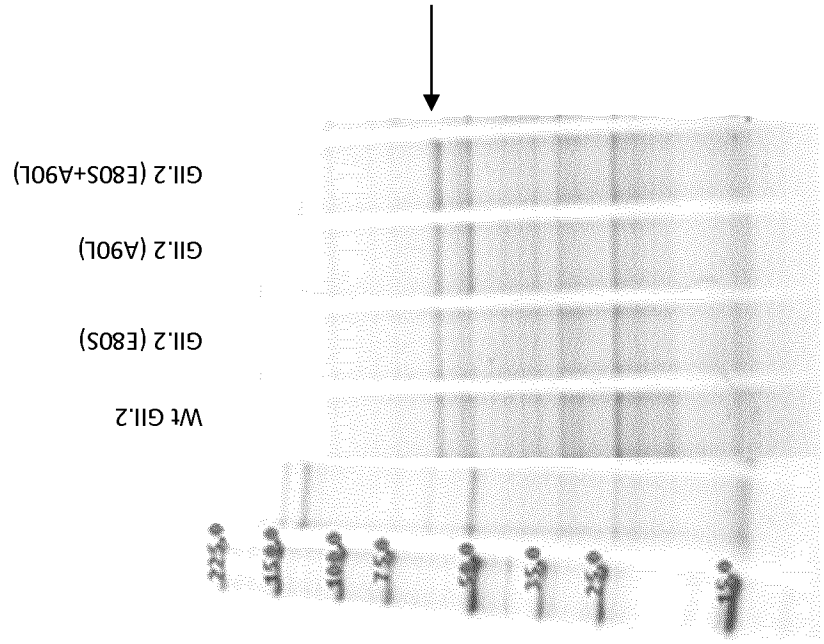


Figure 7B

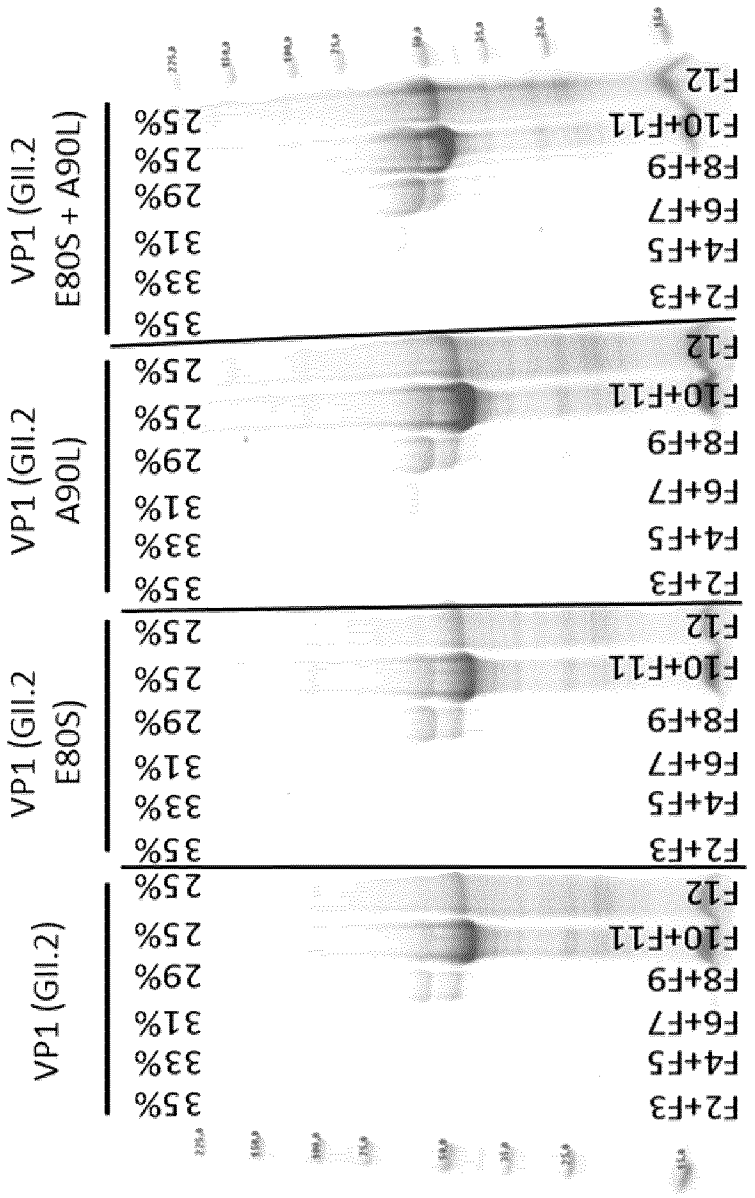
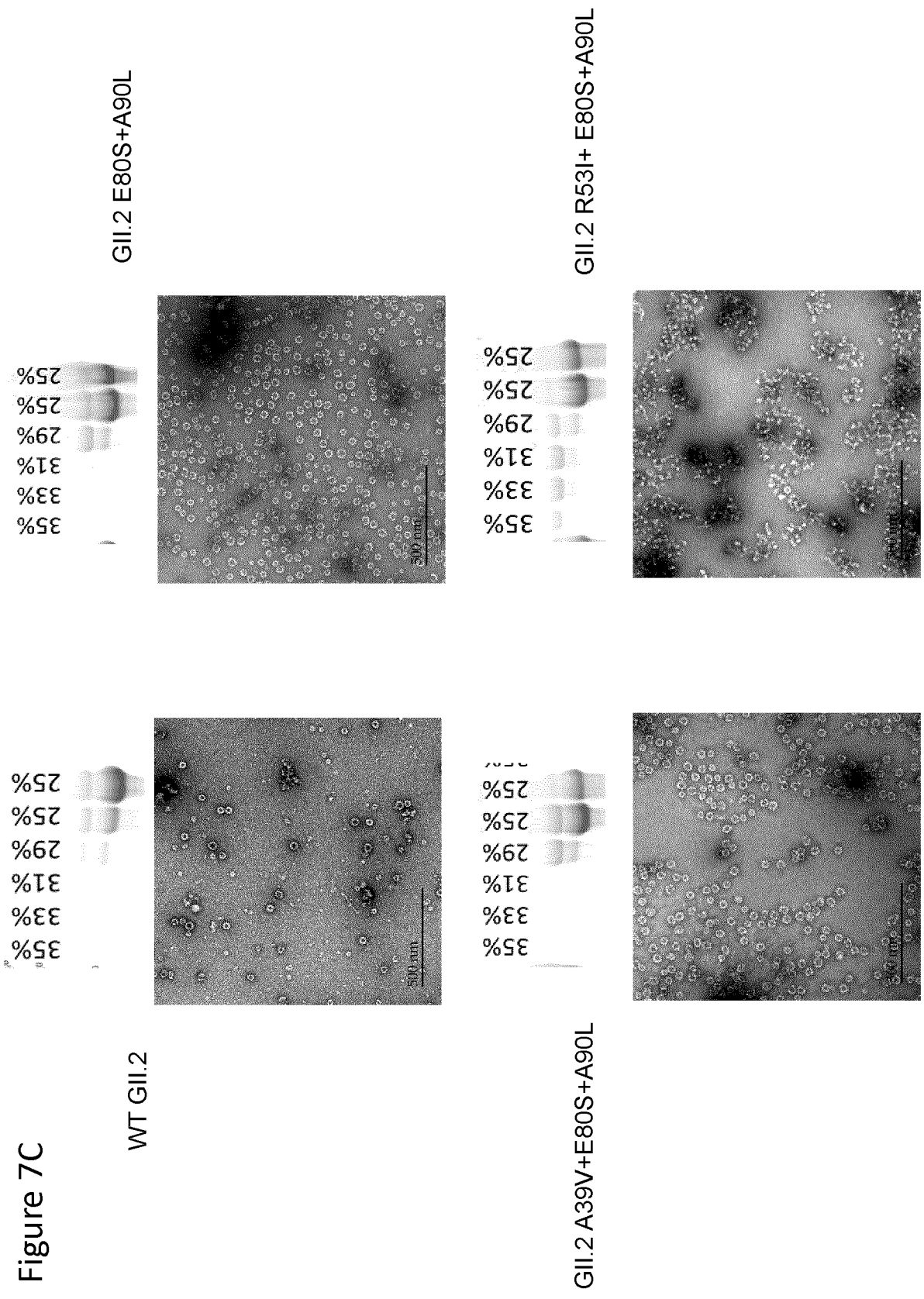

VP1 (GII.2)
VP1 (GII.2 E80S)
VP1 (GII.2 A90L)
VP1 (GII.2 E80S + A90L)
25%
29%
31%
33%
35%
F12
F10+F11
F8+F9
F6+F7
F4+F5
F2+F3

Figure 7C


WT GII.2
GII.2 E80S+A90L
GII.2 R53I+ E80S+A90L
GII.2 A39V+E80S+A90L
35%
33%
31%
29%
25%
25%
500 nm

GII.3/Jingzhou/2013402/CHN

Figure 8A

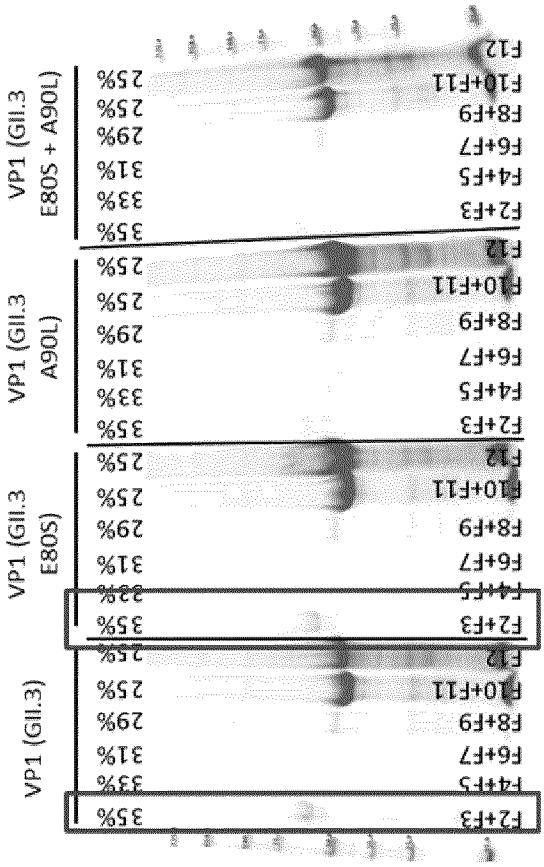
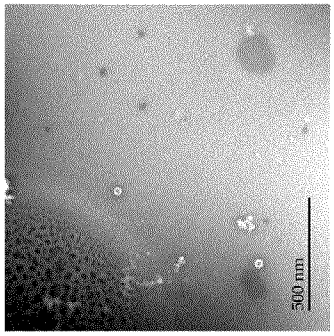
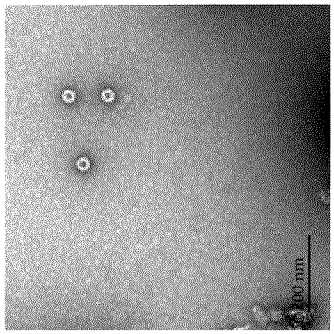


Figure 8B



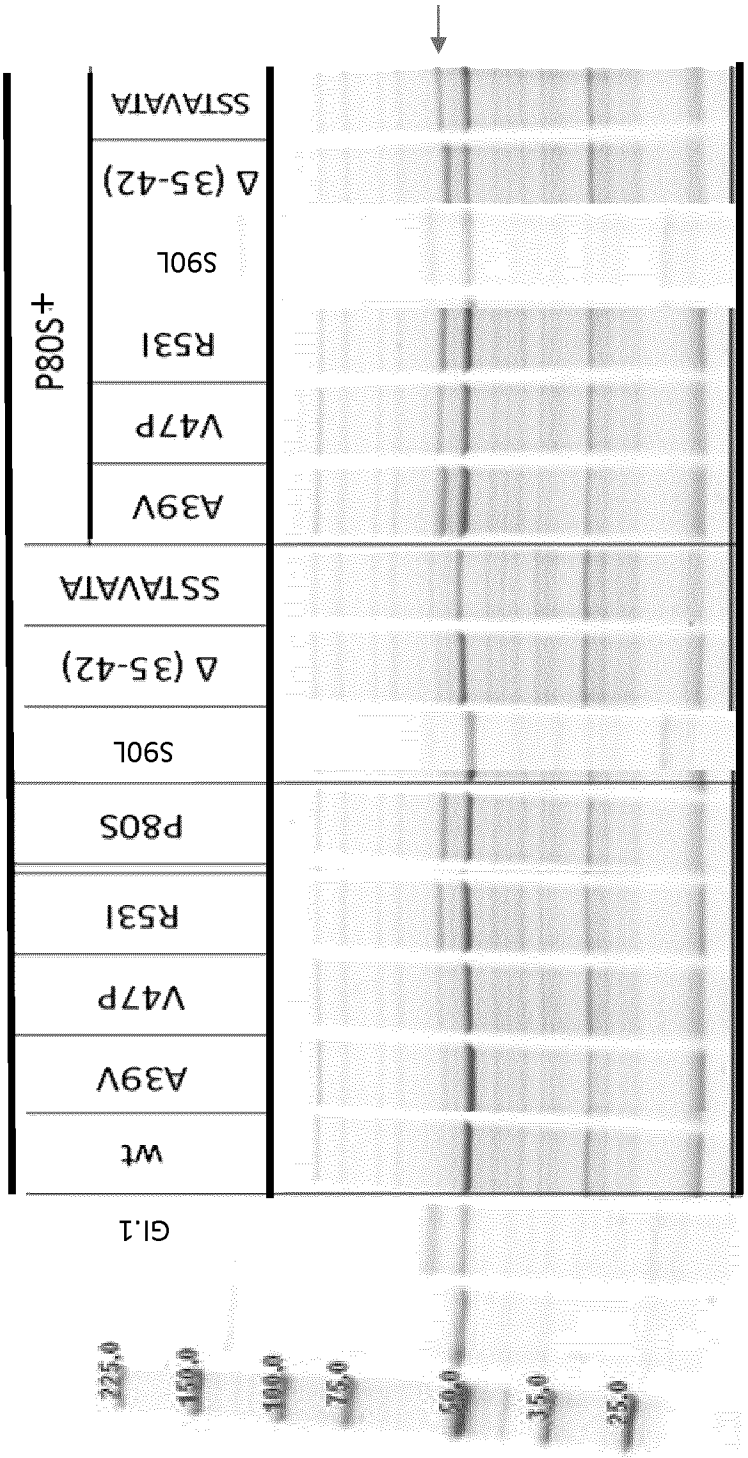
Mag. 15 K, 563-041-8
VP1 (GII.3 E80S)



Mag. 25 K, 563-041-7
VP1 (GII.3)

GII.4/Sydney/SW0514/2012/AU

Figure 9A



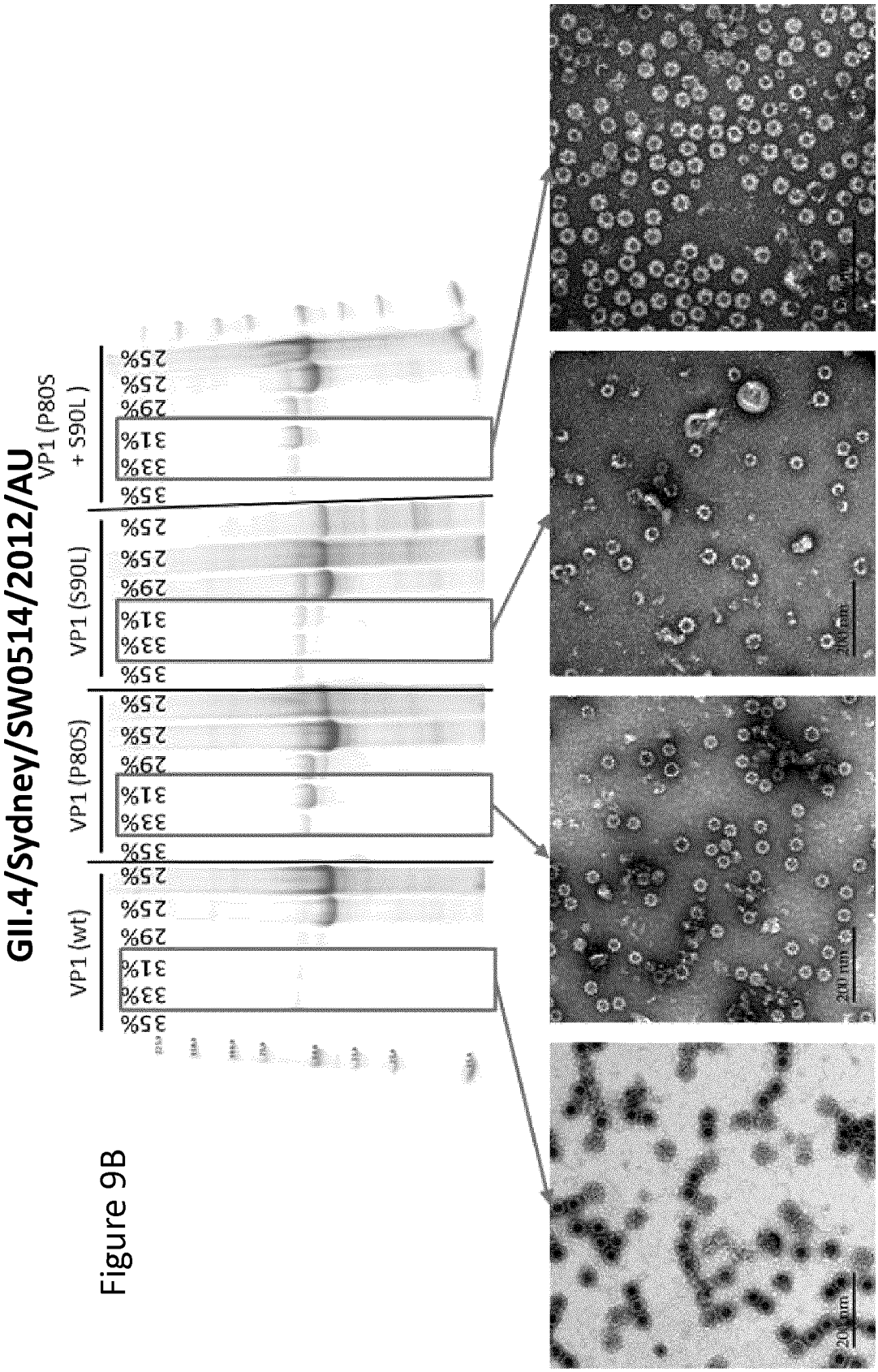
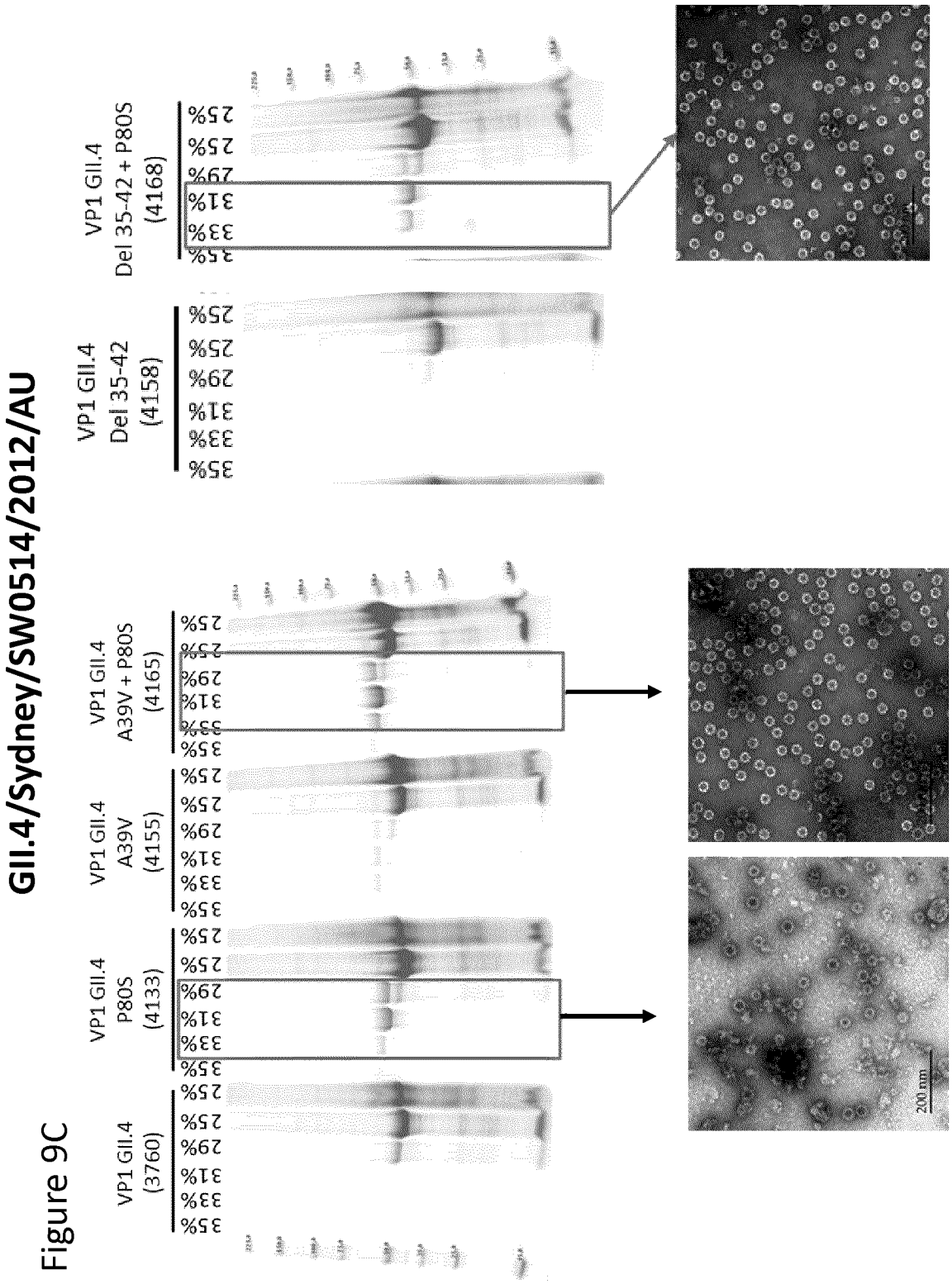

GII.4/Sydney/SW0514/2012/AU
VP1 (wt)
VP1 (P80S)
VP1 (S90L)
VP1 (P80S + S90L)
25%
25%
29%
31%
33%
35%
200 nm

Figure 9B

Figure 9C


GII.4/Sydney/SW0514/2012/AU
VP1 GII.4 (3760)
VP1 GII.4 P80S (4133)
VP1 GII.4 A39V (4155)
VP1 GII.4 A39V + P80S (4165)
VP1 GII.4 Del 35-42 (4158)
VP1 GII.4 Del 35-42 + P80S (4168)
25%
29%
31%
33%
35%
200 nm

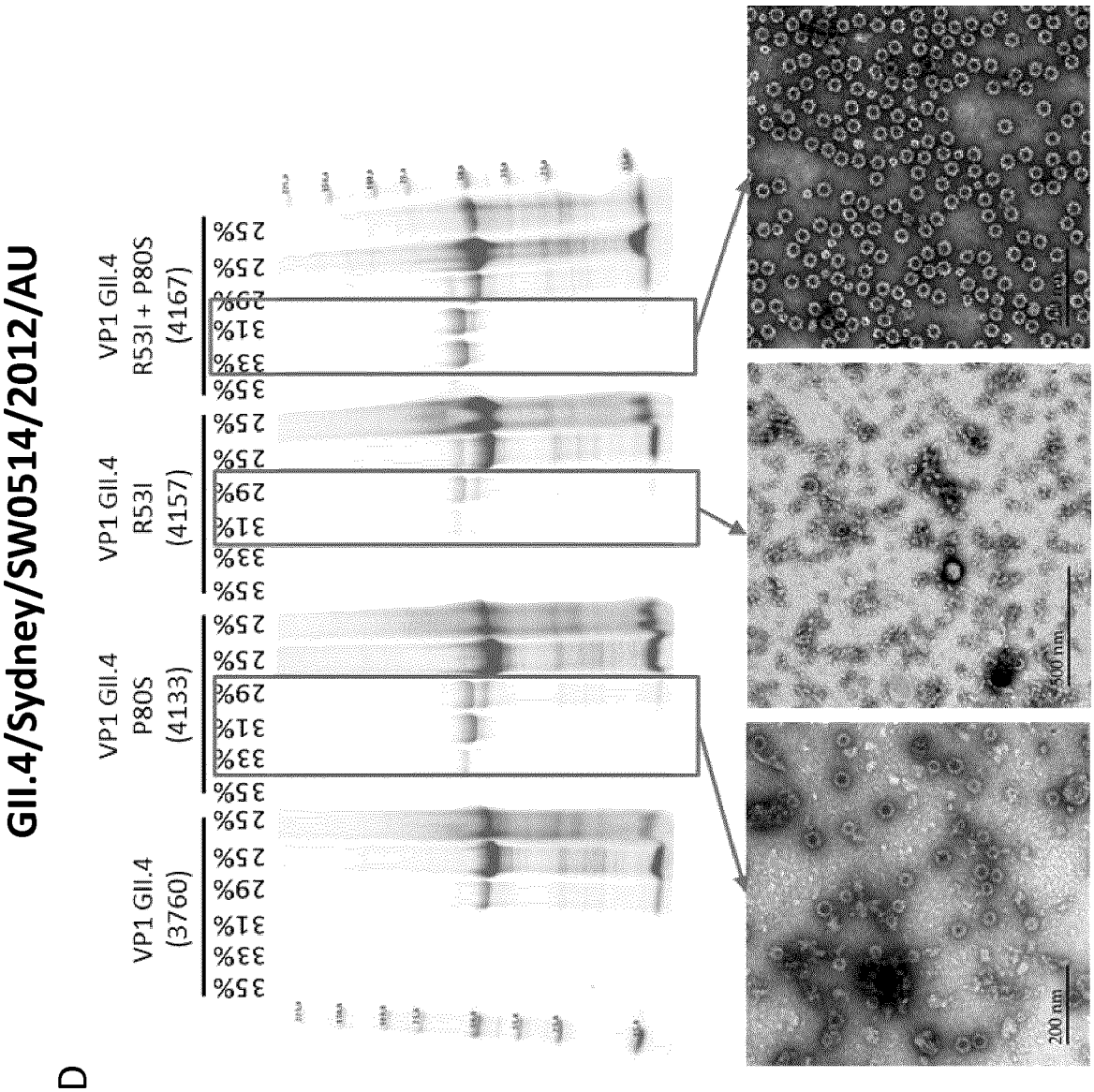

GII.4/Sydney/SW0514/2012/AU
VP1 GII.4 (3760)
VP1 GII.4 P80S (4133)
VP1 GII.4 R53I (4157)
VP1 GII.4 R53I + P80S (4167)
25%
29%
31%
33%
35%
200 nm

Figure 9D

Figure 9E

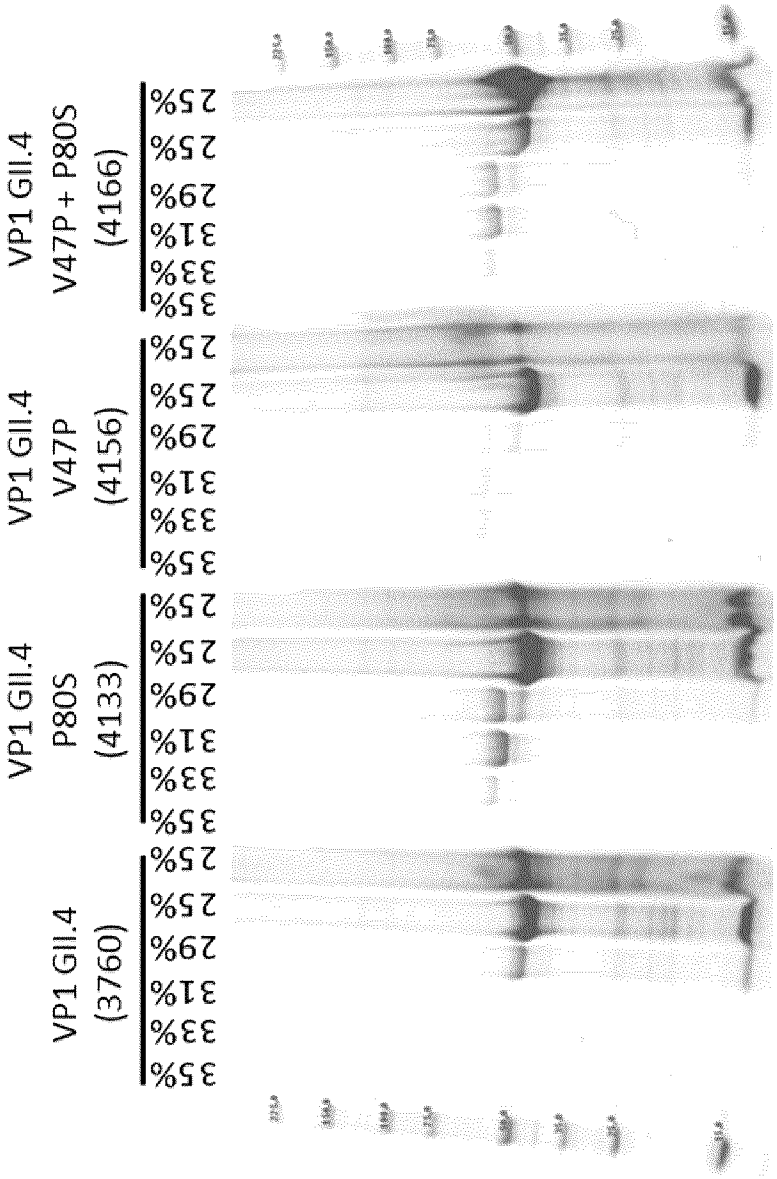

VP1 GII.4 (3760)
VP1 GII.4 P80S (4133)
VP1 GII.4 V47P (4156)
VP1 GII.4 V47P + P80S (4166)
25%
25%
29%
31%
33%
35%

Figure 9F

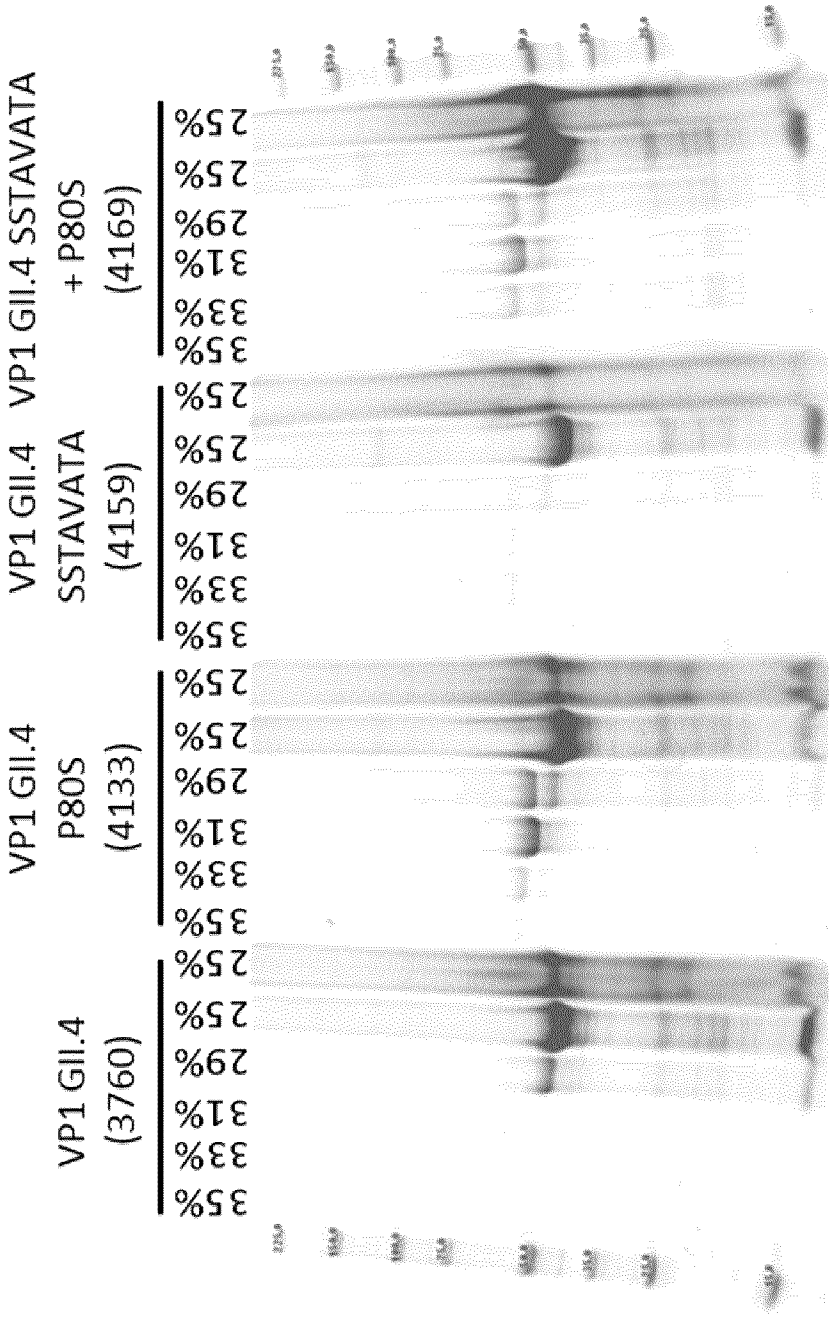

VP1 GII.4 (3760)
VP1 GII.4 P80S (4133)
VP1 GII.4 SSTAVATA (4159)
VP1 GII.4 SSTAVATA + P80S (4169)
25%
25%
29%
31%
33%
35%

Figure 9G

GII.4/Sydney/SW0514/2012/AU

GII.4_A39V+R53I+P80S

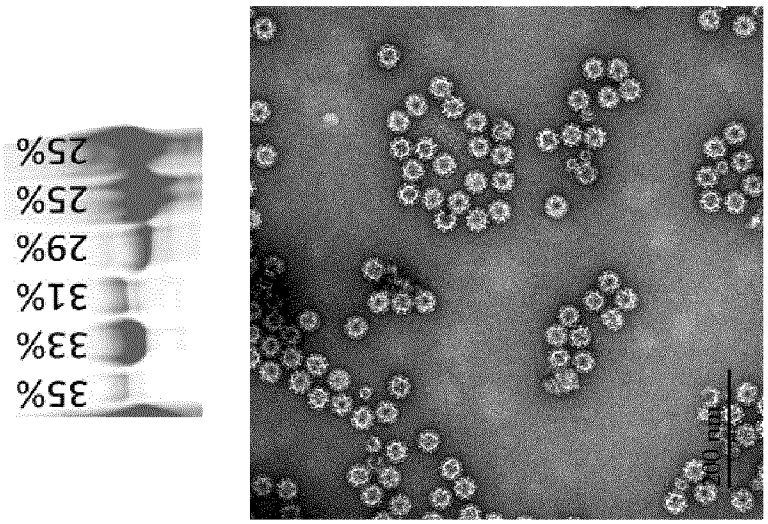


Figure 9H

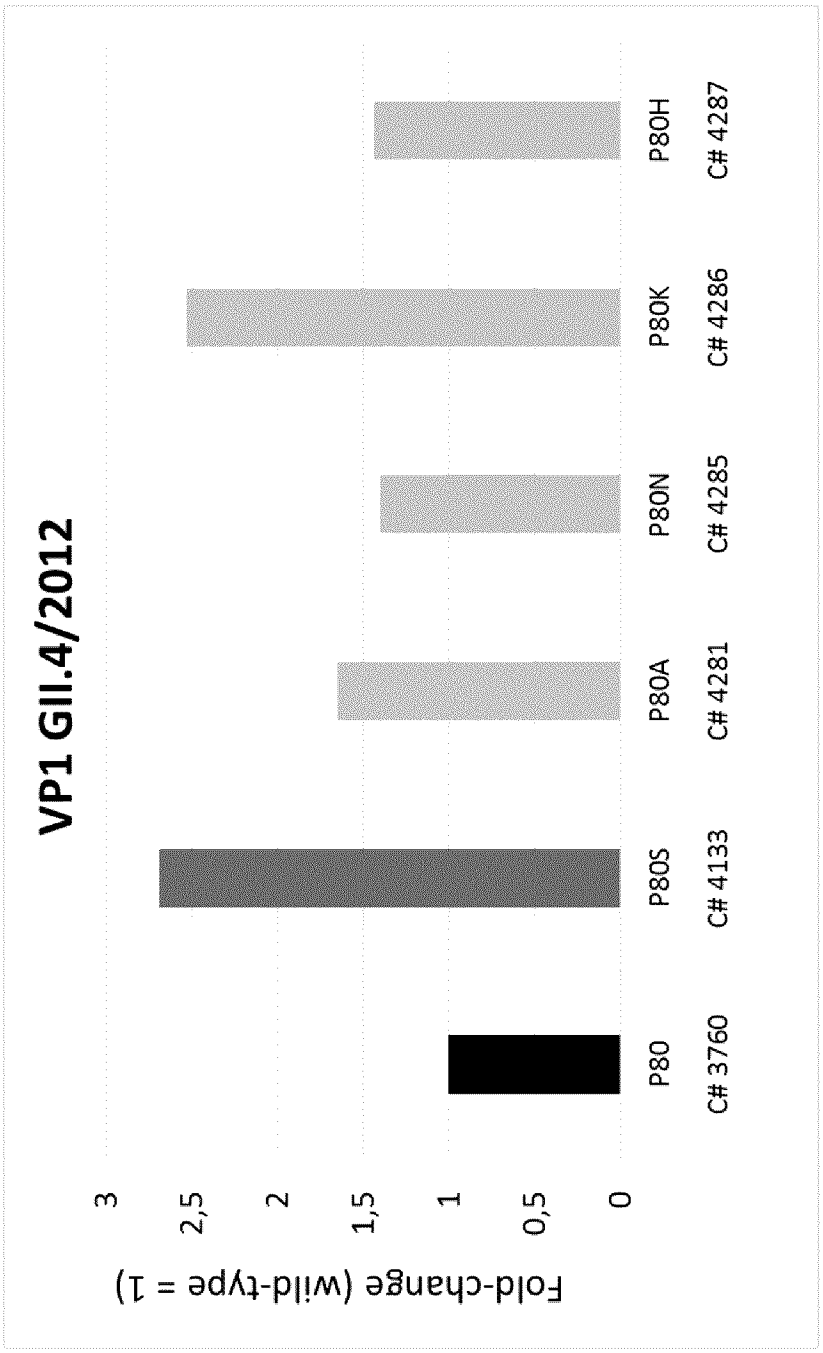
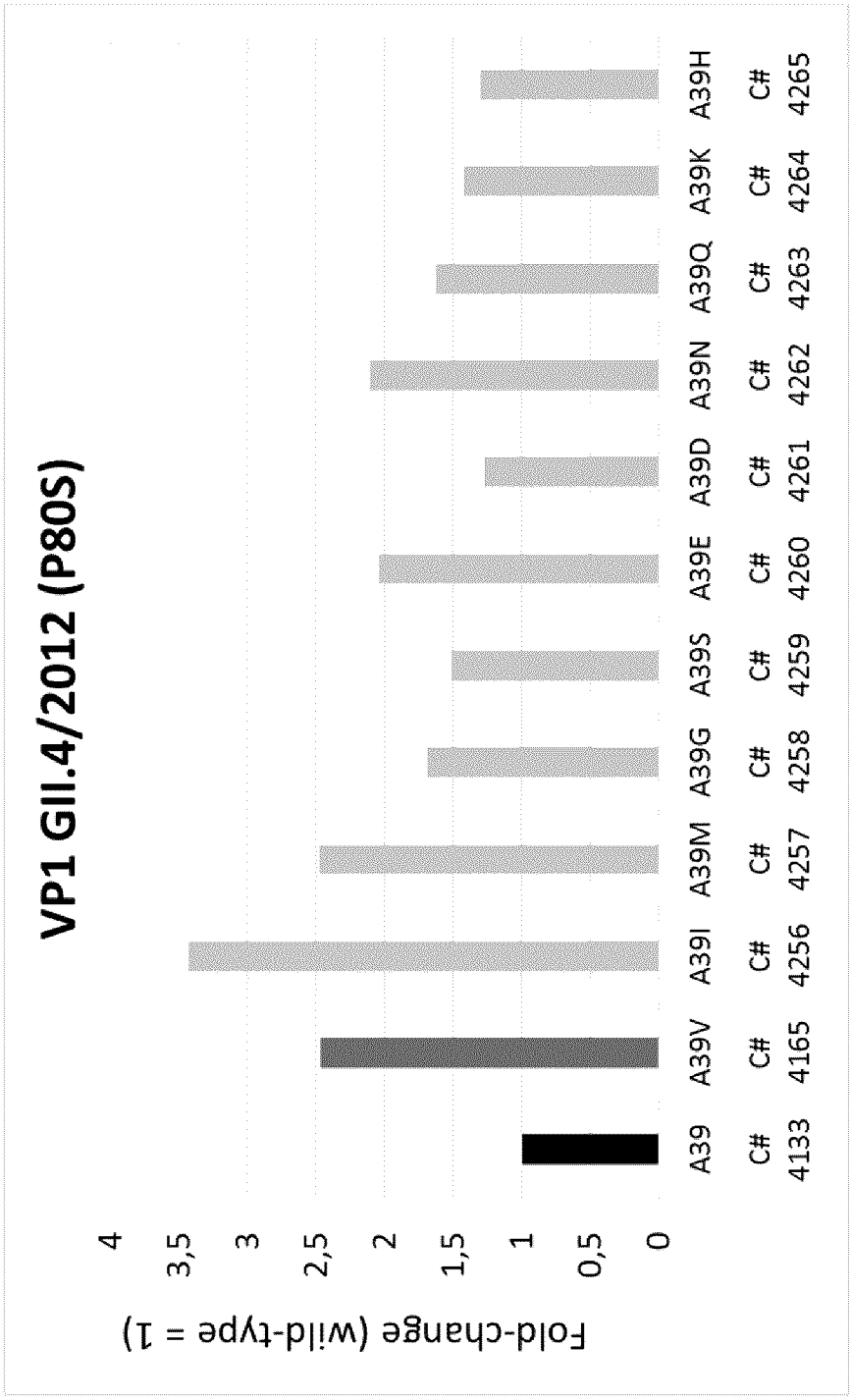

VP1 GII.4/2012
Fold-change (wild-type = 1)
3
2,5
2
1,5
1
0,5
0
P80
C# 3760
P80S
C# 4133
P80A
C# 4281
P80N
C# 4285
P80K
C# 4286
P80H
C# 4287

Figure 9I


VP1 GII.4/2012 (P80S)
Fold-change (wild-type = 1)
4
3,5
3
2,5
2
1,5
1
0,5
0
A39
A39V
A39I
A39M
A39G
A39S
A39E
A39D
A39N
A39Q
A39K
A39H
C# 4133
C# 4165
C# 4256
C# 4257
C# 4258
C# 4259
C# 4260
C# 4261
C# 4262
C# 4263
C# 4264
C# 4265

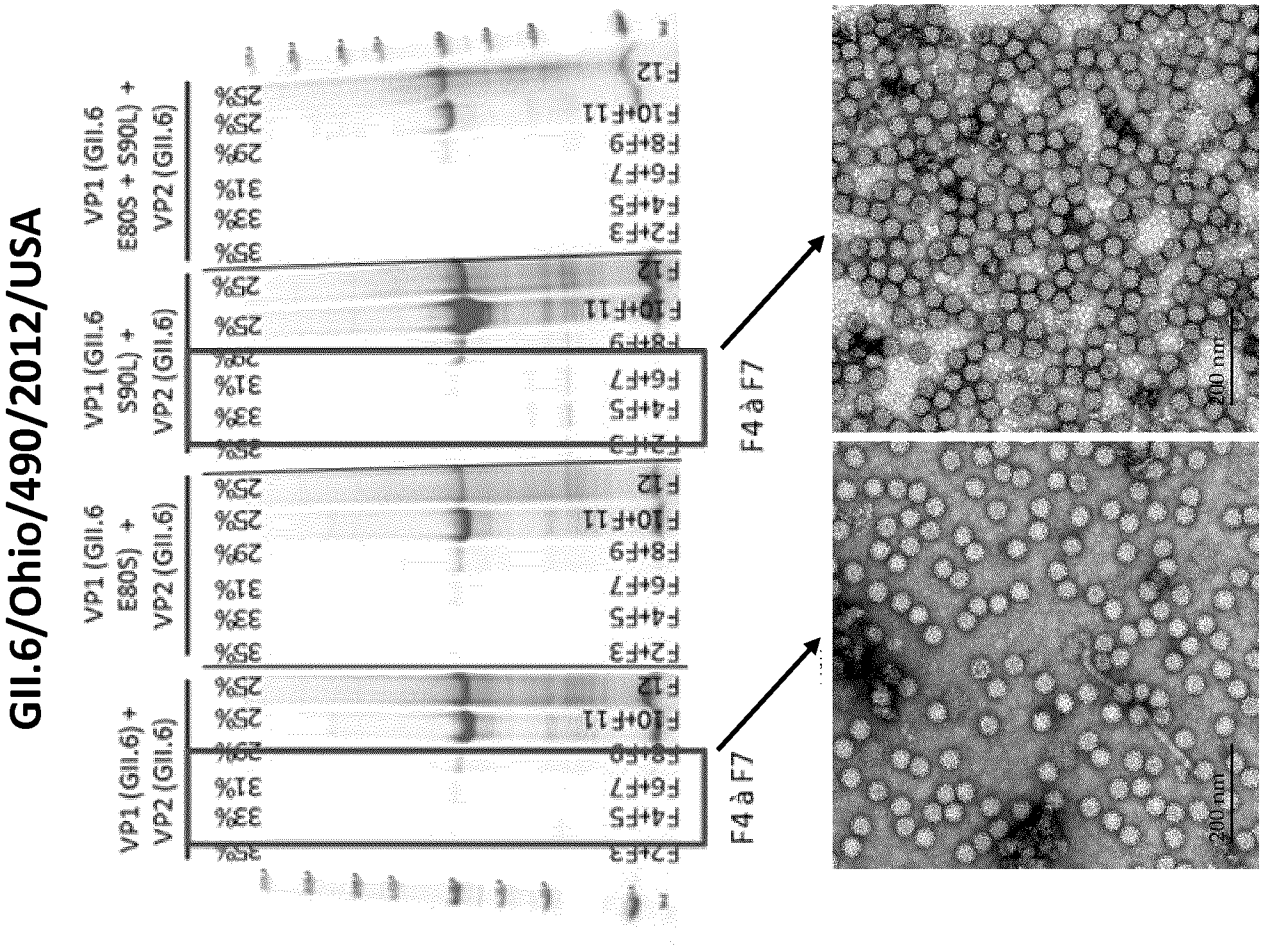
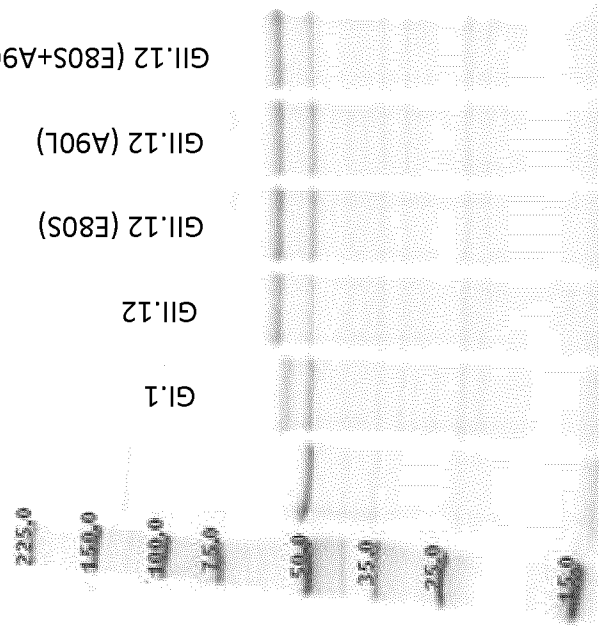


Figure 10A

Figure 10B

GII.12/HS206/2010/USA

Figure 11A



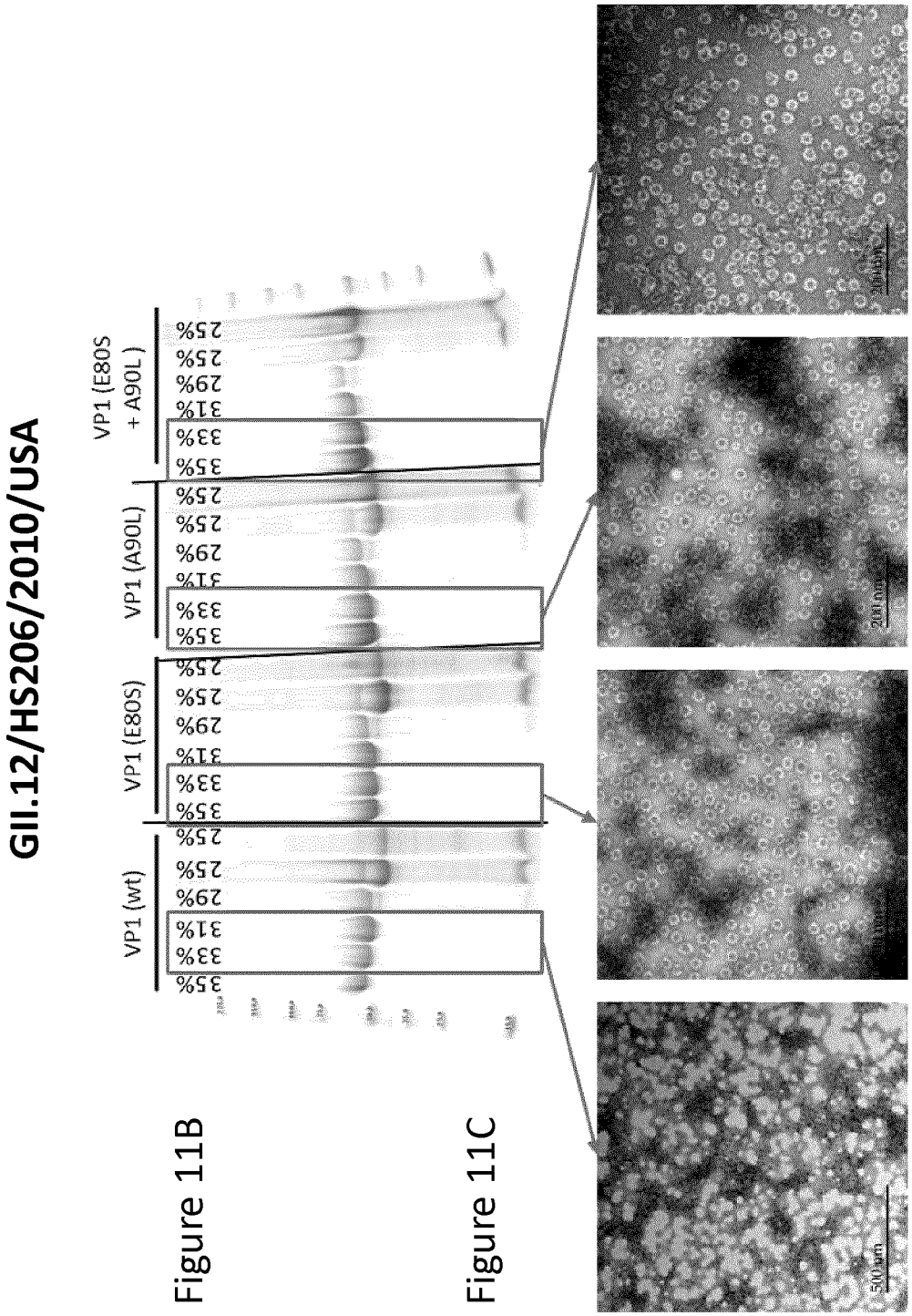


Figure 11B

Figure 11C

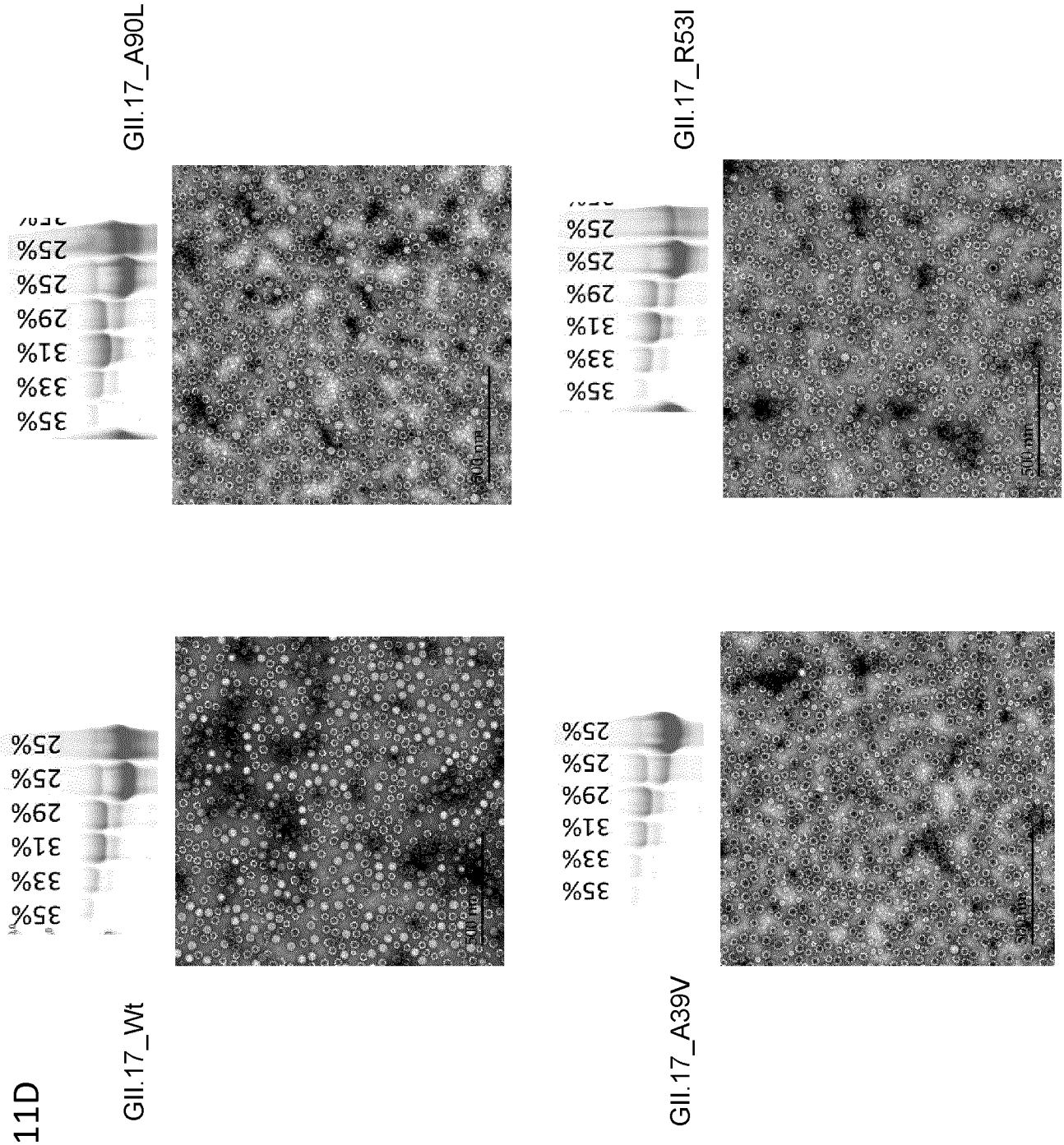

GII.17_A90L
GII.17_R53I
GII.17_Wt
GII.17_A39V
25%
25%
29%
31%
33%
35%
500 nm

Figure 11D

Figure 12A

Amino acid sequence of VP1 G1.1 (SEQ ID NO: 1)

MMMASKDATSSVDGASGAGQLVPEVNASDPLAMDPVAGSSTAVATAGQVNPIDPWIINNFVQAPQGEFTISPNNTP
GDVLFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLTIAQATLFPHVIADVRTLD
PIEVPLEDVRNVLFHNNDRNQQTMRLVCMLYTPLRTGGGTGDSFVVAGRVMTCPSPDFNFLFLVPPTVEQKTRPFTLPN
LPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTLDGRLVGTTPVSLSHVAKIRGTSNGTVINLTELDGTPFHPFEGPAPI
GFPDLGGCDWHINMTQFGHSSQTQYDVDTTPDTFVPHLGSIQANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYG
SSITEATHLAPSVYPPGFGEVLVFFMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVGEAALLHYVDPDTGRNLGEFKAYP
DGFLTCVPNGASSGPQQLPINGVFVFVSWVSRFYQLKPVGTASSARGRLGLRR

Figure 12B

Nucleic acid sequence of wild-type VP1 G1.1 (SEQ ID NO: 2)

ATGATGATGGCGTCTAAGGACGCTACATCAAGCGTGGATGGCGCTAGTGGCGCTGGTCAGTTGGTACCGGAGGTTA
ATGCTTCTGACCCTCTTGCAATGGATCCTGTAGCAGGTTCTTCGACAGCAGTCGCGACTGCTGGACAAGTTAATCCTA
TTGATCCCTGGATAATTAATAATTTTGTGCAAGCCCCCCAAGGTGAATTTACTATTTCCCCAAATAATACCCCCGGTG
ATGTTTTGTTTGATTTGAGTTTGGGTCCCCATCTTAATCCTTTCTTGCTCCATCTATCACAAATGTATAATGGTTGGGTT
GGTAACATGAGAGTCAGGATTATGCTAGCTGGTAATGCCTTTACTGCGGGGAAGATAATAGTTTCCTGCATACCCCC
TGGTTTTGGTTCACATAATCTTACTATAGCACAAGCAACTCTCTTTCCACATGTGATTGCTGATGTTAGGACTCTAGAC
CCCATTGAGGTGCCTTTGGAAGATGTTAGGAATGTTCTCTTTCATAATAATGATAGAAATCAACAAACCATGCGCCTT
GTGTGCATGCTGTACACCCCCCTCCGCACTGGTGGTGGTACTGGTGATTCTTTTGTAGTTGCAGGGCGAGTTATGAC
TTGCCCCAGTCCTGATTTTAATTTCTTGTTTTTAGTCCCTCCTACGGTGGAGCAGAAAACCAGGCCCTTCACACTCCCA
AATCTGCCATTGAGTTCTCTGTCTAACTCACGTGCCCCTCTCCCAATCAGTAGTATGGGCATTTCCCCAGACAATGTCC
AGAGTGTGCAGTTCCAAAATGGTCGGTGTACTCTGGATGGCCGCCTGGTTGGCACCACCCCAGTTTCATTGTCACAT
GTTGCCAAGATAAGAGGGACCTCCAATGGCACTGTAATCAACCTTACTGAATTGGATGGCACACCCTTTCACCCTTTT
GAGGGCCCTGCCCCCATTGGGTTTCCAGACCTCGGTGGTTGTGATTGGCATATCAATATGACACAGTTTGGCCATTC
TAGCCAGACCCAGTATGATGTAGACACCACCCCTGACACTTTTGTCCCCCATCTTGGTTCAATTCAGGCAAATGGCAT
TGGCAGTGGTAATTATGTTGGTGTTCTTAGCTGGATTTCCCCCCCATCACACCCGTCTGGCTCCCAAGTTGACCTTTG
GAAGATCCCCAATTATGGGTCAAGTATTACGGAGGCAACACATCTAGCCCCTTCTGTATACCCCCCTGGTTTCGGAG
AGGTATTGGTCTTTTTCATGTCAAAAATGCCAGGTCCTGGTGCTTATAATTTGCCCTGTCTATTACCACAAGAGTACA
TTTCACATCTTGCTAGTGAACAAGCCCCTACTGTAGGTGAGGCTGCCCTGCTCCACTATGTTGACCCTGATACCGGTC
GGAATCTTGGGGAATTCAAAGCATACCCTGATGGTTTCCTCACTTGTGTCCCCAATGGGGCTAGCTCGGGTCCACAA
CAGCTGCCGATCAATGGGGTCTTTGTCTTTGTTTCATGGGTGTCCAGATTTTATCAATTAAAGCCTGTGGGAACTGCC
AGCTCGGCAAGAGGTAGGCTTGGTCTGCGCCGATAA

Figure 12C

Nucleic acid sequence of human codon-optimized VP1 G1.1 (SEQ ID NO: 3)

ATGATGATGGCTAGTAAAGATGCGACCTCCTCTGTGGATGGTGCGTCAGGGGCAGGACAACTCGTACCCGAGGTAA
ACGCCAGCGACCCACTTGCCATGGACCCCGTTGCCGGAAGTTCCACAGCAGTGGCCACAGCCGGTCAAGTGAATCC
AATTGATCCGTGGATTATCAACAATTTCGTCCAGGCACCCCAGGGCGAGTTCACAATTTCACCAAACAATACACCGG
GCGATGTGCTATTCGATCTTTCCTTGGGTCCTCACCTTAACCCTTTTCTACTCCATCTCTCACAGATGTACAATGGTTG
GGTAGGAAACATGAGAGTCCGGATCATGCTGGCTGGCAATGCCTTTACCGCTGGCAAGATCATCGTCAGTTGTATTC
CTCCCGGATTTGGATCTCATAATCTGACCATTGCTCAAGCGACTCTCTTTCCCCATGTCATCGCCGACGTTAGGACCCT
GGACCCCATCGAGGTGCCCCTGGAGGACGTCCGGAATGTTTTGTTCCACAACAACGACAGAAACCAGCAGACGATG
AGACTTGTCTGTATGCTCTATACCCCACTGCGGACTGGAGGCGGGACTGGAGACTCCTTCGTTGTGGCAGGAAGAG
TGATGACATGCCCCTCCCCCGACTTCAACTTTCTTTTTCTGGTCCCACCAACCGTTGAGCAGAAGACGCGGCCCTTTA
CACTGCCCAATCTCCCGCTTTCAAGTCTGAGTAATTCACGGGCCCCATTGCCGATCTCCTCAATGGGAATCTCCCCCG
ACAACGTCCAGTCTGTCCAATTCCAAAATGGGAGATGCACACTGGACGGTCGCCTGGTGGGAACAACTCCGGTGTC
CCTCTCACATGTCGCCAAAATCCGCGGCACATCAAATGGTACCGTAATCAATCTGACAGAACTTGATGGCACGCCCTT
CCATCCCTTTGAAGGACCAGCCCCTATTGGATTTCCTGATCTGGGAGGTTGCGACTGGCACATAAACATGACACAGT
TTGGCCACTCCAGCCAGACACAGTATGATGTCGATACAACCCCAGATACCTTCGTGCCACACCTGGGATCTATTCAA
GCTAACGGTATTGGATCCGGCAACTACGTGGGAGTCTTATCTTGGATCTCACCACCATCCCACCCCTCAGGATCCCAG
GTTGACTTGTGGAAGATACCGAATTATGGATCCTCGATCACTGAAGCCACGCACCTCGCACCTTCCGTCTACCCACCA
GGTTTTGGAGAAGTCTTGGTGTTTTTCATGAGCAAAATGCCCGGCCCTGGAGCCTACAATCTCCCTTGCCTACTCCCT
CAAGAGTATATTAGTCACCTCGCATCTGAGCAGGCCCCGACCGTTGGCGAGGCAGCCCTGCTGCATTATGTGGATCC
GGACACCGGCAGGAACCTGGGTGAGTTCAAAGCTTATCCTGACGGTTTTCTAACATGTGTACCAAATGGCGCTTCCA
GCGGCCCTCAACAGCTCCCAATCAATGGCGTGTTCGTTTTTGTCAGCTGGGTAAGCCGCTTCTACCAGCTGAAGCCC
GTGGGGACAGCTTCTTCTGCCCGCGGACGCCTCGGTCTGCGGAGATAA

Figure 13A

Amino acid sequence of VP1 G1.2_Leuven_2003_D2DEL3 (SEQ ID NO: 4)

MMMASKDAPQSADGASGAGQLVPEVNTADPLPMEPVAGPTTAVATAGQVNMIDPWIVNNFVQSPQGEFTISPNNT
PGDILFDLQLGPHLNPFLSHLSQMYNGWVGNMRVRILLAGNAFSAGKIIVCCVPPGFTSSSLTIAQATLFPHVIADVRTLEP
IEMPLEDVRNVLYHTNDNQPTMRLVCMLYTPLRTGGGSGNSDSFVVAGRVLTAPSSDFSFLFLVPPTIEQKTRAFTVPNIP
LQTLSNSRFPSLIQGMILSPDASQVVQFQNGRCLIDGQLLGTTPATSGQLFRVRGKINQGARTLNLTEVDGKPFMAFDSP
APVGFPDFGKCDWHMRISKTPNNTSSGDPMRSVDVQTDVQGFVPHLGSIQFDEVFNHPTGDYIGTIEWISQPSTPPGT
DINLWEIPDYGSSLSQAANLAPPVFPPGFGEALVYFVSAFPGPNNRSAPNDVPCLLPQEYVTHFVSEQAPTMGDAALLHY
VDPDTNRNLGEFKLYPGGYLTCVPNGVGAGPQQLPLNGVFLFVSWVSRFYQLKPVGTASTARGRLGVRRI

Figure 13B

Nucleic acid sequence of human codon-optimized VP1 G1.2_Leuven_2003_D2DEL3 (SEQ ID NO: 5)

ATGATGATGGCTTCAAAGGATGCTCCCCAAAGCGCGGACGGAGCTAGCGGCGCCGGACAGTTGGTTCCGGAAGTC
AACACTGCCGATCCACTGCCCATGGAACCCGTAGCTGGTCCAACAACCGCTGTTGCCACCGCCGGCCAGGTTAACAT
GATCGATCCATGGATTGTTAATAACTTTGTACAGAGCCCCCAGGGGGAGTTCACAATTTCTCCGAACAATACCCCTG
GGGACATTCTGTTCGATCTGCAACTGGGCCCACACTTGAATCCTTTCCTGAGCCATCTTTCACAGATGTACAACGGAT
GGGTTGGGAACATGCGTGTTCGGATCCTCCTTGCTGGCAACGCCTTCAGTGCTGGCAAGATTATCGTGTGCTGCGTA
CCACCAGGGTTTACCTCGAGTTCATTAACCATTGCTCAGGCCACCCTTTTCCCTCACGTGATCGCAGACGTGCGTACC
TTAGAACCAATCGAAATGCCCCTGGAAGATGTACGGAACGTGCTGTACCATACTAATGATAACCAGCCAACGATGA
GATTAGTGTGCATGCTGTACACCCCCCTGAGAACTGGAGGAGGTTCTGGAAATTCCGACAGTTTTGTGGTGGCTGG
CAGGGTCCTGACCGCTCCCAGTAGCGACTTCAGCTTTTTGTTCCTCGTTCCTCCTACAATCGAACAAAAAACAAGAGC
ATTCACAGTGCCCAACATTCCACTGCAGACTTTAAGCAATTCCAGGTTTCCCAGCTTGATCCAGGGTATGATCCTTTCT
CCCGACGCCTCCCAAGTTGTGCAGTTCCAGAATGGGAGATGTCTTATCGACGGTCAGCTTCTGGGAACAACCCCTGC
CACCTCCGGGCAACTCTTCCGGGTGAGAGGCAAAATCAATCAGGGCGCCAGAACACTGAATCTGACAGAAGTGGAC
GGGAAACCCTTTATGGCGTTCGATAGCCCCGCGCCCGTTGGATTCCCTGACTTCGGCAAGTGTGATTGGCACATGCG
CATCAGTAAGACTCCCAACAACACTTCATCTGGAGACCCCATGAGGAGCGTGGATGTCCAGACCGACGTGCAGGGC
TTCGTGCCGCACTTGGGATCTATCCAGTTCGATGAGGTGTTCAATCACCCTACTGGCGACTACATAGGCACAATTGA
GTGGATAAGTCAACCATCTACACCTCCAGGGACCGACATAAACCTGTGGGAAATTCCTGATTACGGGTCATCCCTGA
GTCAAGCTGCCAATCTTGCACCCCCTGTCTTTCCCCCCGGCTTTGGTGAGGCTCTTGTTTACTTCGTCTCTGCATTTCCT
GGTCCTAACAACCGCTCCGCCCCTAACGATGTTCCGTGTTTGTTACCCCAGGAATATGTGACTCATTTCGTTTCCGAA
CAGGCACCCACCATGGGGGACGCTGCCCTGCTACACTATGTGGACCCCGACACCAATAGAAACCTCGGCGAGTTCA
AACTCTACCCCGGGGGATACCTGACCTGTGTTCCAAATGGAGTGGGAGCAGGCCCACAACAGCTGCCCCTGAATGG
GGTCTTCCTGTTCGTTTCTTGGGTGTCACGCTTTTACCAGCTGAAGCCCGTTGGCACAGCTTCTACGGCACGCGGCAG
GCTAGGGGTCCGCCGAATCTGA

