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(19) **United States**(12) **Patent Application Publication**
LAVOIE et al.(10) **Pub. No.: US 2023/0293663 A1**(43) **Pub. Date: Sep. 21, 2023**(54) **MODIFIED NOROVIRUS VP1 PROTEINS
AND VLPS COMPRISING MODIFIED
NOROVIRUS VP1 PROTEINS**(71) Applicant: **MEDICAGO INC., QUÉBEC (CA)**(72) Inventors: **Pierre-Olivier LAVOIE, Quebec (CA);
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- (63) Continuation of application No. 16/768,524, filed on May 29, 2020, now Pat. No. 11,602,558, filed as application No. PCT/CA2018/051530 on Nov. 30, 2018.
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(57)

ABSTRACT

Nucleic acids encoding modified norovirus VP1 proteins, and virus-like particles (VLPs) containing one or more of the modified norovirus VP1 proteins, and compositions containing the nucleic acids, VP1 proteins, or the VLPs are provided. Methods for producing modified norovirus VP1 protein, and norovirus VLP, production in plants, portions of the plant or a plant cell, are also provided.

Specification includes a Sequence Listing.

Figure 1A

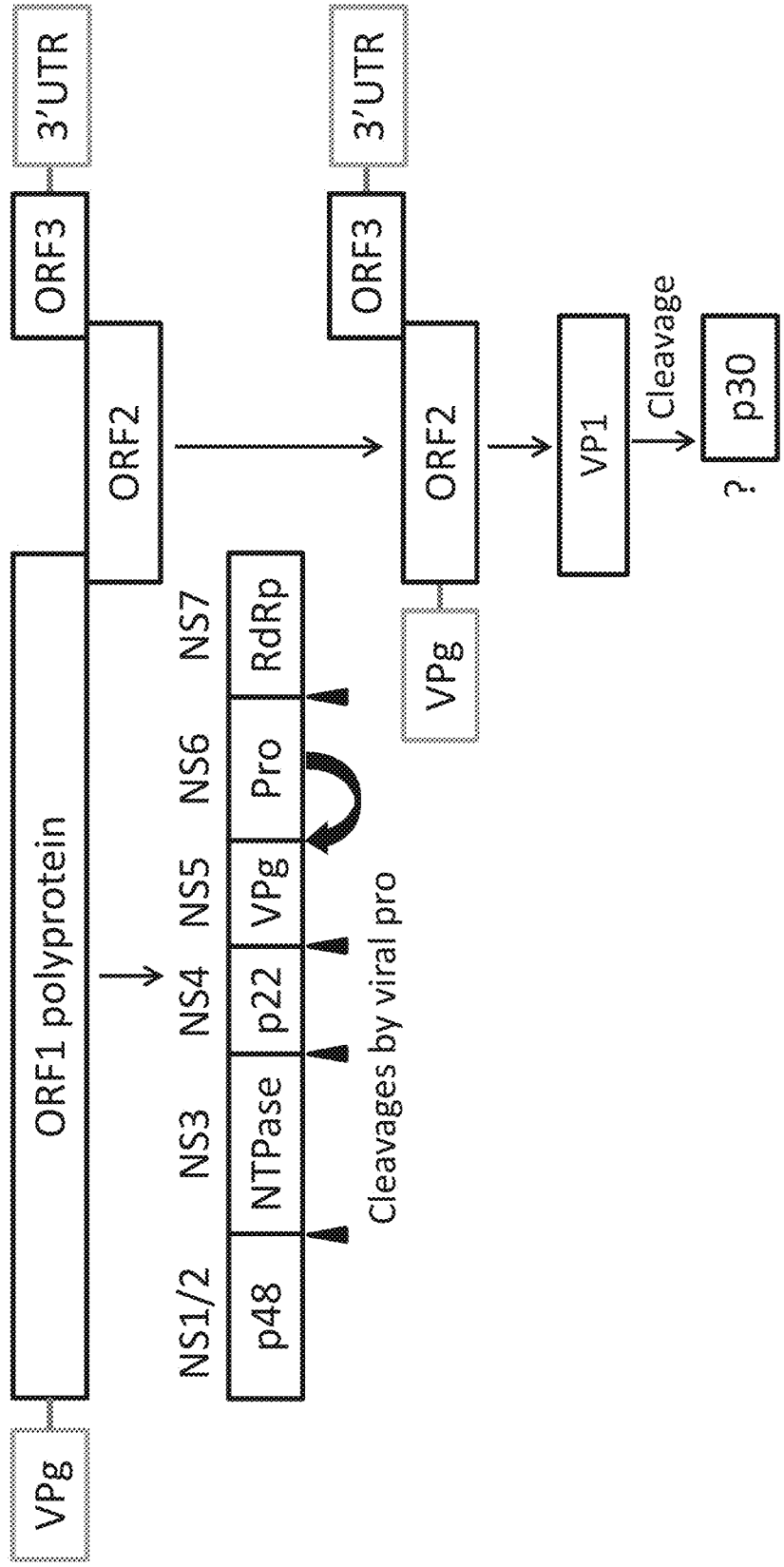


Figure 1B

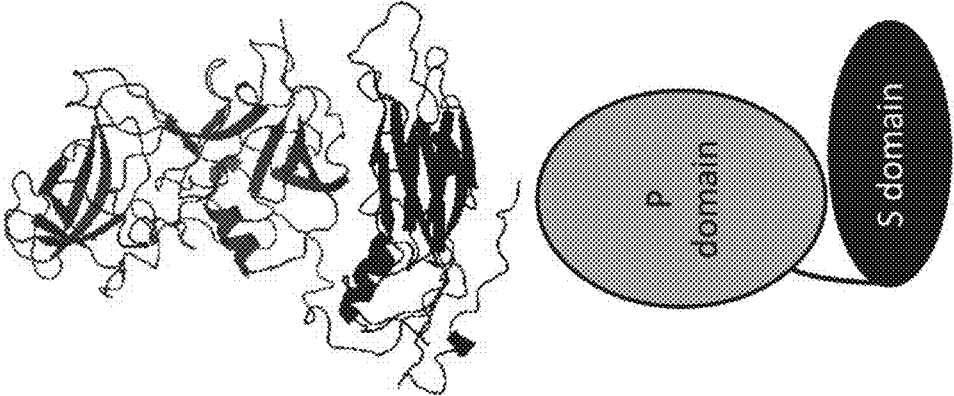


Figure 1C

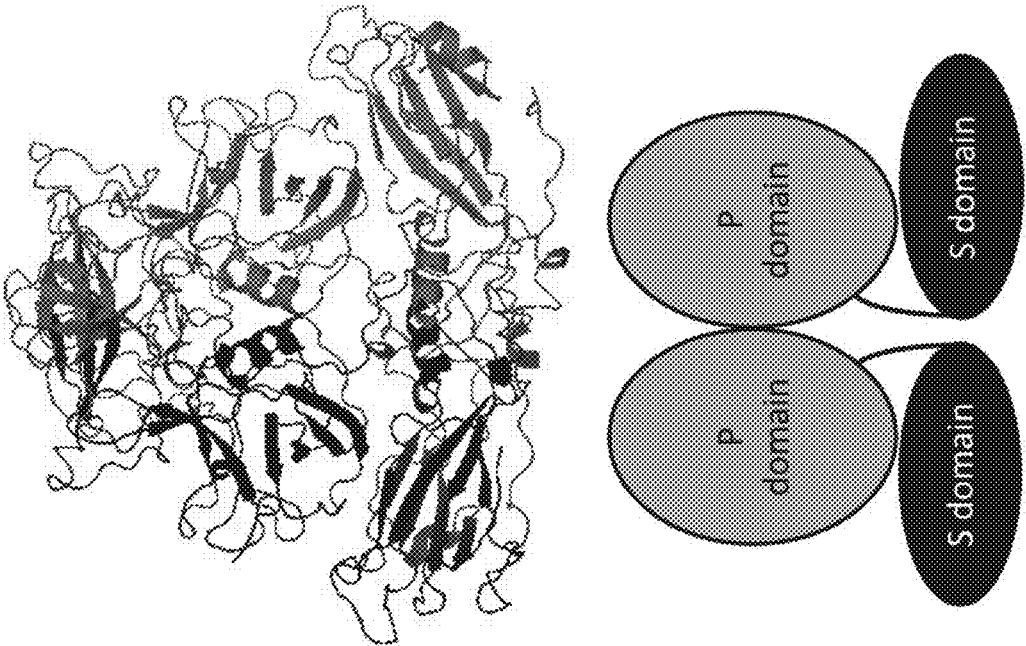


Figure 2A

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
A0A023NFB0	AHW99832	Hu/GI.5/Siklos/HUN5407/2013/HUN
A0A119WIM4	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
A0A119WIL4	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

VP1_G11-SEQ_ID_NO_1	MMMA	SKDA	TS	SV	DG	AG	GA	SG	GA	GQ	L	V	P	E	V	N	A	S	D	P	L	A	M	D	P	V	A	G	S	S	T	A	V	A	T	A	G	G	V	N	P	I	D	P	W	I	I											
VP1_G12-SEQ_ID_NO_4	MMMA	SKDA	PQ	SA	AD	GA	SG	GA	GQ	L	V	P	E	V	N	A	S	D	P	L	A	M	D	P	V	A	G	S	S	T	A	V	A	T	A	G	G	V	N	P	I	D	P	W	I	I												
VP1_G13-SEQ_ID_NO_6	MMMA	SKDA	PT	NM	AD	GT	SG	GA	GQ	L	V	P	E	V	N	A	S	D	P	L	A	M	D	P	V	A	G	S	S	T	A	V	A	T	A	G	G	V	N	P	I	D	P	W	I	I												
VP1_G15-SEQ_ID_NO_12	MMMA	SKDA	PS	SA	AD	GA	NG	GA	GQ	L	V	P	E	V	N	A	S	D	P	L	A	M	D	P	V	A	G	S	S	T	A	V	A	T	A	G	G	V	N	P	I	D	P	W	I	I												
VP1_G17-SEQ_ID_NO_101	MMMA	SKDA	PS	NM	AD	CT	SG	GA	GQ	L	V	P	E	V	N	A	S	D	P	L	A	M	D	P	V	A	G	S	S	T	A	V	A	T	A	G	G	V	N	P	I	D	P	W	I	I												
VP1_G11-SEQ_ID_NO_13	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	N	E	T	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I										
VP1_G12-SEQ_ID_NO_14	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I									
VP1_G13-SEQ_ID_NO_15	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I									
VP1_G15-SEQ_ID_NO_17	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G16-SEQ_ID_NO_20	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G17-SEQ_ID_NO_18	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G12-SEQ_ID_NO_19	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G13-SEQ_ID_NO_22	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G14-SEQ_ID_NO_32	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G17-SEQ_ID_NO_24	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	G	A	G	L	V	P	E	-	-	S	S	E	A	M	A	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I
VP1_G121-SEQ_ID_NO_26	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	T	G	L	V	P	E	-	-	N	T	E	L	P	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I									
Consensus	MKMA	SNDA	A	A	P	S	N	D	-	-	G	A	G	L	V	P	E	-	-	N	T	E	L	P	L	E	P	V	A	G	A	S	I	A	P	L	T	G	G	N	N	V	I	D	P	W	I	I										
VP1_G11-SEQ_ID_NO_1	NNFV	QA	P	Q	G	E	F	T	I	S	P	N	N	T	P	C	D	I	L	F	D	L	Q	L	G	P	H	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A					
VP1_G12-SEQ_ID_NO_4	NNFV	QA	P	Q	G	E	F	T	I	S	P	N	N	T	P	C	D	I	L	F	D	L	Q	L	G	P	H	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A					
VP1_G13-SEQ_ID_NO_6	NNFV	QA	P	Q	G	E	F	T	I	S	P	N	N	T	P	C	D	I	L	F	D	L	Q	L	G	P	H	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A					
VP1_G15-SEQ_ID_NO_12	NNFV	QA	P	Q	G	E	F	T	I	S	P	N	N	T	P	C	D	I	L	F	D	L	Q	L	G	P	H	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A					
VP1_G17-SEQ_ID_NO_101	NNFV	QA	P	Q	G	E	F	T	I	S	P	N	N	T	P	C	D	I	L	F	D	L	Q	L	G	P	H	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A					
VP1_G11-SEQ_ID_NO_13	MNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G12-SEQ_ID_NO_14	MNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G13-SEQ_ID_NO_15	MNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G15-SEQ_ID_NO_16	MNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G17-SEQ_ID_NO_17	TNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G16-SEQ_ID_NO_20	ENFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G12-SEQ_ID_NO_19	NNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G13-SEQ_ID_NO_22	LNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G14-SEQ_ID_NO_32	MNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G17-SEQ_ID_NO_24	TNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
VP1_G121-SEQ_ID_NO_25	NNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				
Consensus	TNFV	QA	P	A	N	G	E	F	T	V	S	P	R	N	S	P	C	E	V	L	L	N	L	E	L	G	P	E	L	N	P	F	L	S	H	L	S	Q	M	Y	N	G	W	V	G	N	M	R	V	R	I	M	L	A				

Figure 2D

VP1_G11-SEQ_ID_NO.1	GN	AF	T	A	G	K	I	I	V	S	C	I	P	P	G	F	T	S	S	S	L	T	I	A	Q	A	T	L	F	P	H	V	I	A	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H	
VP1_G12-SEQ_ID_NO.4	GN	AF	S	A	G	K	I	I	V	C	C	V	P	P	G	F	T	S	S	S	L	T	I	A	Q	A	T	L	F	P	H	V	I	A	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H	
VP1_G13-SEQ_ID_NO.6	GN	AF	T	A	G	K	I	I	S	C	V	P	P	G	F	T	S	S	S	L	T	I	A	Q	A	T	L	F	P	H	V	I	A	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G15-SEQ_ID_NO.12	GN	AF	T	A	G	K	I	I	S	C	V	P	P	G	F	T	S	S	S	L	T	I	A	Q	A	T	L	F	P	H	V	I	A	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G17-SEQ_ID_NO.101	GN	AF	S	A	G	K	I	I	S	C	V	P	P	G	F	T	S	S	S	L	T	I	A	Q	A	T	L	F	P	H	V	I	A	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G11-SEQ_ID_NO.13	GN	AF	T	A	G	K	L	V	F	A	I	P	P	H	F	P	L	E	N	L	S	P	Q	I	T	M	F	P	H	V	I	I	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H			
VP1_G12-SEQ_ID_NO.14	GN	AF	T	A	G	K	L	V	F	A	I	P	P	H	F	P	L	E	N	L	S	P	Q	I	T	M	F	P	H	V	I	I	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H			
VP1_G13-SEQ_ID_NO.15	GN	AF	T	A	G	K	I	I	F	A	I	P	P	N	F	P	T	E	G	L	S	P	S	Q	I	T	M	F	P	H	V	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G14-SEQ_ID_NO.16	GN	AF	T	A	G	K	I	I	F	A	I	P	P	N	F	P	T	E	G	L	S	P	S	Q	I	T	M	F	P	H	V	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G15-SEQ_ID_NO.17	GN	AF	T	A	G	K	I	I	F	A	I	P	P	N	F	P	T	E	G	L	S	P	S	Q	I	T	M	F	P	H	V	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G16-SEQ_ID_NO.20	GN	AF	T	A	G	K	I	I	F	A	I	P	P	H	F	P	L	E	N	L	S	P	S	Q	I	T	M	F	P	H	V	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G17-SEQ_ID_NO.18	GN	AF	T	A	G	K	I	I	F	A	I	P	P	H	F	P	L	E	N	L	S	P	S	Q	I	T	M	F	P	H	V	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G112-SEQ_ID_NO.19	GN	AF	T	A	G	K	L	V	F	A	I	P	P	H	F	P	L	E	N	L	S	P	S	Q	I	T	M	F	P	H	V	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G113-SEQ_ID_NO.22	GN	AF	T	A	G	K	I	L	F	A	I	P	P	N	F	P	T	E	G	L	S	P	A	Q	I	T	M	L	P	H	L	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G114-SEQ_ID_NO.32	GN	AF	T	A	G	K	I	L	F	A	I	P	P	N	F	P	T	E	G	L	S	P	A	Q	I	T	M	L	P	H	L	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G117-SEQ_ID_NO.24	GN	AF	T	A	G	K	I	L	F	A	I	P	P	N	F	P	T	E	G	L	S	P	A	Q	I	T	M	L	P	H	L	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
VP1_G121-SEQ_ID_NO.26	GN	AF	T	A	G	K	I	L	F	A	I	P	P	N	F	P	T	E	G	L	S	P	A	Q	I	T	M	L	P	H	L	I	V	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H		
Consensus	GN	AF	T	A	G	K	I	I	S	C	V	P	P	X	F	P	X	S	S	S	S	L	T	I	A	Q	A	T	L	F	P	H	V	I	A	D	V	R	I	L	D	P	I	E	V	P	L	E	D	V	R	N	V	L	F	H
VP1_G1-SEQ_ID_NO.1	NN	DR	N	Q	O	T	M	R	L	V	C	M	L	Y	T	P	L	R	T	G	G	T	G	-	-	D	S	F	V	I	A	G	R	V	L	T	C	P	S	S	D	F	N	F	L	F	L	V	P	P	T	I	E			
VP1_G2-SEQ_ID_NO.4	TN	D	-	N	Q	P	T	M	R	L	V	C	M	L	Y	T	P	L	R	T	G	G	T	G	-	-	D	S	F	V	I	A	G	R	V	L	T	C	P	S	S	D	F	N	F	L	F	L	V	P	P	T	I	E		
VP1_G3-SEQ_ID_NO.5	TN	D	-	S	T	P	T	M	R	L	V	C	M	L	Y	T	P	L	R	T	G	G	T	G	-	-	D	S	F	V	I	A	G	R	V	L	T	C	P	S	S	D	F	N	F	L	F	L	V	P	P	T	I	E		
VP1_G5-SEQ_ID_NO.12	TN	D	-	N	Q	P	T	M	R	L	V	C	M	L	Y	T	P	L	R	T	G	G	T	G	-	-	D	S	F	V	I	A	G	R	V	L	T	C	P	S	S	D	F	N	F	L	F	L	V	P	P	T	I	E		
VP1_G7-SEQ_ID_NO.101	TN	E	-	N	R	P	T	M	R	L	V	C	M	L	Y	T	P	L	R	T	G	G	T	G	-	-	D	S	F	V	I	A	G	R	V	L	T	C	P	S	S	D	F	N	F	L	F	L	V	P	P	T	I	E		
VP1_G11-SEQ_ID_NO.13	YN	Q	P	E	R	R	M	R	L	V	A	M	L	Y	T	P	L	R	S	N	G	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E			
VP1_G12-SEQ_ID_NO.14	YN	Q	K	D	D	P	R	M	R	L	V	A	M	L	Y	T	P	L	R	S	N	G	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E		
VP1_G13-SEQ_ID_NO.15	YN	Q	S	D	S	R	L	R	L	I	A	M	L	Y	T	P	L	R	A	N	N	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E			
VP1_G14-SEQ_ID_NO.16	YN	Q	S	N	D	P	T	I	K	L	I	A	M	L	Y	T	P	L	R	A	N	N	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E		
VP1_G15-SEQ_ID_NO.17	FN	Q	K	D	E	P	K	M	R	L	V	A	M	L	Y	T	P	L	R	A	N	-	S	G	E	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	A	P	D	F	E	F	T	L	V	P	P	T	I	E		
VP1_G16-SEQ_ID_NO.20	YN	Q	G	N	D	P	K	R	L	I	A	M	L	Y	T	P	L	R	A	N	N	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E			
VP1_G17-SEQ_ID_NO.18	YN	Q	K	D	E	P	K	M	R	L	V	A	M	L	Y	T	P	L	R	A	N	N	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E		
VP1_G112-SEQ_ID_NO.19	YN	Q	K	D	E	P	K	M	R	L	V	A	M	L	Y	T	P	L	R	S	N	G	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	D	F	N	Y	L	V	P	P	T	I	E		
VP1_G113-SEQ_ID_NO.22	FN	N	Q	P	O	P	R	M	R	L	V	A	M	L	Y	T	P	L	R	A	N	N	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	T	P	D	F	E	F	T	L	V	P	P	T	I	E			
VP1_G114-SEQ_ID_NO.32	YN	Q	N	S	P	K	L	R	L	V	A	M	L	Y	T	P	L	R	A	N	N	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	S	P	D	F	E	F	T	L	V	P	P	T	I	E				
VP1_G117-SEQ_ID_NO.24	YN	N	Q	P	N	S	R	M	R	L	V	A	M	L	Y	T	P	L	R	S	N	G	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	T	P	D	F	E	F	T	L	V	P	P	T	I	E			
VP1_G121-SEQ_ID_NO.26	FN	N	Q	P	A	P	R	M	R	L	V	A	M	L	Y	T	P	L	R	S	N	G	S	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	T	P	D	F	E	F	T	L	V	P	P	T	I	E			
Consensus	YN	Q	X	N	X	P	X	M	T	V	A	M	L	Y	T	P	L	R	X	N	G	S	G	G	-	-	D	V	F	T	V	S	C	R	V	L	T	R	P	A	P	D	F	X	F	X	T	L	V	P	P	T	I	E		