Figure 14A

Amino acid sequence of VP1 GI.3_LillaEdet_2008_H2DG70 (SEQ ID NO: 6)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNNT
PGDILFDLQLGPHLNPFLSHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIAQATMFPHVIADVRV
LEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLFLVPPNVEQKTKPFSVPNL
PLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPK
VNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLGEFKLYPEGFMTCVPNSSGSGPQTLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 14B

Nucleic acid sequence of human codon-optimized VP1 GI.3_LillaEdet_2008_H2DG70 (SEQ ID NO: 7)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACCATAAGCCCAAACAACACCCCG
GGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTGAGTCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTCACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCCTTGAGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTTGACTTGTCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCC
ATTCAGCGTGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCCGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC
ATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAAGTTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCACCCCCCATATATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 15A

Amino acid sequence of VP1 GI.5_Siklos_HUN5407_2013_HUN_AHW99832 (SEQ ID NO: 12)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLQLGPHLNPFLAHLSQMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLFPHIIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYTPLRTGGGSGGTDAFVVAGRVLTCPSSDFNFLFLVPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSQILKFRGKVSAGSKVINLTELDGSPFLAFEAPAP
TGFPDLGTSDWHVEMSLNSNSQSSGNPILLRDIHPNSSEFVPHLGSVCVTAAIEVAGDYTGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPPGFGEAIVYFMSPIPGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPQQLPLNGVFVFASWVSRFYQLKPVGTASSARGRLGVRR

Figure 15B

Nucleic acid sequence of human codon-optimized VP1 GI.5_Siklos_HUN5407_2013_HUN AHW99832 (SEQ ID NO: 33)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCTTGGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTTAATATG
ATTGACCCCTGGATTTTCAATAATTTCGTGCAGGCCCCTCAAGGCGAGTTTACTATAAGCCCTAACAACACACCAGGG
GATATTCTGTTCGACCTGCAGTTAGGCCCTCATCTCAACCCCTTCTTGGCCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCTTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTTCCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATACCAACGATAATCAGCCCACTATGAGG
TTACTGTGCATGCTGTACACGCCACTCCGGACTGGTGGGGGCAGTGGGGGGACCGATGCTTTCGTCGTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCCTATTCCTTGTGCCCCCAACGGTGGAACAGAAAACGAGACCTT
TTTCCGTACCTAACATCCCTTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTTCCAGACCTGGGAACATCCGATTGGCATGTCGAGA
TGAGTCTGAATAGCAACTCCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTTGGACAATTCCACACTACGGCTCTAACTTGGCCGA
AGCATCCCAGCTTGCCCCCGTTGTATATCCCCCAGGCTTTGGCGAAGCAATAGTTTATTTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTCGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTCGCATCATGGGTTAGCCGGTTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 16A

Amino acid sequence of VP1_GI.7 (SEQ ID NO:101)

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIMNNFVQAPEGEFTISPNNT
PGDILFDLRLGPHLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICCVPPGFESQNISIGQATMFPHVIADVRVL
EPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPDFNFLFLVPPSVEQKTRQLTIPNI
PLNNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLEGQLLGTTPVSANQVARIRGKVFSTNSGTGLNLTEVDGTPYH
AFESPAPLGFPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGNSFAPHLGSIEFSSENHPSGDQLGTLTWISPLNNASRV
DPWKIPTYGSTLTESTNLAPPIFPPGFGEAIVYFMSDFPIVSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHR
NLGEFKLYPDGFITCVPNTGGGPQNLPSNGVFVFSSWVSRYYQLKPVGTTGPVRRLGVRRV

Figure 16B

Nucleic acid sequence of human codon-optimized VP1 GI.7/GA5043/USA/2014 VP1 (SEQ ID NO:175)

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGCAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAATGAACAATTTCGTTCAGGCACCAGAAGGAGAATTCACC
ATCTCCCCCAATAACACCCCAGGGGATATTCTGTTTGACCTCAGGTTAGGACCCCACTTGAACCCCTTTCT
GCTTCATCTCTCACAAATGTATAATGGCTGGGTCGGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAA
TGCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCCTCCTGGATTCGAATCTCAAAATATCAGCATTG
GTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTCGCGTCCTGGAACCCATTGAAGTTCCTCTCGAC
GACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACA
CCCCATTAAGAGCCGGGGGAGCATCCTCAGGTACTGACCCATTTGTGATTGCCGGGCGGGTGCTCACAT
GCCCGGCTCCAGACTTTAACTTCCTTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCTCACC
ATCCCAAATATCCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCA
GTGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGA
CGACCCCAGTCTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAAACTCCGGCACTG
GCCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTTGAGTCTCCAGCCCCTCTTGGCTTTCCC
GATATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATA
GGTTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCA
TCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCC
CTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGCTCCGCCCATTTTCCCACCCG
GATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCCT
TGCACACTGCCACAAGAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCCC
TCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAGCTGTACCCTGACGGGTTTATT
ACCTGTGTACCCAACACCGGCGGCGGCCCACAAAATTTGCCCAGCAATGGCGTGTTTGTCTTTTCCTCTTG
GGTGTCTCGATACTACCAGCTTAAACCTGTCGGAACTACGGGCCCCGTGCGACGACTCGGCGTGAGGCG
GGTGTGA

Figure 16C

Amino acid sequence of GII.1_Ascension208_2010_USA_AFA55174 native VP1 (SEQ ID NO: 13)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRMNFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPFLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAIPPHFPLENLSPGQITMFPHVIIDVRTLEPVLLPLP
DVRNNFFHYNQQPEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELSNS
RFPVPIDELYTSPNEGVVVQPQNGRSTLDGELLGTTQLVPSNICALRGRINAQVPDDHHQWNLQVTNANGTSFDPTEDV
PAPLGTPDFLANIYGVTSQRNPDNTCRAHDGVLATWSPKFTPKLGSVVLGTWEESDLDLNQPTRFTPVGLYDTGHFDQ
WVLPNYSGRLTLNMNLAPSVAPLFPGEQILFFRSHIPLKGGTSNGAIDCLLPQEWIQHFYQESAPSPTDVALIRYTNPDTG
RVLFEAKLHRQGFITVANSGSRPIVVPPNGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 17A

Amino acid sequence of VP1 GII.2_CGMH47_2011_TW_AGT39206 (SEQ ID NO: 14)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPYLAHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLL
PLPDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGL
NDTDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

Figure 17B

Nucleic acid sequence of human codon-optimized VP1 GII.2 CGMH47 2011 TW AGT39206 (SEQ ID NO: 40)

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCGAGCTGGGACCAGAACTTAATCCGTACCTGGCTCACCTGGCCCGGATGTACAATGGATATGCAGGAG
GGATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCAC
TTCCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTG
TGCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 18A

Amino acid sequence of VP1 GII.3_Jingzhou_2013402_CHN_AGX01095 (SEQ ID NO: 15)

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNFVQAPGGEFTVSPRNSPGEVLLN
LELGPEINPYLAHLARMYNGYAGGFEVQVVLAGNAFTAGKIIFAAIPPNFPIDNLSAAQITMCPHVIVDVRQLEPVNLPMP
DVRNNFFHYNQGSDSRLRLIAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFSFNFLVPPTVESKTKPFSLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLDGELMGTTQLLPSQICAFRGTLTRSTSRASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTPDFRGKVFGVASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNQPTRFTPVGIGVD
HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHKLRFMTIAKSGDSPITVPPNGYFRFESWVNPFYTLAPMGTGNGRRRIQ

Figure 18B

Nucleic acid sequence of human codon-optimized VP1 GII.3_Jingzhou_2013402_CHN AGX01095 (SEQ ID NO: 45)

ATGAAAATGGCTTCCAACGATGCAGCACCCTCTAATGATGGCGCTGCCGGACTTGTGCCGGAGATTAGCTCTGAGG
CTATGGCCCTAGAACCAGTAGCCGGGGCAGCCATAGCTGCCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCGTGCAGGCACCGGGGGGAGAATTCACGGTCTCTCCTCGAAACTCCCCCGGGGAGGTTCTCT
TGAATTTGGAACTGGGCCCTGAAATTAATCCTTATCTGGCCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT
TTCGAGGTCCAGGTGGTGCTCGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCGACGTGCGCAACAACTTCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATTCCGGAGATGACGTTTTCACTGTGAGTTGTCGAGTCCTGACACGTCC
ATCTCCTGACTTTAGCTTTAATTTCCTCGTGCCCCCCACAGTGGAATCCAAAACTAAGCCATTCTCTCTGCCAATTCTT
ACCATTAGCGAAATGTCGAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTCAGAACGGACGCGTGACTCTCGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACTCGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCACCCGGGCCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTCACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTTCGATCAGAACCAGCCAACCCGGTTTACCCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGCAGGCCAGTTCACACATAACATGAATCTTGCCCCCGCTGTGGCCCCCAACTTCCCGGGAG
AACAACTTCTGTTTTTCAGGAGCCAACTGCCTTCCAGCGGCGGCCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATTCGCC
TATTACAGTGCCCCCCAACGGATACTTCAGATTTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 19A

Amino acid sequence of VP1 GII.4_Sydney_2012_K4LM89 (SEQ ID NO: 16)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 19B

Nucleic acid sequence of human codon-optimized VP1 GII.4_Sydney_2012_K4LM89 (SEQ ID NO:52)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 19C

Amino acid sequence of VP1 US96: GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27)

MKMASNDANPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNFYHYNQSNDSTIKLIAMLYTPLKANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFTVPILTVEEMSN
SRFPIPLEKLYTGPSSAFVVQPQNGRCTTDGVLLGTTQLSAVNICTFRGDVTHIAGSHDYTMNLASQNWNNYDPTEEIPA
PLGTPDFVGKIQGMLTQTTREDGSTRAHKATVSTGSVHFTPKLGSVQYTTDTNNDFQTGQNTKFTPVGVIQDGNNHQN
EPQQWVLPNYSGRTGHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMNLDCLLPQEWVQHFYQEAAPAQSDVALL
RFVNPDTGRVLFECKLHKSGYVTVAHTGPHDLVIPPNGYFRFDSWVNQFYTLAPMGNGAGRRRAL

Figure 19D

Amino acid sequence of VP1 FH02: GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28)

MKMASNDANPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKIIFAAVPPNFPTEGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNFYHYNQLNDPTIKLIAMLYTPLRANNAGEDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFTVPILTVEEMTN
SRFPIPLEKLFTGPSGAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHIAGTHNYTMNLASQNWNNYDPTEEIPA
PLGTPDFVGRIQGMLTQTTRGDGSTRGHKATVSTGDVHFTPKLGSIQFNTDTNNDFETGQNTKFTPVGVVQDGNGTH
QNEPQQWVLPSYSGRTGHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMNLDCLLPQEWVQHFYQEAAPAQSDV
ALLRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAL

Figure 19E

Amino acid sequence of VP1 Hnt04:GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29)

MKMASNDATPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKIIFAAVPPNFPTEVLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNLYHYNQSNDPTIRLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPILTVEEMTN
SRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHIAGTQNYTMNLASQNWNNYDPTEEIPA
PLGTPDFVGRIQGVLTQTTRRDGSTRGHKATVSTGSVHFTPKLGSVQFSTDTSNDFETGQNTRFTPVGVVQDGSTTHQN
EPQQWVLPDYSGRDSHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMNLDCLLPQEWVQHFYQESAPAQSDVALL
RFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGAGRRRAL

Figure 19F

Amino acid sequence of VP1 2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30)

MKMASNDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKIIFAAVPPNFPTEGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNFYHYNQSNDSTIKLIAMLYTPLRANNAGEDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFTVPILTVEEMTNS
RFPIPLEKLFTGPSGAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHIAGSRNYTMNLASLKWNKYDPTEEIPAPL
GTPDFVGKIQGVLTQTTKGDGSTRGHKATIYTGSAPFTPKLGSVQFSTDTENDFETHQNTKFTPVGVTQDGSTTHRNEPQ
QWVLPSYSGRNVHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQHFYQEAAPAQSDVALLRFV
NPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAL

Figure 19G

Amino acid sequence of VP1 NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31)

MKMASSDANPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDMNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKIIFAAVPPNFPTEGLSPSQVTMFPHIIVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPILTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHIAGSRNYTMNLASQNWNSYDPTEEIPA
PLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFSPKLGRVQFATDTDNDFDANQNTKFTPVGVIQDGNTAHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAL

Figure 20

Amino acid sequence of VP1 GII.5_Alberta_2013_CA_ALT54485 (SEQ ID NO: 17)

MKMASNDATPSNDGAAGLVPESNNEAMALEPVVGASLAAPVTGQTNIIDPWIRTNFVQAPNGEFTVSPRNSPGEILVN
LELGPELNPYLAHLARMYNGYAGGMEVQVLLAGNAFTAGKIIFAAVPPYFPVENLSPSQITMFPHVIIDVRTLEPVLLPMP
DVRSTLFHFNQKDEPKMRLVAMLYTPLRSNGSGDDVFTVSCRILTRPSPEFDFTYLVPPTVESKTKPFTLPVLTLGELSNSRF
PLSIDEMVTSPNESIVVQPQNGRVTLDGELLGTTQLQACNICSIRGKVTGQVPNEQHMWNLEITNLNGTQFDPTDDVPA
PLGVPDFAGEVFGVLSQRNRGESNPANRAHDAVVATYSDKYTPKLGLVQIGTWNTNDVENQPTKFTPIGLNEVANGHR
FEQWTLPRYSGALTLNMNLAPAVAPLFPGERLLFFRSYVPLKGGFGNPAIDCLVPQEWVQHFYQESAPSLGDVALVRYV
NPDTGRVLFEAKLHKGGFLTVSSTSTGPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRFQ

Figure 21A

Amino acid sequence of VP1 GII.6_Ohio_2012_M9T020 (SEQ ID NO: 20)

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLELGPELNPYLSHLSRMYNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHFPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRFFHYNQENTSRMRLVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSLPILTLGELSNSR
FPAPIDMLYTDPNEGIVVQPQNGRCTLDGTLQGTTQLVPTQICAFRGTLIGQTSRSPDSTDSAPRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVSGQQVGATRAHEVHINTTDPRYTPKLGSILMYSESDDFVTGQPVRFTPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSGNNPIVVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 21B

Nucleic acid sequence of human codon-optimized VP1 GII.6_Ohio_2012_M9T020 (SEQ ID NO: 21)

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGCTCCACAGGGGGAGTTCACAGTCTCCCCCCGGAACTCCCCGGGCGAGATGCTG
CTCAATCTGGAACTCGGCCCTGAACTAAACCCTTATCTGTCACACCTTTCACGGATGTACAATGGCTACGCAGGAGG
AATGCAAGTTCAGGTGGTCCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCCTCCACACT
TCCCTGTCGAAAATATCAACGCCGCCCAGATTACTATGTGCCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCA
GTTCTGCTGCCCCTGCCCGACATCAGAAACCGGTTCTTCCATTACAATCAAGAGAATACTTCACGGATGAGACTTGTT
GCGATGCTGTACACCCCTCTTCGTGCAAATTCCGGCGAAGACGTGTTCACTGTGTCTTGTCGAGTACTTACCCGACCC
GCCCCCGATTTCGAATTCACCTTCCTGGTTCCCCCTACTGTGGAGAGCAAGACAAAACCCTTCAGCCTCCCAATCTTA
ACACTCGGGGAGCTGTCTAATTCACGCTTCCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGT
GGTGCAGCCCCAAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAACTGGTGCCAACCCAGATT
TGTGCATTCAGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGG
ACCACCCACTCCACGTTCAGTTAAAAAACCTGGACGGAACCCAGTACGACCCTACAGACGAGGTCCCCGCTGTCCTC
GGAGCCATCGACTTTAAAGGAACTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGCAGCAGGTGGGAGCT
ACGAGAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCCAAAACTAGGGTCAATTTTAATGTATTC
GGAATCAGACGATTTTGTTACAGGTCAGCCCGTGCGGTTTACCCCGATCGGAATGGGGGACAACGATTGGCACCAG
TGGGAATTGCCCGATTACCCTGGACACCTCACCTTGAATATGAATCTGGCCCCAGCCGTCGCGCCCGCCTTCCCCGGT
GAGCGGATCCTCTTTTTTAGAAGCATAGTGCCCTCCGCAGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCC
CCAAGAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCTAGCCAGTCCGCAGTAGCACTGATCAGATATGTTAATC
CTGATACGGGAAGGAACATCTTCGAAGCAAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAA
CCCTATTGTGGTGCCTCCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTTATACTCTGACTCCCATGGG
GACAGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 22

Amino acid sequence of VP1 GII.7_Musa_2010_AII73774 (SEQ ID NO: 18)

MKMASNDAAPSNDGAAGLVPEINNEVMPLEPVAGASLATPVVGQQNIIDPWIRNNFVQAPAGEFTVSPRNSPGEILLD
LELGPELNPYLAHLARMYNGHAGGMEVQIVLAGNAFTAGKIIFAAIPPGFPYENLSPSQITMCPHVIIDVRQLEPVLLPMP
DIRNNFFHYNQGNDPKLRLIAMLYTPLRANNSGDDVFTVSCRVLTKPSPDFEFTFLVPPTVESKTKQFTLPILKISEMTNSRF
PVPVEMMYTARNENQVVQPQNGRVTLDGELLGTTPLLAVNICKFKGEVIAKNGDVRSYRMDMEITNTDGTPIDPTEDT
PGPIGSPDFQGILFGVASQRNKNEQNPATRAHEANINTGGDQYAPKLAQVKFFSESQDFEVHQPTVFTPVGVAGDTSHP
FRQWVLPRYGGHLTNNTHLAPAVAPLFPGEQILFFRSQIPSSGGHELGYMDCLVPQEWVQHFYQEAATAQSEVALIRFIN
PDTGRVLFEAKLHKQGFITVAHTGDNPIVMPPNGYFRFEAWVNQFYSLAPVGTGNGRRRIQ

Figure 23A

Amino acid sequence of VP1 GII.12_HS206_2010_USA_AEI29586 (SEQ ID NO: 19)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVIIDVRTLEPVLLPLP
DVRNNFFHYNQQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDGELQGTTQLLPTAICSFRGRINQKVSGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTPDFSGKLFGVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTLNMGLAPPVAPTFPGEQILFFRSHIPLKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 23B

Human codon-optimized VP1 GII.12_HS206_2010_USA_AEI29586 (SEQ ID NO: 87)

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCCGTGGCCGGAGCCTCAATTGCCGCCCCCCTCACTGGCCAGAACAACGTGATTGATCCCTGG
ATCAGACTGAACTTCGTTCAGGCTCCTAATGGGGAGTTCACCGTGTCCCCGAGAAACTCCCCCGGCGAAGTGTTATT
GAATTTGGAATTAGGACCAGAACTCAACCCCTATCTGGCACATCTGTCTCGGATGTACAACGGCTATGCGGGCGGA
GTGGAGGTGCAAGTTCTTCTCGCTGGTAATGCATTCACAGCAGGAAAATTAGTATTTGCAGCGGTTCCACCCCATTTT
CCACTTGAAAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGT
GCTGCTACCCCTGCCCGACGTGAGGAACAATTTCTTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCG
CCATGCTCTATACTCCTTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTCGGGTGCTCACCCGA
CCTTCCCCAGATTTCGACTTCAATTATCTGGTCCCCCCCACGGTAGAGTCCAAAACAAAGCCTTTCACTCTTCCAATCC
TTACAATTGGCGAACTGACCAACTCACGCTTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTG
TCGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACTGTTGCCAACCGCTAT
ATGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACCACGTGTGGAACATGCAAGTGACGAATATC
GACGGGACACCTTTCGATCCAACAGAGGATGTCCCAGCGCCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCGG
CGTCCTTTCCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTCATTGCCACCAACTCAGCCAAATTCAC
CCCAAAACTTGGAGCGATACAGATCGGAACTTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCC
CTGTTGGCCTTTTCGAAAGCGAAGGCTTTAACCAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG
GACTCGCACCACCCGTCGCTCCAACGTTTCCTGGTGAGCAGATTTTGTTTTTCCGCAGTCATATTCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTCAGCACTTGTATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCCGATACCGGAAGAGTGTTGTTTGAAGCTAAACTTCATCGCTCC

Figure 23B (cont)

GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCCGGCAAACGGATACTTTCGATTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

Figure 24A

Amino acid sequence of VP1 GII.13_VA173_2010_H9AWU4 (SEQ ID NO: 22)

MKMASNDAAPSNDGAASLVPEAINETMPLEPVAGASIAAPVAGQTNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAIPPNFPVDMISPAQITMLPHLI
VDVRTLEPIMIPLPDVRNVFYHFNNQPQPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFIYLVPP
SVESKTKPFTLPILTISELTNSRFPISIEQLYTAPNENNVVQCQNGRCTLDGELQGTTQLLSSAVCSYRGRTVANS
GDNWDQNVLQLTYPSGASYDPTDEVPAPLGTQDFSGILYGVLTQDNVRENTGEAKNAKGVYISTTSGKFTPK
IGSIGLHSITEDVRPNQQSRFTPVGVAQNENTPFQQWVLPHYAGALALNTNLAPAVAPTFPGEQLLFFRSRVP
CVQGLQGQDAFIDCLLPQEWVNHFYQEAAPSQADVALIRYVNPDTGRTLFEAKLHRSGFITVSHTGAYPLVV
PPNGHFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 24B

Nucleic acid sequence of human codon-optimized VP1 GII.13_VA173_2010_H9AWU4 (SEQ ID NO: 23)

ATGAAAATGGCTTCTAATGATGCCGCGCCCAGCAATGATGGTGCCGCCAGCCTTGTGCCCGAAGCAATTAACGAGA
CAATGCCCTTGGAGCCAGTCGCCGGGGCTTCTATTGCGGCCCCAGTTGCTGGACAGACGAATATCATCGATCCTTGG
ATACGGACTAATTTTGTTCAAGCTCCTAACGGAGAGTTCACTGTCTCCCCCCGTAATAGTCCTGGCGAGATCCTGTTG
AACCTCGAGTTGGGGCCAGATCTCAATCCTTACCTGGCTCATCTGTCGAGAATGTACAACGGGTACGCGGGGGGGG
TTGAGGTGCAGGTCTTACTGGCAGGTAACGCATTCACAGCAGGCAAGATTCTGTTTGCGGCCATCCCTCCTAATTTTC
CAGTGGATATGATATCTCCAGCACAGATTACAATGCTGCCCCATTTGATAGTGGATGTGCGGACACTTGAACCTATC
ATGATCCCTTTGCCCGATGTCCGAAATGTGTTTTATCATTTCAACAACCAGCCGCAGCCAAGAATGCGTCTCGTCGCG
ATGCTGTACACCCCGTTGCGGTCCAACGGCTCTGGCGATGATGTTTTCACAGTGTCGTGTCGAGTGTTAACCCGCCCT
ACCCCAGATTTTGAGTTTATATATCTAGTTCCCCCTTCTGTGGAAAGCAAGACTAAACCCTTTACTCTTCCCATTCTGA
CTATATCCGAGCTTACCAACTCCCGGTTCCCCATCTCAATCGAGCAACTGTACACTGCACCCAACGAGAACAACGTAG
TCCAGTGCCAGAACGGGAGATGTACCCTGGACGGGGAGCTCCAAGGGACCACGCAACTGTTAAGTTCAGCCGTTTG
CAGTTACAGAGGCAGGACTGTGGCGAACTCTGGTGATAACTGGGATCAAAATGTGTTGCAGCTGACTTACCCATCC
GGCGCAAGCTACGATCCAACAGATGAGGTGCCAGCGCCCCTTGGCACACAGGATTTCTCAGGAATTCTATACGGGG
TGCTTACTCAGGATAATGTGCGAGAAAATACTGGCGAGGCCAAGAATGCTAAAGGAGTGTATATAAGCACGACAAG
CGGTAAGTTTACCCCCAAAATTGGCAGTATTGGGCTCCACAGCATTACTGAGGACGTCCGCCCAAACCAGCAGTCTC
GTTTCACTCCCGTGGGGGTGGCACAGAACGAGAACACACCTTTCCAGCAGTGGGTCTTGCCCCATTATGCAGGTGCT
TTGGCGCTCAATACAAATCTGGCACCCGCCGTAGCGCCGACATTTCCTGGGGAGCAATTGCTGTTCTTTAGAAGCCG
CGTCCCGTGTGTTCAGGGCTTGCAGGGCCAGGACGCGTTCATTGATTGCCTCTTGCCCCAGGAATGGGTCAACCACT
TTTATCAGGAGGCAGCGCCCTCTCAAGCAGATGTGGCCCTGATAAGATATGTGAATCCCGACACAGGACGGACTTT
GTTTGAGGCAAAACTCCACCGGTCAGGATTCATTACTGTGAGTCACACAGGAGCCTATCCCCTTGTGGTTCCACCTAA
TGGCCACTTCAGGTTCGACTCTTGGGTCAATCAGTTTTATTCGCTGGCACCAATGGGTACCGGGAATGGTCGCCGTC
GGGTGCAATGA

Figure 25

Amino acid sequence of VP1 GII.14_Saga_2008_JPN_ADE28701 (SEQ ID NO: 32)

MKMASNDATPSDDGAAGLVPEINNEVMALEPVAGASIAAPVVGQQNIIDPWIRNNFVQAPAGEFTVSPRNSPGELLLD
LELGPELNPYLAHLARMYNGHAGGMEVQIVLAGNAFTAGKILFAAIPPSFPYENLSPAQLTMCPHVIVDVRQLEPVLLPM
PDIRNVFYHYNQNNSPKLRLVAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFQFTFLVPPTVESKTKNFTLPVLRVSEMTN
SRFPVVLDQMYTSRNENIIVQPQNGRCTTDGELLGTTILQSVSICNFKGTMQAKLNEEPRYQLQLTNLDGSPIDPTDDMP
APLGTPDFQAMLYGVASQRSSIDNATRAHDAQIDTAGDTFAPKIGQVRFKSSSNDFDLHDPTKFTPIGVNVDDQHPFRQ
WSLPNYGGHLALNNHLAPAVTPLFPGEQILFFRSYIPSAGGHTDGAMDCLLPQEWVEHFYQEAAPSQSDIALVRFINPDT
GRVLFEAKLHKQGFLTIAASGDHPIVMPTNGYFRFEAWVNPFYTLAPVGTGSGRRRIQ

Figure 26A

Amino acid sequence of VP1 GII.17_Kawa_2014_A0A077KVU6 (SEQ ID NO: 24)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLPDVRNTFFHYNNQPNSRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPP
SVESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLDGELQGTTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV
PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

Figure 26B

Human codon-optimized VP1 GII.17_Kawa_2014_A0A077KVU6 (SEQ ID NO: 25)

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAATAATGAG
ACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAATATTATAGACCCTTG
GATTCGGACAAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCCGGAACTCCCCAGGTGAGATACTCC
TGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGCCGCATGTACAATGGTTACGCTGGGGGG
GTCGAAGTGCAGGTCCTCCTGGCCGGAAACGCCTTTACCGCTGGCAAAATTCTGTTTGCCGCCGTTCCACCAAACTTT
CCAGTCGAATTCCTCTCTCCCGCGCAAATAACCATGCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATA
ATGATTCCCCTGCCGGATGTGCGTAACACCTTTTTCCATTATAACAATCAGCCAAACTCTCGGATGAGACTTGTTGCT
ATGCTGTACACCCCCCTGCGGAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCC
CAACCCCGGACTTCGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCT
TAACTCTCTCCGAACTGACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCCA
AGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCAGTGGCATC
TGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAACTCCAAAACTTAAACG
GGACCACCTACGACCCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTTTAAGGGGGTGGTGTTCGGAGT
GGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGCTCACGAGGCCGTTATCTCAACATATAGCC
CCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTAACGACAACGACTTCCAACTGCAACCAACGAAGTTTA
CGCCAGTGGGGATTAATGATGATGGAGACCATCCTTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACC
CTCAATATGAACCTCGCCCCACCCGTGGCCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCA
TGCAGTGGCGGATATAATCAAGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTTACCAGGAAAG

Figure 26B (cont)

TGCGCCCTCCCAGTCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAAT
TGCACAGATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAGGT
TCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCTCAGTAG

Figure 27

Amino acid sequence of VP1 GII.21_Sali_2011_USA_AFC89665 (SEQ ID NO: 26)

MKMASNDAAPSNDGATGLVPEINTETLPLEPVAGAAIAAPVTGQNNIIDPWIRNNFVQAPNGEFTVSPRNSPGEILMNL
ELGPDLNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVDMLSPAQITMLPHLIVDVRTLEPIMIPLP
DVRNVFYHFNNQPAPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPPSVESKTKPFTLPILTIGELTNSR
FPAPIDQLYTSPNADVVVQPQNGRCTLDGELQGTTQLLTTAICSYRGMTSNPTSDYWDDHLLHLVHPNGATYDPTEDVP
APFGTQDFRGILYGMLTQNPRTSGDEAANSHGIYISSTSEKFTPKLGTIGLHQVQGDIASNQQSKFTPVGIAVNGNTPFRQ
WELPNYSGALTLNTNLAPAVGPNFPGEQILFFRSNVPSVQGGQPIEIDCLIPQEWVSHFYQESAPSQSDVALVRYVNPDT
GRTIFEAKLHRQGFITIAATGSNPVVVPPNGYFRFDSWVNQFYALAPMGTGNGRRRVQ

Figure 28A

Amino acid sequence of VP1_GI.3_Lil08_Q84S (SEQ ID NO:98)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNNT
PGDILFDLSLGPHLNPFLSHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIAQATMFPHVIADVRV
LEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLFLVPPNVEQKTKPFSVPNL
PLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPK
VNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLGEFKLYPEGFMTCVPNSSGSGPQTLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 28B

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_Q84S (SEQ ID NO:167)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACCATAAGCCCAAACAACACCCCG
GGTGACATCTTGTTTGACCTGAGCCTAGGACCACACTTGAATCCGTTTCTGAGTCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTCACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCCTTGAGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTTGACTTGTCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCC
ATTCAGCGTGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCCGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC

Figure 28B (cont)

ATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAAGTTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCACCCCCCATATATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 28C

Amino acid sequence of VP1_GI.3_Lil08_S94L (SEQ ID NO:8)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNNT
PGDILFDLQLGPHLNPFLLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIAQATMFPHVIADVRV
LEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLFLVPPNVEQKTKPFSVPNL
PLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPK
VNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLGEFKLYPEGFMTCVPNSSGSGPQTLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 28D

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_S94L (SEQ ID NO:9)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACCATAAGCCCAAACAACACCCCG
GGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTGCTCCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTCACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCCTTGAGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTTGACTTGTCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCC
ATTCAGCGTGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCCGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC
ATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAAGTTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCACCCCCCATATATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT

Figure 28D (cont)

TCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 28E

Amino acid sequence of VP1_GI.3_Lil08_Q84S+S94L (SEQ ID NO:10)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNNT
PGDILFDLSLGPHLNPFLLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIAQATMFPHVIADVRVL
EPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLFLVPPNVEQKTKPFSVPNL
PLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPK
VNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLGEFKLYPEGFMTCVPNSSGSGPQTLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 28F

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_Q84S+S94L (SEQ ID NO:11)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACCATAAGCCCAAACAACACCCCG
GGTGACATCTTGTTTGACCTGAGCCTAGGACCACACTTGAATCCGTTTCTGCTCCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTCACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCCTTGAGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTTGACTTGTCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCC
ATTCAGCGTGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCCGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC
ATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAAGTTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCACCCCCCATATATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 28G

Amino acid sequence of VP1_GI.3_Lil08_A43V+S94L (SEQ ID NO:170)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAVATAGQVNMIDPWIMSNYVQAPQGE
FTISPNNTPGDILFDLQLGPHLNPFLLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIA
QATMFPHVIADVRVLEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPD
FNFLFLVPPNVEQKTKPFSVPNLPLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSA
SQLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDST
FAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPKVNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGEFKLYPEGFMTCVPNSSGSGPQ
TLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 28H

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_A43V+S94L (SEQ ID NO:169)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGTGGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACC
ATAAGCCCAAACAACACCCCGGGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCT
GCTCCACTTGGCTCAGATGTATAATGGATGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAA
TGCATTCACAGCCGGGAAGATTATTATCTCTTGCGTGCCACCTGGATTTGCAGCCCAGAACGTGTCTATC
GCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCCTTG
AGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATAT
ACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGGGCGGGTGTTGACTT
GTCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTCAGC
GTGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCA
CAACCCCAACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGG
GGCTGAATCTTACTGAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCC
GATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCA
TCGCATTGACGTAGCACAGGATAGCACATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGAT
TACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAA
GTTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATAT
ATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGC
CTTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGG
GCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACTCTACCC
TGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTG
TTCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGA
GGCTCGGGATCAGACGGAGCTAG

Figure 28I

Amino acid sequence of VP1_GI.3_Lil08_M57I+S94L (SEQ ID NO:172)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIISNYVQAPQGEFT
ISPNNTPGDILFDLQLGPHLNPFLLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIAQ
ATMFPHVIADVRVLEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDF
NFLFLVPPNVEQKTKPFSVPNLPLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSAS
QLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTF
APHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPKVNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGEFKLYPEGFMTCVPNSSGSGPQ
TLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 28J

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_M57I+S94L (SEQ ID NO:171)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATCTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACCA
TAAGCCCAAACAACACCCCGGGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTG
CTCCACTTGGCTCAGATGTATAATGGATGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAAT
GCATTCACAGCCGGGAAGATTATTATCTCTTGCGTGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCG
CACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCCTTGA
GGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATATA
CTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGGGCGGGTGTTGACTTG
TCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTCAGCG
TGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATCT
CAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCAC
AACCCCAACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGG
GCTGAATCTTACTGAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCCG
ATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCAT
CGCATTGACGTAGCACAGGATAGCACATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATT
ACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAAG
TTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATATA
TCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGCC
TTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGGG
CGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACTCTACCCT
GAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGAG
GCTCGGGATCAGACGGAGCTAG

Figure 28K

Amino acid sequence of VP1_GI.3_Lil08_A43V+M57I+S94L (SEQ ID NO:174)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAVATAGQVNMIDPWIISNYVQAPQGEFT
ISPNNTPGDILFDLQLGPHLNPFLLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIAQ
ATMFPHVIADVRVLEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDF
NFLFLVPPNVEQKTKPFSVPNLPLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSAS
QLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTF
APHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPKVNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGEFKLYPEGFMTCVPNSSGSGPQ
TLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS

Figure 28L

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_A43V+M57I+S94L (SEQ ID NO:173)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGTGGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATCTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACCA
TAAGCCCAAACAACACCCCGGGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTG
CTCCACTTGGCTCAGATGTATAATGGATGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAAT
GCATTCACAGCCGGGAAGATTATTATCTCTTGCGTGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCG
CACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCCTTGA
GGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATATA
CTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGGGCGGGTGTTGACTTG
TCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTCAGCG
TGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATCT
CAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCAC
AACCCCAACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGG
GCTGAATCTTACTGAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCCG
ATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCAT
CGCATTGACGTAGCACAGGATAGCACATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATT
ACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAAG
TTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATATA
TCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGCC
TTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGGG
CGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACTCTACCCT
GAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGAG
GCTCGGGATCAGACGGAGCTAG

Figure 28M (SEQ ID NO:292)

AA sequence of VP1_GI.3_Lil08_S94X; where X = V, I, M, T, E, D, N, Q, K, or H

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGE
FTISPNNTPGDILFDLQLGPHLNPFL**X**HLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIA
QATMFPHVIADVRVLEPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPD
FNFLFLVPPNVEQKTKPFSVPNLPLNVLSNSRVPSLIKSMMVSQDHGQMVQFQNGRVTLDGQLQGTTPTSA
SQLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDST
FAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPKVNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGEFKLYPEGFMTCVPNSSGSGPQ
TLPINGVFTFISWVSRFYQLKPVGTTGPVRRLGIRRS*

Figure 28N (SEQ ID NO:293)

hCod optimized VP1_GI.3_Lil08_S94x; 'x' = V (XXX=GTG), I (XXX=ATC), M (XXX=ATG), T (XXX = ACC), E (XXX=GAG), D (XXX=GAC), N (XXX=AAC), Q (XXX=CAG), K (XXX=AAG), or H (XXX=CAC)

ATGATGATGGCTTCCAAGGATGCTCCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTTACC
ATAAGCCCAAACAACACCCCGGGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCT
G**XXX**CACTTGGCTCAGATGTATAATGGATGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAA
TGCATTCACAGCCGGGAAGATTATTATCTCTTGCGTGCCACCTGGATTTGCAGCCCAGAACGTGTCTATC
GCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCCTTG
AGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATAT
ACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGGGCGGGTGTTGACTT
GTCCTAGCCCTGACTTCAACTTCCTTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTCAGC
GTGCCAAACCTGCCCCTTAACGTGCTGTCGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCA
CAACCCCAACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGG
GGCTGAATCTTACTGAGATCGATGGTACCCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCC
GATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCA
TCGCATTGACGTAGCACAGGATAGCACATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGAT
TACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCTAAA
GTTAACCCATGGGCTATTCCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATAT
ATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGC
CTTAGTGTCCCTTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGG
GCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACTCTACCC
TGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTG
TTCACGTTTATCAGCTGGGTTTCACGGTTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGA
GGCTCGGGATCAGACGGAGCTAG

Figure 29A

Amino acid sequence of VP1_GI.5_Siklos_Q84S (SEQ ID NO:34)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLSLGPHLNPFLAHLSQMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLFPHIIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYTPLRTGGGSGGTDAFVVAGRVLTCPSSDFNFLFLVPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSQILKFRGKVSAGSKVINLTELDGSPFLAFEAPAP
TGFPDLGTSDWHVEMSLNSNSQSSGNPILLRDIHPNSSEFVPHLGSVCVTAAIEVAGDYTGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPPGFGEAIVYFMSPIPGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPQQLPLNGVFVFASWVSRFYQLKPVGTASSARGRLGVRR

Figure 29B

Nucleic acid sequence of human codon optimized VP1_GI.5_Siklos_Q84S (SEQ ID NO:35)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCTTGGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTTAATATG
ATTGACCCCTGGATTTTCAATAATTTCGTGCAGGCCCCTCAAGGCGAGTTTACTATAAGCCCTAACAACACACCAGGG
GATATTCTGTTCGACCTGAGCTTAGGCCCTCATCTCAACCCCTTCTTGGCCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCTTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTTCCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATACCAACGATAATCAGCCCACTATGAGG
TTACTGTGCATGCTGTACACGCCACTCCGGACTGGTGGGGGCAGTGGGGGGACCGATGCTTTCGTCGTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCCTATTCCTTGTGCCCCCAACGGTGGAACAGAAAACGAGACCTT
TTTCCGTACCTAACATCCCTTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTTCCAGACCTGGGAACATCCGATTGGCATGTCGAGA
TGAGTCTGAATAGCAACTCCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTTGGACAATTCCACACTACGGCTCTAACTTGGCCGA
AGCATCCCAGCTTGCCCCCGTTGTATATCCCCCAGGCTTTGGCGAAGCAATAGTTTATTTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTCGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTCGCATCATGGGTTAGCCGGTTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 29C

Amino acid sequence of VP1_GI.5_Siklos_A94L (SEQ ID NO:36)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLQLGPHLNPFLLHLSQMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLFPHIIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYTPLRTGGGSGGTDAFVVAGRVLTCPSSDFNFLFLVPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSQILKFRGKVSAGSKVINLTELDGSPFLAFEAPAP
TGFPDLGTSDWHVEMSLNSNSQSSGNPILLRDIHPNSSEFVPHLGSVCVTAAIEVAGDYTGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPPGFGEAIVYFMSPIPGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPQQLPLNGVFVFASWVSRFYQLKPVGTASSARGRLGVRR

Figure 29D

Nucleic acid sequence of human codon optimized VP1_GI.5_siklos_A94L (SEQ ID NO:37)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCTTGGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTTAATATG
ATTGACCCCTGGATTTTCAATAATTTCGTGCAGGCCCCTCAAGGCGAGTTTACTATAAGCCCTAACAACACACCAGGG
GATATTCTGTTCGACCTGCAGTTAGGCCCTCATCTCAACCCCTTCTTGCTCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCTTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTTCCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATACCAACGATAATCAGCCCACTATGAGG
TTACTGTGCATGCTGTACACGCCACTCCGGACTGGTGGGGGCAGTGGGGGGACCGATGCTTTCGTCGTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCCTATTCCTTGTGCCCCCAACGGTGGAACAGAAAACGAGACCTT
TTTCCGTACCTAACATCCCTTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTTCCAGACCTGGGAACATCCGATTGGCATGTCGAGA
TGAGTCTGAATAGCAACTCCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTTGGACAATTCCACACTACGGCTCTAACTTGGCCGA
AGCATCCCAGCTTGCCCCCGTTGTATATCCCCCAGGCTTTGGCGAAGCAATAGTTTATTTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTCGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTCGCATCATGGGTTAGCCGGTTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 29E

Amino acid sequence of VP1_GI.5_siklos_Q84S+A94L (SEQ ID NO:38)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLFPHIIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYTPLRTGGGSGGTDAFVVAGRVLTCPSSDFNFLFLVPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSQILKFRGKVSAGSKVINLTELDGSPFLAFEAPAP

Figure 29E (cont)

TGFPDLGTSDWHVEMSLNSNSQSSGNPILLRDIHPNSSEFVPHLGSVCVTAAIEVAGDYTGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPPGFGEAIVYFMSPIPGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPQQLPLNGVFVFASWVSRFYQLKPVGTASSARGRLGVRR

Figure 29F

Nucleic acid sequence of human codon optimized VP1_GI.5_siklos_Q84S+A94L (SEQ ID NO:39)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCTTGGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTTAATATG
ATTGACCCCTGGATTTTCAATAATTTCGTGCAGGCCCCTCAAGGCGAGTTTACTATAAGCCCTAACAACACACCAGGG
GATATTCTGTTCGACCTGAGCTTAGGCCCTCATCTCAACCCCTTCTTGCTCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCTTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTTCCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATACCAACGATAATCAGCCCACTATGAGG
TTACTGTGCATGCTGTACACGCCACTCCGGACTGGTGGGGGCAGTGGGGGGACCGATGCTTTCGTCGTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCCTATTCCTTGTGCCCCCAACGGTGGAACAGAAAACGAGACCTT
TTTCCGTACCTAACATCCCTTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTTCCAGACCTGGGAACATCCGATTGGCATGTCGAGA
TGAGTCTGAATAGCAACTCCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTTGGACAATTCCACACTACGGCTCTAACTTGGCCGA
AGCATCCCAGCTTGCCCCCGTTGTATATCCCCCAGGCTTTGGCGAAGCAATAGTTTATTTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTCGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTCGCATCATGGGTTAGCCGGTTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 29G

Amino acid sequence of VP1_ GI.7/GA5043/USA/2014_R84S (SEQ ID NO:177)

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIMNNFVQAPEGE
FTISPNNTPGDILFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICCVPPGFESQNISIG
QATMFPHVIADVRVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAP
DFNFLFLVPPSVEQKTRQLTIPNIPLNNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLEGQLLGTTPVSA
NQVARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFPDIGNCDWHVYAFKVNQNTGDPMYRLDITQG
NSFAPHLGSIEFSSENHPSGDQLGTLTWISPLNNASRVDPWKIPTYGSTLTESTNLAPPIFPPGFGEAIVYFMSD
FPIVSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHRNLGEFKLYPDGFITCVPNTGGGPQNLPS
NGVFVFSSWVSRYYQLKPVGTTGPVRRLGVRRV

Figure 29H

Nucleic acid sequence of human codon optimized VP1_ GI.7/GA5043/USA/2014_R84S (SEQ ID NO:176)

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGCAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAATGAACAATTTCGTTCAGGCACCAGAAGGAGAATTCACC
ATCTCCCCCAATAACACCCCAGGGGATATTCTGTTTGACCTCAGCTTAGGACCCCACTTGAACCCCTTTCT
GCTTCATCTCTCACAAATGTATAATGGCTGGGTCGGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAA
TGCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCCTCCTGGATTCGAATCTCAAAATATCAGCATTG
GTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTCGCGTCCTGGAACCCATTGAAGTTCCTCTCGAC
GACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACA
CCCCATTAAGAGCCGGGGGAGCATCCTCAGGTACTGACCCATTTGTGATTGCCGGGCGGGTGCTCACAT
GCCCGGCTCCAGACTTTAACTTCCTTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCTCACC
ATCCCAAATATCCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCA
GTGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGA
CGACCCCAGTCTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAAACTCCGGCACTG
GCCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTTGAGTCTCCAGCCCCTCTTGGCTTTCCC
GATATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATA
GGTTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCA
TCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCC
CTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGCTCCGCCCATTTTCCCACCCG
GATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCCT
TGCACACTGCCACAAGAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCCC
TCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAGCTGTACCCTGACGGGTTTATT
ACCTGTGTACCCAACACCGGCGGCGGCCCACAAAATTTGCCCAGCAATGGCGTGTTTGTCTTTTCCTCTTG
GGTGTCTCGATACTACCAGCTTAAACCTGTCGGAACTACGGGCCCCGTGCGACGACTCGGCGTGAGGCG
GGTGTGA

Figure 29I

Amino acid sequence of VP1_ GI.7/GA5043/USA/2014_M57I (SEQ ID NO:179)

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIINNFVQAPEGEFT
ISPNNTPGDILFDLRLGPHLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICCVPPGFESQNISIGQA
TMFPHVIADVRVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPDF
NFLFLVPPSVEQKTRQLTIPNIPLNNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLEGQLLGTTPVSANQ
VARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGNSF
APHLGSIEFSSENHPSGDQLGTLTWISPLNNASRVDPWKIPTYGSTLTESTNLAPPIFPPGFGEAIVYFMSDFPI
VSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHRNLGEFKLYPDGFITCVPNTGGGPQNLPSNG
VFVFSSWVSRYYQLKPVGTTGPVRRLGVRRV

Figure 29J

human codon optimized VP1_ GI.7/GA5043/USA/2014_M57I (SEQ ID NO:178)

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGCAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAATCAACAATTTCGTTCAGGCACCAGAAGGAGAATTCACCA
TCTCCCCCAATAACACCCCAGGGGATATTCTGTTTGACCTCAGGTTAGGACCCCACTTGAACCCCTTTCTG
CTTCATCTCTCACAAATGTATAATGGCTGGGTCGGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAAT
GCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCCTCCTGGATTCGAATCTCAAAATATCAGCATTGG
TCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTCGCGTCCTGGAACCCATTGAAGTTCCTCTCGACG
ACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACAC
CCCATTAAGAGCCGGGGGAGCATCCTCAGGTACTGACCCATTTGTGATTGCCGGGCGGGTGCTCACATG
CCCGGCTCCAGACTTTAACTTCCTTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCTCACCA
TCCCAAATATCCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCAG
TGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGAC
GACCCCAGTCTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAAACTCCGGCACTGG
CCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTTGAGTCTCCAGCCCCTCTTGGCTTTCCCGA
TATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATAGG
TTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCATC
CGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCCCT
GGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGCTCCGCCCATTTTCCCACCCGG
ATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCCTT
GCACACTGCCACAAGAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCCCT
CTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAGCTGTACCCTGACGGGTTTATTA
CCTGTGTACCCAACACCGGCGGCGGCCCACAAAATTTGCCCAGCAATGGCGTGTTTGTCTTTTCCTCTTGG
GTGTCTCGATACTACCAGCTTAAACCTGTCGGAACTACGGGCCCCGTGCGACGACTCGGCGTGAGGCGG
GTGTGA

Figure 29K

Amino acid sequence of VP1_ GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:181)

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIINNFVQAPEGEFT
ISPNNTPGDILFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICCVPPGFESQNISIGQA
TMFPHVIADVRVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPDF
NFLFLVPPSVEQKTRQLTIPNIPLNNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLEGQLLGTTPVSANQ
VARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGNSF
APHLGSIEFSSENHPSGDQLGTLTWISPLNNASRVDPWKIPTYGSTLTESTNLAPPIFPPGFGEAIVYFMSDFPI
VSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHRNLGEFKLYPDGFITCVPNTGGGPQNLPSNG
VFVFSSWVSRYYQLKPVGTTGPVRRLGVRRV

Figure 29L

Human codon optimized VP1_ GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:180)

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCCCGAGGTC
AATGCCGCAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCAGGCCAAGTCAATAT
GATCGACCCGTGGATAATCAACAATTTCGTTCAGGCACCAGAAGGAGAATTCACCATCTCCCCCAATAACACCCCAG
GGGATATTCTGTTTGACCTCAGCTTAGGACCCCACTTGAACCCCTTTCTGCTTCATCTCTCACAAATGTATAATGGCTG
GGTCGGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAATGCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTC
CTCCTGGATTCGAATCTCAAAATATCAGCATTGGTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTCGCGTCC
TGGAACCCATTGAAGTTCCTCTCGACGACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGA
CTTCTGTGTATGCTCTACACCCCATTAAGAGCCGGGGGAGCATCCTCAGGTACTGACCCATTTGTGATTGCCGGGCG
GGTGCTCACATGCCCGGCTCCAGACTTTAACTTCCTTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCT
CACCATCCCAAATATCCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCAGTG
CTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGACGACCCCAGT
CTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAAACTCCGGCACTGGCCTTAACCTCACAGAG
GTTGACGGCACTCCCTATCATGCTTTTGAGTCTCCAGCCCCTCTTGGCTTTCCCGATATAGGCAACTGTGACTGGCAC
GTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATAGGTTGGATATAACACAAGGTAATTCATTCGC
CCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCATCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATC
AGCCCTCTGAATAACGCATCAAGAGTGGATCCCTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAA
TTTGGCTCCGCCCATTTTCCCACCCGGATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGG
GAATACAGCCCAGATTCCTTGCACACTGCCACAAGAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTCGAG
GTGAGGCCGCCCTCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAGCTGTACCCTGACGGG
TTTATTACCTGTGTACCCAACACCGGCGGCGGCCCACAAAATTTGCCCAGCAATGGCGTGTTTGTCTTTTCCTCTTGG
GTGTCTCGATACTACCAGCTTAAACCTGTCGGAACTACGGGCCCCGTGCGACGACTCGGCGTGAGGCGGGTGTGA

Figure 29M (SEQ ID NO:290)

AA sequence of VP1_GI.7/GA5043/USA/2014_M57X; where X = L, G, S, T, N, Q, K, or H

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWI**X**NNFVQAPEGEF
TISPNNTPGDILFDLRLGPHLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICCVPPGFESQNISIGQ
ATMFPHVIADVRVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPD
FNFLFLVPPSVEQKTRQLTIPNIPLNNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLEGQLLGTTPVSAN
QVARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGN
SFAPHLGSIEFSSENHPSGDQLGTLTWISPLNNASRVDPWKIPTYGSTLTESTNLAPPIFPPGFGEAIVYFMSDF
PIVSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHRNLGEFKLYPDGFITCVPNTGGGPQNLPSN
GVFVFSSWVSRYYQLKPVGTTGPVRRLGVRRV*

Figure 29N (SEQ ID NO:291)

Human codon optimized VP1_GI.7/GA5043/USA/2014_M57x; 'x' = L (XXX=CTG), G (XXX=GGC), S (XXX=AGC), T (XXX=ACC), N (XXX=AAC), Q (XXX=CAG), K (XXX=AAG), or H (XXX=CAC)

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGCAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATA**XXX**AACAATTTCGTTCAGGCACCAGAAGGAGAATTCACC
ATCTCCCCCAATAACACCCCAGGGGATATTCTGTTTGACCTCAGGTTAGGACCCCACTTGAACCCCTTTCT
GCTTCATCTCTCACAAATGTATAATGGCTGGGTCGGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAA
TGCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCCTCCTGGATTCGAATCTCAAAATATCAGCATTG
GTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTCGCGTCCTGGAACCCATTGAAGTTCCTCTCGAC
GACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACA
CCCCATTAAGAGCCGGGGGAGCATCCTCAGGTACTGACCCATTTGTGATTGCCGGGCGGGTGCTCACAT
GCCCGGCTCCAGACTTTAACTTCCTTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCTCACC
ATCCCAAATATCCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCA
GTGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGA
CGACCCCAGTCTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAAACTCCGGCACTG
GCCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTTGAGTCTCCAGCCCCTCTTGGCTTTCCC
GATATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATA
GGTTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCA
TCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCC
CTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGCTCCGCCCATTTTCCCACCCG
GATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCCT
TGCACACTGCCACAAGAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCCC
TCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAGCTGTACCCTGACGGGTTTATT
ACCTGTGTACCCAACACCGGCGGCGGCCCACAAAATTTGCCCAGCAATGGCGTGTTTGTCTTTTCCTCTTG
GGTGTCTCGATACTACCAGCTTAAACCTGTCGGAACTACGGGCCCCGTGCGACGACTCGGCGTGAGGCG
GGTGTGA

Figure 30A

Amino acid sequence of VP1_GII.2_CGMH47_E80S (SEQ ID NO:85)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLSLGPELNPYLAHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLL
PLPDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGL
NDTDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

Figure 30B

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_E80S_ (SEQ ID NO:86)

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGGCTCACCTGGCCCGGATGTACAATGGATATGCAGGAGG
GATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCACT
TCCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 30C

Amino acid sequence of VP1_GII.2_CGMH47_A90L (SEQ ID NO:41)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLL
PLPDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGL
NDTDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

Figure 30D

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_A90L (SEQ ID NO:42)

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCGAGCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAGG

Figure 30D (cont)

GATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCACT
TCCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 30E

Amino acid sequence of VP1_GII.2_CGMH47_E80S+A90L (SEQ ID NO:43)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLSLGPELNPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLL
PLPDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGL
NDTDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

Figure 30F

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_E80S+A90L (SEQ ID NO:44)

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAGG
GATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCACT
TCCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC

Figure 30F (cont)

TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

FIGURE 30G

Amino acid sequence of VP1_GII.2_CGMH47_A39V+E80S+A90L (SEQ ID NO:182)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAVPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLSLGPELNPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLL
PLPDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGL
NDTDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

FIGURE 30H

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_A39V+E80S+A90L (SEQ ID NO:183)

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGTGCCTGTGACCGGGCAGACAAATATCATCGATCCTT
GGATTAGAGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCT
CCTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAG
GGATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCAC
TTCCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTG
TGCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC

Figure 30H (cont)

CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

FIGURE 30I

Amino acid sequence of VP1_GII.2_CGMH47_ R53I+E80S+A90L (SEQ ID NO:184)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIIANFVQAPNGEFTVSPRNSPGEVLLN
LSLGPELNPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLLPL
PDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELSNS
RFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSEDIP
APLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGLND
TDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVALV
RYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

FIGURE 30J

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_ R53I+E80S+A90L (SEQ ID NO:185)

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTATCGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTCC
TCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAGGG
ATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCACTT
CCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

FIGURE 30K

Amino acid sequence of VP1_GII.2_CGMH47_A39V+ R53I+E80S+A90L (SEQ ID NO:186)

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAVPVTGQTNIIDPWIIANFVQAPNGEFTVSPRNSPGEVLLN
LSLGPELNPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLLPL
PDVRNNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLVPPTVESKTKPFTLPILTLGELSNS
RFPVSIDQMYTSPNEVISVQCQNGRCTLDGELQGTTQLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSEDIP
APLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGLND
TDHFNQWVVPRYAGALNLNTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVALV
RYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

FIGURE 30L (SEQ ID NO:187)

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_A39V+ R53I+E80S+A90L

ATGAAGATGGCATCCAACGACGCCGCACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGTGCCTGTGACCGGGCAGACAAATATCATCGATCCTT
GGATTATCGCTAATTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCT
CCTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAG
GGATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCCTCCCCAC
TTCCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCATGTCATCATCGATGTGCGTACCCTGGAACCTG
TGCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAAACTAAGCCATTCACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTCAGAACGGCAGGTGCACCTTAGACGGTGAACTGCAGGGGACAACGCAGTTGCAGGTCAGTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTCGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 31A

Amino acid sequence of VP1_GII.3_Jing_E80S (SEQ ID NO:46)

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNFVQAPGGEFTVSPRNSPGEVLLN
LSLGPEINPYLAHLARMYNGYAGGFEVQVVLAGNAFTAGKIIFAAIPPNFPIDNLSAAQITMCPHVIVDVRQLEPVNLPMP
DVRNNFFHYNQGSDSRLRLIAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFSFNFLVPPTVESKTKPFSLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLDGELMGTTQLLPSQICAFRGTLTRSTSRASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTPDFRGKVFGVASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNQPTRFTPVGIGVD

Figure 31A (cont)

HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHKLRFMTIAKSGDSPITVPPNGYFRFESWVNPFYTLAPMGTGNGRRRIQ

Figure 31B

Nucleic acid sequence of human codon optimized VP1_GII.3_Jing_E80S (SEQ ID NO:47)

ATGAAAATGGCTTCCAACGATGCAGCACCCTCTAATGATGGCGCTGCCGGACTTGTGCCGGAGATTAGCTCTGAGG
CTATGGCCCTAGAACCAGTAGCCGGGGCAGCCATAGCTGCCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCGTGCAGGCACCGGGGGGGAGAATTCACGGTCTCTCCTCGAAACTCCCCCGGGGAGGTTCTCT
TGAATTTGAGCCTGGGCCCTGAAATTAATCCTTATCTGGCCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT
TTCGAGGTCCAGGTGGTGCTCGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCGACGTGCGCAACAACTTCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATTCCGGAGATGACGTTTTCACTGTGAGTTGTCGAGTCCTGACACGTCC
ATCTCCTGACTTTAGCTTTAATTTCCTCGTGCCCCCCACAGTGGAATCCAAAACTAAGCCATTCTCTCTGCCAATTCTT
ACCATTAGCGAAATGTCGAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTCAGAACGGACGCGTGACTCTCGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACTCGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCACCCGGGCCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTCACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTTCGATCAGAACCAGCCAACCCGGTTTACCCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGCAGGCCAGTTCACACATAACATGAATCTTGCCCCCGCTGTGGCCCCCAACTTCCCGGGAG
AACAACTTCTGTTTTTCAGGAGCCAACTGCCTTCCAGCGGCGGCCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATTCGCC
TATTACAGTGCCCCCCAACGGATACTTCAGATTTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 31C

Amino acid sequence of VP1_GII.3_Jing_A90L (SEQ ID NO:48)

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNFVQAPGGEFTVSPRNSPGEVLLN
LELGPEINPYLLHLARMYNGYAGGFEVQVVLAGNAFTAGKIIFAAIPPNFPIDNLSAAQITMCPHVIVDVRQLEPVNLPMP
DVRNNFFHYNQGSDSRLRLIAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFSFNFLVPPTVESKTKPFSLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLDGELMGTTQLLPSQICAFRGTLTRSTSRASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTPDFRGKVFGVASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNQPTRFTPVGIGVD
HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHKLRFMTIAKSGDSPITVPPNGYFRFESWVNPFYTLAPMGTGNGRRRIQ

Figure 31D

Nucleic acid sequence of human codon optimized VP1_GII.3_Jing_A90L (SEQ ID NO:49)

ATGAAAATGGCTTCCAACGATGCAGCACCCTCTAATGATGGCGCTGCCGGACTTGTGCCGGAGATTAGCTCTGAGG
CTATGGCCCTAGAACCAGTAGCCGGGGCAGCCATAGCTGCCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCGTGCAGGCACCGGGGGGGAGAATTCACGGTCTCTCCTCGAAACTCCCCCGGGGAGGTTCTCT
TGAATTTGGAACTGGGCCCTGAAATTAATCCTTATCTGCTCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT
TTCGAGGTCCAGGTGGTGCTCGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCGACGTGCGCAACAACTTCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATTCCGGAGATGACGTTTTCACTGTGAGTTGTCGAGTCCTGACACGTCC
ATCTCCTGACTTTAGCTTTAATTTCCTCGTGCCCCCCACAGTGGAATCCAAAACTAAGCCATTCTCTCTGCCAATTCTT
ACCATTAGCGAAATGTCGAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTCAGAACGGACGCGTGACTCTCGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACTCGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCACCCGGGCCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTCACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTTCGATCAGAACCAGCCAACCCGGTTTACCCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGCAGGCCAGTTCACACATAACATGAATCTTGCCCCCGCTGTGGCCCCCAACTTCCCGGGAG
AACAACTTCTGTTTTTCAGGAGCCAACTGCCTTCCAGCGGCGGCCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATTCGCC
TATTACAGTGCCCCCCAACGGATACTTCAGATTTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 31E

Amino acid sequence of VP1_GII.3_Jing_E80S+A90L (SEQ ID NO:50)

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNFVQAPGGEFTVSPRNSPGEVLLN
LSLGPEINPYLLHLARMYNGYAGGFEVQVVLAGNAFTAGKIIFAAIPPNFPIDNLSAAQITMCPHVIVDVRQLEPVNLPMP
DVRNNFFHYNQGSDSRLRLIAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFSFNFLVPPTVESKTKPFSLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLDGELMGTTQLLPSQICAFRGTLTRSTSRASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTPDFRGKVFGVASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNQPTRFTPVGIGVD
HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHKLRFMTIAKSGDSPITVPPNGYFRFESWVNPFYTLAPMGTGNGRRRIQ

Figure 31F

Nucleic acid sequence of human codon optimized VP1_GII.3_Jing_E80S+A90L (SEQ ID NO:51)

ATGAAAATGGCTTCCAACGATGCAGCACCCTCTAATGATGGCGCTGCCGGACTTGTGCCGGAGATTAGCTCTGAGG
CTATGGCCCTAGAACCAGTAGCCGGGGCAGCCATAGCTGCCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCGTGCAGGCACCGGGGGGGAGAATTCACGGTCTCTCCTCGAAACTCCCCCGGGGAGGTTCTCT
TGAATTTGAGCCTGGGCCCTGAAATTAATCCTTATCTGCTCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT

Figure 31F (cont)

TTCGAGGTCCAGGTGGTGCTCGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCGACGTGCGCAACAACTTCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATTCCGGAGATGACGTTTTCACTGTGAGTTGTCGAGTCCTGACACGTCC
ATCTCCTGACTTTAGCTTTAATTTCCTCGTGCCCCCCACAGTGGAATCCAAAACTAAGCCATTCTCTCTGCCAATTCTT
ACCATTAGCGAAATGTCGAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTCAGAACGGACGCGTGACTCTCGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACTCGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCACCCGGGCCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTCACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTTCGATCAGAACCAGCCAACCCGGTTTACCCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGCAGGCCAGTTCACACATAACATGAATCTTGCCCCCGCTGTGGCCCCCAACTTCCCGGGAG
AACAACTTCTGTTTTTCAGGAGCCAACTGCCTTCCAGCGGCGGCCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATTCGCC
TATTACAGTGCCCCCCAACGGATACTTCAGATTTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 32A

Amino acid sequence of VP1_GII.4_Syd12_A39V (SEQ ID NO:53)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAVPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32B

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_A39V (SEQ ID NO:54)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC

Figure 32B (cont)

GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32C

Amino acid sequence of VP1_GII.4_Syd12_V47P (SEQ ID NO:55)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNPIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32D

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_V47P (SEQ ID NO:56)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATCCCATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG

Figure 32D (cont)

AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32E

Amino acid sequence of VP1_GII.4_Syd12_R53I (SEQ ID NO:57)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIINNFVQAPGGEFTVSPRNAPGEILW
SAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLIPL
PDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMTN
SRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIPAP
LGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNE
PQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLR
FVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32F

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_R53I (SEQ ID NO:58)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATAATCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32G

Amino acid sequence of VP1_GII.4_Syd12_P80S (SEQ ID NO:59)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32H

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S (SEQ IDNO:60)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32I

Amino acid sequence of VP1_GII.4_Syd12_S90L (SEQ ID NO:61)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLLHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP

Figure 32I (cont)

APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32J

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_S90L (SEQ IDNO:62)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32K

Amino acid sequence of VP1_GII.4_Syd12_Δ35-42 (SEQ ID NO:63)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEILWSAPLGPD
LNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLIPLPDVRNN
FYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMTNSRFPIPLE
KLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFV
GKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVL
PSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTG
RVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32L

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_Δ35-42 (SEQ IDNO:64)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGGTCAGCAGAATGTGATTGACCCGTGGATACGCAACAATTTTGTCCAAGC
CCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTCGGCCCCATTGGGACCCGAT
CTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGC
TGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGTCTCCAA
GCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTA
CGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTCTGCGC
GCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACTTTGACTTTATC
TTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACAGTCGAGGAGATGACAAA
TAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTCGTGGTTCAGCCACAGAACGGACG
CTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGACGTAA
CTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCCAACCGAAGAG
ATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACCGATGG
CTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGCAGTTTG
AGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGACGGGGG
CACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCCGGATATC
CCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCGCACCAGCCCAATCC
GACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTGCAAATTGCACAAATCAGGATA
CGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGATATTTTAGGTTCGACTCCTGGGTGA
ATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCTGTCTGA

Figure 32M

Amino acid sequence of VP1_GII.4_Syd12_SSTAVATA (SEQ ID NO:65)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGSSTAVATAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32N

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_SSTAVATA (SEQ ID NO:66)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCAGCTCCACCGCCGTCGCTACAGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT

Figure 32N (cont)

TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32O

Amino acid sequence of VP1_GII.4_Syd12_P80S+A39V (SEQ ID NO:67)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAVPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32P

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S+A39V (SEQ ID NO:68)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT

Figure 32P (cont)

CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32Q

Amino acid sequence of VP1_GII.4_Syd12_P80S+V47P (SEQ ID NO:69)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNPIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32R

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S+V47P (SEQ ID NO:70)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATCCCATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA

Figure 32R (cont)

ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32S

Amino acid sequence of VP1_GII.4_Syd12_P80S+R53I (SEQID NO:71)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIINNFVQAPGGEFTVSPR
NAPGEILWSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLIPLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFSVPVLTVEEMTNSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLG
RVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHTGQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32T

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S+R53I (SEQ ID NO:72)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATAATCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32U

Amino acid sequence of VP1_GII.4_Syd12_P80S+S90L (SEQ ID NO:73)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPYLLHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32V

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S+S90L (SEQ ID NO:74)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32W

Amino acid sequence of VP1_GII.4_Syd12_P80S+Δ35-42 (SEQ ID NO:75)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEILWSASLGPD
LNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLIPLPDVRNN
FYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMTNSRFPIPLE
KLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFV

Figure 32W (cont)

GKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVL
PSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTG
RVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32X

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S+Δ35-42 (SEQ ID NO:76)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGGTCAGCAGAATGTGATTGACCCGTGGATACGCAACAATTTTGTCCAAGC
CCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTCGGCCAGCTTGGGACCCGAT
CTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGC
TGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGTCTCCAA
GCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTA
CGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTCTGCGC
GCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACTTTGACTTTATC
TTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACAGTCGAGGAGATGACAAA
TAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTCGTGGTTCAGCCACAGAACGGACG
CTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGACGTAA
CTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCCAACCGAAGAG
ATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACCGATGG
CTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGCAGTTTG
AGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGACGGGGG
CACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCCGGATATC
CCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCGCACCAGCCCAATCC
GACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTGCAAATTGCACAAATCAGGATA
CGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGATATTTTAGGTTCGACTCCTGGGTGA
ATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCTGTCTGA

Figure 32Y

Amino acid sequence of VP1_GII.4_Syd12_P80S+SSTAVATA (SEQ ID NO:77)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGSSTAVATAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFSVPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLGRVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32Z

Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S+SSTAVATA (SEQ ID NO:78)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCAGCTCCACCGCCGTCGCTACAGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

FIGURE 32AA

Amino acid sequence of VP1 GII.4 Syd12 A39V+R53I (SEQ ID NO:188)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAVPVAGQQNVIDPWIINNFVQAPGGEFTVSPR
NAPGEILWSAPLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLIPLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFSVPVLTVEEMTNSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLG
RVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHTGQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

FIGURE 32BB

Nucleic acid sequence of human codon optimized VP1 GII.4_Syd12_A39V+R53I (SEQ ID NO:189)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAAT
AATGAGGTGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAA
TGTGATTGACCCGTGGATAATCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGA
AATGCGCCAGGAGAAATCCTGTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCG
CTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTG
CTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCAC
AATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTACGC
AATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTCTG
CGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACT
TTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACA
GTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCAT
TCGTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCC
CTGTTAATATCTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTG
GCATCACAGAATTGGAATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTG
TGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCA
ACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACC
GGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGACGGGGGCACCACTC
ACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCG
CACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTG
CAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAAC
GGATATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCA
GACGCAGGGCTGTCTGA

FIGURE 32CC

Amino acid sequence of VP1 GII.4 Syd12 A39V+R53I+P80S (SEQ ID NO:190)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAVPVAGQQNVIDPWIINNFVQAPGGEFTVSPR
NAPGEILWSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLIPLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFSVPVLTVEEMTNSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLG
RVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHTGQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

FIGURE 32DD

Nucleic acid sequence of human codon optimized VP1 GII.4_Syd12_A39V+R53I+P80S (SEQ ID NO:191)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTG
GATAATCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGT
GGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGA
TTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTT
CCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTG
TCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGC
GATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGAC
CTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACT
CACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTCG
TGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATATC
TGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGAA
TGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTGA
CACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCG
AAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTG
TAGGAGTGATTCAGGACGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGA
GGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAA
CCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATC
AAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGAT
ATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

FIGURE 32EE

Nucleic acid sequence of human codon optimized VP1 GII.4_Syd12_P80X; where X = A (**XXX**=GCC), N (**XXX**=AAC), K(**XXX**=AAG), or H(**XXX**=CAC) (SEQ ID NO:287)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAAT
AATGAGGTGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAA
TGTGATTGACCCGTGGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGA
AATGCGCCAGGAGAAATCCTGTGGTCGGCC**XXX**TTGGGACCCGATCTGAACCCCTATTTGTCACATCTCG
CTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTG
CTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCAC
AATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTACGC
AATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTCTG
CGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACT
TTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACA
GTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCAT
TCGTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCC

FIGURE 32EE (cont)

CTGTTAATATCTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTG
GCATCACAGAATTGGAATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTG
TGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCA
ACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACC
GGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGACGGGGGCACCACTC
ACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCG
CACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTG
CAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAAC
GGATATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCA
GACGCAGGGCTGTCTGA

FIGURE 32FF

Amino acid sequence of VP1_GII.4_Syd12_P80X; where X = A, N, K, or H (SEQ ID NO:286)

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPR
NAPGEILWSA**X**LGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLIPLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFSVPVLTVEEMTNSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLG
RVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHTGQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

FIGURE 32GG (SEQ ID NO:289)

hCod optimize sequence of VP1 GII.4_Syd12_P80S+A39X; X = I(**XXX**=ATC), M(**XXX**=ATG), G(**XXX**=GGC), S(**XXX**=AGC), E(**XXX**=GAG), D(**XXX**=GAC), N(**XXX**=AAC), Q(**XXX**=CAG), K(**XXX**=AAG), or H(**XXX**=CAC)

ATGAAAATGGCCTCGAGTGACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAAT
AATGAGGTGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCA**XXX**CCCGTGGCCGGTCAGCAGAA
TGTGATTGACCCGTGGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGA
AATGCGCCAGGAGAAATCCTGTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCG
CTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTG
CTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCAC
AATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTACGC
AATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTCTG
CGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACT
TTGACTTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACA

FIGURE 32GG (cont)

GTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCAT
TCGTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCC
CTGTTAATATCTGTACGTTTAGAGGCGACGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTG
GCATCACAGAATTGGAATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTG
TGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCA
ACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACC
GGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGACGGGGGCACCACTC
ACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCG
CACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTG
CAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAAC
GGATATTTTAGGTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCA
GACGCAGGGCTGTCTGA

FIGURE 32HH (SEQ ID NO:288)

Amino acid sequence of VP1_GII.4_Syd12_P80S+A39X; where X = I, M, G, S, E, D, N, Q, K, or H

MKMASSDANPSDGSAANLVPEVNNEVMALEPVVGAAIA**X**PVAGQQNVIDPWIRNNFVQAPGGEFTVSPR
NAPGEILWSASLGPDLNPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLIPLPDVRNNFYHYNQSNDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFSVPVLTVEEMTNSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTEEIPAPLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADFAPKLG
RVQFETDTDRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHTGQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 33A

Amino acid sequence of VP1_GII.6_Ohio_E80S (SEQ ID NO:79)

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLSLGPELNPYLSHLSRMYNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHFPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRFFHYNQENTSRMRLVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSLPILTLGELSNSR
FPAPIDMLYTDPNEGIVVQPQNGRCTLDGTLQGTTQLVPTQICAFRGTLIGQTSRSPDSTDSAPRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVSGQQVGATRAHEVHINTTDPRYTPKLGSILMYSESDDFVTGQPVRFTPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSGNNPIVVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 33B

Nucleic acid sequence of human codon optimized VP1_GII.6_Ohio_E80S (SEQ ID NO:80)

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGCTCCACAGGGGGAGTTCACAGTCTCCCCCCGGAACTCCCCGGGCGAGATGCTG
CTCAATCTGAGCCTCGGCCCTGAACTAAACCCTTATCTGTCACACCTTTCACGGATGTACAATGGCTACGCAGGAGG
AATGCAAGTTCAGGTGGTCCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCCTCCACACT
TCCCTGTCGAAAATATCAACGCCGCCCAGATTACTATGTGCCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCA
GTTCTGCTGCCCCTGCCCGACATCAGAAACCGGTTCTTCCATTACAATCAAGAGAATACTTCACGGATGAGACTTGTT
GCGATGCTGTACACCCCTCTTCGTGCAAATTCCGGCGAAGACGTGTTCACTGTGTCTTGTCGAGTACTTACCCGACCC
GCCCCCGATTTCGAATTCACCTTCCTGGTTCCCCCTACTGTGGAGAGCAAGACAAAACCCTTCAGCCTCCCAATCTTA
ACACTCGGGGAGCTGTCTAATTCACGCTTCCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGT
GGTGCAGCCCCAAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAACTGGTGCCAACCCAGATT
TGTGCATTCAGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGG
ACCACCCACTCCACGTTCAGTTAAAAAACCTGGACGGAACCCAGTACGACCCTACAGACGAGGTCCCCGCTGTCCTC
GGAGCCATCGACTTTAAAGGAACTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGCAGCAGGTGGGAGCT
ACGAGAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCCAAAACTAGGGTCAATTTTAATGTATTC
GGAATCAGACGATTTTGTTACAGGTCAGCCCGTGCGGTTTACCCCGATCGGAATGGGGGACAACGATTGGCACCAG
TGGGAATTGCCCGATTACCCTGGACACCTCACCTTGAATATGAATCTGGCCCCAGCCGTCGCGCCCGCCTTCCCCGGT
GAGCGGATCCTCTTTTTTAGAAGCATAGTGCCCTCCGCAGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCC
CCAAGAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCTAGCCAGTCCGCAGTAGCACTGATCAGATATGTTAATC
CTGATACGGGAAGGAACATCTTCGAAGCAAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAA
CCCTATTGTGGTGCCTCCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTTATACTCTGACTCCCATGGG
GACAGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 33C

Amino acid sequence of VP1_GII.6_Ohio_S90L (SEQ ID NO:81)

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLELGPELNPYLLHLSRMYNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHFPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRFFHYNQENTSRMRLVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSLPILTLGELSNSR
FPAPIDMLYTDPNEGIVVQPQNGRCTLDGTLQGTTQLVPTQICAFRGTLIGQTSRSPDSTDSAPRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVSGQQVGATRAHEVHINTTDPRYTPKLGSILMYSESDDFVTGQPVRFTPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSGNNPIVVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 33D

Nucleic acid sequence of human codon optimized VP1_GII.6_Ohio_S90L (SEQ ID NO:82)

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGCTCCACAGGGGGAGTTCACAGTCTCCCCCCGGAACTCCCCGGGCGAGATGCTG
CTCAATCTGGAACTCGGCCCTGAACTAAACCCTTATCTGCTCCACCTTTCACGGATGTACAATGGCTACGCAGGAGG

FIGURE 33D (cont)

AATGCAAGTTCAGGTGGTCCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCCTCCACACT
TCCCTGTCGAAAATATCAACGCCGCCCAGATTACTATGTGCCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCA
GTTCTGCTGCCCCTGCCCGACATCAGAAACCGGTTCTTCCATTACAATCAAGAGAATACTTCACGGATGAGACTTGTT
GCGATGCTGTACACCCCTCTTCGTGCAAATTCCGGCGAAGACGTGTTCACTGTGTCTTGTCGAGTACTTACCCGACCC
GCCCCCGATTTCGAATTCACCTTCCTGGTTCCCCCTACTGTGGAGAGCAAGACAAAACCCTTCAGCCTCCCAATCTTA
ACACTCGGGGAGCTGTCTAATTCACGCTTCCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGT
GGTGCAGCCCCAAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAACTGGTGCCAACCCAGATT
TGTGCATTCAGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGG
ACCACCCACTCCACGTTCAGTTAAAAAACCTGGACGGAACCCAGTACGACCCTACAGACGAGGTCCCCGCTGTCCTC
GGAGCCATCGACTTTAAAGGAACTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGCAGCAGGTGGGAGCT
ACGAGAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCCAAAACTAGGGTCAATTTTAATGTATTC
GGAATCAGACGATTTTGTTACAGGTCAGCCCGTGCGGTTTACCCCGATCGGAATGGGGGACAACGATTGGCACCAG
TGGGAATTGCCCGATTACCCTGGACACCTCACCTTGAATATGAATCTGGCCCCAGCCGTCGCGCCCGCCTTCCCCGGT
GAGCGGATCCTCTTTTTTAGAAGCATAGTGCCCTCCGCAGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCC
CCAAGAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCTAGCCAGTCCGCAGTAGCACTGATCAGATATGTTAATC
CTGATACGGGAAGGAACATCTTCGAAGCAAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAA
CCCTATTGTGGTGCCTCCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTTATACTCTGACTCCCATGGG
GACAGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 33E

Amino acid sequence of VP1_GII.6_Ohio_E80S+S90L (SEQ ID NO:83)

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLSLGPELNPYLLHLSRMYNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHFPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRFFHYNQENTSRMRLVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSLPILTLGELSNSR
FPAPIDMLYTDPNEGIVVQPQNGRCTLDGTLQGTTQLVPTQICAFRGTLIGQTSRSPDSTDSAPRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVSGQQVGATRAHEVHINTTDPRYTPKLGSILMYSESDDFVTGQPVRFTPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSGNNPIVVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 33F

Nucleic acid sequence of human codon optimized VP1_GII.6_Ohio_E80S+S90L (SEQ IDNO:84)

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGCTCCACAGGGGGAGTTCACAGTCTCCCCCCGGAACTCCCCGGGCGAGATGCTG
CTCAATCTGAGCCTCGGCCCTGAACTAAACCCTTATCTGCTCCACCTTTCACGGATGTACAATGGCTACGCAGGAGGA
ATGCAAGTTCAGGTGGTCCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCCTCCACACTTC
CCTGTCGAAAATATCAACGCCGCCCAGATTACTATGTGCCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCAGT
TCTGCTGCCCCTGCCCGACATCAGAAACCGGTTCTTCCATTACAATCAAGAGAATACTTCACGGATGAGACTTGTTGC
GATGCTGTACACCCCTCTTCGTGCAAATTCCGGCGAAGACGTGTTCACTGTGTCTTGTCGAGTACTTACCCGACCCGC
CCCCGATTTCGAATTCACCTTCCTGGTTCCCCCTACTGTGGAGAGCAAGACAAAACCCTTCAGCCTCCCAATCTTAAC
ACTCGGGGAGCTGTCTAATTCACGCTTCCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGTGG

FIGURE 33F (cont)

TGCAGCCCCAAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAACTGGTGCCAACCCAGATTTGT
GCATTCAGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGGACC
ACCCACTCCACGTTCAGTTAAAAAACCTGGACGGAACCCAGTACGACCCTACAGACGAGGTCCCCGCTGTCCTCGGA
GCCATCGACTTTAAAGGAACTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGCAGCAGGTGGGAGCTACGA
GAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCCAAAACTAGGGTCAATTTTAATGTATTCGGAA
TCAGACGATTTTGTTACAGGTCAGCCCGTGCGGTTTACCCCGATCGGAATGGGGGACAACGATTGGCACCAGTGGG
AATTGCCCGATTACCCTGGACACCTCACCTTGAATATGAATCTGGCCCCAGCCGTCGCGCCCGCCTTCCCCGGTGAGC
GGATCCTCTTTTTTAGAAGCATAGTGCCCTCCGCAGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCCCCAA
GAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCTAGCCAGTCCGCAGTAGCACTGATCAGATATGTTAATCCTGA
TACGGGAAGGAACATCTTCGAAGCAAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAACCCT
ATTGTGGTGCCTCCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTTATACTCTGACTCCCATGGGGAC
AGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 34A

Amino acid sequence of VP1_GII.12_HS10_E80S (SEQ ID NO:88)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNFVQAPNGEFTVSPRNSPGEVLL
NLSLGPELNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVIIDVRTLEPVLLPLP
DVRNNFFHYNQQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDGELQGTTQLLPTAICSFRGRINQKVSGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTPDFSGKLFGVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTLNMGLAPPVAPTFPGEQILFFRSHIPLKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 34B

Nucleic acid sequence of human codon optimized VP1_GII.12_HS10_E80S (SEQ ID NO:89)

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCCGTGGCCGGAGCCTCAATTGCCGCCCCCCTCACTGGCCAGAACAACGTGATTGATCCCTGG
ATCAGACTGAACTTCGTTCAGGCTCCTAATGGGGAGTTCACCGTGTCCCCGAGAAACTCCCCCGGCGAAGTGTTATT
GAATTTGAGCTTAGGACCAGAACTCAACCCCTATCTGGCACATCTGTCTCGGATGTACAACGGCTATGCGGGCGGAG
TGGAGGTGCAAGTTCTTCTCGCTGGTAATGCATTCACAGCAGGAAAATTAGTATTTGCAGCGGTTCCACCCCATTTTC
CACTTGAAAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGTG
CTGCTACCCCTGCCCGACGTGAGGAACAATTTCTTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCGC
CATGCTCTATACTCCTTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTCGGGTGCTCACCCGAC
CTTCCCCAGATTTCGACTTCAATTATCTGGTCCCCCCCACGGTAGAGTCCAAAACAAAGCCTTTCACTCTTCCAATCCT
TACAATTGGCGAACTGACCAACTCACGCTTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTGT
CGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACTGTTGCCAACCGCTATA
TGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACCACGTGTGGAACATGCAAGTGACGAATATCG
ACGGGACACCTTTCGATCCAACAGAGGATGTCCCAGCGCCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCGGC
GTCCTTTCCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTCATTGCCACCAACTCAGCCAAATTCACC
CCAAAACTTGGAGCGATACAGATCGGAACTTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCCC
TGTTGGCCTTTTCGAAAGCGAAGGCTTTAACCAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG

FIGURE 34B (cont)

GACTCGCACCACCCGTCGCTCCAACGTTTCCTGGTGAGCAGATTTTGTTTTTCCGCAGTCATATTCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTCAGCACTTGTATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCCGATACCGGAAGAGTGTTGTTTGAAGCTAAACTTCATCGCTCC
GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCCGGCAAACGGATACTTTCGATTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

Figure 34C

Amino acid sequence of VP1_GII.12_HS10_A90L (SEQ ID NO:90)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPYLLHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVIIDVRTLEPVLLPLP
DVRNNFFHYNQQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDGELQGTTQLLPTAICSFRGRINQKVSGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTPDFSGKLFGVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTLNMGLAPPVAPTFPGEQILFFRSHIPLKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 34D

Nucleic acid sequence of human codon optimized VP1_GII.12_HS10_A90L (SEQ ID NO:91)

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCCGTGGCCGGAGCCTCAATTGCCGCCCCCCTCACTGGCCAGAACAACGTGATTGATCCCTGG
ATCAGACTGAACTTCGTTCAGGCTCCTAATGGGGAGTTCACCGTGTCCCCGAGAAACTCCCCCGGCGAAGTGTTATT
GAATTTGGAATTAGGACCAGAACTCAACCCCTATCTGCTCCATCTGTCTCGGATGTACAACGGCTATGCGGGCGGAG
TGGAGGTGCAAGTTCTTCTCGCTGGTAATGCATTCACAGCAGGAAAATTAGTATTTGCAGCGGTTCCACCCCATTTTC
CACTTGAAAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGTG
CTGCTACCCCTGCCCGACGTGAGGAACAATTTCTTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCGC
CATGCTCTATACTCCTTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTCGGGTGCTCACCCGAC
CTTCCCCAGATTTCGACTTCAATTATCTGGTCCCCCCCACGGTAGAGTCCAAAACAAAGCCTTTCACTCTTCCAATCCT
TACAATTGGCGAACTGACCAACTCACGCTTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTGT
CGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACTGTTGCCAACCGCTATA
TGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACCACGTGTGGAACATGCAAGTGACGAATATCG
ACGGGACACCTTTCGATCCAACAGAGGATGTCCCAGCGCCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCGGC
GTCCTTTCCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTCATTGCCACCAACTCAGCCAAATTCACC
CCAAAACTTGGAGCGATACAGATCGGAACTTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCCC
TGTTGGCCTTTTCGAAAGCGAAGGCTTTAACCAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG
GACTCGCACCACCCGTCGCTCCAACGTTTCCTGGTGAGCAGATTTTGTTTTTCCGCAGTCATATTCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTCAGCACTTGTATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCCGATACCGGAAGAGTGTTGTTTGAAGCTAAACTTCATCGCTCC
GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCCGGCAAACGGATACTTTCGATTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

Figure 34E

Amino acid sequence of VP1_GII.12_HS10_E80S+A90L (SEQ ID NO:92)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNFVQAPNGEFTVSPRNSPGEVLL
NLSLGPELNPYLLHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVIIDVRTLEPVLLPLP
DVRNNFFHYNQQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDGELQGTTQLLPTAICSFRGRINQKVSGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTPDFSGKLFGVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTLNMGLAPPVAPTFPGEQILFFRSHIPLKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 34F

Nucleic acid sequence of human codon optimized VP1_GII.12_HS10_E80S+A90L (SEQ ID NO:93)

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCCGTGGCCGGAGCCTCAATTGCCGCCCCCCTCACTGGCCAGAACAACGTGATTGATCCCTGG
ATCAGACTGAACTTCGTTCAGGCTCCTAATGGGGAGTTCACCGTGTCCCCGAGAAACTCCCCCGGCGAAGTGTTATT
GAATTTGAGCTTAGGACCAGAACTCAACCCCTATCTGCTCCATCTGTCTCGGATGTACAACGGCTATGCGGGCGGAG
TGGAGGTGCAAGTTCTTCTCGCTGGTAATGCATTCACAGCAGGAAAATTAGTATTTGCAGCGGTTCCACCCCATTTTC
CACTTGAAAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGTG
CTGCTACCCCTGCCCGACGTGAGGAACAATTTCTTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCGC
CATGCTCTATACTCCTTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTCGGGTGCTCACCCGAC
CTTCCCCAGATTTCGACTTCAATTATCTGGTCCCCCCCACGGTAGAGTCCAAAACAAAGCCTTTCACTCTTCCAATCCT
TACAATTGGCGAACTGACCAACTCACGCTTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTGT
CGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACTGTTGCCAACCGCTATA
TGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACCACGTGTGGAACATGCAAGTGACGAATATCG
ACGGGACACCTTTCGATCCAACAGAGGATGTCCCAGCGCCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCGGC
GTCCTTTCCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTCATTGCCACCAACTCAGCCAAATTCACC
CCAAAACTTGGAGCGATACAGATCGGAACTTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCCC
TGTTGGCCTTTTCGAAAGCGAAGGCTTTAACCAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG
GACTCGCACCACCCGTCGCTCCAACGTTTCCTGGTGAGCAGATTTTGTTTTTCCGCAGTCATATTCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTCAGCACTTGTATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCCGATACCGGAAGAGTGTTGTTTGAAGCTAAACTTCATCGCTCC
GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCCGGCAAACGGATACTTTCGATTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

FIGURE 34G

Amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_A39V (SEQ ID NO:192)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAVPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLPDVRNTFFHYNNQPNSRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPP
SVESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLDGELQGTTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV

FIGURE 34G (cont)

PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34H

Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V (SEQ ID NO:193)

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGTGCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTCGGACAAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGGTCGAAGTGCAGGTCCTCCTGGCCGGAAACGCCTTTACCGCT
GGCAAAATTCTGTTTGCCGCCGTTCCACCAAACTTTCCAGTCGAATTCCTCTCTCCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAAACTCTCGGATGAGACTTGTTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAACTGACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACTTAAACGGGACCACCTACGACCCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACTGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACCCTCAATATGAACCTCGCCCCACCCGTG
GCCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTTACCAGGAAAGTGCGCCCTCCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

FIGURE 34I

Amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:194)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIITNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLPDVRNTFFHYNNQPNSRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPP
SVESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLDGELQGTTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV

FIGURE 34I (cont)

PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34J

Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:195)

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTATCACAAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGGTCGAAGTGCAGGTCCTCCTGGCCGGAAACGCCTTTACCGCT
GGCAAAATTCTGTTTGCCGCCGTTCCACCAAACTTTCCAGTCGAATTCCTCTCTCCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAAACTCTCGGATGAGACTTGTTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAACTGACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACTTAAACGGGACCACCTACGACCCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACTGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACCCTCAATATGAACCTCGCCCCACCCGTG
GCCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTTACCAGGAAAGTGCGCCCTCCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

FIGURE 34K

Amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_A90L (SEQ ID NO:196)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLLHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLIV
DVRTLEPIMIPLPDVRNTFFHYNNQPNSRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPPS
VESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLDGELQGTTQLLPSGICAFRGRVTAET
DHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFVP

FIGURE 34K (cont)

KLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSFV
PCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34L

Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A90L (SEQ ID NO:197)

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTCGGACAAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGCTGCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGGTCGAAGTGCAGGTCCTCCTGGCCGGAAACGCCTTTACCGCT
GGCAAAATTCTGTTTGCCGCCGTTCCACCAAACTTTCCAGTCGAATTCCTCTCTCCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAAACTCTCGGATGAGACTTGTTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAACTGACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACTTAAACGGGACCACCTACGACCCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACTGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACCCTCAATATGAACCTCGCCCCACCCGTG
GCCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTTACCAGGAAAGTGCGCCCTCCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

FIGURE 34M

Amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_A39V+M53I (SEQ ID NO:198)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAVPVTGQNNIIDPWIITNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLPDVRNTFFHYNNQPNSRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPP
SVESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLDGELQGTTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV

FIGURE 34M (cont)

PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34N

Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V+M53I (SEQ ID NO:199)

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGTGCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTATCACAAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGGTCGAAGTGCAGGTCCTCCTGGCCGGAAACGCCTTTACCGCT
GGCAAAATTCTGTTTGCCGCCGTTCCACCAAACTTTCCAGTCGAATTCCTCTCTCCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAAACTCTCGGATGAGACTTGTTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAACTGACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACTTAAACGGGACCACCTACGACCCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACTGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACCCTCAATATGAACCTCGCCCCACCCGTG
GCCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTTACCAGGAAAGTGCGCCCTCCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

FIGURE 34O

Amino acid sequence of VP1GII.17 Kawa 2014 A0A077KVU6_E80S+A90L (SEQ ID NO:200)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLSLGPDLNPYLLHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLIV
DVRTLEPIMIPLPDVRNTFFHYNNQPNSRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPPS
VESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLDGELQGTTQLLPSGICAFRGRVTAET
DHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFVP

FIGURE 34O (cont)

KLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSFV
PCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34P

Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_E80S+A90L (SEQ ID NO:201)

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTCGGACAAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTAGCCTCGGCCCTGACCTCAATCCATATCTGCTGCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGGTCGAAGTGCAGGTCCTCCTGGCCGGAAACGCCTTTACCGCT
GGCAAAATTCTGTTTGCCGCCGTTCCACCAAACTTTCCAGTCGAATTCCTCTCTCCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAAACTCTCGGATGAGACTTGTTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAACTGACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACTTAAACGGGACCACCTACGACCCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACTGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACCCTCAATATGAACCTCGCCCCACCCGTG
GCCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTTACCAGGAAAGTGCGCCCTCCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

Figure 35A

Amino acid sequence of VP2_GI.1_Norwalk (SEQ ID NO:99)

MAQAIIGAIAASTAGSALGAGIQVGGEAALQSQRYQQNLQLQENSFKHDREMIGYQVEASNQLLAKNLATRYSLLRAGG
LTSADAARSVAGAPVTRIVDWNGVRVSAPESSATTLRSGGFMSVPIPFASKQKQVQSSGISNPNYSPSSISRTTSWVESQ
NSSRFGNLSPYHAEALNTVWLTPPGSTASSTLSSVPRGYFNTDRLPLFANNRR

Figure 35B

Nucleic acid sequence of human codon optimized VP.2_GI1_Norwalk (SEQ ID NO:100)

ATGGCTCAGGCCATTATTGGCGCCATCGCTGCAAGTACAGCCGGGAGTGCATTGGGGGCCGGAATACAGGTGGGC
GGGGAAGCTGCATTGCAGAGCCAGCGGTACCAGCAAAACCTGCAGTTACAGGAGAATAGCTTTAAACACGACAGG
GAGATGATTGGATATCAGGTGGAGGCCAGCAATCAGCTGCTCGCCAAAAACTTGGCTACTCGATACTCATTACTGCG
CGCCGGGGGGTTGACTAGCGCCGACGCCGCACGATCTGTCGCAGGCGCCCCCGTGACTCGGATCGTAGACTGGAA
CGGGGTACGAGTCTCGGCTCCCGAGTCGTCTGCAACCACCCTGAGGTCGGGAGGGTTTATGTCCGTGCCCATCCCAT
TCGCTAGCAAACAGAAACAGGTCCAGAGCTCCGGAATCTCCAATCCCAATTACTCCCCTAGCTCTATCTCTCGTACCA
CTTCCTGGGTCGAGAGTCAGAACAGCAGTAGATTTGGCAACCTGAGCCCCTACCATGCTGAAGCCCTGAACACTGTG
TGGTTGACTCCACCTGGTAGCACGGCCTCCTCAACCCTGAGTTCCGTGCCTCGCGGGTACTTCAATACCGACAGACTT
CCTCTGTTCGCTAACAACCGCCGCTGA

Figure 36A

Amino acid sequence of VP2_GI.3_Lil08 (SEQ ID NO:94)

MAQAIFGAIAATAAGSAVGAGIQAGTEAALQHQRFQQDLTLQSNTFKHDKEMLGLQVGASTALLQNSLNTRYNMLTD
AGLSSSDAARMVVGAPATRVVDWNGTRISAPRSTATTLRSGGFMTIPTLYKGKQQQKAPTEIGLSNPNYGSSVSSRVAD
WVSSQNSSHSSLGPYHPSALQTTWVTPPGSSSTSTISSVSTVPRYFNTDRLPLFANMRK

Figure 36B

Nucleic acid sequence of human codon optimized VP2_GI.3_Lil08 (SEQ ID NO:95)

ATGGCTCAGGCAATCTTCGGCGCAATCGCTGCCACTGCTGCCGGATCCGCTGTGGGAGCCGGCATACAGGCCGGAA
CTGAGGCGGCCCTTCAGCATCAGCGGTTCCAGCAGGATCTGACATTACAGAGTAACACATTCAAACATGACAAGGA
GATGCTGGGTCTGCAGGTGGGTGCCAGTACTGCCCTGCTCCAAAACTCTCTGAATACCAGATATAACATGTTAACTG
ATGCGGGACTGTCTAGTAGCGACGCAGCTCGCATGGTCGTGGGCGCCCCAGCTACGAGAGTTGTGGACTGGAATG
GCACCCGAATCAGTGCACCAAGGTCTACAGCCACTACCCTCAGAAGTGGCGGCTTTATGACCATCCCGACTTTATAC
AAGGGCAAACAACAGCAGAAGGCACCTACTGAAATCGGTCTCTCCAATCCCAACTACGGCAGCAGTGTGTCTTCTCG
CGTGGCCGATTGGGTCTCAAGCCAGAACTCCAGTCATAGTTCTCTTGGGCCTTATCATCCATCAGCCTTGCAGACAAC
TTGGGTCACCCCACCCGGGTCCAGTAGCACGTCAACCATCAGTTCCGTCTCCACAGTCCCTCGCTATTTTAATACTGA
TAGGCTTCCCCTGTTCGCAAACATGAGGAAGTGA

Figure 37A

Amino acid sequence of VP2_GII6_HS10 (SEQ ID NO:96)

MASAFLAGLAGDVITNGVGSLINAGANAVNQKVEYDFNKQLQMASFKHDKEMLQSQVLATKQLQQEMMNIRQGVLT
AGGFSPADAARGAVNAPMTKILDWNGTRYWAPNSMKTTSYSGQFSSSPVHKSPAPSQHTALPKSRLQNDFASVYSFPS
SVSSQSTHSTALSAGTGSSRSISPSTATPTLSRTSDWVRGQNERLSPFMDGALQTAFVTPPSSKASSNGTVSTVPKAVLDS
WTPMFNTHRQPLFAHPRRRGESQV

Figure 37B

Nucleic acid sequence of human codon optimized VP2_GII6_HS10 (SEQ ID NO:97)

ATGGCCTCCGCATTTCTAGCTGGATTGGCCGGGGACGTGATCACCAACGGCGTAGGATCGCTGATTAATGCAGGCG
CCAATGCTGTTAATCAGAAGGTTGAATACGACTTCAACAAACAACTGCAGATGGCTTCATTCAAGCACGACAAAGAA
ATGTTGCAGTCACAGGTTCTCGCCACCAAGCAGCTACAACAGGAGATGATGAACATTCGGCAGGGCGTACTGACCG
CTGGAGGATTCAGCCCTGCTGACGCAGCACGGGGGGCCGTGAACGCGCCGATGACCAAGATCCTGGATTGGAACG
GAACTCGGTATTGGGCTCCCAACTCTATGAAAACCACTTCTTACTCTGGTCAGTTCTCCAGCTCGCCAGTCCACAAAA
GTCCGGCCCCTTCACAGCACACAGCACTCCCTAAGTCCAGGCTGCAAAACGACTTTGCCTCCGTGTACTCCTTCCCAT
CCAGCGTGTCATCTCAGAGCACTCATTCAACCGCCCTGTCCGCCGGAACTGGGTCTAGCCGCAGCATTTCCCCAAGC
ACAGCTACTCCAACTCTGAGCAGGACTAGCGATTGGGTCAGAGGACAAAACGAACGACTGTCCCCTTTCATGGACG
GAGCTCTGCAAACCGCCTTCGTCACTCCACCTAGCAGCAAGGCCTCGAGCAACGGTACGGTTAGTACCGTGCCAAAG
GCTGTTCTTGACAGCTGGACCCCCATGTTTAACACACACAGGCAGCCATTGTTTGCACACCCCAGGCGACGGGGAGA
ATCACAAGTTTAG

Figure 38A

Cloning vector 1190 from left to right T-DNA (SEQ ID NO:162)

TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACGTTTTTAATGTACT
GAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTCAAAAACCATAAAAGTTTAAGTTAGCA
AGTGTGTACATTTTTACTTGAACAAAAATATTCACCTACTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAAAT
ATGGATGATAAGAACAAGAGTAGTGATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCTCTC
TTTTCATTGGTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGAGA
AAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGCTACACAAATAAGGGT
TAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTAGAGAATTTTTGGCAAGTCATTAAAAAGA
AAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCATTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGT
TGGATTAAAGTTGTATTAGTAATTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATATATTGCCCCA
TAGAGTCAGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAAAAAAAAA
AAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTAGGAGGATAACATCCAATCC
AACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCACGCATCTGTGGCACATCTACATTATCTAAATCAC
ACATTCTTCCACACATCTGAGCCACACAAAAACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTG
AGTCTACACTTTGATTCCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATG
GAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCAGGAGGTACC
ACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTACATAACGATGAGACGAATTCGAA
TCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTATTTAAGAGATATCTCAGATACGACA
GGACGGAAGCTTCACTGCACAGAGTCCTTGGATCTTGGACGGGAGATTCGGTTAACTATGCAGCATCTCGATTTTTC
GGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAAC
TCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAAGTGGAAAGTA
ATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGTAAGTTAAAATGCTTCTTCGTCTC
CTATTTATAATATGGTTTGTTATTGTTAATTTTGTTCTTGTAGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTAT
TTGTATGAGATGAACTGGTGTAATGTAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTCCATAACTAAC
TAGACATGAAGACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACTTTATA
AGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGTTATCGAAATTCATTAAC
AATCAACTTAACGTTATTAACTACTAATTTTATATCATCCCCTTTGATAAATGATAGTACACCAATTAGGAAGGAGCAT
GCTCGCCTAGGAGATTGTCGTTTCCCGCCTTCAGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAAACCGCCTC

FIGURE 38A (cont)

TCCCCGCGCGTTGGGAATTACTAGCGCGTGTCGACAAGCTTGCATGCCGGTCAACATGGTGGAGCACGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATC
CGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCT
ACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACC
CCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAAC
ATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGA
CTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAG
TGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAG
CAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCT
ATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCC
GAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTC
AACGTTGTCAGATCGTGCTTCGGCACCGCGGATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGT
GTTGGTTCCTTCTCAGATCTTCGCCTGCAGGCTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTG
GATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTG
ACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGC
AGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCAC
CAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTG
TCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACA
TCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACC
CCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCA
AGGAGCGATCGCTCACCATCACCATCACCATCACCATCACCATTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTA
TTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGT
GAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAA
GACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATC
CTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCAT
GACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATA
GCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGAGTCTCAAGCTTGGCGCGC
CCACGTGACTAGTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGC
CTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCG
CAGCCTGAATGGCGAATGCTAGAGCAGCTTGAGCTTGGATCAGATTGTCGTTTCCCGCCTTCAGTTTAAACTATCAG
TGTTTGACAGGATATATTGGCGGGTAAACCTAAGAGAAAAGAGCGTTTA

Figure 38B

Construct 2724 from 2X35S promoter to NOS terminator (SEQ ID NO:163)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAA
TTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTC
TGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGT
CTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAG
CTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAG
GCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAG
AAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCC

FIGURE 38B (cont)

CACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTT
GATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCT
CTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAATGATGATGGCTAGTAAA
GATGCGACCTCCTCTGTGGATGGTGCGTCAGGGGCAGGACAACTCGTACCCGAGGTAAACGCCAGCGACCCACTTG
CCATGGACCCCGTTGCCGGAAGTTCCACAGCAGTGGCCACAGCCGGTCAAGTGAATCCAATTGATCCGTGGATTATC
AACAATTTCGTCCAGGCACCCCAGGGCGAGTTCACAATTTCACCAAACAATACACCGGGCGATGTGCTATTCGATCT
TTCCTTGGGTCCTCACCTTAACCCTTTTCTACTCCATCTCTCACAGATGTACAATGGTTGGGTAGGAAACATGAGAGT
CCGGATCATGCTGGCTGGCAATGCCTTTACCGCTGGCAAGATCATCGTCAGTTGTATTCCTCCCGGATTTGGATCTCA
TAATCTGACCATTGCTCAAGCGACTCTCTTTCCCCATGTCATCGCCGACGTTAGGACCCTGGACCCCATCGAGGTGCC
CCTGGAGGACGTCCGGAATGTTTTGTTCCACAACAACGACAGAAACCAGCAGACGATGAGACTTGTCTGTATGCTCT
ATACCCCACTGCGGACTGGAGGCGGGACTGGAGACTCCTTCGTTGTGGCAGGAAGAGTGATGACATGCCCCTCCCC
CGACTTCAACTTTCTTTTTCTGGTCCCACCAACCGTTGAGCAGAAGACGCGGCCCTTTACACTGCCCAATCTCCCGCTT
TCAAGTCTGAGTAATTCACGGGCCCCATTGCCGATCTCCTCAATGGGAATCTCCCCCGACAACGTCCAGTCTGTCCAA
TTCCAAAATGGGAGATGCACACTGGACGGTCGCCTGGTGGGAACAACTCCGGTGTCCCTCTCACATGTCGCCAAAAT
CCGCGGCACATCAAATGGTACCGTAATCAATCTGACAGAACTTGATGGCACGCCCTTCCATCCCTTTGAAGGACCAG
CCCCTATTGGATTTCCTGATCTGGGAGGTTGCGACTGGCACATAAACATGACACAGTTTGGCCACTCCAGCCAGACA
CAGTATGATGTCGATACAACCCCAGATACCTTCGTGCCACACCTGGGATCTATTCAAGCTAACGGTATTGGATCCGG
CAACTACGTGGGAGTCTTATCTTGGATCTCACCACCATCCCACCCCTCAGGATCCCAGGTTGACTTGTGGAAGATACC
GAATTATGGATCCTCGATCACTGAAGCCACGCACCTCGCACCTTCCGTCTACCCACCAGGTTTTGGAGAAGTCTTGGT
GTTTTTCATGAGCAAAATGCCCGGCCCTGGAGCCTACAATCTCCCTTGCCTACTCCCTCAAGAGTATATTAGTCACCT
CGCATCTGAGCAGGCCCCGACCGTTGGCGAGGCAGCCCTGCTGCATTATGTGGATCCGGACACCGGCAGGAACCTG
GGTGAGTTCAAAGCTTATCCTGACGGTTTTCTAACATGTGTACCAAATGGCGCTTCCAGCGGCCCTCAACAGCTCCCA
ATCAATGGCGTGTTCGTTTTTGTCAGCTGGGTAAGCCGCTTCTACCAGCTGAAGCCCGTGGGGACAGCTTCTTCTGC
CCGCGGACGCCTCGGTCTGCGGAGATAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTA
TGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAG
GTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATAT
CAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCG
ATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGAT
GGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGAT
AAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 38C

Cloning vector 3677 from left to right T-DNA (SEQ ID NO:164)

TGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACATTGCGGACGTTTTTAATGTACT
GAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTCAAAAACCATAAAAGTTTAAGTTAGCA
AGTGTGTACATTTTTACTTGAACAAAAATATTCACCTACTACTGTTATAAATCATTATTAAACATTAGAGTAAAGAAAT
ATGGATGATAAGAACAAGAGTAGTGATATTTTGACAACAATTTTGTTGCAACATTTGAGAAAATTTTGTTGTTCTCTC
TTTTCATTGGTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGAGA
AAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGCTACACAAATAAGGGT
TAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTAGAGAATTTTTGGCAAGTCATTAAAAAGA
AAGAATAAATTATTTTTAAAATTAAAAGTTGAGTCATTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGT
TGGATTAAAGTTGTATTAGTAATTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCCTATATATTGCCCCA
TAGAGTCAGTTAACTCATTTTTATATTTCATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAAAAAAAAA
AAACGGTATATTTACTAAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTAGGAGGATAACATCCAATCC
AACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCACGCATCTGTGGCACATCTACATTATCTAAATCAC
ACATTCTTCCACACATCTGAGCCACACAAAAACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTG
AGTCTACACTTTGATTCCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATG
GAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCAGGAGGTACC

FIGURE 38C (cont)

ACTTCTCCCTTCAAACTTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTACATAACGATGAGACGAATTCGAA
TCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTATTTAAGAGATATCTCAGATACGACA
GGACGGAAGCTTCACTGCACAGAGTCCTTGGATCTTGGACGGGAGATTCGGTTAACTATGCAGCATCTCGATTTTTC
GGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAAC
TCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAAGTGGAAAGTA
ATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGTAAGTTAAAATGCTTCTTCGTCTC
CTATTTATAATATGGTTTGTTATTGTTAATTTTGTTCTTGTAGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTAT
TTGTATGAGATGAACTGGTGTAATGTAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCCTCCATAACTAAC
TAGACATGAAGACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACTTTATA
AGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGTTATCGAAATTCATTAAC
AATCAACTTAACGTTATTAACTACTAATTTTATATCATCCCCTTTGATAAATGATAGTACACCAATTAGGAAGGAGCAT
GCTCGCCTAGGAGATTGTCGTTTCCCGCCTTCAGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAAACCGCCTC
TCCCCGCGCGTTGGGAATTACTAGCGCGTGTCGACAAGCTTGCATGCCGGTCAACATGGTGGAGCACGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATC
CGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCT
ACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACC
CCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAAC
ATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGA
CTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGAAGATAG
TGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAG
CAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCT
ATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCC
GAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCTCTTGTCTTTCTTGCGTGAGCGATCTTC
AACGTTGTCAGATCGTGCTTCGGCACCGCGGATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTCTTCTTGT
GTTGGTTCCTTCTCAGATCTTCGCCTGCAGGCTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCCTG
GATCTGCTGCCCAAACTAACTCCATGGTGACCCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTG
ACCTGGAACTCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCCAGCTGTCCTGCAGTCTGACCTCTACACTCTGAGC
AGCTCAGTGACTGTCCCCTCCAGCACCTGGCCCAGCGAGACCGTCACCTGCAACGTTGCCCACCCGGCCAGCAGCAC
CAAGGTGGACAAGAAAATTGTGCCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTG
TCTTCATCTTCCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACA
TCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACC
CCGGGAGGAGCAGTTCAACAGCACTTTCCGCTCAGTCAGTGAACTTCCCATCATGCACCAGGACTGGCTCAATGGCA
AGGAGCGATCGCTCACCATCACCATCACCATCACCATCACCATTAAAGGCCTATTTTCTTTAGTTTGAATTTACTGTTA
TTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTATTTTATGTAATTTAATTTCTTTGT
GAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTTATTATCGTTCAAACATTTGGCA
ATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATTTCTGTTGAATTACGTTAAGCAT
GTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAA
TACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCT
CTAGGTAAAAATCCCAATTATATTTGGTCTAATTTAGTTTGGTATTGAGTAAAACAAATTCGAACCAAACCAAAATAT
AAATATATAGTTTTTATATATATGCCTTTAAGACTTTTTATAGAATTTTCTTTAAAAAATATCTAGAAATATTTGCGACT
CTTCTGGCATGTAATATTTCGTTAAATATGAAGTGCTCCATTTTTATTAACTTTAAATAATTGGTTGTACGATCACTTTC
TTATCAAGTGTTACTAAAATGCGTCAATCTCTTTGTTCTTCCATATTCATATGTCAAAATCTATCAAAATTCTTATATAT
CTTTTTCGAATTTGAAGTGAAATTTCGATAATTTAAAATTAAATAGAACATATCATTATTTAGGTATCATATTGATTTTT
ATACTTAATTACTAAATTTGGTTAACTTTGAAAGTGTACATCAACGAAAAATTAGTCAAACGACTAAAATAAATAAAT
ATCATGTGTTATTAAGAAAATTCTCCTATAAGAATATTTTAATAGATCATATGTTTGTAAAAAAAATTAATTTTTACTA
ACACATATATTTACTTATCAAAAATTTGACAAAGTAAGATTAAAATAATATTCATCTAACAAAAAAAAAACCAGAAAA
TGCTGAAAACCCGGCAAAACCGAACCAATCCAAACCGATATAGTTGGTTTGGTTTGATTTTGATATAAACCGAACCA
ACTCGGTCCATTTGCACCCCTAATCATAATAGCTTTAATATTTCAAGATATTATTAAGTTAACGTTGTCAATATCCTGG
AAATTTTGCAAAATGAATCAAGCCTATATGGCTGTAATATGAATTTAAAAGCAGCTCGATGTGGTGGTAATATGTAA

FIGURE 38C (cont)

TTTACTTGATTCTAAAAAAATATCCCAAGTATTAATAATTTCTGCTAGGAAGAAGGTTAGCTACGATTTACAGCAAAG
CCAGAATACAAAGAACCATAAAGTGATTGAAGCTCGAAATATACGAAGGAACAAATATTTTTAAAAAAATACGCAAT
GACTTGGAACAAAAGAAAGTGATATATTTTTTGTTCTTAAACAAGCATCCCCTCTAAAGAATGGCAGTTTTCCTTTGC
ATGTAACTATTATGCTCCCTTCGTTACAAAAATTTTGGACTACTATTGGGAACTTCTTCTGAAAATTCTAGAGTCTCAA
GCTTGGCGCGCCCACGTGACTAGTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCCTGGCGTTACCC
AACTTAATCGCCTTGCAGCACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCC
AACAGTTGCGCAGCCTGAATGGCGAATGCTAGAGCAGCTTGAGCTTGGATCAGATTGTCGTTTCCCGCCTTCAGTTT
AAACTATCAGTGTTTGACAGGATATATTGGCGGGTAAACCTAAGAGAAAAGAGCGTTTA

Figure 38D

Construct 4133 from 2X35S promoter to NOS terminator (SEQ ID NO:165)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAA
TTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTC
TGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGT
CTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAG
CTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAG
GCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAG
AAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCC
CACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTT
GATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCT
CTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAATGAAAATGGCCTCGAGT
GACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGGTGATGGCCCTGGAGCCTG
TGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTGGATACGCAACAATTTTGT
CCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTCGGCCAGCTTGGGA
CCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGAT
TCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGT
CTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCT
GATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTC
TGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACTTTGAC
TTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACAGTCGAGGAGATG
ACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTCGTGGTTCAGCCACAGAAC
GGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGA
CGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCCAACCG
AAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACC
GATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGC
AGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGA
CGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTG
CATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCGCACCAGC
CCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTGCAAATTGCACAAAT
CAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGATATTTTAGGTTCGACTCC
TGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCTGTCTGAAGGCCTATTT
TCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTAT
TTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTT
ATTATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATT
TCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAG

FIGURE 38D (cont)

AGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGG
TGTCATCTATGTTACTAGAT

Figure 38E

Construct 4135 from 2X35S promoter to NOS terminator (SEQ ID NO:166)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAA
TTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTC
TGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGT
CTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCCAG
CTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAG
GCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAG
AAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCC
CACTATCCTTCGCAAGACCCTTCCTCTATATAAGGAAGTTCATTTCATTTGGAGAGGTATTAAAATCTTAATAGGTTTT
GATAAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACTTCTCT
CTTGTCTTTCTTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAATGAAAATGGCCTCGAGT
GACGCTAACCCTAGTGACGGCAGCGCCGCCAATCTTGTGCCTGAGGTTAATAATGAGGTGATGGCCCTGGAGCCTG
TGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTGGATACGCAACAATTTTGT
CCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTCGGCCAGCTTGGGA
CCCGATCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGAT
TCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACTTCCCCACTGAAGGACTGT
CTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCT
GATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTC
TGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCATGCAGAGTGCTCACCAGACCTTCACCAGACTTTGAC
TTTATCTTCTTAGTGCCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACAGTCGAGGAGATG
ACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTCACAGGACCTTCCTCGGCATTCGTGGTTCAGCCACAGAAC
GGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGA
CGTAACTCACATAACTGGCTCACGGAACTATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCCAACCG
AAGAGATTCCCGCACCTCTTGGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACC
GATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGC
AGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGA
CGGGGGCACCACTCACCGGAACGAGCCGCAACAATGGGTCCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTG
CATTTGGCTCCTGCAGTGGCTCCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCGCACCAGC
CCAATCCGACGTCGCACTTCTGCGGTTCGTGAATCCAGACACAGGCCGCGTGTTGTTTGAGTGCAAATTGCACAAAT
CAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCCAACGGATATTTTAGGTTCGACTCC
TGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCTGTCTGAAGGCCTATTT
TCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTATGTTTGGTGAGCGGTTTTCTGTGCTCAGAGTGTGTTTAT
TTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAGGTCGTCCCTTCAGCAAGGACACAAAAAGATTTTAATTTT
ATTATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATT
TCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTTATGATTAG
AGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGATAAATTATCGCGCGCGG
TGTCATCTATGTTACTAGAT

Figure 39A

Construct 2724 (VP1 Wt GI.1 hCod)

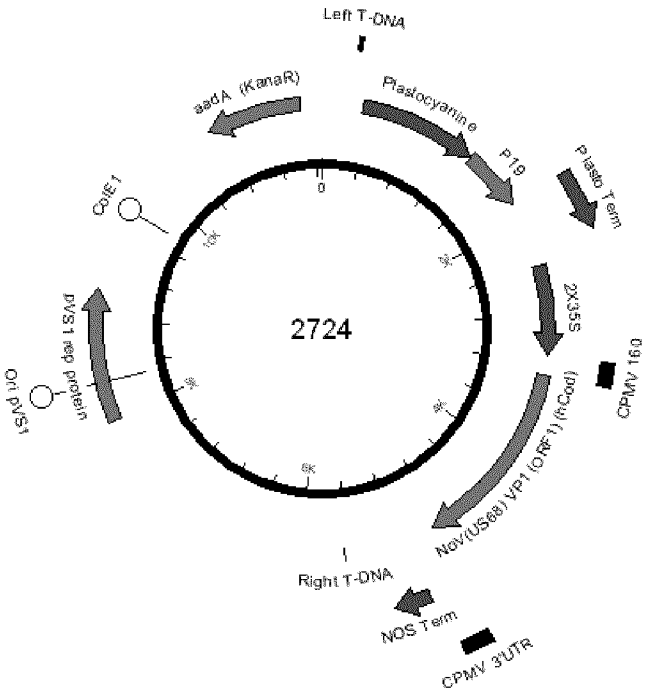


Figure 39B

Construct 3300 (Wt GI.2 hCod)

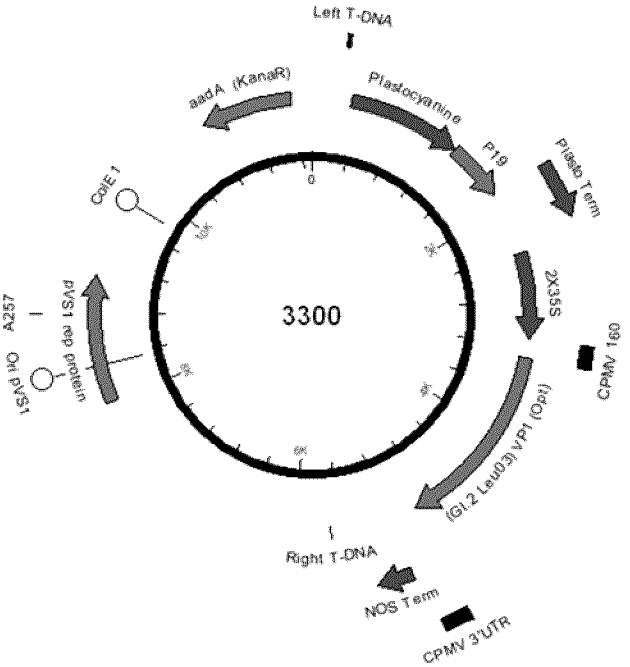


Figure 39C

Construct 3979 (Wt GI.3 hCod)

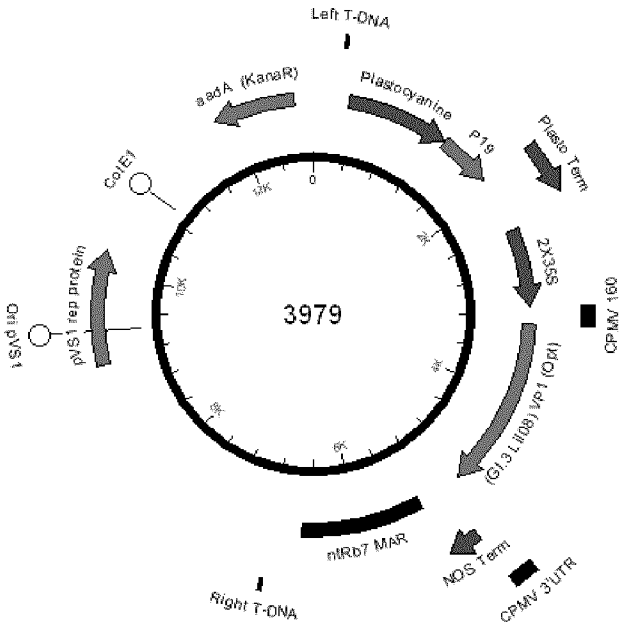


Figure 40A

Construct 4140 (VP1 GI.3_Q84S hCod)

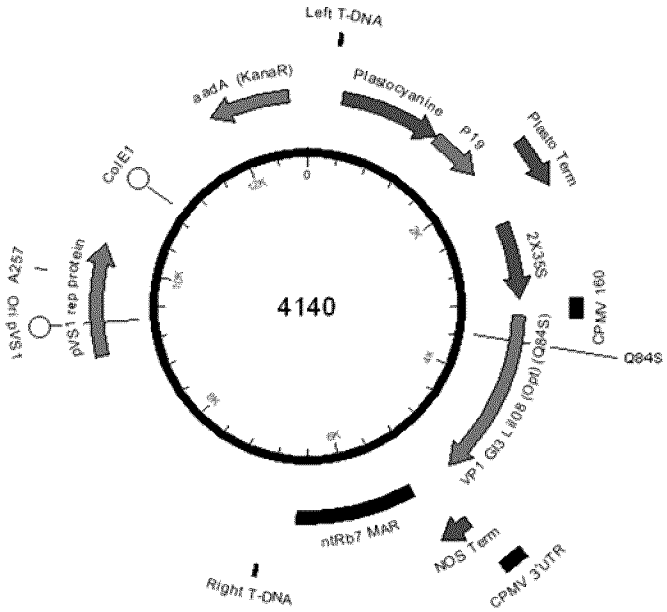


Figure 40B

Construct 4141 (VP1 GI.3_S94L hCod)

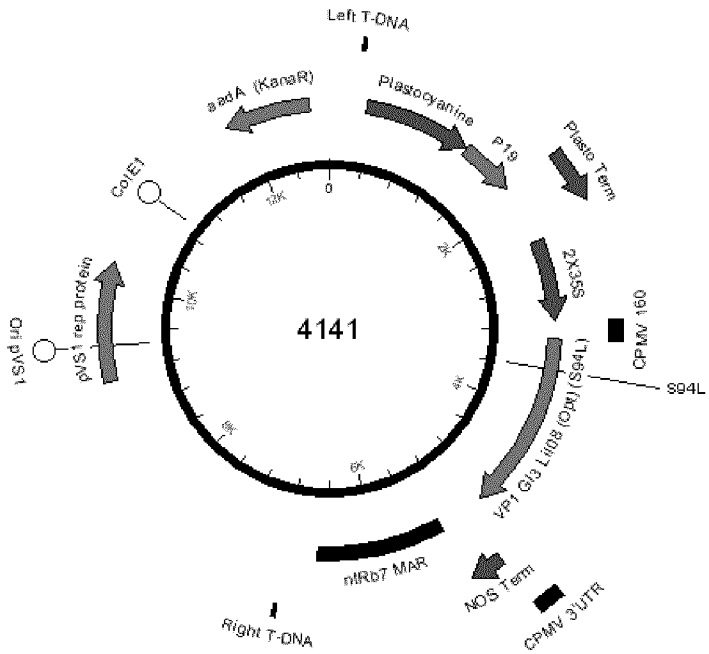


Figure 40C

Construct 4142 (VP1 GI.3_Q84S+S94L hCod)

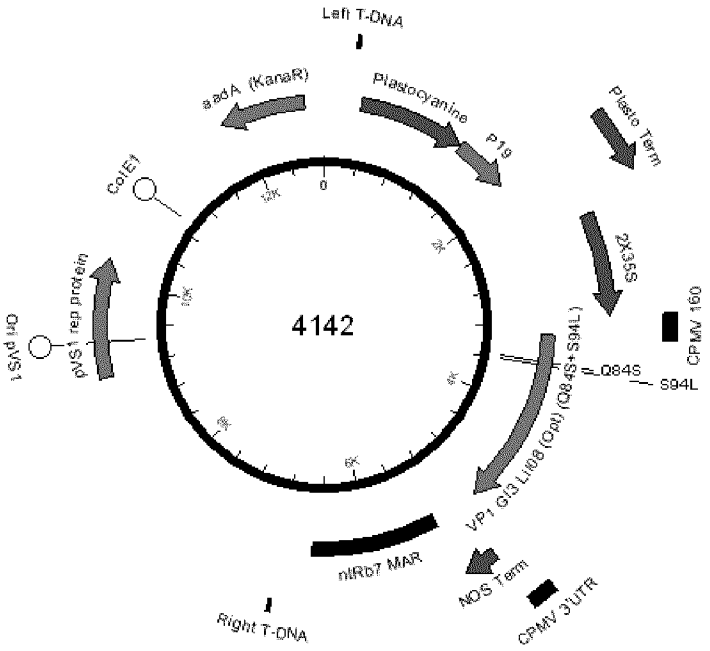


FIGURE 40D

Construct 4179 (VP1 GI.3_A43V+S94L hCod)

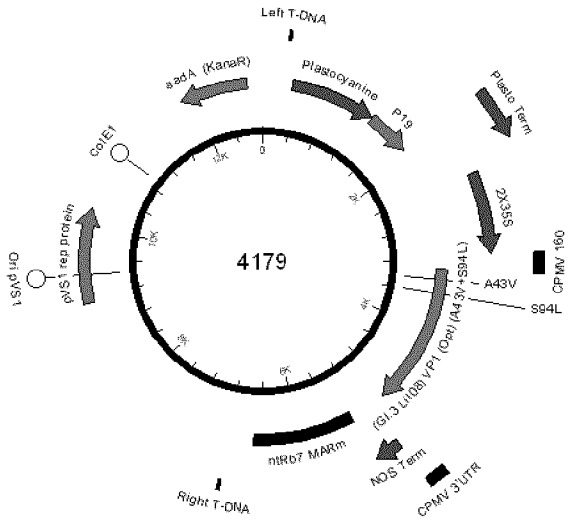


FIGURE 40E

Construct 4180 (VP1 GI.3_M57I+S94L hCod)

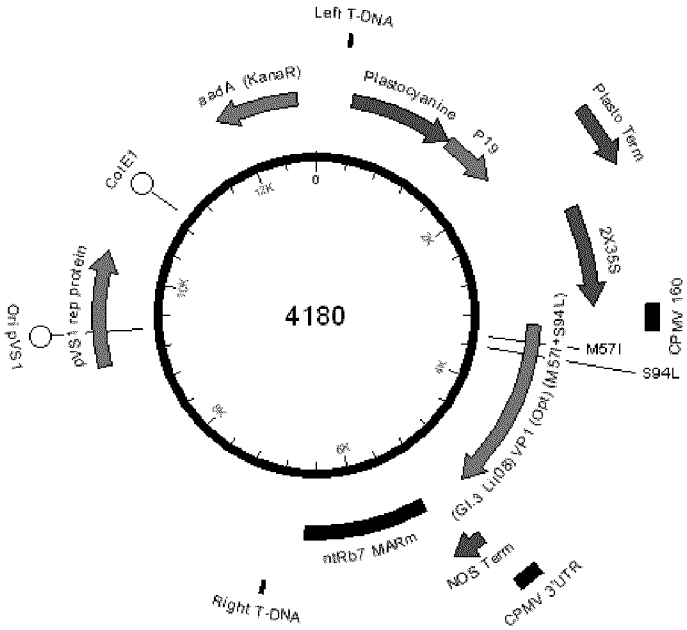


FIGURE 40F

Construct 4181 (VP1 GI.3_A43V+M57I+S94L hCod)

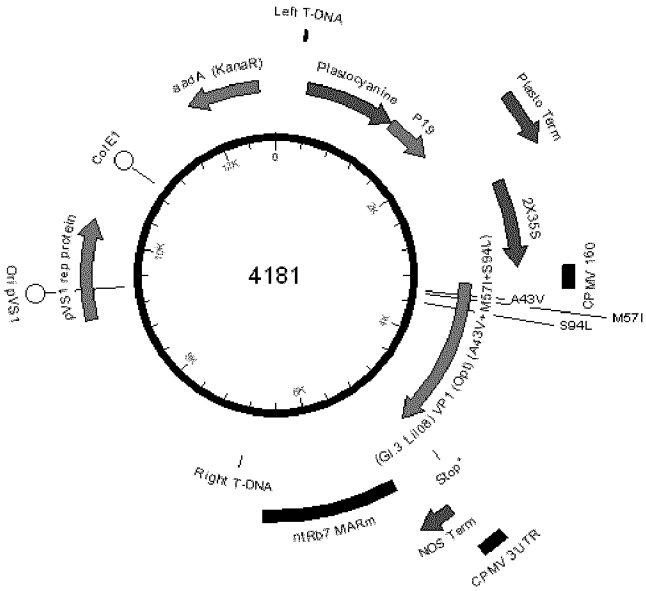


Figure 41A

Construct 3980 (VP1 Wt GI.5 hCod)

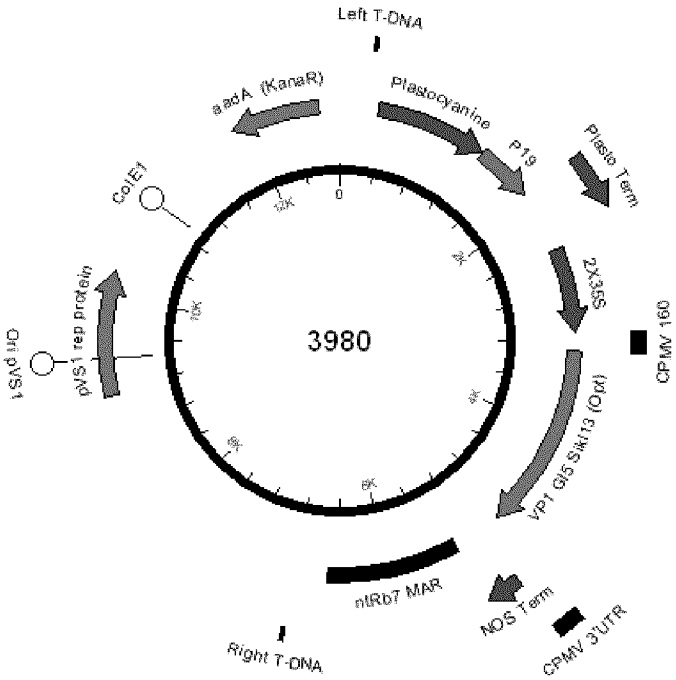


Figure 41B

Construct 4130 (VP1 GI.5_Q84S)

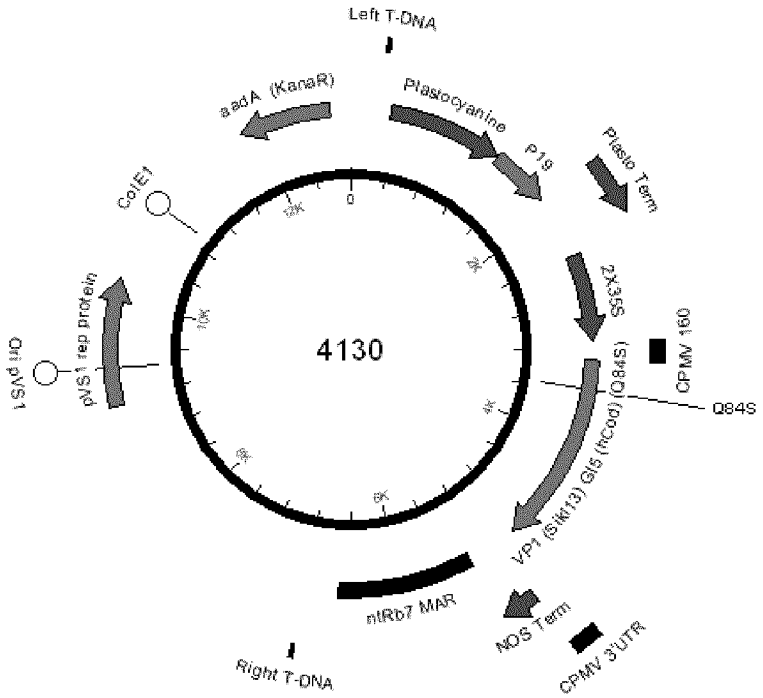


Figure 41C

Construct 4131 (VP1 GI.5_A94L hCod)

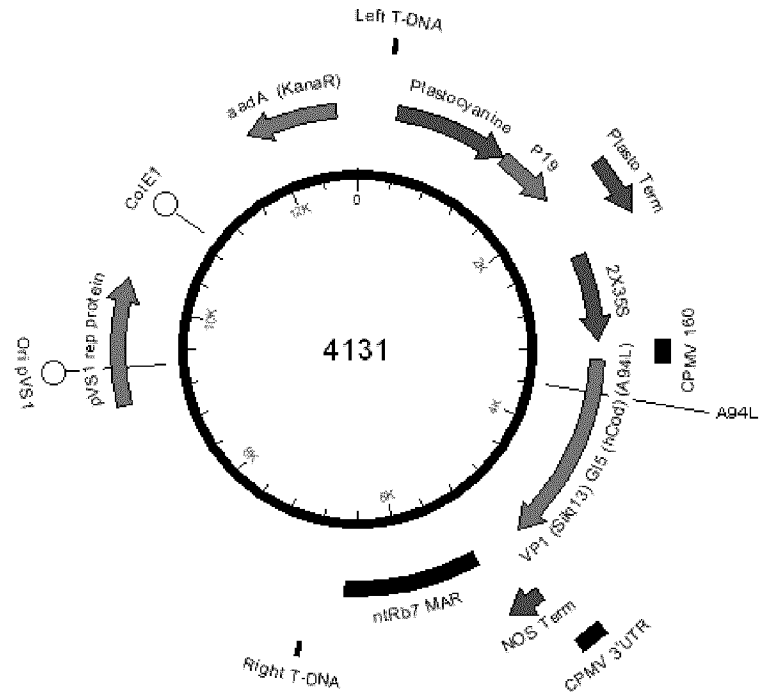


Figure 41D

Construct 4132 (VP1 GI.5_Q84S+A94L hCod)

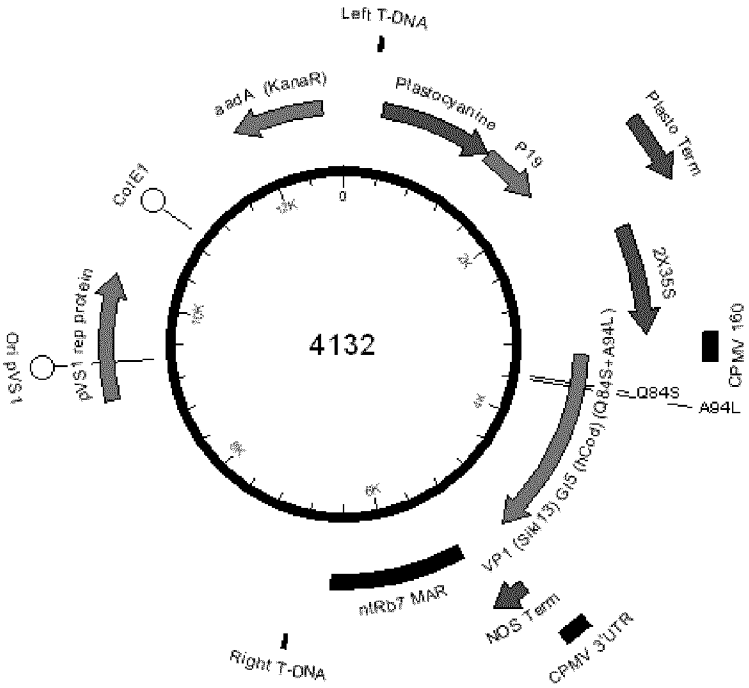


FIGURE 41E

Construct 4210 (VP1 GI.7_R84S hCod)

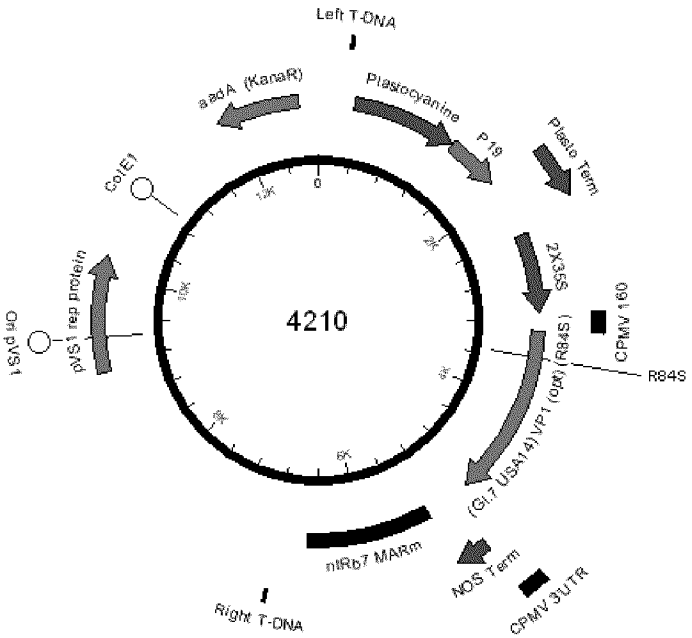


FIGURE 41F

Construct 4217 (VP1 GI.7_M57I hCod)

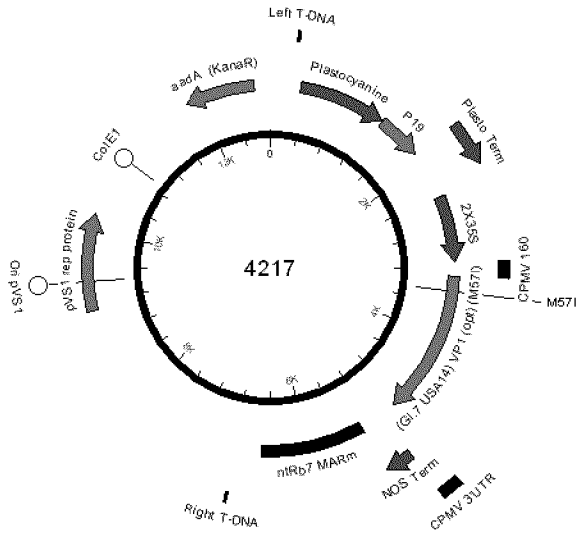


FIGURE 41G

Construct 4218 (VP1 GI.7_M57I+R84S hCod)