Figure 3A

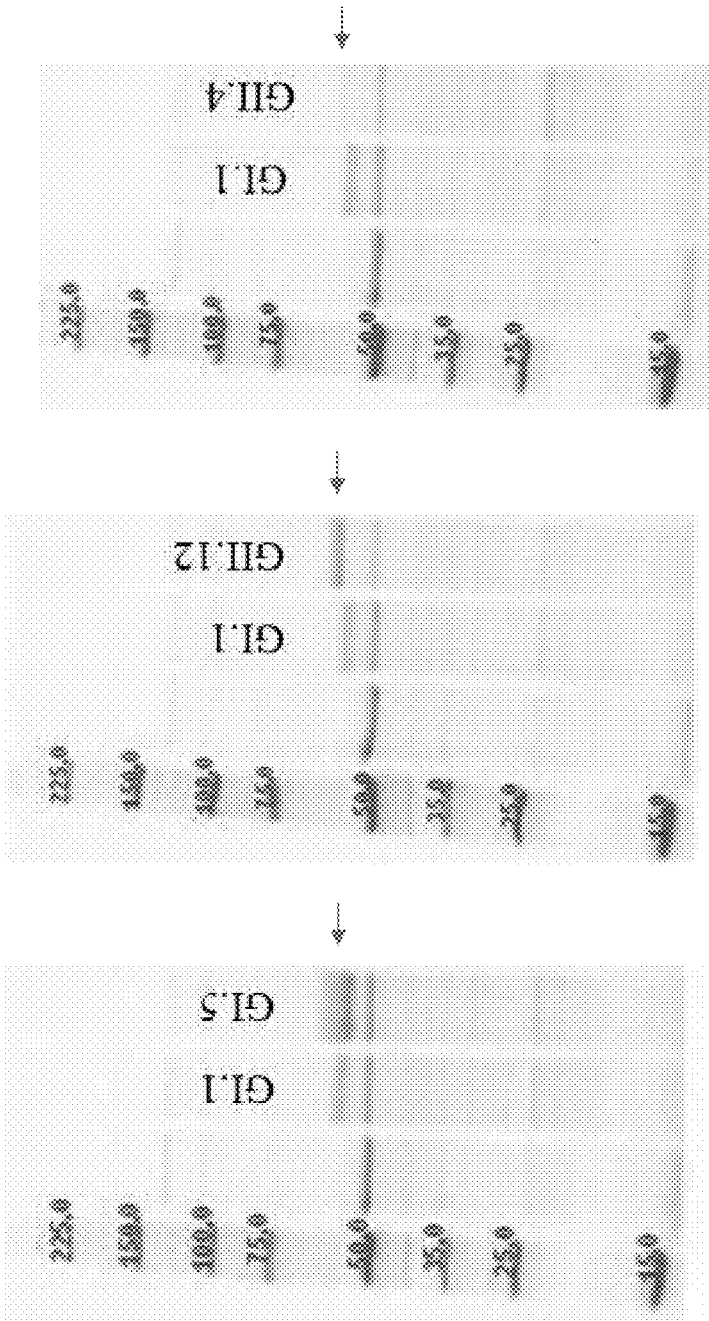


FIGURE 3B

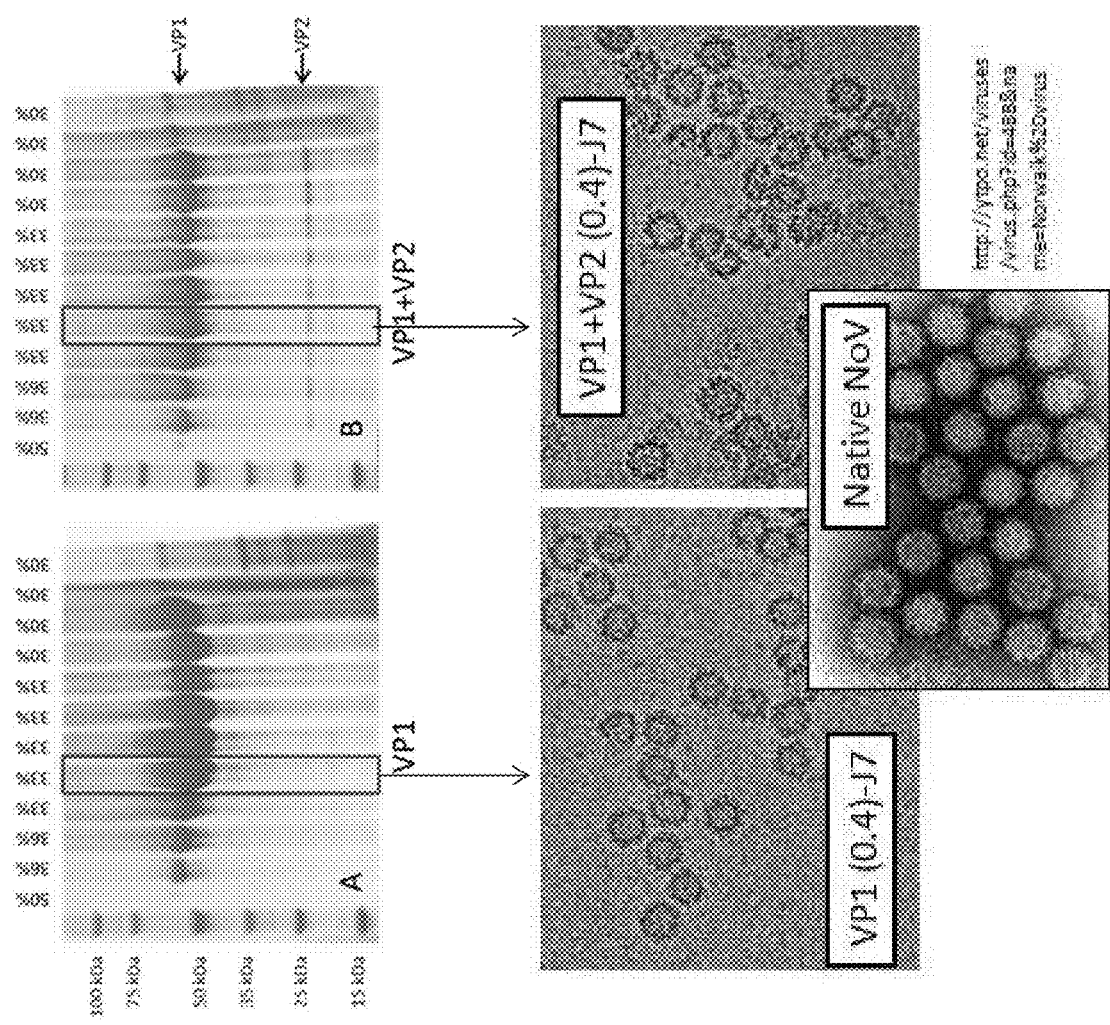


Figure 3C

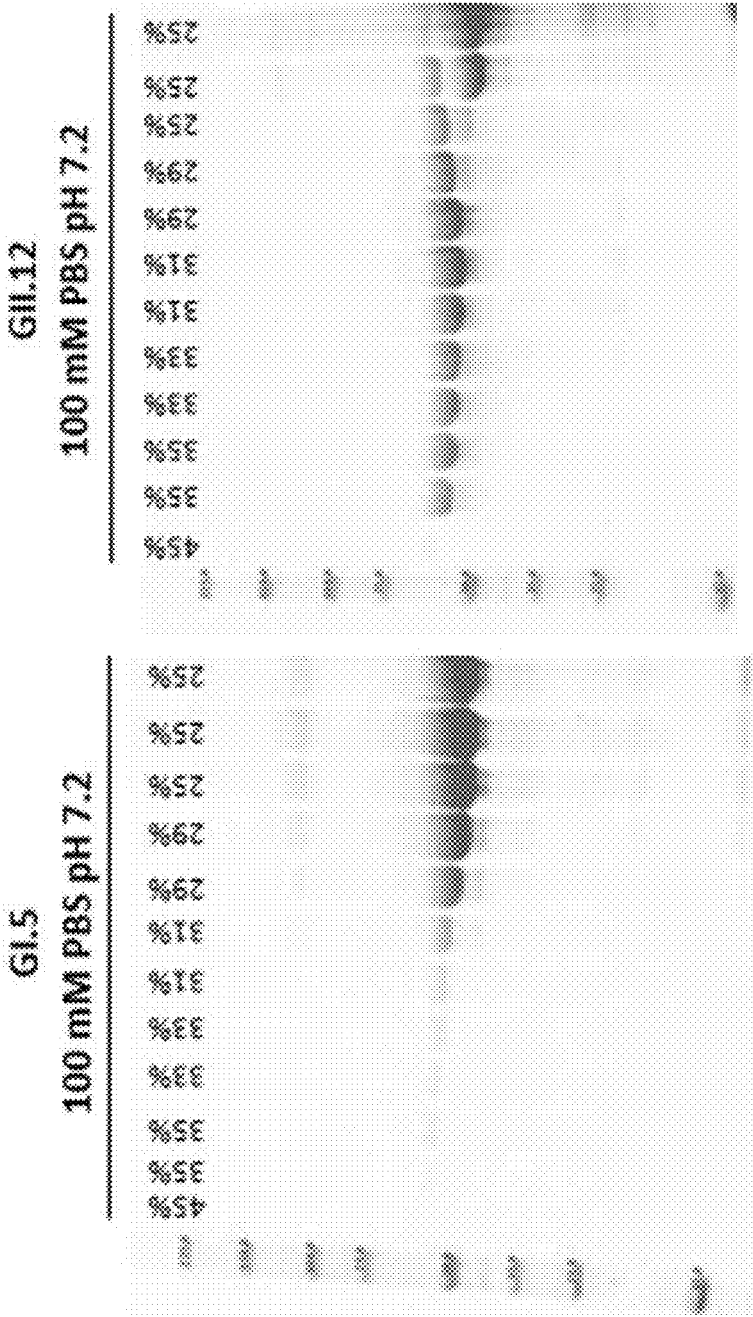


FIGURE 3D

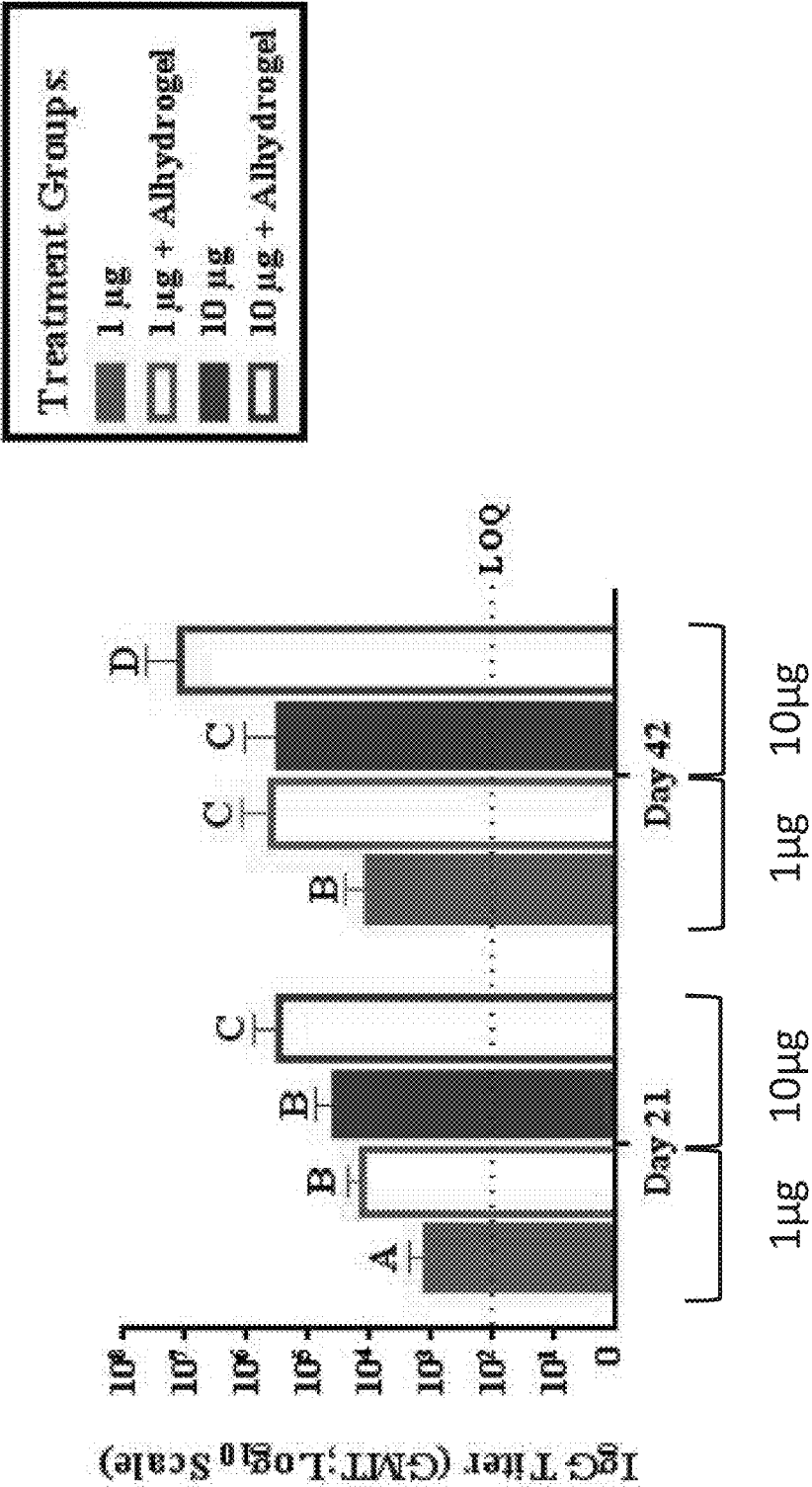


Figure 4B

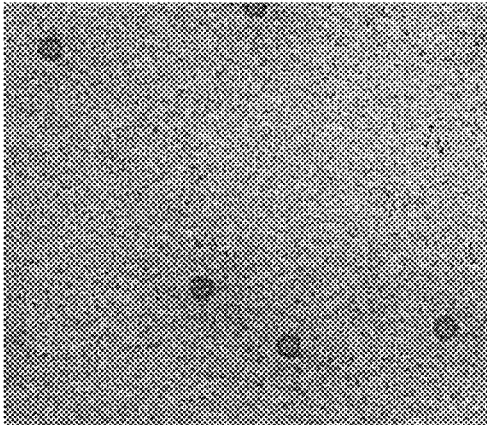
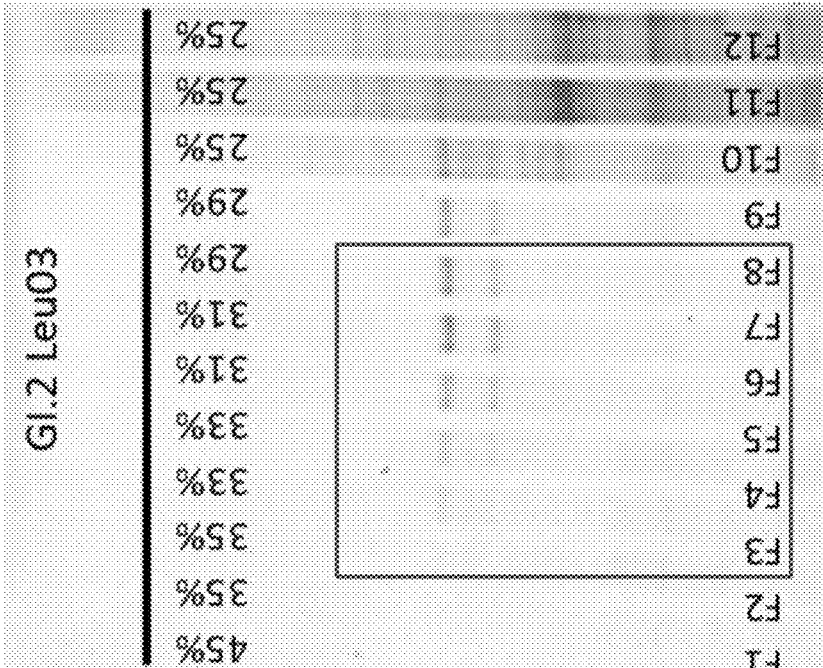
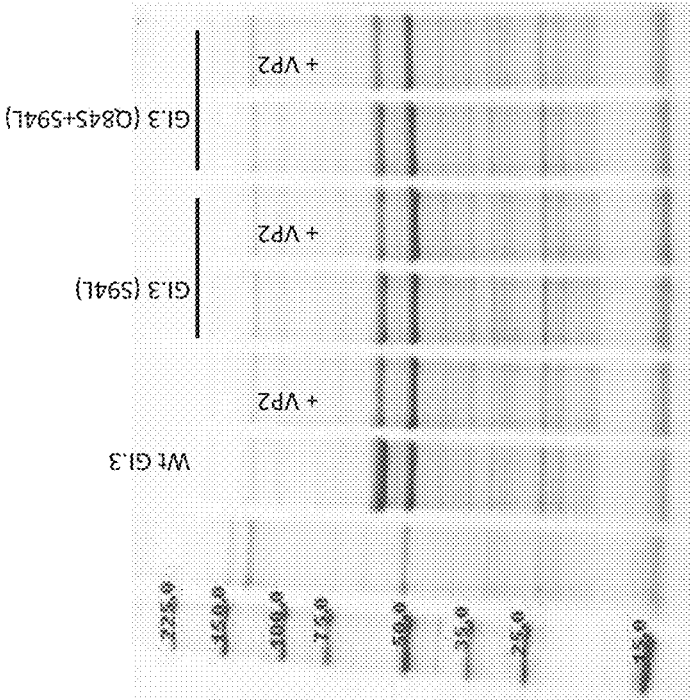


Figure 4A



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

Figure 5A



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

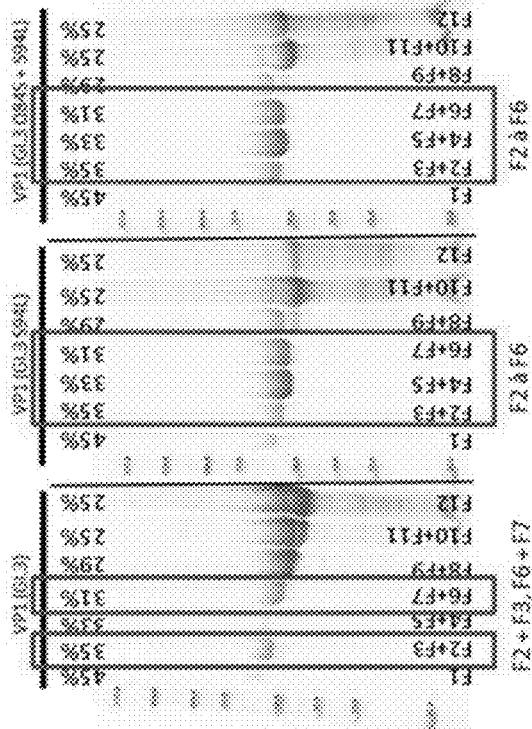


Figure 5B

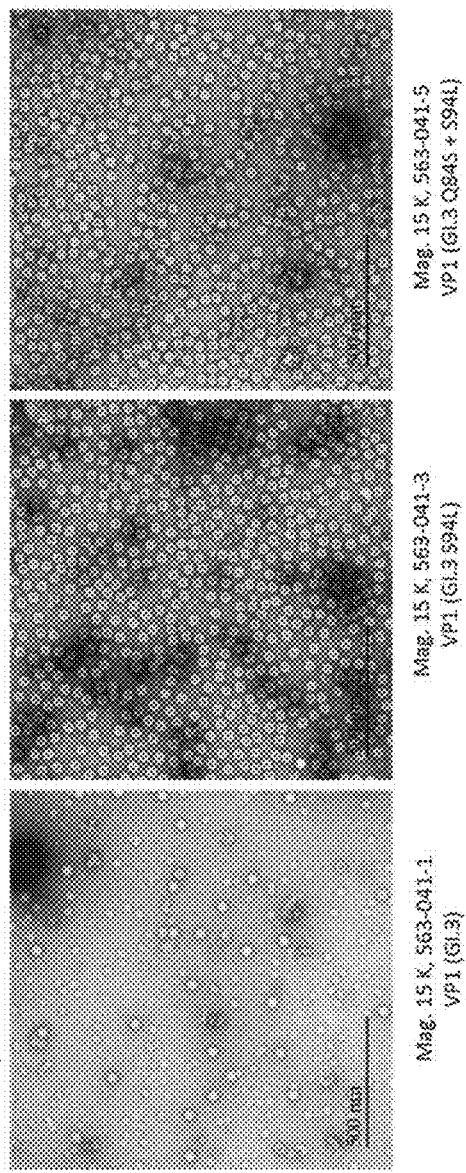


Figure 5C

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

VP1 (GI.3_M57I+S94L)

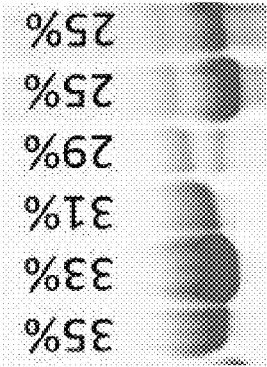


Figure 5D

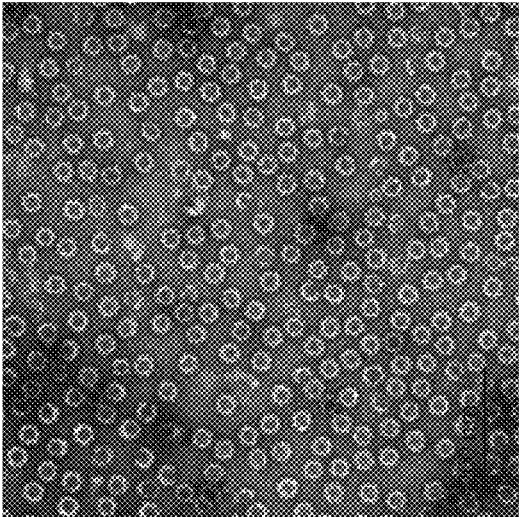
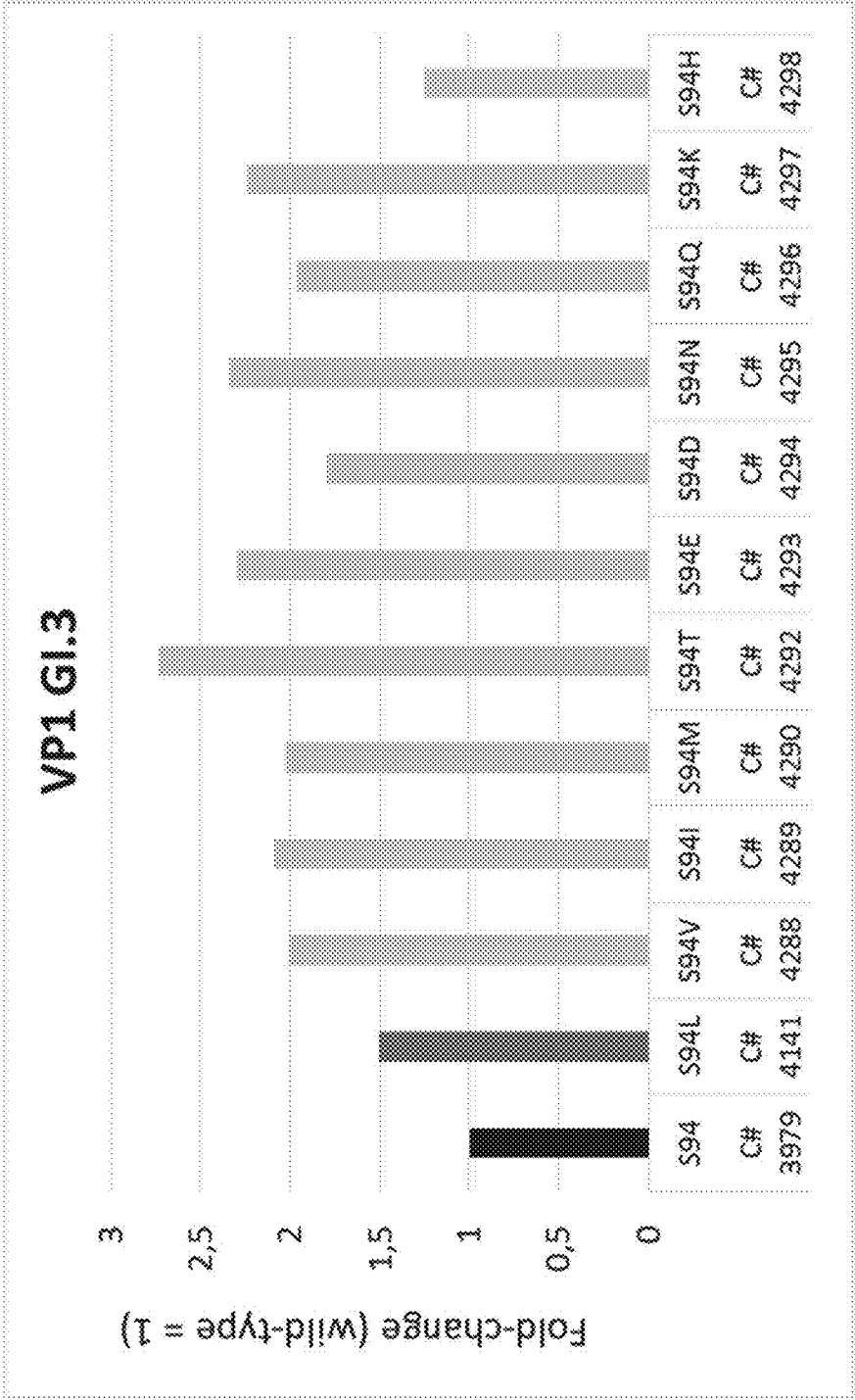


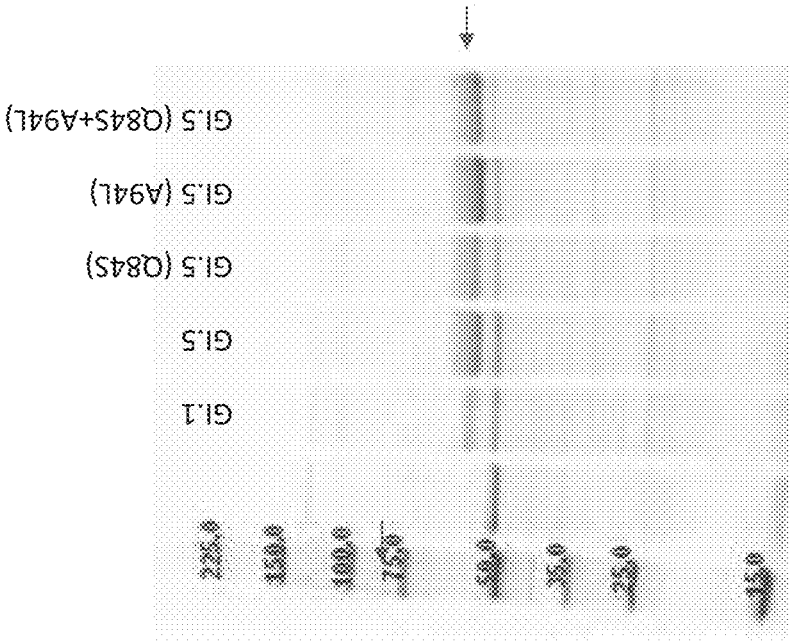
Figure 5E

Figure 5F



GI.5/SIKLOS/HUN54107/2013/HUN

Figure 6A



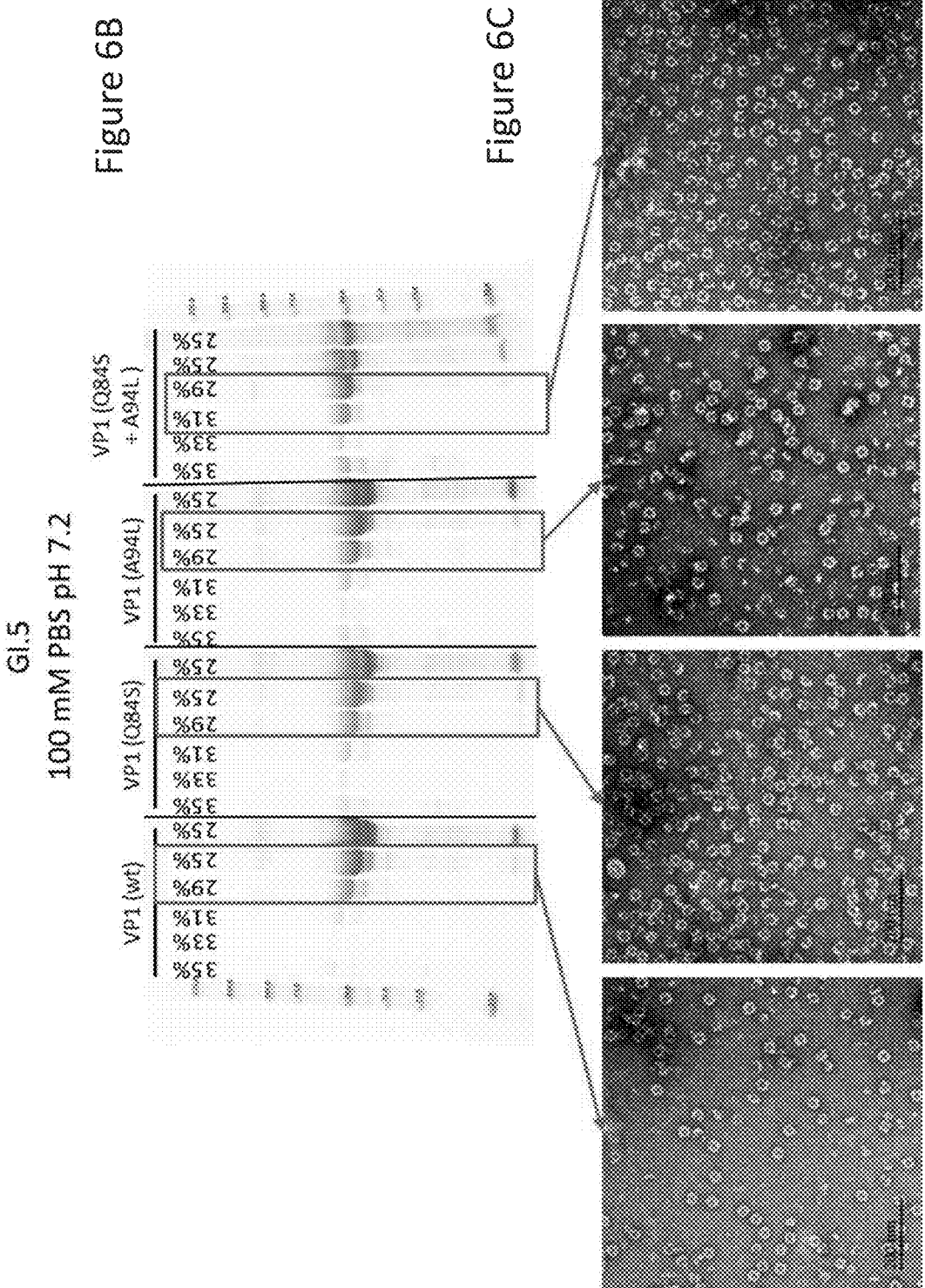
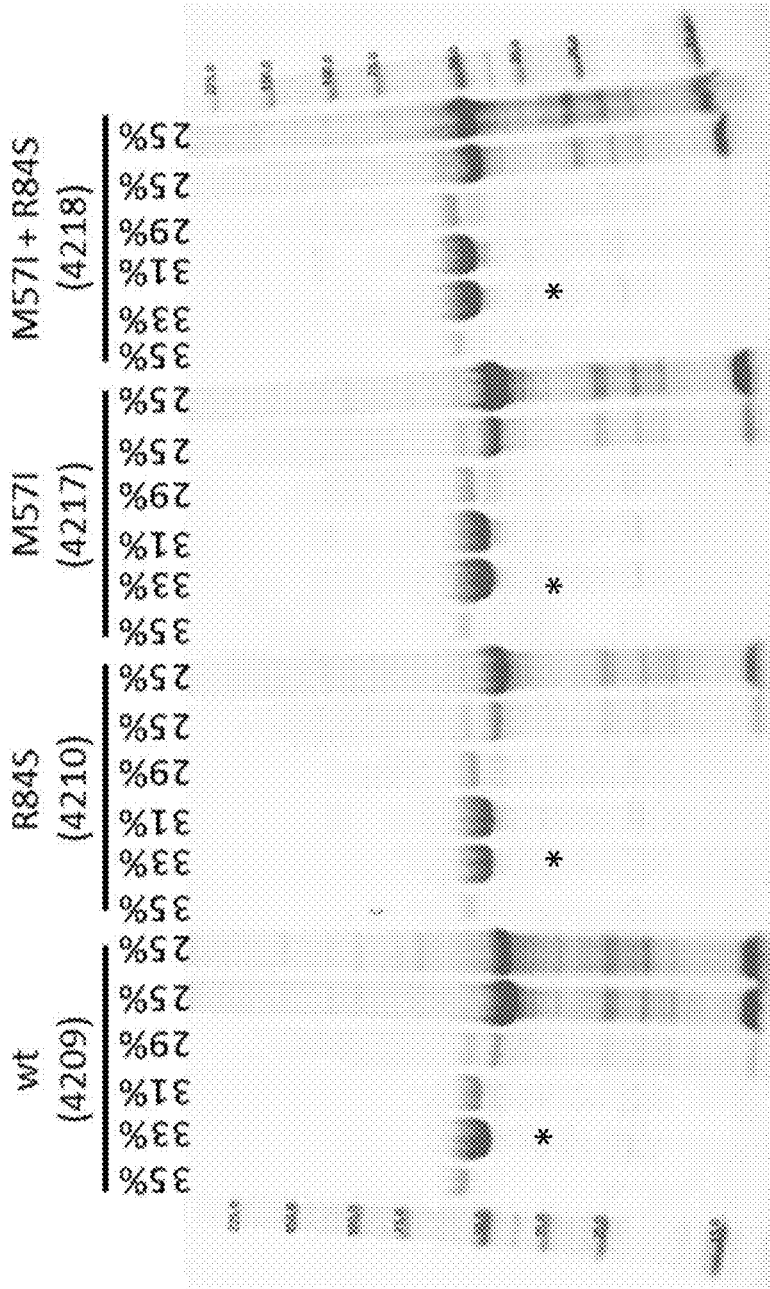


Figure 6D

VP1 (GI.7 USA14)



VP1 GI.7/GA5043/USA/2014

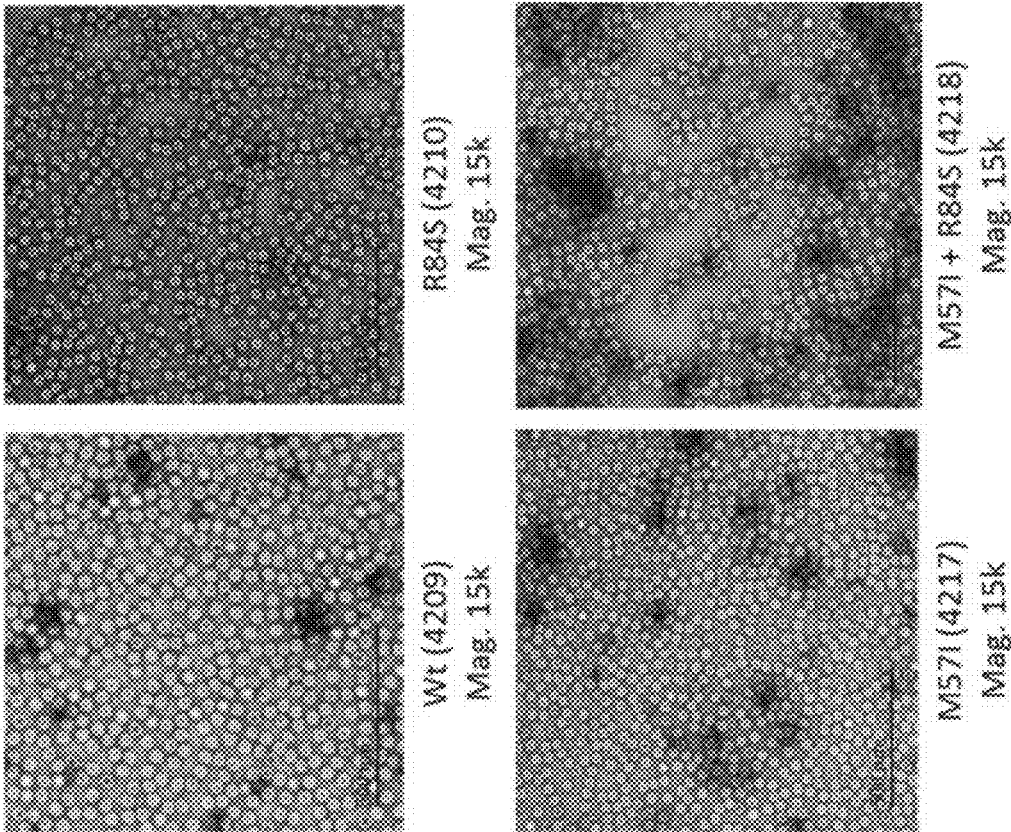


Figure 6E

Figure 6F

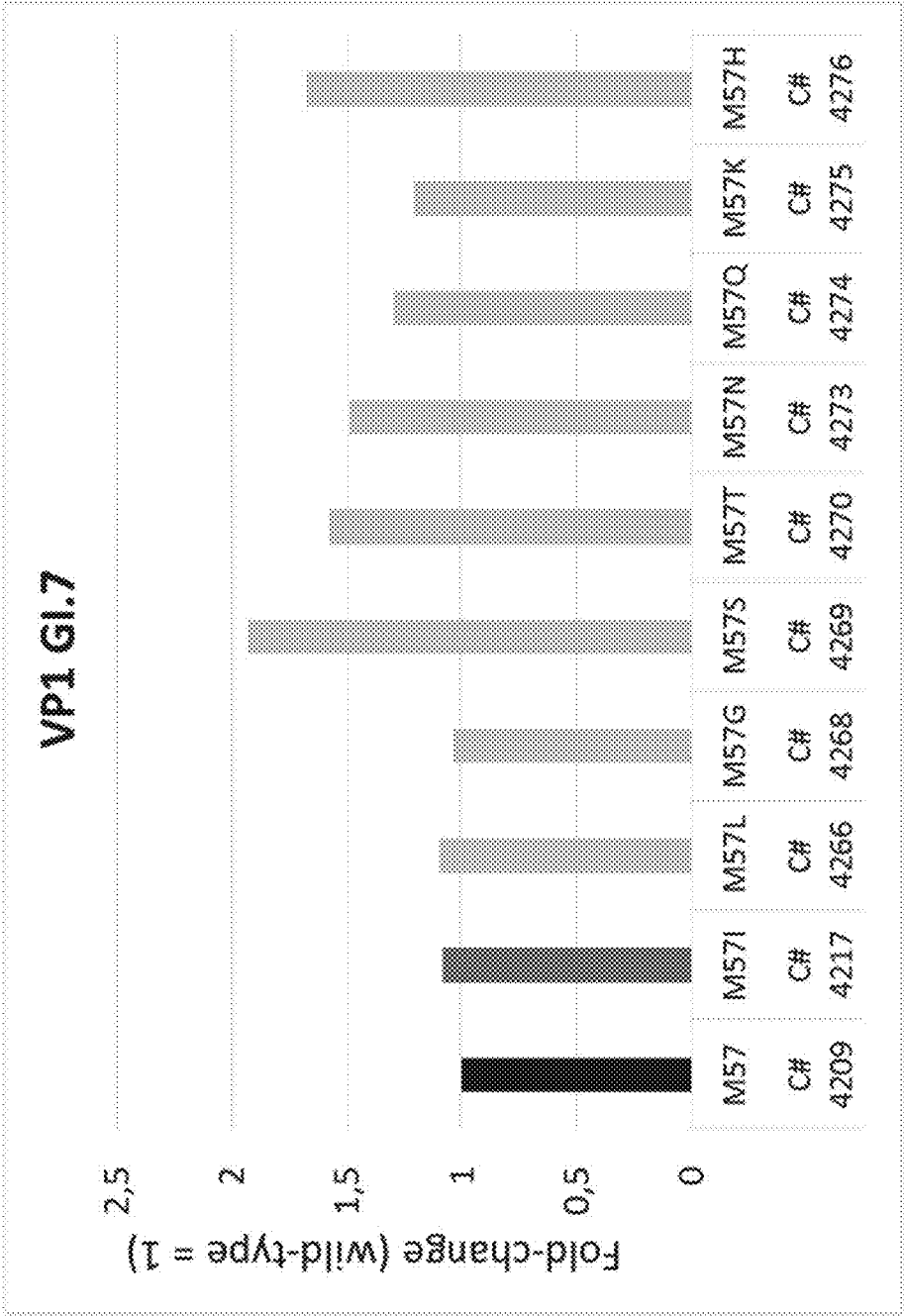


Figure 7A

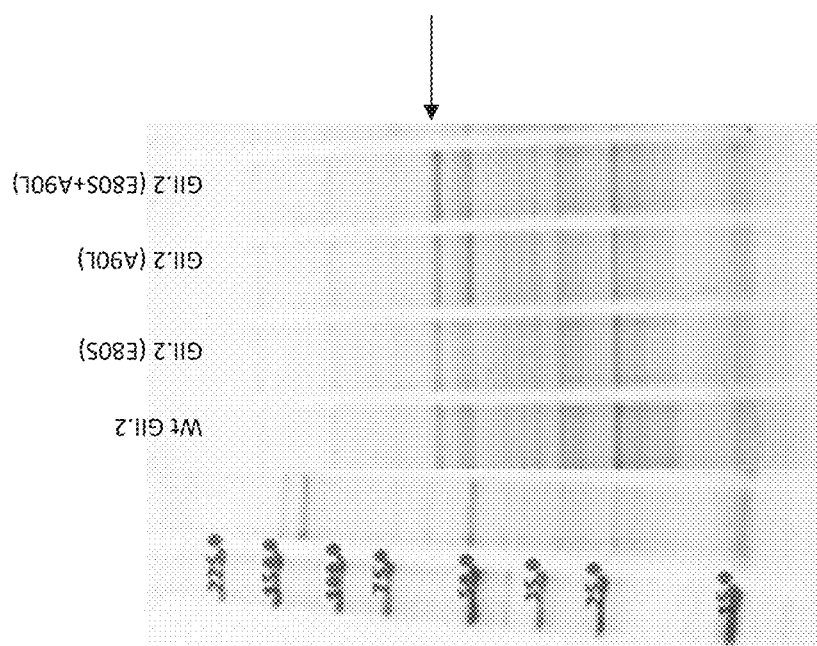
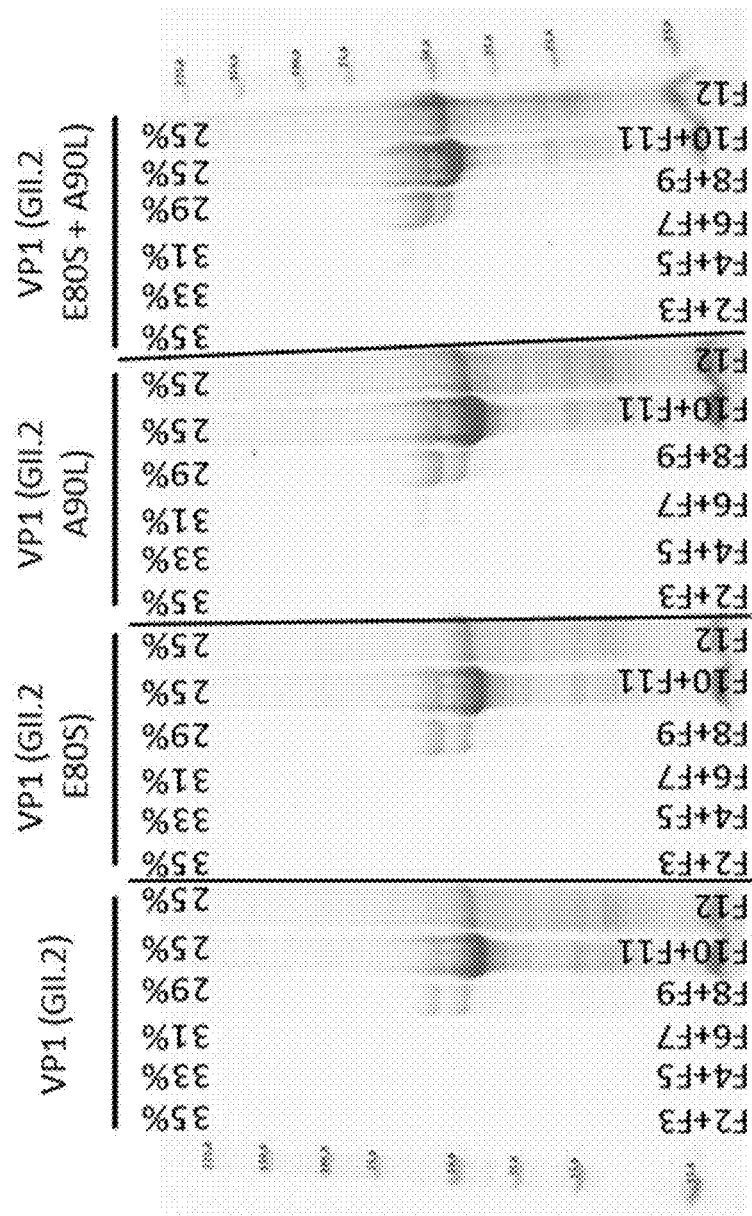
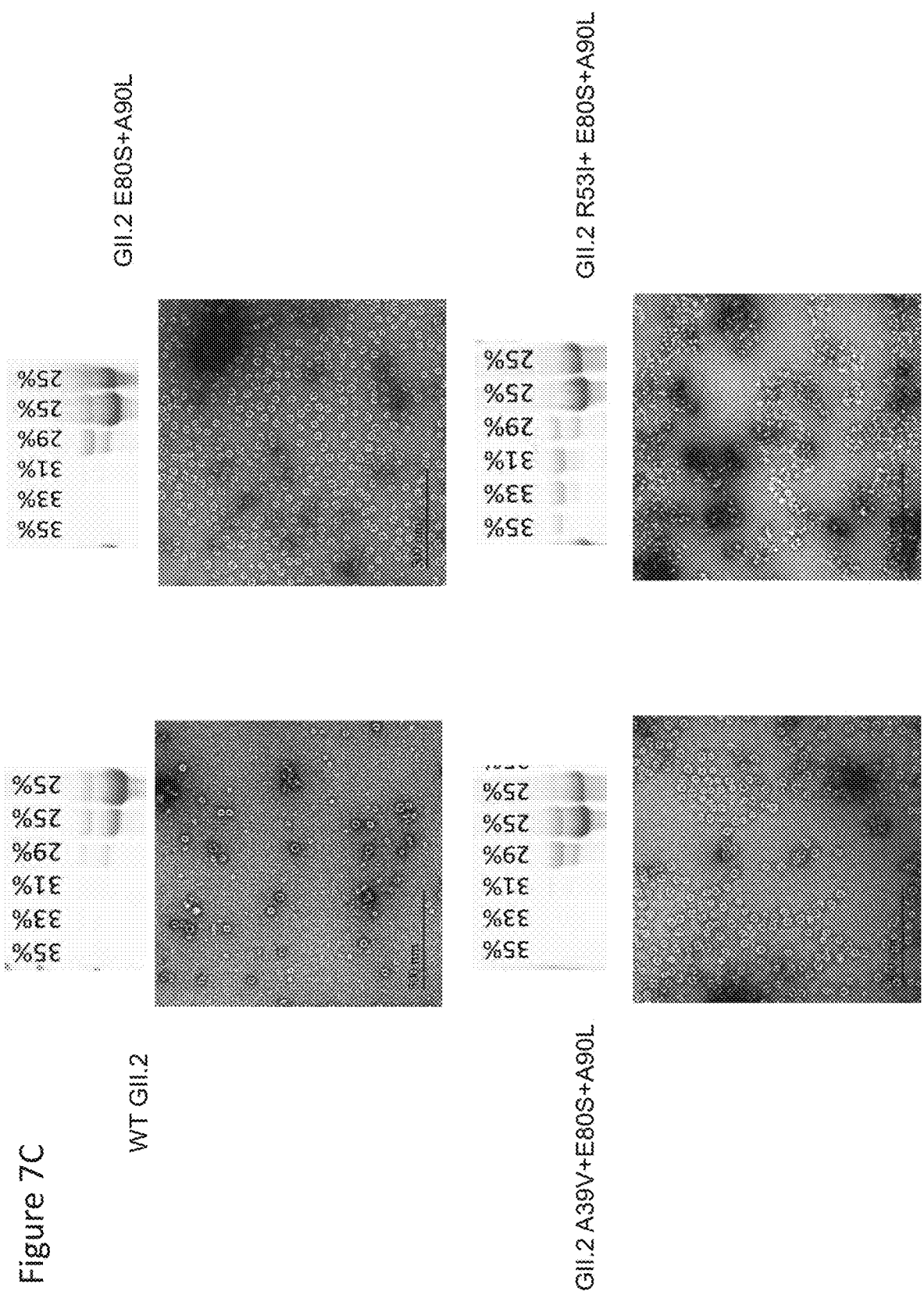


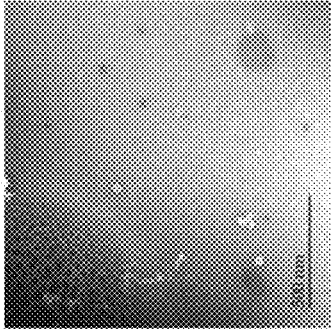
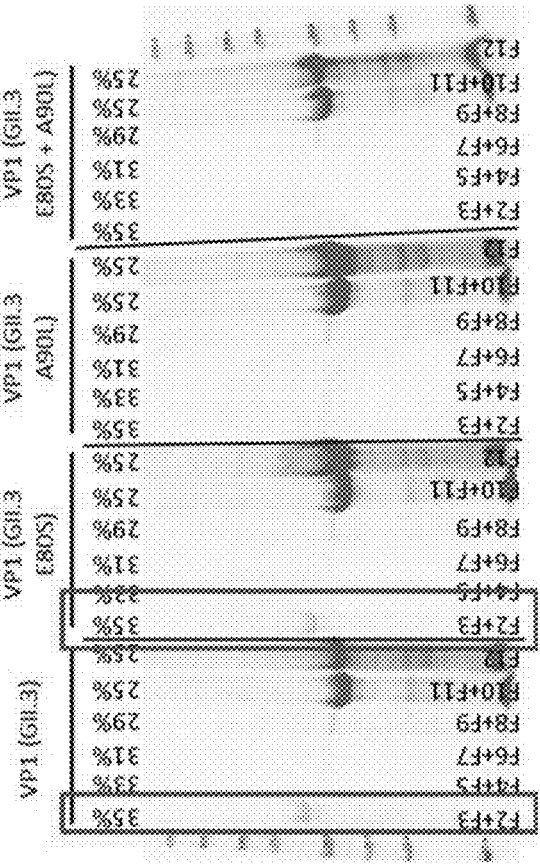
Figure 7B



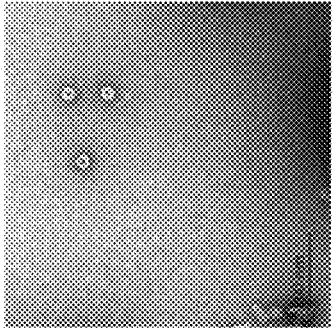


GII.3/Jingzhou/2013402/CHN

Figure 8A



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

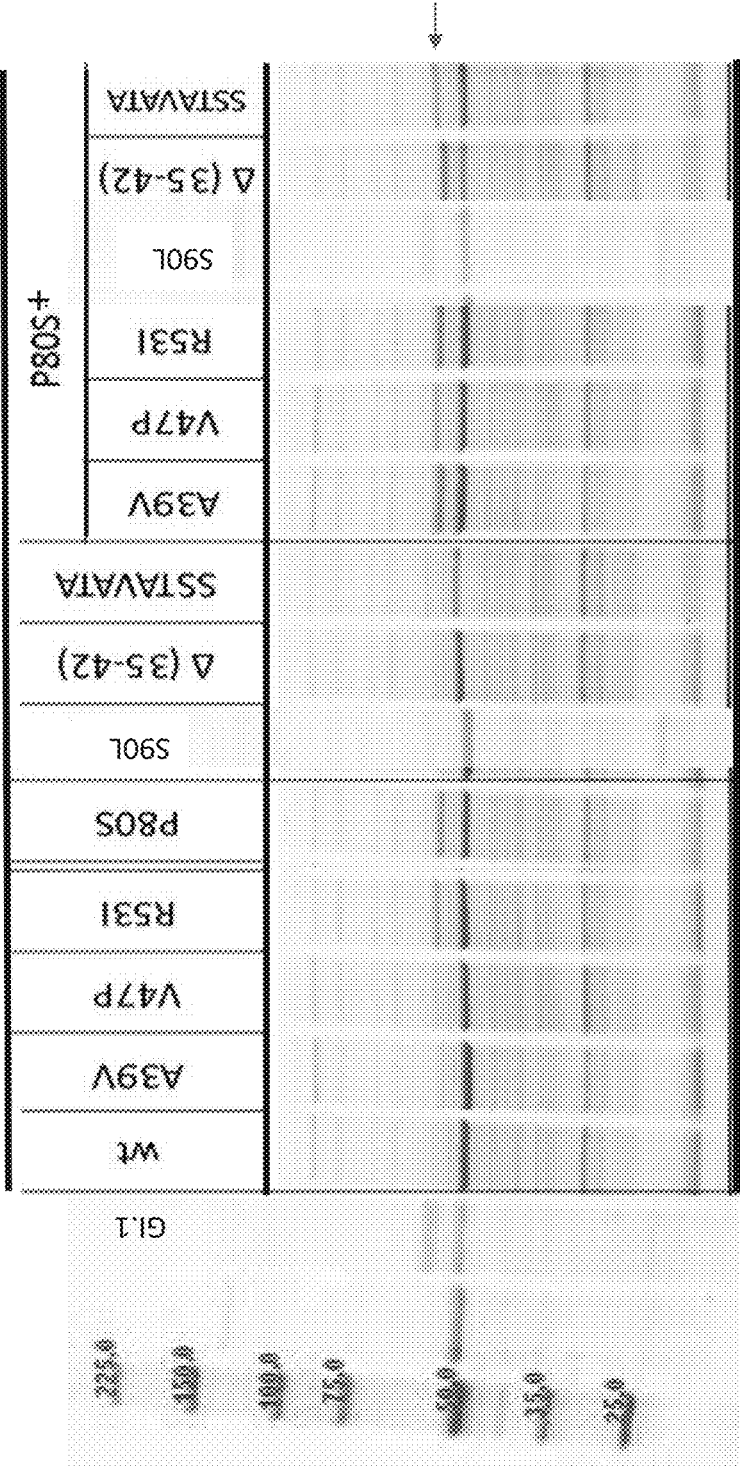


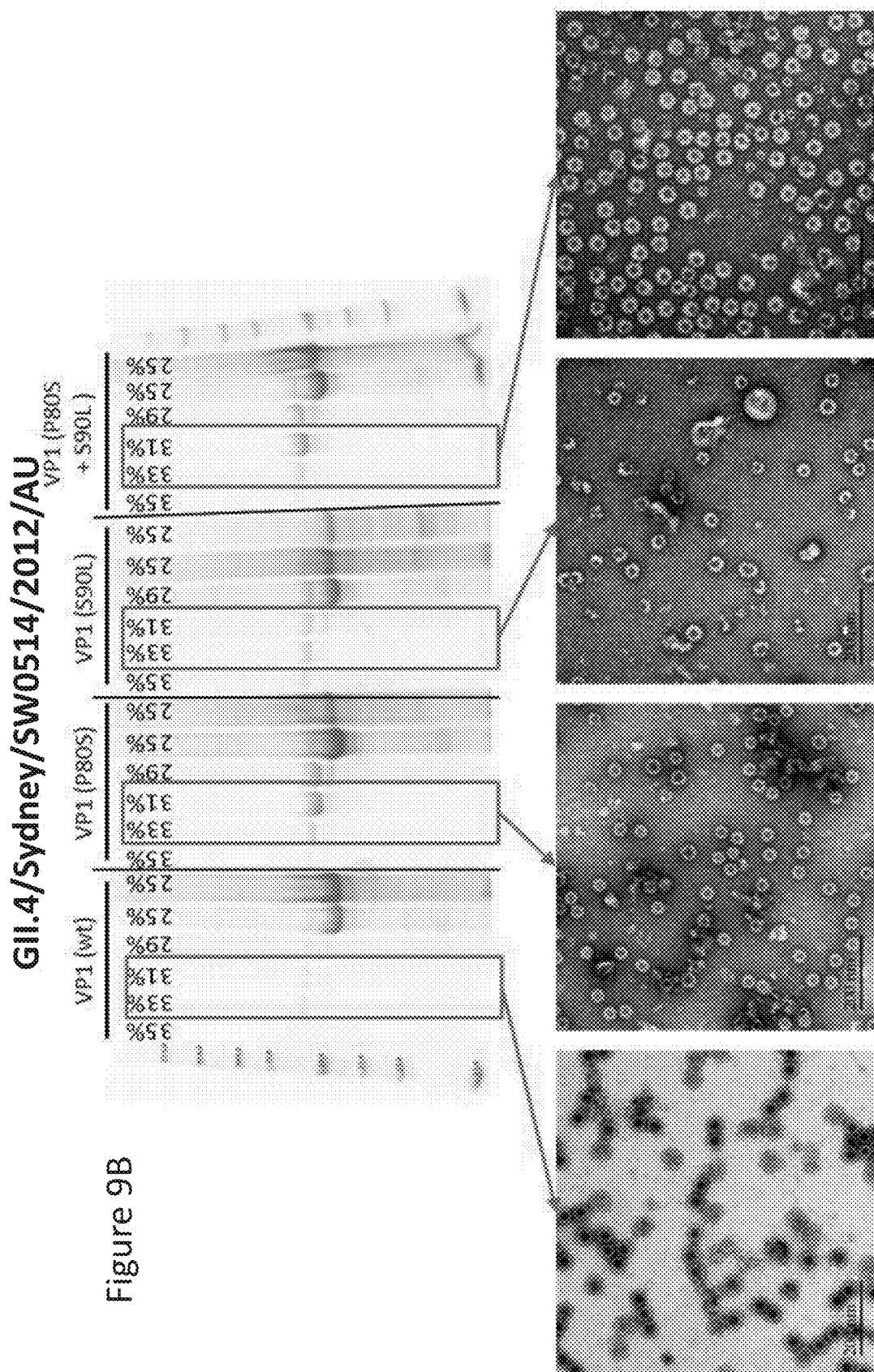
Mag. 25 K, 563-041-7
VP1 (GII.3)

Figure 8B

GII.4/Sydney/SW0514/2012/AU

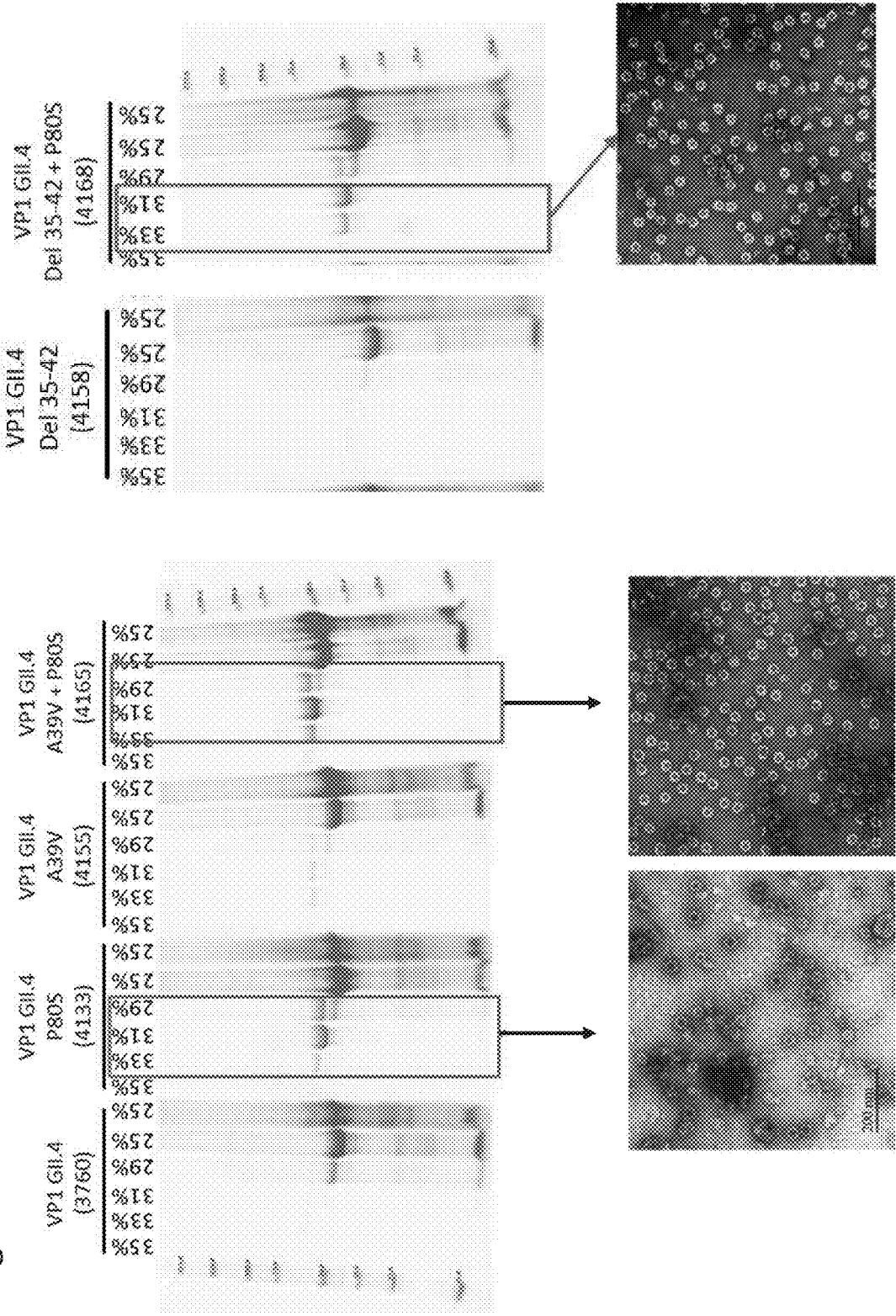
Figure 9A





GII.4/Sydney/SW0514/2012/AU

Figure 9C



GII.4/Sydney/SW0514/2012/AU

Figure 9D

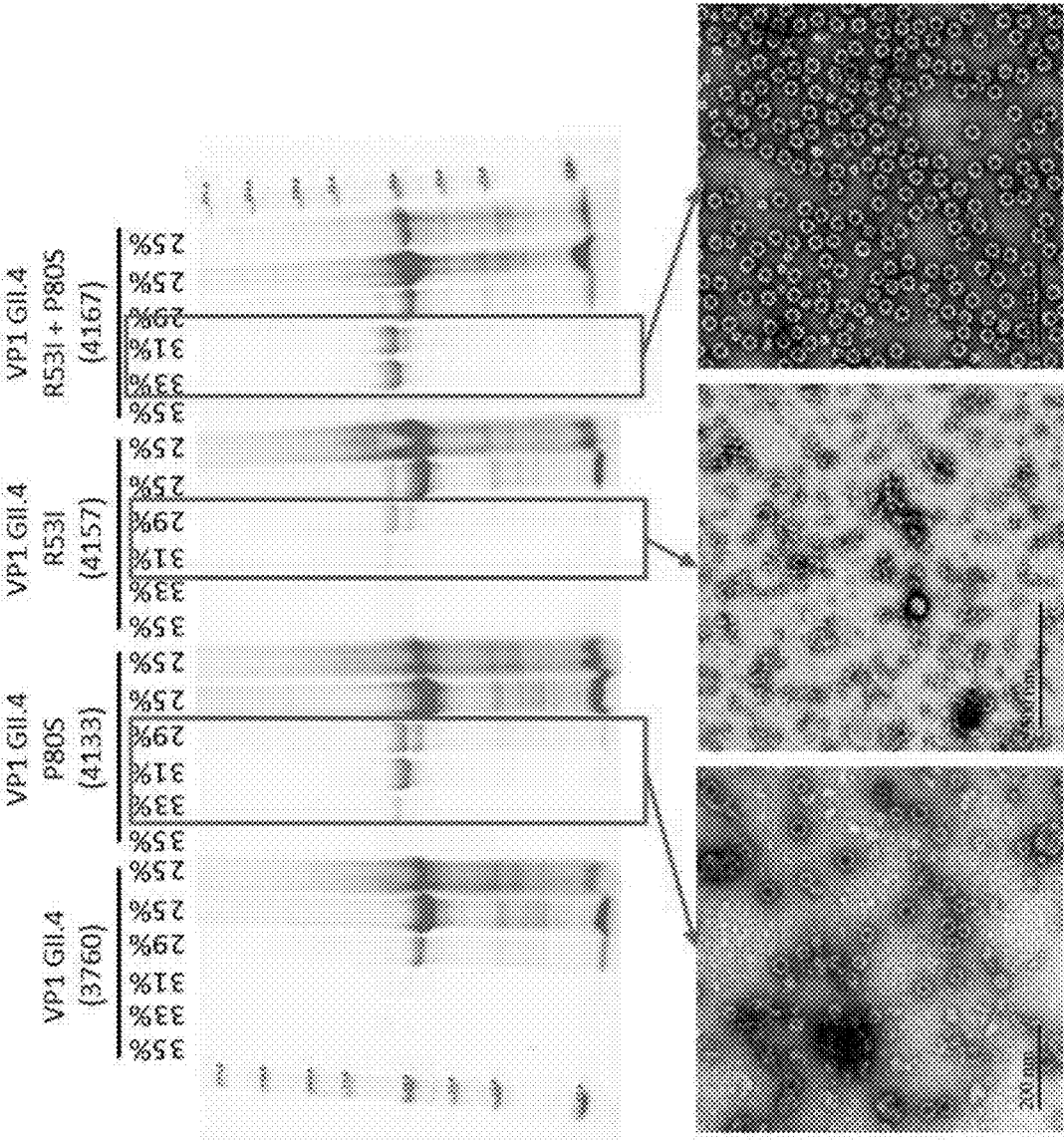


Figure 9E

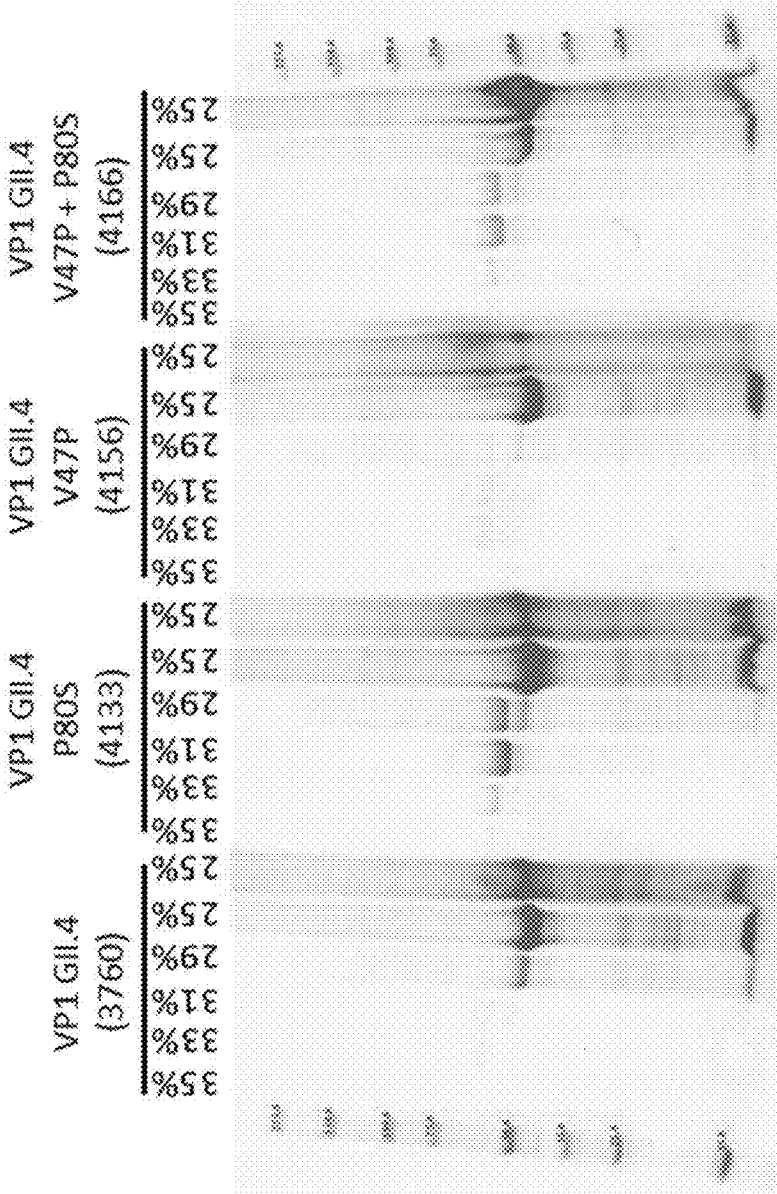


Figure 9F

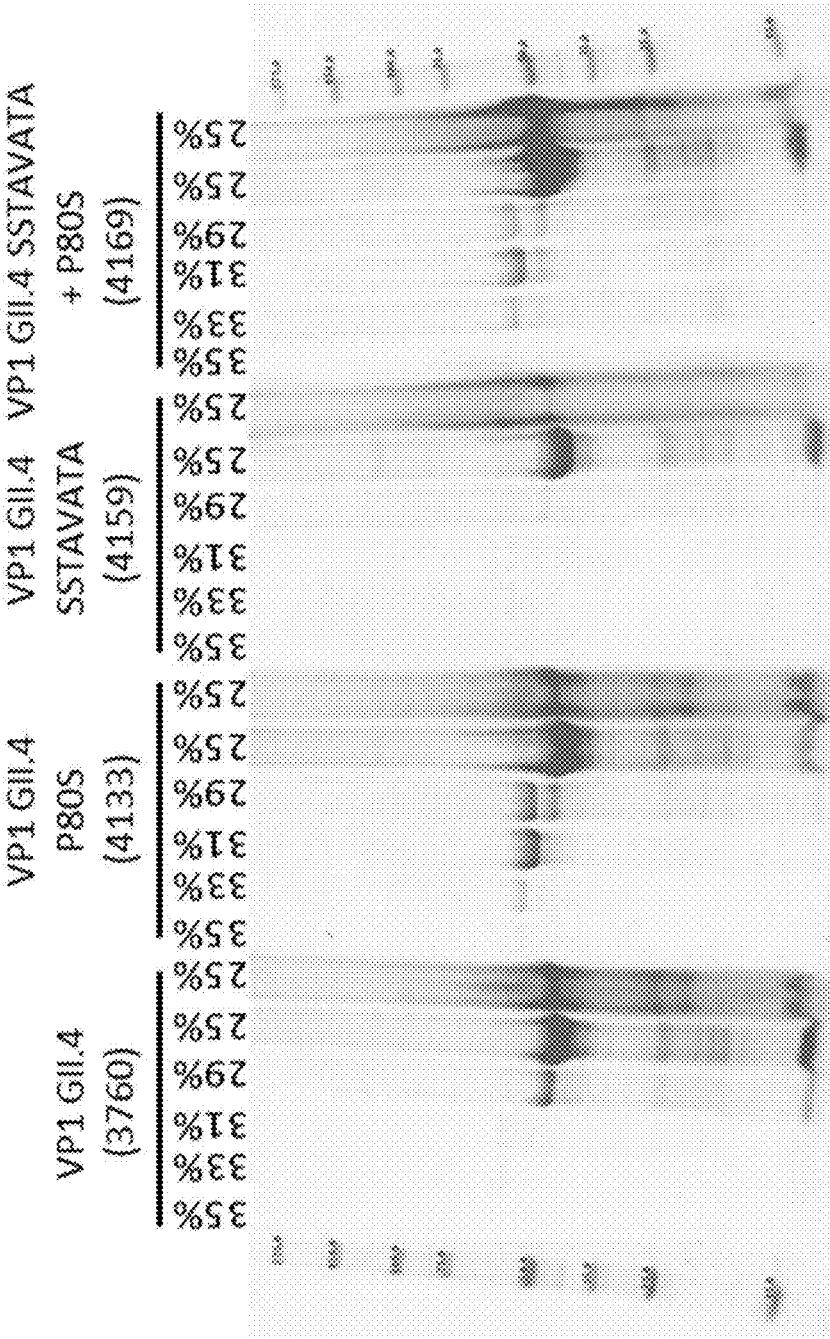


Figure 9G
GII.4/Sydney/SW0514/2012/AU

GII.4_A39V+R53I+P80S

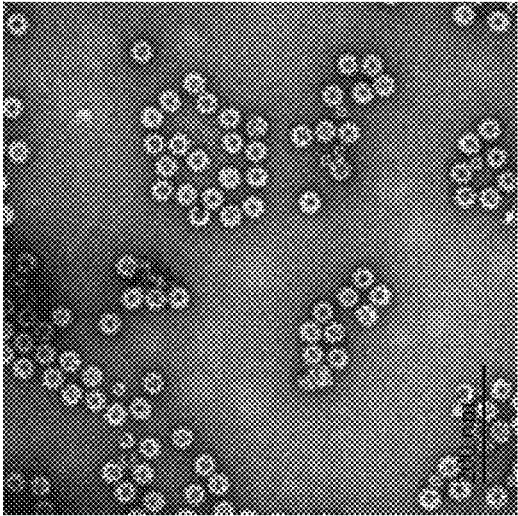
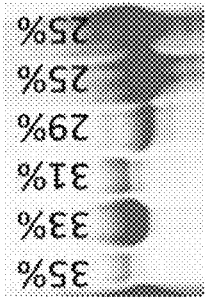


Figure 9H

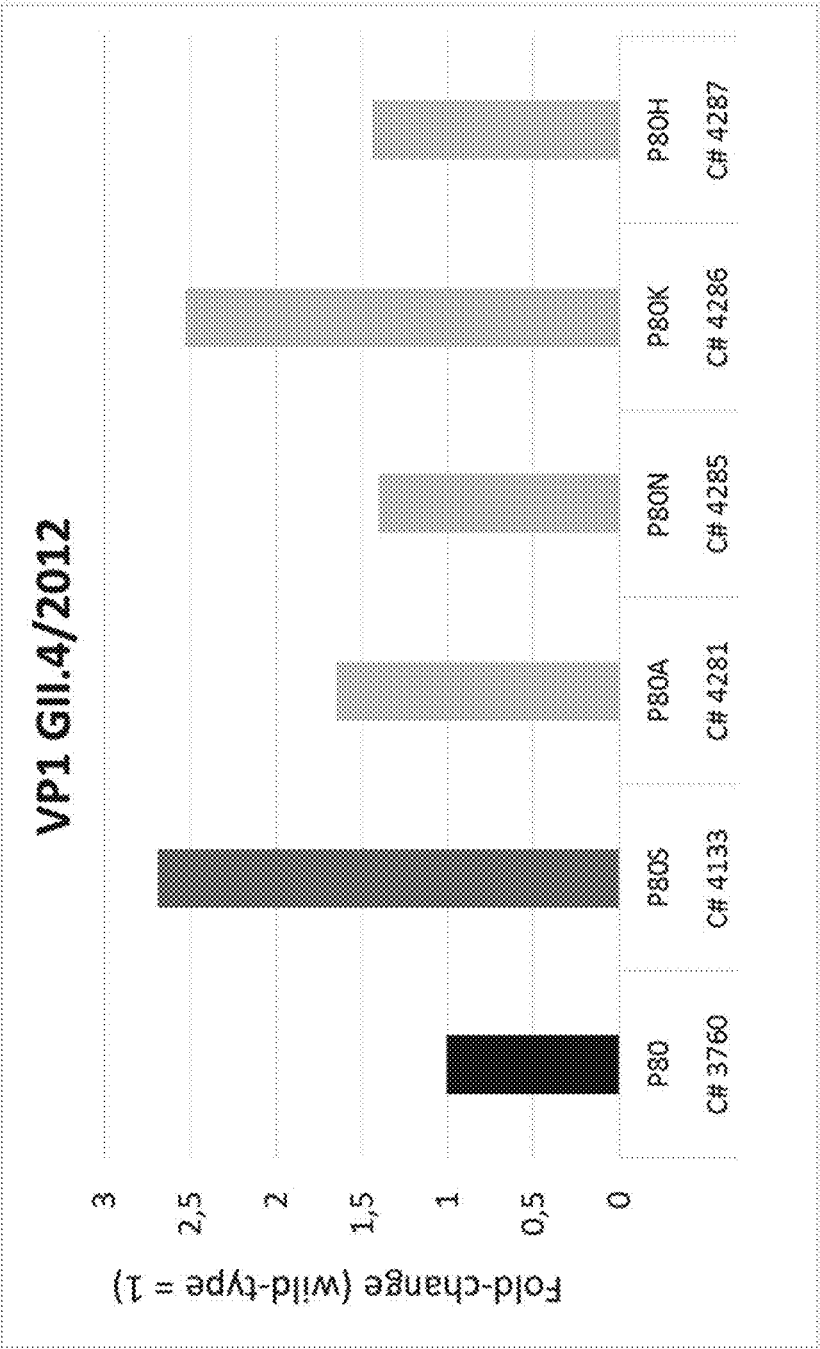
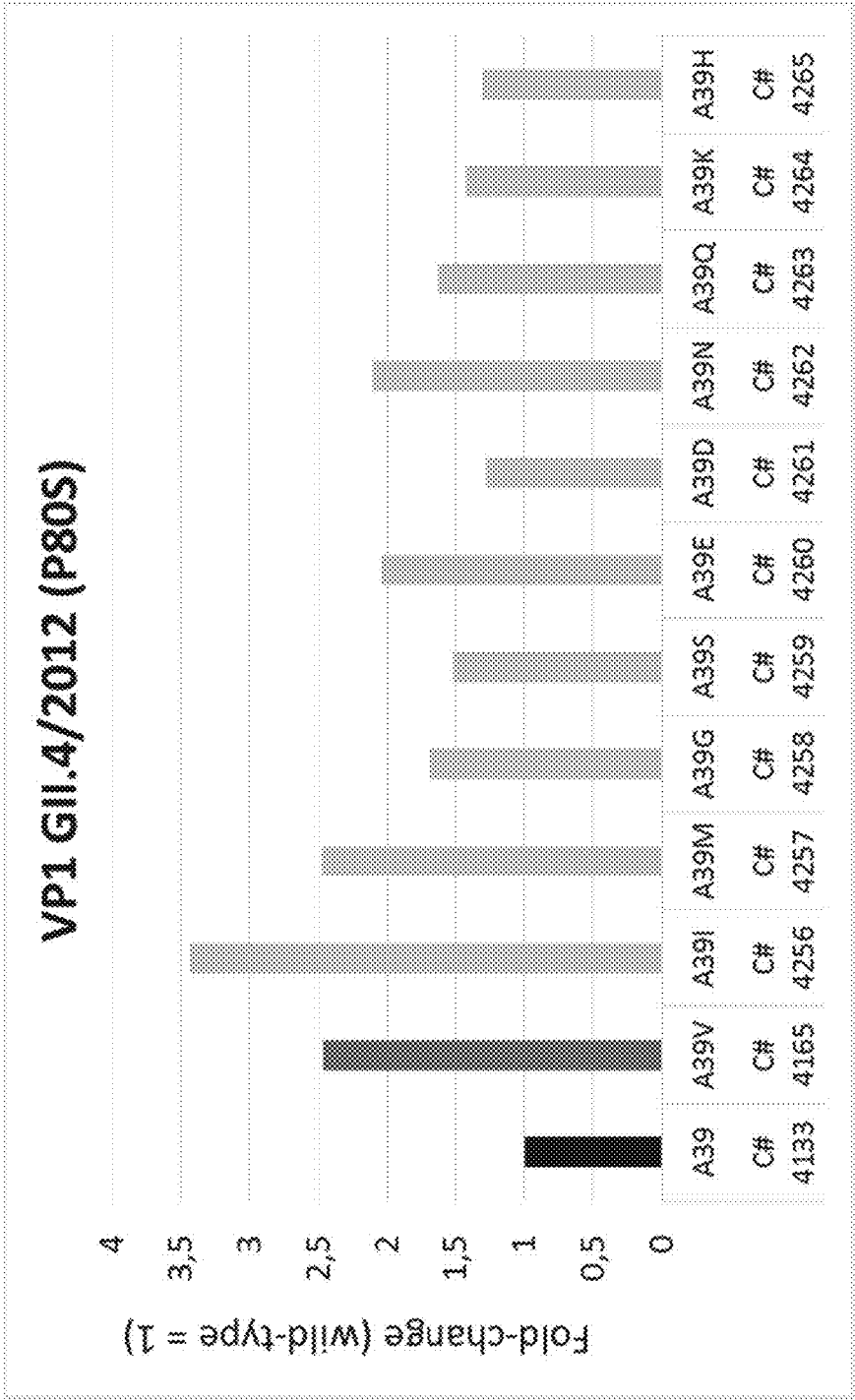