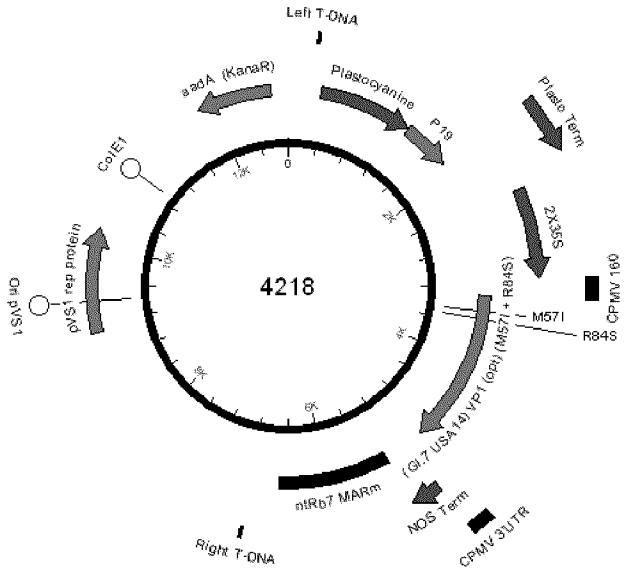


Figure 42A

Construct 3982 (Wt VP1 GII.2 hCod)

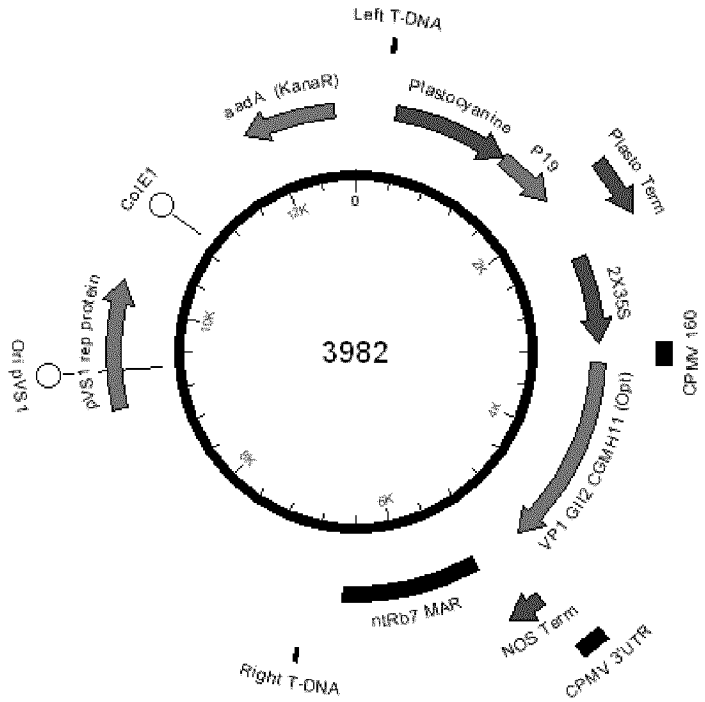


Figure 42B

Construct 4143 (VP1 GII.2_E80S)

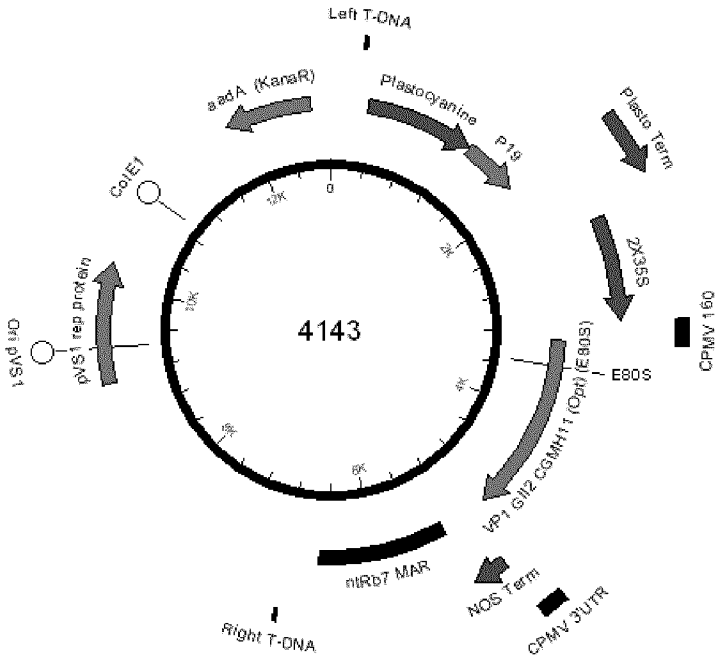


Figure 42C

Construct 4144 (VP1 GII.2_A90L hCod)

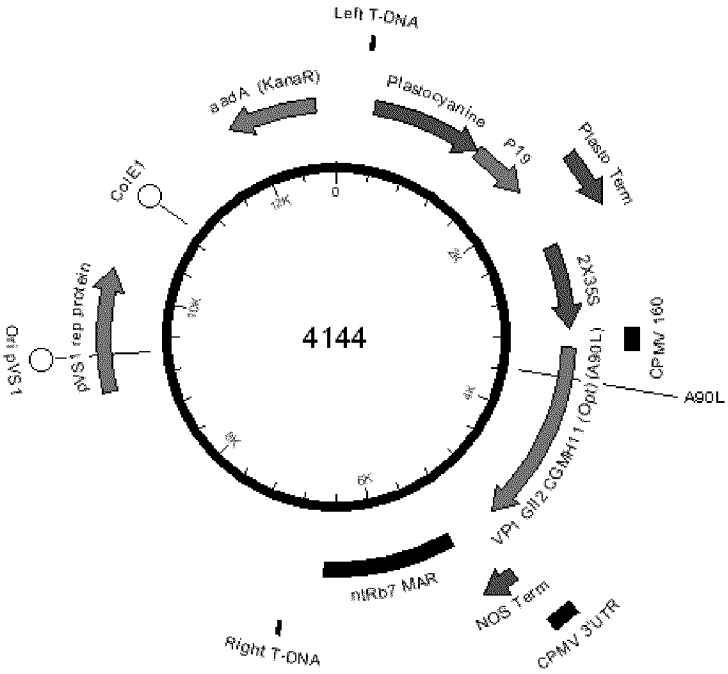


Figure 42D

Construct 4145 (VP1 GII.2_E80S+A90L hCod)

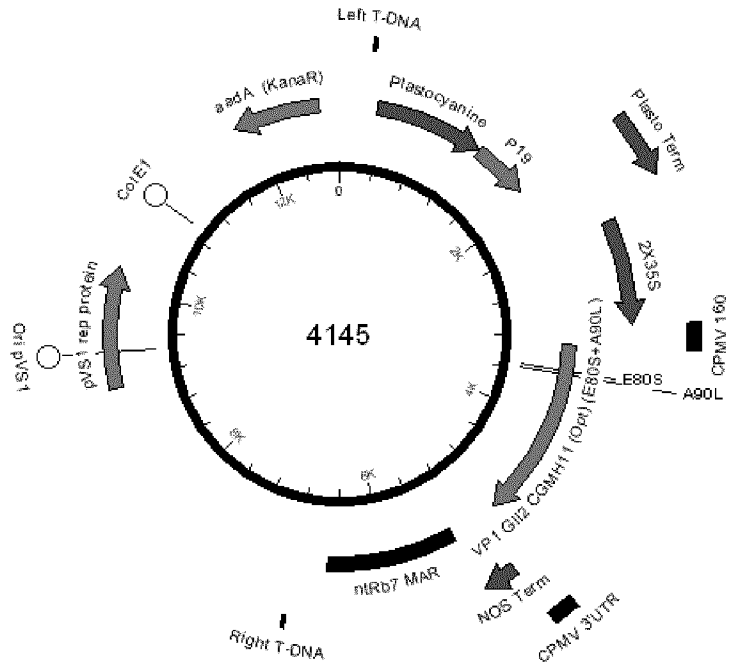


FIGURE 42E

Construct 4182 (VP1 GII.2_A39V+E80S+A90L hCod)

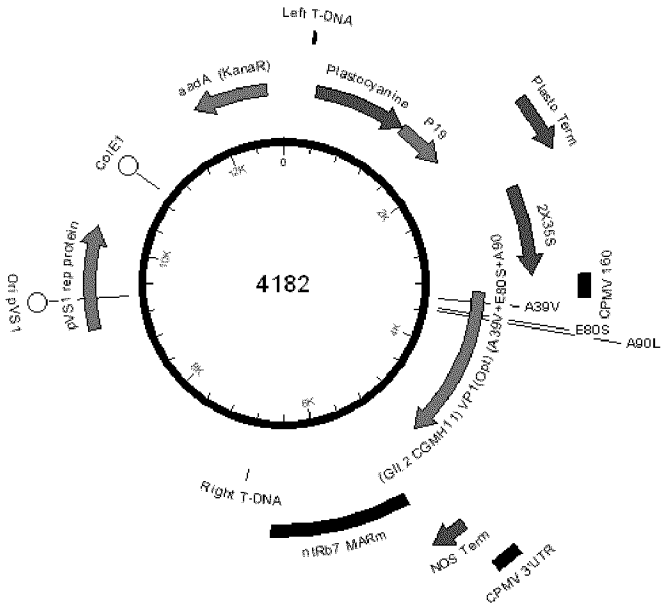


FIGURE 42F

Construct 4183Y (VP1 GII.2_R53I+E80S+A90L hCod)

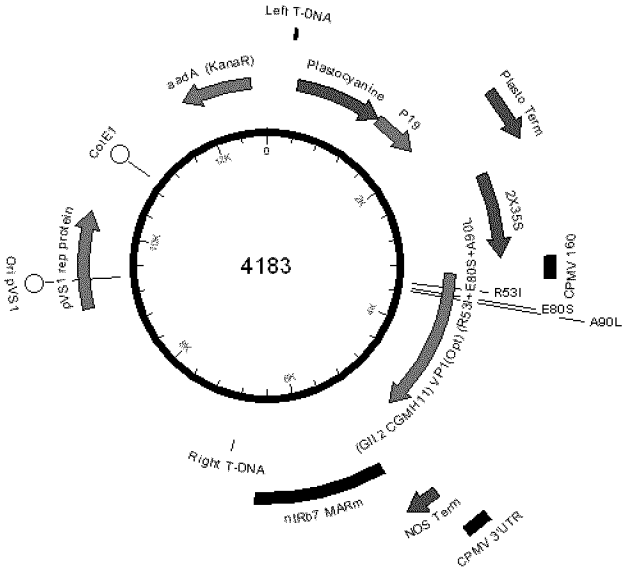


FIGURE 42G

Construct 4184 (VP1 GII.2_A39V+R53I+E80S+A90L hCod).

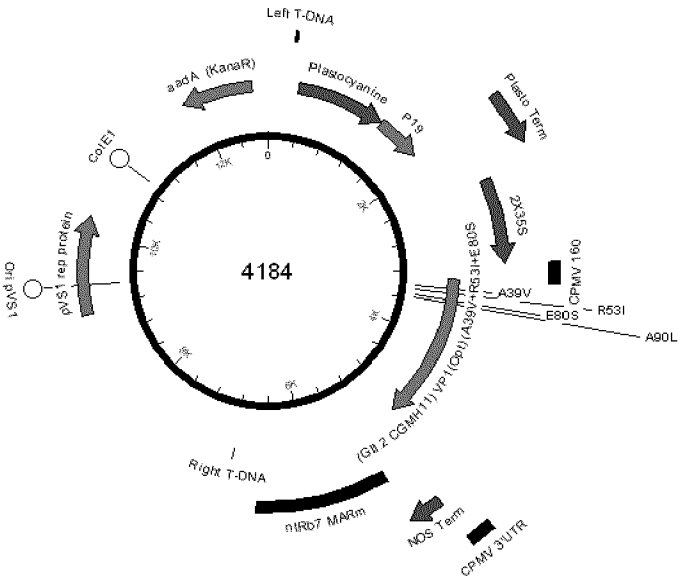


Figure 43A

Construct 3983 (Wt VP1 GII.3 hCod)

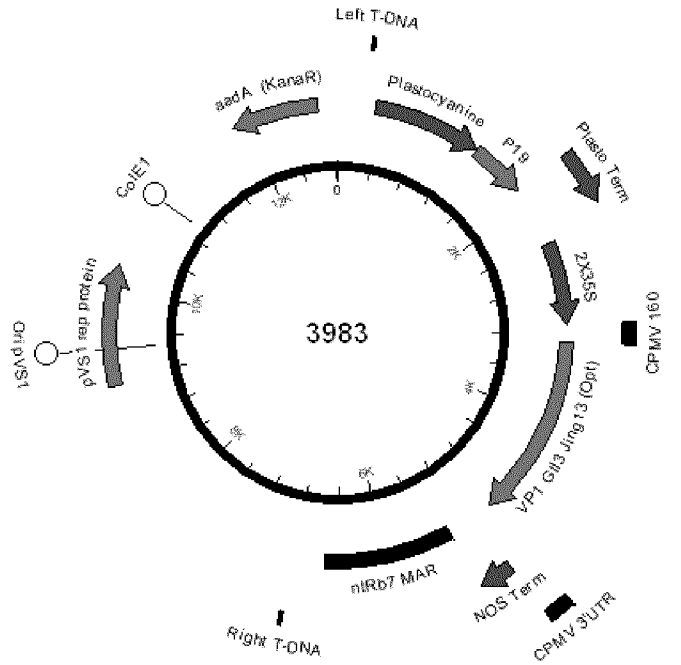


Figure 43B

Construct 4146 (VP1 GII.3_E80S hCod)

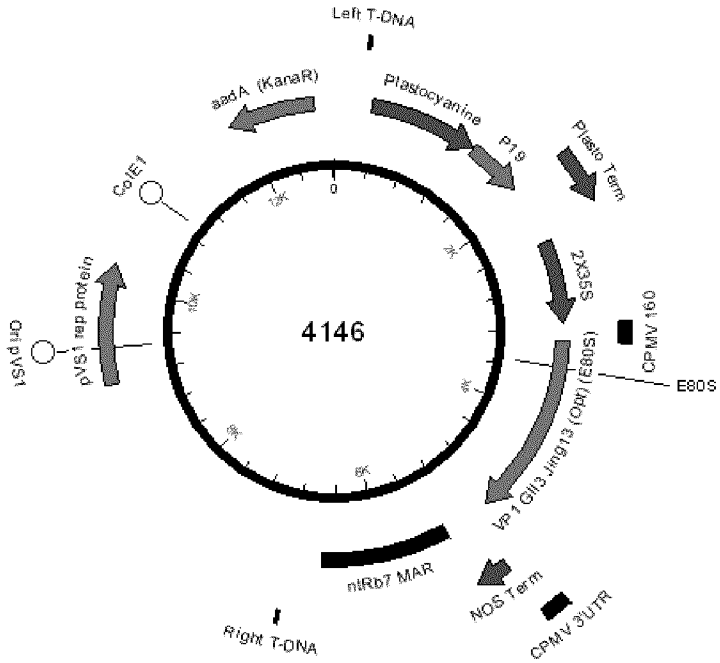


Figure 43C

Construct 4147 (VP1 GII.3_A90L hCod)

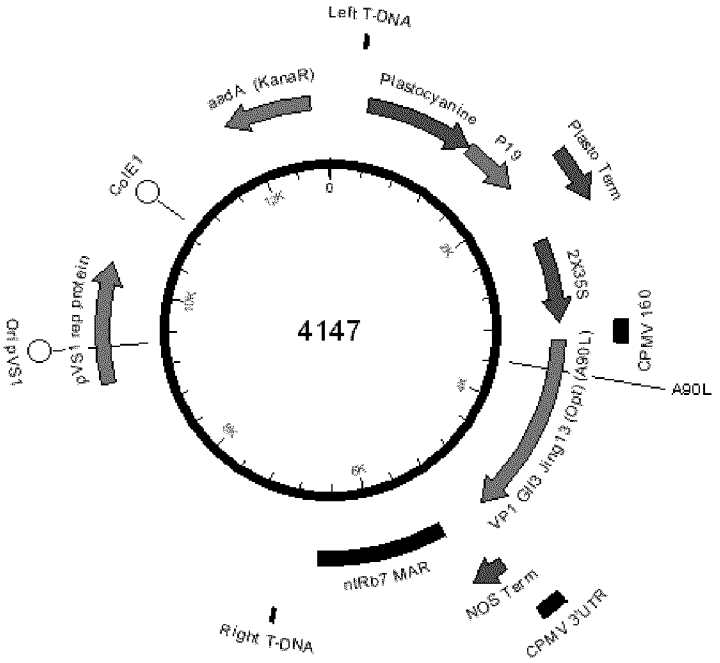


Figure 43D

Construct 4148 (VP1 GII.3_E80S+A90L)

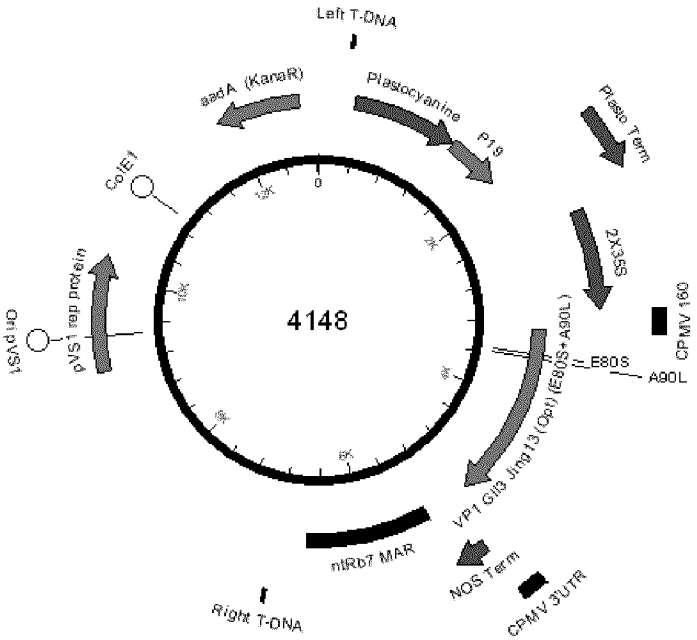


Figure 44A

Construct 3760 (Wt VP1 GII.4 hCod)

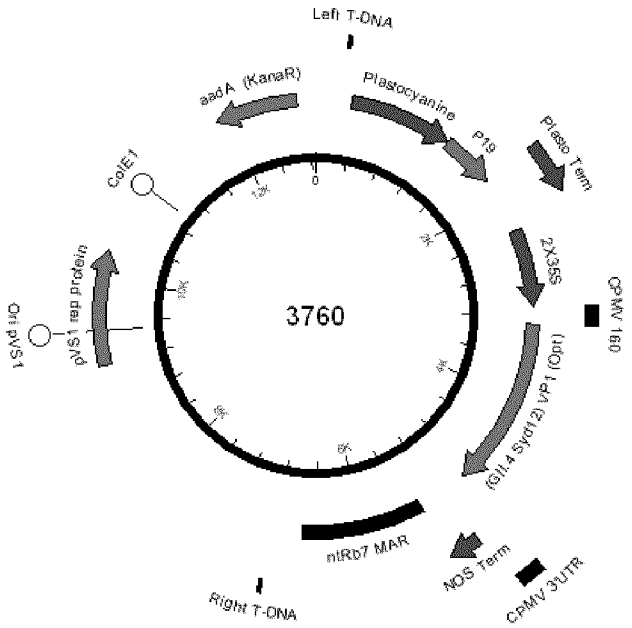


Figure 44B

Construct 4155 (VP1 GII.4_A39V hCod)

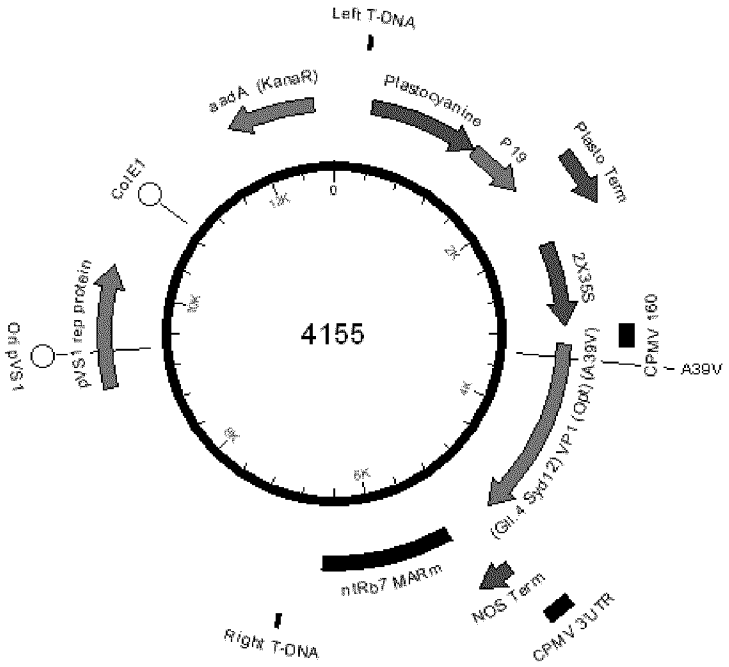


Figure 44C

Construct 4156 (VP1 GII.4_V47P hCod)

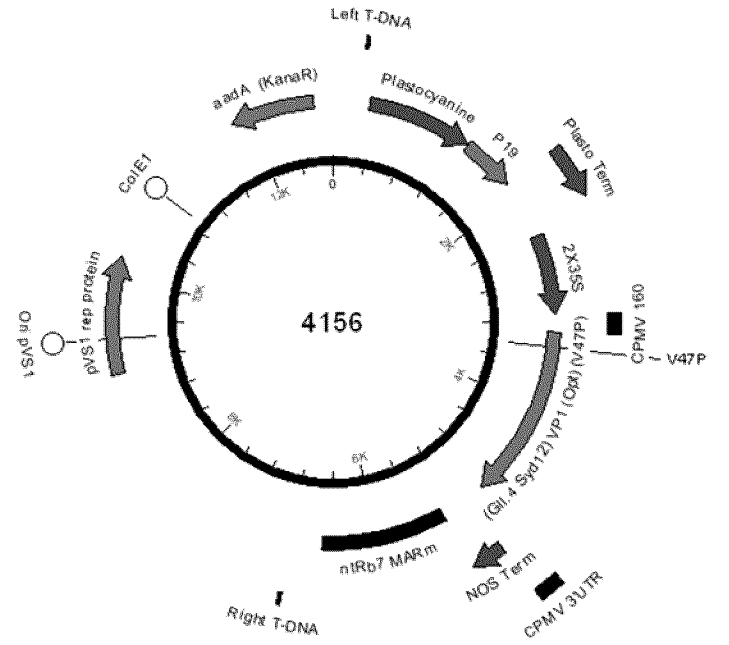


Figure 44D

Construct 4157 (VP1 GII.4_R53I hCod)

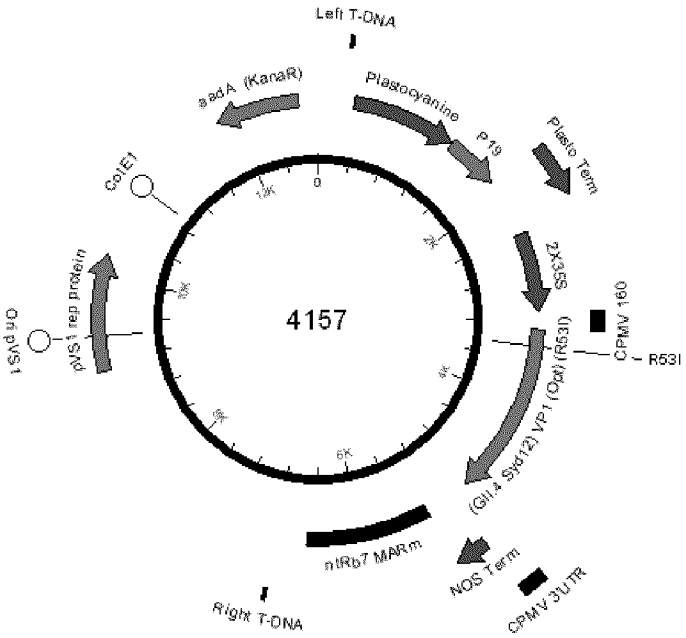


Figure 44E

Construct 4133 (VP1 GII.4_P80S hCod)

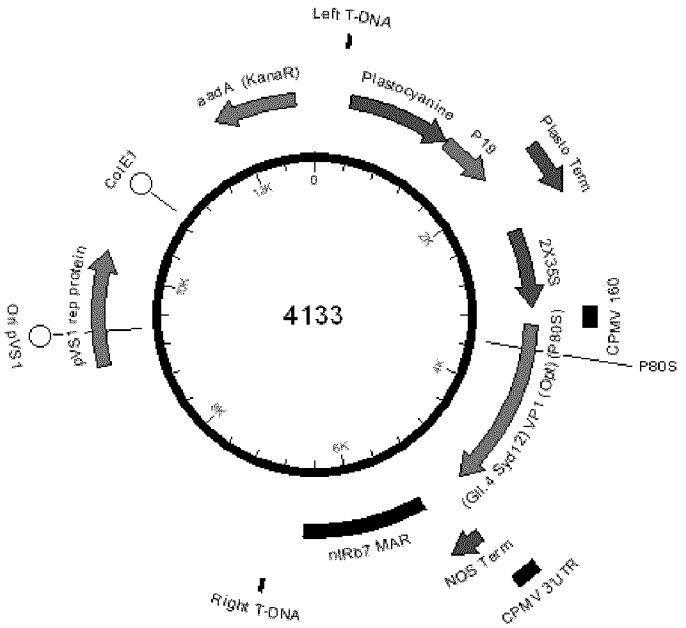


Figure 44F

Construct 4134 (VP1 GII.4_S90L hCod)

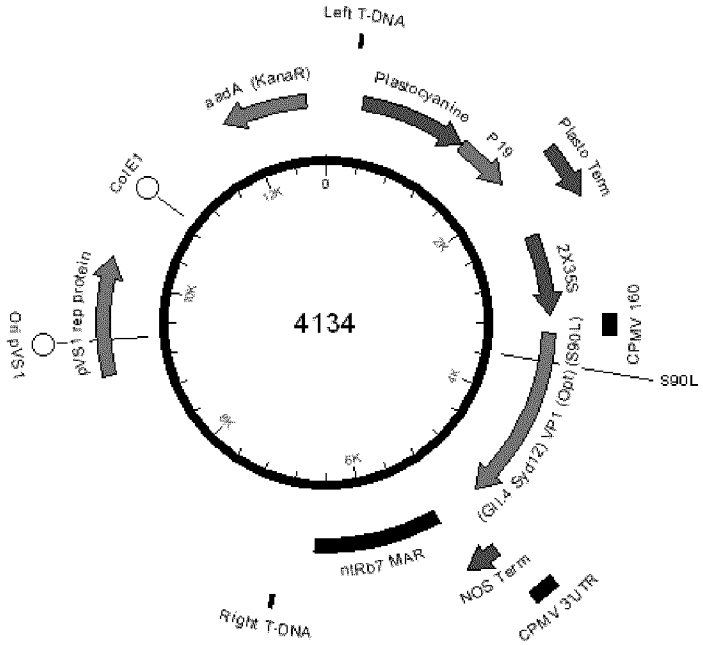


Figure 44G

Construct 4158 (VP1 GII.4_ Δ35-42 hCod)

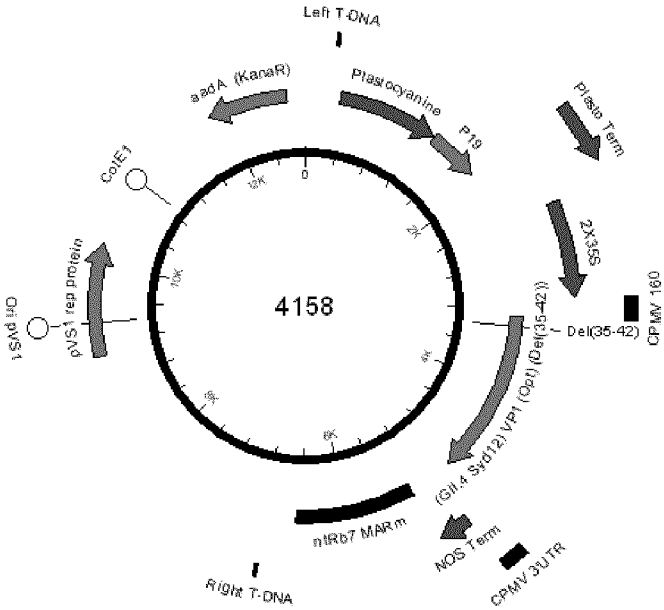


Figure 44H

Construct 4159 (VP1 GII.4_SSTAVATA hCod)

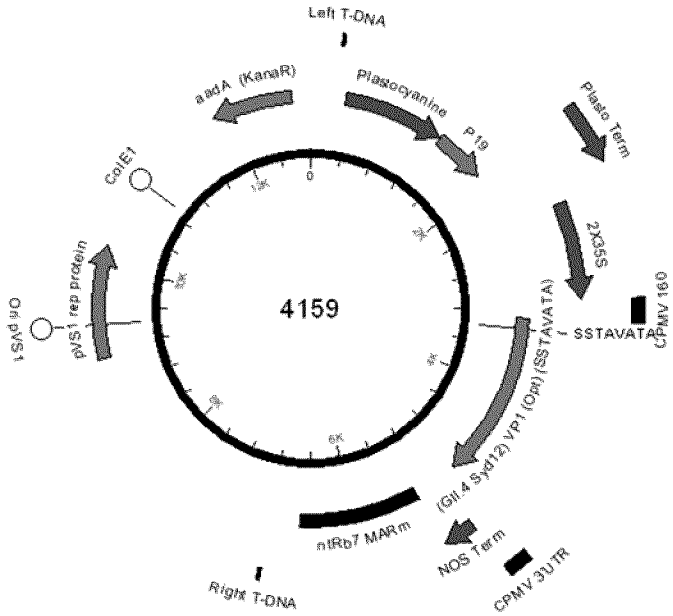


Figure 44I

Construct 4165 (VP1 GII.4_A39V+P80S hCod)

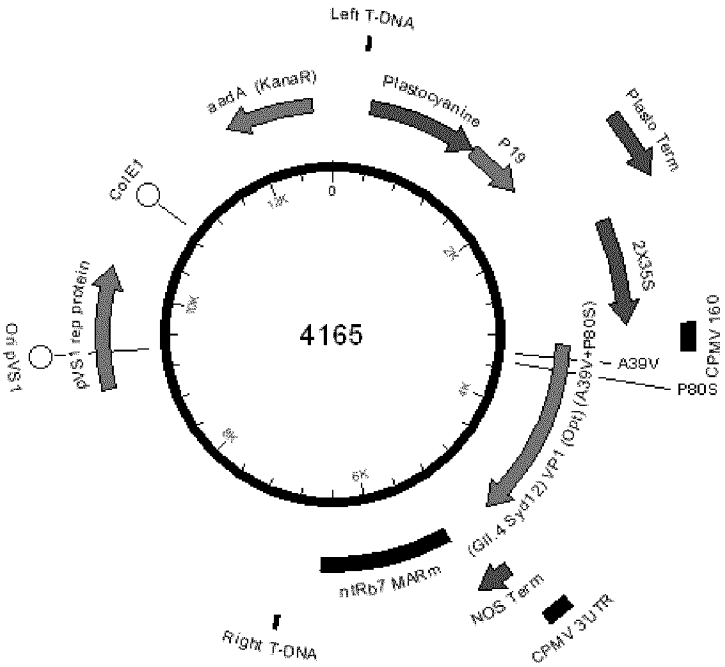


Figure 44J

Construct 4166 (VP1 GII.4_V47P+P80S hCod)

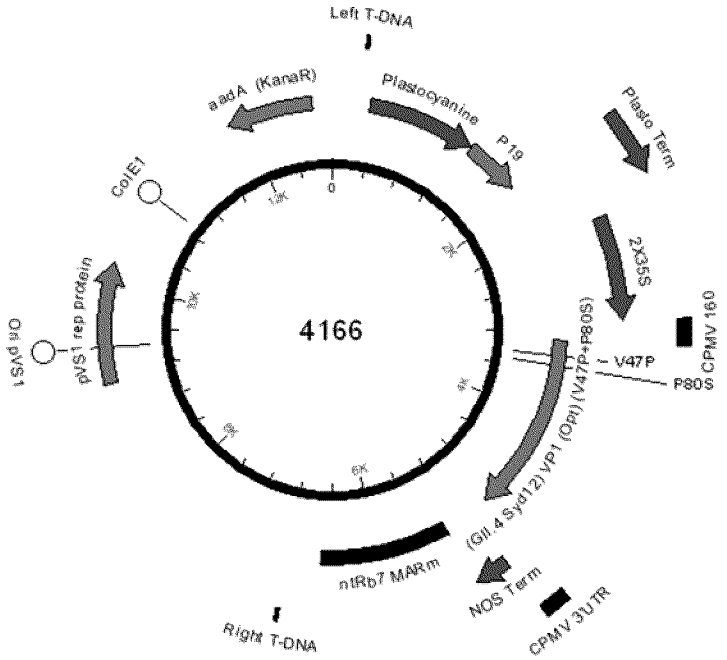


Figure 44K

Construct 4167 (VP1 GII.4_R53I+P80S hCod)

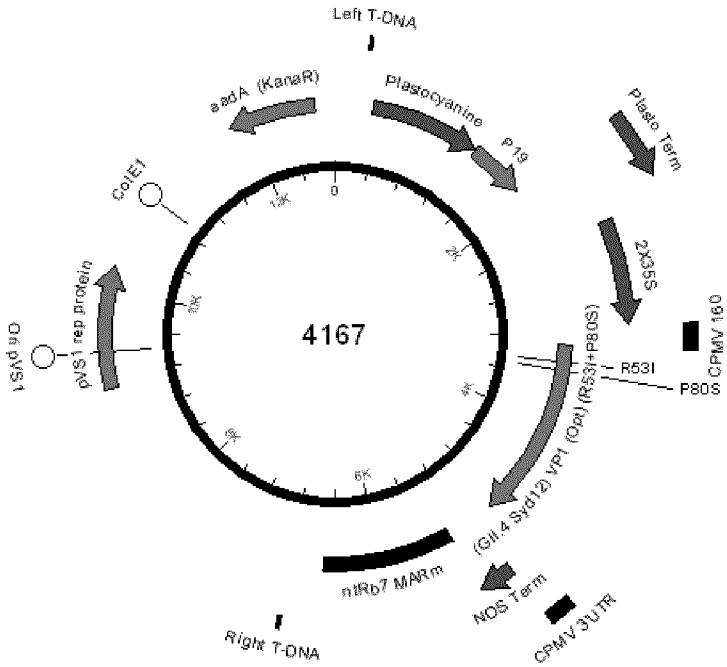


Figure 44L

Construct 4135 (VP1 GII.4_P80S+S90L hCod)

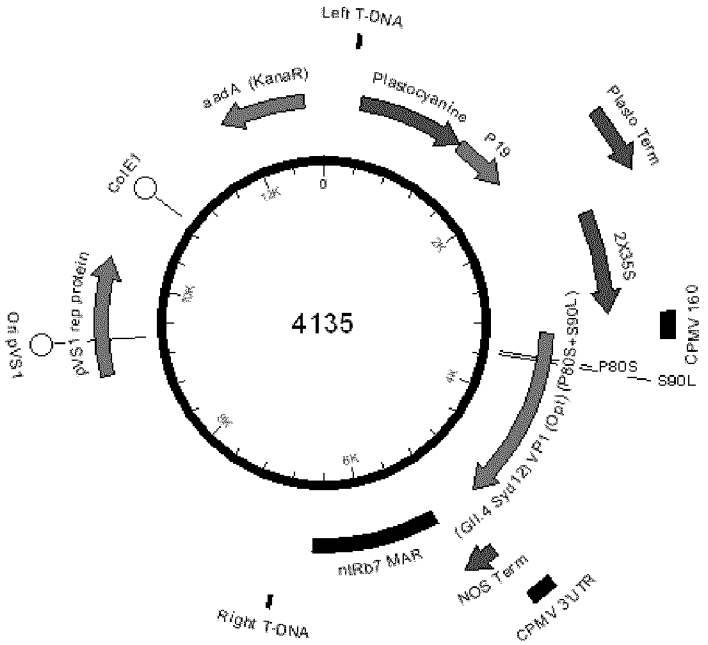


Figure 44M

Construct 4168 (GII.4_ P80S+Δ35-42 hCod)

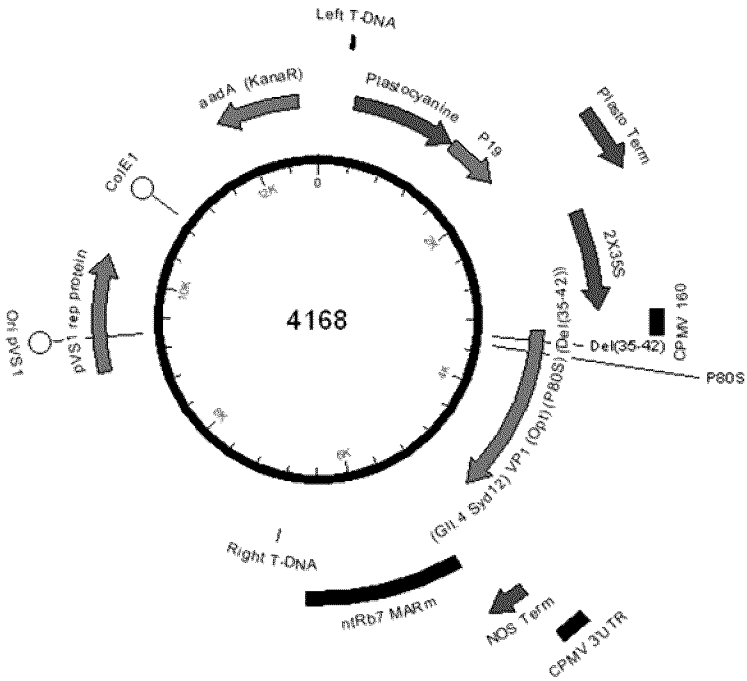


Figure 44N

Construct 4169 (VP1 GII.4_P80S+SSTAVATA hCod)

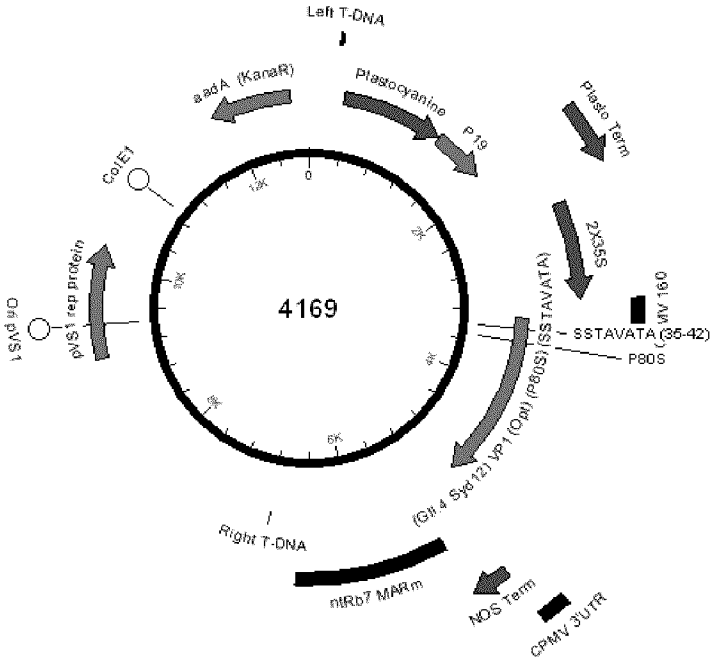


FIGURE 44O

Construct 4185 (VP1 GII.4_A39V+R53I hCod);

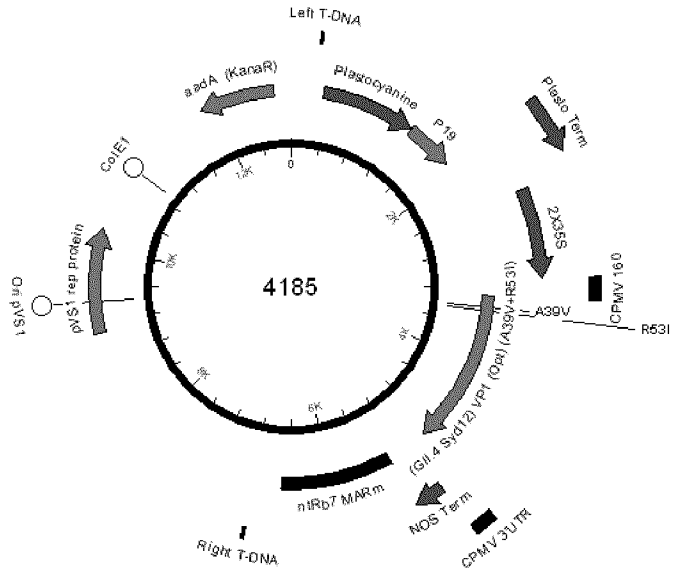


FIGURE 44P

Construct 4186Y (VP1 GII.4_A39V+R53I+P80S hCod)

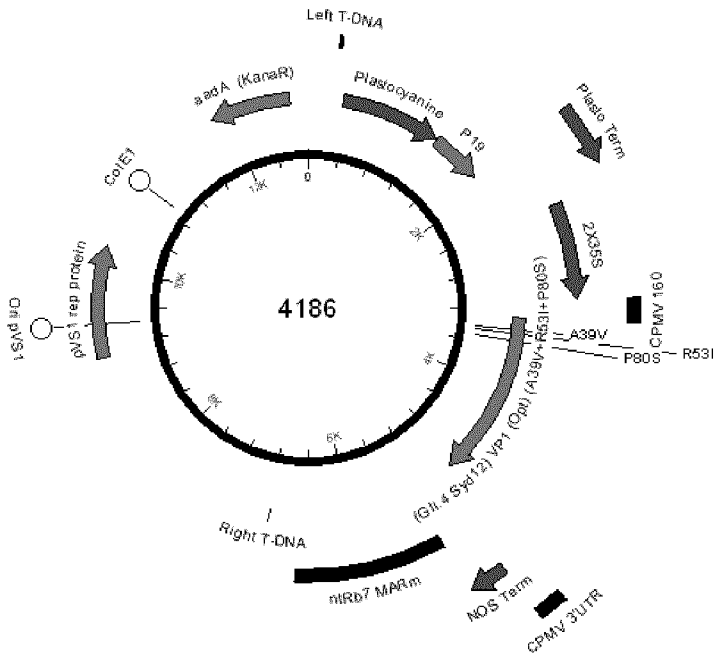


Figure 45A

Construct 3993 (Wt VP1 GII.6 hCod)

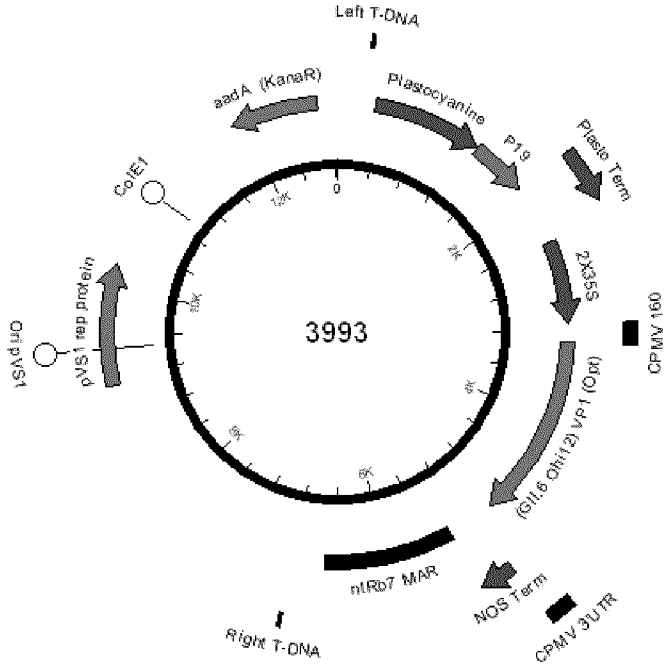


Figure 45B

Construct 4149 (VP1 GII.6_E80S hCod)

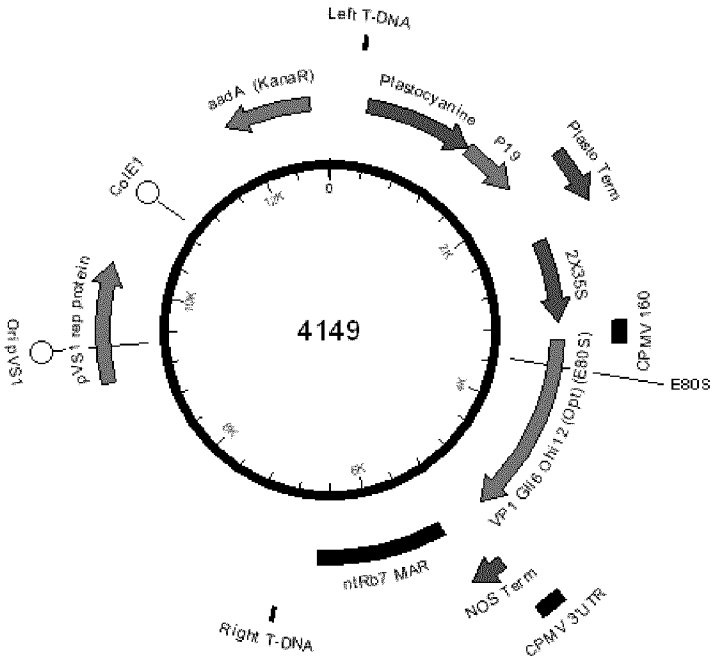


Figure 45C

Construct 4150 (VP1 GII.6_S90L hCod)

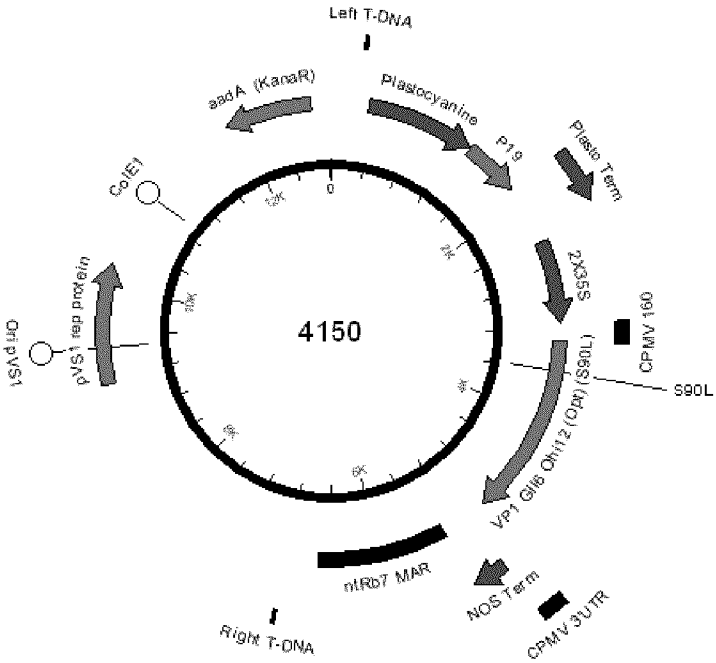


Figure 45D

Construct 4151 (VP1 GII.6_E80S+S90L)

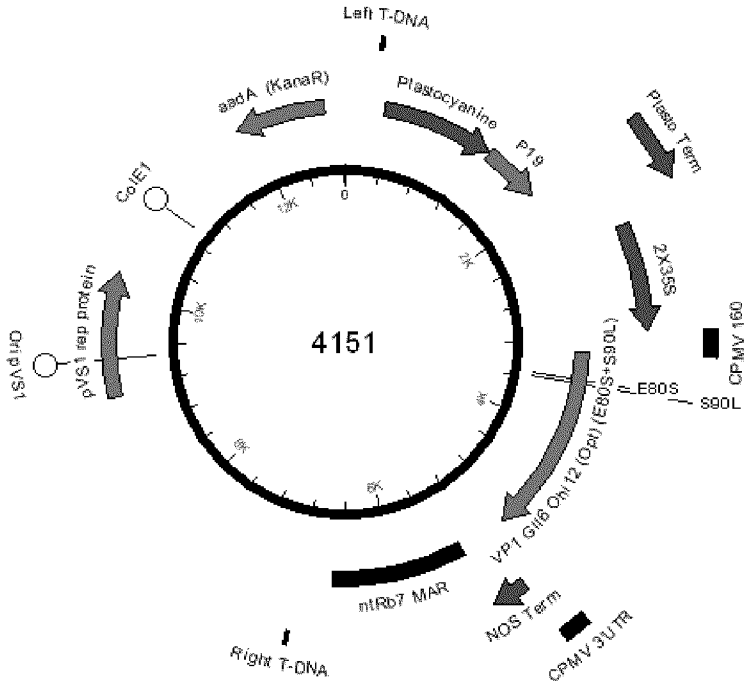


Figure 46A

Construct 3995 (Wt VP1 GII.12 hCod)

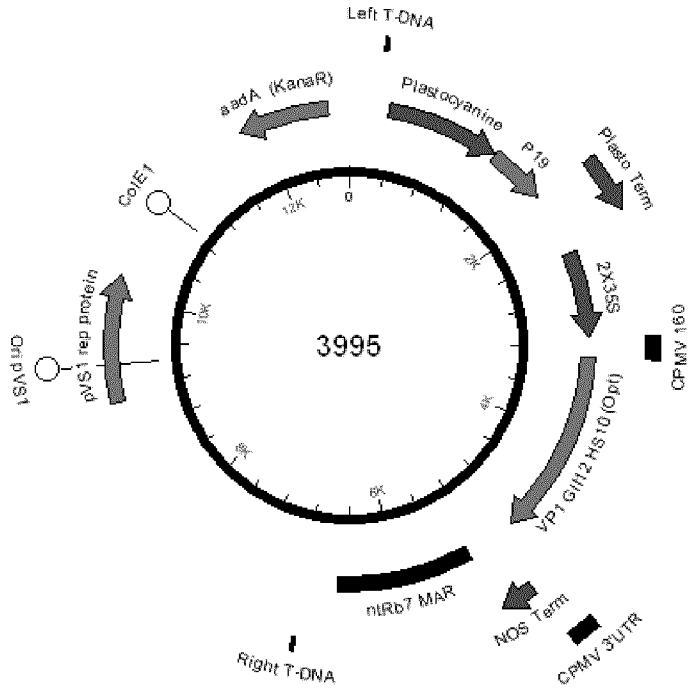


Figure 46B

Construct 4136 (VP1 GII.12_E80S hCod)

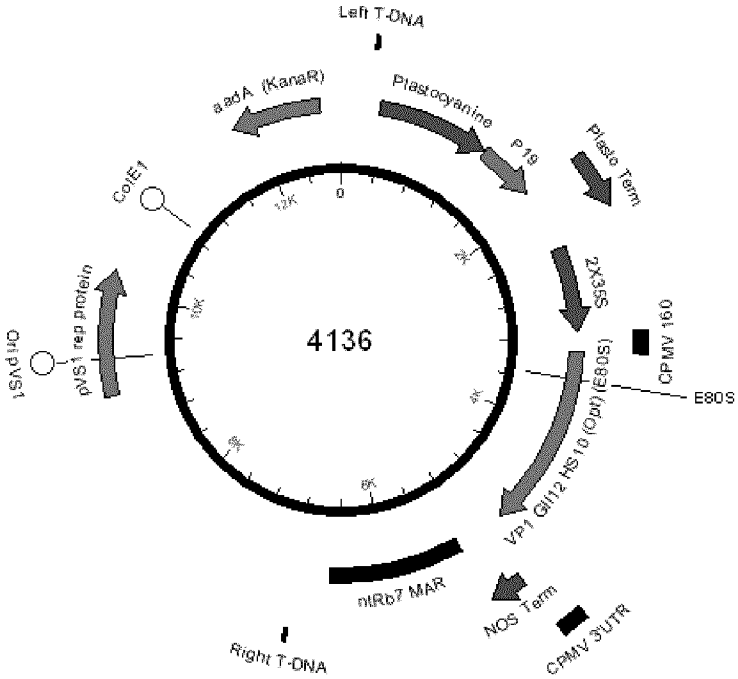


Figure 46C

Construct 4137 (VP1 GII.12_A90L hCod)

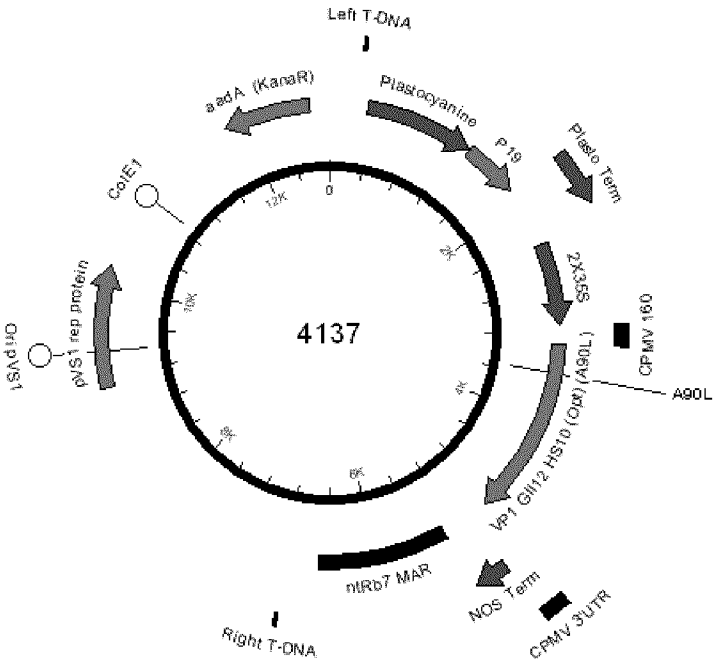


Figure 46D

Construct 4138 (VP1 GII.12_E80S+A90L)

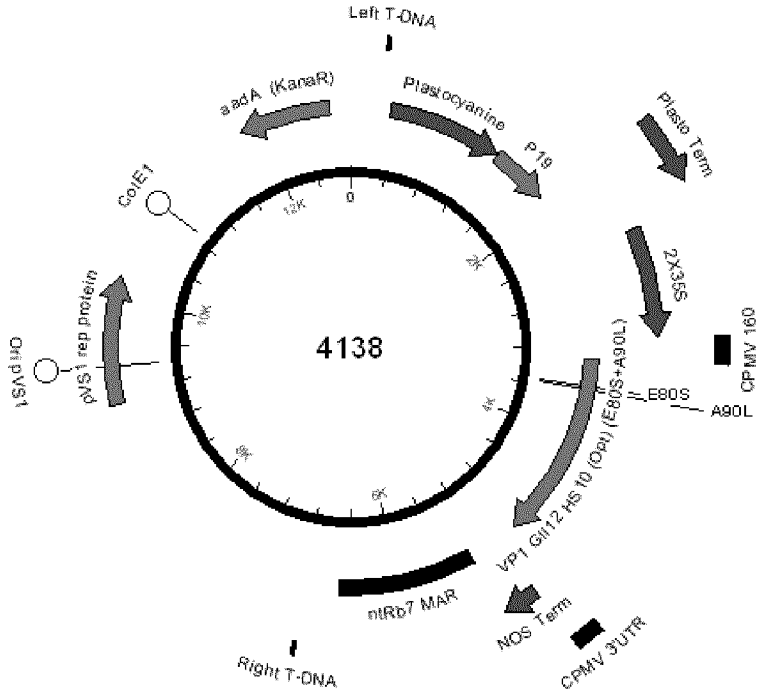


FIGURE 46E

Construct 4234 (VP1 GII.17_A39V hCod)

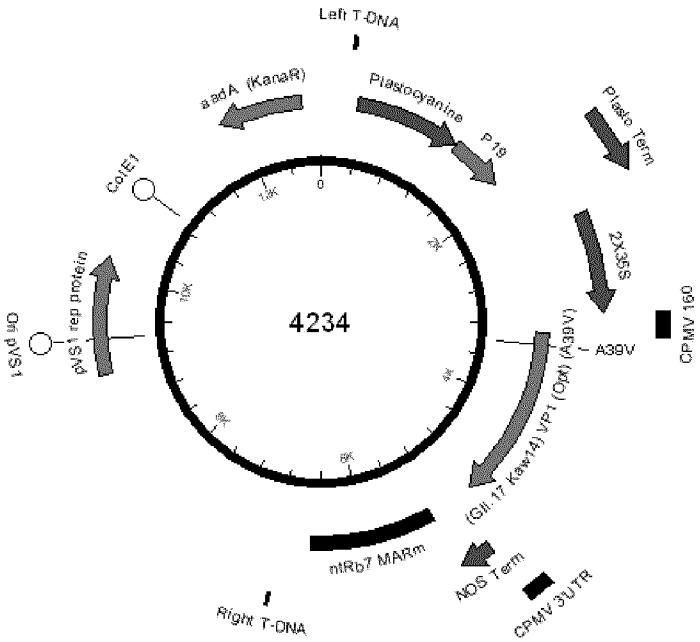


FIGURE 46F

Construct 4235 (VP1 GII.17_R53I hCod)

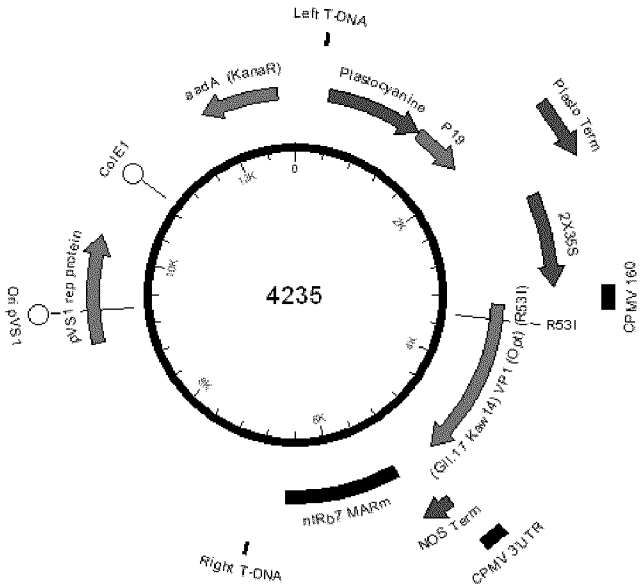


FIGURE 46G

Construct 4232 (VP1 GII.17_ A90L hCod)

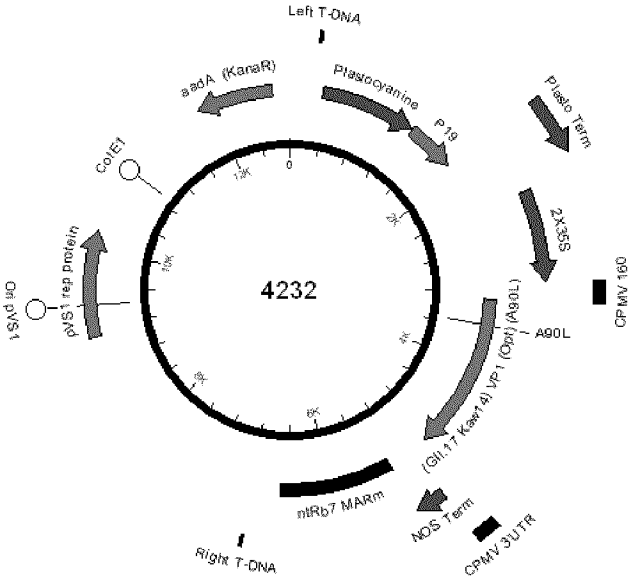


FIGURE 46H

Construct 4236 (VP1 GII.17_A39V+R53I hCod)

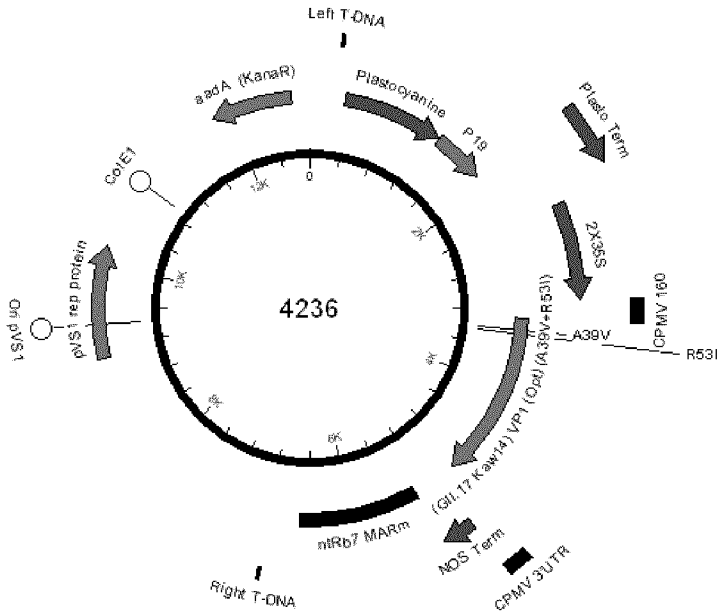


FIGURE 46I

Construct 4233 (VP1 GII.17_E80S+A90L hCod)

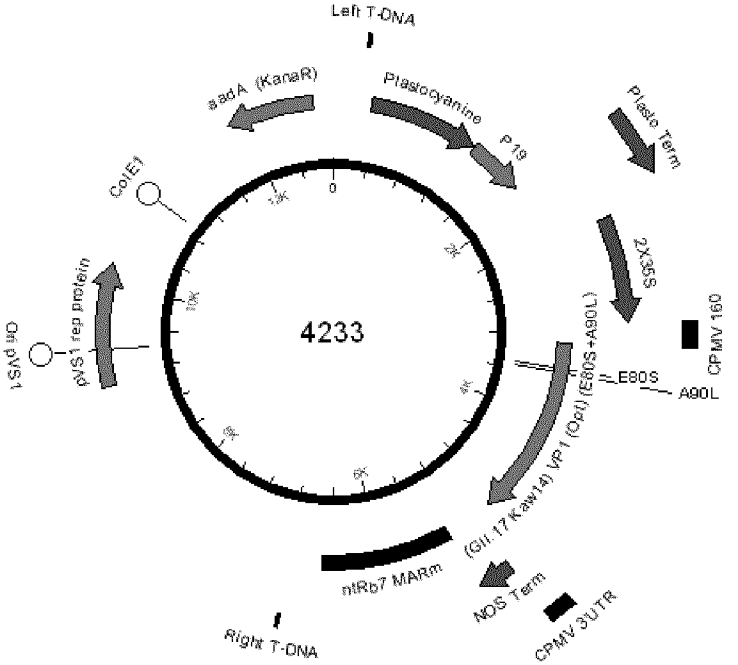


Figure 47A

Construct 2725 (Wt VP2 GI.1)

Figure 47B

Construct 3303 (Wt VP2 GI.3 hCod)

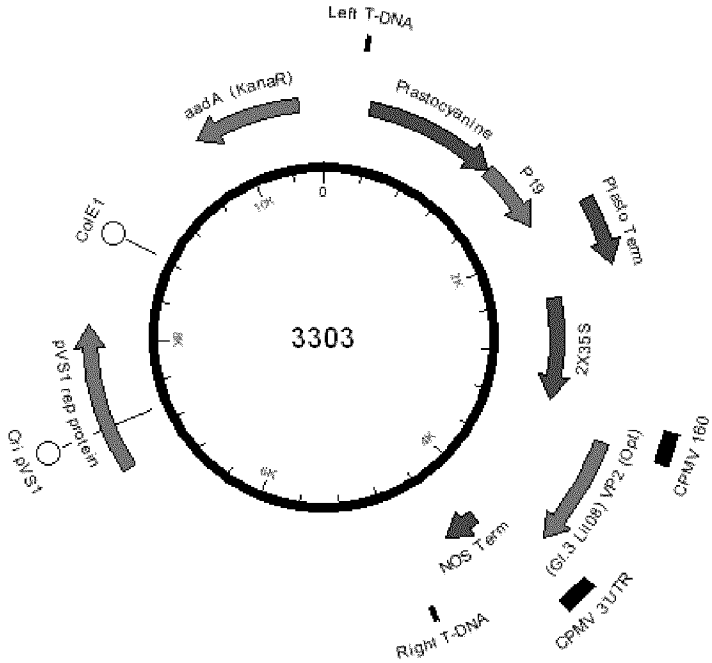


Figure 47C

Construct 3307 (Wt VP2 GII.6)

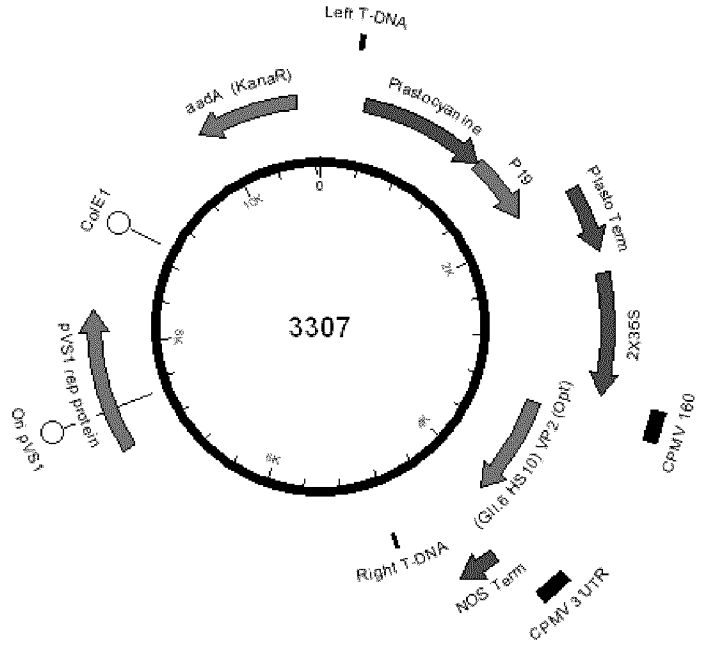


Figure 48

Construct 1190 (Cloning vector 1190)

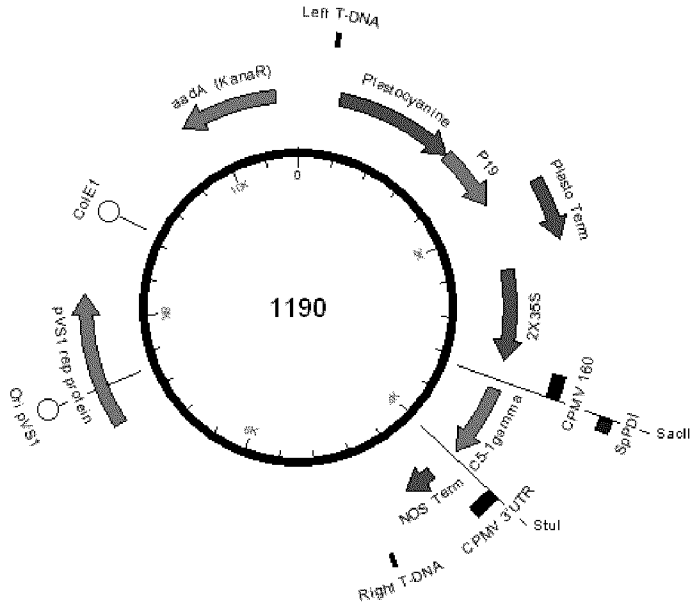


Figure 49

Construct 3677 (Cloning vector 3677)

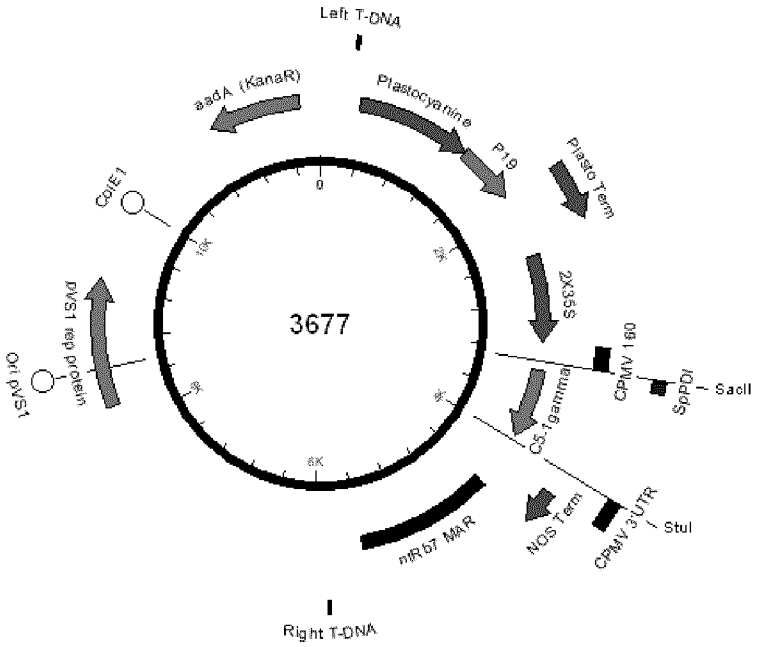


Figure 50A

GII.4 P80X constructs (cloning vectors), wherein X=A (4281); X=N (4285); X=K (4286); X=H (4287)

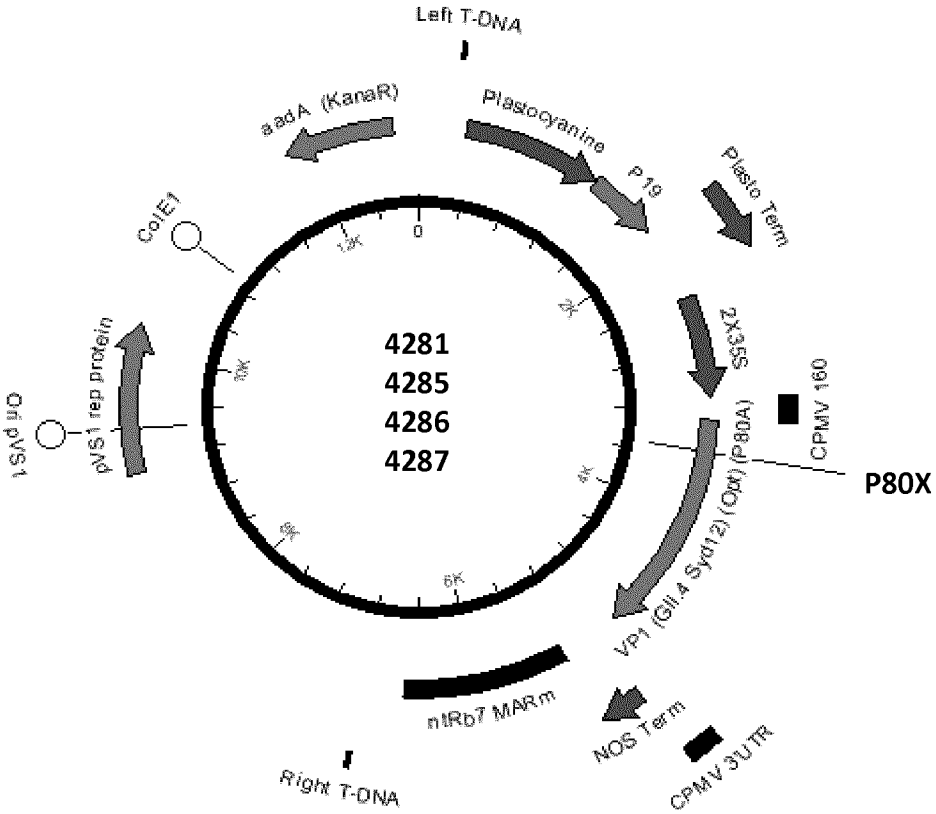


Figure 50B

GII.4 P80s+A39X constructs (cloning vectors), wherein X=I (4256); X=M (4257); X=G (4258); X=S (4259); X=E (4260); X=D (4261); X=N (4262); X=Q (4263); X=K (4264); X=H (4265)

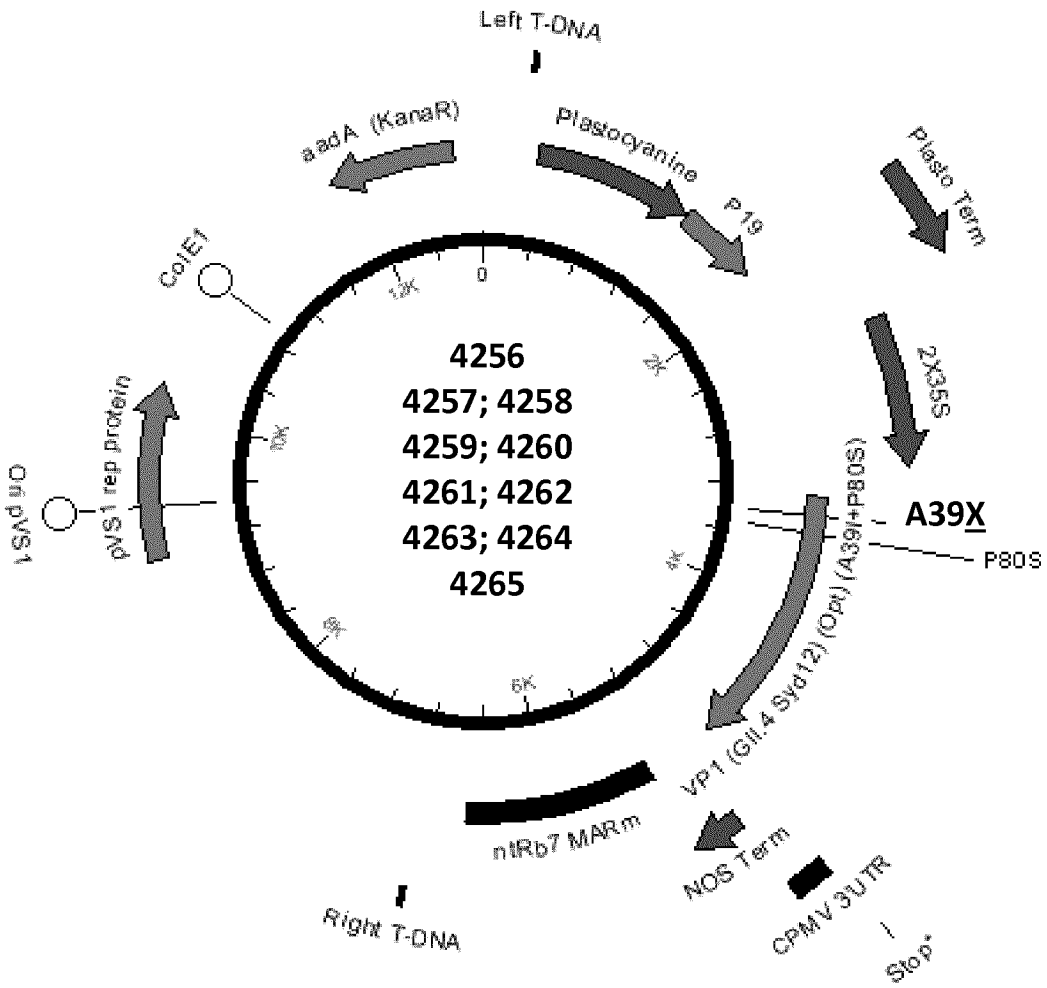


Figure 51

GI.7 M57X constructs (cloning vectors), wherein X= L 4266); G (4268); S (4269); T (4270; N (4273); Q (4274); K (4275); or H (4276).