Figure 9I



GII.6/Ohio/490/2012/USA

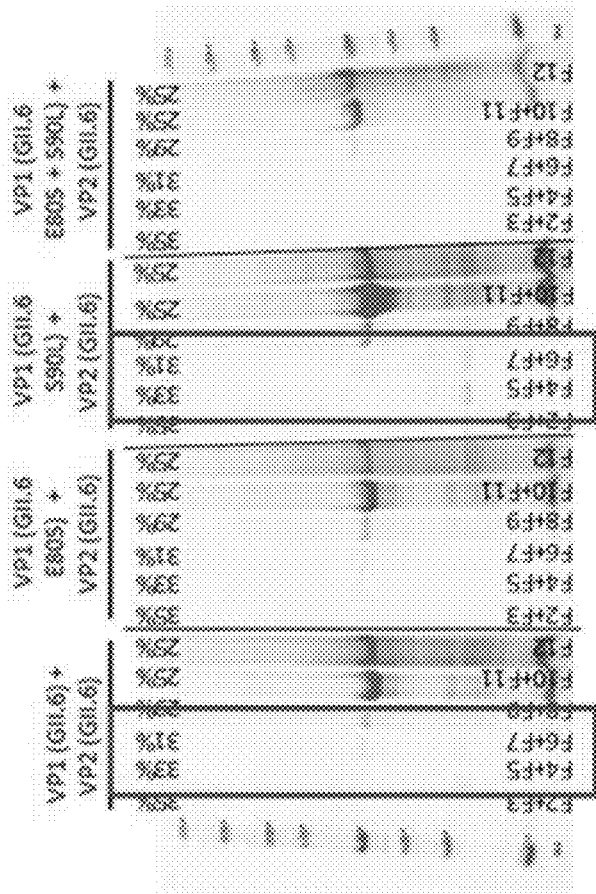


Figure 10A

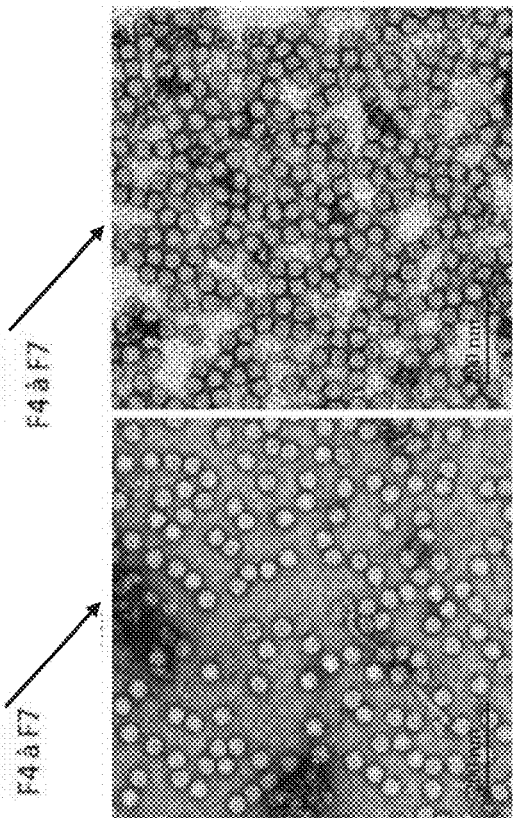
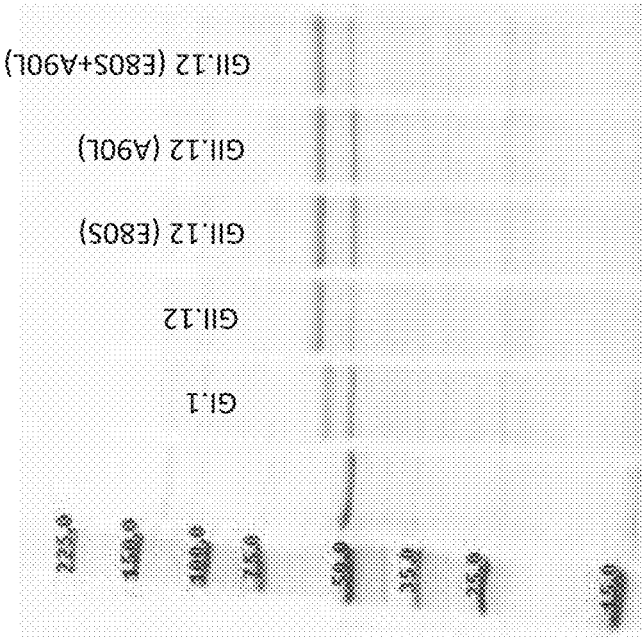


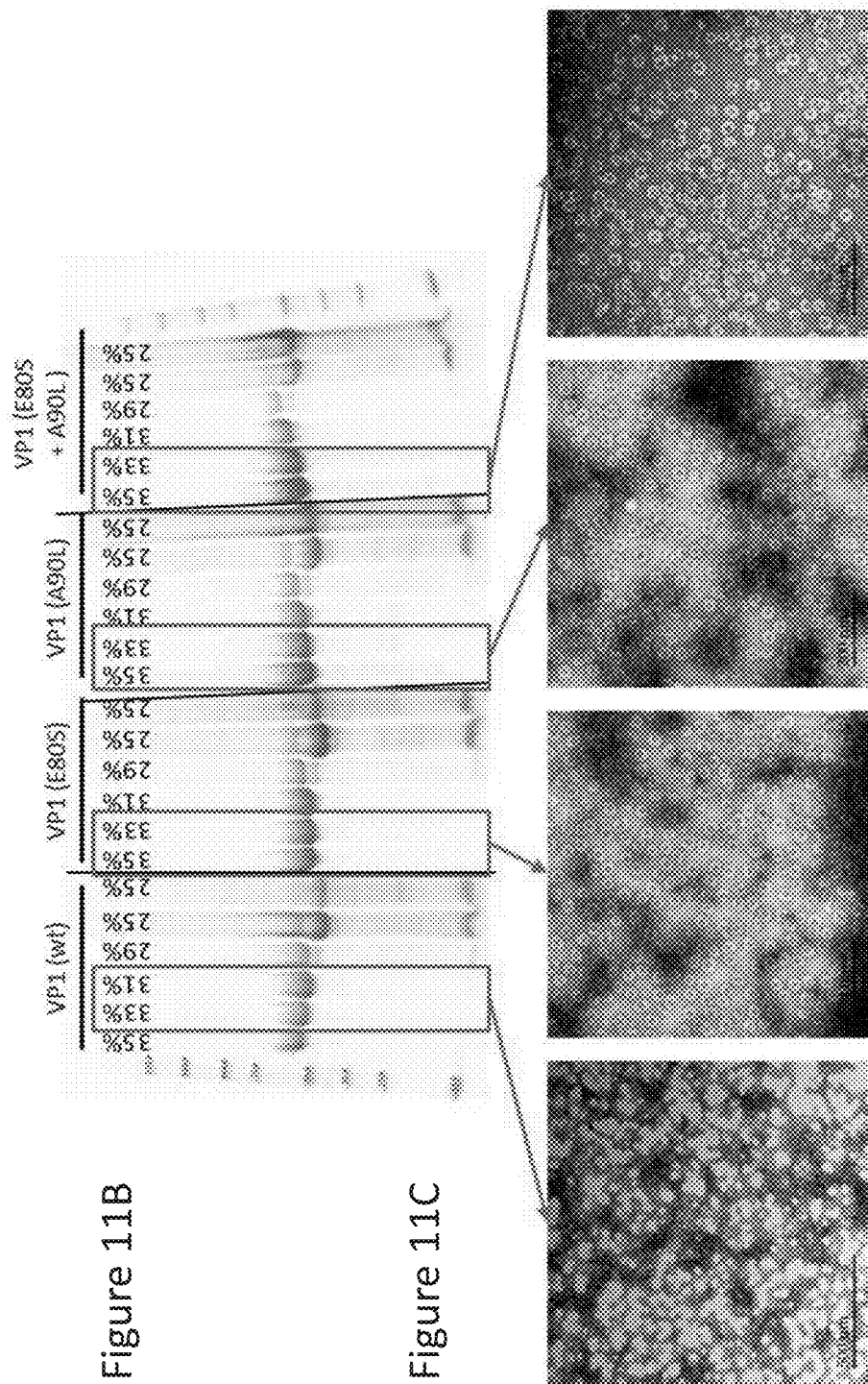
Figure 10B

GII.12/HS206/2010/USA

Figure 11A



GI.12/HS206/2010/USA



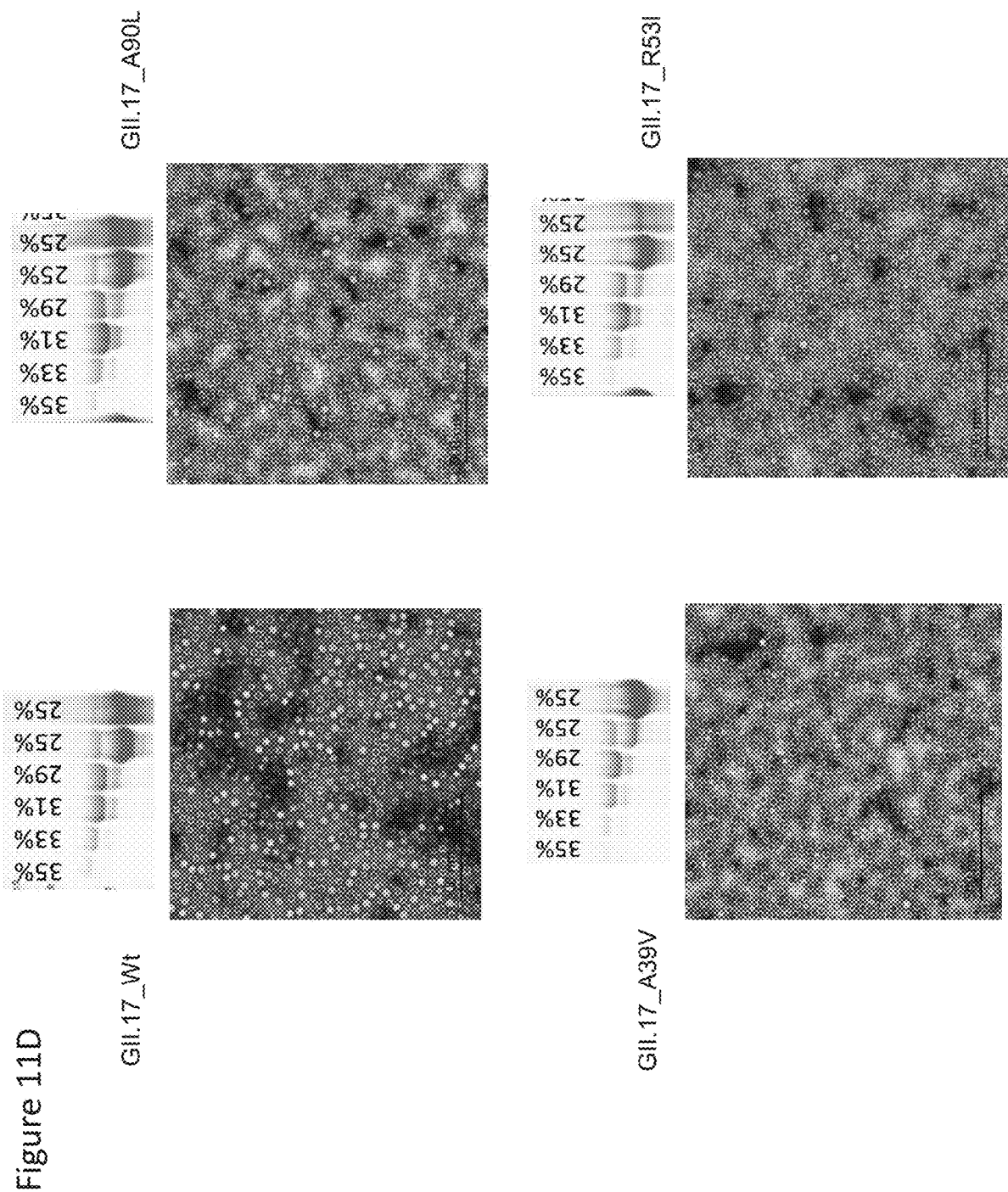


Figure 12A

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

MMMASKDATSSVDGASGAGQLVPEVNASDPLAMDPVAGSSTAVATAGQVNPIDPWIINNFBVQAPQGEFTISPNNTP
GDVLFDSLGLPHLNPFLHLSQMYNGWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLIAQATLFPHVIADVRLD
PIEVPLEDVRNVLFHNDRNQQTMLVCMYLTPLRTGGGTGDSFVVAGRVMTCPSPDFNLFVLPPTVEQKTRPFTLPN
LPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTLGRLVGTTVPVSLSHVAKIRGTSNGTVINLTDLGTPFHPFEGPAPI
GFPDLGGCDWHINMTQFGHSSQTQYDVTDPDTFVPHLGSIQANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYG
SSITEATHLAPSVYPPGFGFVLFVFFMSKMPGPGAYNLPCLLPQEIYISHLASEQAPTVGEAALLHYVDPDTGRNLGEFKAYP
DGFLTCVPNGASSGPQQLPINGVFVFSWVSRYQLKPVGTASSARGRLGLRR

Figure 12B

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

ATGATGATGGCGTCTAAGGACGCTACATCAAGCGTGGATGGCGCTAGTGGCGCTGGTCAGTTGGTACCGGAGGTTA
ATGCTTCTGACCTCTTGCAATGGATCCTGTAGCAGGTTCTTCGACAGCAGTCGCGACTGCTGGACAAGTTAATCCTA
TTGATCCCTGGATAATTAATAATTTGTGCAAGCCCCCAAGGTGAATTTACTATTTCCCAAATAATACCCCCGGTG
ATGTTTTGTTTGATTTGAGTTTGGGTCCCATCTTAATCCTTTCTTGCTCCATCTATCACAAATGTATAATGGTTGGGT
GGTAACATGAGAGTCAGGATTATGCTAGCTGGTAATGCCTTTACTGCGGGGAAGATAATAGTTTCTGCATACCCCC
TGTTTTGGTTCACATAATCTTACTATAGCACAAGCAACTCTTTCCACATGTGATTGCTGATGTTAGGACTCTAGAC
CCCATGAGGTGCCTTTGGAAGATGTTAGGAATGTTCTTTTCATAATAATGATAGAAATCAACAAACCATGCGCCTT
GTGTGCATGCTGTACACCCCCCTCCGCACTGGTGGTGGTACTGGTGATTCTTTGTAGTTGCAGGGCGAGTTATGAC
TTGCCCCAGTCTGATTTTAATTTCTTGTTTTAGTCCCTCCTACGGTGGAGCAGAAAACAGGCCCTTCACACTCCCA
AATCTGCCATTGAGTTCTGTCTAACTCACGTGCCCTCTCCCAATCAGTAGTATGGGCATTTCCCAGACAATGTCC
AGAGTGTGCAGTTCCAAATGGTCGGTGTACTCTGGATGGCCGCCTGGTTGGCACCACCCAGTTTCATTGTCACAT
GTTGCCAAGATAAGAGGGACCTCCAATGGCACTGTAATCAACCTTACTGAATTGGATGGCACACCCTTTCACCTTTT
GAGGGCCCTGCCCATTTGGGTTTCCAGACCTCGGTGGTTGTGATTGGCATATCAATATGACACAGTTTGGCCATTC
TAGCCAGACCCAGTATGATGTAGACACACCCCTGACACTTTTGTCCCCCATCTTGGTTCAATTCAGGCAAATGGCAT
TGGCAGTGGTAATTATGTTGGTGTCTTAGCTGGATTTCCCCCATCACACCCGTCTGGCTCCCAAGTTGACCTTG
GAAGATCCCAATTATGGGTCAAGTATTACGGAGGCAACACATCTAGCCCCCTCTGTATACCCCCCTGGTTTCGGAG
AGGTATTGGTCTTTTTCATGTCAAAAATGCCAGGTCTGGTGTCTATAATTTGCCCTGTCTATTACCACAAGAGTACA
TTTCACATCTTGCTAGTGAACAAGCCCTACTGTAGGTGAGGCTGCCCTGCTCCACTATGTTGACCCTGATACCGGTC
GGAATCTTGGGAATTCAAAGCATACCTGATGTTTTCTCACTTGTGTCCCAATGGGGCTAGCTCGGGTCCACAA
CAGCTGCCGATCAATGGGGTCTTTGTCTTTGTTTCATGGGTGTCCAGATTTTATCAATTAAAGCCTGTGGGAAGTCC
AGCTCGGCAAGAGGTAGGCTTGGTCTGCGCCGATAA

Figure 12C

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

ATGATGATGGCTAGTAAAGATGCGACCTCCTCTGTGGATGGTGCCTCAGGGGCAGGACAACCTCGTACCCGAGGTAA
ACGCCAGCGACCCACTTGCCATGGACCCGTTGCCGGAAGTTCCACAGCAGTGGCCACAGCCGGTCAAGTGAATCC
AATTGATCCGTGGATTATCAACAATTTCTGTCAGGCACCCAGGGCGAGTTCACAATTTACCAAACAATACACCGG
GCGATGTGCTATTCGATCTTTCCTTGGGTCTCACCTTAACCTTTTCTACTCCATCTCTCACAGATGTACAATGGTTG
GGTAGGAAACATGAGAGTCCGGATCATGCTGGCTGGCAATGCCTTTACCGCTGGCAAGATCATCGTCAGTTGTATTC
CTCCCGGATTTGGATCTCATAATCTGACCATTGCTCAAGCGACTCTCTTTCCCATGTTCATCGCCGACGTTAGGACCT
GGACCCCATCGAGGTGCCCCTGGAGGACGTCCGGAATGTTTTGTTCCACAACAACGACAGAAACCAGCAGACGATG
AGACTTGCTGTATGCTCTATACCCCACTGCGGACTGGAGGCGGGACTGGAGACTCCTTCGTTGTGGCAGGAAGAG
TGATGACATGCCCCCTCCCCGACTTCAACTTTCTTTTCTGGTCCCACCAACCGTTGAGCAGAAGACGCGGCCCTTA
CACTGCCCAATCTCCCGCTTTCAAGTCTGAGTAATTCACGGGCCCCATTGCCGATCTCCTCAATGGGAATCTCCCCG
ACAACGTCCAGTCTGTCCAATTCAAAATGGGAGATGCACACTGGACGGTCGCCTGGTGGGAACAACCTCCGGTGT
CCTCTCATATGTCGCAAAATCCGCGGCACATCAAATGGTACCGTAATCAATCTGACAGAACTTGATGGCAGCCCTT
CCATCCCTTTGAAGGACCAGCCCTATTGGATTTCCTGATCTGGGAGGTTGCGACTGGCACATAAACATGACACAGT
TTGGCCACTCCAGCCAGACACAGTATGATGTCGATACAACCCAGATACCTTCGTGCCACACCTGGGATCTATTCAA
GCTAACGGTATTGGATCCGGCAACTACGTGGGAGTCTTATCTTGGATCTCACCACCATCCACCCCTCAGGATCCAG
GTTGACTTGTGGAAGATACCGAATTATGGATCCTCGATCACTGAAGCCACGCACCTCGCACCTTCCGTCTACCCACCA
GGTTTTGGAGAAGTCTTGGTGTTCATGAGCAAAATGCCCGGCCCTGGAGCCTACAATCTCCCTTGCCTACTCCCT
CAAGAGTATATTAGTCACCTCGCATCTGAGCAGGCCCGACCGTTGGCGAGGCAGCCCTGCTGCATTATGTGGATCC
GGACACCGGCAGGAACCTGGGTGAGTTCAAAGCTTATCCTGACGGTTTTCTAACATGTGTACCAAATGGCGCTTCCA
GCGGCCCTCAACAGCTCCAATCAATGGCGTGTTCGTTTTGTGAGCTGGGTAAGCCGCTTCTACCAGCTGAAGCCC
GTGGGGACAGCTTCTTCTGCCCCGGGACGCCTCGGTCTGCGGAGATAA

Figure 13A

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

MMMASKDAPQSADGASGAGQLVPEVNTADPLMEPVAGPTTAVATAGQVNMIDPWIVNNFVQSPQGEFTISPNT
PGDILFDLQLGPHLNPFLSHLSQMYNGWVGNMVRVILLAGNAFSAGKIIVCCVPPGFTSSSLTIAQATLFPVHVIADVRTLEP
IEMPLEDVNRNVLYHTNDNQPTMRLVCMYLTPLRTGGGSGNSD5FVVAGRVLTAPSSDFSFLVPPPTIEQKTRAFTVPNIP
LQTLNSRFPSLIQGMILSPDASQVVFQNGRCLIDGQLLGTTPATSGQLFRVRGKINQGARTLNLTEVDGKPFMAFDSP
APVGFDPDFGKCDWHMRISKTPNNTSSGDPMRSVDVQTDVQGVPHLGSIQFDEVFNHPTGDYIGTIEWISQPSTPPGT
DINLWEIPDYGSSLSQAANLAPPVFPPGFGEALVYFVSAPGPNNSAPNDVPCLLPQEYVTHFVSEQAPTMGDAALLHY
VDPDTNRNLGEFKLYPGGYLTCVPNGVGAGPQQLPLNGVFLVSWVSRFYQLKPVGTASTARGRLGVRR

Figure 13B

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

ATGATGATGGCTTCAAAGGATGCTCCCCAAAGCGCGGACGGAGCTAGCGGCGCCGGACAGTTGGTTCCGGAAGTC
AACACTGCCGATCCACTGCCCATGGAACCCGTAGCTGGTCCAACAACCGCTGTTGCCACCGCCGGCCAGGTAAACAT
GATCGATCCATGGATTGTTAATAACTTTGTACAGAGCCCCCAGGGGGAGTTCACAATTTCTCCGAACAATACCCCTG
GGGACATTCTGTTGATCTGCAACTGGGCCCACACTTGAATCCTTCTGAGCCATCTTTCACAGATGTACAACGGAT
GGGTTGGGAACATGCGTGTTCGGATCCTCCTTGTCTGGCAACGCCTTCAGTGTCTGGCAAGATTATCGTGTCTGCGTA
CCACCAGGGTTTACCTCGAGTTCATTAACCATTTGCTCAGGCCACCCCTTTTCCCTCACGTGATCGCAGACGTGCGTACC
TTAGAACCAATCGAAATGCCCTGGAAGATGTACGGAACGTGCTGTACCATACTAATGATAACCAGCCAACGATGA
GATTAGTGTGCATGCTGTACACCCCCCTGAGAACTGGAGGAGTCTTGAAATTCGACAGTTTTGTGGTGGCTGG
CAGGGTCTGACCGCTCCAGTAGCGACTTCAGCTTTTTGTTCTCTCTCTACAATCGAACAAAAACAAGAGC
ATTCACAGTGCCCAACATCCACTGCAGACTTTAAGCAATTCAGGTTTCCAGCTTGATCCAGGGTATGATCCTTCT
CCCGACGCCTCCCAAGTTGTGCAGTTCAGAATGGGAGATGTCTTATCGACGGTCAGCTTCTGGGAACAACCCCTGC
CACCTCCGGGCAACTCTTCCGGGTGAGAGGCCAAATCAATCAGGGCGCCAGAACACTGAATCTGACAGAAGTGGAC
GGGAAACCCCTTATGGCGTTGATAGCCCCGCGCCGTTGGATTCCCTGACTTCGGCAAGTGTGATTGGCAGATGCG
CATCAGTAAGACTCCCAACAACACTTCATCTGGAGACCCCATGAGGAGCGTGGATGTCCAGACCGACGTGCAGGGC
TTCGTGCCGCACTTGGGATCTATCCAGTTCGATGAGGTGTTCAATCACCTACTGGCGACTACATAGGCACAATTGA
GTGGATAAGTCAACCATCTACACCTCCAGGGACCGACATAAACCTGTGGGAAATCCTGATTACGGSTCATCCCTGA
GTCAAGCTGCCAATCTTGACCCCCCTGTCTTCCCCCGGCTTTGGTGAGGCTCTGTTTACTTCGTCTCTGCATTTCT
GGTCTTAACAACCGCTCCGCCCTAACGATGTTCCGTGTTTGTACCCAGGAATATGTGACTCATTTCTGTTCCGAA
CAGGCACCCACCATGGGGGACGCTGCCCTGCTACACTATGTGGACCCGACACCAATAGAAACCTCGGCGAGTTCA
AACTCTACCCCGGGGGATACCTGACCTGTGTTCCAAATGGAGTGGGAGCAGGCCCAACAGCTGCCCTGAATGG
GGTCTTCTGTGTTCTTGGGTGTACGCTTTTACCAGCTGAAGCCCGTTGGCACAGCTTCTACGGCACGCGGCAG
GCTAGGGGTCCGCCGAATCTGA

Figure 14A

Amino acid sequence of VP1 G1.3_LillaEdet_2008_H2DG70 (SEQ ID NO: 6)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNT
PGDILFDLQLGPLNPLFLSHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSAQATMFPHVIADVRV
LEPIEVPLEDVRNVLFHNNDSTPTMRILCMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLVPPNVEQTKPFVSNL
PLNVLSNSRVPSLIKSMMSVQDHGQMVQFQNGRVTLTGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFPLDGECDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLWLSPPSGGAPK
VNPWAIAPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLGEFKLYPEGFMTCVPNSSSGSPQTLPLINGVFTFISWVSRYQLKPVGTTGPVRRLGIRRS

Figure 14B

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

ATGATGATGGCTTCCAAGGATGCTCCACAAACATGGATGGAACAAGCGGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAAGGCTCCACAGGGGGAGTTTACCATAAGCCCAAACAACACCCCG
GGTGACATCTTGTGTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTGAGTCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCTCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCTTGAGGACGTGCGCAACGTCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTGACTTGTCTAGCCCTGACTTCAACTTCCTTTTCTGGTGCCTCAAATGTAGAACAGAAAACAAAGCC
ATTACGCGTGCCAAACCTGCCCCTTAACGTGCTGTGCAATCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTAGACGGGCAGCTGCAGGGCACAAACCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCTACCATGCATTGAGTCACCTGCACCTATTGGATTTCCCGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC
ATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCAAGCGGTGGGGCCCTAAAGTTAACCCTATGGGCTATTCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCACCCCATATACACCAGGATTCGGGGAAGCCATTGTTTCTTATGTCCGATTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGTCCCTTGACAGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCTACTCGGGGCGAGGCTGCCTTGTGATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCTGAAGGTTTCATGACCTGCGTACCTAAGTCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTACCAACTCAAGCCCGTCGGAACAACCTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 15A

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

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLQLGPHLNPFLAHLNQMYNGWVGNNMRVRVILAGNAFTAGKVIIICVPPGFQSRFLSIAQATLPHIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYPLRTGGGSGGTDAFVAVGRVLTCPSSDFNFLVLPPTVEQKTRPFVSPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSILKFRGKVSAGSKVINLTLDGSPFLAFEAPAP
TGFPDLGTSWVHVEMLNSNSQSSGNPILLRDIHPNSSEFVPHLGSVCVTAIEVAGDYGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPPGFGEAIVYFMSPPIGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPQQLPLNGVVFASWVSRYQLKPVGTASSARGRLGVRR

Figure 15B

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

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCTTGGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTTAATATG
ATTGACCCCTGGATTTTCAATAATTCGTGCAGGCCCTCAAGGCGAGTTTACTATAAGCCCTAACACACACCAGGG
GATATTCTGTTGACCTGCAGTTAGGCCCTCATCTCAACCCCTTCTTGGCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCCTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATAACCAACGATAATCAGCCCACTATGAGG
TACTGTGCATGCTGTACACGCCACTCCGGACTGGTGGGGGGCAGTGGGGGGACCGATGCTTTCGTGCTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCTTCTTGTCGCCCCAACGGTGGAACAGAAAACGAGACCTT
TTTCCGTACCTAACATCCCTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACCTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTCCAGACCTGGGAACATCCGATTGGCATGTGCGAGA
TGAGTCTGAATAGCAACTCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCACTGGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTGGACAATCCACACTACGGCTCTAACTTGCCGA
AGCATCCAGCTTGCCCCGTTGTATATCCCCAGGCTTGGCGAAGCAATAGTTTATTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCGAGGAGTTCGTGACTCATTTGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTGCGATCATGGGTTAGCCGGTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCCGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 16A

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

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIMNMFVQAPERGEFTISPNNT
PGDILFDLRLGPHLNPFLHLSQMYNGWVGNMRRVRVMLAGNAFSAGKIHCCVPPGFESQNISIGQATMFPHVIADVRVL
EPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCAPDFNFLVPPSVEQKTRQLTIPNI
PLNNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLEGQLLGTTPV5ANQVARIRGKVFSTNSGTGLNLTEVDGTPYH
AFESPAPLGFDPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGNSFAPHLGSI EFSSENHPSGDQLGLTLTWISPLNNASRV
DPWKIPTYGSTLTESTNLAPPIFPFGFEAIVYFMSDFPIVSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHR
NLGEFKLYPDGFITCVPNTGGGPQNLPSNGVFVFSSWVSRYQLKPVGTTGPVRRLGVRVV

Figure 16B

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

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGCGAACCCTTCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTGCGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAATGAACAATTTGTTTCAGGCACCAGAAGGAGAATTCACC
ATCTCCCCCAATAACACCCCAGGGGATATTCTGTTTGACCTCAGGTTAGGACCCCACTTGAACCCCTTCT
GCTTCATCTCTCACAAATGTATAATGGCTGGGTGCGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAA
TGCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCTCTGGAATTCGAATCTCAAATATCAGCATTG
GTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTGCGCTCCTGGAACCCATTGAAGTTCCTCTCGAC
GACGTGAGAAATGTTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACA
CCCCATTAAGAGCCGGGGGAGCATCCTCAGGTAAGTACCCATTTGTGATTGCCGGGCGGGTGCTCACAT
GCCCCGCTCCAGACTTTAACTTCTTTTCTTGGTGCCACCCAGTGTGAACAGAAAACAGACAGCTCACC
ATCCCAAATATCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCA
GTGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGA
CGACCCAGTCTCCGCGAACCAGGTGGCCGAATCCGGGGTAAAGTCTTCAGTACAACTCCGGCAGTGT
GCCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTGAGTCTCCAGCCCTCTTGGCTTTCCC
GATATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATA
GGTTGGATATAACACAAGGTAATTCATTGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCA
TCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCC
CTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGTCCGCCCATTTTCCACCCG
GATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCT
TGCACACTGCCACAAGAATTCGTCTCATCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCC
TCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGCGGAGTTTAAGCTGTACCCTGACGGGTTTATT
ACCTGTGTACCAACACCGGCGGGCGGCCACAAAATTTGCCAGCAATGGCGTGTGTTGCTTTTCTCTTG
GGTGTCTCGATACTACCAGCTTAAACCTGTCGGAACCTACGGGCCCCGTGCGACGACTCGGCGTGAGGCG
GGTGTA