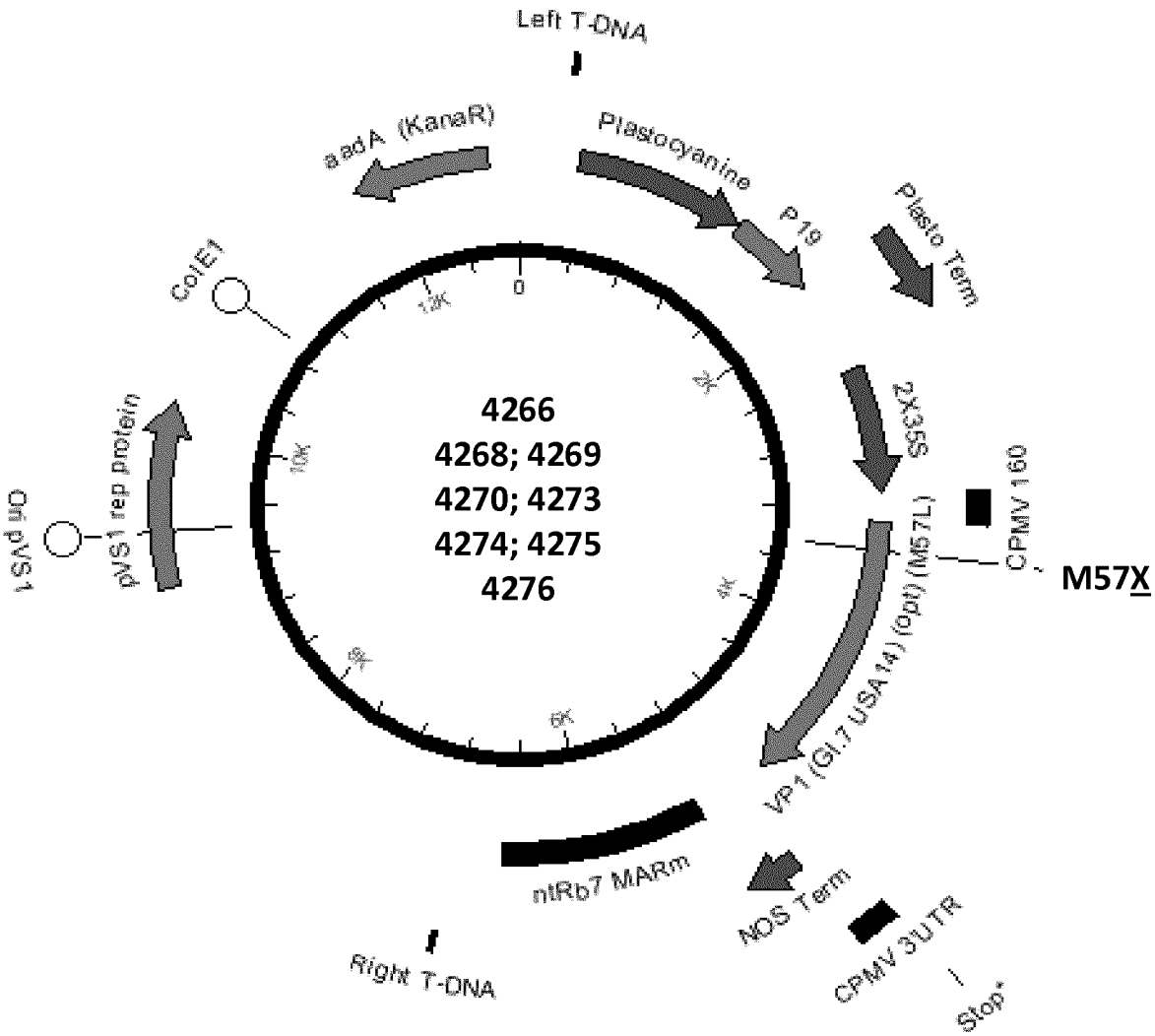
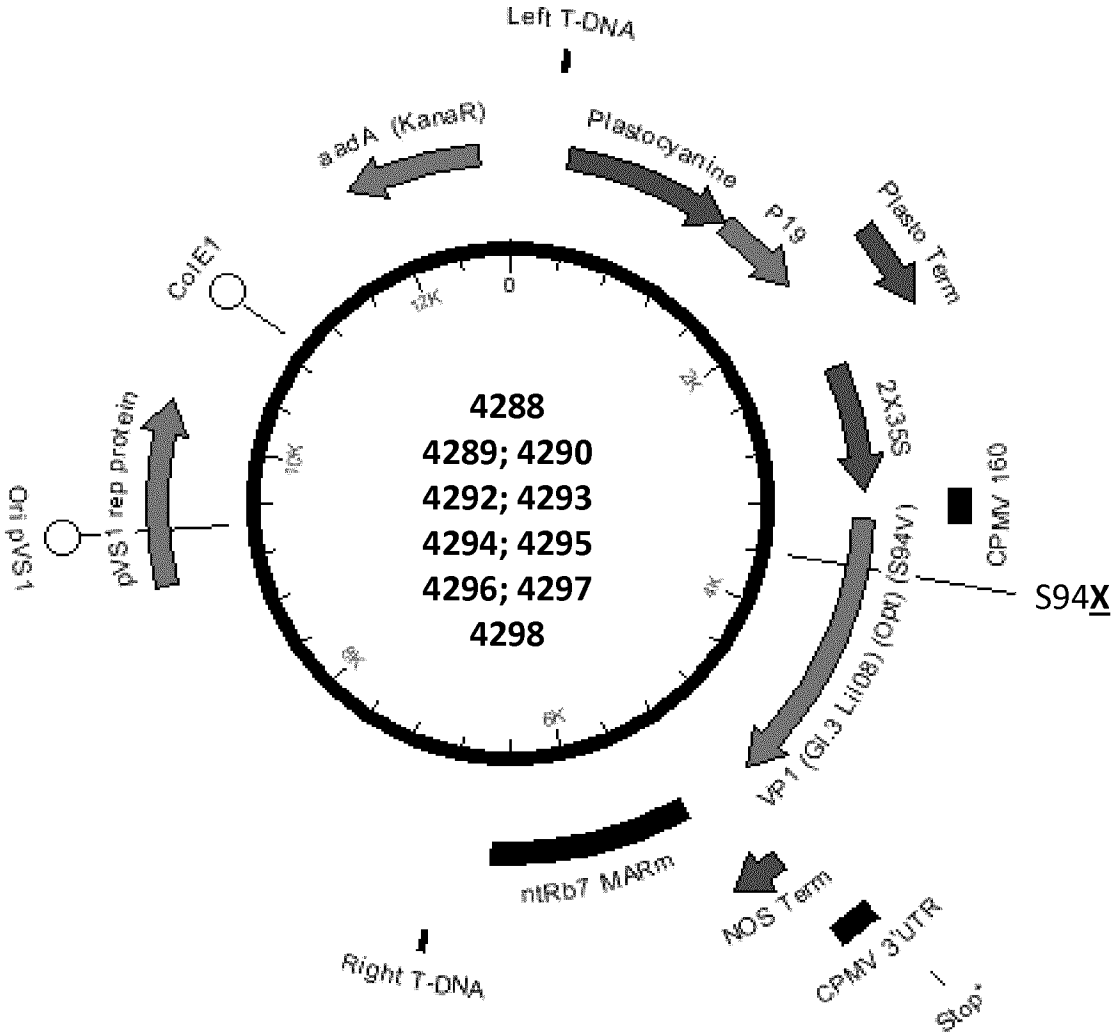


Figure 52

GI.3 S94X constructs (cloning vectors), wherein X=V (4288); I (4289); M (4290); T (4292); E (4293); D (4294); N (4295); Q (4296); K (4297); or H (4298).



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<151> 2018-07-31

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Met Asp Pro Val Ala Gly Ser Ser Thr Ala Val Ala Thr Ala Gly Gln
        35                  40                  45


Val Asn Pro Ile Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro
    50                  55                  60


Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Val Leu
65                  70                  75                  80


Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95


Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Ile Met
            100                 105                 110
```

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Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Val Ser Cys Ile
        115                 120                 125

Pro Pro Gly Phe Gly Ser His Asn Leu Thr Ile Ala Gln Ala Thr Leu
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Thr Leu Asp Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Arg Asn
                165                 170                 175

Gln Gln Thr Met Arg Leu Val Cys Met Leu Tyr Thr Pro Leu Arg Thr
            180                 185                 190

Gly Gly Gly Thr Gly Asp Ser Phe Val Val Ala Gly Arg Val Met Thr
        195                 200                 205

Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Thr Val
    210                 215                 220

Glu Gln Lys Thr Arg Pro Phe Thr Leu Pro Asn Leu Pro Leu Ser Ser
225                 230                 235                 240

Leu Ser Asn Ser Arg Ala Pro Leu Pro Ile Ser Ser Met Gly Ile Ser
                245                 250                 255

Pro Asp Asn Val Gln Ser Val Gln Phe Gln Asn Gly Arg Cys Thr Leu
            260                 265                 270

Asp Gly Arg Leu Val Gly Thr Thr Pro Val Ser Leu Ser His Val Ala
        275                 280                 285

Lys Ile Arg Gly Thr Ser Asn Gly Thr Val Ile Asn Leu Thr Glu Leu
    290                 295                 300

Asp Gly Thr Pro Phe His Pro Phe Glu Gly Pro Ala Pro Ile Gly Phe
305                 310                 315                 320
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Pro Asp Leu Gly Gly Cys Asp Trp His Ile Asn Met Thr Gln Phe Gly
                325                 330                 335

His Ser Ser Gln Thr Gln Tyr Asp Val Asp Thr Thr Pro Asp Thr Phe
            340                 345                 350

Val Pro His Leu Gly Ser Ile Gln Ala Asn Gly Ile Gly Ser Gly Asn
        355                 360                 365

Tyr Val Gly Val Leu Ser Trp Ile Ser Pro Pro Ser His Pro Ser Gly
    370                 375                 380

Ser Gln Val Asp Leu Trp Lys Ile Pro Asn Tyr Gly Ser Ser Ile Thr
385                 390                 395                 400

Glu Ala Thr His Leu Ala Pro Ser Val Tyr Pro Pro Gly Phe Gly Glu
                405                 410                 415

Val Leu Val Phe Phe Met Ser Lys Met Pro Gly Pro Gly Ala Tyr Asn
            420                 425                 430

Leu Pro Cys Leu Leu Pro Gln Glu Tyr Ile Ser His Leu Ala Ser Glu
        435                 440                 445

Gln Ala Pro Thr Val Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro
    450                 455                 460

Asp Thr Gly Arg Asn Leu Gly Glu Phe Lys Ala Tyr Pro Asp Gly Phe
465                 470                 475                 480

Leu Thr Cys Val Pro Asn Gly Ala Ser Ser Gly Pro Gln Gln Leu Pro
                485                 490                 495

Ile Asn Gly Val Phe Val Phe Val Ser Trp Val Ser Arg Phe Tyr Gln
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Leu Lys Pro Val Gly Thr Ala Ser Ser Ala Arg Gly Arg Leu Gly Leu
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Arg Arg
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ccagtttcat tgtcacatgt tgccaagata agagggacct ccaatggcac tgtaatcaac 900

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acagcagtgg ccacagccgg tcaagtgaat ccaattgatc cgtggattat caacaatttc 180

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ccaccaaccg ttgagcagaa gacgcggccc tttacactgc ccaatctccc gctttcaagt 720

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cagtctgtcc aattccaaaa tgggagatgc acactggacg gtcgcctggt gggaacaact 840

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ctgacagaac ttgatggcac gcccttccat ccctttgaag gaccagcccc tattggattt 960

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20 25 30

Met Glu Pro Val Ala Gly Pro Thr Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Val Asn Asn Phe Val Gln Ser Pro
50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

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Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Ser His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Ile Leu
            100                 105                 110

Leu Ala Gly Asn Ala Phe Ser Ala Gly Lys Ile Ile Val Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Thr Ser Ser Ser Leu Thr Ile Ala Gln Ala Thr Leu
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Thr Leu Glu Pro Ile Glu Met
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Tyr His Thr Asn Asp Asn Gln
                165                 170                 175

Pro Thr Met Arg Leu Val Cys Met Leu Tyr Thr Pro Leu Arg Thr Gly
            180                 185                 190

Gly Gly Ser Gly Asn Ser Asp Ser Phe Val Val Ala Gly Arg Val Leu
        195                 200                 205

Thr Ala Pro Ser Ser Asp Phe Ser Phe Leu Phe Leu Val Pro Pro Thr
    210                 215                 220

Ile Glu Gln Lys Thr Arg Ala Phe Thr Val Pro Asn Ile Pro Leu Gln
225                 230                 235                 240

Thr Leu Ser Asn Ser Arg Phe Pro Ser Leu Ile Gln Gly Met Ile Leu
                245                 250                 255

Ser Pro Asp Ala Ser Gln Val Val Gln Phe Gln Asn Gly Arg Cys Leu
            260                 265                 270

Ile Asp Gly Gln Leu Leu Gly Thr Thr Pro Ala Thr Ser Gly Gln Leu
        275                 280                 285
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Phe Arg Val Arg Gly Lys Ile Asn Gln Gly Ala Arg Thr Leu Asn Leu
    290                 295                 300

Thr Glu Val Asp Gly Lys Pro Phe Met Ala Phe Asp Ser Pro Ala Pro
305                 310                 315                 320

Val Gly Phe Pro Asp Phe Gly Lys Cys Asp Trp His Met Arg Ile Ser
                325                 330                 335

Lys Thr Pro Asn Asn Thr Ser Ser Gly Asp Pro Met Arg Ser Val Asp
            340                 345                 350

Val Gln Thr Asp Val Gln Gly Phe Val Pro His Leu Gly Ser Ile Gln
        355                 360                 365

Phe Asp Glu Val Phe Asn His Pro Thr Gly Asp Tyr Ile Gly Thr Ile
    370                 375                 380

Glu Trp Ile Ser Gln Pro Ser Thr Pro Pro Gly Thr Asp Ile Asn Leu
385                 390                 395                 400

Trp Glu Ile Pro Asp Tyr Gly Ser Ser Leu Ser Gln Ala Ala Asn Leu
                405                 410                 415

Ala Pro Pro Val Phe Pro Pro Gly Phe Gly Glu Ala Leu Val Tyr Phe
            420                 425                 430

Val Ser Ala Phe Pro Gly Pro Asn Asn Arg Ser Ala Pro Asn Asp Val
        435                 440                 445

Pro Cys Leu Leu Pro Gln Glu Tyr Val Thr His Phe Val Ser Glu Gln
    450                 455                 460

Ala Pro Thr Met Gly Asp Ala Ala Leu Leu His Tyr Val Asp Pro Asp
465                 470                 475                 480

Thr Asn Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Gly Gly Tyr Leu
                485                 490                 495
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Thr Cys Val Pro Asn Gly Val Gly Ala Gly Pro Gln Gln Leu Pro Leu
500 505 510

Asn Gly Val Phe Leu Phe Val Ser Trp Val Ser Arg Phe Tyr Gln Leu
515 520 525

Lys Pro Val Gly Thr Ala Ser Thr Ala Arg Gly Arg Leu Gly Val Arg
530 535 540

Arg Ile
545

<210> 5
<211> 1641
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1 G1.2 Leuven 2003 D2DEL3

<400> 5
atgatgatgg cttcaaagga tgctccccaa agcgcggacg gagctagcgg cgccggacag 60

ttggttccgg aagtcaacac tgccgatcca ctgcccatgg aacccgtagc tggtccaaca 120

accgctgttg ccaccgccgg ccaggttaac atgatcgatc catggattgt taataacttt 180

gtacagagcc cccaggggga gttcacaatt tctccgaaca ataccctgg ggacattctg 240

ttcgatctgc aactgggccc acacttgaat cctttcctga gccatctttc acagatgtac 300

aacggatggg ttgggaacat gcgtgttcgg atcctccttg ctggcaacgc cttcagtgct 360

ggcaagatta tcgtgtgctg cgtaccacca gggtttacct cgagttcatt aaccattgct 420

caggccaccc ttttccctca cgtgatcgca gacgtgcgta ccttagaacc aatcgaaatg 480

cccctggaag atgtacggaa cgtgctgtac catactaatg ataaccagcc aacgatgaga 540

ttagtgtgca tgctgtacac ccccctgaga actggaggag gttctggaaa ttccgacagt 600

tttgtggtgg ctggcagggt cctgaccgct cccagtagcg acttcagctt tttgttcctc 660

gttcctccta caatcgaaca aaaaacaaga gcattcacag tgcccaacat tccactgcag 720

actttaagca attccaggtt tcccagcttg atccagggta tgatcctttc tcccgacgcc 780

tcccaagttg tgcagttcca gaatgggaga tgtcttatcg acggtcagct tctgggaaca 840

acccctgcca cctccgggca actcttccgg gtgagaggca aaatcaatca gggcgccaga 900

acactgaatc tgacagaagt ggacgggaaa ccctttatgg cgttcgatag ccccgcgccc 960

gttggattcc ctgacttcgg caagtgtgat tggcacatgc gcatcagtaa gactcccaac 1020

aacacttcat ctggagaccc catgaggagc gtggatgtcc agaccgacgt gcagggcttc 1080

gtgccgcact tgggatctat ccagttcgat gaggtgttca atcaccctac tggcgactac 1140

ataggcacaa ttgagtggat aagtcaacca tctacacctc cagggaccga cataaacctg 1200

tgggaaattc ctgattacgg gtcatccctg agtcaagctg ccaatcttgc acccccctgtc 1260

tttccccccg gctttggtga ggctcttgtt tacttcgtct ctgcatttcc tggtcctaac 1320

aaccgctccg cccctaacga tgttccgtgt ttgttacccc aggaatatgt gactcatttc 1380

gtttccgaac aggcacccac catgggggac gctgccctgc tacactatgt ggaccccgac 1440

accaatagaa acctcggcga gttcaaactc taccccgggg gatacctgac ctgtgttcca 1500

aatggagtgg gagcaggccc acaacagctg cccctgaatg gggtcttcct gttcgtttct 1560

tgggtgtcac gcttttacca gctgaagccc gttggcacag cttctacggc acgcggcagg 1620

ctaggggtcc gccgaatctg a 1641

<210> 6
<211> 543
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of VP1 GI.3 LillaEdet 2008 H2DG70

<400> 6

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
20 25 30

Met Glu Pro Val Ala Gly Ala Ala Thr Ala Ala Ala Thr Ala Gly Gln

```
        35                  40                  45

Val Asn Met Ile Asp Pro Trp Ile Met Ser Asn Tyr Val Gln Ala Pro
    50                  55                  60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Ser His Leu
                85                  90                  95

Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
            100                 105                 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
        115                 120                 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
                165                 170                 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
            180                 185                 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
    210                 215                 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225                 230                 235                 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
```

245 250 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
260 265 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
275 280 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
290 295 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305 310 315 320

Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
325 330 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
340 345 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
355 360 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
370 375 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385 390 395 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
405 410 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
420 425 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
435 440 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro

```
    450                 455                 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465                 470                 475                 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
                485                 490                 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
            500                 505                 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
        515                 520                 525

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
    530                 535                 540
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<210> 7
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1 GI.3 LillaEdet 2008 H2DG70

<400> 7

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cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc      120

actgctgccg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac      180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg      240

tttgacctgc agctaggacc acacttgaat ccgtttctga gtcacttggc tcagatgtat      300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc      360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca      420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg      480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc      540

ttgatatgta tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct      600
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tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt ccttttttctg 660

gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720

gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggtatc tcaggatcac 780

ggtcaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840

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aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140

atctgtagcc tagagtggct atctccgcca agcggtgggg cccctaaagt taacccatgg 1200

gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 8
<211> 543
<212> PRT
<213> Norovirus

<400> 8

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
20 25 30

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Met Glu Pro Val Ala Gly Ala Ala Thr Ala Ala Ala Thr Ala Gly Gln
        35                  40                  45

Val Asn Met Ile Asp Pro Trp Ile Met Ser Asn Tyr Val Gln Ala Pro
    50                  55                  60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95

Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
            100                 105                 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
        115                 120                 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
                165                 170                 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
            180                 185                 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
    210                 215                 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225                 230                 235                 240
```

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Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
                245                 250                 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
            260                 265                 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
        275                 280                 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
    290                 295                 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
                325                 330                 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
            340                 345                 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
        355                 360                 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
    370                 375                 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385                 390                 395                 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
                405                 410                 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
            420                 425                 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
        435                 440                 445
```

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
450 455 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465 470 475 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
485 490 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
500 505 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 9
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1 GI.3 Lil08 S94L

<400> 9
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cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc 120

actgctgccg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctgc agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca 420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg 480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc 540

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gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gcccccttaac 720

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aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

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gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 10
<211> 543
<212> PRT
<213> Norovirus

<400> 10

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser

20 25 30

Met Glu Pro Val Ala Gly Ala Ala Thr Ala Ala Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Met Ser Asn Tyr Val Gln Ala Pro
50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
85 90 95

Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
100 105 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
115 120 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
130 135 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145 150 155 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
165 170 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
180 185 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
195 200 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
210 215 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn

225 230 235 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
245 250 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
260 265 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
275 280 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
290 295 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305 310 315 320

Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
325 330 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
340 345 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
355 360 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
370 375 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385 390 395 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
405 410 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
420 425 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys

435 440 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
450 455 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465 470 475 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
485 490 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
500 505 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 11
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1 GI.3 Lil08 Q84S plus sign S94L

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actgctgccg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctga gcctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300

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aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

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gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 12
<211> 543
<212> PRT
<213> Norovirus

<400> 12

Met Met Met Ala Ser Lys Asp Ala Pro Ser Ser Ala Asp Gly Ala Asn
1 5 10 15

```
Gly Ala Gly Gln Leu Val Pro Glu Val Asn Asn Ala Glu Pro Leu Pro
            20                  25                  30

Leu Asp Pro Val Ala Gly Ala Ser Thr Ala Leu Ala Thr Ala Gly Gln
        35                  40                  45

Val Asn Met Ile Asp Pro Trp Ile Phe Asn Asn Phe Val Gln Ala Pro
    50                  55                  60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Ala His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Ile
            100                 105                 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Val Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Gln Ser Arg Thr Leu Ser Ile Ala Gln Ala Thr Leu
    130                 135                 140

Phe Pro His Ile Ile Ala Asp Val Arg Thr Leu Glu Pro Ile Glu Ile
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Thr Leu Tyr His Thr Asn Asp Asn Gln
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Thr Gly
            180                 185                 190

Gly Gly Ser Gly Gly Thr Asp Ala Phe Val Val Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Ser Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Thr
    210                 215                 220
```

```
Val Glu Gln Lys Thr Arg Pro Phe Ser Val Pro Asn Ile Pro Leu Gln
225                 230                 235                 240

Leu Leu Ser Asn Ser Arg Val Pro Asn Leu Ile Gln Ser Met Val Leu
                245                 250                 255

Ser Pro Asp Gln Ala Gln Asn Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270

Thr Asp Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Val Ser Gln Ile
        275                 280                 285

Leu Lys Phe Arg Gly Lys Val Ser Ala Gly Ser Lys Val Ile Asn Leu
    290                 295                 300

Thr Glu Leu Asp Gly Ser Pro Phe Leu Ala Phe Glu Ala Pro Ala Pro
305                 310                 315                 320

Thr Gly Phe Pro Asp Leu Gly Thr Ser Asp Trp His Val Glu Met Ser
                325                 330                 335

Leu Asn Ser Asn Ser Gln Ser Ser Gly Asn Pro Ile Leu Leu Arg Asp
            340                 345                 350

Ile His Pro Asn Ser Ser Glu Phe Val Pro His Leu Gly Ser Val Cys
        355                 360                 365

Val Thr Ala Ala Ile Glu Val Ala Gly Asp Tyr Thr Gly Thr Ile Gln
    370                 375                 380

Trp Thr Ser Gln Pro Ser Asn Val Thr Pro Val Pro Asp Val Asn Phe
385                 390                 395                 400

Trp Thr Ile Pro His Tyr Gly Ser Asn Leu Ala Glu Ala Ser Gln Leu
                405                 410                 415

Ala Pro Val Val Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe
            420                 425                 430
```

```
Met Ser Pro Ile Pro Gly Pro Asn Thr Ala His Lys Pro Asn Leu Val
        435                 440                 445

Pro Cys Leu Leu Pro Gln Glu Phe Val Thr His Phe Val Ser Glu Gln
    450                 455                 460

Ala Pro Ser Met Gly Glu Ala Ala Leu Val His Tyr Val Asp Pro Asp
465                 470                 475                 480

Thr Asn Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Ile
                485                 490                 495

Thr Cys Val Pro Asn Gly Thr Gly Pro Gln Gln Leu Pro Leu Asn Gly
            500                 505                 510

Val Phe Val Phe Ala Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
        515                 520                 525

Val Gly Thr Ala Ser Ser Ala Arg Gly Arg Leu Gly Val Arg Arg
    530                 535                 540
```

<210> 13
<211> 535
<212> PRT
<213> Norovirus

<400> 13

```
Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                   10                  15

Gly Leu Val Pro Glu Val Asn Asn Glu Thr Met Ala Leu Glu Pro Val
            20                  25                  30

Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Val Ile
        35                  40                  45

Asp Pro Trp Ile Arg Met Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60
```

```
Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65                  70                  75                  80

Leu Gly Pro Glu Leu Asn Pro Phe Leu Ala His Leu Ser Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Ile Pro Pro His Phe
        115                 120                 125

Pro Leu Glu Asn Leu Ser Pro Gly Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Pro Glu Pro Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Gly
                245                 250                 255

Val Val Val Gln Pro Gln Asn Gly Arg Ser Thr Leu Asp Gly Glu Leu
            260                 265                 270
```

```
Leu Gly Thr Thr Gln Leu Val Pro Ser Asn Ile Cys Ala Leu Arg Gly
        275                 280                 285

Arg Ile Asn Ala Gln Val Pro Asp Asp His His Gln Trp Asn Leu Gln
    290                 295                 300

Val Thr Asn Ala Asn Gly Thr Ser Phe Asp Pro Thr Glu Asp Val Pro
305                 310                 315                 320

Ala Pro Leu Gly Thr Pro Asp Phe Leu Ala Asn Ile Tyr Gly Val Thr
                325                 330                 335

Ser Gln Arg Asn Pro Asp Asn Thr Cys Arg Ala His Asp Gly Val Leu
            340                 345                 350

Ala Thr Trp Ser Pro Lys Phe Thr Pro Lys Leu Gly Ser Val Val Leu
        355                 360                 365

Gly Thr Trp Glu Glu Ser Asp Leu Asp Leu Asn Gln Pro Thr Arg Phe
    370                 375                 380

Thr Pro Val Gly Leu Tyr Asp Thr Gly His Phe Asp Gln Trp Val Leu
385                 390                 395                 400

Pro Asn Tyr Ser Gly Arg Leu Thr Leu Asn Met Asn Leu Ala Pro Ser
                405                 410                 415

Val Ala Pro Leu Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser His
            420                 425                 430

Ile Pro Leu Lys Gly Gly Thr Ser Asn Gly Ala Ile Asp Cys Leu Leu
        435                 440                 445

Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala Pro Ser Pro
    450                 455                 460

Thr Asp Val Ala Leu Ile Arg Tyr Thr Asn Pro Asp Thr Gly Arg Val
465                 470                 475                 480
```

Leu Phe Glu Ala Lys Leu His Arg Gln Gly Phe Ile Thr Val Ala Asn
485 490 495

Ser Gly Ser Arg Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe
500 505 510

Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly
515 520 525

Asn Gly Arg Arg Arg Val Gln
530 535

<210> 14
<211> 542
<212> PRT
<213> Norovirus

<400> 14

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe

```
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300

Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320

Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
```

325 330 335

Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
340 345 350

Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
355 360 365

Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
370 375 380

Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385 390 395 400

His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
405 410 415

Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
420 425 430

Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
435 440 445

Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
450 455 460

Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465 470 475 480

Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
485 490 495

Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
500 505 510

Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
515 520 525

Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln

530 535 540

<210> 15
<211> 548
<212> PRT
<213> Norovirus

<400> 15

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ile Ser Ser Glu Ala Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65 70 75 80

Leu Gly Pro Glu Ile Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Val Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Ile Pro Pro Asn Phe
115 120 125

Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr Met Cys Pro His Val
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Asn Leu Pro Met Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Ser Asp Ser Arg Leu
165 170 175

```
Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Ser Phe Asn Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Ile Ser Glu Met Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Ser Leu His Thr Ser Pro Thr Glu Asn
                245                 250                 255

Ile Val Val Gln Cys Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu
            260                 265                 270

Met Gly Thr Thr Gln Leu Leu Pro Ser Gln Ile Cys Ala Phe Arg Gly
        275                 280                 285

Thr Leu Thr Arg Ser Thr Ser Arg Ala Ser Asp Gln Ala Asp Thr Ala
    290                 295                 300

Thr Pro Arg Leu Phe Asn Tyr Tyr Trp His Ile Gln Leu Asp Asn Leu
305                 310                 315                 320

Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp Ile Pro Ala Pro Leu Gly
                325                 330                 335

Thr Pro Asp Phe Arg Gly Lys Val Phe Gly Val Ala Ser Gln Arg Asn
            340                 345                 350

Pro Asp Ala Thr Thr Arg Ala His Glu Ala Lys Ile Asp Thr Thr Ser
        355                 360                 365

Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu Ile Ser Thr Glu Ser
    370                 375                 380
```

```
Gly Asp Phe Asp Gln Asn Gln Pro Thr Arg Phe Thr Pro Val Gly Ile
385                 390                 395                 400

Gly Val Asp His Glu Pro Asp Phe Gln Gln Trp Ala Leu Pro Asp Tyr
                405                 410                 415

Ala Gly Gln Phe Thr His Asn Met Asn Leu Ala Pro Ala Val Ala Pro
            420                 425                 430

Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Gln Leu Pro Ser
        435                 440                 445

Ser Gly Gly Arg Ser Asn Gly Ile Leu Asp Cys Leu Val Pro Gln Glu
    450                 455                 460

Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ser Gln Thr Gln Val
465                 470                 475                 480

Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu
                485                 490                 495

Ala Lys Leu His Lys Leu Arg Phe Met Thr Ile Ala Lys Ser Gly Asp
            500                 505                 510

Ser Pro Ile Thr Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ser Trp
        515                 520                 525

Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Asn Gly Arg
    530                 535                 540

Arg Arg Ile Gln
545
```

<210> 16
<211> 540
<212> PRT
<213> Norovirus

<400> 16

```
Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1               5                  10                  15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
        35                  40                  45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65                  70                  75                  80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205
```

```
Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415
```

```
His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430


Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445


Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460


Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480


Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495


Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510


Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525


Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540


<210>  17
<211>  540
<212>  PRT
<213>  Norovirus

<400>  17

Met Lys Met Ala Ser Asn Asp Ala Thr Pro Ser Asn Asp Gly Ala Ala
1               5                   10                  15


Gly Leu Val Pro Glu Ser Asn Asn Glu Ala Met Ala Leu Glu Pro Val
            20                  25                  30


Val Gly Ala Ser Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile
        35                  40                  45
```

```
Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Val Asn Leu Glu
65                  70                  75                  80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Tyr Phe
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Ser Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Met Pro Asp
145                 150                 155                 160

Val Arg Ser Thr Leu Phe His Phe Asn Gln Lys Asp Glu Pro Lys Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Ile Leu Thr Arg Pro Ser Pro
        195                 200                 205

Glu Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Val Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Leu Ser Ile Asp Glu Met Val Thr Ser Pro Asn Glu Ser
                245                 250                 255
```

```
Ile Val Val Gln Pro Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Gln Ala Cys Asn Ile Cys Ser Ile Arg Gly
        275                 280                 285

Lys Val Thr Gly Gln Val Pro Asn Glu Gln His Met Trp Asn Leu Glu
    290                 295                 300

Ile Thr Asn Leu Asn Gly Thr Gln Phe Asp Pro Thr Asp Asp Val Pro
305                 310                 315                 320

Ala Pro Leu Gly Val Pro Asp Phe Ala Gly Glu Val Phe Gly Val Leu
                325                 330                 335

Ser Gln Arg Asn Arg Gly Glu Ser Asn Pro Ala Asn Arg Ala His Asp
            340                 345                 350

Ala Val Val Ala Thr Tyr Ser Asp Lys Tyr Thr Pro Lys Leu Gly Leu
        355                 360                 365

Val Gln Ile Gly Thr Trp Asn Thr Asn Asp Val Glu Asn Gln Pro Thr
    370                 375                 380

Lys Phe Thr Pro Ile Gly Leu Asn Glu Val Ala Asn Gly His Arg Phe
385                 390                 395                 400

Glu Gln Trp Thr Leu Pro Arg Tyr Ser Gly Ala Leu Thr Leu Asn Met
                405                 410                 415

Asn Leu Ala Pro Ala Val Ala Pro Leu Phe Pro Gly Glu Arg Leu Leu
            420                 425                 430

Phe Phe Arg Ser Tyr Val Pro Leu Lys Gly Gly Phe Gly Asn Pro Ala
        435                 440                 445

Ile Asp Cys Leu Val Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu
    450                 455                 460
```

Ser Ala Pro Ser Leu Gly Asp Val Ala Leu Val Arg Tyr Val Asn Pro
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Ala Lys Leu His Lys Gly Gly Phe
485 490 495

Leu Thr Val Ser Ser Thr Ser Thr Gly Pro Val Val Val Pro Ala Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala
515 520 525

Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Phe Gln
530 535 540

<210> 18
<211> 540
<212> PRT
<213> Norovirus

<400> 18

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ile Asn Asn Glu Val Met Pro Leu Glu Pro Val
20 25 30

Ala Gly Ala Ser Leu Ala Thr Pro Val Val Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Ala Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asp Leu Glu
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
85 90 95

Asn Gly His Ala Gly Gly Met Glu Val Gln Ile Val Leu Ala Gly Asn

100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Ile Pro Pro Gly Phe
115 120 125

Pro Tyr Glu Asn Leu Ser Pro Ser Gln Ile Thr Met Cys Pro His Val
130 135 140

Ile Ile Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Met Pro Asp
145 150 155 160

Ile Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Asn Asp Pro Lys Leu
165 170 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Lys Pro Ser Pro
195 200 205

Asp Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr
210 215 220

Lys Gln Phe Thr Leu Pro Ile Leu Lys Ile Ser Glu Met Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Val Glu Met Met Tyr Thr Ala Arg Asn Glu Asn
245 250 255

Gln Val Val Gln Pro Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu
260 265 270

Leu Gly Thr Thr Pro Leu Leu Ala Val Asn Ile Cys Lys Phe Lys Gly
275 280 285

Glu Val Ile Ala Lys Asn Gly Asp Val Arg Ser Tyr Arg Met Asp Met
290 295 300

Glu Ile Thr Asn Thr Asp Gly Thr Pro Ile Asp Pro Thr Glu Asp Thr

```
305                 310                 315                 320

Pro Gly Pro Ile Gly Ser Pro Asp Phe Gln Gly Ile Leu Phe Gly Val
                325                 330                 335

Ala Ser Gln Arg Asn Lys Asn Glu Gln Asn Pro Ala Thr Arg Ala His
            340                 345                 350

Glu Ala Asn Ile Asn Thr Gly Gly Asp Gln Tyr Ala Pro Lys Leu Ala
        355                 360                 365

Gln Val Lys Phe Phe Ser Glu Ser Gln Asp Phe Glu Val His Gln Pro
    370                 375                 380

Thr Val Phe Thr Pro Val Gly Val Ala Gly Asp Thr Ser His Pro Phe
385                 390                 395                 400

Arg Gln Trp Val Leu Pro Arg Tyr Gly Gly His Leu Thr Asn Asn Thr
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Leu Phe Pro Gly Glu Gln Ile Leu
            420                 425                 430

Phe Phe Arg Ser Gln Ile Pro Ser Ser Gly Gly His Glu Leu Gly Tyr
        435                 440                 445

Met Asp Cys Leu Val Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Thr Ala Gln Ser Glu Val Ala Leu Ile Arg Phe Ile Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Ala Lys Leu His Lys Gln Gly Phe
                485                 490                 495

Ile Thr Val Ala His Thr Gly Asp Asn Pro Ile Val Met Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Glu Ala Trp Val Asn Gln Phe Tyr Ser Leu Ala
```

515 520 525

Pro Val Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
530 535 540

<210> 19
<211> 535
<212> PRT
<213> Norovirus

<400> 19

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Val Asn Asn Glu Thr Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Leu Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
115 120 125

Pro Leu Glu Asn Ile Ser Pro Gly Gln Ile Thr Met Phe Pro His Val
130 135 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145 150 155 160

```
Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Asn Glu Pro Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Ser
                245                 250                 255

Leu Val Val Gln Pro Gln Asn Gly Arg Cys Ala Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Leu Pro Thr Ala Ile Cys Ser Phe Arg Gly
        275                 280                 285

Arg Ile Asn Gln Lys Val Ser Gly Glu Asn His Val Trp Asn Met Gln
    290                 295                 300

Val Thr Asn Ile Asp Gly Thr Pro Phe Asp Pro Thr Glu Asp Val Pro
305                 310                 315                 320

Ala Pro Leu Gly Thr Pro Asp Phe Ser Gly Lys Leu Phe Gly Val Leu
                325                 330                 335

Ser Gln Arg Asp His Asp Asn Ala Cys Arg Ser His Asp Ala Val Ile
            340                 345                 350

Ala Thr Asn Ser Ala Lys Phe Thr Pro Lys Leu Gly Ala Ile Gln Ile
        355                 360                 365
```

```
Gly Thr Trp Glu Gln Asp Asp Val His Ile Asn Gln Pro Thr Lys Phe
    370                 375                 380

Thr Pro Val Gly Leu Phe Glu Ser Glu Gly Phe Asn Gln Trp Thr Leu
385                 390                 395                 400

Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Met Gly Leu Ala Pro Pro
                405                 410                 415

Val Ala Pro Thr Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser His
            420                 425                 430

Ile Pro Leu Lys Gly Gly Val Ala Asp Pro Val Ile Asp Cys Leu Leu
        435                 440                 445

Pro Gln Glu Trp Ile Gln His Leu Tyr Gln Glu Ser Ala Pro Ser Gln
    450                 455                 460

Thr Asp Val Ala Leu Ile Arg Phe Thr Asn Pro Asp Thr Gly Arg Val
465                 470                 475                 480

Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr Val Ala Asn
                485                 490                 495

Thr Gly Ser Arg Pro Ile Val Val Pro Ala Asn Gly Tyr Phe Arg Phe
            500                 505                 510

Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly
        515                 520                 525

Asn Gly Arg Arg Arg Val Gln
    530                 535
```

<210> 20
<211> 547
<212> PRT
<213> Norovirus

<400> 20

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                  10                  15

Asn Leu Val Pro Glu Ala Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30

Val Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile
        35                  40                  45

Asp Pro Trp Ile Arg Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Met Leu Leu Asn Leu Glu
65                  70                  75                  80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ser His Leu Ser Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Met Gln Val Gln Val Val Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Ile Asn Ala Ala Gln Ile Thr Met Cys Pro His Val
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Ile Arg Asn Arg Phe Phe His Tyr Asn Gln Glu Asn Thr Ser Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Ser Gly Glu
            180                 185                 190

Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ala Pro Asp
        195                 200                 205
```

```
Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr Lys
    210                 215                 220

Pro Phe Ser Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser Arg
225                 230                 235                 240

Phe Pro Ala Pro Ile Asp Met Leu Tyr Thr Asp Pro Asn Glu Gly Ile
                245                 250                 255

Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Thr Leu Gln
            260                 265                 270

Gly Thr Thr Gln Leu Val Pro Thr Gln Ile Cys Ala Phe Arg Gly Thr
        275                 280                 285

Leu Ile Gly Gln Thr Ser Arg Ser Pro Asp Ser Thr Asp Ser Ala Pro
    290                 295                 300

Arg Arg Arg Asp His Pro Leu His Val Gln Leu Lys Asn Leu Asp Gly
305                 310                 315                 320

Thr Gln Tyr Asp Pro Thr Asp Glu Val Pro Ala Val Leu Gly Ala Ile
                325                 330                 335

Asp Phe Lys Gly Thr Val Phe Gly Val Ala Ser Gln Arg Asp Val Ser
            340                 345                 350

Gly Gln Gln Val Gly Ala Thr Arg Ala His Glu Val His Ile Asn Thr
        355                 360                 365

Thr Asp Pro Arg Tyr Thr Pro Lys Leu Gly Ser Ile Leu Met Tyr Ser
    370                 375                 380

Glu Ser Asp Asp Phe Val Thr Gly Gln Pro Val Arg Phe Thr Pro Ile
385                 390                 395                 400

Gly Met Gly Asp Asn Asp Trp His Gln Trp Glu Leu Pro Asp Tyr Pro
                405                 410                 415
```

Gly His Leu Thr Leu Asn Met Asn Leu Ala Pro Ala Val Ala Pro Ala
420 425 430

Phe Pro Gly Glu Arg Ile Leu Phe Phe Arg Ser Ile Val Pro Ser Ala
435 440 445

Gly Gly Tyr Gly Ser Gly Gln Ile Asp Cys Leu Ile Pro Gln Glu Trp
450 455 460

Val Gln His Phe Tyr Gln Glu Ala Ala Pro Ser Gln Ser Ala Val Ala
465 470 475 480

Leu Ile Arg Tyr Val Asn Pro Asp Thr Gly Arg Asn Ile Phe Glu Ala
485 490 495

Lys Leu His Arg Glu Gly Phe Ile Thr Val Ala Asn Ser Gly Asn Asn
500 505 510

Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ala Trp Val
515 520 525

Asn Gln Phe Tyr Thr Leu Thr Pro Met Gly Thr Gly Gln Gly Arg Arg
530 535 540

Arg Asp Gln
545

<210> 21
<211> 1644
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1 GII.6 Ohio 2012 M9T020

<400> 21
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gaagctaata atgaggtgat ggcgttagag ccggtggttg gcgcatctat tgcagcgcct 120

gtggtcggac agcagaacat cattgatccc tggattcgcg agaacttcgt acaagctcca 180

caggggagt tcacagtctc cccccggaac tccccgggcg agatgctgct caatctggaa 240

ctcggccctg aactaaaccc ttatctgtca cacctttcac ggatgtacaa tggctacgca 300

ggaggaatgc aagttcaggt ggtcctggcc ggcaatgctt tcaccgcggg caaaatcatc 360

tttgcggccg ttcctccaca cttccctgtc gaaaatatca acgccgccca gattactatg 420

tgcccccacg tgattgtgga tgtgcgacag ttagagccag ttctgctgcc cctgcccgac 480

atcagaaacc ggttcttcca ttacaatcaa gagaatactt cacggatgag acttgttgcg 540

atgctgtaca cccctcttcg tgcaaattcc ggcgaagacg tgttcactgt gtcttgtcga 600

gtacttaccc gacccgcccc cgatttcgaa ttcaccttcc tggttccccc tactgtggag 660

agcaagacaa aacccttcag cctcccaatc ttaacactcg gggagctgtc taattcacgc 720

ttccccgcac ctattgatat gctgtatact gaccccaacg aggggatagt ggtgcagccc 780

caaaatggac ggtgtactct cgacggcacg ctccagggca caacccaact ggtgccaacc 840

cagatttgtg cattcagggg cactttgatt gggcagacat cgagatctcc agattctact 900

gattccgcgc caaggaggag ggaccaccca ctccacgttc agttaaaaaa cctggacgga 960

acccagtacg accctacaga cgaggtcccc gctgtcctcg gagccatcga ctttaaagga 1020

actgtatttg gagtggcatc ccaaagggat gtctcggggc agcaggtggg agctacgaga 1080

gcacatgaag tccacattaa caccacagac ccaagatata ccccaaaact agggtcaatt 1140

ttaatgtatt cggaatcaga cgattttgtt acaggtcagc ccgtgcggtt taccccgatc 1200

ggaatggggg acaacgattg gcaccagtgg gaattgcccg attaccctgg acacctcacc 1260

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tttagaagca tagtgccctc cgcaggtggg tatggatcag ggcagattga ttgcctgatc 1380

ccccaagaat gggtacagca tttctaccag gaagcagccc ctagccagtc cgcagtagca 1440

ctgatcagat atgttaatcc tgatacggga aggaacatct tcgaagcaaa actgcaccgt 1500

gagggcttca ttaccgtcgc caacagtggt aataacccta ttgtggtgcc tcctaatgga 1560

tacttcaggt ttgaggcatg ggtgaatcag ttttatactc tgactcccat ggggacaggc 1620

caggggcgac gccgggatca gtga 1644

<210> 22
<211> 542
<212> PRT
<213> Norovirus

<400> 22

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                  10                  15

Ser Leu Val Pro Glu Ala Ile Asn Glu Thr Met Pro Leu Glu Pro Val
            20                  25                  30

Ala Gly Ala Ser Ile Ala Ala Pro Val Ala Gly Gln Thr Asn Ile Ile
        35                  40                  45

Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu
65                  70                  75                  80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Ile Pro Pro Asn Phe
        115                 120                 125

Pro Val Asp Met Ile Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
    130                 135                 140

Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Val Phe Tyr His Phe Asn Asn Gln Pro Gln Pro Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
```

180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
195 200 205

Asp Phe Glu Phe Ile Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Ser Glu Leu Thr Asn Ser
225 230 235 240

Arg Phe Pro Ile Ser Ile Glu Gln Leu Tyr Thr Ala Pro Asn Glu Asn
245 250 255

Asn Val Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
260 265 270

Gln Gly Thr Thr Gln Leu Leu Ser Ser Ala Val Cys Ser Tyr Arg Gly
275 280 285

Arg Thr Val Ala Asn Ser Gly Asp Asn Trp Asp Gln Asn Val Leu Gln
290 295 300

Leu Thr Tyr Pro Ser Gly Ala Ser Tyr Asp Pro Thr Asp Glu Val Pro
305 310 315 320

Ala Pro Leu Gly Thr Gln Asp Phe Ser Gly Ile Leu Tyr Gly Val Leu
325 330 335

Thr Gln Asp Asn Val Arg Glu Asn Thr Gly Glu Ala Lys Asn Ala Lys
340 345 350

Gly Val Tyr Ile Ser Thr Thr Ser Gly Lys Phe Thr Pro Lys Ile Gly
355 360 365

Ser Ile Gly Leu His Ser Ile Thr Glu Asp Val Arg Pro Asn Gln Gln
370 375 380

Ser Arg Phe Thr Pro Val Gly Val Ala Gln Asn Glu Asn Thr Pro Phe

385 390 395 400

Gln Gln Trp Val Leu Pro His Tyr Ala Gly Ala Leu Ala Leu Asn Thr
405 410 415

Asn Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
420 425 430

Phe Phe Arg Ser Arg Val Pro Cys Val Gln Gly Leu Gln Gly Gln Asp
435 440 445

Ala Phe Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Asn His Phe Tyr
450 455 460

Gln Glu Ala Ala Pro Ser Gln Ala Asp Val Ala Leu Ile Arg Tyr Val
465 470 475 480

Asn Pro Asp Thr Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser
485 490 495

Gly Phe Ile Thr Val Ser His Thr Gly Ala Tyr Pro Leu Val Val Pro
500 505 510

Pro Asn Gly His Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
515 520 525

Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Val Gln
530 535 540

<210> 23
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1
GII.17_Kawa_2014_A0A077KVU6

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gttgctggac agacgaatat catcgatcct tggatacgga ctaattttgt tcaagctcct 180

aacggagagt tcactgtctc cccccgtaat agtcctggcg agatcctgtt gaacctcgag 240

ttggggccag atctcaatcc ttacctggct catctgtcga gaatgtacaa cgggtacgcg 300

gggggggttg aggtgcaggt cttactggca ggtaacgcat tcacagcagg caagattctg 360

tttgcggcca tccctcctaa ttttccagtg gatatgatat ctccagcaca gattacaatg 420

ctgccccatt tgatagtgga tgtgcggaca cttgaaccta tcatgatccc tttgcccgat 480

gtccgaaatg tgttttatca tttcaacaac cagccgcagc caagaatgcg tctcgtcgcg 540

atgctgtaca ccccgttgcg gtccaacggc tctggcgatg atgttttcac agtgtcgtgt 600

cgagtgttaa cccgccctac cccagatttt gagtttatat atctagttcc cccttctgtg 660

gaaagcaaga ctaaaccctt tactcttccc attctgacta tatccgagct taccaactcc 720

cggttcccca tctcaatcga gcaactgtac actgcaccca acgagaacaa cgtagtccag 780

tgccagaacg ggagatgtac cctggacggg gagctccaag ggaccacgca actgttaagt 840

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aatgtgttgc agctgactta cccatccggc gcaagctacg atccaacaga tgaggtgcca 960

gcgccccttg gcacacagga tttctcagga attctatacg gggtgcttac tcaggataat 1020

gtgcgagaaa atactggcga ggccaagaat gctaaaggag tgtatataag cacgacaagc 1080

ggtaagttta cccccaaaat tggcagtatt gggctccaca gcattactga ggacgtccgc 1140

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cagcagtggg tcttgcccca ttatgcaggt gctttggcgc tcaatacaaa tctggcaccc 1260

gccgtagcgc cgacatttcc tggggagcaa ttgctgttct ttagaagccg cgtcccgtgt 1320

gttcagggct tgcagggcca ggacgcgttc attgattgcc tcttgcccca ggaatgggtc 1380

aaccactttt atcaggaggc agcgccctct caagcagatg tggccctgat aagatatgtg 1440

aatcccgaca caggacggac tttgtttgag gcaaaactcc accggtcagg attcattact 1500

gtgagtcaca caggagccta tccccttgtg gttccaccta atggccactt caggttcgac 1560

tcttgggtca atcagtttta ttcgctggca ccaatgggta ccgggaatgg tcgccgtcgg 1620

gtgcaatga 1629

<210> 24
<211> 538
<212> PRT
<213> Norovirus

<400> 24

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                   10                  15


Gly Leu Val Pro Glu Gly Asn Asn Glu Thr Leu Pro Leu Glu Pro Val
            20                  25                  30


Ala Gly Ala Ala Ile Ala Ala Pro Val Thr Gly Gln Asn Asn Ile Ile
        35                  40                  45


Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu
65                  70                  75                  80


Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125


Pro Val Glu Phe Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
    130                 135                 140


Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Thr Phe Phe His Tyr Asn Asn Gln Pro Asn Ser Arg Met
                165                 170                 175
```

```
Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
        195                 200                 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Leu Ser Glu Leu Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Ser Leu Phe Thr Ala Gln Asn Asn Val
                245                 250                 255

Leu Gln Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Leu Pro Ser Gly Ile Cys Ala Phe Arg Gly
        275                 280                 285

Arg Val Thr Ala Glu Thr Asp His Arg Asp Lys Trp His Met Gln Leu
    290                 295                 300

Gln Asn Leu Asn Gly Thr Thr Tyr Asp Pro Thr Asp Asp Val Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Lys Gly Val Val Phe Gly Val Ala Ser
                325                 330                 335

Gln Arg Asn Val Gly Asn Asp Ala Pro Gly Ser Thr Arg Ala His Glu
            340                 345                 350

Ala Val Ile Ser Thr Tyr Ser Pro Gln Phe Val Pro Lys Leu Gly Ser
        355                 360                 365

Val Asn Phe Arg Ser Asn Asp Asn Asp Phe Gln Leu Gln Pro Thr Lys
    370                 375                 380
```

```
Phe Thr Pro Val Gly Ile Asn Asp Asp Gly Asp His Pro Phe Arg Gln
385                 390                 395                 400


Trp Glu Leu Pro Asp Tyr Ser Gly Leu Leu Thr Leu Asn Met Asn Leu
                405                 410                 415


Ala Pro Pro Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe
            420                 425                 430


Arg Ser Phe Val Pro Cys Ser Gly Gly Tyr Asn Gln Gly Ile Val Asp
        435                 440                 445


Cys Leu Ile Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala
    450                 455                 460


Pro Ser Gln Ser Asp Val Ala Leu Ile Arg Tyr Val Asn Pro Asp Thr
465                 470                 475                 480


Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr
                485                 490                 495


Val Ala His Ser Gly Asp Tyr Pro Leu Val Val Pro Ala Asn Gly Tyr
            500                 505                 510


Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met
        515                 520                 525


Gly Thr Gly Asn Gly Arg Arg Arg Ala Gln
    530                 535


<210>  25
<211>  1617
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon-optimized VP1
       GII.17_Kawa_2014_A0A077KVU6

<400>  25
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gtgacagggc agaataatat tatagaccct tggattcgga caaacttcgt gcaggcaccc 180

aacggcgagt ttacagtatc cccccggaac tccccaggtg agatactcct gaatcttgag 240

ctcggccctg acctcaatcc atatctggct catctgagcc gcatgtacaa tggttacgct 300

gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360

tttgccgccg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420

ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480

gtgcgtaaca ccttttcca ttataacaat cagccaaact ctcggatgag acttgttgct 540

atgctgtaca ccccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600

agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660

gaatctaaga ccaaaccgtt ttcactgcca atcttaactc tctccgaact gactaacagc 720

cggtttccag tacccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780

tgccagaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840

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cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960

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caatttgtgc ccaagctcgg atccgttaat tttcgtagta acgacaacga cttccaactg 1140

caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc tttccgccaa 1200

tgggaactac cagattattc tgggctgctc accctcaata tgaacctcgc cccacccgtg 1260

gcccctaatt tccccggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320

ggatataatc aaggcatcgt agactgcttg attccccaag agtggataca acatttttac 1380

caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440

ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500

ggcgattatc ccctggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560

cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

<210> 26
<211> 539
<212> PRT
<213> Norovirus

<400> 26

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Thr
1               5                   10                  15


Gly Leu Val Pro Glu Ile Asn Thr Glu Thr Leu Pro Leu Glu Pro Val
            20                  25                  30


Ala Gly Ala Ala Ile Ala Ala Pro Val Thr Gly Gln Asn Asn Ile Ile
        35                  40                  45


Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Met Asn Leu Glu
65                  70                  75                  80


Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125


Pro Val Asp Met Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
    130                 135                 140


Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Val Phe Tyr His Phe Asn Asn Gln Pro Ala Pro Arg Met
                165                 170                 175
```

```
Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
        195                 200                 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ala Pro Ile Asp Gln Leu Tyr Thr Ser Pro Asn Ala Asp
                245                 250                 255

Val Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Leu Thr Thr Ala Ile Cys Ser Tyr Arg Gly
        275                 280                 285

Met Thr Ser Asn Pro Thr Ser Asp Tyr Trp Asp Asp His Leu Leu His
    290                 295                 300

Leu Val His Pro Asn Gly Ala Thr Tyr Asp Pro Thr Glu Asp Val Pro
305                 310                 315                 320

Ala Pro Phe Gly Thr Gln Asp Phe Arg Gly Ile Leu Tyr Gly Met Leu
                325                 330                 335

Thr Gln Asn Pro Arg Thr Ser Gly Asp Glu Ala Ala Asn Ser His Gly
            340                 345                 350

Ile Tyr Ile Ser Ser Thr Ser Glu Lys Phe Thr Pro Lys Leu Gly Thr
        355                 360                 365

Ile Gly Leu His Gln Val Gln Gly Asp Ile Ala Ser Asn Gln Gln Ser
    370                 375                 380
```

```
Lys Phe Thr Pro Val Gly Ile Ala Val Asn Gly Asn Thr Pro Phe Arg
385                 390                 395                 400


Gln Trp Glu Leu Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Thr Asn
                405                 410                 415


Leu Ala Pro Ala Val Gly Pro Asn Phe Pro Gly Glu Gln Ile Leu Phe
            420                 425                 430


Phe Arg Ser Asn Val Pro Ser Val Gln Gly Gly Gln Pro Ile Glu Ile
        435                 440                 445


Asp Cys Leu Ile Pro Gln Glu Trp Val Ser His Phe Tyr Gln Glu Ser
    450                 455                 460


Ala Pro Ser Gln Ser Asp Val Ala Leu Val Arg Tyr Val Asn Pro Asp
465                 470                 475                 480


Thr Gly Arg Thr Ile Phe Glu Ala Lys Leu His Arg Gln Gly Phe Ile
                485                 490                 495


Thr Ile Ala Ala Thr Gly Ser Asn Pro Val Val Val Pro Pro Asn Gly
            500                 505                 510


Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ala Leu Ala Pro
        515                 520                 525


Met Gly Thr Gly Asn Gly Arg Arg Arg Val Gln
    530                 535


<210>  27
<211>  539
<212>  PRT
<213>  Norovirus

<400>  27

Met Lys Met Ala Ser Asn Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala
1               5                   10                  15
```

```
Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
        35                  40                  45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65                  70                  75                  80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Ser Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Lys Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220
```

```
Lys Pro Phe Thr Val Pro Ile Leu Thr Val Glu Glu Met Ser Asn Ser
225                 230                 235                 240


Arg Phe Pro Ile Pro Leu Glu Lys Leu Tyr Thr Gly Pro Ser Ser Ala
                245                 250                 255


Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270


Leu Gly Thr Thr Gln Leu Ser Ala Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285


Asp Val Thr His Ile Ala Gly Ser His Asp Tyr Thr Met Asn Leu Ala
    290                 295                 300


Ser Gln Asn Trp Asn Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320


Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Met Leu Thr Gln
                325                 330                 335


Thr Thr Arg Glu Asp Gly Ser Thr Arg Ala His Lys Ala Thr Val Ser
            340                 345                 350


Thr Gly Ser Val His Phe Thr Pro Lys Leu Gly Ser Val Gln Tyr Thr
        355                 360                 365


Thr Asp Thr Asn Asn Asp Phe Gln Thr Gly Gln Asn Thr Lys Phe Thr
    370                 375                 380


Pro Val Gly Val Ile Gln Asp Gly Asn Asn His Gln Asn Glu Pro Gln
385                 390                 395                 400


Gln Trp Val Leu Pro Asn Tyr Ser Gly Arg Thr Gly His Asn Val His
                405                 410                 415


Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu Phe
            420                 425                 430
```

Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asn Leu
435 440 445

Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu Ala
450 455 460

Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro Asp
465 470 475 480

Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr Val
485 490 495

Thr Val Ala His Thr Gly Pro His Asp Leu Val Ile Pro Pro Asn Gly
500 505 510

Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala Pro
515 520 525

Met Gly Asn Gly Ala Gly Arg Arg Arg Ala Leu
530 535

<210> 28
<211> 540
<212> PRT
<213> Norovirus

<400> 28

Met Lys Met Ala Ser Asn Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro

65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Leu Asn Asp Pro Thr Ile
165 170 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
180 185 190

Glu Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
195 200 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
210 215 220

Lys Pro Phe Thr Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser
225 230 235 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Gly Ala
245 250 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
260 265 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly

```
        275                 280                 285

Asp Val Thr His Ile Ala Gly Thr His Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Arg Ile Gln Gly Met Leu Thr Gln
                325                 330                 335

Thr Thr Arg Gly Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Ser
            340                 345                 350

Thr Gly Asp Val His Phe Thr Pro Lys Leu Gly Ser Ile Gln Phe Asn
        355                 360                 365

Thr Asp Thr Asn Asn Asp Phe Glu Thr Gly Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Val Gln Asp Gly Asn Gly Thr His Gln Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Thr Gly His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asn
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
```

485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Leu
530 535 540

<210> 29
<211> 540
<212> PRT
<213> Norovirus

<400> 29

Met Lys Met Ala Ser Asn Asp Ala Thr Pro Ser Asp Gly Ser Thr Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

```
Pro Thr Glu Val Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Leu Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Ala Gly Thr Gln Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asn Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Arg Ile Gln Gly Val Leu Thr Gln
                325                 330                 335
```

```
Thr Thr Arg Arg Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Ser
            340                 345                 350

Thr Gly Ser Val His Phe Thr Pro Lys Leu Gly Ser Val Gln Phe Ser
        355                 360                 365

Thr Asp Thr Ser Asn Asp Phe Glu Thr Gly Gln Asn Thr Arg Phe Thr
    370                 375                 380

Pro Val Gly Val Val Gln Asp Gly Ser Thr Thr His Gln Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Asp Tyr Ser Gly Arg Asp Ser His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asn
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu
    450                 455                 460

Ser Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Ala Gly Arg Arg Arg Ala Leu
    530                 535                 540
```

<210> 30
<211> 540
<212> PRT
<213> Norovirus

<400> 30

Met Lys Met Ala Ser Asn Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Ser Thr Ile
165 170 175

```
Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Glu Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Thr Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Gly Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Ala Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Leu Lys Trp Asn Lys Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Lys Gly Asp Gly Ser Thr Arg Gly His Lys Ala Thr Ile Tyr
            340                 345                 350

Thr Gly Ser Ala Pro Phe Thr Pro Lys Leu Gly Ser Val Gln Phe Ser
        355                 360                 365

Thr Asp Thr Glu Asn Asp Phe Glu Thr His Gln Asn Thr Lys Phe Thr
    370                 375                 380
```

```
Pro Val Gly Val Thr Gln Asp Gly Ser Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400


Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Val His Asn Val
                405                 410                 415


His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430


Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445


Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr Gln Glu
    450                 455                 460


Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480


Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495


Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510


Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525


Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Leu
    530                 535                 540


<210>  31
<211>  540
<212>  PRT
<213>  Norovirus

<400>  31

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Thr Ala
1               5                   10                  15
```

```
Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
        35                  40                  45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65                  70                  75                  80

Leu Gly Pro Asp Met Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220
```

```
Lys Pro Phe Ser Val Pro Ile Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240


Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255


Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270


Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285


Asp Val Thr His Ile Ala Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300


Ser Gln Asn Trp Asn Ser Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320


Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335


Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350


Thr Gly Ser Ala Asp Phe Ser Pro Lys Leu Gly Arg Val Gln Phe Ala
        355                 360                 365


Thr Asp Thr Asp Asn Asp Phe Asp Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380


Pro Val Gly Val Ile Gln Asp Gly Asn Thr Ala His Arg Asn Glu Pro
385                 390                 395                 400


Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415


His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430
```

```
Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Leu
    530                 535                 540
```

<210> 32
<211> 536
<212> PRT
<213> Norovirus

<400> 32

```
Met Lys Met Ala Ser Asn Asp Ala Thr Pro Ser Asp Asp Gly Ala Ala
1               5                   10                  15

Gly Leu Val Pro Glu Ile Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30

Ala Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile
        35                  40                  45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Ala Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Leu Leu Leu Asp Leu Glu
```

65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
85 90 95

Asn Gly His Ala Gly Gly Met Glu Val Gln Ile Val Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Ile Pro Pro Ser Phe
115 120 125

Pro Tyr Glu Asn Leu Ser Pro Ala Gln Leu Thr Met Cys Pro His Val
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Met Pro Asp
145 150 155 160

Ile Arg Asn Val Phe Tyr His Tyr Asn Gln Asn Asn Ser Pro Lys Leu
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
195 200 205

Asp Phe Gln Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr
210 215 220

Lys Asn Phe Thr Leu Pro Val Leu Arg Val Ser Glu Met Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Val Leu Asp Gln Met Tyr Thr Ser Arg Asn Glu Asn
245 250 255

Ile Ile Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Glu Leu
260 265 270

Leu Gly Thr Thr Ile Leu Gln Ser Val Ser Ile Cys Asn Phe Lys Gly

```
        275                 280                 285

Thr Met Gln Ala Lys Leu Asn Glu Glu Pro Arg Tyr Gln Leu Gln Leu
    290                 295                 300

Thr Asn Leu Asp Gly Ser Pro Ile Asp Pro Thr Asp Asp Met Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Gln Ala Met Leu Tyr Gly Val Ala Ser
                325                 330                 335

Gln Arg Ser Ser Ile Asp Asn Ala Thr Arg Ala His Asp Ala Gln Ile
            340                 345                 350

Asp Thr Ala Gly Asp Thr Phe Ala Pro Lys Ile Gly Gln Val Arg Phe
        355                 360                 365

Lys Ser Ser Ser Asn Asp Phe Asp Leu His Asp Pro Thr Lys Phe Thr
    370                 375                 380

Pro Ile Gly Val Asn Val Asp Asp Gln His Pro Phe Arg Gln Trp Ser
385                 390                 395                 400

Leu Pro Asn Tyr Gly Gly His Leu Ala Leu Asn Asn His Leu Ala Pro
                405                 410                 415

Ala Val Thr Pro Leu Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser
            420                 425                 430

Tyr Ile Pro Ser Ala Gly Gly His Thr Asp Gly Ala Met Asp Cys Leu
        435                 440                 445

Leu Pro Gln Glu Trp Val Glu His Phe Tyr Gln Glu Ala Ala Pro Ser
    450                 455                 460

Gln Ser Asp Ile Ala Leu Val Arg Phe Ile Asn Pro Asp Thr Gly Arg
465                 470                 475                 480

Val Leu Phe Glu Ala Lys Leu His Lys Gln Gly Phe Leu Thr Ile Ala
```

485 490 495

Ala Ser Gly Asp His Pro Ile Val Met Pro Thr Asn Gly Tyr Phe Arg
500 505 510

Phe Glu Ala Trp Val Asn Pro Phe Tyr Thr Leu Ala Pro Val Gly Thr
515 520 525

Gly Ser Gly Arg Arg Arg Ile Gln
530 535

<210> 33
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1 GI.5 Siklos HUN5407 2013 HUN AHW99832

<400> 33
atgatgatgg cctccaaaga cgctcctagc agtgctgatg gcgctaacgg tgccggccag 60

ctggtccccg aggtgaataa cgccgagcct ctccccttgg acccagtagc cggagcttca 120

acggccctag ctactgccgg acaggttaat atgattgacc cctggatttt caataatttc 180

gtgcaggccc ctcaaggcga gtttactata agccctaaca acacaccagg ggatattctg 240

ttcgacctgc agttaggccc tcatctcaac cccttcttgg cccacctgag ccagatgtac 300

aatggctggg tgggcaacat gcgagtgaga gttatcctcg cagggaacgc ctttaccgct 360

ggtaaggtga tcatttgttg cgtaccacct ggattccagt ctaggacatt aagtattgcg 420

caagctaccc tctttcctca tatcatcgcc gacgtgcgga cactagagcc catcgagatc 480

ccactggagg atgtccggaa taccctgtac cataccaacg ataatcagcc cactatgagg 540

ttactgtgca tgctgtacac gccactccgg actggtgggg gcagtggggg gaccgatgct 600

ttcgtcgttg ccggtagggt gctcacttgc ccgtcatctg actttaactt cctattcctt 660

gtgcccccaa cggtggaaca gaaaacgaga ccttttttccg tacctaacat ccctttacag 720

ctcctaagca atagcagagt acctaacctg atccaatcca tggttcttag ccctgatcaa 780

gcgcagaacg tacagtttca gaacgggcgg tgcaccacag atggccagct gcttggtaca 840

actcccgtct ccgtgtctca gatacttaag tttcgcggca aggtctccgc tggatccaaa 900

gtaatcaacc tcactgagct tgatggctct ccctttctgg cgttcgaggc gcccgcccca 960

acaggctttc cagacctggg aacatccgat tggcatgtcg agatgagtct gaatagcaac 1020

tcccagtctt ctggcaatcc aatactgctc cgcgatatcc atcctaattc tagcgagttc 1080

gttccacacc tgggttctgt gtgcgtgacg gctgcaatag aggtggctgg cgactacacg 1140

ggtaccattc agtggacctc tcagccaagt aacgtgaccc ctgtgccaga cgttaacttt 1200

tggacaattc cacactacgg ctctaacttg gccgaagcat cccagcttgc ccccgttgta 1260

tatcccccag gctttggcga agcaatagtt tattttatgt ccccaatccc tggacctaac 1320

acagcacaca agccaaacct cgtcccatgc ctgctgcccc aggagttcgt gactcatttc 1380

gtttcggaac aagccccatc aatgggggag gccgccctgg tccactacgt ggatccagat 1440

accaatcgga atctgggaga attcaaactc taccctgaag gattcattac atgtgtgccc 1500

aatggaacag gaccgcagca gctcccactg aacggtgtct ttgtattcgc atcatgggtt 1560

agccggttct atcaacttaa acccgtgggg acagcttcat ctgcccgggg gcgccttggc 1620

gtgcggcgct ga 1632

<210> 34
<211> 543
<212> PRT
<213> Norovirus

<400> 34

Met Met Met Ala Ser Lys Asp Ala Pro Ser Ser Ala Asp Gly Ala Asn
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Asn Ala Glu Pro Leu Pro
20 25 30

Leu Asp Pro Val Ala Gly Ala Ser Thr Ala Leu Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Phe Asn Asn Phe Val Gln Ala Pro
50 55 60

```
Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Ala His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Ile
            100                 105                 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Val Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Gln Ser Arg Thr Leu Ser Ile Ala Gln Ala Thr Leu
    130                 135                 140

Phe Pro His Ile Ile Ala Asp Val Arg Thr Leu Glu Pro Ile Glu Ile
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Thr Leu Tyr His Thr Asn Asp Asn Gln
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Thr Gly
            180                 185                 190

Gly Gly Ser Gly Gly Thr Asp Ala Phe Val Val Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Ser Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Thr
    210                 215                 220

Val Glu Gln Lys Thr Arg Pro Phe Ser Val Pro Asn Ile Pro Leu Gln
225                 230                 235                 240

Leu Leu Ser Asn Ser Arg Val Pro Asn Leu Ile Gln Ser Met Val Leu
                245                 250                 255

Ser Pro Asp Gln Ala Gln Asn Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270
```

```
Thr Asp Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Val Ser Gln Ile
        275                 280                 285

Leu Lys Phe Arg Gly Lys Val Ser Ala Gly Ser Lys Val Ile Asn Leu
    290                 295                 300

Thr Glu Leu Asp Gly Ser Pro Phe Leu Ala Phe Glu Ala Pro Ala Pro
305                 310                 315                 320

Thr Gly Phe Pro Asp Leu Gly Thr Ser Asp Trp His Val Glu Met Ser
                325                 330                 335

Leu Asn Ser Asn Ser Gln Ser Ser Gly Asn Pro Ile Leu Leu Arg Asp
            340                 345                 350

Ile His Pro Asn Ser Ser Glu Phe Val Pro His Leu Gly Ser Val Cys
        355                 360                 365

Val Thr Ala Ala Ile Glu Val Ala Gly Asp Tyr Thr Gly Thr Ile Gln
    370                 375                 380

Trp Thr Ser Gln Pro Ser Asn Val Thr Pro Val Pro Asp Val Asn Phe
385                 390                 395                 400

Trp Thr Ile Pro His Tyr Gly Ser Asn Leu Ala Glu Ala Ser Gln Leu
                405                 410                 415

Ala Pro Val Val Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe
            420                 425                 430

Met Ser Pro Ile Pro Gly Pro Asn Thr Ala His Lys Pro Asn Leu Val
        435                 440                 445

Pro Cys Leu Leu Pro Gln Glu Phe Val Thr His Phe Val Ser Glu Gln
    450                 455                 460

Ala Pro Ser Met Gly Glu Ala Ala Leu Val His Tyr Val Asp Pro Asp
465                 470                 475                 480
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Thr Asn Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Ile
485 490 495

Thr Cys Val Pro Asn Gly Thr Gly Pro Gln Gln Leu Pro Leu Asn Gly
500 505 510

Val Phe Val Phe Ala Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Ala Ser Ser Ala Arg Gly Arg Leu Gly Val Arg Arg
530 535 540

<210> 35
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1 GI.5 Siklos Q84S

<400> 35
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acggccctag ctactgccgg acaggttaat atgattgacc cctggatttt caataatttc 180

gtgcaggccc ctcaaggcga gtttactata agccctaaca acacaccagg ggatattctg 240

ttcgacctga gcttaggccc tcatctcaac cccttcttgg cccacctgag ccagatgtac 300

aatggctggg tgggcaacat gcgagtgaga gttatcctcg cagggaacgc ctttaccgct 360

ggtaaggtga tcatttgttg cgtaccacct ggattccagt ctaggacatt aagtattgcg 420

caagctaccc tctttcctca tatcatcgcc gacgtgcgga cactagagcc catcgagatc 480

ccactggagg atgtccggaa taccctgtac cataccaacg ataatcagcc cactatgagg 540

ttactgtgca tgctgtacac gccactccgg actggtgggg gcagtggggg gaccgatgct 600

ttcgtcgttg ccggtagggt gctcacttgc ccgtcatctg actttaactt cctattcctt 660

gtgcccccaa cggtggaaca gaaaacgaga cctttttccg tacctaacat ccctttacag 720

ctcctaagca atagcagagt acctaacctg atccaatcca tggttcttag ccctgatcaa 780

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gtaatcaacc tcactgagct tgatggctct ccctttctgg cgttcgaggc gcccgcccca 960

acaggctttc cagacctggg aacatccgat tggcatgtcg agatgagtct gaatagcaac 1020

tcccagtctt ctggcaatcc aatactgctc cgcgatatcc atcctaattc tagcgagttc 1080

gttccacacc tgggttctgt gtgcgtgacg gctgcaatag aggtggctgg cgactacacg 1140

ggtaccattc agtggacctc tcagccaagt aacgtgaccc ctgtgccaga cgttaacttt 1200

tggacaattc cacactacgg ctctaacttg gccgaagcat cccagcttgc ccccgttgta 1260

tatcccccag gctttggcga agcaatagtt tattttatgt ccccaatccc tggacctaac 1320

acagcacaca agccaaacct cgtcccatgc ctgctgcccc aggagttcgt gactcatttc 1380

gtttcggaac aagccccatc aatgggggag gccgccctgg tccactacgt ggatccagat 1440

accaatcgga atctgggaga attcaaactc taccctgaag gattcattac atgtgtgccc 1500

aatggaacag gaccgcagca gctcccactg aacggtgtct ttgtattcgc atcatgggtt 1560

agccggttct atcaacttaa acccgtgggg acagcttcat ctgcccgggg gcgccttggc 1620

gtgcggcgct ga 1632

<210> 36
<211> 543
<212> PRT
<213> Norovirus

<400> 36

Met Met Met Ala Ser Lys Asp Ala Pro Ser Ser Ala Asp Gly Ala Asn
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Asn Ala Glu Pro Leu Pro
20 25 30

Leu Asp Pro Val Ala Gly Ala Ser Thr Ala Leu Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Phe Asn Asn Phe Val Gln Ala Pro

50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
85 90 95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Ile
100 105 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Val Ile Ile Cys Cys Val
115 120 125

Pro Pro Gly Phe Gln Ser Arg Thr Leu Ser Ile Ala Gln Ala Thr Leu
130 135 140

Phe Pro His Ile Ile Ala Asp Val Arg Thr Leu Glu Pro Ile Glu Ile
145 150 155 160

Pro Leu Glu Asp Val Arg Asn Thr Leu Tyr His Thr Asn Asp Asn Gln
165 170 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Thr Gly
180 185 190

Gly Gly Ser Gly Gly Thr Asp Ala Phe Val Val Ala Gly Arg Val Leu
195 200 205

Thr Cys Pro Ser Ser Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Thr
210 215 220

Val Glu Gln Lys Thr Arg Pro Phe Ser Val Pro Asn Ile Pro Leu Gln
225 230 235 240

Leu Leu Ser Asn Ser Arg Val Pro Asn Leu Ile Gln Ser Met Val Leu
245 250 255

Ser Pro Asp Gln Ala Gln Asn Val Gln Phe Gln Asn Gly Arg Cys Thr

260 265 270

Thr Asp Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Val Ser Gln Ile
275 280 285

Leu Lys Phe Arg Gly Lys Val Ser Ala Gly Ser Lys Val Ile Asn Leu
290 295 300

Thr Glu Leu Asp Gly Ser Pro Phe Leu Ala Phe Glu Ala Pro Ala Pro
305 310 315 320

Thr Gly Phe Pro Asp Leu Gly Thr Ser Asp Trp His Val Glu Met Ser
325 330 335

Leu Asn Ser Asn Ser Gln Ser Ser Gly Asn Pro Ile Leu Leu Arg Asp
340 345 350

Ile His Pro Asn Ser Ser Glu Phe Val Pro His Leu Gly Ser Val Cys
355 360 365

Val Thr Ala Ala Ile Glu Val Ala Gly Asp Tyr Thr Gly Thr Ile Gln
370 375 380

Trp Thr Ser Gln Pro Ser Asn Val Thr Pro Val Pro Asp Val Asn Phe
385 390 395 400

Trp Thr Ile Pro His Tyr Gly Ser Asn Leu Ala Glu Ala Ser Gln Leu
405 410 415

Ala Pro Val Val Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe
420 425 430

Met Ser Pro Ile Pro Gly Pro Asn Thr Ala His Lys Pro Asn Leu Val
435 440 445

Pro Cys Leu Leu Pro Gln Glu Phe Val Thr His Phe Val Ser Glu Gln
450 455 460

Ala Pro Ser Met Gly Glu Ala Ala Leu Val His Tyr Val Asp Pro Asp

465 470 475 480

Thr Asn Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Ile
485 490 495

Thr Cys Val Pro Asn Gly Thr Gly Pro Gln Gln Leu Pro Leu Asn Gly
500 505 510

Val Phe Val Phe Ala Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Ala Ser Ser Ala Arg Gly Arg Leu Gly Val Arg Arg
530 535 540

<210> 37
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1 GI.5 siklos A94L

<400> 37
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acggccctag ctactgccgg acaggttaat atgattgacc cctggatttt caataatttc 180

gtgcaggccc ctcaaggcga gtttactata agccctaaca acacaccagg ggatattctg 240

ttcgacctgc agttaggccc tcatctcaac cccttcttgc tccacctgag ccagatgtac 300

aatggctggg tgggcaacat gcgagtgaga gttatcctcg cagggaacgc ctttaccgct 360

ggtaaggtga tcatttgttg cgtaccacct ggattccagt ctaggacatt aagtattgcg 420

caagctaccc tctttcctca tatcatcgcc gacgtgcgga cactagagcc catcgagatc 480

ccactggagg atgtccggaa taccctgtac cataccaacg ataatcagcc cactatgagg 540

ttactgtgca tgctgtacac gccactccgg actggtgggg gcagtggggg gaccgatgct 600

ttcgtcgttg ccggtagggt gctcacttgc ccgtcatctg actttaactt cctattcctt 660

gtgcccccaa cggtggaaca gaaaacgaga ccttttccg tacctaacat ccctttacag 720

ctcctaagca atagcagagt acctaacctg atccaatcca tggttcttag ccctgatcaa 780

gcgcagaacg tacagtttca gaacgggcgg tgcaccacag atggccagct gcttggtaca 840

actcccgtct ccgtgtctca gatacttaag tttcgcggca aggtctccgc tggatccaaa 900

gtaatcaacc tcactgagct tgatggctct ccctttctgg cgttcgaggc gcccgcccca 960

acaggctttc cagacctggg aacatccgat tggcatgtcg agatgagtct gaatagcaac 1020

tcccagtctt ctggcaatcc aatactgctc cgcgatatcc atcctaattc tagcgagttc 1080

gttccacacc tgggttctgt gtgcgtgacg gctgcaatag aggtggctgg cgactacacg 1140

ggtaccattc agtggacctc tcagccaagt aacgtgaccc ctgtgccaga cgttaacttt 1200

tggacaattc cacactacgg ctctaacttg gccgaagcat cccagcttgc ccccgttgta 1260

tatcccccag gctttggcga agcaatagtt tattttatgt ccccaatccc tggacctaac 1320

acagcacaca agccaaacct cgtcccatgc ctgctgcccc aggagttcgt gactcatttc 1380

gtttcggaac aagccccatc aatgggggag gccgccctgg tccactacgt ggatccagat 1440

accaatcgga atctgggaga attcaaactc taccctgaag gattcattac atgtgtgccc 1500

aatggaacag gaccgcagca gctcccactg aacggtgtct ttgtattcgc atcatgggtt 1560

agccggttct atcaacttaa acccgtgggg acagcttcat ctgcccgggg gcgccttggc 1620

gtgcggcgct ga 1632

<210> 38
<211> 543
<212> PRT
<213> Norovirus

<400> 38

Met Met Met Ala Ser Lys Asp Ala Pro Ser Ser Ala Asp Gly Ala Asn
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Asn Ala Glu Pro Leu Pro
20 25 30

Leu Asp Pro Val Ala Gly Ala Ser Thr Ala Leu Ala Thr Ala Gly Gln
35 40 45

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Val Asn Met Ile Asp Pro Trp Ile Phe Asn Asn Phe Val Gln Ala Pro
    50                  55                  60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Ile
            100                 105                 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Val Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Gln Ser Arg Thr Leu Ser Ile Ala Gln Ala Thr Leu
    130                 135                 140

Phe Pro His Ile Ile Ala Asp Val Arg Thr Leu Glu Pro Ile Glu Ile
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Thr Leu Tyr His Thr Asn Asp Asn Gln
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Thr Gly
            180                 185                 190

Gly Gly Ser Gly Gly Thr Asp Ala Phe Val Val Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Ser Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Thr
    210                 215                 220

Val Glu Gln Lys Thr Arg Pro Phe Ser Val Pro Asn Ile Pro Leu Gln
225                 230                 235                 240

Leu Leu Ser Asn Ser Arg Val Pro Asn Leu Ile Gln Ser Met Val Leu
                245                 250                 255
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Ser Pro Asp Gln Ala Gln Asn Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270

Thr Asp Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Val Ser Gln Ile
        275                 280                 285

Leu Lys Phe Arg Gly Lys Val Ser Ala Gly Ser Lys Val Ile Asn Leu
    290                 295                 300

Thr Glu Leu Asp Gly Ser Pro Phe Leu Ala Phe Glu Ala Pro Ala Pro
305                 310                 315                 320

Thr Gly Phe Pro Asp Leu Gly Thr Ser Asp Trp His Val Glu Met Ser
                325                 330                 335

Leu Asn Ser Asn Ser Gln Ser Ser Gly Asn Pro Ile Leu Leu Arg Asp
            340                 345                 350

Ile His Pro Asn Ser Ser Glu Phe Val Pro His Leu Gly Ser Val Cys
        355                 360                 365

Val Thr Ala Ala Ile Glu Val Ala Gly Asp Tyr Thr Gly Thr Ile Gln
    370                 375                 380

Trp Thr Ser Gln Pro Ser Asn Val Thr Pro Val Pro Asp Val Asn Phe
385                 390                 395                 400

Trp Thr Ile Pro His Tyr Gly Ser Asn Leu Ala Glu Ala Ser Gln Leu
                405                 410                 415

Ala Pro Val Val Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe
            420                 425                 430

Met Ser Pro Ile Pro Gly Pro Asn Thr Ala His Lys Pro Asn Leu Val
        435                 440                 445

Pro Cys Leu Leu Pro Gln Glu Phe Val Thr His Phe Val Ser Glu Gln
    450                 455                 460
```

```
Ala Pro Ser Met Gly Glu Ala Ala Leu Val His Tyr Val Asp Pro Asp
465                 470                 475                 480


Thr Asn Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Ile
                485                 490                 495


Thr Cys Val Pro Asn Gly Thr Gly Pro Gln Gln Leu Pro Leu Asn Gly
            500                 505                 510


Val Phe Val Phe Ala Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
        515                 520                 525


Val Gly Thr Ala Ser Ser Ala Arg Gly Arg Leu Gly Val Arg Arg
    530                 535                 540


<210>  39
<211>  1632
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized VP1 GI.5 siklos
       Q84S plus sign A94L

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ctggtccccg aggtgaataa cgccgagcct ctccccttgg acccagtagc cggagcttca      120

acggccctag ctactgccgg acaggttaat atgattgacc cctggatttt caataatttc      180

gtgcaggccc ctcaaggcga gtttactata agccctaaca acacaccagg ggatattctg      240

ttcgacctga gcttaggccc tcatctcaac cccttcttgc tccacctgag ccagatgtac      300

aatggctggg tgggcaacat gcgagtgaga gttatcctcg cagggaacgc ctttaccgct      360

ggtaaggtga tcatttgttg cgtaccacct ggattccagt ctaggacatt aagtattgcg      420

caagctaccc tctttcctca tatcatcgcc gacgtgcgga cactagagcc catcgagatc      480

ccactggagg atgtccggaa taccctgtac cataccaacg ataatcagcc cactatgagg      540

ttactgtgca tgctgtacac gccactccgg actggtgggg gcagtggggg gaccgatgct      600

ttcgtcgttg ccggtagggt gctcacttgc ccgtcatctg actttaactt cctattcctt      660
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ctcctaagca atagcagagt acctaacctg atccaatcca tggttcttag ccctgatcaa 780

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acaggctttc cagacctggg aacatccgat tggcatgtcg agatgagtct gaatagcaac 1020

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gttccacacc tgggttctgt gtgcgtgacg gctgcaatag aggtggctgg cgactacacg 1140

ggtaccattc agtggacctc tcagccaagt aacgtgaccc ctgtgccaga cgttaacttt 1200

tggacaattc cacactacgg ctctaacttg gccgaagcat cccagcttgc ccccgttgta 1260

tatcccccag gctttggcga agcaatagtt tattttatgt ccccaatccc tggacctaac 1320

acagcacaca agccaaacct cgtcccatgc ctgctgcccc aggagttcgt gactcatttc 1380

gtttcggaac aagccccatc aatgggggag gccgccctgg tccactacgt ggatccagat 1440

accaatcgga atctgggaga attcaaactc taccctgaag gattcattac atgtgtgccc 1500

aatggaacag gaccgcagca gctcccactg aacggtgtct ttgtattcgc atcatgggtt 1560

agccggttct atcaacttaa acccgtgggg acagcttcat ctgcccgggg gcgccttggc 1620

gtgcggcgct ga 1632

<210> 40
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1 GII.2 CGMH47 2011 TW AGT39206

<400> 40
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gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcgag 240

ctgggaccag aacttaatcc gtacctggct cacctggccc ggatgtacaa tggatatgca 300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480

gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcat ttctgtgcag 780

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tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

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cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

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cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

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gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

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atccagtaa 1629

<210> 41

<211> 542
<212> PRT
<213> Norovirus

<400> 41

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1               5                  10                  15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30

Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile
        35                  40                  45

Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65                  70                  75                  80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190
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Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300

Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320

Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
                325                 330                 335

Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
            340                 345                 350

Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
        355                 360                 365

Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
    370                 375                 380

Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385                 390                 395                 400
```

His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
405 410 415

Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
420 425 430

Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
435 440 445

Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
450 455 460

Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465 470 475 480

Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
485 490 495

Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
500 505 510

Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
515 520 525

Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
530 535 540

<210> 42
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1 GII.2 CGMH47 A90L

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gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcgag 240

ctgggaccag aacttaatcc gtacctgctc cacctggccc ggatgtacaa tggatatgca 300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480

gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcat ttctgtgcag 780

tgtcagaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840

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tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

aagcataaca cacccggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080

acctatacgg ctcagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140

gatgacctca ctgtgaatca acctgtgaaa ttcactccag taggtctgaa tgatacagac 1200

cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

gcccttccg ttgcacctgt gtttccgggg gagcggttgc tcttctttag aagctatatt 1320

cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

aatccagaca caggaagagc actgttcgag gccaagctgc acagagccgg cttcatgacc 1500

gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

agttgggtga atcagtttta ctcgttggcc cccatgggca cagggaacgg tcgccgacgg 1620

atccagtaa 1629

<210> 43
<211> 542
<212> PRT
<213> Norovirus

<400> 43

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1               5                  10                  15


Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30


Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile
        35                  40                  45


Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65                  70                  75                  80


Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125


Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140


Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175
```

```
Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190


Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205


Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220


Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240


Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255


Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270


Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285


Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300


Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320


Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
                325                 330                 335


Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
            340                 345                 350


Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
        355                 360                 365


Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
    370                 375                 380
```

```
Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385                 390                 395                 400


His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
                405                 410                 415


Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
            420                 425                 430


Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
        435                 440                 445


Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
    450                 455                 460


Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465                 470                 475                 480


Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
                485                 490                 495


Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
            500                 505                 510


Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
        515                 520                 525


Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
    530                 535                 540


<210>  44
<211>  1629
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized VP1 GII.2 CGMH47
       E80S plus sign A90L

<400>  44
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gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcagc 240

ctgggaccag aacttaatcc gtacctgctc cacctggccc ggatgtacaa tggatatgca 300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480

gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

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tgtcagaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840

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tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

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acctatacgg ctcagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140

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cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

gcccttccg ttgcacctgt gtttccgggg gagcggttgc tcttctttag aagctatatt 1320

cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

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gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

agttgggtga atcagtttta ctcgttggcc cccatgggca cagggaacgg tcgccgacgg 1620

atccagtaa 1629

<210> 45
<211> 1647
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1
GII.3_Jingzhou_2013402_CHN AGX01095

<400> 45
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gagattagct ctgaggctat ggccctagaa ccagtagccg gggcagccat agctgcccca 120

ctgactggcc agcagaatat cattgacccc tggataatga acaatttcgt gcaggcaccg 180

gggggagaat tcacggtctc tcctcgaaac tcccccgggg aggttctctt gaatttggaa 240

ctgggccctg aaattaatcc ttatctggcc catctagccc gaatgtacaa cggctacgcc 300

ggaggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360

tttgcagcaa tccctccaaa cttccctatc gataatctta gtgccgccca gatcacaatg 420

tgccctcacg ttatcgtaga tgtgaggcag ctggaacctg tcaatctccc aatgcccgac 480

gtgcgcaaca acttctttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540

atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600

cgagtcctga cacgtccatc tcctgacttt agctttaatt tcctcgtgcc ccccacagtg 660

gaatccaaaa ctaagccatt ctctctgcca attcttacca ttagcgaaat gtcgaatagt 720

aggttcccgg tgcccataga ttcactgcat accagtccaa cagaaaacat cgtcgtacag 780

tgtcagaacg gacgcgtgac tctcgacggg gagcttatgg gcactaccca gctgctgccc 840

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gcagatacag ctacaccaag gctgttcaat tattattggc atatacaact cgataatctg 960

aatggcactc cttatgaccc agccgaggac atccccgccc cacttggcac cccggacttt 1020

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ggggttgacc acgaaccgga tttccagcag tgggctctgc ctgattacgc aggccagttc 1260

acacataaca tgaatcttgc ccccgctgtg gcccccaact tcccgggaga acaacttctg 1320

tttttcagga gccaactgcc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380

gtgccccagg aatgggtgca gcatttttac caggagtccg cgccctccca gacgcaggtg 1440

gctctggtta gatatgtcaa tcccgacacc ggcagggtgc tatttgaggc aaagctgcac 1500

aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gccccccaac 1560

ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620

ggcaatggca gacggcggat ccagtaa 1647

<210> 46
<211> 548
<212> PRT
<213> Norovirus

<400> 46

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ile Ser Ser Glu Ala Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65 70 75 80

Leu Gly Pro Glu Ile Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Val Leu Ala Gly Asn
100 105 110

```
Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Ile Pro Pro Asn Phe
        115                 120                 125

Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr Met Cys Pro His Val
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Asn Leu Pro Met Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Ser Asp Ser Arg Leu
                165                 170                 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Ser Phe Asn Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Ile Ser Glu Met Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Ser Leu His Thr Ser Pro Thr Glu Asn
                245                 250                 255

Ile Val Val Gln Cys Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu
            260                 265                 270

Met Gly Thr Thr Gln Leu Leu Pro Ser Gln Ile Cys Ala Phe Arg Gly
        275                 280                 285

Thr Leu Thr Arg Ser Thr Ser Arg Ala Ser Asp Gln Ala Asp Thr Ala
    290                 295                 300

Thr Pro Arg Leu Phe Asn Tyr Tyr Trp His Ile Gln Leu Asp Asn Leu
305                 310                 315                 320
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Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp Ile Pro Ala Pro Leu Gly
                325                 330                 335

Thr Pro Asp Phe Arg Gly Lys Val Phe Gly Val Ala Ser Gln Arg Asn
            340                 345                 350

Pro Asp Ala Thr Thr Arg Ala His Glu Ala Lys Ile Asp Thr Thr Ser
        355                 360                 365

Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu Ile Ser Thr Glu Ser
    370                 375                 380

Gly Asp Phe Asp Gln Asn Gln Pro Thr Arg Phe Thr Pro Val Gly Ile
385                 390                 395                 400

Gly Val Asp His Glu Pro Asp Phe Gln Gln Trp Ala Leu Pro Asp Tyr
                405                 410                 415

Ala Gly Gln Phe Thr His Asn Met Asn Leu Ala Pro Ala Val Ala Pro
            420                 425                 430

Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Gln Leu Pro Ser
        435                 440                 445

Ser Gly Gly Arg Ser Asn Gly Ile Leu Asp Cys Leu Val Pro Gln Glu
    450                 455                 460

Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ser Gln Thr Gln Val
465                 470                 475                 480

Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu
                485                 490                 495

Ala Lys Leu His Lys Leu Arg Phe Met Thr Ile Ala Lys Ser Gly Asp
            500                 505                 510

Ser Pro Ile Thr Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ser Trp
        515                 520                 525
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Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Asn Gly Arg
530 535 540

Arg Arg Ile Gln
545

<210> 47
<211> 1647
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.3_Jing_E80S

<400> 47
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gagattagct ctgaggctat ggccctagaa ccagtagccg gggcagccat agctgcccca 120

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gggggagaat tcacggtctc tcctcgaaac tcccccgggg aggttctctt gaatttgagc 240

ctgggccctg aaattaatcc ttatctggcc catctagccc gaatgtacaa cggctacgcc 300

ggaggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360

tttgcagcaa tccctccaaa cttccctatc gataatctta gtgccgccca gatcacaatg 420

tgccctcacg ttatcgtaga tgtgaggcag ctggaacctg tcaatctccc aatgcccgac 480

gtgcgcaaca acttctttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540

atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600

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gaatccaaaa ctaagccatt ctctctgcca attcttacca ttagcgaaat gtcgaatagt 720

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ggggttgacc acgaaccgga tttccagcag tgggctctgc ctgattacgc aggccagttc 1260

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tttttcagga gccaactgcc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380

gtgccccagg aatgggtgca gcatttttac caggagtccg cgccctccca gacgcaggtg 1440

gctctggtta gatatgtcaa tcccgacacc ggcagggtgc tatttgaggc aaagctgcac 1500

aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gccccccaac 1560

ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620

ggcaatggca gacggcggat ccagtaa 1647

<210> 48
<211> 548
<212> PRT
<213> Norovirus

<400> 48

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ile Ser Ser Glu Ala Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65 70 75 80

Leu Gly Pro Glu Ile Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr

85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Val Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Ile Pro Pro Asn Phe
115 120 125

Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr Met Cys Pro His Val
130 135 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Asn Leu Pro Met Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Ser Asp Ser Arg Leu
165 170 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
195 200 205

Asp Phe Ser Phe Asn Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Ile Ser Glu Met Ser Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu His Thr Ser Pro Thr Glu Asn
245 250 255

Ile Val Val Gln Cys Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu
260 265 270

Met Gly Thr Thr Gln Leu Leu Pro Ser Gln Ile Cys Ala Phe Arg Gly
275 280 285

Thr Leu Thr Arg Ser Thr Ser Arg Ala Ser Asp Gln Ala Asp Thr Ala

290 295 300

Thr Pro Arg Leu Phe Asn Tyr Tyr Trp His Ile Gln Leu Asp Asn Leu
305 310 315 320

Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp Ile Pro Ala Pro Leu Gly
325 330 335

Thr Pro Asp Phe Arg Gly Lys Val Phe Gly Val Ala Ser Gln Arg Asn
340 345 350

Pro Asp Ala Thr Thr Arg Ala His Glu Ala Lys Ile Asp Thr Thr Ser
355 360 365

Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu Ile Ser Thr Glu Ser
370 375 380

Gly Asp Phe Asp Gln Asn Gln Pro Thr Arg Phe Thr Pro Val Gly Ile
385 390 395 400

Gly Val Asp His Glu Pro Asp Phe Gln Gln Trp Ala Leu Pro Asp Tyr
405 410 415

Ala Gly Gln Phe Thr His Asn Met Asn Leu Ala Pro Ala Val Ala Pro
420 425 430

Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Gln Leu Pro Ser
435 440 445

Ser Gly Gly Arg Ser Asn Gly Ile Leu Asp Cys Leu Val Pro Gln Glu
450 455 460

Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ser Gln Thr Gln Val
465 470 475 480

Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu
485 490 495

Ala Lys Leu His Lys Leu Arg Phe Met Thr Ile Ala Lys Ser Gly Asp

500 505 510

Ser Pro Ile Thr Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ser Trp
515 520 525

Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Asn Gly Arg
530 535 540

Arg Arg Ile Gln
545

<210> 49
<211> 1647
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.3_Jing_A90L

<400> 49
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gagattagct ctgaggctat ggccctagaa ccagtagccg gggcagccat agctgcccca 120

ctgactggcc agcagaatat cattgacccc tggataatga acaatttcgt gcaggcaccg 180

gggggagaat tcacggtctc tcctcgaaac tcccccgggg aggttctctt gaatttggaa 240

ctgggccctg aaattaatcc ttatctgctc catctagccc gaatgtacaa cggctacgcc 300

ggaggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360

tttgcagcaa tccctccaaa cttccctatc gataatctta gtgccgccca gatcacaatg 420

tgccctcacg ttatcgtaga tgtgaggcag ctggaacctg tcaatctccc aatgcccgac 480

gtgcgcaaca acttctttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540

atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600

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tttttcagga gccaactgcc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380

gtgccccagg aatgggtgca gcatttttac caggagtccg cgccctccca gacgcaggtg 1440

gctctggtta gatatgtcaa tcccgacacc ggcagggtgc tatttgaggc aaagctgcac 1500

aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gccccccaac 1560

ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620

ggcaatggca gacggcggat ccagtaa 1647

<210> 50
<211> 548
<212> PRT
<213> Norovirus

<400> 50

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ile Ser Ser Glu Ala Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Leu Thr Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

```
Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65                  70                  75                  80

Leu Gly Pro Glu Ile Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Val Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Ile Pro Pro Asn Phe
        115                 120                 125

Pro Ile Asp Asn Leu Ser Ala Ala Gln Ile Thr Met Cys Pro His Val
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Asn Leu Pro Met Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gly Ser Asp Ser Arg Leu
                165                 170                 175

Arg Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Ser Phe Asn Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Ile Ser Glu Met Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Ser Leu His Thr Ser Pro Thr Glu Asn
                245                 250                 255

Ile Val Val Gln Cys Gln Asn Gly Arg Val Thr Leu Asp Gly Glu Leu
            260                 265                 270
```

```
Met Gly Thr Thr Gln Leu Leu Pro Ser Gln Ile Cys Ala Phe Arg Gly
        275                 280                 285

Thr Leu Thr Arg Ser Thr Ser Arg Ala Ser Asp Gln Ala Asp Thr Ala
    290                 295                 300

Thr Pro Arg Leu Phe Asn Tyr Tyr Trp His Ile Gln Leu Asp Asn Leu
305                 310                 315                 320

Asn Gly Thr Pro Tyr Asp Pro Ala Glu Asp Ile Pro Ala Pro Leu Gly
                325                 330                 335

Thr Pro Asp Phe Arg Gly Lys Val Phe Gly Val Ala Ser Gln Arg Asn
            340                 345                 350

Pro Asp Ala Thr Thr Arg Ala His Glu Ala Lys Ile Asp Thr Thr Ser
        355                 360                 365

Gly Arg Phe Thr Pro Lys Leu Gly Ser Leu Glu Ile Ser Thr Glu Ser
    370                 375                 380

Gly Asp Phe Asp Gln Asn Gln Pro Thr Arg Phe Thr Pro Val Gly Ile
385                 390                 395                 400

Gly Val Asp His Glu Pro Asp Phe Gln Gln Trp Ala Leu Pro Asp Tyr
                405                 410                 415

Ala Gly Gln Phe Thr His Asn Met Asn Leu Ala Pro Ala Val Ala Pro
            420                 425                 430

Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Gln Leu Pro Ser
        435                 440                 445

Ser Gly Gly Arg Ser Asn Gly Ile Leu Asp Cys Leu Val Pro Gln Glu
    450                 455                 460

Trp Val Gln His Phe Tyr Gln Glu Ser Ala Pro Ser Gln Thr Gln Val
465                 470                 475                 480
```

Ala Leu Val Arg Tyr Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu
485 490 495

Ala Lys Leu His Lys Leu Arg Phe Met Thr Ile Ala Lys Ser Gly Asp
500 505 510

Ser Pro Ile Thr Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ser Trp
515 520 525

Val Asn Pro Phe Tyr Thr Leu Ala Pro Met Gly Thr Gly Asn Gly Arg
530 535 540

Arg Arg Ile Gln
545

<210> 51
<211> 1647
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.3_Jing_E80S+A90L

<400> 51
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gagattagct ctgaggctat ggccctagaa ccagtagccg gggcagccat agctgcccca 120

ctgactggcc agcagaatat cattgacccc tggataatga acaatttcgt gcaggcaccg 180

gggggagaat tcacggtctc tcctcgaaac tcccccgggg aggttctctt gaatttgagc 240

ctgggccctg aaattaatcc ttatctgctc catctagccc gaatgtacaa cggctacgcc 300

ggaggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360

tttgcagcaa tccctccaaa cttccctatc gataatctta gtgccgccca gatcacaatg 420

tgccctcacg ttatcgtaga tgtgaggcag ctggaacctg tcaatctccc aatgcccgac 480

gtgcgcaaca acttctttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540

atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600

cgagtcctga cacgtccatc tcctgacttt agctttaatt tcctcgtgcc ccccacagtg 660

gaatccaaaa ctaagccatt ctctctgcca attcttacca ttagcgaaat gtcgaatagt 720

aggttcccgg tgcccataga ttcactgcat accagtccaa cagaaaacat cgtcgtacag 780

tgtcagaacg gacgcgtgac tctcgacggg gagcttatgg gcactaccca gctgctgccc 840

agccagatat gcgccttccg cggcacactg actagaagca cttcgcgtgc ttctgaccag 900

gcagatacag ctacaccaag gctgttcaat tattattggc atatacaact cgataatctg 960

aatggcactc cttatgaccc agccgaggac atccccgccc cacttggcac cccggacttt 1020

agagggaagg tctttggagt ggcttctcaa agaaatcccg acgcaaccac ccgggcccac 1080

gaggccaaaa tcgatactac atcagggcgt ttcaccccta agttaggcag tctggagata 1140

tctaccgaaa gtggagattt cgatcagaac cagccaaccc ggtttacccc cgtgggaatc 1200

ggggttgacc acgaaccgga tttccagcag tgggctctgc ctgattacgc aggccagttc 1260

acacataaca tgaatcttgc ccccgctgtg gcccccaact tcccgggaga acaacttctg 1320

tttttcagga gccaactgcc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380

gtgccccagg aatgggtgca gcatttttac caggagtccg cgccctccca gacgcaggtg 1440

gctctggtta gatatgtcaa tcccgacacc ggcagggtgc tatttgaggc aaagctgcac 1500

aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gccccccaac 1560

ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620

ggcaatggca gacggcggat ccagtaa 1647

<210> 52
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1
GII.4_Sydney_2012_K4LM89

<400> 52
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 53

<211> 540
<212> PRT
<213> Norovirus

<400> 53

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Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1               5                  10                  15


Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30


Val Gly Ala Ala Ile Ala Val Pro Val Ala Gly Gln Gln Asn Val Ile
        35                  40                  45


Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65                  70                  75                  80


Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125


Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140


Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175


Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190
```

```
Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400
```

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
405 410 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
420 425 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
435 440 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
450 455 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 54
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_A39V

<400> 54
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagtcccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 55
<211> 540
<212> PRT
<213> Norovirus

<400> 55

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Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1               5                  10                  15


Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
            20                  25                  30


Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Pro Ile
        35                  40                  45


Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65                  70                  75                  80


Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125


Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140


Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175
```

```
Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380
```

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385 390 395 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
405 410 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
420 425 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
435 440 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
450 455 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 56
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_V47P

<400> 56
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gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatcc cattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

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catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 57
<211> 540
<212> PRT
<213> Norovirus

<400> 57

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
165 170 175

```
Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380
```

```
Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
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<210> 58
<211> 1623
<212> DNA
<213> Artificial Sequqence

<220>
<223> Nucleic acid sequence of human codon optimized
       VP1_GII.4_Syd12_R53I

<400> 58

atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggataatca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 59
<211> 540
<212> PRT
<213> Norovirus

<400> 59

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

```
Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365
```

```
Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
```

<210> 60
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S

<400> 60
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 61
<211> 540
<212> PRT
<213> Norovirus

<400> 61

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

```
Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365
```

```
Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
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<210> 62
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>

<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_S90L

<400> 62

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gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgctg catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

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gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 63
<211> 532
<212> PRT
<213> Norovirus

<400> 63

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Gly Gln Gln Asn Val Ile Asp Pro Trp Ile Arg Asn Asn Phe
35 40 45

Val Gln Ala Pro Gly Gly Glu Phe Thr Val Ser Pro Arg Asn Ala Pro
50 55 60

Gly Glu Ile Leu Trp Ser Ala Pro Leu Gly Pro Asp Leu Asn Pro Tyr
65 70 75 80

Leu Ser His Leu Ala Arg Met Tyr Asn Gly Tyr Ala Gly Gly Phe Glu
85 90 95

Val Gln Val Ile Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Val Ile
100 105 110

Phe Ala Ala Val Pro Pro Asn Phe Pro Thr Glu Gly Leu Ser Pro Ser
115 120 125

Gln Val Thr Met Phe Pro His Ile Val Val Asp Val Arg Gln Leu Glu
130 135 140

```
Pro Val Leu Ile Pro Leu Pro Asp Val Arg Asn Asn Phe Tyr His Tyr
145                 150                 155                 160


Asn Gln Ser Asn Asp Pro Thr Ile Lys Leu Ile Ala Met Leu Tyr Thr
                165                 170                 175


Pro Leu Arg Ala Asn Asn Ala Gly Asp Asp Val Phe Thr Val Ser Cys
            180                 185                 190


Arg Val Leu Thr Arg Pro Ser Pro Asp Phe Asp Phe Ile Phe Leu Val
        195                 200                 205


Pro Pro Thr Val Glu Ser Arg Thr Lys Pro Phe Ser Val Pro Val Leu
    210                 215                 220


Thr Val Glu Glu Met Thr Asn Ser Arg Phe Pro Ile Pro Leu Glu Lys
225                 230                 235                 240


Leu Phe Thr Gly Pro Ser Ser Ala Phe Val Val Gln Pro Gln Asn Gly
                245                 250                 255


Arg Cys Thr Thr Asp Gly Val Leu Leu Gly Thr Thr Gln Leu Ser Pro
            260                 265                 270


Val Asn Ile Cys Thr Phe Arg Gly Asp Val Thr His Ile Thr Gly Ser
        275                 280                 285


Arg Asn Tyr Thr Met Asn Leu Ala Ser Gln Asn Trp Asn Asp Tyr Asp
    290                 295                 300


Pro Thr Glu Glu Ile Pro Ala Pro Leu Gly Thr Pro Asp Phe Val Gly
305                 310                 315                 320


Lys Ile Gln Gly Val Leu Thr Gln Thr Thr Arg Thr Asp Gly Ser Thr
                325                 330                 335


Arg Gly His Lys Ala Thr Val Tyr Thr Gly Ser Ala Asp Phe Ala Pro
            340                 345                 350
```

```
Lys Leu Gly Arg Val Gln Phe Glu Thr Asp Thr Asp Arg Asp Phe Glu
        355                 360                 365

Ala Asn Gln Asn Thr Lys Phe Thr Pro Val Gly Val Ile Gln Asp Gly
    370                 375                 380

Gly Thr Thr His Arg Asn Glu Pro Gln Gln Trp Val Leu Pro Ser Tyr
385                 390                 395                 400

Ser Gly Arg Asn Thr His Asn Val His Leu Ala Pro Ala Val Ala Pro
                405                 410                 415

Thr Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Thr Met Pro Gly
            420                 425                 430

Cys Ser Gly Tyr Pro Asn Met Asp Leu Asp Cys Leu Leu Pro Gln Glu
        435                 440                 445

Trp Val Gln Tyr Phe Tyr Gln Glu Ala Ala Pro Ala Gln Ser Asp Val
    450                 455                 460

Ala Leu Leu Arg Phe Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu
465                 470                 475                 480

Cys Lys Leu His Lys Ser Gly Tyr Val Thr Val Ala His Thr Gly Gln
                485                 490                 495

His Asp Leu Val Ile Pro Pro Asn Gly Tyr Phe Arg Phe Asp Ser Trp
            500                 505                 510

Val Asn Gln Phe Tyr Thr Leu Ala Pro Met Gly Asn Gly Thr Gly Arg
        515                 520                 525

Arg Arg Ala Val
    530
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<210> 64
<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_
delta 35-42

<400> 64
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gaggttaata atgaggtgat ggccctggag cctgtggtgg gcggtcagca gaatgtgatt 120

gacccgtgga tacgcaacaa ttttgtccaa gcccctggtg gggagttcac cgttagcccg 180

agaaatgcgc caggagaaat cctgtggtcg gccccattgg gacccgatct gaacccctat 240

ttgtcacatc tcgctcggat gtacaacggg tatgccggcg gatttgaagt gcaggtgatt 300

ctggctggga acgcgttcac tgctggcaaa gtgatctttg cagcggtgcc tcccaacttc 360

cccactgaag gactgtctcc aagccaggtc acaatgtttc cacacatcgt ggtggacgta 420

cggcagctag agcctgtcct gattcccctc cctgatgtac gcaataattt ctaccactac 480

aatcaatcca atgatccgac cattaaactc atcgcgatgt tgtacacccc tctgcgcgct 540

aacaatgctg gagacgacgt attcaccgtg tcatgcagag tgctcaccag accttcacca 600

gactttgact ttatcttctt agtgcccccc actgttgaga gccgaaccaa gcccttttagt 660

gtccccgtac tcacagtcga ggagatgaca aatagccgct ttccaatccc ccttgagaaa 720

ctgttcacag gaccttcctc ggcattcgtg gttcagccac agaacggacg ctgcacaact 780

gacggcgtgc tgctcggaac cacccagctt agccctgtta atatctgtac gtttagaggc 840

gacgtaactc acataactgg ctcacggaac tataccatga atctggcatc acagaattgg 900

aatgactacg acccaaccga agagattccc gcacctcttg gaacccccga ctttgtggga 960

aaaatacagg gcgtcctgac acaaaccacc agaaccgatg gctccacacg gggacacaag 1020

gcaaccgtct acactggctc tgccgatttt gccccgaaac tgggtagagt gcagtttgag 1080

accgacactg accgggactt tgaagccaat cagaatacta agttcacacc tgtaggagtg 1140

attcaggacg ggggcaccac tcaccggaac gagccgcaac aatgggtcct gccctcttat 1200

agcgggagga atactcataa tgtgcatttg gctcctgcag tggctcccac gtttcccggg 1260

gaacaactgc tctttttttcg ttcaaccatg cctggatgct ccggatatcc caatatggat 1320

ctcgattgcc tgctcccaca ggaatgggtg cagtattttt atcaagaggc cgcaccagcc 1380

caatccgacg tcgcacttct gcggttcgtg aatccagaca caggccgcgt gttgtttgag 1440

tgcaaattgc acaaatcagg atacgttaca gtggctcata ctggacagca tgacctggtg 1500

atcccaccca acggatattt taggttcgac tcctgggtga atcagtttta tacattagcc 1560

cccatgggga atgggactgg cagacgcagg gctgtctga 1599

<210> 65
<211> 540
<212> PRT
<213> Norovirus

<400> 65

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ser Ser Thr Ala Val Ala Thr Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

```
Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175


Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190


Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205


Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220


Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240


Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255


Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270


Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285


Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300


Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320


Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335


Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350
```

```
Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
```

<210> 66
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized
VP1_GII.4_Syd12_SSTAVATA

<400> 66
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcagctccac cgccgtcgct 120

acagccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 67
<211> 540
<212> PRT
<213> Norovirus

<400> 67

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Val Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

```
Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350
```

```
Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
```

<210> 68
<211> 1623

<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized
VP1_GII.4_Syd12_P80S plus sign A39V

<400> 68
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagtcccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 69
<211> 540
<212> PRT
<213> Norovirus

<400> 69

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Pro Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

```
Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335
```

```
Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
```

<210> 70
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S plus sign V47P

<400> 70
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatcc cattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 71
<211> 540
<212> PRT
<213> Norovirus

<400> 71

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

```
Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335
```

```
Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
    530                 535                 540
```

<210> 72
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized
VP1_GII.4_Syd12_P80S plus sign R53I

<400> 72
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gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggataatca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

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tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

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gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 73
<211> 540
<212> PRT
<213> Norovirus

<400> 73

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

```
Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320
```

```
Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525
```

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 74
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S plus sign S90L

<400> 74
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgctg catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 75
<211> 532
<212> PRT
<213> Norovirus

<400> 75

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Gly Gln Gln Asn Val Ile Asp Pro Trp Ile Arg Asn Asn Phe
35 40 45

Val Gln Ala Pro Gly Gly Glu Phe Thr Val Ser Pro Arg Asn Ala Pro
50 55 60

Gly Glu Ile Leu Trp Ser Ala Ser Leu Gly Pro Asp Leu Asn Pro Tyr
65 70 75 80

Leu Ser His Leu Ala Arg Met Tyr Asn Gly Tyr Ala Gly Gly Phe Glu
85 90 95

Val Gln Val Ile Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Val Ile
100 105 110

```
Phe Ala Ala Val Pro Pro Asn Phe Pro Thr Glu Gly Leu Ser Pro Ser
        115                 120                 125

Gln Val Thr Met Phe Pro His Ile Val Val Asp Val Arg Gln Leu Glu
    130                 135                 140

Pro Val Leu Ile Pro Leu Pro Asp Val Arg Asn Asn Phe Tyr His Tyr
145                 150                 155                 160

Asn Gln Ser Asn Asp Pro Thr Ile Lys Leu Ile Ala Met Leu Tyr Thr
                165                 170                 175

Pro Leu Arg Ala Asn Asn Ala Gly Asp Asp Val Phe Thr Val Ser Cys
            180                 185                 190

Arg Val Leu Thr Arg Pro Ser Pro Asp Phe Asp Phe Ile Phe Leu Val
        195                 200                 205

Pro Pro Thr Val Glu Ser Arg Thr Lys Pro Phe Ser Val Pro Val Leu
    210                 215                 220

Thr Val Glu Glu Met Thr Asn Ser Arg Phe Pro Ile Pro Leu Glu Lys
225                 230                 235                 240

Leu Phe Thr Gly Pro Ser Ser Ala Phe Val Val Gln Pro Gln Asn Gly
                245                 250                 255

Arg Cys Thr Thr Asp Gly Val Leu Leu Gly Thr Thr Gln Leu Ser Pro
            260                 265                 270

Val Asn Ile Cys Thr Phe Arg Gly Asp Val Thr His Ile Thr Gly Ser
        275                 280                 285

Arg Asn Tyr Thr Met Asn Leu Ala Ser Gln Asn Trp Asn Asp Tyr Asp
    290                 295                 300

Pro Thr Glu Glu Ile Pro Ala Pro Leu Gly Thr Pro Asp Phe Val Gly
305                 310                 315                 320
```

```
Lys Ile Gln Gly Val Leu Thr Gln Thr Thr Arg Thr Asp Gly Ser Thr
                325                 330                 335

Arg Gly His Lys Ala Thr Val Tyr Thr Gly Ser Ala Asp Phe Ala Pro
            340                 345                 350

Lys Leu Gly Arg Val Gln Phe Glu Thr Asp Thr Asp Arg Asp Phe Glu
        355                 360                 365

Ala Asn Gln Asn Thr Lys Phe Thr Pro Val Gly Val Ile Gln Asp Gly
    370                 375                 380

Gly Thr Thr His Arg Asn Glu Pro Gln Gln Trp Val Leu Pro Ser Tyr
385                 390                 395                 400

Ser Gly Arg Asn Thr His Asn Val His Leu Ala Pro Ala Val Ala Pro
                405                 410                 415

Thr Phe Pro Gly Glu Gln Leu Leu Phe Phe Arg Ser Thr Met Pro Gly
            420                 425                 430

Cys Ser Gly Tyr Pro Asn Met Asp Leu Asp Cys Leu Leu Pro Gln Glu
        435                 440                 445

Trp Val Gln Tyr Phe Tyr Gln Glu Ala Ala Pro Ala Gln Ser Asp Val
    450                 455                 460

Ala Leu Leu Arg Phe Val Asn Pro Asp Thr Gly Arg Val Leu Phe Glu
465                 470                 475                 480

Cys Lys Leu His Lys Ser Gly Tyr Val Thr Val Ala His Thr Gly Gln
                485                 490                 495

His Asp Leu Val Ile Pro Pro Asn Gly Tyr Phe Arg Phe Asp Ser Trp
            500                 505                 510

Val Asn Gln Phe Tyr Thr Leu Ala Pro Met Gly Asn Gly Thr Gly Arg
        515                 520                 525
```

Arg Arg Ala Val
530

<210> 76
<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80Splus sign delta 35-42

<400> 76
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcggtcagca gaatgtgatt 120

gacccgtgga tacgcaacaa ttttgtccaa gcccctggtg gggagttcac cgttagcccg 180

agaaatgcgc caggagaaat cctgtggtcg gccagcttgg gacccgatct gaacccctat 240

ttgtcacatc tcgctcggat gtacaacggg tatgccggcg gatttgaagt gcaggtgatt 300

ctggctggga acgcgttcac tgctggcaaa gtgatctttg cagcggtgcc tcccaacttc 360

cccactgaag gactgtctcc aagccaggtc acaatgtttc cacacatcgt ggtggacgta 420

cggcagctag agcctgtcct gattcccctc cctgatgtac gcaataattt ctaccactac 480

aatcaatcca atgatccgac cattaaactc atcgcgatgt tgtacacccc tctgcgcgct 540

aacaatgctg gagacgacgt attcaccgtg tcatgcagag tgctcaccag accttcacca 600

gactttgact ttatcttctt agtgcccccc actgttgaga gccgaaccaa gcccttttagt 660

gtccccgtac tcacagtcga ggagatgaca aatagccgct ttccaatccc ccttgagaaa 720

ctgttcacag gaccttcctc ggcattcgtg gttcagccac agaacggacg ctgcacaact 780

gacggcgtgc tgctcggaac cacccagctt agccctgtta atatctgtac gtttagaggc 840

gacgtaactc acataactgg ctcacggaac tataccatga atctggcatc acagaattgg 900

aatgactacg acccaaccga agagattccc gcacctcttg gaacccccga ctttgtggga 960

aaaatacagg gcgtcctgac acaaaccacc agaaccgatg gctccacacg gggacacaag 1020

gcaaccgtct acactggctc tgccgatttt gccccgaaac tgggtagagt gcagtttgag 1080

accgacactg accgggactt tgaagccaat cagaatacta agttcacacc tgtaggagtg 1140

attcaggacg ggggcaccac tcaccggaac gagccgcaac aatgggtcct gccctcttat 1200

agcgggagga atactcataa tgtgcatttg gctcctgcag tggctcccac gtttcccggg 1260

gaacaactgc tctttttcg ttcaaccatg cctggatgct ccggatatcc caatatggat 1320

ctcgattgcc tgctcccaca ggaatgggtg cagtattttt atcaagaggc cgcaccagcc 1380

caatccgacg tcgcacttct gcggttcgtg aatccagaca caggccgcgt gttgtttgag 1440

tgcaaattgc acaaatcagg atacgttaca gtggctcata ctggacagca tgacctggtg 1500

atcccaccca acggatattt taggttcgac tcctgggtga atcagtttta tacattagcc 1560

cccatgggga atgggactgg cagacgcagg gctgtctga 1599

<210> 77
<211> 540
<212> PRT
<213> Norovirus

<400> 77

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ser Ser Thr Ala Val Ala Thr Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

```
Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320
```

```
Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
            500                 505                 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
        515                 520                 525
```

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 78
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.4_Syd12_P80S plus sign SSTAVATA

<400> 78
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcagctccac cgccgtcgct 120

acagccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 79
<211> 547
<212> PRT
<213> Norovirus

<400> 79

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Ala Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Met Leu Leu Asn Leu Ser
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ser His Leu Ser Arg Met Tyr
85 90 95

```
Asn Gly Tyr Ala Gly Gly Met Gln Val Gln Val Val Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Ile Asn Ala Ala Gln Ile Thr Met Cys Pro His Val
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Ile Arg Asn Arg Phe Phe His Tyr Asn Gln Glu Asn Thr Ser Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Ser Gly Glu
            180                 185                 190

Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ala Pro Asp
        195                 200                 205

Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr Lys
    210                 215                 220

Pro Phe Ser Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser Arg
225                 230                 235                 240

Phe Pro Ala Pro Ile Asp Met Leu Tyr Thr Asp Pro Asn Glu Gly Ile
                245                 250                 255

Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Thr Leu Gln
            260                 265                 270

Gly Thr Thr Gln Leu Val Pro Thr Gln Ile Cys Ala Phe Arg Gly Thr
        275                 280                 285

Leu Ile Gly Gln Thr Ser Arg Ser Pro Asp Ser Thr Asp Ser Ala Pro
    290                 295                 300
```

```
Arg Arg Arg Asp His Pro Leu His Val Gln Leu Lys Asn Leu Asp Gly
305                 310                 315                 320


Thr Gln Tyr Asp Pro Thr Asp Glu Val Pro Ala Val Leu Gly Ala Ile
                325                 330                 335


Asp Phe Lys Gly Thr Val Phe Gly Val Ala Ser Gln Arg Asp Val Ser
            340                 345                 350


Gly Gln Gln Val Gly Ala Thr Arg Ala His Glu Val His Ile Asn Thr
        355                 360                 365


Thr Asp Pro Arg Tyr Thr Pro Lys Leu Gly Ser Ile Leu Met Tyr Ser
    370                 375                 380


Glu Ser Asp Asp Phe Val Thr Gly Gln Pro Val Arg Phe Thr Pro Ile
385                 390                 395                 400


Gly Met Gly Asp Asn Asp Trp His Gln Trp Glu Leu Pro Asp Tyr Pro
                405                 410                 415


Gly His Leu Thr Leu Asn Met Asn Leu Ala Pro Ala Val Ala Pro Ala
            420                 425                 430


Phe Pro Gly Glu Arg Ile Leu Phe Phe Arg Ser Ile Val Pro Ser Ala
        435                 440                 445


Gly Gly Tyr Gly Ser Gly Gln Ile Asp Cys Leu Ile Pro Gln Glu Trp
    450                 455                 460


Val Gln His Phe Tyr Gln Glu Ala Ala Pro Ser Gln Ser Ala Val Ala
465                 470                 475                 480


Leu Ile Arg Tyr Val Asn Pro Asp Thr Gly Arg Asn Ile Phe Glu Ala
                485                 490                 495


Lys Leu His Arg Glu Gly Phe Ile Thr Val Ala Asn Ser Gly Asn Asn
            500                 505                 510
```

Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ala Trp Val
515 520 525

Asn Gln Phe Tyr Thr Leu Thr Pro Met Gly Thr Gly Gln Gly Arg Arg
530 535 540

Arg Asp Gln
545

<210> 80
<211> 1644
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.6_Ohio_E80S

<400> 80
atgaagatgg caagcaacga cgcagctccc tccaatgatg gtgccgccaa cctggtcccc 60

gaagctaata atgaggtgat ggcgttagag ccggtggttg gcgcatctat tgcagcgcct 120

gtggtcggac agcagaacat cattgatccc tggattcgcg agaacttcgt acaagctcca 180

cagggggagt tcacagtctc cccccggaac tccccgggcg agatgctgct caatctgagc 240

ctcggccctg aactaaaccc ttatctgtca cacctttcac ggatgtacaa tggctacgca 300

ggaggaatgc aagttcaggt ggtcctggcc ggcaatgctt tcaccgcggg caaaatcatc 360

tttgcggccg ttcctccaca cttccctgtc gaaaatatca acgccgccca gattactatg 420

tgcccccacg tgattgtgga tgtgcgacag ttagagccag ttctgctgcc cctgcccgac 480

atcagaaacc ggttcttcca ttacaatcaa gagaatactt cacggatgag acttgttgcg 540

atgctgtaca cccctcttcg tgcaaattcc ggcgaagacg tgttcactgt gtcttgtcga 600

gtacttaccc gacccgcccc cgatttcgaa ttcaccttcc tggttccccc tactgtggag 660

agcaagacaa aacccttcag cctcccaatc ttaacactcg gggagctgtc taattcacgc 720

ttccccgcac ctattgatat gctgtatact gaccccaacg aggggatagt ggtgcagccc 780

caaaatggac ggtgtactct cgacggcacg ctccagggca caacccaact ggtgccaacc 840

cagatttgtg cattcagggg cactttgatt gggcagacat cgagatctcc agattctact 900

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ttaatgtatt cggaatcaga cgattttgtt acaggtcagc ccgtgcggtt taccccgatc 1200

ggaatggggg acaacgattg gcaccagtgg gaattgcccg attaccctgg acacctcacc 1260

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tttagaagca tagtgccctc cgcaggtggg tatggatcag ggcagattga ttgcctgatc 1380

ccccaagaat gggtacagca tttctaccag gaagcagccc ctagccagtc cgcagtagca 1440

ctgatcagat atgttaatcc tgatacggga aggaacatct tcgaagcaaa actgcaccgt 1500

gagggcttca ttaccgtcgc caacagtggt aataacccta ttgtggtgcc tcctaatgga 1560

tacttcaggt ttgaggcatg ggtgaatcag ttttatactc tgactcccat ggggacaggc 1620

caggggcgac gccgggatca gtga 1644

<210> 81
<211> 547
<212> PRT
<213> Norovirus

<400> 81

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Ala Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Met Leu Leu Asn Leu Glu
65 70 75 80

```
Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ser Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Met Gln Val Gln Val Val Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Ile Asn Ala Ala Gln Ile Thr Met Cys Pro His Val
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Ile Arg Asn Arg Phe Phe His Tyr Asn Gln Glu Asn Thr Ser Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Ser Gly Glu
            180                 185                 190

Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ala Pro Asp
        195                 200                 205

Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr Lys
    210                 215                 220

Pro Phe Ser Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser Arg
225                 230                 235                 240

Phe Pro Ala Pro Ile Asp Met Leu Tyr Thr Asp Pro Asn Glu Gly Ile
                245                 250                 255

Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Thr Leu Gln
            260                 265                 270

Gly Thr Thr Gln Leu Val Pro Thr Gln Ile Cys Ala Phe Arg Gly Thr
        275                 280                 285
```

```
Leu Ile Gly Gln Thr Ser Arg Ser Pro Asp Ser Thr Asp Ser Ala Pro
    290                 295                 300

Arg Arg Arg Asp His Pro Leu His Val Gln Leu Lys Asn Leu Asp Gly
305                 310                 315                 320

Thr Gln Tyr Asp Pro Thr Asp Glu Val Pro Ala Val Leu Gly Ala Ile
                325                 330                 335

Asp Phe Lys Gly Thr Val Phe Gly Val Ala Ser Gln Arg Asp Val Ser
            340                 345                 350

Gly Gln Gln Val Gly Ala Thr Arg Ala His Glu Val His Ile Asn Thr
        355                 360                 365

Thr Asp Pro Arg Tyr Thr Pro Lys Leu Gly Ser Ile Leu Met Tyr Ser
    370                 375                 380

Glu Ser Asp Asp Phe Val Thr Gly Gln Pro Val Arg Phe Thr Pro Ile
385                 390                 395                 400

Gly Met Gly Asp Asn Asp Trp His Gln Trp Glu Leu Pro Asp Tyr Pro
                405                 410                 415

Gly His Leu Thr Leu Asn Met Asn Leu Ala Pro Ala Val Ala Pro Ala
            420                 425                 430

Phe Pro Gly Glu Arg Ile Leu Phe Phe Arg Ser Ile Val Pro Ser Ala
        435                 440                 445

Gly Gly Tyr Gly Ser Gly Gln Ile Asp Cys Leu Ile Pro Gln Glu Trp
    450                 455                 460

Val Gln His Phe Tyr Gln Glu Ala Ala Pro Ser Gln Ser Ala Val Ala
465                 470                 475                 480

Leu Ile Arg Tyr Val Asn Pro Asp Thr Gly Arg Asn Ile Phe Glu Ala
                485                 490                 495
```

Lys Leu His Arg Glu Gly Phe Ile Thr Val Ala Asn Ser Gly Asn Asn
500 505 510

Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ala Trp Val
515 520 525

Asn Gln Phe Tyr Thr Leu Thr Pro Met Gly Thr Gly Gln Gly Arg Arg
530 535 540

Arg Asp Gln
545

<210> 82
<211> 1644
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.6_Ohio_S90L

<400> 82
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gaagctaata atgaggtgat ggcgttagag ccggtggttg gcgcatctat tgcagcgcct 120

gtggtcggac agcagaacat cattgatccc tggattcgcg agaacttcgt acaagctcca 180

cagggggagt tcacagtctc cccccggaac tccccgggcg agatgctgct caatctggaa 240

ctcggccctg aactaaaccc ttatctgctc cacctttcac ggatgtacaa tggctacgca 300

ggaggaatgc aagttcaggt ggtcctggcc ggcaatgctt tcaccgcggg caaaatcatc 360

tttgcggccg ttcctccaca cttccctgtc gaaaatatca acgccgccca gattactatg 420

tgcccccacg tgattgtgga tgtgcgacag ttagagccag ttctgctgcc cctgcccgac 480

atcagaaacc ggttcttcca ttacaatcaa gagaatactt cacggatgag acttgttgcg 540

atgctgtaca cccctcttcg tgcaaattcc ggcgaagacg tgttcactgt gtcttgtcga 600

gtacttaccc gacccgcccc cgatttcgaa ttcaccttcc tggttccccc tactgtggag 660

agcaagacaa aacccttcag cctcccaatc ttaacactcg gggagctgtc taattcacgc 720

ttccccgcac ctattgatat gctgtatact gaccccaacg aggggatagt ggtgcagccc 780

caaaatggac ggtgtactct cgacggcacg ctccagggca caacccaact ggtgccaacc 840

cagatttgtg cattcagggg cactttgatt gggcagacat cgagatctcc agattctact 900

gattccgcgc caaggaggag ggaccaccca ctccacgttc agttaaaaaa cctggacgga 960

acccagtacg accctacaga cgaggtcccc gctgtcctcg gagccatcga ctttaaagga 1020

actgtatttg gagtggcatc ccaaagggat gtctcggggc agcaggtggg agctacgaga 1080

gcacatgaag tccacattaa caccacagac ccaagatata ccccaaaact agggtcaatt 1140

ttaatgtatt cggaatcaga cgattttgtt acaggtcagc ccgtgcggtt taccccgatc 1200

ggaatggggg acaacgattg gcaccagtgg gaattgcccg attaccctgg acacctcacc 1260

ttgaatatga atctggcccc agccgtcgcg cccgccttcc ccggtgagcg gatcctcttt 1320

tttagaagca tagtgccctc cgcaggtggg tatggatcag ggcagattga ttgcctgatc 1380

ccccaagaat gggtacagca tttctaccag gaagcagccc ctagccagtc cgcagtagca 1440

ctgatcagat atgttaatcc tgatacggga aggaacatct tcgaagcaaa actgcaccgt 1500

gagggcttca ttaccgtcgc caacagtggt aataacccta ttgtggtgcc tcctaatgga 1560

tacttcaggt ttgaggcatg ggtgaatcag ttttatactc tgactcccat ggggacaggc 1620

caggggcgac gccgggatca gtga 1644

<210> 83
<211> 547
<212> PRT
<213> Norovirus

<400> 83

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Ala Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ser Ile Ala Ala Pro Val Val Gly Gln Gln Asn Ile Ile
35 40 45

```
Asp Pro Trp Ile Arg Glu Asn Phe Val Gln Ala Pro Gln Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Met Leu Leu Asn Leu Ser
65                  70                  75                  80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ser Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Met Gln Val Gln Val Val Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Ile Ile Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Ile Asn Ala Ala Gln Ile Thr Met Cys Pro His Val
    130                 135                 140

Ile Val Asp Val Arg Gln Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Ile Arg Asn Arg Phe Phe His Tyr Asn Gln Glu Asn Thr Ser Arg Met
                165                 170                 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Ser Gly Glu
            180                 185                 190

Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ala Pro Asp
        195                 200                 205

Phe Glu Phe Thr Phe Leu Val Pro Pro Thr Val Glu Ser Lys Thr Lys
    210                 215                 220

Pro Phe Ser Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser Arg
225                 230                 235                 240

Phe Pro Ala Pro Ile Asp Met Leu Tyr Thr Asp Pro Asn Glu Gly Ile
                245                 250                 255
```

```
Val Val Gln Pro Gln Asn Gly Arg Cys Thr Leu Asp Gly Thr Leu Gln
            260                 265                 270