Figure 16C

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

MKMASNDAAPSNDDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRNMNFVQAPNGEFTVSPRNSPGEVLL
NLELGPENPFLAHLRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAIPPHFPLENLSPGQITMFPVHIIDVRTLEPVLLPLP
DVRNFFHYNQQPEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELSNS
RFPVPIDELTYSPNEGVSQVQPNQGRSTLDGELLGTTQLVPSNICALRGRINAQVPDDHHQWNLQVTNANGTSFDPTEDEV
PAPLGTDFLANIYGVTSQRNPNTCRAHDGVLATWSPKFTPKLGSVVLGTWEESDLNQPTRFTPVGLYDTHGFDQ
WVLPNYSGRLLTNMNLAPSVAPLFPGEQILFFRSHIPLKGGTSNGAIDCLLPQEWIQHFYQESAPSPTDVALIRYTNPDGT
RVLFEAKLHRQGFITVANSGRPIVPPNGYFRFDSWVNQFYS LAPMGTGNGRRRVQ

Figure 17A

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

MKMASNDAAPSTDGAAGLPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPLYLAHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPVHVIDVRTLEPVLL
PLPDVRNFFHYNQKDDPKMRIVAMLYTPLR5NGSGDDVFTVSCRVLTRPSPDFDFTYLPPTVESKTKPFTLPILTLGELS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLGELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVTITNLNGSPFDPSSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDDLTVNQPVKFTPVGL
NDTDHFNQWVVPYAGALNLTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

Figure 17B

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

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTTCGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCGAGCTGGGACCAGAACTTAATCCGTACCTGGCTCACCTGGCCCCGGATGTACAATGGATATGCAGGAG
GGATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCCTTACAGCAGGCAAACCTCGTTTTTCGACGCCGTCCCTCCCCAC
TTCCAGTTGAAAATCTTTCCCTCAGCAGATTACCATGTTTCCCATGTCATCATCGATGTGCGTACCCTGGAACCTG
TGCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAACTAAGCCATTACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTT
TGTGCACTGTCAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTCACTGGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATTCCTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACCTAACCTTGCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTGCAGAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 18A

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

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNEFVQAPGGFTVSPRNSPGEVLLN
LELGPEINPYLAHLARMYNGYAGGFVQVVLAGNAFTAGKIIFAAIPPNFIDNL5AAQITMCPHVIVDVRQLEPVNLPMP
DVRNNFFHYNQGSDSRLRIAMLYTLRANNSGDDVFTVSCRVLTRPSPDFSNFLVPPTVESKTKPFSLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLDGELMGTQQLPSQJCAFRGTLTRSTSASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTPDFRGKVFVVASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNPTRFTPVGIGVD
HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHLRFMTIAKSGDSPITVPPNGYFRFESWVNPFTLAPMGTGNGRRRIQ

Figure 18B

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

ATGAAAATGGCTTCCAACGATGCAGCACCTCTAATGATGGCGCTGCCGACTTGTGCCGAGATTAGCTCTGAGG
CTATGGCCCTAGAACCAGTAGCCGGGGCAGCCATAGCTGCCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCTGTCAGGCACCGGGGGGAGAATTCACGGTCTCTCCTCGAACTCCCCGGGGAGGTTCTCT
TGAATTTGGAACCTGGGCCCTGAAATTAATCCTTATCTGGCCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT
TTCGAGGTCCAGGTGGTGCTCGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAACTTC
CCTATCGATAATCTTAGTGCCGCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCGACGTGCGCAACAACCTCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATCCGGAGATGACGTTTTCACTGTGAGTTGTCGAGTCCTGACACGTCC
ATCTCCTGACTTTAGCTTTAATTTCTCGTGCCCCCACAGTGGAATCCAAACTAAGCCATTCTCTCTGCCAATTCTT
ACCATTAGCGAAATGTGCAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTGAGAACGGACGCGTGACTCTCGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACCTGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCACCCGGGCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTTGATCAGAACAGCAACCCGGTTTACCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGACAGGCCAGTTCACACATAACATGAATCTTGCCCCGCTGTGGCCCCCACTTCCCGGAG
AACAACCTCTGTTTTTCAGGAGCCAACTGCCTTCAGCGGCGCGGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATCGCC
TATTACAGTGCCCCCAACGGATACTTCAGATTTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 19A

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGGEFTVSPRNAPGEIL
WSAPLGPDLNPLYSLHARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFTEGLSPSQVTMFPHIVVDVRQLEPVL
PLPDVRNNFYHYNQSDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRSPDFDFIFLVPPTVESRTKPFVSPVLTVEEMT
NSRFPIPLEKLTGPSSAFVVQPQNGRCTTDGVLGGTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAFAPKLRVQFETDTRDFEANTKFTPVGVIQDGGTTHR
NEPQQWVLPYSYGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDLVPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 19B

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCCTGCTGGCAAAGTGATCTTTCAGCGGTGCCTCCCAAC
TTCCCACTGAAGGACTGTCTCAAGCCAGGTACAAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTATGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCTCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCATTG
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAATATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCCAACGAAGAGATTCCCGCACCTCTTGAACCCCCGACTTTGTGGGAAAATACAGGGCGTCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTGCCCC
GAACTGGGTAGAGTGCAAGTTGAGACCGACACTGACCGGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTACAGGACGGGGGACCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACTGCTCTTTTTCGTTCA
ACCATGCCTGGATGCTCCGATATCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGCAGTATTTTAT
CAAGAGGCCGACCAAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCAACGGAT
ATTTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 19C

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

MKMASNDANPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGGFTVSPRNAPGEIL
WSAPLGPDLPYLSHLARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFPTGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNFYHYNQSNDSSTIKLIAMLYTPLKANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFTVPILTVEEMSN
SRFPIPLEKLYTGPSSAFVVQPQNGRCTTDGVLGGTTQLSAVNICTFRGDVTHIAGSHDYTMNLASQNWNNYDPTTEEIPA
PLGTPDFVGGIKQGMILTQTTRDGSTRAHKATVSTGSHVFTPKLGSVQYTTDTNNDFTGQNTKFTPVGVQQDGNHQN
EPQQWVLPNYSGRGTGHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMNLDCLLPQEWVQHFYQEAAPASDVALL
RFVNPDTGRVLFECKLHKSGYVTVAHGTGPHDLVIPPNGYFRFDSWVNQFYTLAPMGNGAGRRRAL

Figure 19D

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

MKMASNDANPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGGFTVSPRNAPGEIL
WSAPLGPDLPYLSHLARMYNGYAGGFVQVILAGNAFTAGKIIFAAPVPPNFPTGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNFYHYNQLNDPTIKLIAMLYTPLRANNAGEDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFTVPILTVEEMTN
SRFPIPLEKLTGPSSAFVVQPQNGRCTTDGVLGGTTQLSPVNICTFRGDVTHIAGTHNYTMNLASQNWNNYDPTTEEIPA
PLGTPDFVGRIQGMILTQTTRDGSTRGHKATVSTGDVHFTPKLGSIQFNTDTNNDFTGQNTKFTPVGVVQDGNHGH
QNEPQQWVLPNYSGRGTGHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMNLDCLLPQEWVQHFYQEAAPASDV
ALLRFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAL

Figure 19E

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

MKMASNDATPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGGFTVSPRNAPGEIL
WSAPLGPDLPYLSHLARMYNGYAGGFVQVILAGNAFTAGKIIFAAPVPPNFPTGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNLYHYNQSNDSPTIRLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFVPILTVEEMTN
SRFPIPLEKLTGPSSAFVVQPQNGRCTTDGVLGGTTQLSPVNICTFRGDVTHIAGTQNYTMNLASQNWNNYDPTTEEIPA
PLGTPDFVGRIQGVLTQTTRRDGSTRGHKATVSTGSHVFTPKLGSVQFSTDTNNDFTGQNTKFTPVGVVQDGSSTTHQN
EPQQWVLPDYSGRDSHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMNLDCLLPQEWVQHFYQESAPASDVALL
RFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDVIPPNGYFRFDSWVNQFYTLAPMGNGAGRRRAL

Figure 19F

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

MKMASNDANPSDGSAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGFTVSPRNAPGEIL
WSAPLGPDLPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKHFAAVPPNFPTEGLSPSQVTMFPHIIVDVRQLEPVLIP
LPDVRNNFYHYNQSNDSSTIKLIAMLYTPLRANNAGEDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFVTPILTVEEMTNS
RFPIPLEKLFTGPSGAFVVPQNGRCTTDGVLGTTQLSPVNICTFRGDVTHIAGSRNYTMNLASLKWNYDPTTEEIPAPL
GTPDFVGKIQGVLTQTTKGDGSTRGHKATYTGSAFPTPKLGSVQFSTDTENDFETHQNTKFTPVGVTQDGSSTHRNEPQ
QWVLPSSYGRNVHNVHLAPAVAPTFPGEQLLFRSTMPGCSGYPNMDLCLLPQEWVQHFYQEAAPAQSDVALLRFV
NPDTGRVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAL

Figure 19G

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

MKMASSDANPSDGSTANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGFTVSPRNAPGEIL
WSAPLGPDMPYLSHLARMYNGYAGGFEVQVILAGNAFTAGKHFAAVPPNFPTEGLSPSQVTMFPHIIVDVRQLEPVLIP
PLPDVRNNFYHYNQSNDSPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFVTPILTVEEMT
NSRFPIPLEKLFTGPSSAFVVPQNGRCTTDGVLGTTQLSPVNICTFRGDVTHIAGSRNYTMNLASQNWNSYDPTTEEIPA
PLGTPDFVGKIQGVLTQTTTRTDGSTRGHKATVYTGSAFSPKLGVRVQFATDNDNDFDANQNTKFTPVGVIQDGNHTAHR
NEPQQWVLPSSYGRNTHNVHLAPAVAPTFPGEQLLFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAL

Figure 20

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

MKMASNDATPSNDGAAGLVPESNNEAMALEPVVGASLAAPVTGQTNIIDPWIRTNFVQAPNGFTVSPRNAPGEILVN
LELGPELNPYLAHLARMYNGYAGGMEVQVLLAGNAFTAGKHFAAVPPYFPVENLSP5QITMFPHVIIDVRTLEPVLLPMP
DVRSTLFHFNQKDEPKMRLVAMLYTPLRSNGSGDDVFTVSCRILTRPSPDFDFTYLPPTVESKTKPFTLPVLTGELSNSRF
PLSIDEMVTSPNESIVVQPNQNGRVTLDGELLGTTQLQACNICSIRGKVTGQVPNEQHMWNLEITNLNGTQFDPDTDDVPA
PLGVPDFAGEVFGVLSQRNRGESNPANRAHDAVVATYSKYTPKLGLVQIGTWNTNDVENQPTKFTPIGLNEVANGHR
FEQWTLPRYSGALTINMNLAPAVAPLFPGERLLFRSYVPLKGGFGNPAIDCLVPQEWVQHFYQESAPSLGDVALVRVY
NPDTGRVLFEAKLHKGGLTVSSTSTGPVVVPANGYFRFDSWVNQFYSLAPMGNGTGRRRRFQ

Figure 21A

Amino acid sequence of VP1 GII.6 Ohio 2012 M9T020 (SEQ ID NO: 20)

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGFEVTVSPRNSPGEMILL
NLELGPENLPYLSHLRMYNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRRFFHYNQENTSRMLVAMLYTPLRANSGEDVFTVSCRVLTRPADFEFTFLVPPTVESKTKPFSLPILTGLGELSNSR
FPAPIDMLYTDPNEGIVVQPPQNGRCTLDTGLQGTTQLVPTQICAFRGTIGQTSRSPDSTDSAPRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVS6QQVGATRAHEVHINTTDPRTYTKLGSILMYSESDDFVTGQPVRFPTPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSGNNPVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 21B

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

ATGAAGATGGCAAGCAACGACGAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGCTCCACAGGGGGAGTTACAGTCTCCCCCGGAACTCCCCGGGCGAGATGCTG
CTCAATCTGGAATCGGCCCTGAACTAAACCTTATCTGTACACCTTTACGGGATGTACAATGGCTACGCAGGAGG
AATGCAAGTTCAGGTGGTCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCCTCCACACT
TCCCTGTGCAAAATATCAACGCCGCCAGATTACTATGTGCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCA
GTTCTGCTGCCCTGCCCGACATCAGAAACCGTTCTTCATTACAATCAAGAGAATACTTCACGGATGAGACTTGT
GCGATGCTGTACACCCCTCTTCGTGCAAATCCGGCGAAGACGTGTTCACTGTGTCTTGTGAGTACTTACCCGACCC
GCCCCGATTTGCAATTCACCTTCTGGTCCCCCTACTGTGGAGAGCAAGACAAAACCTTCAGCCTCCCAATCTTA
ACACTCGGGGAGCTGTCTAATTCACGCTTCCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGT
GGTGCGAGCCCCAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAACTGGTGCCAACCCAGATT
TGTGCATTACGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGG
ACCACCCACTCCACGTTCAAGTTAAAAAACCTGGACGGAACCCAGTACGACCTACAGACGAGGTCCCCGCTGTCTC
GGAGCCATCGACTTTAAAGGAAGTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGCAGCAGGTGGGAGCT
ACGAGAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCCAAACCTAGGGTCAATTTTAATGTATTC
GGAATCAGACGATTTTGTACAGGTCAGCCCGTGCGTTTACCCCGATCGGAATGGGGGACAACGATTGGCACCAG
TGGAATTTGCCGATTACCCCTGGACACCTCACCTTGAATATGAATCTGGCCCCAGCCGTCGCGCCCGCTTCCCCGT
GAGCGGATCCTCTTTTTAGAAAGCATAGTGCCTCCCGCAGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCC
CCAAGAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCCTAGCCAGTCCGCAGTAGCACTGATCAGATATGTTAATC
CTGATACGGGAAGGAACATCTTGAAGCAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAA
CCCTATTGTGGTGCTCCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTTATACTCTGACTCCCATGGG
GACAGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 22

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

MKMASNDAAPSNDGAAGLVPEINNEVMPLEPVAGASLATPVVGQNIIDPWIRNNFVQAPAGEFTVSPRNSPGEILLD
LELGPELNPYLAHLARMYNGHAGGMEVQIVLAGNAFTAGKIIFAAIPPGFPYENLSPSQITMCPHVIIDVRQLEPVLLPMP
DIRNNFFHYNQGNPKRLIAMLYTPLRANN5GDDVFTVSCRVLTKP5PDFEFTFLVPPTVESKTKQFTLPILKISEMTNSRF
PVPVEMMYTARNENQVVPQNGRVTLDGELLGTTPLAVNICKFKGEVIAKNGDVRSYRMDMEITNTDGTPIDPTEDT
PGPIGSPDFQGILFGVASQRNKNEQNPATRAHEANINTGGDQYAPKLAQVKFFSESQDFEVHQPTVFTPVGVAGDTSHP
FRQWVLPRYGGHLTNNTHLAPAVAPLFPGEQILFFRSQIPSSGGHELGYMDCLVPQEWVQHIFYQEAATAQSEVALIRFIN
PDTGRVLFEAKLHKQGFITVAHTGDNPIVMPPNGYFRFEAWVNQFYSLAPVGTGNGRRRIQ

Figure 23A

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

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNFVQAPNGEFTVSPRNSPGEVLL
NLELGPELNPYLAHLARMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVIIDVRTLEPVLLPLP
DVRNNFFHYNQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDGELOQTQLLPTAICSFGRINQKVSGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTPDFSGKLFQVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTINMGLAPPVAPTFPGEQILFFRSHIPLKGGVADPVIDCLLPQEWIQLHYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 23B

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

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCCGTGGCCGGAGCCTCAATTGCCGCCCTCACTGGCCAGAACAACGTGATTGATCCCTGG
ATCAGACTGAACTTCGTTCAAGGCTCCTAATGGGGAGTTCACCGTGTCCCCGAGAACTCCCCGGCGAAGTGTTATT
GAATTTGGAATTAGGACCAGAACTCAACCCCTATCTGGCACATCTGTCTCGGATGTACAACGGCTATGCGGGCGGA
GTGGAGGTGCAAGTCTTCTCGCTGGTAATGCATTACAGCAGGAAAATTAGTATTTGCAGCGGTTCACCCCATTTT
CCACTTGAAAAACATAAGCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGT
GCTGCTACCCCTGCCGACGTGAGGAACAATTTCTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCG
CCATGCTCTATACTCTTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTCGGGTGCTCACCCGA
CCTTCCCCAGATTTGACTTCAATTATCTGGTCCCCCAGGTAGAGTCCAAAACAAAGCCTTCACTCTTCCAATCC
TTACAATTGGCGAACTGACCAACTCACGCTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTG
TCGTTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACCTGTTGCCAACCCTAT
ATGCTCTTTAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACACGTGTGGAACATGCAAGTGACGAATATC
GACGGGACACCTTCGATCCAACAGAGGATGTCCAGCGCCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCCG
CGTCTTTCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTGATTGCCACCAACTCAGCCAAATTCAC
CCAAAACCTGGAGCGATACAGATCGGAACCTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCC
CTGTTGGCCTTTTCGAAAGCGAAGGCTTTAACCAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG
GACTCGACCAACCCGTCGCTCAACGTTTCTGGTGAGCAGATTTTGTGTTTCCGCGATCATATCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTACAGCACTTGATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCTGATACGCTTCACAAACCCGATACCGGAAGAGTGTTGTTGAAGCTAACTTCATCGCTCC

Figure 23B (cont)

GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCGGGCAAACGGATACTTTCGATTTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

Figure 24A

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

MKMASNDAAPSNDGAASLVPEAINETMPLEPVAGASIAAPVAGQTNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLAHLRMYNGYAGGVEVQVLLAGNAFTAGKILFAAIPPNFPVDMISPAQITMLPHLI
VDVRTLEPIMIPDPVRNVFYHFNNQPQPRMRLVAMLYTLR5NGSGDDVFTVSCRVLTRPTPDFEYIYLVPP
SVESKTPFTLPILTISELTNSRFPISIEQLYTAPNENNVVQCQNGRCTLDGELQGTQQLSSAVCSYRGRTVANS
GDNWDQNVQLTYPGASYDPTDEVPAPLGTQDFSGILYGVLTQDNVRENTGEAKNAKGVYISTTS GKFTPK
IGSIGLHSITEDVRPNQQRFTPVGVAQNENTPFQQWVLPHYAGALALNTNLAPAVAPTFFGEQLLFFRSRVP
CVQGLQGQDAFIDCLLPQEWVNHFYQEAAPSQADVALIRYVNPDTGRTLFEAKLHRS GFITVSHTGAYPLVV
PPNGHFRFDSWVNQFYSLAPMGTGNRRRVQ

Figure 24B

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

ATGAAAATGGCTTCTAATGATGCCGCGCCAGCAATGATGGTGCCGCCAGCCTTGTCGCCGAAGCAATTAACGAGA
CAATGCCCTTGAGCCAGTCGCCGGGGCTTCTATTGCCGCCAGTTGCTGGACAGACGAATATCATCGATCCTTGG
ATACGGACTAATTTTGTCAAGCTCCTAACGGAGAGTTCACTGTCTCCCCCGTAATAGTCCTGGCGAGATCCTGTTG
AACCTCGAGTTGGGGCCAGATCTCAATCCTTACCTGGCTCATCTGTCGAGAATGTACAACGGGTACGCGGGGGGG
TTGAGGTGCAGGTCTTACTGGCAGGTAAACGCATTACAGCAGGCAAGATTCTGTTTGGCGCCATCCCTCCTAATTTT
CAGTGGATATGATATCTCCAGCACAGATTACAATGCTGCCCCATTTGATAGTGGATGTGCGGACACTTGAACCTATC
ATGATCCCTTTGCCGATGTCCGAAATGTGTTTATCATTTCAACAACAGCCGAGCCAAGAATGCGTCTCGTCGCG
ATGCTGTACACCCGTTGCGGTCCAACGGCTCTGGCGATGATGTTTTACAGTGTGTCGTGTCGAGTGTTAACCCGCCCT
ACCCAGATTTTGAGTTTATATATCTAGTTCCCCCTTCTGTGGAAAGCAAGACTAAACCTTTACTCTCCCATTTCTGA
CTATATCCGAGCTTACCAACTCCCGGTTCCCATCTCAATCGAGCAACTGTACACTGCACCAACGAGAAACAACGTAG
TCCAGTGCCAGAACGGGAGATGTACCCTGGACGGGGAGCTCCAAGGGACCACGCAACTGTAAAGTTCAGCCGTTTG
CAGTTACAGAGGCAGGACTGTGGCGAACTCTGGTGATAACTGGGATCAAAATGTGTTGCAGCTGACTTACCCATCC
GGCGCAAGCTACGATCCAACAGATGAGGTGCCAGCGCCCTTGGCACACAGGATTTCTCAGGAATTTCTATACGGGG
TGCTTACTCAGGATAATGTGCGAGAAAATACTGGCGAGGCCAAGAATGCTAAAGGAGTGATATAAGCACGACAAG
CGGTAAGTTTACCCCCAAAATTGGCAGTATTGGGCTCCACAGCATTACTGAGGACGTCCGCCCAAACAGCAGTCTC
GTTTCACTCCCGTGGGGTGGCACAGAACGAGAACACACCTTCCAGCAGTGGGTCTTGCCCCATTATGCAAGGTGCT
TTGGCGCTCAATACAAATCTGGCACCCGCCGTAGCGCCGACATTTCTGGGGAGCAATTGCTGTTCTTTAGAAGCCG
CGTCCCGTGTGTTCAAGGCTTGACAGGCGCAGGACGCGTTTCATTGATTGCCTCTTGCCCCAGGAATGGGTCAACCACT
TTTATCAGGAGGCAGCGCCCTCTCAAGCAGATGTGGCCCTGATAAGATATGTGAATCCCGACACAGGACGGACTTT
GTTTGAGGCAAACTCCACCGGTCAAGATTCACTGTGAGTCACACAGGAGCCTATCCCTTGTGGTTCCACCTAA
TGGCCACTTCAGGTTCTGACTCTTGGGTCAATCAGTTTTATTCGCTGGCACCAATGGGTACCGGGAATGGTGCCTGTC
GGGTGCAATGA

Figure 25

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

MKMASNDATPSDDGAAGLVPEINNEVMALEPVAGASIAAPVVGQQNIIDPWIRNNFVQAPAGEFTVSPRNSPGELLDD
LELGPELNPLYLAHLARMYNGHAGGMEVQIVLAGNAFTAGKILFAAIPPSFPYENLSPAQLTMCPHVIVDVRQLEPVLLPM
PDIRNVFHYHNQNNSPKLRLVAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFQFTFLVPPTVESKTKNFTLPVLRVSEMTN
SRFPVVDQMYTSRNENIIVQPQNGRCTTDGELLGTTILQSVSICNFKGTMQAKLNNEEPYQLQLTNLDGSPIDPTDDMP
APLGTPDFQAMLYGVASQRSSIDNATRAHDAQIDTAGDTFAPKIGQVRFKSSSNDFDLHDPKFTPIGVNVDDQHPFRQ
WSLPNYGGHLALNNHLAPAVTPLFPGEQILFFRSYIPSAGGHTDGAMDCLLPQEWVEHFYQEAAPSQSDIALVRFINPDT
GRVLFEAKLHKQGLTIAASGDHPVIMPTNGYFRFEAWVNPFTYLPVGTGSGRRRIQ

Figure 26A

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

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPLYLAHLARMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLDVRNTFFHYNNQPNRMLRVAMLYTPLRNSGSGDDVFTVSCRVLTRPTDFEFTYLVPP
SVESKTKPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLGELQGTTLQPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTGDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV
PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTLNMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSYITVAHSGDYPLVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

Figure 26B

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

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAATAATGAG
ACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAATATTATAGACCCCTTG
GATTCGGACAACTTCGTGCAGGCACCAACGGCGAGTTTACAGTATCCCCCGGAACTCCCCAGGTGAGATACTCC
TGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGCCGCATGTACAATGGTTACGCTGGGGGG
GTCGAAGTGCAGGTCTCTCTGGCCGAAACGCCTTTACCGCTGGCAAAATTCTGTTTGCCGCCGTTCCACCAAACCTTT
CCAGTCGAATTCTCTCTCCCGCGCAAATAACCATGCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATA
ATGATTCCCCTGCCGGATGTGCGTAACACCTTTTCCATTATAACAATCAGCCAACTCTCGGATGAGACTTGTTGCT
ATGCTGTACACCCCCCTGCGGAGCAACGGCAGTGCGCATGATGTGTTTACCGTGAGTTGCAGAGTCTGACGCGCC
CAACCCCGGACTTCGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTTCACTGCCAATCT
TAACTCTCTCCGAAGTACTAACAGCCGTTTCCAGTACCCATAGATTCTCTTTTACCGCTCAAACAACGTAAGTCCA
AGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCAGTGCGCATC
TGTGCATTCCGGGGCCGCGTGACCGTGAGACAGACCATCGTGACAAATGGCACATGCAACTCCAAAACCTTAAACG
GGACCACCTACGACCAACCGACGACGTCCTGCTCCGCTAGGGACTCCTGACTTTAAGGGGGTGGTGTTCGGAGT
GGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCGAGCTCACGAGGCCGTTATCTCAACATATAGCC
CCCAATTTGTGCCAAGCTCGGATCCGTTAATTTTCGTAGTAACGACAACGACTTCCAAGTCAACCAACGAAGTTTA
CGCCAGTGGGGATTAATGATGATGGAGACCATCTTCCGCCAATGGGAAGTACCAGATTATTCTGGGCTGCTCACC
CTCAATATGAACCTCGCCCCACCGTGGCCCTAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCA
TGCAGTGGCGGATATAATCAAGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTACCAGGAAAG

Figure 26B (cont)

TGCGCCCTCCAGTCCGATGTGGCCCTGATACGGTACGTAAACCCGATACCGGAAGAACATTATTCGAAGCGAAAT
TGCACAGATCAGGGTACATTACCGTTGCACATTCGGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAGGT
TCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCTCAGTAG

Figure 27

Amino acid sequence of VP1_GII.21_Sali_2011_USA_AFC89665 (SEQ ID NO: 26)

MKMASNDAAPSNDGATGLVPEINTETLPLEPVAGAAIAAPVTGQNNIIDPWIRNNFVQAPNGEFTVSPRNSPGEILMNL
ELGPDNLNYPYLAHLRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVDMLSPAQITMPLHLIVDVRTLEPIMILP
DVRNVFYHFNNQAPRMLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTDFEFTYLVPPSVESKTKPFTLPILTIGELTNSR
FPAPIDQLYTSNADVVVQPQNGRCTLGELQGTQLLTTAICSYRGMTSNPTSDYWDDHLLHLVHPNGATYDPTEDVP
APFGTQDFRGILYGMILTQNPRTSGDEAANSHGIYISSTSEKFTPKLGTIGLHQVQGDIAASNQSKFTPVGIAVNGNTPFRQ
WELPNYSGALTINTNLAPAVGPNFPGEQILFFRSNVPSVQGGQPIEDCLIPQEWVSHFYQESAPSQSDVALVRYVNPDT
GRTIFEAKLHRQGFITIAATGSNPVVPPNGYFRFDSWVNQFYALAPMGTGNGRRRVQ

Figure 28A

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

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNN
PGDILFDLSLGPLNPLFLSLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIQAQTMFPHVIADVRV
LEPIEVPLEDVNRVLFHNNDSTPTMRILCMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLVPPNVEQKTKPFSV
PLNVLSNSRVPSLIKSMMSVQDHGQMVQFQNGRVTLGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFDPDLGECDDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLWLSPPSGGAPK
VNPWAIPIRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPTIPQEFVTHFVNEQAPTREGAALLHYVDP
DTHRNLEGEFKLYPEGFMTCVPNSSSGSPQTLPIINGVFTFISWVSRYQLKPVGTTGPVRRLGIRRS

Figure 28B

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

ATGATGATGGCTTCAAGGATGCTCCCAACAACATGGATGGAACAAGCGGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGGAGTTACCATAAGCCCAACAACACCCCG
GGTGACATCTTGTGTGACCTGAGCCTAGGACCACACTGAATCCGTTTCTGAGTCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTGTCAGCCAGAACGTGTCTATCGACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCATCGAGGTGCCCTTGAGGACGTGCGCAACGTCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTTGACTTGCTAGCCCTGACTTCAACTTCTTTTCTGGTGCCTCAAATGTAGAACAGAAAACAAGCC
ATTACGCGTGCCAAACCTGCCCTTAACGTGCTGTCGAATCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCGGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC

Figure 28B (cont)

ATTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAAGTTAACCCTATGGGCTATTCCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCAGCCCCCATATATCCACCAGGATTCCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGCCCTTGACAGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTACCAACTCAAGCCCCTCGGAACAACCTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 28C

Amino acid sequence of VP1_GI.3_Lil08_594L (SEQ ID NO:8)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNN
PGDILFDLQLGPHLNPFLHLAQMNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVISIAQATMFPHVIADVRV
LEPIEVPLEDVRNVLFHNNDSTPTMRILCMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLVPPNVEQTKPFVSPNL
PLNVLNSRVPSLIKSMMSVQDHGQMVQFQNGRVTLDGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFPDLGECDDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPK
VNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLVSPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLGFEKLYPEGFMTCVPSNSSGSGPQTLPIINGVFTFISWVSRYQLKPVGTTGPVRRLGIRRS

Figure 28D

Nucleic acid sequence of human codon optimized VP1_GI.3_Lil08_594L (SEQ ID NO:9)

ATGATGATGGCTTCAAGGATGCTCCACAAACATGGATGGAACAAGCGGCGGGGCAACTTGTGCCGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAAGGCTCCACAGGGGAGTTTACCATAAGCCCCAAACAACCCCCG
GGTGACATCTTGTGACCTGCAGCTAGGACCACACTGAATCCGTTTCTGCTCCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAAACATGAAGGTGCGCGTGTCTTGGCGGGCAATGCATTACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCCCTGAGGACGTGCGCAACGTCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGG
GCGGGTGTGACTTGTCTAGCCCTGACTTCAACTTCCTTTTCTGGTGCCTCAAATGTAGAACAGAAAACAAAGCC
ATTCAGCGTGCCAAACCTGCCCCCTAACGTGCTGTGCAATCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCTACCATGCATTGAGTCACCTGCACCTATTGGATTTCGGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC
ATTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAAGTTAACCCTATGGGCTATTCCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCAGCCCCCATATATCCACCAGGATTCCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGCCCTTGACAGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTTGCATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT

Figure 28D (cont)

TCACGTTTATCAGCTGGGTTTCACGGTTTACCAACTCAAGCCCCTCGGAACAACTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 28E

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

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGEFTISPNN
PGDILFDLSLGPLNPFLLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIQAQTMFPHVIADVRVL
EPIEVPLEDVRNVLFHNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDFNFLVPPNVEQKTKPFVSNL
PLNVLSNSRVPSLIKSMVVSQDHGQMVQFQNGRVTLDGQLQGTTPTSASQLCKIRGTVYHATGGQGLNLTEIDGTPYH
AFESPAPIGFDPDLGECDWHINASPANAFTDGSIIHRIDVAQDSTFAPHLGTHYTNADYNANVGLICSLWLSPPSGGAPK
VNPWAIPIRYGSTLTEAAQLAPPIYPPGFGEAIVFFMSDFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDP
DTHRNLEGEFKLYPEGFMTCVPNSSGSGPQTLPIINGVFTFISWVSIFYQLKPVGTTGPVRRLGIRRS

Figure 28F

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

ATGATGATGGCTTCCAAGGATGCTCCACAAACATGGATGGAACAAGCGCGCGGGGCAACTTGTGCCGGAGGTG
TCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCAGGACAGGTAAACA
TGATCGACCCCTGGATCATGTCAAATTACGTTCAGGCTCCACAGGGGAGTTTACCATAAGCCCCAAACACCCCCG
GGTGACATCTTGTGTGACCTGAGCCTAGGACCACACTTGAATCCGTTTCTGCTCCACTTGGCTCAGATGTATAATGGA
TGGGTTGGAACATGAAGGTGCGCGTGCTCCTGGCGGGCAATGCATTACAGCCGGGAAGATTATTATCTCTTGCG
TGCCACCTGGATTTGCAGCCAGAACGTGTCTATCGCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGC
GTGCTAGAGCCCATCGAGGTGCCCCCTGAGGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCAT
GCGCTTGATATGTATGTTATATACTCCCTCCGCGCCAGTGCGGTCCAGCTCCGGGACCGATCCTTTTGATTGCTGG
GCGGGTGTTGACTTGTCTAGCCCTGACTTCAACTTCTTTTCTGGTGCTCCAAATGTAGAACAGAAAACAAAGCC
ATTCAGCGTGCCAAACCTGCCCTTAACGTGCTGTCGAATCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCACAACCCC
AACCAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGGGCTGAATCTTACT
GAGATCGATGGTACCCCTACCATGCATTGAGTCACCTGCACCTATTGGATTTCCTGATCTTGGGGAGTGTGATTG
GCATATCAATGCTTACCTGCCAACGCTTTCACAGACGGGTCTATTATTCATCGCATTGACGTAGCACAGGATAGCAC
ATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATTACAACGCAAACGTGGGTCTTATCTGTAGCCTAG
AGTGGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAAGTTAACCCATGGGCTATTCTCGGTACGGGTCTACGCTGACT
GAGGCCGCTCAGCTGGCACCCCCATATATCCACCAGGATTCGGGGAAGCCATTGTTTCTTTATGTCCGATTTCCG
ATAGCCAACGGTTCAGATGGCCTTAGTGCCCTGCACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCA
GGCTCCTACTCGGGGCGAGGCTGCCTTGTGATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAAC
TCTACCCTGAAGGTTTCATGACCTGCGTACCTAACTCTCCGGCAGTGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTCACGGTTTACCAACTCAAGCCCCTCGGAACAACTGGGCCAGTTCGGAGGCTCGGG
ATCAGACGGAGCTAG

Figure 28G

Amino acid sequence of VP1_Gl.3_Lil08_A43V+S94L (SEQ ID NO:170)

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAVATAGQVNMIDPWIMSNYVQAPQGE
FTISPNNTPGDILFDLQLGPHLNPFLHQAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIA
QATMFPHVIADVRLVLEPIEVPLEDVRNVLFHNNDSTPTMRILCMLYTPLRASGSSSGTDPFVIAGRVLTCPSPD
FNFLFLVPPNVEQKTKPFSVPLNPLNVLSNSRVPSLIKSMMSQDHGQMVQFQNGRVTLTGQLQGTTPTSA
SQLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDDWHINASPANAFTDGSIIHRIDVAQDST
FAPHLGTIHYTNADYNANVGLICSLWLSPPSGGAPKVNPNWAIAPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGFEKLYPEGFMTCPVNSSGSGPQ
TLPINGVFTFISWVSRYQLKPVGTTGPVRRLGIRRS

Figure 28H

Nucleic acid sequence of human codon optimized VP1_Gl.3_Lil08_A43V+S94L (SEQ ID NO:169)

ATGATGATGGCTTCCAAGGATGCTCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGTGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATGTCAAATTACGTTGAGGCTCCACAGGGGGAGTTTACC
ATAAGCCCCAAACAACACCCCGGGTGACATCTTGTGGACCTGCAGCTAGGACCACACTTGAATCCGTTTCT
GCTCCACTTGGCTCAGATGTATAATGGATGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAA
TGCATTCACAGCCGGGAAGATTATTCTCTTGCCTGCCACCTGGATTGTCAGCCAGAACGTGTCTATC
GCACAGGCAACCATGTTTCCGATGTATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCTTG
AGGACGTGCGCAACGTCTATTCCATAACAATGATAGCACCCCAACCATGCGCTTGATATGTATGTTATAT
ACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGGGCGGGTGTGACTT
GTCCTAGCCCTGACTTCAACTTCCTTTTCTGGTGCCCTCAAATGTAGAACAGAAAACAAAGCCATTACAGC
GTGCCAAACCTGCCCTTAACGTGCTGTGAATTCCCGAGTGCCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCA
CAACCCCAACAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGG
GGCTGAATCTTACTGAGATCGATGGTACCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCC
GATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCA
TCGATTGACGTAGCACAGGATAGCACATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGAT
TACAACGCAAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAA
GTTAACCCATGGGCTATTCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATAT
ATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGC
CTTAGTGTCCCTTGACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGG
GCGAGGCTGCCTTGTGATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACCTCTACCC
TGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTG
TTCACGTTTATCAGCTGGGTTTACAGGTTTACCAACTCAAGCCCGTCGGAACAACCTGGGCCAGTTCGGA
GGCTCGGGATCAGACGGAGCTAG

Figure 28I

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

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIISNYVQAPQGEFT
ISPNNTPGDILFDLQLGPHLNPFLHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVSIQAQ
ATMFPHVIADVRVLEPIEVPLEDVRNVLFHNNDSTPTMRILICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDF
NFLFLVPPNVEQKTKPF5VPNLPLNVLSNSRVPSLIKSMMSVQDHGQMVQFQNGRVTLDGQLQGTTPTSAS
QLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDDWHINASPANAFTDGSIIHRIDVAQDSTF
APHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPKVPNPWAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGEFKLYPEGFMTCVPNSSSGSGPQ
TLPINGVFTFISWVSRYQLKPVGTTGPVRRLGIRRS

Figure 28J

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

ATGATGATGGCTTCCAAGGATGCTCCACAAACATGGATGGAACAAGCGGCGGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATCTCAAATTACGTTGAGGCTCCACAGGGGGAGTTTACCA
TAAGCCCAAACAACACCCCGGGTGACATCTTGTGTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTG
CTCCACTTGGCTCAGATGTATAATGGATGGGTTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAAT
GCATTCACAGCCGGGAAGATTATTATCTCTTGCCTGCCACCTGGATTTGCAGCCCAGAACGTGTCTATCG
CACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCTTGA
GGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATATA
CTCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTGTGATTGCTGGGCGGGTGTGACTTG
TCCTAGCCCTGACTTCAACTTCTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTCAGCG
TGCCAAACCTGCCCCCTAACGTGCTGTCGAATTCCCGAGTGCCCTCCCTTATTAAGTCCATGATGGTATCT
CAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCAC
AACCCCAACAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGG
GCTGAATCTTACTGAGATCGATGGTACCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCTG
ATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCAT
CGCATTGACGTAGCACAGGATAGCACATTTGCCCCGCACCTGGGTACCATCCACTATACGAACGCAGATT
ACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAAG
TTAACCCATGGGCTATTCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATATA
TCCACCAGGATTCGGGGAAGCCATTGTTTTCTTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGCC
TTAGTGTCCCTTGACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGGG
CGAGGCTGCCTTGTGATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACCTTACCCCT
GAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTACGGTTTACCAACTCAAGCCCGTCGGAACAACCTGGGCCAGTTCGGAG
GCTCGGGATCAGACGGAGCTAG

Figure 28K

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

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAVATAGQVNMIDPWIIISNYVQAPQGEFT
ISPNNTPGDILFDLQLGPHLNPFLHHLAQMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNVISIAQ
ATMFPHVIADVRVLEPIEVPLEDVNRNVLHFNNDSTPTMRLICMLYTPLRASGSSSGTDPFVIAGRVLTCPSPDF
NFLFLVPPNVEQKTKPFSVPNLPLNVLSNSRVPSLIKSMMSQDHGQMVQFQNGRVTLDGQLQGTTPTSAS
QLCKIRGTVYHATGGQGLNLTEIDGTPYHAFESPAPIGFDPDLGECDDWHINASPANAFTDGSIIHRIDVAQDSTF
APHLGTIHYTNADYNANVGLICSLEWLSPPSGGAPKVNPAIPRYGSTLTEAAQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRNLGFEKLYPEGFMTCPVNPSSGSGPQ
TLPINGVFTFISWVSRYQLKPVGTTGPVRRLGIRRS

Figure 28L

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

ATGATGATGGCTTCCAAGGATGCTCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGCGCAGCCACTGCTGTGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATCTCAAATTACGTTGAGGCTCCACAGGGGGAGTTTACCA
TAAGCCCAAAACACCCCCGGGTGACATCTTGTTTGACCTGCAGCTAGGACCACACTTGAATCCGTTTCTG
CTCCACTTGGCTCAGATGTATAATGGATGGGTGGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAAT
GCATTCACAGCCGGAAGATTATTATCTCTTGCGTGCCACCTGGATTTGCAGCCAGAACGTGTCTATCG
CACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCCCTGA
GGACGTGCGCAACGTCCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATATA
CTCCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGATTGCTGGGCGGGTGTGACTTG
TCCTAGCCCTGACTTCAACTTCTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTGAGCG
TGCCAAACCTGCCCCCTAACGTGCTGTGAATTCGAGTGCCCTTCCCTTATTAAGTCCATGATGGTATCT
CAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCAC
AACCCCAACAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGGG
GCTGAATCTTACTGAGATCGATGGTACCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCGG
ATCTTGGGGAGTGTGATTGGCATATCAATGCTTCACCTGCCAACGCTTTCACAGACGGGTCTATTATTCAT
CGCATTGACGTAGCACAGGATAGCACATTTGCCCCGACCTGGGTACCATCCACTATACGAACGCAGATT
ACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAAG
TTAACCCATGGGCTATTCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATATA
TCCACCAGGATTCGGGGAAGCCATTGTTTTCTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGCC
TTAGTGCCCTTGACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGGG
CGAGGCTGCCTTGTGATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACCTTACCCT
GAAGGTTTCATGACCTGCGTACCTAACTCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTGT
TCACGTTTATCAGCTGGGTTTACGAGTTTACCAACTCAAGCCCGTCGGAACAACCTGGGCCAGTTCGGAG
GCTCGGGATCAGACGGAGCTAG

Figure 28M (SEQ ID NO:292)

AA sequence of VP1_Gl.3_Lil08_S94X; where X = V, I, M, T, E, D, N, Q, K, or H

MMMASKDAPTNMDGTSGAGQLVPEVSTAEPISMEPVAGAATAAATAGQVNMIDPWIMSNYVQAPQGE
FTISPNNTPGDILFDLQLGPHLNPF~~X~~H~~LA~~QMYNGWVGNMKVRVLLAGNAFTAGKIIISCVPPGFAAQNV~~SIA~~
QATMFPHVIADVRLVLEPIEVPLEDVRNVLFHNNNDSTPTMR~~LIC~~MLYTPLRASGSSSGTDPFVIAGRVLTCPSPD
FNFLFLVPPNVEQKTKPFSV~~PNL~~PLNVLSNSRVPSLIKSM~~MM~~V5QDHGQMVQFQNGRVTL~~DG~~QLQGTTPTSA
SQLCKIRGT~~VY~~HATGGQGLNLTEIDGTPYHAFESPAPIGFPDLGECDWHINASPANAFTDGSIIHRIDVAQDST
FAPHLGTIHYTNADYNANVGLICSLEWLSP~~PS~~GGAPKVN~~PWA~~IPRYGSTL~~TEA~~AQLAPPIYPPGFGEAIVFFMS
DFPIANGSDGLSVPCTIPQEFVTHFVNEQAPTRGEAALLHYVDPDTHRN~~LGE~~FLYPEGFMTCPVNSSSGSGPQ
TLPINGVFTFISWVS~~RFY~~QLKPVGTTGPVRR~~LGI~~RRS*

Figure 28N (SEQ ID NO:293)

hCod optimized VP1_Gl.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)

ATGATGATGGCTTCCAAGGATGCTCCACAAACATGGATGGAACAAGCGGCGCGGGGCAACTTGTGCCG
GAGGTGTCCACGGCGGAACCCATTTCCATGGAACCTGTGGCCGGCGCAGCCACTGCTGCCGCCACCGCA
GGACAGGTAAACATGATCGACCCCTGGATCATGTCAAATTACGTTCAAGGCTCCACAGGGGGAGTTTACC
ATAAGCCCCAAACAACACCCCGGTGACATCTTGTGGACCTGCAGCTAGGACCACACTTGAATCCGTTTCT
G~~XXX~~CACTTGGCTCAGATGTATAATGGATGGGTTGAAACATGAAGGTGCGCGTGCTCCTGGCGGGCAA
TGCATTACAGCCGGGAAGATTATTATCTCTTGCCTGCCACCTGGATTTGCAGCCAGAACGTGTCTATC
GCACAGGCAACCATGTTTCCGCATGTCATCGCAGATGTGCGCGTGCTAGAGCCCATCGAGGTGCCCTTG
AGGACGTGCGCAACGTCTATTCCATAACAATGATAGCACCCCCACCATGCGCTTGATATGTATGTTATAT
ACTCCCCTCCGCGCCAGTGGGTCCAGCTCCGGGACCGATCCTTTTGTGATTGCTGGGCGGGTGTGACTT
GTCCTAGCCCTGACTTCAACTTCCTTTTCTGGTGCCTCCAAATGTAGAACAGAAAACAAAGCCATTCAGC
GTGCCAAACCTGCCCTTAACGTGCTGTGCAATTCCCGAGTGCTTCCCTTATTAAGTCCATGATGGTATC
TCAGGATCACGGTCAAATGGTGCAGTTTCAGAACGGCCGAGTGACGTTAGACGGGCAGCTGCAGGGCA
CAACCCCAACAGTGCCAGTCAGCTGTGTAAGATCAGAGGCACCGTCTACCACGCAACTGGCGGACAGG
GGCTGAATCTTACTGAGATCGATGGTACCCCTACCATGCATTCGAGTCACCTGCACCTATTGGATTTCCT
GATCTTGGGGAGTGTGATTGGCATATCAATGCTTACCTGCCAACGCTTTCACAGACGGGTCTATTATTCA
TCGATTGACGTAGCACAGGATAGCACATTTGCCCGCACCTGGGTACCATCCACTATACGAACGCAGAT
TACAACGCAAACGTGGGTCTTATCTGTAGCCTAGAGTGGCTATCTCCGCCAAGCGGTGGGGCCCCCTAAA
GTTAACCCATGGGCTATTCTCGGTACGGGTCTACGCTGACTGAGGCCGCTCAGCTGGCACCCCCCATAT
ATCCACCAGGATTCGGGGAAGCCATTGTTTTCTTATGTCCGATTTTCCGATAGCCAACGGTTCAGATGGC
CTTAGTGTCCCTTGACGATTCCACAGGAATTTGTGACACACTTCGTAAACGAGCAGGCTCCTACTCGGG
GCGAGGCTGCCTTGTGATTACGTAGACCCCGATACCCATAGAAACCTGGGCGAATTCAAACCTCTACCC
TGAAGGTTTCATGACCTGCGTACCTAACTCCTCCGGCAGTGGCCCTCAAACCTTGCCGATCAACGGCGTG
TTCACGTTTATCAGCTGGGTTTACGTTTACCAACTCAAGCCCGTCGGAACAACTGGGCCAGTTCGGA
GGCTCGGGATCAGACGGAGCTAG

Figure 29A

Amino acid sequence of VP1_Gl.5_Siklos_Q84S (SEQ ID NO:34)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLSLGPLNPLLAHL5QMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLFPHIIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYTPLRTGGGSGGTDADFVAGRVLTCPSSDFNFLFLVPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTTPVSVSQILKFRGKVSAGSKVINLTLDGSPFLAFEAPAP
TGFPDLGTSWDWHVEMSLNSNSQSSGNPILLRDIHPN5SEFVPHLG5VCVTAIEVAGDYGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPGFGAIVYFMSPGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPOQLPLNGVVFVASFVWSRFYQLKPVGTASSARGRLGVRR

Figure 29B

Nucleic acid sequence of human codon optimized VP1_Gl.5_Siklos_Q84S (SEQ ID NO:35)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCCTTGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTAAATATG
ATTGACCCCTGGATTTTCAATAATTCGTGCAGGCCCTCAAGGCGAGTTTACTATAAGCCCTAACAACACACCAGGG
GATATTCTGTTCGACCTGAGCTTAGGCCCTCATCTCAACCCCTTCTTGCCCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAAACGCCTTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATACCAACGATAATCAGCCCACTATGAGG
TTACTGTGCATGCTGTACACGCCACTCCGGAAGTGGTGGGGGGCAGTGGGGGGACCGATGCTTTCGTGCTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCTATTCCTTGTCGCCCCAACGGTGGAACAGAAAACGAGACCTT
TTCCGTACCTAACATCCCTTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACCTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTCCAGACCTGGGAACATCCGATTGGCATGTCGAGA
TGAGTCTGAATAGCAACTCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTGGACAATTCCACACTACGGCTCTAACTTGGCCGA
AGCATCCCAGCTTGCCCCGTTGTATATCCCCCAGGCTTTGGCGAAGCAATAGTTTATTTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTCGCATCATGGGTTAGCCGTTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 29C

Amino acid sequence of VP1_Gl.5_Siklos_A94L (SEQ ID NO:36)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLQLGPHLNPFLHLSQMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLPHIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYPLRTGGGSGGTDAFVAVAGRVLTCPSSDFNLFVLPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSQILKFRGKVSAGSKVINLTLDGSPFLAFEAPAP
TGFPDLGTSWDHVMESLNSNSQSSGNPILLRDIHPNSSEFVPHLGSCVTAIEVAGDYGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPGFGAIVYFMSPIGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPQQLPLNGVVFASWVSRFYQLKPVGTASSARGRLGVRR

Figure 29D

Nucleic acid sequence of human codon optimized VP1_Gl.5_siklos_A94L (SEQ ID NO:37)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCTTGGACCCAGTAGCCGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTAAATATG
ATTGACCCCTGGATTTTCAATAATTCGTGCAGGCCCTCAAGGCGAGTTTACTATAAGCCCTAACACACACAGGG
GATATTCTGTTTCGACCTGCAGTTAGGCCCTCATCTCAACCCCTTCTTGCTCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCTTTACCGCTGGTAAGGTGATCATTTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCCACTGGAGGATGTCCGGAATACCCTGTACCATACCAACGATAATCAGCCCACTATGAGG
TTACTGTGCATGCTGTACACGCCACTCCGGACTGGTGGGGGACAGTGGGGGGACCGATGCTTTCGTCGTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCTATTCTTGTCGCCCCAACGGTGGAACAGAAAACGAGACCTT
TTTCCGTACCTAACATCCCTTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACCTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTCCAGACCTGGGAACATCCGATTGGCATGTGCGAGA
TGAGTCTGAATAGCAACTCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTGGACAATTCACACTACGGCTCTAATTGGCCGA
AGCATCCCAGCTTGCCCCGTTGTATATCCCCAGGCTTTGGCGAAGCAATAGTTTATTTATGTCCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTCTGTTCCGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTACATATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGTGTCTTTGT
ATTGCGCATCATGGTTAGCCGTTCTATCAACTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 29E

Amino acid sequence of VP1_Gl.5_siklos_Q84S+A94L (SEQ ID NO:38)

MMMASKDAPSSADGANGAGQLVPEVNNAEPLPLDPVAGASTALATAGQVNMIDPWIFNNFVQAPQGEFTISPNNTP
GDILFDLSLGPLNPFLLHLSQMYNGWVGNMRVRVILAGNAFTAGKVIICCVPPGFQSRTLSIAQATLPHIADVRTLEPI
EIPLEDVRNTLYHTNDNQPTMRLLCMLYPLRTGGGSGGTDAFVAVAGRVLTCPSSDFNLFVLPPTVEQKTRPFSVPNIPL
QLLSNSRVPNLIQSMVLSPDQAQNVQFQNGRCTTDGQLLGTTPVSVSQILKFRGKVSAGSKVINLTLDGSPFLAFEAPAP

Figure 29E (cont)

TGFPDLGTSDWHVEMSLNSNSQSSGNPILLRDIHPNSSEFVPHLGSVCTAAIEVAGDYTGTIQWTSQPSNVTPVPDVNF
WTIPHYGSNLAEASQLAPVVYPGFGGEAIVYFMSPIPGPNTAHKPNLVPCLLPQEFVTHFVSEQAPSMGEAALVHYVDPD
TNRNLGEFKLYPEGFITCVPNGTGPOQLPLNGVVFVASFVSRFYQLKPVGTASSARGRLGVRR

Figure 29F

Nucleic acid sequence of human codon optimized VP1_GI.5_siklos_Q845+A94L (SEQ ID NO:39)

ATGATGATGGCCTCCAAAGACGCTCCTAGCAGTGCTGATGGCGCTAACGGTGCCGGCCAGCTGGTCCCCGAGGTGA
ATAACGCCGAGCCTCTCCCCCTGGACCCAGTAGCCGGAGCTTCAACGGCCCTAGCTACTGCCGGACAGGTAAATATG
ATTGACCCCTGGATTTCATAATTCCTGTCAGGCCCCCTCAAGGCGAGTTTACTATAAGCCCTAACAAACACACCAGGG
GATATTCTGTTGACCTGAGCTTAGGCCCTCATCTCAACCCCTTCTGCTCCACCTGAGCCAGATGTACAATGGCTGG
GTGGGCAACATGCGAGTGAGAGTTATCCTCGCAGGGAACGCCTTTACCGCTGGTAAGGTGATCATTGTTGCGTAC
CACCTGGATTCCAGTCTAGGACATTAAGTATTGCGCAAGCTACCCTCTTCTCATATCATCGCCGACGTGCGGACAC
TAGAGCCCATCGAGATCCACTGGAGGATGTCCGGAATACCCTGTACCATAACCAACGATAATCAGCCCACTATGAGG
TACTGTGCATGCTGTACACGCCACTCCGACTGGTGGGGGGCAGTGGGGGGACCGATGCTTTCGTCGTTGCCGGTA
GGGTGCTCACTTGCCCGTCATCTGACTTTAACTTCCTATTCTTGTGCCCCCAACGGTGGAACAGAAAACGAGACCTT
TTCCGTACCTAACATCCCTTACAGCTCCTAAGCAATAGCAGAGTACCTAACCTGATCCAATCCATGTTCTTAGCCC
TGATCAAGCGCAGAACGTACAGTTTCAGAACGGGCGGTGCACCACAGATGGCCAGCTGCTTGGTACAACTCCCGTC
TCCGTGTCTCAGATACTTAAGTTTCGCGGCAAGGTCTCCGCTGGATCCAAAGTAATCAACCTCACTGAGCTTGATGG
CTCTCCCTTCTGGCGTTCGAGGCGCCCGCCCCAACAGGCTTCCAGACCTGGGAACATCCGATTGGCATGTCGAGA
TGAGTCTGAATAGCAACTCCAGTCTTCTGGCAATCCAATACTGCTCCGCGATATCCATCCTAATTCTAGCGAGTTCG
TTCCACACCTGGGTTCTGTGTGCGTGACGGCTGCAATAGAGGTGGCTGGCGACTACACGGGTACCATTCAGTGGAC
CTCTCAGCCAAGTAACGTGACCCCTGTGCCAGACGTTAACTTTGGACAATCCACACTACGGCTCTAACTTGGCCGA
AGCATCCCAGCTTGCCCCGTTGTATATCCCCCAGGCTTTGGCGAAGCAATAGTTTATTTATGTCCCAATCCCTGG
ACCTAACACAGCACACAAGCCAAACCTCGTCCCATGCCTGCTGCCCCAGGAGTTCGTGACTCATTTGTTTCGGAACA
AGCCCCATCAATGGGGGAGGCCGCCCTGGTCCACTACGTGGATCCAGATACCAATCGGAATCTGGGAGAATTCAAA
CTCTACCCTGAAGGATTCATTACATGTGTGCCCAATGGAACAGGACCGCAGCAGCTCCCACTGAACGGGTGCTTTGT
ATTGCGATCATGGGTTAGCCGTTCTATCAACTTAAACCCGTGGGGACAGCTTCATCTGCCCGGGGGCGCCTTGGCG
TGCGGCGCTGA

Figure 29G

Amino acid sequence of VP1_GI.7/GA5043/USA/2014_R845 (SEQ ID NO:177)

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVGAATAVATAGQVNMIDPWIMNNFVQAPEGE
FTISPNNTPGDILFDLSLGPLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICVPPGFESQNISIG
QATMFPHVIADVRLPEIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAP
DFNFLFLVPPSVEQKTRQLTIPNIPNLNANSRVPAMINKMTVSADQNQVVFQNGRCTLGQLLGTTPVSA
NQVARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFPDIGNCDWHVYAFKVNQNTGDPMYRLDITQG
NSFAPHLGSIEFSSENHPSGDQLGTLTWISPLNNASRVDPWKIPTYGSTLTSTNLAPPIFPFGFGGEAIVYFMSD
FPIVSGNTAQIPCTLPQEFVSSFVEQQAPIRGEAALLHYVDPDTHRNLEFKLYPDGFITCVPNTGGGPQNLPS
NGVVFSSWVSRYQLKPVGTTGPVRRRLGVRRV

Figure 29H

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

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGCGAGAACCCTTCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTGCGAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAATGAACAATTTGTTTCAGGCACCAGAAGGAGAATTCACC
ATCTCCCCCAATAACACCCCAGGGGATATTCTGTTTGACCTCAGCTTAGGACCCCACTTGAACCCCTTCT
GCTTCATCTCTCACAAATGTATAATGGCTGGGTGCGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAA
TGCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCCTCTGGATTCTGAATCTCAAATATCAGCATTG
GTCAAGCAACCATTGTTCCACATGTGATCGCTGATGTTGCGCTCCTGGAACCCATTGAAGTTCCTCTCGAC
GACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACA
CCCCATTAAGAGCCGGGGGAGCATCCTCAGGTAAGTACCCATTTGTGATTGCCGGGCGGGTGCTCACAT
GCCCCGCTCCAGACTTTAACTTCCTTTTCTTGGTGCCACCCAGTGTGAACAGAAAACCAGACAGCTCACC
ATCCCAAATATCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCA
GTGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACCTGCTGGGA
CGACCCAGTCTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAACTCCGGCACTG
GCCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTGAGTCTCCAGCCCTCTTGGCTTTCCC
GATATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATA
GGTTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCA
TCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCC
CTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGTCCGCCCCATTTTCCACCCG
GATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCT
TGCACACTGCCACAAGAATTCGTCTCATCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCC
TCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAAGTGTACCCTGACGGGTTTATT
ACCTGTGTACCAACACCGGCGGGCGGCCACAAAATTTGCCAGCAATGGCGTGTGTCTTTCTCTTG
GGTGTCTCGATACTACCAGCTTAAACCTGTCGGAACCTACGGGCCCCGTGCGACGACTCGGCGTGAGGCG
GGTGTA

Figure 29I

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

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVGAATAVATAGQVNMIDPWIINNFVQAPEGEFT
ISPNNTPGDILFDLRLGPLNPFLLHLSQMYNGWVGNNMRVRVMLAGNAFSAAGKIIICVPPGFESQNISIGQA
TMFPHVIADVRLVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPDF
NFLFLVPPSVEQKTRQLTIPNIPNLANSRVPAMINKMTVSADQNQVVFQNGRCTLEGQLLGTTVPVSANQ
VARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFDPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGNSE
APHLGSIEFSSNHPSGDQLGTLTWISPLNNASRVDPWKIPTYGSTLTSTNLAPPIFPFGGEAIVYFMSDFPI
VSGNTAQIPCTLPQEFVSSFEQQAPIRGEAALLHYVDPDTHRNLFGEFKLYPDGFITCVPNTGGGPQNLPSNG
VVFSSWVSRYYQLKPVGTTGPVRRLLGVRRV

Figure 29J

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

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGCGCGGGGCAGCTGGTGCC
CGAGGTCAATGCCGAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAATCAACAATTTCTGTTAGGCACCAGAAAGGAGAATTCACCA
TCTCCCCAATAACACCCAGGGGATATTCTGTTTGACCTCAGGTTAGGACCCCACTTGAACCCCTTTCTG
CTTCATCTCTCACAAATGTATAATGGCTGGGTGCGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAAT
GCTTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCTCCTGGATTGCAATCTCAAATATCAGCATTGG
TCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTGCGCTCCTGGAACCCATTGAAGTTCCTCTCGACG
ACGTGAGAAATGTTCTCTTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACAC
CCCATTAAGAGCCGGGGGAGCATCCTCAGGTACTGACCCATTTGTGATTGCCGGGCGGGTGCTCACATG
CCCGGCTCCAGACTTTAACTTCCTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCTCACCA
TCCAAATATCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCAG
TGCTGACCAGAACCAGGTAGTCCAGTTTCAAGACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGAC
GACCCAGTCTCCGCGAACCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAACTCCGGCACTGG
CCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTTGTGCTCTCCAGCCCTCTTGGCTTTCCCGA
TATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATAGG
TTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCATC
CGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCCCT
GGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGCTCCGCCCATTTTCCACCCGG
ATTCGGCGAGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCAGATTCTT
GCACACTGCCACAAGAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTCGAGGTGAGGCCGCCCT
CTTGCACTACGTGGACCTGACACCCACCGCAATCTTGGCGAGTTTAAAGCTGTACCCTGACGGGTTTATTA
CCTGTGTACCCAACACCGGCGGCGGCCCAAAAATTTGCCAGCAATGGCGTGTTTGTCTTTCTCTTGG
GTGTCTCGATACTACCAGCTTAAACCTGTCGGAACCTACGGGCCCCGTGCGACGACTCGGCGTGAGGCGG
GTGTGA

Figure 29K

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

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIINNFEVQAPEGEFT
ISPNNTPGDILFDLSLGPLNPFLLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICVPPGFESQNISIGQA
TMFPHVIADVRLVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYTPLRAGGASSGTDPFVIAGRVLTCPAPDF
NFLFLVPPSVEQKTRQLTIPNIPNLNLANSRVPAMINKMTVSADQNQVVQFQNGRCTLGQLLGTTVPVSANQ
VARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFDPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGNSE
APHLGSIEFSSENHPSGDQLGLTLTWISPLNNASRVDPWKIPTYGSTLTSTNLAPPIFPFGFEAIVYFMSDFPI
VSGNTAQIPCTLPQEFVSSFEQQAPIRGEAALLHYVDPDTHRNLGEFKLYPDGFITCVPNTGGGPQNLPSNG
VVFVSSWVSRYQLKPVGTGTPVRRLLGVRV

Figure 29L

Human codon optimized VP1_GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:180)

ATGATGATGGCCAGCAAGGACGCTCCGAGTAACATGGACGGCACTTCGGGGCGCGGGGCAGCTGGTGCCCCGAGGTC
AATGCCGCAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTCGCAACTGCAGGCCAAGTCAATAT
GATCGACCCGTGGATAATCAACAATTTCTGTCAGGCACCAGAAGGAGAATTCACCATCTCCCCAATAACACCCAG
GGGATATTCTGTTTGACCTCAGCTTAGGACCCCACTTGAACCCCTTTCTGCTTCATCTCTCACAATGTATAATGGCTG
GGTCGGGAATATGCGCGTGCAGGTGATGCTAGCCGGCAATGCTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTC
CTCCTGGATTCTGAATCTCAAAATATCAGCATTGGTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTGCGCTCC
TGGAACCCATTGAAGTTCCTCTCGACGACGTGAGAAATGTTCTCTCCACACCAACGAGAATAGGCCGACTATGAGA
CTTCTGTGTATGCTCTACCCCCATTAAGAGCCGGGGGAGCATCTCAGGTAAGTACCCATTGTGATTGCCGGGCG
GGTGCTCACATGCCCCGGCTCCAGACTTTAACTTCTTTCTTGGTGCCACCCAGTGTTGAACAGAAAACCAGACAGCT
CACCATCCCCAAATATCCCATTTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCAGTG
CTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGACGACCCAGT
CTCCGCGAACCCAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAACTCCGGCACTGGCCTTAACCTCACAGAG
GTTGACGGCACTCCCTATCATGCTTTTGAAGTCTCCAGCCCTCTTGGCTTTCCTGATATAGGCAACTGTGACTGGCAC
GTTTATGCGTTTAAAGTAAACAGAACACCGGCGATCCTATGTATAGTTGGATATAACACAAGGTAATTCATTGCG
CCCACACTTGGGTAGCATCGAGTTCAGTTCAGAGAACCATCCGAGTGTTGATCAGCTAGGCACATTGACGTGGATC
AGCCCTCTGAATAACGCATCAAGAGTGGATCCCTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAA
TTTGGCTCCGCCCATTTTCCACCCGATTCCGGCGAGGCCATAGTGTAATTTATGTCTGACTTTCCTATCGTCAGCGG
GAATACAGCCCAGATTCTTGCACTGCCACAAGAAATTCGTCTCATCCTTTGTAGAGCAGCAGGCACCTATTTCGAG
GTGAGGCCGCCCTCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGGCGAGTTTAAAGCTGTACCCTGACGGG
TTTATTACCTGTGTACCAACACCGGCGGCGGCCCAAAATTTGCCAGCAATGGCGTGTGTTCTTTCTCTTGG
GTGTCTCGATACTACCAGCTTAAACCTGTCGGAACCTACGGGCCCGTGGACGACTCGGCGTGAGGCGGGTGTGA

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

MMMASKDAPSNMDGTSGAGQLVPEVNAAEPLPLEPVVGAATAVATAGQVNMIDPWIXNNFVQAPGEGF
TISPNTPGDILFDLRLGPHLNPFLHLSQMYNGWVGNMRVRVMLAGNAFSAGKIIICCVPPGFESQNISIGQ
ATMFPHVIADVRVLEPIEVPLDDVRNVLFHTNENRPTMRLLCMLYPLRAGGASSGTDPFVIAGRVLTCPAPD
FNFLFLVPPSVEQKTRQLTIPNIPLNNLANSRVPAMINKMTVSADQNQVVFQNGRCTLEGQLLGTTPVSAN
QVARIRGKVFSTNSGTGLNLTEVDGTPYHAFESPAPLGFDPDIGNCDWHVYAFKVNQNTGDPMYRLDITQGN
SFAPHLGSIEFSSSENHPSGDQLGLTLTWISPLNNASRVDPWKIPTYGSTLTESTNLAPPIFPFGFEAIVYFMSDF
PIVSGNTAQIPCTLPQEFVSSFVEQQAIRGEAALLHYVDPDTHRNLGEFKLYPDGFITCVPNTGGGPQNLPNSN
GVFVFSSWVSRYQLKPVGTTGPVRRLLGVRRV*