Gly Thr Thr Gln Leu Val Pro Thr Gln Ile Cys Ala Phe Arg Gly Thr
        275                 280                 285

Leu Ile Gly Gln Thr Ser Arg Ser Pro Asp Ser Thr Asp Ser Ala Pro
    290                 295                 300

Arg Arg Arg Asp His Pro Leu His Val Gln Leu Lys Asn Leu Asp Gly
305                 310                 315                 320

Thr Gln Tyr Asp Pro Thr Asp Glu Val Pro Ala Val Leu Gly Ala Ile
                325                 330                 335

Asp Phe Lys Gly Thr Val Phe Gly Val Ala Ser Gln Arg Asp Val Ser
            340                 345                 350

Gly Gln Gln Val Gly Ala Thr Arg Ala His Glu Val His Ile Asn Thr
        355                 360                 365

Thr Asp Pro Arg Tyr Thr Pro Lys Leu Gly Ser Ile Leu Met Tyr Ser
    370                 375                 380

Glu Ser Asp Asp Phe Val Thr Gly Gln Pro Val Arg Phe Thr Pro Ile
385                 390                 395                 400

Gly Met Gly Asp Asn Asp Trp His Gln Trp Glu Leu Pro Asp Tyr Pro
                405                 410                 415

Gly His Leu Thr Leu Asn Met Asn Leu Ala Pro Ala Val Ala Pro Ala
            420                 425                 430

Phe Pro Gly Glu Arg Ile Leu Phe Phe Arg Ser Ile Val Pro Ser Ala
        435                 440                 445

Gly Gly Tyr Gly Ser Gly Gln Ile Asp Cys Leu Ile Pro Gln Glu Trp
    450                 455                 460
```

```
Val Gln His Phe Tyr Gln Glu Ala Ala Pro Ser Gln Ser Ala Val Ala
465                 470                 475                 480


Leu Ile Arg Tyr Val Asn Pro Asp Thr Gly Arg Asn Ile Phe Glu Ala
                485                 490                 495


Lys Leu His Arg Glu Gly Phe Ile Thr Val Ala Asn Ser Gly Asn Asn
            500                 505                 510


Pro Ile Val Val Pro Pro Asn Gly Tyr Phe Arg Phe Glu Ala Trp Val
        515                 520                 525


Asn Gln Phe Tyr Thr Leu Thr Pro Met Gly Thr Gly Gln Gly Arg Arg
    530                 535                 540


Arg Asp Gln
545


<210>  84
<211>  1644
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized
       VP1_GII.6_Ohio_E80S plus sign S90L

<400>  84
atgaagatgg caagcaacga cgcagctccc tccaatgatg gtgccgccaa cctggtcccc       60

gaagctaata atgaggtgat ggcgttagag ccggtggttg gcgcatctat tgcagcgcct      120

gtggtcggac agcagaacat cattgatccc tggattcgcg agaacttcgt acaagctcca      180

cagggggagt tcacagtctc cccccggaac tccccgggcg agatgctgct caatctgagc      240

ctcggccctg aactaaaccc ttatctgctc cacctttcac ggatgtacaa tggctacgca      300

ggaggaatgc aagttcaggt ggtcctggcc ggcaatgctt tcaccgcggg caaaatcatc      360

tttgcggccg ttcctccaca cttccctgtc gaaaatatca acgccgccca gattactatg      420

tgcccccacg tgattgtgga tgtgcgacag ttagagccag ttctgctgcc cctgcccgac      480

atcagaaacc ggttcttcca ttacaatcaa gagaatactt cacggatgag acttgttgcg      540
```

atgctgtaca cccctcttcg tgcaaattcc ggcgaagacg tgttcactgt gtcttgtcga 600

gtacttaccc gacccgcccc cgatttcgaa ttcaccttcc tggttccccc tactgtggag 660

agcaagacaa aacccttcag cctcccaatc ttaacactcg gggagctgtc taattcacgc 720

ttccccgcac ctattgatat gctgtatact gaccccaacg aggggatagt ggtgcagccc 780

caaaatggac ggtgtactct cgacggcacg ctccagggca caacccaact ggtgccaacc 840

cagatttgtg cattcagggg cactttgatt gggcagacat cgagatctcc agattctact 900

gattccgcgc caaggaggag ggaccaccca ctccacgttc agttaaaaaa cctggacgga 960

acccagtacg accctacaga cgaggtcccc gctgtcctcg gagccatcga ctttaaagga 1020

actgtatttg gagtggcatc ccaaagggat gtctcggggc agcaggtggg agctacgaga 1080

gcacatgaag tccacattaa caccacagac ccaagatata ccccaaaact agggtcaatt 1140

ttaatgtatt cggaatcaga cgattttgtt acaggtcagc ccgtgcggtt taccccgatc 1200

ggaatggggg acaacgattg gcaccagtgg gaattgcccg attaccctgg acacctcacc 1260

ttgaatatga atctggcccc agccgtcgcg cccgccttcc ccggtgagcg gatcctcttt 1320

tttagaagca tagtgccctc cgcaggtggg tatggatcag ggcagattga ttgcctgatc 1380

ccccaagaat gggtacagca tttctaccag gaagcagccc ctagccagtc cgcagtagca 1440

ctgatcagat atgttaatcc tgatacggga aggaacatct tcgaagcaaa actgcaccgt 1500

gagggcttca ttaccgtcgc caacagtggt aataacccta ttgtggtgcc tcctaatgga 1560

tacttcaggt ttgaggcatg ggtgaatcag ttttatactc tgactcccat ggggacaggc 1620

caggggcgac gccgggatca gtga 1644

<210> 85
<211> 542
<212> PRT
<213> Norovirus

<400> 85

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

```
Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile
        35                  40                  45

Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65                  70                  75                  80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240
```

```
Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300

Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320

Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
                325                 330                 335

Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
            340                 345                 350

Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
        355                 360                 365

Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
    370                 375                 380

Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385                 390                 395                 400

His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
                405                 410                 415

Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
            420                 425                 430

Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
        435                 440                 445
```

```
Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
    450                 455                 460


Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465                 470                 475                 480


Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
                485                 490                 495


Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
            500                 505                 510


Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
        515                 520                 525


Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
    530                 535                 540


<210>  86
<211>  1629
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized
       VP1_GII.2_CGMH47_E80S_

<400>  86
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc       60

gagtctaata acgaggtgat ggccttggag cctgttgcag gggctgccct cgcagctcct      120

gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca      180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcagc      240

ctgggaccag aacttaatcc gtacctggct cacctggccc ggatgtacaa tggatatgca      300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt      360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg      420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac      480
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gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcat ttctgtgcag 780

tgtcagaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840

agtggaattt gcgcctttaa gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900

tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

aagcataaca cacccggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080

acctatacgg ctcagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140

gatgacctca ctgtgaatca acctgtgaaa ttcactccag taggtctgaa tgatacagac 1200

cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

gcccttccg ttgcacctgt gtttccgggg gagcggttgc tcttctttag aagctatatt 1320

cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

aatccagaca caggaagagc actgttcgag gccaagctgc acagagccgg cttcatgacc 1500

gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

agttgggtga atcagtttta ctcgttggcc cccatgggca cagggaacgg tcgccgacgg 1620

atccagtaa 1629

<210> 87
<211> 1608
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon-optimized VP1
GII.12_HS206_2010_USA_

<400> 87
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gaagtgaata acgagactat ggctctcgaa cccgtggccg gagcctcaat tgccgccccc 120

ctcactggcc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180

aatggggagt tcaccgtgtc cccgagaaac tcccccggcg aagtgttatt gaatttggaa 240

ttaggaccag aactcaaccc ctatctggca catctgtctc ggatgtacaa cggctatgcg 300

ggcggagtgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360

tttgcagcgg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420

ttccctcacg tgataatcga cgtgcggaca ttagagcccg tgctgctacc cctgcccgac 480

gtgaggaaca atttctttca ctacaatcag caaaatgaac caagaatgcg cctggtcgcc 540

atgctctata ctcctttaag aagtaatggc agtggggatg acgtgtttac tgttagctgt 600

cgggtgctca cccgaccttc cccagatttc gacttcaatt atctggtccc ccccacggta 660

gagtccaaaa caaagccttt cactcttcca atccttacaa ttggcgaact gaccaactca 720

cgctttccag tgcctattga tgagctgtac acaagtccaa atgaatccct tgtcgttcag 780

ccacagaatg ggcgctgcgc gcttgacggt gagctccagg gcacaacaca actgttgcca 840

accgctatat gctctttcag ggggcgtatt aatcagaagg tctccgggga gaaccacgtg 900

tggaacatgc aagtgacgaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960

gcgcctctag gtacccctga cttctcaggc aagttgttcg gcgtcctttc ccagcgcgac 1020

catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaattcacc 1080

ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140

ccaacaaagt ttacccctgt tggccttttc gaaagcgaag gctttaacca gtggacactt 1200

cccaattaca gcggggctct cactcttaat atgggactcg caccacccgt cgctccaacg 1260

tttcctggtg agcagatttt gtttttccgc agtcatattc cactgaaggg tggagttgct 1320

gatcccgtga tagactgcct cctccctcag gaatggattc agcacttgta tcaggagtcc 1380

gctccctcgc agaccgatgt ggccctgata cgcttcacaa accccgatac cggaagagtg 1440

ttgtttgaag ctaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500

ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560

agcctggctc caatgggaac aggaaatggg aggaggcgtg tgcagtaa 1608

<210> 88
<211> 535
<212> PRT
<213> Norovirus

<400> 88

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                   10                  15


Gly Leu Val Pro Glu Val Asn Asn Glu Thr Met Ala Leu Glu Pro Val
            20                  25                  30


Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Val Ile
        35                  40                  45


Asp Pro Trp Ile Arg Leu Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65                  70                  75                  80


Leu Gly Pro Glu Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125


Pro Leu Glu Asn Ile Ser Pro Gly Gln Ile Thr Met Phe Pro His Val
    130                 135                 140


Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Asn Glu Pro Arg Met
                165                 170                 175
```

```
Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Ser
                245                 250                 255

Leu Val Val Gln Pro Gln Asn Gly Arg Cys Ala Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Leu Pro Thr Ala Ile Cys Ser Phe Arg Gly
        275                 280                 285

Arg Ile Asn Gln Lys Val Ser Gly Glu Asn His Val Trp Asn Met Gln
    290                 295                 300

Val Thr Asn Ile Asp Gly Thr Pro Phe Asp Pro Thr Glu Asp Val Pro
305                 310                 315                 320

Ala Pro Leu Gly Thr Pro Asp Phe Ser Gly Lys Leu Phe Gly Val Leu
                325                 330                 335

Ser Gln Arg Asp His Asp Asn Ala Cys Arg Ser His Asp Ala Val Ile
            340                 345                 350

Ala Thr Asn Ser Ala Lys Phe Thr Pro Lys Leu Gly Ala Ile Gln Ile
        355                 360                 365

Gly Thr Trp Glu Gln Asp Asp Val His Ile Asn Gln Pro Thr Lys Phe
    370                 375                 380
```

```
Thr Pro Val Gly Leu Phe Glu Ser Glu Gly Phe Asn Gln Trp Thr Leu
385                 390                 395                 400


Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Met Gly Leu Ala Pro Pro
                405                 410                 415


Val Ala Pro Thr Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser His
            420                 425                 430


Ile Pro Leu Lys Gly Gly Val Ala Asp Pro Val Ile Asp Cys Leu Leu
        435                 440                 445


Pro Gln Glu Trp Ile Gln His Leu Tyr Gln Glu Ser Ala Pro Ser Gln
    450                 455                 460


Thr Asp Val Ala Leu Ile Arg Phe Thr Asn Pro Asp Thr Gly Arg Val
465                 470                 475                 480


Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr Val Ala Asn
                485                 490                 495


Thr Gly Ser Arg Pro Ile Val Val Pro Ala Asn Gly Tyr Phe Arg Phe
            500                 505                 510


Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly
        515                 520                 525


Asn Gly Arg Arg Arg Val Gln
    530                 535


<210>  89
<211>  1608
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized
       VP1_GII.12_HS10_E80S

<400>  89
atgaagatgg cgtctaatga tgctgctcct tccaatgatg gcgcagccgg cctggtccct       60
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gaagtgaata acgagactat ggctctcgaa cccgtggccg gagcctcaat tgccgccccc 120

ctcactggcc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180

aatggggagt tcaccgtgtc cccgagaaac tcccccggcg aagtgttatt gaatttgagc 240

ttaggaccag aactcaaccc ctatctggca catctgtctc ggatgtacaa cggctatgcg 300

ggcggagtgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360

tttgcagcgg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420

ttccctcacg tgataatcga cgtgcggaca ttagagcccg tgctgctacc cctgcccgac 480

gtgaggaaca atttctttca ctacaatcag caaaatgaac caagaatgcg cctggtcgcc 540

atgctctata ctcctttaag aagtaatggc agtggggatg acgtgtttac tgttagctgt 600

cgggtgctca cccgaccttc cccagatttc gacttcaatt atctggtccc ccccacggta 660

gagtccaaaa caaagccttt cactcttcca atccttacaa ttggcgaact gaccaactca 720

cgctttccag tgcctattga tgagctgtac acaagtccaa atgaatccct tgtcgttcag 780

ccacagaatg ggcgctgcgc gcttgacggt gagctccagg gcacaacaca actgttgcca 840

accgctatat gctctttcag ggggcgtatt aatcagaagg tctccgggga gaaccacgtg 900

tggaacatgc aagtgacgaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960

gcgcctctag gtacccctga cttctcaggc aagttgttcg gcgtcctttc ccagcgcgac 1020

catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaattcacc 1080

ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140

ccaacaaagt ttacccctgt tggccttttc gaaagcgaag gctttaacca gtggacactt 1200

cccaattaca gcggggctct cactcttaat atgggactcg caccacccgt cgctccaacg 1260

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gatcccgtga tagactgcct cctccctcag gaatggattc agcacttgta tcaggagtcc 1380

gctccctcgc agaccgatgt ggccctgata cgcttcacaa accccgatac cggaagagtg 1440

ttgtttgaag ctaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500

ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560

agcctggctc caatgggaac aggaaatggg aggaggcgtg tgcagtaa 1608

<210> 90
<211> 535
<212> PRT
<213> Norovirus

<400> 90

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                   10                  15


Gly Leu Val Pro Glu Val Asn Asn Glu Thr Met Ala Leu Glu Pro Val
            20                  25                  30


Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Val Ile
        35                  40                  45


Asp Pro Trp Ile Arg Leu Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Glu
65                  70                  75                  80


Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ser Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125


Pro Leu Glu Asn Ile Ser Pro Gly Gln Ile Thr Met Phe Pro His Val
    130                 135                 140


Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Asn Glu Pro Arg Met
                165                 170                 175
```

```
Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Ser
                245                 250                 255

Leu Val Val Gln Pro Gln Asn Gly Arg Cys Ala Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Leu Pro Thr Ala Ile Cys Ser Phe Arg Gly
        275                 280                 285

Arg Ile Asn Gln Lys Val Ser Gly Glu Asn His Val Trp Asn Met Gln
    290                 295                 300

Val Thr Asn Ile Asp Gly Thr Pro Phe Asp Pro Thr Glu Asp Val Pro
305                 310                 315                 320

Ala Pro Leu Gly Thr Pro Asp Phe Ser Gly Lys Leu Phe Gly Val Leu
                325                 330                 335

Ser Gln Arg Asp His Asp Asn Ala Cys Arg Ser His Asp Ala Val Ile
            340                 345                 350

Ala Thr Asn Ser Ala Lys Phe Thr Pro Lys Leu Gly Ala Ile Gln Ile
        355                 360                 365

Gly Thr Trp Glu Gln Asp Asp Val His Ile Asn Gln Pro Thr Lys Phe
    370                 375                 380
```

```
Thr Pro Val Gly Leu Phe Glu Ser Glu Gly Phe Asn Gln Trp Thr Leu
385                 390                 395                 400


Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Met Gly Leu Ala Pro Pro
                405                 410                 415


Val Ala Pro Thr Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser His
            420                 425                 430


Ile Pro Leu Lys Gly Gly Val Ala Asp Pro Val Ile Asp Cys Leu Leu
        435                 440                 445


Pro Gln Glu Trp Ile Gln His Leu Tyr Gln Glu Ser Ala Pro Ser Gln
    450                 455                 460


Thr Asp Val Ala Leu Ile Arg Phe Thr Asn Pro Asp Thr Gly Arg Val
465                 470                 475                 480


Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr Val Ala Asn
                485                 490                 495


Thr Gly Ser Arg Pro Ile Val Val Pro Ala Asn Gly Tyr Phe Arg Phe
            500                 505                 510


Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly
        515                 520                 525


Asn Gly Arg Arg Arg Val Gln
    530                 535


<210>  91
<211>  1608
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized
       VP1_GII.12_HS10_A90L

<400>  91
atgaagatgg cgtctaatga tgctgctcct tccaatgatg gcgcagccgg cctggtccct       60
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gaagtgaata acgagactat ggctctcgaa cccgtggccg gagcctcaat tgccgccccc 120

ctcactggcc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180

aatggggagt tcaccgtgtc cccgagaaac tcccccggcg aagtgttatt gaatttggaa 240

ttaggaccag aactcaaccc ctatctgctc catctgtctc ggatgtacaa cggctatgcg 300

ggcggagtgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360

tttgcagcgg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420

ttccctcacg tgataatcga cgtgcggaca ttagagcccg tgctgctacc cctgcccgac 480

gtgaggaaca atttctttca ctacaatcag caaaatgaac caagaatgcg cctggtcgcc 540

atgctctata ctcctttaag aagtaatggc agtggggatg acgtgtttac tgttagctgt 600

cgggtgctca cccgaccttc cccagatttc gacttcaatt atctggtccc ccccacggta 660

gagtccaaaa caaagccttt cactcttcca atccttacaa ttggcgaact gaccaactca 720

cgctttccag tgcctattga tgagctgtac acaagtccaa atgaatccct tgtcgttcag 780

ccacagaatg ggcgctgcgc gcttgacggt gagctccagg gcacaacaca actgttgcca 840

accgctatat gctctttcag ggggcgtatt aatcagaagg tctccgggga gaaccacgtg 900

tggaacatgc aagtgacgaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960

gcgcctctag gtacccctga cttctcaggc aagttgttcg gcgtcctttc ccagcgcgac 1020

catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaattcacc 1080

ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140

ccaacaaagt ttacccctgt tggccttttc gaaagcgaag gctttaacca gtggacactt 1200

cccaattaca gcggggctct cactcttaat atgggactcg caccacccgt cgctccaacg 1260

tttcctggtg agcagatttt gtttttccgc agtcatattc cactgaaggg tggagttgct 1320

gatcccgtga tagactgcct cctccctcag gaatggattc agcacttgta tcaggagtcc 1380

gctccctcgc agaccgatgt ggccctgata cgcttcacaa accccgatac cggaagagtg 1440

ttgtttgaag ctaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500

ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560

agcctggctc caatgggaac aggaaatggg aggaggcgtg tgcagtaa 1608

<210> 92
<211> 535
<212> PRT
<213> Norovirus

<400> 92

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Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1               5                  10                  15


Gly Leu Val Pro Glu Val Asn Asn Glu Thr Met Ala Leu Glu Pro Val
            20                  25                  30


Ala Gly Ala Ser Ile Ala Ala Pro Leu Thr Gly Gln Asn Asn Val Ile
        35                  40                  45


Asp Pro Trp Ile Arg Leu Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
    50                  55                  60


Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65                  70                  75                  80


Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ser Arg Met Tyr
                85                  90                  95


Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
            100                 105                 110


Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125


Pro Leu Glu Asn Ile Ser Pro Gly Gln Ile Thr Met Phe Pro His Val
    130                 135                 140


Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160


Val Arg Asn Asn Phe Phe His Tyr Asn Gln Gln Asn Glu Pro Arg Met
                165                 170                 175
```

```
Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Asn Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Ile Gly Glu Leu Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Pro Ile Asp Glu Leu Tyr Thr Ser Pro Asn Glu Ser
                245                 250                 255

Leu Val Val Gln Pro Gln Asn Gly Arg Cys Ala Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Leu Pro Thr Ala Ile Cys Ser Phe Arg Gly
        275                 280                 285

Arg Ile Asn Gln Lys Val Ser Gly Glu Asn His Val Trp Asn Met Gln
    290                 295                 300

Val Thr Asn Ile Asp Gly Thr Pro Phe Asp Pro Thr Glu Asp Val Pro
305                 310                 315                 320

Ala Pro Leu Gly Thr Pro Asp Phe Ser Gly Lys Leu Phe Gly Val Leu
                325                 330                 335

Ser Gln Arg Asp His Asp Asn Ala Cys Arg Ser His Asp Ala Val Ile
            340                 345                 350

Ala Thr Asn Ser Ala Lys Phe Thr Pro Lys Leu Gly Ala Ile Gln Ile
        355                 360                 365

Gly Thr Trp Glu Gln Asp Asp Val His Ile Asn Gln Pro Thr Lys Phe
    370                 375                 380
```

```
Thr Pro Val Gly Leu Phe Glu Ser Glu Gly Phe Asn Gln Trp Thr Leu
385                 390                 395                 400


Pro Asn Tyr Ser Gly Ala Leu Thr Leu Asn Met Gly Leu Ala Pro Pro
                405                 410                 415


Val Ala Pro Thr Phe Pro Gly Glu Gln Ile Leu Phe Phe Arg Ser His
            420                 425                 430


Ile Pro Leu Lys Gly Gly Val Ala Asp Pro Val Ile Asp Cys Leu Leu
        435                 440                 445


Pro Gln Glu Trp Ile Gln His Leu Tyr Gln Glu Ser Ala Pro Ser Gln
    450                 455                 460


Thr Asp Val Ala Leu Ile Arg Phe Thr Asn Pro Asp Thr Gly Arg Val
465                 470                 475                 480


Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr Val Ala Asn
                485                 490                 495


Thr Gly Ser Arg Pro Ile Val Val Pro Ala Asn Gly Tyr Phe Arg Phe
            500                 505                 510


Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met Gly Thr Gly
        515                 520                 525


Asn Gly Arg Arg Arg Val Gln
    530                 535


<210>  93
<211>  1608
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Nucleic acid sequence of human codon optimized
       VP1_GII.12_HS10_E80S plus sign A90L

<400>  93
atgaagatgg cgtctaatga tgctgctcct tccaatgatg gcgcagccgg cctggtccct       60
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ctcactggcc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180

aatggggagt tcaccgtgtc cccgagaaac tcccccggcg aagtgttatt gaatttgagc 240

ttaggaccag aactcaaccc ctatctgctc catctgtctc ggatgtacaa cggctatgcg 300

ggcggagtgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360

tttgcagcgg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420

ttccctcacg tgataatcga cgtgcggaca ttagagcccg tgctgctacc cctgcccgac 480

gtgaggaaca atttctttca ctacaatcag caaaatgaac caagaatgcg cctggtcgcc 540

atgctctata ctcctttaag aagtaatggc agtggggatg acgtgtttac tgttagctgt 600

cgggtgctca cccgaccttc cccagatttc gacttcaatt atctggtccc ccccacggta 660

gagtccaaaa caaagccttt cactcttcca atccttacaa ttggcgaact gaccaactca 720

cgctttccag tgcctattga tgagctgtac acaagtccaa atgaatccct tgtcgttcag 780

ccacagaatg ggcgctgcgc gcttgacggt gagctccagg gcacaacaca actgttgcca 840

accgctatat gctctttcag ggggcgtatt aatcagaagg tctccgggga gaaccacgtg 900

tggaacatgc aagtgacgaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960

gcgcctctag gtacccctga cttctcaggc aagttgttcg gcgtcctttc ccagcgcgac 1020

catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaattcacc 1080

ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140

ccaacaaagt ttacccctgt tggccttttc gaaagcgaag gctttaacca gtggacactt 1200

cccaattaca gcggggctct cactcttaat atgggactcg caccacccgt cgctccaacg 1260

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gatcccgtga tagactgcct cctccctcag gaatggattc agcacttgta tcaggagtcc 1380

gctccctcgc agaccgatgt ggccctgata cgcttcacaa accccgatac cggaagagtg 1440

ttgtttgaag ctaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500

ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560

agcctggctc caatgggaac aggaaatggg aggaggcgtg tgcagtaa 1608

<210> 94
<211> 215
<212> PRT
<213> Norovirus

<400> 94

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Met Ala Gln Ala Ile Phe Gly Ala Ile Ala Ala Thr Ala Ala Gly Ser
1               5                   10                  15


Ala Val Gly Ala Gly Ile Gln Ala Gly Thr Glu Ala Ala Leu Gln His
            20                  25                  30


Gln Arg Phe Gln Gln Asp Leu Thr Leu Gln Ser Asn Thr Phe Lys His
        35                  40                  45


Asp Lys Glu Met Leu Gly Leu Gln Val Gly Ala Ser Thr Ala Leu Leu
    50                  55                  60


Gln Asn Ser Leu Asn Thr Arg Tyr Asn Met Leu Thr Asp Ala Gly Leu
65                  70                  75                  80


Ser Ser Ser Asp Ala Ala Arg Met Val Val Gly Ala Pro Ala Thr Arg
                85                  90                  95


Val Val Asp Trp Asn Gly Thr Arg Ile Ser Ala Pro Arg Ser Thr Ala
            100                 105                 110


Thr Thr Leu Arg Ser Gly Gly Phe Met Thr Ile Pro Thr Leu Tyr Lys
        115                 120                 125


Gly Lys Gln Gln Gln Lys Ala Pro Thr Glu Ile Gly Leu Ser Asn Pro
    130                 135                 140


Asn Tyr Gly Ser Ser Val Ser Ser Arg Val Ala Asp Trp Val Ser Ser
145                 150                 155                 160


Gln Asn Ser Ser His Ser Ser Leu Gly Pro Tyr His Pro Ser Ala Leu
                165                 170                 175
```

Gln Thr Thr Trp Val Thr Pro Pro Gly Ser Ser Ser Thr Ser Thr Ile
180 185 190

Ser Ser Val Ser Thr Val Pro Arg Tyr Phe Asn Thr Asp Arg Leu Pro
195 200 205

Leu Phe Ala Asn Met Arg Lys
210 215

<210> 95
<211> 648
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP2_GI.3_Lil08

<400> 95
atggctcagg caatcttcgg cgcaatcgct gccactgctg ccggatccgc tgtgggagcc 60

ggcatacagg ccggaactga ggcggccctt cagcatcagc ggttccagca ggatctgaca 120

ttacagagta acacattcaa acatgacaag gagatgctgg gtctgcaggt gggtgccagt 180

actgccctgc tccaaaactc tctgaatacc agatataaca tgttaactga tgcgggactg 240

tctagtagcg acgcagctcg catggtcgtg ggcgccccag ctacgagagt tgtggactgg 300

aatggcaccc gaatcagtgc accaaggtct acagccacta ccctcagaag tggcggcttt 360

atgaccatcc cgactttata caagggcaaa caacagcaga aggcacctac tgaaatcggt 420

ctctccaatc ccaactacgg cagcagtgtg tcttctcgcg tggccgattg ggtctcaagc 480

cagaactcca gtcatagttc tcttgggcct tatcatccat cagccttgca gacaacttgg 540

gtcaccccac ccgggtccag tagcacgtca accatcagtt ccgtctccac agtccctcgc 600

tattttaata ctgataggct tcccctgttc gcaaacatga ggaagtga 648

<210> 96
<211> 259
<212> PRT
<213> Norovirus

<400> 96

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Met Ala Ser Ala Phe Leu Ala Gly Leu Ala Gly Asp Val Ile Thr Asn
1               5                  10                  15

Gly Val Gly Ser Leu Ile Asn Ala Gly Ala Asn Ala Val Asn Gln Lys
            20                  25                  30

Val Glu Tyr Asp Phe Asn Lys Gln Leu Gln Met Ala Ser Phe Lys His
        35                  40                  45

Asp Lys Glu Met Leu Gln Ser Gln Val Leu Ala Thr Lys Gln Leu Gln
    50                  55                  60

Gln Glu Met Met Asn Ile Arg Gln Gly Val Leu Thr Ala Gly Gly Phe
65                  70                  75                  80

Ser Pro Ala Asp Ala Ala Arg Gly Ala Val Asn Ala Pro Met Thr Lys
                85                  90                  95

Ile Leu Asp Trp Asn Gly Thr Arg Tyr Trp Ala Pro Asn Ser Met Lys
            100                 105                 110

Thr Thr Ser Tyr Ser Gly Gln Phe Ser Ser Ser Pro Val His Lys Ser
        115                 120                 125

Pro Ala Pro Ser Gln His Thr Ala Leu Pro Lys Ser Arg Leu Gln Asn
    130                 135                 140

Asp Phe Ala Ser Val Tyr Ser Phe Pro Ser Ser Val Ser Ser Gln Ser
145                 150                 155                 160

Thr His Ser Thr Ala Leu Ser Ala Gly Thr Gly Ser Ser Arg Ser Ile
                165                 170                 175

Ser Pro Ser Thr Ala Thr Pro Thr Leu Ser Arg Thr Ser Asp Trp Val
            180                 185                 190

Arg Gly Gln Asn Glu Arg Leu Ser Pro Phe Met Asp Gly Ala Leu Gln
        195                 200                 205
```

Thr Ala Phe Val Thr Pro Pro Ser Ser Lys Ala Ser Ser Asn Gly Thr
210 215 220

Val Ser Thr Val Pro Lys Ala Val Leu Asp Ser Trp Thr Pro Met Phe
225 230 235 240

Asn Thr His Arg Gln Pro Leu Phe Ala His Pro Arg Arg Arg Gly Glu
245 250 255

Ser Gln Val

<210> 97
<211> 780
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP2_GII6_HS10

<400> 97
atggcctccg catttctagc tggattggcc ggggacgtga tcaccaacgg cgtaggatcg 60

ctgattaatg caggcgccaa tgctgttaat cagaaggttg aatacgactt caacaaacaa 120

ctgcagatgg cttcattcaa gcacgacaaa gaaatgttgc agtcacaggt tctcgccacc 180

aagcagctac aacaggagat gatgaacatt cggcagggcg tactgaccgc tggaggattc 240

agccctgctg acgcagcacg gggggccgtg aacgcgccga tgaccaagat cctggattgg 300

aacggaactc ggtattgggc tcccaactct atgaaaacca cttcttactc tggtcagttc 360

tccagctcgc cagtccacaa aagtccggcc ccttcacagc acacagcact ccctaagtcc 420

aggctgcaaa acgactttgc ctccgtgtac tccttcccat ccagcgtgtc atctcagagc 480

actcattcaa ccgccctgtc cgccggaact gggtctagcc gcagcatttc cccaagcaca 540

gctactccaa ctctgagcag gactagcgat tgggtcagag gacaaaacga acgactgtcc 600

cctttcatgg acggagctct gcaaaccgcc ttcgtcactc cacctagcag caaggcctcg 660

agcaacggta cggttagtac cgtgccaaag gctgttcttg acagctggac ccccatgttt 720

aacacacaca ggcagccatt gtttgcacac cccaggcgac ggggagaatc acaagtttag 780

<210> 98
<211> 543
<212> PRT
<213> Norovirus

<400> 98

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Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1               5                   10                  15


Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
            20                  25                  30


Met Glu Pro Val Ala Gly Ala Ala Thr Ala Ala Ala Thr Ala Gly Gln
        35                  40                  45


Val Asn Met Ile Asp Pro Trp Ile Met Ser Asn Tyr Val Gln Ala Pro
    50                  55                  60


Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80


Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Ser His Leu
                85                  90                  95


Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
            100                 105                 110


Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
        115                 120                 125


Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
    130                 135                 140


Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160


Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
                165                 170                 175


Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
```

180 185 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
195 200 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
210 215 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225 230 235 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
245 250 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
260 265 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
275 280 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
290 295 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305 310 315 320

Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
325 330 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
340 345 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
355 360 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
370 375 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp

385 390 395 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
405 410 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
420 425 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
435 440 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
450 455 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465 470 475 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
485 490 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
500 505 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 99
<211> 212
<212> PRT
<213> Norovirus

<400> 99

Met Ala Gln Ala Ile Ile Gly Ala Ile Ala Ala Ser Thr Ala Gly Ser
1 5 10 15

Ala Leu Gly Ala Gly Ile Gln Val Gly Gly Glu Ala Ala Leu Gln Ser
20 25 30

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Gln Arg Tyr Gln Gln Asn Leu Gln Leu Gln Glu Asn Ser Phe Lys His
        35                  40                  45

Asp Arg Glu Met Ile Gly Tyr Gln Val Glu Ala Ser Asn Gln Leu Leu
    50                  55                  60

Ala Lys Asn Leu Ala Thr Arg Tyr Ser Leu Leu Arg Ala Gly Gly Leu
65                  70                  75                  80

Thr Ser Ala Asp Ala Ala Arg Ser Val Ala Gly Ala Pro Val Thr Arg
                85                  90                  95

Ile Val Asp Trp Asn Gly Val Arg Val Ser Ala Pro Glu Ser Ser Ala
            100                 105                 110

Thr Thr Leu Arg Ser Gly Gly Phe Met Ser Val Pro Ile Pro Phe Ala
        115                 120                 125

Ser Lys Gln Lys Gln Val Gln Ser Ser Gly Ile Ser Asn Pro Asn Tyr
    130                 135                 140

Ser Pro Ser Ser Ile Ser Arg Thr Thr Ser Trp Val Glu Ser Gln Asn
145                 150                 155                 160

Ser Ser Arg Phe Gly Asn Leu Ser Pro Tyr His Ala Glu Ala Leu Asn
                165                 170                 175

Thr Val Trp Leu Thr Pro Pro Gly Ser Thr Ala Ser Ser Thr Leu Ser
            180                 185                 190

Ser Val Pro Arg Gly Tyr Phe Asn Thr Asp Arg Leu Pro Leu Phe Ala
        195                 200                 205

Asn Asn Arg Arg
    210
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<210> 100
<211> 639

<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP.2_GI1_Norwalk

<400> 100
atggctcagg ccattattgg cgccatcgct gcaagtacag ccgggagtgc attgggggcc 60

ggaatacagg tgggcgggga agctgcattg cagagccagc ggtaccagca aaacctgcag 120

ttacaggaga atagctttaa acacgacagg gagatgattg gatatcaggt ggaggccagc 180

aatcagctgc tcgccaaaaa cttggctact cgatactcat tactgcgcgc cgggggttg 240

actagcgccg acgccgcacg atctgtcgca ggcgcccccg tgactcggat cgtagactgg 300

aacggggtac gagtctcggc tcccgagtcg tctgcaacca ccctgaggtc gggagggttt 360

atgtccgtgc ccatcccatt cgctagcaaa cagaaacagg tccagagctc cggaatctcc 420

aatcccaatt actcccctag ctctatctct cgtaccactt cctgggtcga gagtcagaac 480

agcagtagat ttggcaacct gagcccctac catgctgaag ccctgaacac tgtgtggttg 540

actccacctg gtagcacggc ctcctcaacc ctgagttccg tgcctcgcgg gtacttcaat 600

accgacagac ttcctctgtt cgctaacaac cgccgctga 639

<210> 101
<211> 538
<212> PRT
<213> Norovirus

<400> 101

Met Met Met Ala Ser Lys Asp Ala Pro Ser Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Ala Ala Glu Pro Leu Pro
20 25 30

Leu Glu Pro Val Val Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro
50 55 60

```
Glu Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Arg Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Met
            100                 105                 110

Leu Ala Gly Asn Ala Phe Ser Ala Gly Lys Ile Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Glu Ser Gln Asn Ile Ser Ile Gly Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Asp Asp Val Arg Asn Val Leu Phe His Thr Asn Glu Asn Arg
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Ala Gly
            180                 185                 190

Gly Ala Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ala Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Ser
    210                 215                 220

Val Glu Gln Lys Thr Arg Gln Leu Thr Ile Pro Asn Ile Pro Leu Asn
225                 230                 235                 240

Asn Leu Ala Asn Ser Arg Val Pro Ala Met Ile Asn Lys Met Thr Val
                245                 250                 255

Ser Ala Asp Gln Asn Gln Val Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270
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Leu Glu Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Ala Asn Gln Val
        275                 280                 285

Ala Arg Ile Arg Gly Lys Val Phe Ser Thr Asn Ser Gly Thr Gly Leu
    290                 295                 300

Asn Leu Thr Glu Val Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Leu Gly Phe Pro Asp Ile Gly Asn Cys Asp Trp His Val Tyr
                325                 330                 335

Ala Phe Lys Val Asn Gln Asn Thr Gly Asp Pro Met Tyr Arg Leu Asp
            340                 345                 350

Ile Thr Gln Gly Asn Ser Phe Ala Pro His Leu Gly Ser Ile Glu Phe
        355                 360                 365

Ser Ser Glu Asn His Pro Ser Gly Asp Gln Leu Gly Thr Leu Thr Trp
    370                 375                 380

Ile Ser Pro Leu Asn Asn Ala Ser Arg Val Asp Pro Trp Lys Ile Pro
385                 390                 395                 400

Thr Tyr Gly Ser Thr Leu Thr Glu Ser Thr Asn Leu Ala Pro Pro Ile
                405                 410                 415

Phe Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe Met Ser Asp Phe
            420                 425                 430

Pro Ile Val Ser Gly Asn Thr Ala Gln Ile Pro Cys Thr Leu Pro Gln
        435                 440                 445

Glu Phe Val Ser Ser Phe Val Glu Gln Gln Ala Pro Ile Arg Gly Glu
    450                 455                 460

Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His Arg Asn Leu Gly
465                 470                 475                 480
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Glu Phe Lys Leu Tyr Pro Asp Gly Phe Ile Thr Cys Val Pro Asn Thr
485 490 495

Gly Gly Gly Pro Gln Asn Leu Pro Ser Asn Gly Val Phe Val Phe Ser
500 505 510

Ser Trp Val Ser Arg Tyr Tyr Gln Leu Lys Pro Val Gly Thr Thr Gly
515 520 525

Pro Val Arg Arg Leu Gly Val Arg Arg Val
530 535

<210> 102
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-NoV(US68)VP1(ORF1)(hCod).c

<400> 102
tcgtgcttcg gcaccagtac aatgatgatg gctagtaaag atgcgacct 49

<210> 103
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-NoV(US68)VP1(ORF1)(hCod).r

<400> 103
actaaagaaa ataggccttt atctccgcag accgaggcgt ccgcgggcag aa 52

<210> 104
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GI3Lil08VP1.c

<400> 104
tcgtgcttcg gcaccagtac aatgatgatg gcttccaagg atgctccca 49

<210> 105
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GI3Lil08VP1.r

<400> 105
actaaagaaa ataggcctct agctccgtct gatcccgagc ctccgaact 49

<210> 106
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GI.3Lil08(S94L).r

<400> 106
ctgagccaag tggagcagaa acggattcaa gtgtggtcct agctgcaggt caaacaaga 59

<210> 107
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GI.3Lil08(S94L).c

<400> 107
aggaccacac ttgaatccgt ttctgctcca cttggctcag atgtataatg gatggg 56

<210> 108
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GI.3Lil08(Q84S).r

<400> 108
gtgtggtcct aggctcaggt caaacaagat gtcacccggg gtgttgtttg ggcttat 57

<210> 109
<211> 48
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer VP1_GI.3Lil08(Q84S).c

<400> 109
ggtgacatct tgtttgacct gagcctagga ccacacttga atccgttt 48

<210> 110
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GI3Lil08VP2.c

<400> 110
tcgtgcttcg gcaccagtac aatggctcag gcaatcttcg gcgcaatc 48

<210> 111
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GI3Lil08VP2.r

<400> 111
actaaagaaa ataggccttc acttcctcat gtttgcgaac aggggaagc 49

<210> 112
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-(160)GI.5_Sikl13_VP1.c

<400> 112
tcgtgcttcg gcaccagtac aatgatgatg gcctccaaag acgctcct 48

<210> 113
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GI.5_Sikl13_VP1.r

<400> 113
actaaagaaa ataggccttc agcgccgcac gccaaggcgc ccccgggcag atg 53

<210> 114
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.5(hCod)(Q84S).r

<400> 114
gatgagggcc taagctcagg tcgaacagaa tatcccctgg tgtgttgtta g 51

<210> 115
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.5(hCod)(Q84S).c

<400> 115
tattctgttc gacctgagct taggccctca tctcaacccc ttcttggccc a 51

<210> 116
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.5(hCod)(A94L).r

<400> 116
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<210> 117
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.5(hCod)(A94L).c

<400> 117
tctcaacccc ttcttgctcc acctgagcca gatgtacaat ggctgggtgg g 51

<210> 118
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-(160)GII.2_CGMH11_VP1.c

<400> 118
tcgtgcttcg gcaccagtac aatgaagatg gcatccaacg acgccgcacc cagc 54

<210> 119
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.2_CGMH11_VP1.r

<400> 119
actaaagaaa ataggccttt actggatccg tcggcgaccg ttccctgtgc cca 53

<210> 120
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.2CGMH11(E80S).r

<400> 120
ttctggtccc aggctgagat tgaggagcac ttccccaggg ctatttctag ggctgaccg 59

<210> 121
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.2CGMH11(E80S).c

<400> 121
ggaagtgctc ctcaatctca gcctgggacc agaacttaat ccgtacct 48

<210> 122
<211> 59
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer VP1_GII.2CGMH11(A90L).r

<400> 122
tccgggccag gtggagcagg tacggattaa gttctggtcc cagctcgaga ttgaggagc 59

<210> 123
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.2CGMH11(A90L).c

<400> 123
gggaccagaa cttaatccgt acctgctcca cctggcccgg atgtacaatg gatatgcag 59

<210> 124
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-(160)GII.3_Jing13_VP1.c

<400> 124
tcgtgcttcg gcaccagtac aatgaaaatg gcttccaacg atgcagcacc ct 52

<210> 125
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.3_Jing13_VP1.r

<400> 125
actaaagaaa ataggccttt actggatccg ccgtctgcca ttgcctgtac 50

<210> 126
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.3Jing13(E80S).r

<400> 126
atttcagggc ccaggctcaa attcaagaga acctccccgg gggagtttcg aggagagac 59

<210> 127
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.3Jing13(E80S).c

<400> 127
ggaggttctc ttgaatttga gcctgggccc tgaaattaat ccttatct 48

<210> 128
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.3Jing13(A90L).r

<400> 128
attcgggcta gatggagcag ataaggatta atttcagggc ccagttccaa attcaagag 59

<210> 129
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.3Jing13(A90L).c

<400> 129
gggccctgaa attaatcctt atctgctcca tctagcccga atgtacaacg gctacg 56

<210> 130
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.4Syd12VP1.c

<400> 130
tcgtgcttcg gcaccagtac aatgaaaatg gcctcgagtg acgctaacc 49

<210> 131
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.4Syd12VP1.r

<400> 131
actaaagaaa ataggccttc agacagccct gcgtctgcca gtcccatt 48

<210> 132
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(A39V).r

<400> 132
gaccggccac ggggactgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 133
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(A39V).c

<400> 133
gggcgcagcc atagcagtcc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 134
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(V47P).r

<400> 134
cgtatccacg ggtcaatggg attctgctga ccggccacgg gcgctgctat g 51

<210> 135
<211> 53
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(V47P).c

<400> 135
ggccggtcag cagaatccca ttgacccgtg gatacgcaac aattttgtcc aag 53

<210> 136
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(R53I).r

<400> 136
tggacaaaat tgttgattat ccacgggtca atcacattct gctgaccg 48

<210> 137
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(R53I).c

<400> 137
gattgacccg tggataatca acaattttgt ccaagcccct ggtggggagt 50

<210> 138
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4(P80S).r

<400> 138
gatcgggtcc caagctggcc gaccacagga tttctcctgg cgcatttctc 50

<210> 139
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4(P80S).c

<400> 139
aatcctgtgg tcggccagct tgggacccga tctgaacccc tatttgtcac 50

<210> 140
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4(S90L).r

<400> 140
atccgagcga gatgcagcaa ataggggttc agatcgggtc ccaatggggc cgacca 56

<210> 141
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4(S90L).c

<400> 141
tctgaacccc tatttgctgc atctcgctcg gatgtacaac gggtatgc 48

<210> 142
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(Del(35-42)).r

<400> 142
cacattctgc tgaccgccca ccacaggctc cagggccatc acctcattat 50

<210> 143
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(Del(35-42)).c

<400> 143
ggagcctgtg gtgggcggtc agcagaatgt gattgacccg tggatacg 48

<210> 144
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(SSTAVATA).r

<400> 144
ctgaccggct gtagcgacgg cggtggagct gcccaccaca ggctccaggg ccatcacctc 60

<210> 145
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.4Syd12(SSTAVATA).c

<400> 145
tgtggtgggc agctccaccg ccgtcgctac agccggtcag cagaatgtga ttgacccgtg 60

<210> 146
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.6Ohi12VP1.c

<400> 146
tcgtgcttcg gcaccagtac aatgaagatg gcaagcaacg acgcagctc 49

<210> 147
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.6Ohi12VP1.r

<400> 147
actaaagaaa ataggccttc actgatcccg gcgtcgcccc tggcctgtcc ccat 54

<210> 148
<211> 51
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer IF-GII.6HS10VP2.c

<400> 148
tcgtgcttcg gcaccagtac aatggcctcc gcatttctag ctggattggc c 51

<210> 149
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.6HS10VP2.r

<400> 149
actaaagaaa ataggcctct aaacttgtga ttctccccgt cgcctggggt gtg 53

<210> 150
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.6Ohi12(E80S).r

<400> 150
agttcagggc cgaggctcag attgagcagc atctcgcccg gggagttccg gggggagac 59

<210> 151
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.6Ohi12(E80S).c

<400> 151
cgagatgctg ctcaatctga gcctcggccc tgaactaaac ccttatct 48

<210> 152
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer VP1_GII.6Ohi12(S90L).c

<400> 152
ccctgaacta aacccttatc tgctccacct ttcacggatg tacaatggct acgcaggag 59

<210> 153
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-(160)GII.12_HS10_VP1.c

<400> 153
tcgtgcttcg gcaccagtac aatgaagatg gcgtctaatg atgctgctcc tt 52

<210> 154
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-GII.12_HS10_VP1.r

<400> 154
actaaagaaa ataggccttt actgcacacg cctcctccca tttcctgttc ccat 54

<210> 155
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.12(E80S).r

<400> 155
agttctggtc ctaagctcaa attcaataac acttcgccgg gggagttt 48

<210> 156
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.12(E80S).c

<400> 156
agtgttattg aatttgagct taggaccaga actcaacccc tatctggca 49

<210> 157
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.12(A90L).r

<400> 157
atccgagaca gatggagcag ataggggttg agttctggtc ctaattccaa 50

<210> 158
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.12(A90L).c

<400> 158
actcaacccc tatctgctcc atctgtctcg gatgtacaac ggctatgcgg gcggagt 57

<210> 159
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-NoV(US68)VP2(ORF3)(hCod).c

<400> 159
tcgtgcttcg gcaccagtac aatggctcag gccattattg gcgccat 47

<210> 160
<211> 47
<212> DNA
<213> Artificial Sequqence

<220>
<223> Primer IF-NoV(US68)VP2(ORF3)(hCod).c

<400> 160
tcgtgcttcg gcaccagtac aatggctcag gccattattg gcgccat 47

<210> 161
<211> 50
<212> DNA

<213> Artificial Sequence

<220>
<223> Primer IF-NoV(US68)VP2(ORF3)(hCod).r

<400> 161
actaaagaaa ataggccttc agcggcggtt gttagcgaac agaggaagtc 50

<210> 162
<211> 4540
<212> DNA
<213> Artificial Sequence

<220>
<223> Cloning vector 1190 from left to right T-DNA

<400> 162
tggcaggata tattgtggtg taaacaaatt gacgcttaga caacttaata acacattgcg 60

gacgttttta atgtactgaa ttaacgccga atcccgggct ggtatattta tatgttgtca 120

aataactcaa aaaccataaa agtttaagtt agcaagtgtg tacattttta cttgaacaaa 180

aatattcacc tactactgtt ataaatcatt attaaacatt agagtaaaga aatatggatg 240

ataagaacaa gagtagtgat attttgacaa caattttgtt gcaacatttg agaaaatttt 300

gttgttctct cttttcattg gtcaaaaaca atagagagag aaaaaggaag agggagaata 360

aaaacataat gtgagtatga gagagaaagt tgtacaaaag ttgtaccaaa atagttgtac 420

aaatatcatt gaggaatttg acaaaagcta cacaaataag ggttaattgc tgtaaataaa 480

taaggatgac gcattagaga gatgtaccat tagagaattt ttggcaagtc attaaaaaga 540

aagaataaat tatttttaaa attaaaagtt gagtcatttg attaaacatg tgattattta 600

atgaattgat gaaagagttg gattaaagtt gtattagtaa ttagaatttg gtgtcaaatt 660

taatttgaca tttgatcttt tcctatatat tgccccatag agtcagttaa ctcattttta 720

tatttcatag atcaaataag agaaataacg gtatattaat ccctccaaaa aaaaaaaacg 780

gtatatttac taaaaaatct aagccacgta ggaggataac aggatccccg taggaggata 840

acatccaatc caaccaatca caacaatcct gatgagataa cccactttaa gcccacgcat 900

ctgtggcaca tctacattat ctaaatcaca cattcttcca cacatctgag ccacacaaaa 960

accaatccac atctttatca cccattctat aaaaaatcac actttgtgag tctacacttt 1020

gattcccttc aaacacatac aaagagaaga gactaattaa ttaattaatc atcttgagag 1080

aaaatggaac gagctataca aggaaacgac gctagggaac aagctaacag tgaacgttgg 1140

gatggaggat caggaggtac cacttctccc ttcaaacttc ctgacgaaag tccgagttgg 1200

actgagtggc ggctacataa cgatgagacg aattcgaatc aagataatcc ccttggtttc 1260

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tagccctgtt aatatctgta cgtttagagg cgacgtaact cacataactg gctcacggaa 1800

ctataccatg aatctggcat cacagaattg gaatgactac gacccaaccg aagagattcc 1860

cgcacctctt ggaacccccg actttgtggg aaaaatacag ggcgtcctga cacaaaccac 1920

cagaaccgat ggctccacac ggggacacaa ggcaaccgtc tacactggct ctgccgattt 1980

tgccccgaaa ctgggtagag tgcagtttga gaccgacact gaccgggact ttgaagccaa 2040

tcagaatact aagttcacac ctgtaggagt gattcaggac gggggcacca ctcaccggaa 2100

cgagccgcaa caatgggtcc tgccctctta tagcgggagg aatactcata atgtgcattt 2160

ggctcctgca gtggctccca cgtttcccgg ggaacaactg ctctttttttc gttcaaccat 2220

gcctggatgc tccggatatc ccaatatgga tctcgattgc ctgctcccac aggaatgggt 2280

gcagtatttt tatcaagagg ccgcaccagc ccaatccgac gtcgcacttc tgcggttcgt 2340

gaatccagac acaggccgcg tgttgtttga gtgcaaattg cacaaatcag gatacgttac 2400

agtggctcat actggacagc atgacctggt gatcccaccc aacggatatt ttaggttcga 2460

ctcctgggtg aatcagtttt atacattagc ccccatgggg aatgggactg gcagacgcag 2520

ggctgtctga aggcctattt tctttagttt gaatttactg ttattcggtg tgcatttcta 2580

tgtttggtga gcggttttct gtgctcagag tgtgtttatt ttatgtaatt taatttcttt 2640

gtgagctcct gtttagcagg tcgtcccttc agcaaggaca caaaaagatt ttaattttat 2700

tatcgttcaa acatttggca ataaagtttc ttaagattga atcctgttgc cggtcttgcg 2760

atgattatca tataatttct gttgaattac gttaagcatg taataattaa catgtaatgc 2820

atgacgttat ttatgagatg ggtttttatg attagagtcc cgcaattata catttaatac 2880

gcgatagaaa acaaaatata gcgcgcaaac taggataaat tatcgcgcgc ggtgtcatct 2940

atgttactag at 2952

<210> 166
<211> 2952
<212> DNA
<213> Artificial Sequence

<220>
<223> Construct 4135 from 2X35S promoter to NOS terminator

<400> 166
gtcaacatgg tggagcacga cacacttgtc tactccaaaa atatcaaaga tacagtctca 60

gaagaccaaa gggcaattga gacttttcaa caaagggtaa tatccggaaa cctcctcgga 120

ttccattgcc cagctatctg tcactttatt gtgaagatag tggaaaagga aggtggctcc 180

tacaaatgcc atcattgcga taaaggaaag gccatcgttg aagatgcctc tgccgacagt 240

ggtcccaaag atggaccccc acccacgagg agcatcgtgg aaaaagaaga cgttccaacc 300

acgtcttcaa agcaagtgga ttgatgtgat aacatggtgg agcacgacac acttgtctac 360

tccaaaaata tcaaagatac agtctcagaa gaccaaaggg caattgagac ttttcaacaa 420

agggtaatat ccggaaacct cctcggattc cattgcccag ctatctgtca ctttattgtg 480

aagatagtgg aaaaggaagg tggctcctac aaatgccatc attgcgataa aggaaaggcc 540

atcgttgaag atgcctctgc cgacagtggt cccaaagatg gacccccacc cacgaggagc 600

atcgtggaaa aagaagacgt tccaaccacg tcttcaaagc aagtggattg atgtgatatc 660

tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc ttcctctata 720

taaggaagtt catttcattt ggagaggtat taaaatctta ataggttttg ataaaagcga 780

acgtggggaa acccgaacca aaccttcttc taaactctct ctcatctctc ttaaagcaaa 840

cttctctctt gtctttcttg cgtgagcgat cttcaacgtt gtcagatcgt gcttcggcac 900

cagtacaatg aaaatggcct cgagtgacgc taaccctagt gacggcagcg ccgccaatct 960

tgtgcctgag gttaataatg aggtgatggc cctggagcct gtggtgggcg cagccatagc 1020

agcgcccgtg gccggtcagc agaatgtgat tgacccgtgg atacgcaaca attttgtcca 1080

agcccctggt ggggagttca ccgttagccc gagaaatgcg ccaggagaaa tcctgtggtc 1140

ggccagcttg ggacccgatc tgaaccccta tttgctgcat ctcgctcgga tgtacaacgg 1200

gtatgccggc ggatttgaag tgcaggtgat tctggctggg aacgcgttca ctgctggcaa 1260

agtgatcttt gcagcggtgc ctcccaactt ccccactgaa ggactgtctc caagccaggt 1320

cacaatgttt ccacacatcg tggtggacgt acggcagcta gagcctgtcc tgattcccct 1380

ccctgatgta cgcaataatt tctaccacta caatcaatcc aatgatccga ccattaaact 1440

catcgcgatg ttgtacaccc ctctgcgcgc taacaatgct ggagacgacg tattcaccgt 1500

gtcatgcaga gtgctcacca gaccttcacc agactttgac tttatcttct tagtgccccc 1560

cactgttgag agccgaacca agccctttag tgtccccgta ctcacagtcg aggagatgac 1620

aaatagccgc tttccaatcc cccttgagaa actgttcaca ggaccttcct cggcattcgt 1680

ggttcagcca cagaacggac gctgcacaac tgacggcgtg ctgctcggaa ccacccagct 1740

tagccctgtt aatatctgta cgtttagagg cgacgtaact cacataactg gctcacggaa 1800

ctataccatg aatctggcat cacagaattg gaatgactac gacccaaccg aagagattcc 1860

cgcacctctt ggaacccccg actttgtggg aaaaatacag ggcgtcctga cacaaaccac 1920

cagaaccgat ggctccacac ggggacacaa ggcaaccgtc tacactggct ctgccgattt 1980

tgccccgaaa ctgggtagag tgcagtttga gaccgacact gaccgggact ttgaagccaa 2040

tcagaatact aagttcacac ctgtaggagt gattcaggac gggggcacca ctcaccggaa 2100

cgagccgcaa caatgggtcc tgccctctta tagcgggagg aatactcata atgtgcattt 2160

ggctcctgca gtggctccca cgtttcccgg ggaacaactg ctctttttttc gttcaaccat 2220

gcctggatgc tccggatatc ccaatatgga tctcgattgc ctgctcccac aggaatgggt 2280

gcagtatttt tatcaagagg ccgcaccagc ccaatccgac gtcgcacttc tgcggttcgt 2340

gaatccagac acaggccgcg tgttgtttga gtgcaaattg cacaaatcag gatacgttac 2400

agtggctcat actggacagc atgacctggt gatcccaccc aacggatatt ttaggttcga 2460

ctcctgggtg aatcagtttt atacattagc ccccatgggg aatgggactg gcagacgcag 2520

ggctgtctga aggcctattt tctttagttt gaatttactg ttattcggtg tgcatttcta 2580

tgtttggtga gcggttttct gtgctcagag tgtgtttatt ttatgtaatt taatttcttt 2640

gtgagctcct gtttagcagg tcgtcccttc agcaaggaca caaaaagatt ttaattttat 2700

tatcgttcaa acatttggca ataaagtttc ttaagattga atcctgttgc cggtcttgcg 2760

atgattatca tataatttct gttgaattac gttaagcatg taataattaa catgtaatgc 2820

atgacgttat ttatgagatg ggtttttatg attagagtcc cgcaattata catttaatac 2880

gcgatagaaa acaaaatata gcgcgcaaac taggataaat tatcgcgcgc ggtgtcatct 2940

atgttactag at 2952

<210> 167
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_Q84S

<400> 167
atgatgatgg cttccaagga tgctcccaca aacatggatg gaacaagcgg cgcggggcaa 60

cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc 120

actgctgccg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctga gcctaggacc acacttgaat ccgtttctga gtcacttggc tcagatgtat 300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca 420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg 480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc 540

ttgatatgta tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct 600

tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt ccttttttctg 660

gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720

gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggtatc tcaggatcac 780

ggtcaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840

accccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900

ggacaggggc tgaatcttac tgagatcgat ggtaccccct accatgcatt cgagtcacct 960

gcacctattg gatttcccga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020

aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140

atctgtagcc tagagtggct atctccgcca agcggtgggg cccctaaagt taacccatgg 1200

gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 168
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Mutation of SEQ ID NO;1 at positions 39-46

<400> 168

Ser Ser Thr Ala Val Ala Thr Ala
1 5

<210> 169
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized
VP1_GI.3_Lil08_A43V plus sign

<400> 169
atgatgatgg cttccaagga tgctcccaca aacatggatg gaacaagcgg cgcggggcaa 60

cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc 120

actgctgtgg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctgc agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca 420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg 480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc 540

ttgatatgta tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct 600

tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt ccttttttctg 660

gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720

gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggtatc tcaggatcac 780

ggtcaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840

accccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900

ggacaggggc tgaatcttac tgagatcgat ggtaccccct accatgcatt cgagtcacct 960

gcacctattg gatttcccga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020

aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140

atctgtagcc tagagtggct atctccgcca agcggtgggg cccctaaagt taacccatgg 1200

gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 170
<211> 543
<212> PRT
<213> Norovirus

<400> 170

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
20 25 30

Met Glu Pro Val Ala Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Met Ser Asn Tyr Val Gln Ala Pro
50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
85 90 95

Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
100 105 110

```
Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
        115                 120                 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
                165                 170                 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
            180                 185                 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
    210                 215                 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225                 230                 235                 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
                245                 250                 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
            260                 265                 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
        275                 280                 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
    290                 295                 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320
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Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
                325                 330                 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
            340                 345                 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
        355                 360                 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
    370                 375                 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385                 390                 395                 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
                405                 410                 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
            420                 425                 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
        435                 440                 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
    450                 455                 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465                 470                 475                 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
                485                 490                 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
            500                 505                 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
        515                 520                 525
```

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 171
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_M57I plus sign S94L

<400> 171
atgatgatgg cttccaagga tgctcccaca aacatggatg gaacaagcgg cgcggggcaa 60

cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc 120

actgctgccg ccaccgcagg acaggtaaac atgatcgacc cctggatcat ctcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctgc agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca 420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg 480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc 540

ttgatatgta tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct 600

tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt ccttttttctg 660

gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720

gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggtatc tcaggatcac 780

ggtcaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840

accccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900

ggacaggggc tgaatcttac tgagatcgat ggtaccccct accatgcatt cgagtcacct 960

gcacctattg gatttcccga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020

aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140

atctgtagcc tagagtggct atctccgcca agcggtgggg cccctaaagt taacccatgg 1200

gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 172
<211> 543
<212> PRT
<213> Norovirus

<400> 172

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
20 25 30

Met Glu Pro Val Ala Gly Ala Ala Thr Ala Ala Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Ile Ser Asn Tyr Val Gln Ala Pro
50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
85 90 95

Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
100 105 110

```
Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
        115                 120                 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
                165                 170                 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
            180                 185                 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
    210                 215                 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225                 230                 235                 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
                245                 250                 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
            260                 265                 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
        275                 280                 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
    290                 295                 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320
```

```
Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
                325                 330                 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
            340                 345                 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
        355                 360                 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
    370                 375                 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385                 390                 395                 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
                405                 410                 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
            420                 425                 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
        435                 440                 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
    450                 455                 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465                 470                 475                 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
                485                 490                 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
            500                 505                 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
        515                 520                 525
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Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 173
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_A43Vplus sign M57Iplus sign S94L

<400> 173
atgatgatgg cttccaagga tgctcccaca aacatggatg gaacaagcgg cgcggggcaa 60

cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc 120

actgctgtgg ccaccgcagg acaggtaaac atgatcgacc cctggatcat ctcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctgc agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca 420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg 480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc 540

ttgatatgta tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct 600

tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt ccttttttctg 660

gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720

gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggtatc tcaggatcac 780

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ggacaggggc tgaatcttac tgagatcgat ggtaccccct accatgcatt cgagtcacct 960

gcacctattg gatttcccga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020

aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140

atctgtagcc tagagtggct atctccgcca agcggtgggg cccctaaagt taacccatgg 1200

gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632

<210> 174
<211> 543
<212> PRT
<213> Norovirus

<400> 174

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
20 25 30

Met Glu Pro Val Ala Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Ile Ser Asn Tyr Val Gln Ala Pro
50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
85 90 95

```
Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
            100                 105                 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
        115                 120                 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
                165                 170                 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
            180                 185                 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
    210                 215                 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225                 230                 235                 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
                245                 250                 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
            260                 265                 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu
        275                 280                 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
    290                 295                 300
```

```
Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
                325                 330                 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
            340                 345                 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
        355                 360                 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
    370                 375                 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385                 390                 395                 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
                405                 410                 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
            420                 425                 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
        435                 440                 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
    450                 455                 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465                 470                 475                 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
                485                 490                 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
            500                 505                 510
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Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 175
<211> 1617
<212> DNA
<213> Norovirus

<400> 175
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ctggtgcccg aggtcaatgc cgcagaacca cttcctcttg agcccgtcgt tggcgccgcc 120

acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat gaacaatttc 180

gttcaggcac cagaaggaga attcaccatc tcccccaata acaccccagg ggatattctg 240

tttgacctca ggttaggacc ccacttgaac ccctttctgc ttcatctctc acaaatgtat 300

aatggctggg tcgggaatat gcgcgtgcgg gtgatgctag ccggcaatgc tttttctgca 360

ggcaagatta tcatttgctg cgttcctcct ggattcgaat ctcaaaatat cagcattggt 420

caagcaacca tgtttccaca tgtgatcgct gatgttcgcg tcctggaacc cattgaagtt 480

cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540

cttctgtgta tgctctacac cccattaaga gccgggggag catcctcagg tactgaccca 600

tttgtgattg ccgggcgggt gctcacatgc ccggctccag actttaactt ccttttcttg 660

gtgccaccca gtgttgaaca gaaaaccaga cagctcacca tcccaaatat cccattgaac 720

aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780

aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840

accccagtct ccgcgaacca ggtggcccga atccggggta aagtcttcag tacaaactcc 900

ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960

gcccctcttg gctttcccga tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020

aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080

ccacacttgg gtagcatcga gttcagttca gagaaccatc cgagtggtga tcagctaggc 1140

acattgacgt ggatcagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200

acctatgggt ccactctgac agagagcaca aatttggctc cgcccatttt cccacccgga 1260

ttcggcgagg ccatagtgta ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320

cagattcctt gcacactgcc acaagaattc gtctcatcct ttgtagagca gcaggcacct 1380

attcgaggtg aggccgccct cttgcactac gtggaccctg acacccaccg caatcttggc 1440

gagtttaagc tgtaccctga cgggtttatt acctgtgtac ccaacaccgg cggcggccca 1500

caaaatttgc ccagcaatgg cgtgtttgtc ttttcctctt gggtgtctcg atactaccag 1560

cttaaacctg tcggaactac gggccccgtg cgacgactcg gcgtgaggcg ggtgtga 1617

<210> 176
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_
GI.7/GA5043/USA/2014_R84S

<400> 176
atgatgatgg ccagcaagga cgctccgagt aacatggacg gcacttcggg cgcggggcag 60

ctggtgcccg aggtcaatgc cgcagaacca cttcctcttg agcccgtcgt tggcgccgcc 120

acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat gaacaatttc 180

gttcaggcac cagaaggaga attcaccatc tcccccaata acaccccagg ggatattctg 240

tttgacctca gcttaggacc ccacttgaac ccctttctgc ttcatctctc acaaatgtat 300

aatggctggg tcgggaatat gcgcgtgcgg gtgatgctag ccggcaatgc tttttctgca 360

ggcaagatta tcatttgctg cgttcctcct ggattcgaat ctcaaaatat cagcattggt 420

caagcaacca tgtttccaca tgtgatcgct gatgttcgcg tcctggaacc cattgaagtt 480

cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540

cttctgtgta tgctctacac cccattaaga gccgggggag catcctcagg tactgaccca 600

tttgtgattg ccgggcgggt gctcacatgc ccggctccag actttaactt ccttttcttg 660

gtgccaccca gtgttgaaca gaaaaccaga cagctcacca tcccaaatat cccattgaac 720

aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780

aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840

accccagtct ccgcgaacca ggtggcccga atccggggta aagtcttcag tacaaactcc 900

ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960

gcccctcttg gctttcccga tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020

aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080

ccacacttgg gtagcatcga gttcagttca gagaaccatc cgagtggtga tcagctaggc 1140

acattgacgt ggatcagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200

acctatgggt ccactctgac agagagcaca aatttggctc cgcccatttt cccacccgga 1260

ttcggcgagg ccatagtgta ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320

cagattcctt gcacactgcc acaagaattc gtctcatcct ttgtagagca gcaggcacct 1380

attcgaggtg aggccgccct cttgcactac gtggaccctg acacccaccg caatcttggc 1440

gagtttaagc tgtaccctga cgggtttatt acctgtgtac ccaacaccgg cggcggccca 1500

caaaatttgc ccagcaatgg cgtgtttgtc ttttcctctt gggtgtctcg atactaccag 1560

cttaaacctg tcggaactac gggccccgtg cgacgactcg gcgtgaggcg ggtgtga 1617

<210> 177
<211> 538
<212> PRT
<213> Norovirus

<400> 177

Met Met Met Ala Ser Lys Asp Ala Pro Ser Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Ala Ala Glu Pro Leu Pro
20 25 30

Leu Glu Pro Val Val Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Met Asn Asn Phe Val Gln Ala Pro
50 55 60

```
Glu Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Met
            100                 105                 110

Leu Ala Gly Asn Ala Phe Ser Ala Gly Lys Ile Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Glu Ser Gln Asn Ile Ser Ile Gly Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Asp Asp Val Arg Asn Val Leu Phe His Thr Asn Glu Asn Arg
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Ala Gly
            180                 185                 190

Gly Ala Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ala Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Ser
    210                 215                 220

Val Glu Gln Lys Thr Arg Gln Leu Thr Ile Pro Asn Ile Pro Leu Asn
225                 230                 235                 240

Asn Leu Ala Asn Ser Arg Val Pro Ala Met Ile Asn Lys Met Thr Val
                245                 250                 255

Ser Ala Asp Gln Asn Gln Val Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270
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```
Leu Glu Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Ala Asn Gln Val
        275                 280                 285

Ala Arg Ile Arg Gly Lys Val Phe Ser Thr Asn Ser Gly Thr Gly Leu
    290                 295                 300

Asn Leu Thr Glu Val Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Leu Gly Phe Pro Asp Ile Gly Asn Cys Asp Trp His Val Tyr
                325                 330                 335

Ala Phe Lys Val Asn Gln Asn Thr Gly Asp Pro Met Tyr Arg Leu Asp
            340                 345                 350

Ile Thr Gln Gly Asn Ser Phe Ala Pro His Leu Gly Ser Ile Glu Phe
        355                 360                 365

Ser Ser Glu Asn His Pro Ser Gly Asp Gln Leu Gly Thr Leu Thr Trp
    370                 375                 380

Ile Ser Pro Leu Asn Asn Ala Ser Arg Val Asp Pro Trp Lys Ile Pro
385                 390                 395                 400

Thr Tyr Gly Ser Thr Leu Thr Glu Ser Thr Asn Leu Ala Pro Pro Ile
                405                 410                 415

Phe Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe Met Ser Asp Phe
            420                 425                 430

Pro Ile Val Ser Gly Asn Thr Ala Gln Ile Pro Cys Thr Leu Pro Gln
        435                 440                 445

Glu Phe Val Ser Ser Phe Val Glu Gln Gln Ala Pro Ile Arg Gly Glu
    450                 455                 460

Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His Arg Asn Leu Gly
465                 470                 475                 480
```