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
CGAGGTCAATGCCGAGAACCACTTCCTCTTGAGCCCGTCGTTGGCGCCGCCACAGCTGTGCAACTGCA
GGCCAAGTCAATATGATCGACCCGTGGATAXXXAACAATTTCTGTTAGGCACCAAGGAGAATTCACC
ATCTCCCCAATAACACCCAGGGGATATTCTGTTTGACCTCAGGTTAGGACCCCACTGAACCCCTTCT
GCTTCATCTCTCACAAATGTATAATGGCTGGGTGCGGAATATGCGCGTGCGGGTGATGCTAGCCGGCAA
TGCTTTTCTGCAGGCAAGATTATCATTTGCTGCGTTCCTCTGGATTCTGAATCTCAAATATCAGCATTG
GTCAAGCAACCATGTTTCCACATGTGATCGCTGATGTTGCGCTCCTGGAACCCATTGAAGTTCCTCTCGAC
GACGTGAGAAATGTTCTCTCCACACCAACGAGAATAGGCCGACTATGAGACTTCTGTGTATGCTCTACA
CCCCATTAAGAGCCGGGGGAGCATCCTCAGGTAAGTACCCATTTGTGATTGCCGGGCGGGTGCTCACAT
GCCCCGCTCCAGACTTTAACTTCCTTTCTTGGTGCCACCCAGTGTGAACAGAAAACCAGACAGCTCACC
ATCCCAAATATCCATTGAACAATCTCGCCAACAGCAGGGTGCCAGCAATGATAAACAAAATGACAGTCA
GTGCTGACCAGAACCAGGTAGTCCAGTTTCAGAACGGCAGATGCACGCTTGAGGGCCAACTGCTTGGGA
CGACCCAGTCTCCGCGAACCAAGGTGGCCCGAATCCGGGGTAAAGTCTTCAGTACAACTCCGGCACTG
GCCTTAACCTCACAGAGGTTGACGGCACTCCCTATCATGCTTTGAGTCTCCAGCCCTCTTGGCTTTCC
GATATAGGCAACTGTGACTGGCACGTTTATGCGTTTAAAGTAAACCAGAACACCGGCGATCCTATGTATA
GGTTGGATATAACACAAGGTAATTCATTCGCCCCACACTTGGGTAGCATCGAGTTCAGTTTCAGAGAACCA
TCCGAGTGGTGATCAGCTAGGCACATTGACGTGGATCAGCCCTCTGAATAACGCATCAAGAGTGGATCC
CTGGAAGATCCCTACCTATGGGTCCACTCTGACAGAGAGCACAAATTTGGCTCCGCCCATTTTCCACCCG
GATTCGGCGAGGGCCATAGTGTACTTTATGTCTGACTTTCCTATCGTCAGCGGGAATACAGCCCAGATTCT
TGCACACTGCCACAAGAATTCGTCTCATCTTTGTAGAGCAGCAGGCACCTATTCAGAGGTGAGGCCGCC
TCTTGCACTACGTGGACCCTGACACCCACCGCAATCTTGCGAGTTTAAGCTGTACCCTGACGGGTTTATT
ACCTGTGTACCAACACCGGCGGGCGGCCACAAAATTTGCCAGCAATGGCGTGTGTCTTTCTCTTG
GGTGTCTCGATACTACCAGCTTAAACCTGTCGGAACCTACGGGCCCCGTGCGACGACTCGGCGTGAGGCG
GGTGTGA

Figure 30A

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

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLSLGPENLPYLAHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPVHVIDVRTLEPVLL
PLPDVRNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPPTVESKTKPFTLPILTGLGS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLGDELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDLTVNQPVKFTPVGL
NDTDHFNQWVVPYAGALNLTNLAAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNRRRIQ

Figure 30B

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

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCTGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGGCTCACCTGGCCCGGATGTACAATGGATATGCAGGAGG
GATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACCTCGTTTTTCGAGCCGCTCCCTCCCCACT
TCCCAGTTGAAAATCTTTCCCTCAGCAGATTACCATGTTTCCCATGTCATCATCGATGTGCGTACCCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCACTGTCGAAAAGCAAACTAAGCCATTACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCTGTTTCAATTGATCAGATGTACACGTCTCAAATGAAGTCATTTT
TGTGCAGTGTGAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTGAGTGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTCGACCCCTCGGAAGATATTCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATCACTCCAGTAGGTCTGAATGATACAGACCCTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACCTAACCTTGCCCCCTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTCAACATT
TCTATCAAGAGGCCGACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTGACAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 30C

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

MKMASNDAA PSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLELGPENPYLLHARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPVHIIDVRTLEPVLL
PLPDVRNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPPTVESKTKPFTLPILTGLS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVTTNLNGSPFDPSD
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDLTVNQPVKFTPVGL
NDTDHFNQWVVPYAGALNLTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNRRRIQ

Figure 30D

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

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGAGCCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCTGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCAGCTGGGACCAGAACTTAATCCGTACCTGCTCACCTGGCCCGGATGTACAATGGATATGCAGGAGG

Figure 30D (cont)

GATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACCTCGTTTTTCGAGCCGTCCTCCCCACT
TCCCAGTTGAAAATCTTTCCCTCAGCAGATTACCATGTTTCCCATGTCATCATCGATGTGCGTACCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTAATACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAACTAAGCCATTACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTC
TGTGCAGTGTGAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTGAGTGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCTTTGACCCCTCGGAAGATATCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATCACTCCAGTAGGTCTGAATGATACAGACCCTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACACTAACCTTGCCCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTAG
AAGCTATATCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTCAACATT
TCTATCAAGAGGCCGACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTGCAGAGTTGGGTGAATCAGTTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 30E

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

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL
NLSLGPENPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLL
PLPDVRNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPPTVESKTKPFTLPILTGLS
NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVITNLNGSPFDPSED
IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDLTVNQPVKFTPVGL
NDTDHFNQWVVPYAGALNLTNLAPSVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA
LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNRRRIQ

Figure 30F

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

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGAGAGCTGTTGCAGGGGCTGCCCTGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTAGAGCTAATTTCTGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTC
CTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAGG
GATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACCTCGTTTTTCGAGCCGTCCTCCCCACT
TCCCAGTTGAAAATCTTTCCCTCAGCAGATTACCATGTTTCCCATGTCATCATCGATGTGCGTACCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTAATACTCGC
CCTTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAACTAAGCCATTACACTTCCCATCC

Figure 30F (cont)

TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTCTGTGTCAGTGTGAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTGAGTGAATTTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG TGATATCACAACGAGATAAGCATAACACACCCCGACATAATGAGCCAGCCAATAGAGCCACGACGCAGTCGTTCC GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG AATCAACCTGTGAAATTCACCTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC CGGAGCCTTGAACCTAAACCTAACCTTGCCCTTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG AAGCTATATTCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTCAACATT TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT GTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCAATACATCCGCACCCGTAGTAGTCCCCGCCA ACGGGTACTTCAGATTGACAGTTGGGTGAATCAGTTTACTCGTTGGCCCCATGGGCACAGGGAACGGTCGCCG ACGGATCCAGTAA

FIGURE 30G

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

MKMASNDAA PSTDGAAGLPESNNEVMALEPVAGAALAVPVTGQTNIIDPWIRANFVQAPNGEFTVSPRNSPGEVLL NLSLGPENPYLLHARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSQQITMFPVHVIDVRTLEPVLL PLPDVRNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPPTVESKTKPFTLPILTGE LS NSRFPVSIDQMYTSPNEVISVQCQNGRCTLDELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVITITNLNGSPFDPSED IPAPLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDLTVNQPVKFTPVGL NDTDFHNQWVVPYAGALNLTNLPASVAPVFPGERLLFFRSYIPLKGGYGTPAIDCLLPQEWVQHFYQEAAPSMSEVA LVRYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRIQ

FIGURE 30H

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

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGATTGGTACCCGAGTCTAATAACGAG GTGATGGCCTTGAGAGCTGTTGCAGGGGCTGCCCTCGCAGTGCCTGTGACCGGGCAGACAAATATCATCGATCCTT GGATTAGAGCTAATTTCTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCT CCTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAG GGATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACCTCGTTTTCGCAGCCGTCCCTCCCCAC TTCCAGTTGAAAATCTTTCCCTCAGCAGATTACCATGTTTCCCATGTGCATCATCGATGTGCGTACCCTGGAACCTG TGCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTCACTATAATCAGAAGGATGACCCAAAATGCGGATCGTTG CGATGCTTTATACTCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTACTAACTCGC CCTTACCAGACTTCGACTTTACGTACTTGGTGCCTCCCACTGTCGAAAGCAAACTAAGCCATTCACACTTCCCATCC TCACCCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTTCAATTGATCAGATGTACACGTCTCCAAATGAAGTCATTTCTGTGTCAGTGTGAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTGAGTGAAT TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA TGGAAGTCCTTTCGACCCCTCGGAAGATATTCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG TGATATCACAACGAGATAAGCATAACACACCCCGACATAATGAGCCAGCCAATAGAGCCACGACGCAGTCGTTCC GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG AATCAACCTGTGAAATTCACCTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC

Figure 30H (cont)

CGGAGCCTTGAACTAAACACTAACCTTGCCCCCTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCACATT
TCTATCAAGAGGCCGACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTTCAGAGTTGGGTGAATCAGTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

FIGURE 30I

Amino acid sequence of VP1_GII.2_CGMH47_R53I+E80S+A90L (SEQ ID NO:184)

MKMASNDAA PSTDGAAGLVPESNNEVMALEPVAGAALAAPVTGQTNIIDPWIIANFVQAPNGEFTVSPRNSPGEVLLN
LSLGPENPYLLHLARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLLPL
PDVRNFFHYNQDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFTYLPPTVESKTKPFTLPILTGLSLS
RFPVSIDQMYTSPNEVISVQCQNGRCTLGDELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVITITNLNGSPFDPSEDIP
APLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVPTYTAQYTPKLGQIQIGTWQTDLTVNQPVKFTPVGLND
TDHFNQWVVPYAGALNLTNLPVAPVFPGERLLFFRSYIPLKGGYGTAPIDCLLPQEWVQHFYQEAAPSMSEVALV
RYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYS LAPMGTGNGRRRIQ

FIGURE 30J

Nucleic acid sequence of human codon optimized VP1_GII.2_CGMH47_R53I+E80S+A90L (SEQ ID NO:185)

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGAGAGCTGTTGCAGGGGCTGCCCTCGCAGCTCCTGTGACCGGGCAGACAAATATCATCGATCCTTG
GATTATCGTAATTTCTGTCAAGCCCCAAATGGGGAGTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCTCC
TCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAGGG
ATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTTCGAGCCGTCCTCCCCACTT
CCCAGTTGAAAATCTTTCCCCTCAGCAGATTACCATGTTTCCCCTGTCATCATCGATGTGCGTACCCTGGAACCTGT
GCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTGCGGTACTAAGTCGC
CCTTACCAGACTTCGACTTTACGTACTTGGTGCCTCCACTGTGCAAGCAAACTAAGCCATTACACTTCCCATCC
TCACCCTCGGAGAACTCTCGAACTCCCGCTCCCTGTTTCAATTGATCAGATGTACACGTCTCAAATGAAGTCATTT
TGTGCAGTGTGAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTGAGTGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCCTTTGACCCCTCGGAAGATATCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCACGACGCGAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATCACTCCAGTAGGTCTGAATGATACAGACCACTTAACCAAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACTAAACACTAACCTTGCCCCCTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTTCTTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTTCACATT
TCTATCAAGAGGCCGACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTTCAGAGTTGGGTGAATCAGTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

FIGURE 30K

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

MKMASNDAAPSTDGAAGLVPESNNEVMALEPVAGAALAVPVTGQTNIIDPWIIANFVQAPNGEFTVSPRNSPGEVLLN
LSLGPELNPYLLHARMYNGYAGGMEVQVMLAGNAFTAGKLVFAAVPPHFPVENLSPQQITMFPHVIIDVRTLEPVLLPL
PDVRNFFHYNQKDDPKMRIVAMLYTPLRSNGSGDDVFTVSCRVLTRSPDFDFTYLPPTVESKTKPFTLPILTGLSLSNS
RFPVSIDQMYTSPNEVISVQCQNGRCTLGELQGTTLQVSGICAFKGEVTAHLHDNDHLYNVTTITNLNGSPFDPSEDIP
APLGVPDFQGRVFGVISQRDKHNTPGHNEPANRAHDAVVPTYTAQYTPKLGQIQIGTWQTDLTVNQPVKFTPVGLND
TDHFNQWVVPYAGALNLTNLAAPSVAPVFPGERLLFFRSYIPLKGGYGTAPIDCLLPQEWVQHFYQEAAPSMSEVALV
RYINPDTGRALFEAKLHRAGFMTVSSNTSAPVVVPANGYFRFDSWVNQFYSLAPMGTGNRRRIQ

FIGURE 30L (SEQ ID NO:187)

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

ATGAAGATGGCATCCAACGACGCCGACCCAGCACAGACGGAGCTGCCGGATTGGTACCCGAGTCTAATAACGAG
GTGATGGCCTTGAGCCTGTTGCAGGGGCTGCCCTCGCAGTGCCTGTGACCGGGCAGACAAATATCATCGATCCTT
GGATTATCGCTAATTTCTGTGCAAGCCCCAAATGGGGAGTTTACGGTCAGCCCTAGAAATAGCCCTGGGGAAGTGCT
CCTCAATCTCAGCCTGGGACCAGAACTTAATCCGTACCTGCTCCACCTGGCCCGGATGTACAATGGATATGCAGGAG
GGATGGAGGTGCAGGTTATGCTGGCTGGCAATGCCTTTACAGCAGGCAAACTCGTTTTCGCAGCCGTCCTCCCCAC
TTCCAGTTGAAAATCTTTCCCTCAGCAGATTACCATGTTTCCCATGTGCATCATCGATGTGCGTACCCTGGAACCTG
TGCTGTTGCCTTTACCAGACGTGCGGAATAATTTCTTCACTATAATCAGAAGGATGACCCAAAAATGCGGATCGTTG
CGATGCTTTATACTCCCTGCGTAGCAATGGTAGTGGGGATGACGTTTTTACAGTGAGTTGTCGGGTAATACTCGC
CCTCACCAGACTTCGACTTTACGTACTTGGTGCCTCCACTGTCGAAAGCAAACTAAGCCATTACACTTCCCATCC
TCACCTCGGAGAACTCTCGAACTCCCGCTTCCCTGTTCAATTGATCAGATGTACACGTCTCAAATGAAGTCATTTT
TGTGCAGTGTGAGAACGGCAGGTGCACCTTAGACGGTGAAGTGCAGGGGACAACGCAGTTGCAGGTGAGTGAAT
TTGCGCCTTTAAGGGCGAAGTGACAGCTCACCTCCACGACAACGATCATCTCTACAATGTTACTATTACTAATCTCAA
TGGAAGTCTTTGACCCCTCGGAAGATATCCCGCTCCACTCGGAGTACCTGACTTTCAGGGACGCGTCTTCGGCG
TGATATCACAACGAGATAAGCATAACACACCCGGACATAATGAGCCAGCCAATAGAGCCACGACGCAGTCGTTCC
GACCTATACGGCTCAGTACACCCCAAAGCTCGGCCAGATACAAATCGGGACTTGGCAGACCGATGACCTCACTGTG
AATCAACCTGTGAAATCACTCCAGTAGGTCTGAATGATACAGACCACTTTAACCAGTGGGTGGTCCCTAGATACGC
CGGAGCCTTGAACCTAAACCTAACCTTGCCCCCTCCGTTGCACCTGTGTTTCCGGGGGAGCGGTTGCTCTCTTAG
AAGCTATATTCCTCTGAAGGGCGGGTATGGTACTCCAGCAATCGACTGCCTGCTACCTCAGGAGTGGGTCAACATT
TCTATCAAGAGGCCGCACCTAGTATGAGCGAGGTGGCTTTGGTCAGATACATCAATCCAGACACAGGAAGAGCACT
GTTTCGAGGCCAAGCTGCACAGAGCCGGCTTCATGACCGTCTCATCAATACATCCGCACCCGTAGTAGTCCCCGCCA
ACGGGTACTTCAGATTGCAGAGTTGGGTGAATCAGTTTACTCGTTGGCCCCCATGGGCACAGGGAACGGTCGCCG
ACGGATCCAGTAA

Figure 31A

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

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNMFVQAPNGEFTVSPRNSPGEVLLN
LSLGPEINPYLAHLARMYNGYAGGFEVQVVLAGNAFTAGKIIFAAIPPNFIDNLSAAQITMCPHVIVDVRQLEPVNLMP
DVRNFFHYNQGSDSLRLIAMLYTPLRANNSGDDVFTVSCRVLTRSPDFSFNFLVPTVESKTKPFTLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLGELMGTTLQVSGICAFRGTLTRSTSRASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTDFRGKVFVGASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNPQTRFTPVGIGVD

Figure 31A (cont)

HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHLRFMTIAKSGDSPITVPPNGYFRFESWVNPFTLAPMGTGNGRRRIQ

Figure 31B

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

ATGAAAATGGCTTCCAACGATGCAGCACCCCTAATGATGGCGCTGCCGACTTGTGCCGAGATTAGCTCTGAGG
CTATGGCCCTAGAACCAGTAGCCGGGGCAGCCATAGCTGCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCTGTCAGGCACCGGGGGGAGAATTCACGGTCTCTCCTCGAACTCCCCCGGGGAGGTTCTCT
TGAATTTGAGCCTGGGCCCTGAAATTAATCCTTATCTGGCCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT
TTCGAGGTCCAGGTGGTGTCTGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCGACGTGCGCAACAACCTCTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATCCGGAGATGACGTTTTCACTGTGAGTTGTGAGTCTGACACGTCC
ATCTCTGACTTTAGCTTTAATTTCTCTGTGCCCCCACAGTGGAATCCAAAATAAGCCATTCTCTGCCAATTCTT
ACCATTAGCGAAATGTGCAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTGAGAACGGACGCGTACTCTGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCAGCCAGATA
TGCGCCTTCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACCTGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCACCGGGGCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTCACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAAGTGGAG
ATTTGATCAGAACAGCAACCCCGTTTACCCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGCAGGCCAGTTCACACATAACATGAATCTTCCCCCGCTGTGGCCCCCACTTCCCGGGAG
AACAACCTCTGTTTTTCAGGAGCCAACCTGCCTTCAGCGGCGGCCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATTCCGCC
TATTACAGTGCCCCCAACGGATACTTCAGATTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 31C

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

MKMASNDAAPSNDGAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNFVQAPGGFTVSPRNSPGEVLLN
LELGPEINPYLLHARMYNGYAGGFVQVVLAGNAFTAGKIIFAAIPPNFIDNLSAAQITMCPHVIVDVRQLEPVNLMP
DVRNNFFHYNQSGDSRLRIAMLYTPLRANNSGDDVFTVSCRVLTRSPDFSFNFLVPPTVESKTKPFSLPILTISEMSNSRF
PVPIDSLHTSPTENIVVQCQNGRVTLDGELMGTTLQLLPSQJCAFRGTLTRSTSRSASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTDFRGKVFGVASQRNPDATTRAHEAKIDTTSGRFTPKLGSLEISTESGDFDQNPTRFTPVGIGVD
HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFEAKLHLRFMTIAKSGDSPITVPPNGYFRFESWVNPFTLAPMGTGNGRRRIQ

Figure 31D

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

ATGAAAATGGCTTCCAACGATGCAGCACCCCTAATGATGGCGCTGCCGGACTTGTGCCGGAGATTAGCTCTGAGG
CTATGGCCCTAGAACAGTAGCCGGGGCAGCCATAGCTGCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCTGTCAGGCACCGGGGGGAGAATTCACGGTCTCTCTCGAAACTCCCCCGGGGAGGTTCTCT
TGAATTTGGAAGTGGGCCCTGAAATTAATCCTTATCTGCTCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT
TTCGAGGTCAGGTGGTCTGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCCAGCTGCGCAACAATCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATCCGGAGATGACGTTTTCACTGTGAGTTGTGAGTCTGACACGTCC
ATCTCTGACTTTAGCTTTAATTTCTCTGTCGCCCCACAGTGGAAATCCAAAATAAGCCATTCTCTGCCAATTCTT
ACCATTAGCGAAATGTCGAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTGAGAACGGACGCGTACTCTGACGGGGAGCTTATGGGCACTACCCAGCTGTGCCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACCTGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACACCCGGGCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTCGATCAGAACAGCCAACCCGGTTTACCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGCAGGCCAGTTCACACATAACATGAATCTTGCCCCGCTGTGGCCCCAACTTCCGGGAG
AACAACCTCTGTTTTTCAGGAGCCAACCTGCCTTCAGCGGCGGCCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTACCAGGAGTCCGCGCCCTCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACGGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTATGACTATCGCTAAGAGCGGTGATTGCC
TATTACAGTGCCCCCAACGGATACTTCAGATTTGAGAGTTGGGTGAACCCATTCTATACCCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGGCGGATCCAGTAA

Figure 31E

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

MKMASNDAAPSNDAAGLVPEISSEAMALEPVAGAAIAAPLTGQQNIIDPWIMNNFVQAPGGEFTVSPRNSPGEVLLN
LSLGPINPYLLHARMYNGYAGGFEVQVVLGNAFTAGKIIFAAIPNFPIDNLSAAQITMCPHVIVDVRQLEPVNLMP
DVRNNFFHYNQGSRLRLIAMLYTPLRANNSGDDVFTVSCRVLTRPSPDFSNFLVPPTVESKTKPFLPILTISEMSNRF
PVPIDSLHTSPTENIVVQCQNGRVTLTGELMGTQLLPSQICAFRGTLTRSTSRASDQADTATPRLFNYYWHIQLDNLNG
TPYDPAEDIPAPLGTDFRGKVFVGASQRNPDATTRAHEAKIDTTSGRFTPKLSLEISTESGDFDQNPTRFTPVGIGVD
HEPDFQQWALPDYAGQFTHNMNLAPAVAPNFPGEQLLFFRSQLPSSGGRSNGILDCLVPQEWVQHFYQESAPSQTQV
ALVRYVNPDTGRVLFELKHLKRFMTIAKSGDSPITVPPNGYFRFESWVNPFTLAPMGTGNGRRRIQ

Figure 31F

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

ATGAAAATGGCTTCCAACGATGCAGCACCCCTAATGATGGCGCTGCCGGACTTGTGCCGGAGATTAGCTCTGAGG
CTATGGCCCTAGAACAGTAGCCGGGGCAGCCATAGCTGCCCACTGACTGGCCAGCAGAATATCATTGACCCCTG
GATAATGAACAATTTCTGTCAGGCACCGGGGGGAGAATTCACGGTCTCTCTCGAAACTCCCCCGGGGAGGTTCTCT
TGAATTTGAGCCTGGGCCCTGAAATTAATCCTTATCTGCTCCATCTAGCCCGAATGTACAACGGCTACGCCGGAGGT

Figure 31F (cont)

TTCGAGGTCCAGGTGGTCTGCTGGTAACGCCTTCACAGCTGGCAAGATCATTTTTGCAGCAATCCCTCCAACTTC
CCTATCGATAATCTTAGTGCCGCCCAGATCACAATGTGCCCTCACGTTATCGTAGATGTGAGGCAGCTGGAACCTGT
CAATCTCCCAATGCCCCAGCTGCGCAACAATCTTTCACTATAACCAGGGATCTGACTCCCGCCTTCGCCTTATCGCT
ATGCTGTACACCCCTCTGAGGGCTAACAATCCGGAGATGACGTTTTCACTGTGAGTTGTGAGTCTCTGACACGTCC
ATCTCCTGACTTTAGCTTTAATTTCTCGTGCCCCCACAGTGGAATCCAAAATAAGCCATTCTCTCTGCCAATTCTT
ACCATTAGCGAAATGTGAATAGTAGGTTCCCGGTGCCCATAGATTCACTGCATACCAGTCCAACAGAAAACATCGT
CGTACAGTGTGAGAACGGACGCGTGAAGTCTCGACGGGGAGCTTATGGGCACTACCCAGCTGCTGCCAGCCAGATA
TGCGCCTTCCGCGGCACACTGACTAGAAGCACTTCGCGTGCTTCTGACCAGGCAGATACAGCTACACCAAGGCTGTT
CAATTATTATTGGCATATACAACCTCGATAATCTGAATGGCACTCCTTATGACCCAGCCGAGGACATCCCCGCCCCACT
TGGCACCCCGGACTTTAGAGGGAAGGTCTTTGGAGTGGCTTCTCAAAGAAATCCCGACGCAACCAACCCGGGCCAC
GAGGCCAAAATCGATACTACATCAGGGCGTTTACCCCTAAGTTAGGCAGTCTGGAGATATCTACCGAAAGTGGAG
ATTTGATCAGAACCAGCCAACCCGGTTTACCCCGTGGGAATCGGGGTTGACCACGAACCGGATTTCCAGCAGTG
GGCTCTGCCTGATTACGACAGGCCAGTTCACACATAACATGAATCTTCCCCCGCTGTGGCCCCCACTTCCCGGGAG
AACAACCTCTGTTTTTCAGGAGCCAACCTGCCTTCAGCGCGCGCGATCTAACGGGATTTTGGACTGTCTCGTGCCCC
AGGAATGGGTGCAGCATTTTTACCAGGAGTCCGCGCCCTCCAGACGCAGGTGGCTCTGGTTAGATATGTCAATCCC
GACACCGGCAGGGTGCTATTTGAGGCAAAGCTGCACAAGCTTCGCTTTATGACTATCGCTAAGAGCGGTGATTGCC
TATTACAGTGCCCCCAACGGATACTTCAGATTGAGAGTTGGGTGAACCCATTCTATACCTGGCCCCCATGGGTAC
AGGCAATGGCAGACGCGGATCCAGTAA

Figure 32A

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAIAVPVAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPLYSLHARMYNGYAGGFEVQVILAGNAFTAGKVIFAAPPNFPTTEGLSPSQVTMFPHIVVDVRQLEPVL
PLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFVSPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVQPNQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
APLGTDPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAADFAPKLRVQFETDTRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPYSYGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTRVLFECKLHKSGYVTVAHGTQHDLVIPPNGYFRFDSWVNQFYTLAPMNGTGRRRAV

Figure 32B

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTGTCCAAGCCCCTGGTGGGGAGTTACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTCAGCGGTGCCTCCCACT
TCCCCACTGAAGGACTGTCTCAAGCCAGGTACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACATCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTGATGCAGAGTGCTCACCAGA
CCTTACCAGACTTTGACTTTATCTTCTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTATGTGCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTC

Figure 32B (cont)

GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACACATAACTGGCTCACGGAACATATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGAGTTTGTAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTTACACCT
GTAGGAGTGATTGAGGACGGGGGCCCACTCACCAGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTAT
CAAGAGGCCGACCAAGCCCAATCCGACGTCGCACTTCTCGGTTCTGTGAATCCAGACACAGGCCGCGTGTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32C

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAIAAPVAGQQNPIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSAPLGPDLNPLYSLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAPVPPNFTEGLSPSQVTMFPHIVVDVRQLEPVL
PLPDVRNNFYHYNQSDPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILVPPTVESRTKPFSPVPLTVEEMT
NSRFPIPLEKLTGPSSAFVQPPQNGRCTTDGVLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
APLGTDPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAFAPKLRVQFETDTRDFEANTQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSSYGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTRVLFECKLHKSGYVTVAHGTQHDLVPPNGYFRFDSWVNQFYTLAPMNGTGRRRAV

Figure 32D

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATCCCATTGACCCGTG
GATACGCAACAATTTGTCCAAGCCCCCTGGTGGGGAGTTACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGACGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACT
TCCCCACTGAAGGACTGTCTCAAGCCAGGTACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACCTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTACCGTGTGATGCAGAGTGCTCACCAGA
CCTTACCAGACTTTGACTTTATCTTCTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCGCTTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACACATAACTGGCTCACGGAACATATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGAGTTTGTAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTTACACCT
GTAGGAGTGATTGAGGACGGGGGCCCACTCACCAGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG

Figure 32D (cont)

AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTCGTTCA
 ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTAT
 CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTGAATCCAGACACAGGCCGCGTGTGTTTGA
 GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCAACGGAT
 ATTTTAGGTTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
 GTCTGA

Figure 32E

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAIAAPVAGQQNVIDPWIIINNFVQAPGGEFTVSPRNAPGEILW
 SAPLGPDLPYLSHLARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLPL
 PDVRNNFYHYNQSNDPITIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPF5VPVLTEEMTN
 SRFPIPLEKLTGPSSAFVVPQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEIPAP
 LGTPDFVGKIQGVLTQTTTRTDGSTRGHKATVYTGSADEFAPKLGRVQFETDTRDFEANQNTKFTPVGVQDGGTTHRNE
 PQQWVLPSSYGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAPAQSDVALLR
 FVNPDTRVLFECKLHKSGYVTVAHGTQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32F

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
 TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
 GGATAATCAACAATTTTGTCCAAGCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
 GTGGTGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
 GATTTGAAGTGCAGGTGATTCTGGCTGGGAACCGCTTCACTGCTGGCAAAGTGATCTTTCAGCGGTGCCTCCCAAC
 TTCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
 TGCTCTGATTCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
 GCGATGTTGTACCCCTCTGCGCGCTAACAAATGCTGGAGACGACGTATTCACCGTGTGATGCAGAGTGCTCACCAG
 ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCTCGTA
 CTCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAAACTGTTACAGGACCTTCTCGGCATTC
 GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCAGCTTAGCCCTGTTAATAT
 CTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAATATACCATGAATCTGGCATCACAGAATTGGA
 ATGACTACGACCCAACCGAAGAGATCCCGCACCTTTGGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
 ACACAAACCACCAAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
 GAAACTGGGTAGAGTGACGTTTGAACCGACACTGACGGGACTTTGAAGCCAATCAGAATACTAAGTTTCACACCT
 GTAGGAGTGATTACAGGACGGGGGCCCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
 AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTCGTTCA
 ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTAT
 CAAGAGGCCGCACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTGAATCCAGACACAGGCCGCGTGTGTTTGA
 GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCACCAACGGAT
 ATTTTAGGTTTCGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
 GTCTGA

Figure 32G

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGGFTVSPRNAPGEIL
WSASLGPDLNPLYSLHARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILVPPTVESRTKPFVSPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVQPNQGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
APLGTPDFVKGKIQGVLTQTTTRTDGSTRGHKATVYTGSAFAPKLGRVQFETDTRDFEANQNTKFTPVGVQDGGGTTTHR
NEPQQWVLPYSYGRNTHNVHLAPAVAPTFPGEQLLFR5TMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMNGTGRRAV

Figure 32H

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTGCAGCGGTGCCTCCCAAC
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGCTCTGATTCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCTGTCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCTCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACACATAACTGGCTCACGGAACATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCGCGACCTCTTGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAACTGGGTAGAGTGACGTTTGAACCGACACTGACGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTACGACGGGGGACCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGATTTGGCTCTGCACTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTCGTTCA
ACCATGCCTGGATGCTCCGATATCCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGCAGTATTTTAT
CAAGAGGCCGACCAAGCCCAATCCGACGTGCGACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32I

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGGFTVSPRNAPGEIL
WSAPLGPDLNPLYLLHARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILVPPTVESRTKPFVSPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVQPNQGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP

Figure 32I (cont)

APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADEFAPKLGRVQFETDTRDFEANQNTKFTPVGVIQDGGTTTHR
NEPQQWVLPYSYGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAQAQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32J

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCCTGCTGGCAAAGTGATCTTTCAGCGGTGCCTCCCAAC
TTCCCCACTGAAGGACTGTCTCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGCTCTGATTCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACCCCTCTGCGCGCTAACAAATGCTGGAGACGACGTATTACCGTGTCTGTCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTACAGGACCTTCTCGGCATTG
GTGGTTCAGCCACAGAACGGACGCTGCACAACGACGGCGTGTCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACACATAACTGGCTCACGGAACATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCGCGACCTCTTGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCTCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTGCCCC
GAAACTGGGTAGAGTGACGTTTGAAGCCAAATCAGAATACTAAGTTTACACCT
GTAGGAGTGATTGAGGACGGGGGCACCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTAT
CAAGAGGCCGACCAAGCCCAATCCGACGTCGCACTTCTCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGA
GTGCAAATGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGACGGGCT
GTCTGA