Glu Phe Lys Leu Tyr Pro Asp Gly Phe Ile Thr Cys Val Pro Asn Thr
485 490 495

Gly Gly Gly Pro Gln Asn Leu Pro Ser Asn Gly Val Phe Val Phe Ser
500 505 510

Ser Trp Val Ser Arg Tyr Tyr Gln Leu Lys Pro Val Gly Thr Thr Gly
515 520 525

Pro Val Arg Arg Leu Gly Val Arg Arg Val
530 535

<210> 178
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_
GI.7/GA5043/USA/2014_M57I

<400> 178
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ctggtgcccg aggtcaatgc cgcagaacca cttcctcttg agcccgtcgt tggcgccgcc 120

acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat caacaatttc 180

gttcaggcac cagaaggaga attcaccatc tcccccaata acaccccagg ggatattctg 240

tttgacctca ggttaggacc ccacttgaac ccctttctgc ttcatctctc acaaatgtat 300

aatggctggg tcgggaatat gcgcgtgcgg gtgatgctag ccggcaatgc tttttctgca 360

ggcaagatta tcatttgctg cgttcctcct ggattcgaat ctcaaaatat cagcattggt 420

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cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540

cttctgtgta tgctctacac cccattaaga gccgggggag catcctcagg tactgaccca 600

tttgtgattg ccgggcgggt gctcacatgc ccggctccag actttaactt ccttttcttg 660

gtgccaccca gtgttgaaca gaaaaccaga cagctcacca tcccaaatat cccattgaac 720

aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780

aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840

accccagtct ccgcgaacca ggtggcccga atccggggta aagtcttcag tacaaactcc 900

ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960

gcccctcttg gctttcccga tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020

aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080

ccacacttgg gtagcatcga gttcagttca gagaaccatc cgagtggtga tcagctaggc 1140

acattgacgt ggatcagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200

acctatgggt ccactctgac agagagcaca aatttggctc cgcccatttt cccacccgga 1260

ttcggcgagg ccatagtgta ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320

cagattcctt gcacactgcc acaagaattc gtctcatcct ttgtagagca gcaggcacct 1380

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caaaatttgc ccagcaatgg cgtgtttgtc ttttcctctt gggtgtctcg atactaccag 1560

cttaaacctg tcggaactac gggccccgtg cgacgactcg gcgtgaggcg ggtgtga 1617

<210> 179
<211> 538
<212> PRT
<213> Norovirus

<400> 179

Met Met Met Ala Ser Lys Asp Ala Pro Ser Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Ala Ala Glu Pro Leu Pro
20 25 30

Leu Glu Pro Val Val Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro
50 55 60

```
Glu Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Arg Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Met
            100                 105                 110

Leu Ala Gly Asn Ala Phe Ser Ala Gly Lys Ile Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Glu Ser Gln Asn Ile Ser Ile Gly Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Asp Asp Val Arg Asn Val Leu Phe His Thr Asn Glu Asn Arg
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Ala Gly
            180                 185                 190

Gly Ala Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ala Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Ser
    210                 215                 220

Val Glu Gln Lys Thr Arg Gln Leu Thr Ile Pro Asn Ile Pro Leu Asn
225                 230                 235                 240

Asn Leu Ala Asn Ser Arg Val Pro Ala Met Ile Asn Lys Met Thr Val
                245                 250                 255

Ser Ala Asp Gln Asn Gln Val Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270
```

```
Leu Glu Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Ala Asn Gln Val
        275                 280                 285

Ala Arg Ile Arg Gly Lys Val Phe Ser Thr Asn Ser Gly Thr Gly Leu
    290                 295                 300

Asn Leu Thr Glu Val Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Leu Gly Phe Pro Asp Ile Gly Asn Cys Asp Trp His Val Tyr
                325                 330                 335

Ala Phe Lys Val Asn Gln Asn Thr Gly Asp Pro Met Tyr Arg Leu Asp
            340                 345                 350

Ile Thr Gln Gly Asn Ser Phe Ala Pro His Leu Gly Ser Ile Glu Phe
        355                 360                 365

Ser Ser Glu Asn His Pro Ser Gly Asp Gln Leu Gly Thr Leu Thr Trp
    370                 375                 380

Ile Ser Pro Leu Asn Asn Ala Ser Arg Val Asp Pro Trp Lys Ile Pro
385                 390                 395                 400

Thr Tyr Gly Ser Thr Leu Thr Glu Ser Thr Asn Leu Ala Pro Pro Ile
                405                 410                 415

Phe Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe Met Ser Asp Phe
            420                 425                 430

Pro Ile Val Ser Gly Asn Thr Ala Gln Ile Pro Cys Thr Leu Pro Gln
        435                 440                 445

Glu Phe Val Ser Ser Phe Val Glu Gln Gln Ala Pro Ile Arg Gly Glu
    450                 455                 460

Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His Arg Asn Leu Gly
465                 470                 475                 480
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Glu Phe Lys Leu Tyr Pro Asp Gly Phe Ile Thr Cys Val Pro Asn Thr
485 490 495

Gly Gly Gly Pro Gln Asn Leu Pro Ser Asn Gly Val Phe Val Phe Ser
500 505 510

Ser Trp Val Ser Arg Tyr Tyr Gln Leu Lys Pro Val Gly Thr Thr Gly
515 520 525

Pro Val Arg Arg Leu Gly Val Arg Arg Val
530 535

<210> 180
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_
GI.7/GA5043/USA/2014_M57I plus sign R84S

<400> 180
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ctggtgcccg aggtcaatgc cgcagaacca cttcctcttg agcccgtcgt tggcgccgcc 120

acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat caacaatttc 180

gttcaggcac cagaaggaga attcaccatc tcccccaata acaccccagg ggatattctg 240

tttgacctca gcttaggacc ccacttgaac ccctttctgc ttcatctctc acaaatgtat 300

aatggctggg tcgggaatat gcgcgtgcgg gtgatgctag ccggcaatgc tttttctgca 360

ggcaagatta tcatttgctg cgttcctcct ggattcgaat ctcaaaatat cagcattggt 420

caagcaacca tgtttccaca tgtgatcgct gatgttcgcg tcctggaacc cattgaagtt 480

cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540

cttctgtgta tgctctacac cccattaaga gccgggggag catcctcagg tactgaccca 600

tttgtgattg ccgggcgggt gctcacatgc ccggctccag actttaactt ccttttcttg 660

gtgccaccca gtgttgaaca gaaaaccaga cagctcacca tcccaaatat cccattgaac 720

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aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840

accccagtct ccgcgaacca ggtggcccga atccggggta aagtcttcag tacaaactcc 900

ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960

gcccctcttg gctttcccga tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020

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acctatgggt ccactctgac agagagcaca aatttggctc cgcccatttt cccacccgga 1260

ttcggcgagg ccatagtgta ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320

cagattcctt gcacactgcc acaagaattc gtctcatcct ttgtagagca gcaggcacct 1380

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caaaatttgc ccagcaatgg cgtgtttgtc ttttcctctt gggtgtctcg atactaccag 1560

cttaaacctg tcggaactac gggccccgtg cgacgactcg gcgtgaggcg ggtgtga 1617

<210> 181
<211> 538
<212> PRT
<213> Norovirus

<400> 181

Met Met Met Ala Ser Lys Asp Ala Pro Ser Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Asn Ala Ala Glu Pro Leu Pro
20 25 30

Leu Glu Pro Val Val Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro
50 55 60

```
Glu Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65                  70                  75                  80

Phe Asp Leu Ser Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
                85                  90                  95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Met
            100                 105                 110

Leu Ala Gly Asn Ala Phe Ser Ala Gly Lys Ile Ile Ile Cys Cys Val
        115                 120                 125

Pro Pro Gly Phe Glu Ser Gln Asn Ile Ser Ile Gly Gln Ala Thr Met
    130                 135                 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160

Pro Leu Asp Asp Val Arg Asn Val Leu Phe His Thr Asn Glu Asn Arg
                165                 170                 175

Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Ala Gly
            180                 185                 190

Gly Ala Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205

Thr Cys Pro Ala Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Ser
    210                 215                 220

Val Glu Gln Lys Thr Arg Gln Leu Thr Ile Pro Asn Ile Pro Leu Asn
225                 230                 235                 240

Asn Leu Ala Asn Ser Arg Val Pro Ala Met Ile Asn Lys Met Thr Val
                245                 250                 255

Ser Ala Asp Gln Asn Gln Val Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270
```

```
Leu Glu Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Ala Asn Gln Val
        275                 280                 285

Ala Arg Ile Arg Gly Lys Val Phe Ser Thr Asn Ser Gly Thr Gly Leu
    290                 295                 300

Asn Leu Thr Glu Val Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Leu Gly Phe Pro Asp Ile Gly Asn Cys Asp Trp His Val Tyr
                325                 330                 335

Ala Phe Lys Val Asn Gln Asn Thr Gly Asp Pro Met Tyr Arg Leu Asp
            340                 345                 350

Ile Thr Gln Gly Asn Ser Phe Ala Pro His Leu Gly Ser Ile Glu Phe
        355                 360                 365

Ser Ser Glu Asn His Pro Ser Gly Asp Gln Leu Gly Thr Leu Thr Trp
    370                 375                 380

Ile Ser Pro Leu Asn Asn Ala Ser Arg Val Asp Pro Trp Lys Ile Pro
385                 390                 395                 400

Thr Tyr Gly Ser Thr Leu Thr Glu Ser Thr Asn Leu Ala Pro Pro Ile
                405                 410                 415

Phe Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe Met Ser Asp Phe
            420                 425                 430

Pro Ile Val Ser Gly Asn Thr Ala Gln Ile Pro Cys Thr Leu Pro Gln
        435                 440                 445

Glu Phe Val Ser Ser Phe Val Glu Gln Gln Ala Pro Ile Arg Gly Glu
    450                 455                 460

Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His Arg Asn Leu Gly
465                 470                 475                 480
```

Glu Phe Lys Leu Tyr Pro Asp Gly Phe Ile Thr Cys Val Pro Asn Thr
485 490 495

Gly Gly Gly Pro Gln Asn Leu Pro Ser Asn Gly Val Phe Val Phe Ser
500 505 510

Ser Trp Val Ser Arg Tyr Tyr Gln Leu Lys Pro Val Gly Thr Thr Gly
515 520 525

Pro Val Arg Arg Leu Gly Val Arg Arg Val
530 535

<210> 182
<211> 542
<212> PRT
<213> Norovirus

<400> 182

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Leu Ala Val Pro Val Thr Gly Gln Thr Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
100 105 110

```
Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300

Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320
```

```
Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
                325                 330                 335

Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
            340                 345                 350

Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
        355                 360                 365

Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
    370                 375                 380

Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385                 390                 395                 400

His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
                405                 410                 415

Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
            420                 425                 430

Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
        435                 440                 445

Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
    450                 455                 460

Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465                 470                 475                 480

Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
                485                 490                 495

Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
            500                 505                 510

Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
        515                 520                 525
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Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
530 535 540

<210> 183
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_A39V plus sign E80S plus sign A90L

<400> 183
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc 60

gagtctaata acgaggtgat ggccttggag cctgttgcag gggctgccct cgcagtgcct 120

gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcagc 240

ctgggaccag aacttaatcc gtacctgctc cacctggccc ggatgtacaa tggatatgca 300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480

gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcat ttctgtgcag 780

tgtcagaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840

agtggaattt gcgcctttaa gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900

tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

aagcataaca cacccggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080

acctatacgg ctcagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140

gatgacctca ctgtgaatca acctgtgaaa ttcactccag taggtctgaa tgatacagac 1200

cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

gcccttccg ttgcacctgt gtttccgggg gagcggttgc tcttctttag aagctatatt 1320

cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

aatccagaca caggaagagc actgttcgag gccaagctgc acagagccgg cttcatgacc 1500

gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

agttgggtga atcagtttta ctcgttggcc cccatgggca cagggaacgg tcgccgacgg 1620

atccagtaa 1629

<210> 184
<211> 542
<212> PRT
<213> Norovirus

<400> 184

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Leu Ala Ala Pro Val Thr Gly Gln Thr Asn Ile Ile
35 40 45

Asp Pro Trp Ile Ile Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
100 105 110

```
Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300

Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320
```

```
Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
                325                 330                 335

Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
            340                 345                 350

Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
        355                 360                 365

Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
    370                 375                 380

Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385                 390                 395                 400

His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
                405                 410                 415

Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
            420                 425                 430

Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
        435                 440                 445

Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
    450                 455                 460

Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465                 470                 475                 480

Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
                485                 490                 495

Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
            500                 505                 510

Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
        515                 520                 525
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Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
530 535 540

<210> 185
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_R53I plus sign E80S plus sign A90L

<400> 185
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc 60

gagtctaata acgaggtgat ggccttggag cctgttgcag gggctgccct cgcagctcct 120

gtgaccgggc agacaaatat catcgatcct tggattatcg ctaatttcgt gcaagcccca 180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcagc 240

ctgggaccag aacttaatcc gtacctgctc cacctggccc ggatgtacaa tggatatgca 300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480

gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcat ttctgtgcag 780

tgtcagaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840

agtggaattt gcgcctttaa gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900

tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

aagcataaca cacccggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080

acctatacgg ctcagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140

gatgacctca ctgtgaatca acctgtgaaa ttcactccag taggtctgaa tgatacagac 1200

cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

gccccttccg ttgcacctgt gtttccgggg gagcggttgc tcttctttag aagctatatt 1320

cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

aatccagaca caggaagagc actgttcgag gccaagctgc acagagccgg cttcatgacc 1500

gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

agttgggtga atcagtttta ctcgttggcc cccatgggca cagggaacgg tcgccgacgg 1620

atccagtaa 1629

<210> 186
<211> 542
<212> PRT
<213> Norovirus

<400> 186

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Thr Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Ser Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Leu Ala Val Pro Val Thr Gly Gln Thr Asn Ile Ile
35 40 45

Asp Pro Trp Ile Ile Ala Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Val Leu Leu Asn Leu Ser
65 70 75 80

Leu Gly Pro Glu Leu Asn Pro Tyr Leu Leu His Leu Ala Arg Met Tyr
85 90 95

```
Asn Gly Tyr Ala Gly Gly Met Glu Val Gln Val Met Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Leu Val Phe Ala Ala Val Pro Pro His Phe
        115                 120                 125

Pro Val Glu Asn Leu Ser Pro Gln Gln Ile Thr Met Phe Pro His Val
    130                 135                 140

Ile Ile Asp Val Arg Thr Leu Glu Pro Val Leu Leu Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Phe His Tyr Asn Gln Lys Asp Asp Pro Lys Met
                165                 170                 175

Arg Ile Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Thr Tyr Leu Val Pro Pro Thr Val Glu Ser Lys Thr
    210                 215                 220

Lys Pro Phe Thr Leu Pro Ile Leu Thr Leu Gly Glu Leu Ser Asn Ser
225                 230                 235                 240

Arg Phe Pro Val Ser Ile Asp Gln Met Tyr Thr Ser Pro Asn Glu Val
                245                 250                 255

Ile Ser Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
            260                 265                 270

Gln Gly Thr Thr Gln Leu Gln Val Ser Gly Ile Cys Ala Phe Lys Gly
        275                 280                 285

Glu Val Thr Ala His Leu His Asp Asn Asp His Leu Tyr Asn Val Thr
    290                 295                 300
```

```
Ile Thr Asn Leu Asn Gly Ser Pro Phe Asp Pro Ser Glu Asp Ile Pro
305                 310                 315                 320


Ala Pro Leu Gly Val Pro Asp Phe Gln Gly Arg Val Phe Gly Val Ile
                325                 330                 335


Ser Gln Arg Asp Lys His Asn Thr Pro Gly His Asn Glu Pro Ala Asn
            340                 345                 350


Arg Ala His Asp Ala Val Val Pro Thr Tyr Thr Ala Gln Tyr Thr Pro
        355                 360                 365


Lys Leu Gly Gln Ile Gln Ile Gly Thr Trp Gln Thr Asp Asp Leu Thr
    370                 375                 380


Val Asn Gln Pro Val Lys Phe Thr Pro Val Gly Leu Asn Asp Thr Asp
385                 390                 395                 400


His Phe Asn Gln Trp Val Val Pro Arg Tyr Ala Gly Ala Leu Asn Leu
                405                 410                 415


Asn Thr Asn Leu Ala Pro Ser Val Ala Pro Val Phe Pro Gly Glu Arg
            420                 425                 430


Leu Leu Phe Phe Arg Ser Tyr Ile Pro Leu Lys Gly Gly Tyr Gly Thr
        435                 440                 445


Pro Ala Ile Asp Cys Leu Leu Pro Gln Glu Trp Val Gln His Phe Tyr
    450                 455                 460


Gln Glu Ala Ala Pro Ser Met Ser Glu Val Ala Leu Val Arg Tyr Ile
465                 470                 475                 480


Asn Pro Asp Thr Gly Arg Ala Leu Phe Glu Ala Lys Leu His Arg Ala
                485                 490                 495


Gly Phe Met Thr Val Ser Ser Asn Thr Ser Ala Pro Val Val Val Pro
            500                 505                 510
```

Ala Asn Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser
515 520 525

Leu Ala Pro Met Gly Thr Gly Asn Gly Arg Arg Arg Ile Gln
530 535 540

<210> 187
<211> 1629
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_A39Vplus sign R53I plus sign E80S plus sign A90L

<400> 187
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc 60

gagtctaata acgaggtgat ggccttggag cctgttgcag gggctgccct cgcagtgcct 120

gtgaccgggc agacaaatat catcgatcct tggattatcg ctaatttcgt gcaagcccca 180

aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgctcct caatctcagc 240

ctgggaccag aacttaatcc gtacctgctc cacctggccc ggatgtacaa tggatatgca 300

ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360

ttcgcagccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420

tttccccatg tcatcatcga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480

gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540

atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600

cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

gaaagcaaaa ctaagccatt cacacttccc atcctcaccc tcggagaact ctcgaactcc 720

cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcat ttctgtgcag 780

tgtcagaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840

agtggaattt gcgcctttaa gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900

tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960

gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020

aagcataaca cacccggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080

acctatacgg ctcagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140

gatgacctca ctgtgaatca acctgtgaaa ttcactccag taggtctgaa tgatacagac 1200

cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260

gccccttccg ttgcacctgt gtttccgggg gagcggttgc tcttctttag aagctatatt 1320

cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440

aatccagaca caggaagagc actgttcgag gccaagctgc acagagccgg cttcatgacc 1500

gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560

agttgggtga atcagtttta ctcgttggcc cccatgggca cagggaacgg tcgccgacgg 1620

atccagtaa 1629

<210> 188
<211> 540
<212> PRT
<213> Norovirus

<400> 188

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Val Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Pro
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr

85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
165 170 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
195 200 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
210 215 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225 230 235 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
245 250 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
260 265 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
275 280 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala

```
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
```

500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 189
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1 GII.4_Syd12_A39V plus sign R53I

<400> 189
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gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagtcccc 120

gtggccggtc agcagaatgt gattgacccg tggataatca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 190
<211> 540
<212> PRT
<213> Norovirus

<400> 190

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Val Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Ile Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

```
Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
                85                  90                  95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
            100                 105                 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
        115                 120                 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
    130                 135                 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145                 150                 155                 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
                165                 170                 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
            180                 185                 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
        195                 200                 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
    210                 215                 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225                 230                 235                 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
                245                 250                 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
            260                 265                 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
        275                 280                 285
```

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Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
    290                 295                 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305                 310                 315                 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
                325                 330                 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
            340                 345                 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
        355                 360                 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
    370                 375                 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385                 390                 395                 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
                405                 410                 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
            420                 425                 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
        435                 440                 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
    450                 455                 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465                 470                 475                 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
                485                 490                 495
```

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 191
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1
GII.4_Syd12_A39V plus sign R53I plus sign P80S

<400> 191
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gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagtcccc 120

gtggccggtc agcagaatgt gattgacccg tggataatca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 192
<211> 538
<212> PRT
<213> Norovirus

<400> 192

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Gly Asn Asn Glu Thr Leu Pro Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Val Pro Val Thr Gly Gln Asn Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu

65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Val Glu Phe Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
130 135 140

Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Thr Phe Phe His Tyr Asn Asn Gln Pro Asn Ser Arg Met
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
195 200 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Leu Ser Glu Leu Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu Phe Thr Ala Gln Asn Asn Val
245 250 255

Leu Gln Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
260 265 270

Gln Gly Thr Thr Gln Leu Leu Pro Ser Gly Ile Cys Ala Phe Arg Gly

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        275                 280                 285

Arg Val Thr Ala Glu Thr Asp His Arg Asp Lys Trp His Met Gln Leu
    290                 295                 300

Gln Asn Leu Asn Gly Thr Thr Tyr Asp Pro Thr Asp Asp Val Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Lys Gly Val Val Phe Gly Val Ala Ser
                325                 330                 335

Gln Arg Asn Val Gly Asn Asp Ala Pro Gly Ser Thr Arg Ala His Glu
            340                 345                 350

Ala Val Ile Ser Thr Tyr Ser Pro Gln Phe Val Pro Lys Leu Gly Ser
        355                 360                 365

Val Asn Phe Arg Ser Asn Asp Asn Asp Phe Gln Leu Gln Pro Thr Lys
    370                 375                 380

Phe Thr Pro Val Gly Ile Asn Asp Asp Gly Asp His Pro Phe Arg Gln
385                 390                 395                 400

Trp Glu Leu Pro Asp Tyr Ser Gly Leu Leu Thr Leu Asn Met Asn Leu
                405                 410                 415

Ala Pro Pro Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe
            420                 425                 430

Arg Ser Phe Val Pro Cys Ser Gly Gly Tyr Asn Gln Gly Ile Val Asp
        435                 440                 445

Cys Leu Ile Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala
    450                 455                 460

Pro Ser Gln Ser Asp Val Ala Leu Ile Arg Tyr Val Asn Pro Asp Thr
465                 470                 475                 480

Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr
```

485 490 495

Val Ala His Ser Gly Asp Tyr Pro Leu Val Val Pro Ala Asn Gly Tyr
500 505 510

Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met
515 520 525

Gly Thr Gly Asn Gly Arg Arg Arg Ala Gln
530 535

<210> 193
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V

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gaggggaata atgagacact tccactagag ccggttgcag gcgccgctat agctgtgcca 120

gtgacagggc agaataatat tatagaccct tggattcgga caaacttcgt gcaggcaccc 180

aacggcgagt ttacagtatc cccccggaac tccccaggtg agatactcct gaatcttgag 240

ctcggccctg acctcaatcc atatctggct catctgagcc gcatgtacaa tggttacgct 300

gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360

tttgccgccg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420

ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480

gtgcgtaaca ccttttcca ttataacaat cagccaaact ctcggatgag acttgttgct 540

atgctgtaca ccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600

agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660

gaatctaaga ccaaaccgtt ttcactgcca atcttaactc tctccgaact gactaacagc 720

cggtttccag tacccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780

tgccagaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840

agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaaatgg 900

cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960

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gggaatgacg cccccggctc tacccgagct cacgaggccg ttatctcaac atatagcccc 1080

caatttgtgc ccaagctcgg atccgttaat tttcgtagta acgacaacga cttccaactg 1140

caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc tttccgccaa 1200

tgggaactac cagattattc tgggctgctc accctcaata tgaacctcgc cccacccgtg 1260

gcccctaatt tccccggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320

ggatataatc aaggcatcgt agactgcttg attccccaag agtggataca acatttttac 1380

caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440

ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500

ggcgattatc ccctggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560

cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

<210> 194
<211> 538
<212> PRT
<213> Norovirus

<400> 194

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Gly Asn Asn Glu Thr Leu Pro Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Val Thr Gly Gln Asn Asn Ile Ile
35 40 45

Asp Pro Trp Ile Ile Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu

65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Val Glu Phe Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
130 135 140

Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Thr Phe Phe His Tyr Asn Asn Gln Pro Asn Ser Arg Met
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
195 200 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Leu Ser Glu Leu Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu Phe Thr Ala Gln Asn Asn Val
245 250 255

Leu Gln Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
260 265 270

Gln Gly Thr Thr Gln Leu Leu Pro Ser Gly Ile Cys Ala Phe Arg Gly

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        275                 280                 285

Arg Val Thr Ala Glu Thr Asp His Arg Asp Lys Trp His Met Gln Leu
    290                 295                 300

Gln Asn Leu Asn Gly Thr Thr Tyr Asp Pro Thr Asp Asp Val Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Lys Gly Val Val Phe Gly Val Ala Ser
                325                 330                 335

Gln Arg Asn Val Gly Asn Asp Ala Pro Gly Ser Thr Arg Ala His Glu
            340                 345                 350

Ala Val Ile Ser Thr Tyr Ser Pro Gln Phe Val Pro Lys Leu Gly Ser
        355                 360                 365

Val Asn Phe Arg Ser Asn Asp Asn Asp Phe Gln Leu Gln Pro Thr Lys
    370                 375                 380

Phe Thr Pro Val Gly Ile Asn Asp Asp Gly Asp His Pro Phe Arg Gln
385                 390                 395                 400

Trp Glu Leu Pro Asp Tyr Ser Gly Leu Leu Thr Leu Asn Met Asn Leu
                405                 410                 415

Ala Pro Pro Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe
            420                 425                 430

Arg Ser Phe Val Pro Cys Ser Gly Gly Tyr Asn Gln Gly Ile Val Asp
        435                 440                 445

Cys Leu Ile Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala
    450                 455                 460

Pro Ser Gln Ser Asp Val Ala Leu Ile Arg Tyr Val Asn Pro Asp Thr
465                 470                 475                 480

Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr
```

485 490 495

Val Ala His Ser Gly Asp Tyr Pro Leu Val Val Pro Ala Asn Gly Tyr
500 505 510

Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met
515 520 525

Gly Thr Gly Asn Gly Arg Arg Arg Ala Gln
530 535

<210> 195
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_R53I

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gaggggaata atgagacact tccactagag ccggttgcag gcgccgctat agctgcccca 120

gtgacagggc agaataatat tatagaccct tggattatca caaacttcgt gcaggcaccc 180

aacggcgagt ttacagtatc cccccggaac tccccaggtg agatactcct gaatcttgag 240

ctcggccctg acctcaatcc atatctggct catctgagcc gcatgtacaa tggttacgct 300

gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360

tttgccgccg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420

ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480

gtgcgtaaca ccttttcca ttataacaat cagccaaact ctcggatgag acttgttgct 540

atgctgtaca ccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600

agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660

gaatctaaga ccaaaccgtt ttcactgcca atcttaactc tctccgaact gactaacagc 720

cggtttccag tacccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780

tgccagaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840

agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaaatgg 900

cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960

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caatttgtgc ccaagctcgg atccgttaat tttcgtagta acgacaacga cttccaactg 1140

caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc tttccgccaa 1200

tgggaactac cagattattc tgggctgctc accctcaata tgaacctcgc cccacccgtg 1260

gcccctaatt tccccggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320

ggatataatc aaggcatcgt agactgcttg attccccaag agtggataca acatttttac 1380

caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440

ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500

ggcgattatc ccctggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560

cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

<210> 196
<211> 538
<212> PRT
<213> Norovirus

<400> 196

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Gly Asn Asn Glu Thr Leu Pro Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Val Thr Gly Gln Asn Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu

65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Leu His Leu Ser Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Val Glu Phe Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
130 135 140

Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Thr Phe Phe His Tyr Asn Asn Gln Pro Asn Ser Arg Met
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
195 200 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Leu Ser Glu Leu Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu Phe Thr Ala Gln Asn Asn Val
245 250 255

Leu Gln Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
260 265 270

Gln Gly Thr Thr Gln Leu Leu Pro Ser Gly Ile Cys Ala Phe Arg Gly

```
        275                 280                 285

Arg Val Thr Ala Glu Thr Asp His Arg Asp Lys Trp His Met Gln Leu
    290                 295                 300

Gln Asn Leu Asn Gly Thr Thr Tyr Asp Pro Thr Asp Asp Val Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Lys Gly Val Val Phe Gly Val Ala Ser
                325                 330                 335

Gln Arg Asn Val Gly Asn Asp Ala Pro Gly Ser Thr Arg Ala His Glu
            340                 345                 350

Ala Val Ile Ser Thr Tyr Ser Pro Gln Phe Val Pro Lys Leu Gly Ser
        355                 360                 365

Val Asn Phe Arg Ser Asn Asp Asn Asp Phe Gln Leu Gln Pro Thr Lys
    370                 375                 380

Phe Thr Pro Val Gly Ile Asn Asp Asp Gly Asp His Pro Phe Arg Gln
385                 390                 395                 400

Trp Glu Leu Pro Asp Tyr Ser Gly Leu Leu Thr Leu Asn Met Asn Leu
                405                 410                 415

Ala Pro Pro Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe
            420                 425                 430

Arg Ser Phe Val Pro Cys Ser Gly Gly Tyr Asn Gln Gly Ile Val Asp
        435                 440                 445

Cys Leu Ile Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala
    450                 455                 460

Pro Ser Gln Ser Asp Val Ala Leu Ile Arg Tyr Val Asn Pro Asp Thr
465                 470                 475                 480

Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr
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485 490 495

Val Ala His Ser Gly Asp Tyr Pro Leu Val Val Pro Ala Asn Gly Tyr
500 505 510

Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met
515 520 525

Gly Thr Gly Asn Gly Arg Arg Arg Ala Gln
530 535

<210> 197
<211> 1617
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A90L

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gtgacagggc agaataatat tatagaccct tggattcgga caaacttcgt gcaggcaccc 180

aacggcgagt ttacagtatc cccccggaac tccccaggtg agatactcct gaatcttgag 240

ctcggccctg acctcaatcc atatctgctg catctgagcc gcatgtacaa tggttacgct 300

gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360

tttgccgccg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420

ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480

gtgcgtaaca ccttttcca ttataacaat cagccaaact ctcggatgag acttgttgct 540

atgctgtaca ccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600

agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660

gaatctaaga ccaaaccgtt ttcactgcca atcttaactc tctccgaact gactaacagc 720

cggtttccag tacccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780

tgccagaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840

agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaaatgg 900

cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960

ccgctaggga ctcctgactt taaggggtg gtgttcggag tggcctctca gcggaatgtt 1020

gggaatgacg cccccggctc tacccgagct cacgaggccg ttatctcaac atatagcccc 1080

caatttgtgc ccaagctcgg atccgttaat tttcgtagta acgacaacga cttccaactg 1140

caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc tttccgccaa 1200

tgggaactac cagattattc tgggctgctc accctcaata tgaacctcgc cccacccgtg 1260

gcccctaatt tccccggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320

ggatataatc aaggcatcgt agactgcttg attccccaag agtggataca acatttttac 1380

caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440

ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500

ggcgattatc ccctggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560

cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

<210> 198
<211> 538
<212> PRT
<213> Norovirus

<400> 198

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Gly Leu Val Pro Glu Gly Asn Asn Glu Thr Leu Pro Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Val Pro Val Thr Gly Gln Asn Asn Ile Ile
35 40 45

Asp Pro Trp Ile Ile Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Glu

65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ala His Leu Ser Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Val Glu Phe Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
130 135 140

Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Thr Phe Phe His Tyr Asn Asn Gln Pro Asn Ser Arg Met
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
195 200 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Leu Ser Glu Leu Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu Phe Thr Ala Gln Asn Asn Val
245 250 255

Leu Gln Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
260 265 270

Gln Gly Thr Thr Gln Leu Leu Pro Ser Gly Ile Cys Ala Phe Arg Gly

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        275                 280                 285

Arg Val Thr Ala Glu Thr Asp His Arg Asp Lys Trp His Met Gln Leu
    290                 295                 300

Gln Asn Leu Asn Gly Thr Thr Tyr Asp Pro Thr Asp Asp Val Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Lys Gly Val Val Phe Gly Val Ala Ser
                325                 330                 335

Gln Arg Asn Val Gly Asn Asp Ala Pro Gly Ser Thr Arg Ala His Glu
            340                 345                 350

Ala Val Ile Ser Thr Tyr Ser Pro Gln Phe Val Pro Lys Leu Gly Ser
        355                 360                 365

Val Asn Phe Arg Ser Asn Asp Asn Asp Phe Gln Leu Gln Pro Thr Lys
    370                 375                 380

Phe Thr Pro Val Gly Ile Asn Asp Asp Gly Asp His Pro Phe Arg Gln
385                 390                 395                 400

Trp Glu Leu Pro Asp Tyr Ser Gly Leu Leu Thr Leu Asn Met Asn Leu
                405                 410                 415

Ala Pro Pro Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe
            420                 425                 430

Arg Ser Phe Val Pro Cys Ser Gly Gly Tyr Asn Gln Gly Ile Val Asp
        435                 440                 445

Cys Leu Ile Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala
    450                 455                 460

Pro Ser Gln Ser Asp Val Ala Leu Ile Arg Tyr Val Asn Pro Asp Thr
465                 470                 475                 480

Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr
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485 490 495

Val Ala His Ser Gly Asp Tyr Pro Leu Val Val Pro Ala Asn Gly Tyr
500 505 510

Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met
515 520 525

Gly Thr Gly Asn Gly Arg Arg Arg Ala Gln
530 535

<210> 199
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<220>
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gtgacagggc agaataatat tatagaccct tggattatca caaacttcgt gcaggcaccc 180

aacggcgagt ttacagtatc cccccggaac tccccaggtg agatactcct gaatcttgag 240

ctcggccctg acctcaatcc atatctggct catctgagcc gcatgtacaa tggttacgct 300

gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360

tttgccgccg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420

ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480

gtgcgtaaca ccttttcca ttataacaat cagccaaact ctcggatgag acttgttgct 540

atgctgtaca ccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600

agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660

gaatctaaga ccaaaccgtt ttcactgcca atcttaactc tctccgaact gactaacagc 720

cggtttccag tacccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780

tgccagaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840

agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaaatgg 900

cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960

ccgctaggga ctcctgactt taaggggtg gtgttcggag tggcctctca gcggaatgtt 1020

gggaatgacg cccccggctc tacccgagct cacgaggccg ttatctcaac atatagcccc 1080

caatttgtgc ccaagctcgg atccgttaat tttcgtagta acgacaacga cttccaactg 1140

caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc tttccgccaa 1200

tgggaactac cagattattc tgggctgctc accctcaata tgaacctcgc cccacccgtg 1260

gcccctaatt tccccggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320

ggatataatc aaggcatcgt agactgcttg attccccaag agtggataca acatttttac 1380

caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440

ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500

ggcgattatc ccctggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560

cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

<210> 200
<211> 538
<212> PRT
<213> Norovirus

<400> 200

Met Lys Met Ala Ser Asn Asp Ala Ala Pro Ser Asn Asp Gly Ala Ala
1 5 10 15

Gly Leu Val Pro Glu Gly Asn Asn Glu Thr Leu Pro Leu Glu Pro Val
20 25 30

Ala Gly Ala Ala Ile Ala Ala Pro Val Thr Gly Gln Asn Asn Ile Ile
35 40 45

Asp Pro Trp Ile Arg Thr Asn Phe Val Gln Ala Pro Asn Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ser Pro Gly Glu Ile Leu Leu Asn Leu Ser

65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Leu His Leu Ser Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Val Glu Val Gln Val Leu Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Ile Leu Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Val Glu Phe Leu Ser Pro Ala Gln Ile Thr Met Leu Pro His Leu
130 135 140

Ile Val Asp Val Arg Thr Leu Glu Pro Ile Met Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Thr Phe Phe His Tyr Asn Asn Gln Pro Asn Ser Arg Met
165 170 175

Arg Leu Val Ala Met Leu Tyr Thr Pro Leu Arg Ser Asn Gly Ser Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Thr Pro
195 200 205

Asp Phe Glu Phe Thr Tyr Leu Val Pro Pro Ser Val Glu Ser Lys Thr
210 215 220

Lys Pro Phe Ser Leu Pro Ile Leu Thr Leu Ser Glu Leu Thr Asn Ser
225 230 235 240

Arg Phe Pro Val Pro Ile Asp Ser Leu Phe Thr Ala Gln Asn Asn Val
245 250 255

Leu Gln Val Gln Cys Gln Asn Gly Arg Cys Thr Leu Asp Gly Glu Leu
260 265 270

Gln Gly Thr Thr Gln Leu Leu Pro Ser Gly Ile Cys Ala Phe Arg Gly

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        275                 280                 285

Arg Val Thr Ala Glu Thr Asp His Arg Asp Lys Trp His Met Gln Leu
    290                 295                 300

Gln Asn Leu Asn Gly Thr Thr Tyr Asp Pro Thr Asp Asp Val Pro Ala
305                 310                 315                 320

Pro Leu Gly Thr Pro Asp Phe Lys Gly Val Val Phe Gly Val Ala Ser
                325                 330                 335

Gln Arg Asn Val Gly Asn Asp Ala Pro Gly Ser Thr Arg Ala His Glu
            340                 345                 350

Ala Val Ile Ser Thr Tyr Ser Pro Gln Phe Val Pro Lys Leu Gly Ser
        355                 360                 365

Val Asn Phe Arg Ser Asn Asp Asn Asp Phe Gln Leu Gln Pro Thr Lys
    370                 375                 380

Phe Thr Pro Val Gly Ile Asn Asp Asp Gly Asp His Pro Phe Arg Gln
385                 390                 395                 400

Trp Glu Leu Pro Asp Tyr Ser Gly Leu Leu Thr Leu Asn Met Asn Leu
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Ala Pro Pro Val Ala Pro Asn Phe Pro Gly Glu Gln Leu Leu Phe Phe
            420                 425                 430

Arg Ser Phe Val Pro Cys Ser Gly Gly Tyr Asn Gln Gly Ile Val Asp
        435                 440                 445

Cys Leu Ile Pro Gln Glu Trp Ile Gln His Phe Tyr Gln Glu Ser Ala
    450                 455                 460

Pro Ser Gln Ser Asp Val Ala Leu Ile Arg Tyr Val Asn Pro Asp Thr
465                 470                 475                 480

Gly Arg Thr Leu Phe Glu Ala Lys Leu His Arg Ser Gly Tyr Ile Thr
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485 490 495

Val Ala His Ser Gly Asp Tyr Pro Leu Val Val Pro Ala Asn Gly Tyr
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Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Ser Leu Ala Pro Met
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Gly Thr Gly Asn Gly Arg Arg Arg Ala Gln
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<220>
<223> Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_E80S plus sign A90L

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gtgacagggc agaataatat tatagaccct tggattcgga caaacttcgt gcaggcaccc 180

aacggcgagt ttacagtatc cccccggaac tccccaggtg agatactcct gaatcttagc 240

ctcggccctg acctcaatcc atatctgctg catctgagcc gcatgtacaa tggttacgct 300

gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360

tttgccgccg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420

ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480

gtgcgtaaca ccttttcca ttataacaat cagccaaact ctcggatgag acttgttgct 540

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agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660

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cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960

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caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440

ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500

ggcgattatc ccctggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560

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<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(M57I).r

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<210> 203
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<212> DNA
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<220>
<223> Primer GI.3Lil08(M57I).c

<400> 203
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<210> 204
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-(GI.7USA14)VP1.c

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<210> 205
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer IF-(GI.7USA14)VP1.r

<400> 205
actaaagaaa ataggccttc acacccgcct cacgccgagt cgtcgcacg 49

<210> 206
<211> 48
<212> DNA
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<220>
<223> Primer GI.7USA14_VP1(R84S).r

<400> 206
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<211> 50
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<223> Primer GI.7USA14_VP1(R84S).c

<400> 207
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<210> 208
<211> 51
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<220>
<223> Primer GI.7USA14_VP1(M57I).r

<400> 208
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<210> 209
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<223> Primer GI.7USA14_VP1(M57I).c

<400> 209
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<210> 210
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<220>
<223> Primer GII.2CGMH11(A39V).r

<400> 210
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<210> 211
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<212> DNA
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<400> 211
gttgcagggg ctgccctcgc agtgcctgtg accgggcaga caaatatcat cgatccttg 59

<210> 212
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<212> DNA
<213> Artificial Sequence

<220>

<223> Primer GII.2CGMH11(R53I).r

<400> 212
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<210> 213
<211> 59
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<223> Primer GII.2CGMH11(R53I).c

<400> 213
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<210> 214
<211> 53
<212> DNA
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<220>
<223> Primer IF-GII17Kaw14VP1.c

<400> 214
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<212> DNA
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<220>
<223> Primer IF-GII17Kaw14VP1.r

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<220>
<223> Primer GII.17Kaw14(A90L).r

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<220>
<223> Primer GII.17Kaw14(A90L).c

<400> 217
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<210> 218
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<213> Artificial Sequence

<220>
<223> Primer GII.17Kaw14(A39V).r

<400> 218
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<210> 219
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<212> DNA
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<220>
<223> Primer GII.17Kaw14(A39V).c

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<220>
<223> Primer GII.17Kaw14(R53I).r

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<210> 221
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<212> DNA
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<220>
<223> Primer GII.17Kaw14(R53I).c

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<212> DNA
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<220>
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<223> Primer GII.4Syd12(P80A).c

<400> 223
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<211> 50
<212> DNA
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<223> Primer GII.4Syd12(P80N).r

<400> 224
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<210> 225
<211> 50
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<223> Primer GII.4Syd12(P80N).c

<400> 225
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<210> 226
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(P80K).r

<400> 226
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<210> 227
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(P80K).c

<400> 227
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<210> 228
<211> 50
<212> DNA
<213> Artificial /Sequence

<220>
<223> Primer GII.4Syd12(P80H).r

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<210> 229
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(P80H).c

<400> 229
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<210> 230
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39I).r

<400> 230
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<210> 231
<211> 54
<212> DNA
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<220>
<223> Primer GII.4Syd12(A39I).c

<400> 231
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<220>
<223> Primer GII.4Syd12(A39M).r

<400> 232
gaccggccac gggcattgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 233
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39M).c

<400> 233
gggcgcagcc atagcaatgc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 234
<211> 54

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39G).r

<400> 234
gaccggccac ggggcctgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 235
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39G).c

<400> 235
gggcgcagcc atagcaggcc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 236
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39S).r

<400> 236
gaccggccac ggggcttgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 237
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39S).c

<400> 237
gggcgcagcc atagcaagcc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 238
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer GII.4Syd12(A39E).r

<400> 238
gaccggccac gggctctgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 239
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39E).c

<400> 239
gggcgcagcc atagcagagc ccgtggccgg tcagcagaat gtgattgac 49

<210> 240
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39D).r

<400> 240
gaccggccac ggggtctgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 241
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39D).c

<400> 241
gggcgcagcc atagcagacc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 242
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39N).r

<400> 242
accggccacg gggtttgcta tggctgcgcc caccacaggc tccagggcca tcac 54

<210> 243
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39N).c

<400> 243
gggcgcagcc atagcaaacc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 244
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39Q).r

<400> 244
gaccggccac gggctgtgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 245
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39Q).c

<400> 245
gggcgcagcc atagcacagc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 246
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39K).r

<400> 246
gaccggccac gggctttgct atggctgcgc ccaccacagg ctccagggcc atca 54

<210> 247
<211> 54

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39K).c

<400> 247
gggcgcagcc atagcaaagc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 248
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39H).r

<400> 248
gaccggccac ggggtgtgct atggctgcgc ccaccacagg ctccagggcc a 51

<210> 249
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GII.4Syd12(A39H).c

<400> 249
gggcgcagcc atagcacacc ccgtggccgg tcagcagaat gtgattgacc cgtg 54

<210> 250
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57L).r

<400> 250
gaacgaaatt gttcagtatc cacgggtcga tcatattgac ttggcctgca 50

<210> 251
<211> 48
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer GI.7USA14_VP1(M57L).c

<400> 251
gatcgacccg tggatactga acaatttcgt tcaggcacca gaaggaga 48

<210> 252
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57G).r

<400> 252
gaacgaaatt gttgcctatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 253
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57G).c

<400> 253
gatcgacccg tggataggca acaatttcgt tcaggcacca gaaggaga 48

<210> 254
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57S).r

<400> 254
gaacgaaatt gttgcttatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 255
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57S).c

<400> 255
gatcgacccg tggataagca acaatttcgt tcaggcacca gaaggaga 48

<210> 256
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57T).r

<400> 256
gaacgaaatt gttggttatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 257
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57T).c

<400> 257
gatcgacccg tggataacca acaatttcgt tcaggcacca gaaggaga 48

<210> 258
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57N).r

<400> 258
gaacgaaatt gttgtttatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 259
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57N).c

<400> 259
gatcgacccg tggataaaca acaatttcgt tcaggcacca gaaggaga 48

<210> 260
<211> 52

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57Q).r

<400> 260
gaacgaaatt gttctgtatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 261
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57Q).c

<400> 261
gatcgacccg tggatacaga acaatttcgt tcaggcacca gaaggaga 48

<210> 262
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57K).r

<400> 262
gaacgaaatt gttctttatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 263
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57K).c

<400> 263
gatcgacccg tggataaaga acaatttcgt tcaggcacca gaaggaga 48

<210> 264
<211> 52
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer GI.7USA14_VP1(M57H).r

<400> 264
gaacgaaatt gttgtgtatc cacgggtcga tcatattgac ttggcctgca gt 52

<210> 265
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.7USA14_VP1(M57H).c

<400> 265
gatcgacccg tggatacaca acaatttcgt tcaggcacca gaaggaga 48

<210> 266
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94V).r

<400> 266
tctgagccaa gtgcaccaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 267
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94V).c

<400> 267
cttgaatccg tttctggtgc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 268
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94I).r

<400> 268
tctgagccaa gtggatcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 269
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94I).c

<400> 269
cttgaatccg tttctgatcc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 270
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94M).r

<400> 270
tctgagccaa gtgcatcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 271
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94M).c

<400> 271
cttgaatccg tttctgatgc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 272
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94T).r

<400> 272
tctgagccaa gtgggtcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 273
<211> 54

<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94T).c

<400> 273
cttgaatccg tttctgaccc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 274
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94E).r

<400> 274
tctgagccaa gtgctccaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 275
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94E).c

<400> 275
cttgaatccg tttctggagc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 276
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94D).r

<400> 276
tctgagccaa gtggtccaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 277
<211> 54
<212> DNA
<213> Artificial Sequence

<220>

<223> Primer GI.3Lil08(S94D).c

<400> 277
cttgaatccg tttctggacc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 278
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94N).r

<400> 278
tctgagccaa gtggttcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 279
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94N).c

<400> 279
cttgaatccg tttctgaacc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 280
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94Q).r

<400> 280
tctgagccaa gtgctgcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 281
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94Q).c

<400> 281
cttgaatccg tttctgcagc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 282
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94K).r

<400> 282
tctgagccaa gtgcttcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 283
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94K).c

<400> 283
cttgaatccg tttctgaagc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 284
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94H).r

<400> 284
tctgagccaa gtggtgcaga aacggattca agtgtggtcc tagctgcagg tcaa 54

<210> 285
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer GI.3Lil08(S94H).c

<400> 285
cttgaatccg tttctgcacc acttggctca gatgtataat ggatgggttg gaaa 54

<210> 286
<211> 540

<212> PRT
<213> Norovirus

<220>
<221> MISC_FEATURE
<222> (80)..(80)
<223> X may be Ala, Asn, Lys or His

<400> 286

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Ala Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Xaa
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile
130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile

165 170 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
195 200 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
210 215 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225 230 235 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
245 250 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
260 265 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
275 280 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
290 295 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305 310 315 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
325 330 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr
340 345 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
355 360 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr

370 375 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385 390 395 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
405 410 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
420 425 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
435 440 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
450 455 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 287
<211> 1623
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleic acid sequence of human codon optimized VP1
GII.4_Syd12_P80X

<400> 287

atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120

gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180

ggtggggagt tcaccgttag cccgagaaat gcgccaggag aaatcctgtg gtcggccvms 240

ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300

ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcactgctgg caaagtgatc 360

tttgcagcgg tgcctcccaa cttccccact gaaggactgt ctccaagcca ggtcacaatg 420

tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcctgattcc cctccctgat 480

gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540

atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600

agagtgctca ccagaccttc accagacttt gactttatct tcttagtgcc ccccactgtt 660

gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

cgctttccaa tccccttga gaaactgttc acaggacctt cctcggcatt cgtggttcag 780

ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840

gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900

atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960

cttggaaccc ccgactttgt gggaaaaata cagggcgtcc tgacacaaac caccagaacc 1020

gatggctcca cacggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080

aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140

actaagttca cacctgtagg agtgattcag gacgggggca ccactcaccg gaacgagccg 1200

caacaatggg tcctgccctc ttatagcggg aggaatactc ataatgtgca tttggctcct 1260

gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320

tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380

ttttatcaag aggccgcacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440

gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500

catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560

gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620

tga 1623

<210> 288
<211> 540
<212> PRT
<213> Norovirus

<220>
<221> MOD_RES
<222> (39)..(39)
<223> X may be Ile, Met, Gly, Ser, Glu, Asp, Asn, Gln, Lys or His

<400> 288

Met Lys Met Ala Ser Ser Asp Ala Asn Pro Ser Asp Gly Ser Ala Ala
1 5 10 15

Asn Leu Val Pro Glu Val Asn Asn Glu Val Met Ala Leu Glu Pro Val
20 25 30

Val Gly Ala Ala Ile Ala Xaa Pro Val Ala Gly Gln Gln Asn Val Ile
35 40 45

Asp Pro Trp Ile Arg Asn Asn Phe Val Gln Ala Pro Gly Gly Glu Phe
50 55 60

Thr Val Ser Pro Arg Asn Ala Pro Gly Glu Ile Leu Trp Ser Ala Ser
65 70 75 80

Leu Gly Pro Asp Leu Asn Pro Tyr Leu Ser His Leu Ala Arg Met Tyr
85 90 95

Asn Gly Tyr Ala Gly Gly Phe Glu Val Gln Val Ile Leu Ala Gly Asn
100 105 110

Ala Phe Thr Ala Gly Lys Val Ile Phe Ala Ala Val Pro Pro Asn Phe
115 120 125

Pro Thr Glu Gly Leu Ser Pro Ser Gln Val Thr Met Phe Pro His Ile

130 135 140

Val Val Asp Val Arg Gln Leu Glu Pro Val Leu Ile Pro Leu Pro Asp
145 150 155 160

Val Arg Asn Asn Phe Tyr His Tyr Asn Gln Ser Asn Asp Pro Thr Ile
165 170 175

Lys Leu Ile Ala Met Leu Tyr Thr Pro Leu Arg Ala Asn Asn Ala Gly
180 185 190

Asp Asp Val Phe Thr Val Ser Cys Arg Val Leu Thr Arg Pro Ser Pro
195 200 205

Asp Phe Asp Phe Ile Phe Leu Val Pro Pro Thr Val Glu Ser Arg Thr
210 215 220

Lys Pro Phe Ser Val Pro Val Leu Thr Val Glu Glu Met Thr Asn Ser
225 230 235 240

Arg Phe Pro Ile Pro Leu Glu Lys Leu Phe Thr Gly Pro Ser Ser Ala
245 250 255

Phe Val Val Gln Pro Gln Asn Gly Arg Cys Thr Thr Asp Gly Val Leu
260 265 270

Leu Gly Thr Thr Gln Leu Ser Pro Val Asn Ile Cys Thr Phe Arg Gly
275 280 285

Asp Val Thr His Ile Thr Gly Ser Arg Asn Tyr Thr Met Asn Leu Ala
290 295 300

Ser Gln Asn Trp Asn Asp Tyr Asp Pro Thr Glu Glu Ile Pro Ala Pro
305 310 315 320

Leu Gly Thr Pro Asp Phe Val Gly Lys Ile Gln Gly Val Leu Thr Gln
325 330 335

Thr Thr Arg Thr Asp Gly Ser Thr Arg Gly His Lys Ala Thr Val Tyr

340 345 350

Thr Gly Ser Ala Asp Phe Ala Pro Lys Leu Gly Arg Val Gln Phe Glu
355 360 365

Thr Asp Thr Asp Arg Asp Phe Glu Ala Asn Gln Asn Thr Lys Phe Thr
370 375 380

Pro Val Gly Val Ile Gln Asp Gly Gly Thr Thr His Arg Asn Glu Pro
385 390 395 400

Gln Gln Trp Val Leu Pro Ser Tyr Ser Gly Arg Asn Thr His Asn Val
405 410 415

His Leu Ala Pro Ala Val Ala Pro Thr Phe Pro Gly Glu Gln Leu Leu
420 425 430

Phe Phe Arg Ser Thr Met Pro Gly Cys Ser Gly Tyr Pro Asn Met Asp
435 440 445

Leu Asp Cys Leu Leu Pro Gln Glu Trp Val Gln Tyr Phe Tyr Gln Glu
450 455 460

Ala Ala Pro Ala Gln Ser Asp Val Ala Leu Leu Arg Phe Val Asn Pro
465 470 475 480

Asp Thr Gly Arg Val Leu Phe Glu Cys Lys Leu His Lys Ser Gly Tyr
485 490 495

Val Thr Val Ala His Thr Gly Gln His Asp Leu Val Ile Pro Pro Asn
500 505 510

Gly Tyr Phe Arg Phe Asp Ser Trp Val Asn Gln Phe Tyr Thr Leu Ala
515 520 525

Pro Met Gly Asn Gly Thr Gly Arg Arg Arg Ala Val
530 535 540

<210> 289

<211> 1620
<212> DNA
<213> Artificial Sequence

<220>
<223> hCod optimize sequence of VP1 GII.4_Syd12_P80S+A39X

<400> 289
atgaaaatgg cctcgagtga cgctaaccct agtgacggca gcgccgccaa tcttgtgcct 60

gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcavdsgtg 120

gccggtcagc agaatgtgat tgacccgtgg atacgcaaca attttgtcca agcccctggt 180

ggggagttca ccgttagccc gagaaatgcg ccaggagaaa tcctgtggtc ggccagcttg 240

ggacccgatc tgaaccccta tttgtcacat ctcgctcgga tgtacaacgg gtatgccggc 300

ggatttgaag tgcaggtgat tctggctggg aacgcgttca ctgctggcaa agtgatcttt 360

gcagcggtgc ctcccaactt ccccactgaa ggactgtctc caagccaggt cacaatgttt 420

ccacacatcg tggtggacgt acggcagcta gagcctgtcc tgattcccct ccctgatgta 480

cgcaataatt tctaccacta caatcaatcc aatgatccga ccattaaact catcgcgatg 540

ttgtacaccc ctctgcgcgc taacaatgct ggagacgacg tattcaccgt gtcatgcaga 600

gtgctcacca gaccttcacc agactttgac tttatcttct tagtgccccc cactgttgag 660

agccgaacca agcccttag tgtccccgta ctcacagtcg aggagatgac aaatagccgc 720

tttccaatcc cccttgagaa actgttcaca ggaccttcct cggcattcgt ggttcagcca 780

cagaacggac gctgcacaac tgacggcgtg ctgctcggaa ccacccagct tagccctgtt 840

aatatctgta cgtttagagg cgacgtaact cacataactg gctcacggaa ctataccatg 900

aatctggcat cacagaattg gaatgactac gacccaaccg aagagattcc cgcacctctt 960

ggaacccccg actttgtggg aaaaatacag ggcgtcctga cacaaaccac cagaaccgat 1020

ggctccacac ggggacacaa ggcaaccgtc tacactggct ctgccgattt tgccccgaaa 1080

ctgggtagag tgcagtttga gaccgacact gaccgggact ttgaagccaa tcagaatact 1140

aagttcacac ctgtaggagt gattcaggac gggggcacca ctcaccggaa cgagccgcaa 1200

caatgggtcc tgccctctta tagcgggagg aatactcata atgtgcattt ggctcctgca 1260

gtggctccca cgtttcccgg ggaacaactg ctctttttttc gttcaaccat gcctggatgc 1320

tccggatatc ccaatatgga tctcgattgc ctgctcccac aggaatgggt gcagtatttt 1380

tatcaagagg ccgcaccagc ccaatccgac gtcgcacttc tgcggttcgt gaatccagac 1440

acaggccgcg tgttgtttga gtgcaaattg cacaaatcag gatacgttac agtggctcat 1500

actggacagc atgacctggt gatcccaccc aacggatatt ttaggttcga ctcctgggtg 1560

aatcagtttt atacattagc ccccatgggg aatgggactg gcagacgcag ggctgtctga 1620

<210> 290
<211> 538
<212> PRT
<213> Norovirus

<220>
<221> MOD_RES
<222> (57)..(57)
<223> X ma be Leu, Gly, Ser, Thr, Asn, Gln, Lys or His

<400> 290

Met Met Met Ala Ser Lys Asp Ala Pro Ser Asn Met Asp Gly Thr Ser
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Gly Ala Gly Gln Leu Val Pro Glu Val Asn Ala Ala Glu Pro Leu Pro
20 25 30

Leu Glu Pro Val Val Gly Ala Ala Thr Ala Val Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Xaa Asn Asn Phe Val Gln Ala Pro
50 55 60

Glu Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu
65 70 75 80

Phe Asp Leu Arg Leu Gly Pro His Leu Asn Pro Phe Leu Leu His Leu
85 90 95

Ser Gln Met Tyr Asn Gly Trp Val Gly Asn Met Arg Val Arg Val Met
100 105 110

```
Leu Ala Gly Asn Ala Phe Ser Ala Gly Lys Ile Ile Ile Cys Cys Val
        115                 120                 125


Pro Pro Gly Phe Glu Ser Gln Asn Ile Ser Ile Gly Gln Ala Thr Met
    130                 135                 140


Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145                 150                 155                 160


Pro Leu Asp Asp Val Arg Asn Val Leu Phe His Thr Asn Glu Asn Arg
                165                 170                 175


Pro Thr Met Arg Leu Leu Cys Met Leu Tyr Thr Pro Leu Arg Ala Gly
            180                 185                 190


Gly Ala Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
        195                 200                 205


Thr Cys Pro Ala Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Ser
    210                 215                 220


Val Glu Gln Lys Thr Arg Gln Leu Thr Ile Pro Asn Ile Pro Leu Asn
225                 230                 235                 240


Asn Leu Ala Asn Ser Arg Val Pro Ala Met Ile Asn Lys Met Thr Val
                245                 250                 255


Ser Ala Asp Gln Asn Gln Val Val Gln Phe Gln Asn Gly Arg Cys Thr
            260                 265                 270


Leu Glu Gly Gln Leu Leu Gly Thr Thr Pro Val Ser Ala Asn Gln Val
        275                 280                 285


Ala Arg Ile Arg Gly Lys Val Phe Ser Thr Asn Ser Gly Thr Gly Leu
    290                 295                 300


Asn Leu Thr Glu Val Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320
```

```
Ala Pro Leu Gly Phe Pro Asp Ile Gly Asn Cys Asp Trp His Val Tyr
                325                 330                 335

Ala Phe Lys Val Asn Gln Asn Thr Gly Asp Pro Met Tyr Arg Leu Asp
            340                 345                 350

Ile Thr Gln Gly Asn Ser Phe Ala Pro His Leu Gly Ser Ile Glu Phe
        355                 360                 365

Ser Ser Glu Asn His Pro Ser Gly Asp Gln Leu Gly Thr Leu Thr Trp
    370                 375                 380

Ile Ser Pro Leu Asn Asn Ala Ser Arg Val Asp Pro Trp Lys Ile Pro
385                 390                 395                 400

Thr Tyr Gly Ser Thr Leu Thr Glu Ser Thr Asn Leu Ala Pro Pro Ile
                405                 410                 415

Phe Pro Pro Gly Phe Gly Glu Ala Ile Val Tyr Phe Met Ser Asp Phe
            420                 425                 430

Pro Ile Val Ser Gly Asn Thr Ala Gln Ile Pro Cys Thr Leu Pro Gln
        435                 440                 445

Glu Phe Val Ser Ser Phe Val Glu Gln Gln Ala Pro Ile Arg Gly Glu
    450                 455                 460

Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His Arg Asn Leu Gly
465                 470                 475                 480

Glu Phe Lys Leu Tyr Pro Asp Gly Phe Ile Thr Cys Val Pro Asn Thr
                485                 490                 495

Gly Gly Gly Pro Gln Asn Leu Pro Ser Asn Gly Val Phe Val Phe Ser
            500                 505                 510

Ser Trp Val Ser Arg Tyr Tyr Gln Leu Lys Pro Val Gly Thr Thr Gly
        515                 520                 525
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Pro Val Arg Arg Leu Gly Val Arg Arg Val
530 535

<210> 291
<211> 1614
<212> DNA
<213> Artificial Sequence

<220>
<223> Human codon optimized VP1_GI.7/GA5043/USA/2014_M57x

<220>
<221> misc_feature
<222> (170)..(170)
<223> n is a, c, g, or t

<400> 291
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ctggtgcccg aggtcaatgc cgcagaacca cttcctcttg agcccgtcgt tggcgccgcc 120

acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggatavn saatttcgtt 180

caggcaccag aaggagaatt caccatctcc cccaataaca ccccagggga tattctgttt 240

gacctcaggt taggacccca cttgaacccc tttctgcttc atctctcaca aatgtataat 300

ggctgggtcg ggaatatgcg cgtgcgggtg atgctagccg gcaatgcttt ttctgcaggc 360

aagattatca tttgctgcgt tcctcctgga ttcgaatctc aaaatatcag cattggtcaa 420

gcaaccatgt ttccacatgt gatcgctgat gttcgcgtcc tggaacccat tgaagttcct 480

ctcgacgacg tgagaaatgt tctcttccac accaacgaga ataggccgac tatgagactt 540

ctgtgtatgc tctacacccc attaagagcc gggggagcat cctcaggtac tgacccattt 600

gtgattgccg ggcgggtgct cacatgcccg gctccagact ttaacttcct tttcttggtg 660

ccacccagtg ttgaacagaa aaccagacag ctcaccatcc caaatatccc attgaacaat 720

ctcgccaaca gcagggtgcc agcaatgata aacaaaatga cagtcagtgc tgaccagaac 780

caggtagtcc agtttcagaa cggcagatgc acgcttgagg gccaactgct tgggacgacc 840

ccagtctccg cgaaccaggt ggcccgaatc cggggtaaag tcttcagtac aaactccggc 900

actggcctta acctcacaga ggttgacggc actccctatc atgcttttga gtctccagcc 960

cctcttggct ttcccgatat aggcaactgt gactggcacg tttatgcgtt taaagtaaac 1020

cagaacaccg gcgatcctat gtataggttg gatataacac aaggtaattc attcgcccca 1080

cacttgggta gcatcgagtt cagttcagag aaccatccga gtggtgatca gctaggcaca 1140

ttgacgtgga tcagccctct gaataacgca tcaagagtgg atccctggaa gatccctacc 1200

tatgggtcca ctctgacaga gagcacaaat ttggctccgc ccattttccc acccggattc 1260

ggcgaggcca tagtgtactt tatgtctgac tttcctatcg tcagcgggaa tacagcccag 1320

attccttgca cactgccaca agaattcgtc tcatcctttg tagagcagca ggcacctatt 1380

cgaggtgagg ccgccctctt gcactacgtg gaccctgaca cccaccgcaa tcttggcgag 1440

tttaagctgt accctgacgg gtttattacc tgtgtaccca acaccggcgg cggcccacaa 1500

aatttgccca gcaatggcgt gtttgtcttt tcctcttggg tgtctcgata ctaccagctt 1560

aaacctgtcg gaactacggg ccccgtgcga cgactcggcg tgaggcgggt gtga 1614

<210> 292
<211> 543
<212> PRT
<213> Norovirus

<220>
<221> MOD_RES
<222> (94)..(94)
<223> X may be Val, Ile, Met, Thr, Glu, Asp, Asn, Gln, Lys or His

<400> 292

Met Met Met Ala Ser Lys Asp Ala Pro Thr Asn Met Asp Gly Thr Ser
1 5 10 15

Gly Ala Gly Gln Leu Val Pro Glu Val Ser Thr Ala Glu Pro Ile Ser
20 25 30

Met Glu Pro Val Ala Gly Ala Ala Thr Ala Ala Ala Thr Ala Gly Gln
35 40 45

Val Asn Met Ile Asp Pro Trp Ile Met Ser Asn Tyr Val Gln Ala Pro
50 55 60

Gln Gly Glu Phe Thr Ile Ser Pro Asn Asn Thr Pro Gly Asp Ile Leu

65 70 75 80

Phe Asp Leu Gln Leu Gly Pro His Leu Asn Pro Phe Leu Xaa His Leu
85 90 95

Ala Gln Met Tyr Asn Gly Trp Val Gly Asn Met Lys Val Arg Val Leu
100 105 110

Leu Ala Gly Asn Ala Phe Thr Ala Gly Lys Ile Ile Ile Ser Cys Val
115 120 125

Pro Pro Gly Phe Ala Ala Gln Asn Val Ser Ile Ala Gln Ala Thr Met
130 135 140

Phe Pro His Val Ile Ala Asp Val Arg Val Leu Glu Pro Ile Glu Val
145 150 155 160

Pro Leu Glu Asp Val Arg Asn Val Leu Phe His Asn Asn Asp Ser Thr
165 170 175

Pro Thr Met Arg Leu Ile Cys Met Leu Tyr Thr Pro Leu Arg Ala Ser
180 185 190

Gly Ser Ser Ser Gly Thr Asp Pro Phe Val Ile Ala Gly Arg Val Leu
195 200 205

Thr Cys Pro Ser Pro Asp Phe Asn Phe Leu Phe Leu Val Pro Pro Asn
210 215 220

Val Glu Gln Lys Thr Lys Pro Phe Ser Val Pro Asn Leu Pro Leu Asn
225 230 235 240

Val Leu Ser Asn Ser Arg Val Pro Ser Leu Ile Lys Ser Met Met Val
245 250 255

Ser Gln Asp His Gly Gln Met Val Gln Phe Gln Asn Gly Arg Val Thr
260 265 270

Leu Asp Gly Gln Leu Gln Gly Thr Thr Pro Thr Ser Ala Ser Gln Leu

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        275                 280                 285

Cys Lys Ile Arg Gly Thr Val Tyr His Ala Thr Gly Gly Gln Gly Leu
    290                 295                 300

Asn Leu Thr Glu Ile Asp Gly Thr Pro Tyr His Ala Phe Glu Ser Pro
305                 310                 315                 320

Ala Pro Ile Gly Phe Pro Asp Leu Gly Glu Cys Asp Trp His Ile Asn
                325                 330                 335

Ala Ser Pro Ala Asn Ala Phe Thr Asp Gly Ser Ile Ile His Arg Ile
            340                 345                 350

Asp Val Ala Gln Asp Ser Thr Phe Ala Pro His Leu Gly Thr Ile His
        355                 360                 365

Tyr Thr Asn Ala Asp Tyr Asn Ala Asn Val Gly Leu Ile Cys Ser Leu
    370                 375                 380

Glu Trp Leu Ser Pro Pro Ser Gly Gly Ala Pro Lys Val Asn Pro Trp
385                 390                 395                 400

Ala Ile Pro Arg Tyr Gly Ser Thr Leu Thr Glu Ala Ala Gln Leu Ala
                405                 410                 415

Pro Pro Ile Tyr Pro Pro Gly Phe Gly Glu Ala Ile Val Phe Phe Met
            420                 425                 430

Ser Asp Phe Pro Ile Ala Asn Gly Ser Asp Gly Leu Ser Val Pro Cys
        435                 440                 445

Thr Ile Pro Gln Glu Phe Val Thr His Phe Val Asn Glu Gln Ala Pro
    450                 455                 460

Thr Arg Gly Glu Ala Ala Leu Leu His Tyr Val Asp Pro Asp Thr His
465                 470                 475                 480

Arg Asn Leu Gly Glu Phe Lys Leu Tyr Pro Glu Gly Phe Met Thr Cys
```

485 490 495

Val Pro Asn Ser Ser Gly Ser Gly Pro Gln Thr Leu Pro Ile Asn Gly
500 505 510

Val Phe Thr Phe Ile Ser Trp Val Ser Arg Phe Tyr Gln Leu Lys Pro
515 520 525

Val Gly Thr Thr Gly Pro Val Arg Arg Leu Gly Ile Arg Arg Ser
530 535 540

<210> 293
<211> 1632
<212> DNA
<213> Artificial Sequence

<220>
<223> hCod optimized VP1_GI.3_Lil08_S94x

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cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcagcc 120

actgctgccg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180

gttcaggctc cacaggggga gtttaccata agcccaaaca acaccccggg tgacatcttg 240

tttgacctgc agctaggacc acacttgaat ccgtttctgv hscacttggc tcagatgtat 300

aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360

gggaagatta ttatctcttg cgtgccacct ggatttgcag cccagaacgt gtctatcgca 420

caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgaggtg 480

ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcacccc caccatgcgc 540

ttgatatgta tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct 600

tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt ccttttttctg 660

gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720

gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggtatc tcaggatcac 780

ggtcaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840

accccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900

ggacaggggc tgaatcttac tgagatcgat ggtaccccct accatgcatt cgagtcacct 960

gcacctattg gatttcccga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020

aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080

gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140

atctgtagcc tagagtggct atctccgcca agcggtgggg cccctaaagt taacccatgg 1200

gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260

ccaccaggat tcggggaagc cattgttttc tttatgtccg attttccgat agccaacggt 1320

tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380

gagcaggctc ctactcgggg cgaggctgcc ttgttgcatt acgtagaccc cgatacccat 1440

agaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaactcc 1500

tccggcagtg gccctcaaac cttgccgatc aacggcgtgt tcacgtttat cagctgggtt 1560

tcacggtttt accaactcaa gcccgtcgga acaactgggc cagttcggag gctcgggatc 1620

agacggagct ag 1632