Figure 32K

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGGQQNVDPWIRNNFVQAPGGEFTVSPRNAPGEILWSAPLGPD
LNPYLSHLARMYNGYAGGFVQVILAGNAFTAGKVIFAAPPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLIPDPVRNN
FYHYNQSNDPKTIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFVSPVLTVEEMTNSRPIPLE
KLFTGPSSAFVVPQNGRCTTDGVLLGTTQLSPVNICFRGDVTHITGSRNYTMNLASQNWNDYDPTEEIPAPLGPDPFV
GKIQGVLTQTTRTDGSTRGHKATVYTGSADEFAPKLGRVQFETDTRDFEANQNTKFTPVGVIQDGGTTTHRNEPQQWV
PYSYGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAQAQSDVALLRFVNPDTG
RVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32L

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGGTGACGAGAATGTGATTGACCCGTGGATACGCAACAATTTGTCCAAGC
CCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTGGGCCCATTTGGGACCCGAT
CTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGC
TGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCAACTTCCCACTGAAGGACTGTCTCCAA
GCCAGGTACACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGCTCTGATTCCCTCCCTGATGTA
CGCAATAATTTCTACCACTACAATCAATCAATGATCCGACCATTAACCTCATCGCGATGTTGTACACCCCTCTGCGC
GCTAACAAATGCTGGAGACGACGATTACCGGTGTCATGCAGAGTGCTCACCAGACCTTACCAGACTTTGACTTTATC
TTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCGTACTCACAGTCGAGGAGATGACAAA
TAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTCTGTGGTTCAGCCACAGAACGGACG
CTGCACAACTGACGGCGTGTCTCGGAACCAACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGACGTAA
CTCACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCAACCGAAGAG
ATTCGCCGACCTCTTGGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCTGACACAAACCACCAGAACCGATGG
CTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAAACTGGGTAGAGTGACGTTG
AGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTACAGGACGGGGG
CACCCTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTTCGTTCAACCATGCCTGGATGCTCCGATATC
CCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTATCAAGAGGCCGACCCAGCCCAATCC
GACGTGCACTTCTGCGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGAGTGCAAATTGCACAAATCAGGATA
CGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCAACCGGATATTTAGGTTGACTCCTGGGTGA
ATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCTGTCTGA

Figure 32M

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGSSTAVATAGQQNVIDPWIRNNFVQAPGGGFTVSPRNAPGEIL
WSAPLGPDLNPLYSLHARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVL
PLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILVPPTVESRTKPFVSVPLTVEEMT
NSRFPIPLEKLTGPSSAFVVQPQNGRCTTDGVLGTTQLSPVNICTFRGDVTHITGSRNYTMNLAQNWNNDYDPTEEIP
APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAADFAPKLGRVQFETDTRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLP5YSGRNTHNVHLAPAVAPTFPGEQLLFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSgyvtvahtgqhdlvipngyfrfDSWVNQFYTLAPMGNGTGRRRAV

Figure 32N

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGAGCTCCACCGCCGTGCTACAGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCCGGCCCATTTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCCTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACT

Figure 32N (cont)

TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
 GTCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACTCATCG
 CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTATGCAGAGTGCTCACCAGA
 CCTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
 TCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCATTCTC
 GTGGTTCAGCCACAGAACGGACGCTGCACAACGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
 CTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGA
 ATGACTACGACCCAAACGAAGAGATTCCCGCACCTCTTGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCTG
 ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTGCCCT
 GAAACTGGGTAGAGTGACGTTTGAAGCCAATCAGAATACTAAGTTCACACCT
 GTAGGAGTGATTACAGGACGGGGGACCACTACCCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
 AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTCGTTCA
 ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTAT
 CAAGAGGCCCGACCAACCGAATCCGACGTCGACTTCTGCGGTTCTGTGAATCCAGACACAGGCCGCGTGTGTTTGA
 GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
 ATTTTAGGTTTCGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
 GTCTGA

Figure 32O

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAVPVAGQQNVIDPWIRNPFVQAPGGEFTVSPRNAPGEIL
 WSASLGPDLNPLYSLHARMYNGYAGGFEVQVILAGNAFTAGKVIFAAVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVL
 PLPDVRNPFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLPPTVESRTKPFVSVPLTVEEMT
 NSRFPIPLEKLTGPSSAFVQPNQNGRCTTDGVLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
 APLGTPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAADFAPKLGRVQFETDTRDFEANTQNTKFTPVGVIQDGGTTHR
 NEPQQWVLPSSYGRNTHNVHLAPAVAPTFPGEQLLFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPASDVAL
 LRFVNPDTGRVLFECKLHKSQYVTVAGTQHDVLPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32P

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCCAATCTTGTGCCTGAGGTTAATAATGAGG
 TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCTGGCCGGTCAGCAGAATGTGATTGACCCGTG
 GATACGCAACAATTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
 TGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
 ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCAGTCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCAACT
 TCCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
 GTCCTGATTCCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACTCATCG
 CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTATGCAGAGTGCTCACCAGA
 CCTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
 TCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCATTCTC
 GTGGTTCAGCCACAGAACGGACGCTGCACAACGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT

Figure 32P (cont)

CTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGGCCC
GAAACTGGGTAGAGTGACGTTTGAAGCCAATCAGAATACTAAGTTTCACACCT
GTAGGAGTGATTACAGGACGGGGGCACCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCCGACCGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTGCACTCCTGGGTGAATCAGTTTATACATTAGCCCCATGGGGAAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32Q

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNPIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPLYSLHARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVL
PLPDVRNPFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLPPTVESRTKPFVSPVLTVEEMT
NSRFPIPLEKLTGPSSAFVQPNQGRCTTDGVLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEIP
APLGTDPDFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAADFAPKLGRVQFETDTRDFEANQNTKFTPVGVIQDGGTT
NEPQQWVLPSSYGRNTHNVHLAPAVAPTFPGEQLLFRSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSQYVTVAGTGHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32R

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATCCCATTGACCCGTG
GATACGCAACAATTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCAGTCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTACACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACCTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCATT
GTGGTTCAGCCACAGAACGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGGCCC
GAAACTGGGTAGAGTGACGTTTGAAGCCAATCAGAATACTAAGTTTCACACCT
GTAGGAGTGATTACAGGACGGGGGCACCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTCGTTCA

Figure 32R (cont)

ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTTCTGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32S

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIINNFEVQAPGGEFTVSPR
NAPGEILWSASLGPLNPLYSHLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAPVPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLPLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFVSVPLTVEEMTNSRFPIPLEKLTGPSSAFVVPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTTEIPAPLGPDPFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAFAPKLG
RVQFETDTRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPYSYGRNTHNVHLAPAVAPTFFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPQSDVALLRFVNPDTGRVLFECKLHKSQYVTVAHGTGQ
HDLVIPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32T

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATAATCAACAATTTTGTCCAAGCCCCTGGTGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACCGCTTACTGCTGGCAAAGTGATCTTGCAGCGGTGCCTCCCAAC
TTCCCACTGAAGGACTGTCTCAAGCCAGGTCAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGTCCTGATTCCCCTCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTACCGTGTCTGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTCT
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGTCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAATATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCCCGACCTTGGAAACCCCGACTTTGTGGGAAAAATACAGGGCGTCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTGCCCC
GAACTGGGTAGAGTGACGTTTGTAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTACAGGACGGGGGCACTCACCAGAACGAGCCGCAACAATGGGTCTGCCCCTCTATAGCGGG
AGGAATACTCATAATGTGCATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTAT
CAAGAGGCCGACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTTCTGACTCCTGGGTGAATCAGTTTTATACATTAGCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32U

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAAPVAGQQNVIDPWIRNNFVQAPGGFTVSPRNAPGEIL
WSASLGPDLNPLYLHARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFTEGLSPSQVTMFPHIVVDVRQLEPVL
PLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILVPPTVESRTKPFVSPVLTVEEMT
NSRFPIPLEKLFTGPSSAFVQPNQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
APLGTPDFVQKIQGVLTQTTTGDSTRGHKATVYTGSAFAPKLGRVQFETDTRDFEANTKFTPVGVQDGGTTHR
NEPQQWVLPYSYGRNTHNVHLAPAVAPTFPGEQLLFR5TMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVAL
LRFVNPDTGRVLFECKLHKSQYVTVAHGTGQHDLPVPPNGYFRFDSWVNFYTLAPMNGTGRRAV

Figure 32V

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTAAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGT
GGATACGCAACAATTTTGTCCAAGCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCT
GTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGCCGGCG
GATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCAGTCTGGCAAAGTGATCTTGCAGCGGTGCCTCCCAAC
TTCCCACTGAAGGACTGTCTCCAAGCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCC
TGCTCTGATTCCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATC
GCGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTGCAGAGTGCTCACCAG
ACCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGCCCCGTA
CTCACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTACAGGACCTTCTCGGCATT
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGCGACGTAACACATAACTGGCTCACGGAATATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAAACGAAGAGATCCCGCACCTCTTGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAACTGGGTAGAGTGACGTTTGAACCGACACTGACGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCT
GTAGGAGTGATTACGACGGGGGACCACTACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGG
AGGAATACTCATAATGTGATTTGGCTCTGCACTGGCTCCACGTTTCCCGGGGAACAAGTCTCTTTTTCGTTCA
ACCATGCCTGGATGCTCCGATATCCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGCAGTATTTTAT
CAAGAGGCCGACACGCCAATCCGACGTGCGACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

Figure 32W

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGGQQNVIDPWIRNNFVQAPGGFTVSPRNAPGEILWSASLGP
DLNPLYLHARMYNGYAGGFVQVILAGNAFTAGKVIFAAPVPPNFTEGLSPSQVTMFPHIVVDVRQLEPVLPLPDVRNN
FYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILVPPTVESRTKPFVSPVLTVEEMTNSRFP
IPLEKLFTGPSSAFVQPNQNGRCTTDGVLLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
APLGTPDFV

Figure 32W (cont)

GKIQGVLTQTTRTDGSTRGHKATVYTGSADEFAPKLGRVQFETDTRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVL
PSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAPASQSDVALLRFVNPDTG
RVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32X

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTAAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGGTGAGCAGAATGTGATTGACCCGTGGATACGCAACAATTTGTCCAAGC
CCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTCGGCCAGCTTGGGACCCGAT
CTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGC
TGGGAACGCGTTCAGTCTGGCAAAGTGATCTTGCAGCGGTGCCTCCCACTCCCACTGAAGGACTGTCTCAA
GCCAGGTCACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCTCCCTGATGTA
CGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACCTCATCGCGATGTTGTACACCCCTCTGCGC
GCTAACAATGCTGGAGACGACGTATTCACCGTGTCTGAGAGTGCTCACCAGACCTTACCAGACTTTGACTTTATC
TTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCTGACTCACAGTCGAGGAGATGACAAA
TAGCCGCTTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTCGTGGTTCAGCCACAGAACGGACG
CTGCACAACTGACGGCGTGTCTCGGAACCAACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGACGTAA
CTCACATAACTGGCTCACGGAACATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCAACCGAAGAG
ATTCCCGCACCTCTTGGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCTGACACAAACCACCAAGAACCGATGG
CTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAACTGGGTAGAGTGCAAGTTG
AGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTGAGGACGGGGG
CACCCTCACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCTTCAACCATGCCTGGATGCTCCGATATC
CCAATATGGATCTCGATTGCTCTCCACAGGAATGGGTGCGATTTTTATCAAGAGGCCGACCAAGCCCAATCC
GACGTGCGACTTCTGCGGTTCTGAATCCAGACACAGGCCGCGTGTGTTGAGTGCAAAATGCACAAATCAGGATA
CGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCAACCGATATTTAGGTTGACTCTGGGTGA
ATCAGTTTTATACATTAGCCCCATGGGGAATGGGACTGGCAGACGCGGGCTGTCTGA

Figure 32Y

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGSSTAVATAGQQNVIDPWIRNNFVQAPGGEFTVSPRNAPGEIL
WSASLGPDLNPLYSLHARMYNGYAGGFEVQVILAGNAFTAGKVIFAAPPNFPTEGLSPSQVTMFPHIVVDVRQLEPVLI
PLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLVPPTVESRTKPFVSPVLVEEMT
NSRFPIPLEKLTGPSSAFVQVQPNGRCTTDGVLGTTQLSPVNICTFRGDVTHITGSRNYTMNLASQNWNDYDPTTEEIP
APLGPDPFVGKIQGVLTQTTRTDGSTRGHKATVYTGSADEFAPKLGRVQFETDTRDFEANQNTKFTPVGVIQDGGTTHR
NEPQQWVLPSYSGRNTHNVHLAPAVAPTFPGEQLLFFRSTMPGCSGYPNMDLCLLPQEWVQYFYQEAAPASQSDVAL
LRFVNPDTGRVLFECKLHKSGYVTVAHGTGQHDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 32Z

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCAGCTCCACCGCCGTCGCTACAGCCGGTCAGCAGAATGTGATTGACCCGTG
GATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTG
TGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGG
ATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCAGTCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACT
TCCCCACTGAAGGACTGTCTCCAAGCCAGGTACAAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCT
GTCCTGATTCCTCCCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACCTCATCG
CGATGTTGTACACCCCTCTGCGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTGCATGCAGAGTGCTCACCAGA
CCTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTAC
TCACAGTCGAGGAGATGACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCATTC
GTGGTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGTCTCGGAACCAACCCAGCTTAGCCCTGTTAATAT
CTGTACGTTTAGAGGGCAGCTAACTCACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGA
ATGACTACGACCCAACCGAAGAGATTCGCGACCTCTTGAACCCCGACTTTGTGGGAAAAATACAGGGCGTCTG
ACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCC
GAAACTGGGTAGAGTGCAAGTTTGAAGCCAACTCAGAATACTAAGTTTCACACCT
GTAGGAGTGATTACAGACGGGGGCACCACTCACCGAACGAGCCGCAACAATGGGTCTGCCCTCTATAGCGGG
AGGAATACTCATAATGTGCAATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACTGCTCTTTTTTCGTTCA
ACCATGCCTGGATGCTCCGGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTAT
CAAGAGGCCGACCAAGCCCAATCCGACGTGCACTTCTGCGGTTGCTGAATCCAGACACAGGCCGCGTGTGTTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTTCGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
GTCTGA

FIGURE 32AA

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAAIAPVPVAGQQNVIDPWIINNPFVQAPGGEFTVSPR
NAPGEILWSAPLGPDLNPYLSHLARMYNGYAGGFVQVILAGNAFTAGKVIFAAPPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLPLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFVSVPLTVEEMTNSRFPIPLEKLTGPSSAFVVPQNGRCTTDGVLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTTEIPAPLGPDPFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAADFAPKLG
RVQFETDTRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPYSYGRNTHNVHLAPAVAPTFFGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPASQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHGTGQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRAV

FIGURE 32BB

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTAAAT
AATGAGGTGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAA
TGTGATTGACCCGTGGATAATCAACAATTTTGTCCAAGCCCCCTGGTGGGGAGTTCACCGTTAGCCCCGAGA
AATGCGCCAGGAGAAATCCTGTGGTCGGCCCCATTGGGACCCGATCTGAACCCCTATTTGTCACATCTCG
CTCGGATGTACAACGGGTATGCCGGCGGATTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTG
CTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACTTCCCCACTGAAGGACTGTCTCCAAGCCAGGTAC
AATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTACGC
AATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACTCATCGCGATGTTGTACACCCCTCTG
CGCGCTAACAATGCTGGAGACGACGTATTCACCGTGTCTGCAGAGTGCTCACCAGACCTTCACCAGACT
TTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCCGTACTCACA
GTCGAGGAGATGACAAATAGCCGCTTTCGAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCAT
TCGTGGTTCAGCCACAGAACGGACGCTGCACAACCTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCC
CTGTTAATATCTGTACGTTTAGAGGCGACGTAACCTCACATAACTGGCTCACGGAACCTATACCATGAATCTG
GCATCACAGAATTGGAATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGAACCCCCGACTTTG
TGGGAAAAATACAGGGCGTCTGACACAAACCACAGAACCGATGGCTCCACACGGGGACACAAGGCA
ACCGTCTACACTGGCTCTGCCGATTTTCCCCGAACTGGGTAGAGTGCAGTTTGAGACCGACACTGACC
GGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGACGGGGGCACCACTC
ACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTCTGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCG
CACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGAGTG
CAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCAACCAAC
GGATATTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGAATGGGACTGGCA
GACGCAGGGCTGTCTGA

FIGURE 32CC

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAIAVPVAGQQNVIDPWIINNFEVQAPGGGEFTVSPR
NAPGEILWSASLGPLNPNYLSHARMYNGYAGGFEVQVILAGNAFTAGKVIFAAPPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLPLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFSPVLTVEEMTNSRFPIPLEKLFTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTTEIPAPLGTDPFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAFAPKLG
RVQFETDTRDFEANQNTKFTPVGVIQDGGTTHRNEPQQWVLPYSYGRNTHNVHLAPAVAPTFFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPAQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHGTGQ
HDLVIPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

FIGURE 32DD

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

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGG
TGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTG
GATAATCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGT
GGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGA
TTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACTT
CCCCACTGAAGGACTGTCTCCAAGCCAGGTCAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTG
TCCTGATTCCCCCTCTGATGTACGCAATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGC
GATGTTGTACACCCCTCTGCGCGCTAACAAATGCTGGAGACGACGTATTCACCGTGTGATGCAGAGTGCTCACCAGAC
CTTCACCAGACTTTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCGTACT
CACAGTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTACAGGACCTTCTCGGCATTCTG
TGGTTCAGCCACAGAACGGACGCTGCACAACCTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATATC
TGACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGAA
TGACTACGACCAACCGAAGAGATTTCCCGCACCTCTTGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCTCTGA
CACAACCAACAGAACCGATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGGCCCG
AAACTGGGTAGAGTGCAGTTTGAACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTG
TAGGAGTGATTCAGGACGGGGGACCACTCACGGGAACGAGCCGCAACAATGGGTCTGCTCTTATAGCGGGA
GGAATACTCATAATGTGCATTTGGCTCCTGCACTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTCGTTCAA
CCATGCTCGGATGCTCCGATATCCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGCAGTATTTTATC
AAGAGGCCGACACAGCCCAATCCGACGTGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGA
GTGCAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGAT
ATTTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGCAGGGCT
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)

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAAT
AATGAGGTGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAA
TGTGATTGACCCGTGGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGA
AATGCGCCAGGAGAAATCCTGTGGTCCGCCCXXXTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCG
CTCGGATGTACAACGGGTATGCCGGCGGATTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTG
CTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACTTCCCCACTGAAGGACTGTCTCCAAGCCAGGTCAC
AATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGCTGATTCCCCCTCCCTGATGTACGC
AATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAAACTCATCGCGATGTTGTACACCCCTCTG
CGCGCTAACAAATGCTGGAGACGACGTATTCACCGTGTGATGCAGAGTGCTCACCAGACCTTACCAGACT
TTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCGTACTCACA
GTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAAACTGTTACAGGACCTTCTCGGCAT
TCGTGGTTCAGCCACAGAACGGACGCTGCACAACCTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCC

FIGURE 32EE (cont)

CTGTTAATATCTGTACGTTTAGAGGCGACGTAACCTCACATAACTGGCTCACGGAACCTATACCATGAATCTG
GCATCACAGAATTGGAATGACTACGACCCAACCGAAGAGATCCCCGCACCTCTTGAACCCCCGACTTTG
TGGGAAAAATACAGGGCGTCCTGACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCA
ACCGTCTACACTGGCTCTGCCGATTTTGGCCCCGAACTGGGTAGAGTGCAGTTTGAACCGACACTGACC
GGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTGAGGACGGGGGCACCACTC
ACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGCAGTATTTTATCAAGAGGCCG
CACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGAGTG
CAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAAC
GGATATTTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGGAATGGGACTGGCA
GACGCAGGGCTGTCTGA

FIGURE 32FF

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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAIAAPVAGQQNVIDPWIRNNFVQAPGGEFTVSPR
NAPGEILWSAXLGPDLNPLYSLARMYNGYAGGFEVQVILAGNAFTAGKVIFAAPPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLPLPDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFILV
PPTVESRTKPFVSVPLTVEEMTNSRFPIPLEKLTGPSSAFVVQPQNGRCTTDGVLGTTQLSPVNICFRGDVT
HITGSRNYTMNLASQNWNDYDPTTEIPAPLGPDPFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAFAPKLG
RVQFETDTRDFEANQNTKFTPVGVIQDGGTTHRNPPQWVLPSSYSGRNTHNVHLAPAVAPTFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPQSDVALLRFVNPDTGRVLFECKLHKSQYVTVAHGTGQ
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)

ATGAAAATGGCCTCGAGTGACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTAAAT
AATGAGGTGATGGCCCTGGAGCCTGTGGTGGGCGCAGCCATAGCAXXXCCCGTGGCCGGTCAGCAGAA
TGTGATTGACCCGTGGATACGCAACAATTTTGTCCAAGCCCCTGGTGGGGAGTTCACCGTTAGCCCCGAGA
AATGCGCCAGGAGAAATCCTGTGGTCGGCCAGCTTGGGACCCGATCTGAACCCCTATTTGTCACATCTCG
CTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGATTCTGGCTGGGAACGCGTTCACTG
CTGGCAAAGTGATCTTTGCAGCGGTGCCTCCCACTTCCCCACTGAAGGACTGTCTCAAGCCAGGTACAC
AATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCCTGATTCCCCTCCCTGATGTACGC
AATAATTTCTACCACTACAATCAATCCAATGATCCGACCATTAACCTCATCGCGATGTTGTACACCCCTCTG
CGCGCTAACAATGCTGGAGACGACGTATTACCGTGTGATGCAGAGTGCTCACCAGACCTTACCAGACT
TTGACTTTATCTTCTTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCTCCGTAATCACA

FIGURE 32GG (cont)

GTCGAGGAGATGACAAATAGCCGCTTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCCTCGGCAT
TCGTGGTTTCAGCCACAGAACGGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCC
CTGTTAATATCTGTACGTTTAGAGGCGACGTAACCTACATAACTGGCTCACGGAACCTATACCATGAATCTG
GCATCACAGAATTGGAATGACTACGACCCAACCGAAGAGATTCCCGCACCTCTTGAACCCCCGACTTTG
TGGGAAAAATACAGGGCGTCTGACACAAACCACCAGAACCGATGGCTCCACACGGGGACACAAGGCA
ACCGTCTACACTGGCTCTGCCGATTTTGGCCCCGAACTGGGTAGAGTGACAGTTTGAGACCGACACTGACC
GGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTACAGGACGGGGGCACCACTC
ACCGGAACGAGCCGCAACAATGGGTCTGCCCTCTTATAGCGGGAGGAATACTCATAATGTGCATTTGG
CTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACCTGCTCTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCCTGCTCCACAGGAATGGGTGCAGTATTTTATCAAGAGGCCG
CACCAGCCCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTTGAGTG
CAAATTGCACAAATCAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCAACCAAC
GGATATTTAGGTTGACTCCTGGGTGAATCAGTTTATACATTAGCCCCCATGGGGAATGGGACTGGCA
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

MKMASSDANPSDGSAAANLVPEVNNEVMALEPVVGAIAIXPVAGQQNVIDPWIRNNFVQAPGGEFTVSPR
NAPGEILWSASLGPLNLYSHLARMYNGYAGGFVQVILAGNAFTAGKVIFAAPPPNFPTEGLSPSQVTMF
PHIVVDVRQLEPVLIPLDVRNNFYHYNQSNPTIKLIAMLYTPLRANNAGDDVFTVSCRVLTRPSPDFDFIFLV
PPTVESRTKPFVSVPLTVEEMTNSRFPIPLEKLTGPSSAFVVQPQNGRCTTDGVLLGTTQLSPVNICTFRGDVT
HITGSRNYTMNLASQNWNDYDPTTEIPAPLGPDPFVGKIQGVLTQTTRTDGSTRGHKATVYTGSAFAPKLG
RVQFETDTRDFEANQNTKFTPVGVIQDGGTTHRNPPQWVLPYSYGRNTHNVHLAPAVAPTFFPGEQLLFF
RSTMPGCSGYPNMDLDCLLPQEWVQYFYQEAAPQSDVALLRFVNPDTGRVLFECKLHKSGYVTVAHGTQ
HDLVIPPNGYFRFDSWVNQFYTLAPMGNGTGRRRAV

Figure 33A

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

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGSIAAPVVGGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLSLGPENLYSHLSRMVNGYAGGMQVQVVLAGNAFTAGKIIFAAPPPHFPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRRFFHYNQENTSRMRVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSLPILTGLSLSNR
FPAPIDMLYTDPNEGIVVQPQNGRCTLDTLQGTTLQVPTQICAFRGTLIGQTSRSPDSTDSAPRRRDHPLHVQLKNDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVSGQQVGATRAHEVHINTTDPRYTPKLGSILMYSESDDFVTGQPVRFPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSNNPIVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 33B

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

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGTCCACAGGGGGAGTTACAGTCTCCCCCGGAACCTCCCGGGCGAGATGCTG
CTCAATCTGAGCCTCGGCCCTGAACTAAACCCTTATCTGTACACCTTTCACGGATGTACAATGGCTACGCAGGAGG
AATGCAAGTTCAGGTGGTCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTCGGGCCGTTCTCCACACT
TCCCTGTGCGAAAATATCAACGCCGCCAGATTACTATGTGCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCA
GTTCTGTGCCCCGCCCCGACATCAGAAACCGGTTCTTCCATTACAATCAAGAGAATACTTCACGGATGAGACTTGTT
GCGATGCTGTACCCCTCTTCGTGCAAATTCGGCGAAGACGTGTTCACTGTGTCTTGTGAGTACTTACCCGACCC
GCCCCGATTTTGAATTCACCTTCTGGTTCCCCCTACTGTGGAGAGCAAGACAAAACCTTCAGCCTCCCAATCTTA
ACACTCGGGGAGCTGTCTAATTCACGCTTCCCCGACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGT
GGTGACGCCCCAAATGGACGGTGTACTCTGACGGCAGCTCCAGGGCACAACCCAAGTGGTCCAACCCAGATT
TGTGCATTACAGGGGCACCTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGG
ACCACCACTCCACGTTCAAGTAAAAAACCTGGACGGAACCCAGTACGACCTACAGACGAGGTCCCCGCTGTCTC
GGAGCCATCGACTTTAAAGGAAGTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGACGAGGTGGGAGCT
ACGAGAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCCAAACTAGGGTCAATTTTAATGTATTC
GGAATCAGACGATTTTGTACAGGTACGCGCTGCGGTTTACCCGATCGGAATGGGGGACAACGATTGGCACCAG
TGGGAATTGCCGATTACCTGGACACCTACCTTGAATATGAATCTGGCCCCAGCGTCGCGCCCGCTTCCCCGGT
GAGCGGATCCTCTTTTTAGAACATAGTGCCCTCCGACGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCC
CCAAGAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCTAGCCAGTCCGACGTAGCACTGATCAGATATGTTAATC
CTGATACGGGAAGGAACATCTTGAAGCAAACTGCACCGTGAGGGCTTCAATACCGTCGCCAACAGTGGTAATAA
CCCTATTGTGGTGCCTCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTATACTCTGACTCCCATGGG
GACAGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 33C

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

MKMASNDAAPSNDGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLELGPENPYLLHLSRMYNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHFPVENINAAQITMCPHVIVDVRQLEPVLLP
LPDIRNRFFHYNQENTSRMRLVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSPLITLGELSNSR
FPAPIDMLYTDPNEGIVVQPQNGRCTLGTLQGTTLQVPTQICAFRGTLIGQTSRSPDSTDSAPRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGTVFGVASQRDVSGQVQVGAATRAHEVHINTTDPRTYTPKLGSILMYSESDDFVTGQPVRFPTPI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSNNPIVPPNGYFRFEAWVNQFYTLTPMGTGQGRRRDQ

Figure 33D

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

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGTCCACAGGGGGAGTTACAGTCTCCCCCGGAACCTCCCGGGCGAGATGCTG
CTCAATCTGGAAGTTCGGCCCTGAACTAAACCCTTATCTGTCTCACCTTTCACGGATGTACAATGGCTACGCAGGAGG

FIGURE 33D (cont)

AATGCAAGTTCAGGTGGTCTCTGGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCTCCACACT
TCCCTGTCGAAAAATATCAACGCCGCCAGATTACTATGTGCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCA
GTTCTGCTGCCCTGCCCGACATCAGAAACCGTTCTTCCATTACAATCAAGAGAATACTTCACGGATGAGACTTGT
GCGATGCTGTACACCCCTCTTCGTGCAAATCCGGCGAAGACGTGTTCACTGTGTCTTGTGCGAGTACTTACCCGACCC
GCCCCCGATTTCGAATTCACCTTCTGGTCCCCCTACTGTGGAGAGCAAGACAAAACCTTCAGCCTCCCAATCTTA
ACACTCGGGGAGCTGTCTAATTCACGCTTCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGATAGT
GGTGCAGCCCCAAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAACCTGGTGCCAACCCAGATT
TGTGCATTAGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGG
ACCACCACTCCACGTTCAAGTAAAAAACCTGGACGGAAACCCAGTACGACCTACAGACGAGGTCCCCGCTGTCTC
GGAGCCATCGACTTTAAAGGAACTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGACAGAGGTGGGAGCT
ACGAGAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCAAAACCTAGGGTCAATTTTAATGTATTC
GGAATCAGACGATTTTGTTACAGGTACGCGCTGCGGTTTACCCCGATCGGAATGGGGGACAACGATTGGCACCAG
TGGAATTGCCGATTACCCTGGACACCTCACCTGAATATGAATCTGCCCCAGCCGTCGCGCCCGCCTCCCCGGT
GAGCGGATCCTCTTTTTAGAAAGCATAGTGCCCTCCGAGGTGGGTATGGATCAGGGCAGATTGATTGCCTGATCCC
CCAAGAATGGGTACAGCATTTCTACCAGGAAGCAGCCCCCTAGCCAGTCCGCAGTAGCACTGATCAGATATGTTAATC
CTGATACGGGAAGGAACATCTTCAAGCAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAA
CCCTATTGTGGTGCCCTCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTTATACTCTGACTCCCATGGG
GACAGGCCAAGGGGCGACGCCGGGATCAGTGA

Figure 33E

Amino acid sequence of VP1 GII.6 Ohio E80S+590L (SEQ ID NO:83)

MKMASNDAAPSN DGAANLVPEANNEVMALEPVVGASIAAPVVGQQNIIDPWIRENFVQAPQGEFTVSPRNSPGEMLL
NLSLGP ELPYPYLLHLSRMVNGYAGGMQVQVVLAGNAFTAGKIIFAAVPPHFPVENINAAQJTMCPHVIVDVRQLEPVLLP
LPDIRNRFHHYNQENTSRMRLVAMLYTPLRANSGEDVFTVSCRVLTRPAPDFEFTFLVPPTVESKTKPFSLPILTGLGELSNSR
FPAPIDMLYTDPN EGVVQPQNGRCTL DGT LQGTTQLVPTQICAFRGT LIGQTSRSPDSTD S APRRRDHPLHVQLKNLDG
TQYDPTDEVPAVLGAIDFKGT VFGVASQRDVS GQQV GATRAHEVHINTTDP RYTPKLSILMYSEDDFVTGQPVRFPTI
GMGDNDWHQWELPDYPGHLTLNMNLAPAVAPAFPGERILFFRSIVPSAGGYGSGQIDCLIPQEWVQHIFYQEAAPSQS
AVALIRYVNPDTGRNIFEAKLHREGFITVANSGNNPIVPPNGYERFEAWVNOFYTLTPMGTGGGRRRDO

Figure 33F

Nucleic acid sequence of human codon optimized VP1 GII.6 Ohio E80S+S90L (SEQ IDNO:84)

ATGAAGATGGCAAGCAACGACGCAGCTCCCTCCAATGATGGTGCCGCCAACCTGGTCCCCGAAGCTAATAATGAGG
TGATGGCGTTAGAGCCGGTGTTGGCGCATCTATTGCAGCGCCTGTGGTCGGACAGCAGAACATCATTGATCCCTG
GATTCGCGAGAACTTCGTACAAGCTCCACAGGGGGAGTTCACAGTCTCCCCCGGAACTCCCCGGGCGAGATGCTG
CTCAATCTGAGCCTCGGCCCTGAACTAAACCTTATCTGCTCCACCTTTCACGGATGTACAATGGCTACGCAGGAGGA
ATGCAAGTTCAGGTGGTCTGCGCCGGCAATGCTTTCACCGCGGGCAAAATCATCTTTGCGGCCGTTCTCTCCACACTTC
CCTGTGCAAAATATCAACGCCGCCAGATTACTATGTGCCCCACGTGATTGTGGATGTGCGACAGTTAGAGCCAGT
TCTGCTGCCCTGCCCGACATCAGAAACCGTTCTTCATTACAATCAAGAGAATACTTCACGGATGAGACTTGTTGC
GATGCTGTACACCCCTCTTCGTGCAAATTCGGCGAAGACGTGTTCACTGTGTCTTGTCGAGTACTTACCCGACCCGC
CCCCGATTCGAATTCACCTTCTGGTCCCCCTACTGTGGAGAGCAAGACAAAACCTTCAGCCTCCCAATCTTAAC
ACTCGGGGAGCTGTCTAATTCAGCTTCCCCGCACCTATTGATATGCTGTATACTGACCCCAACGAGGGGGATAGTGG

FIGURE 33F (cont)

TGCAGCCCCAAAATGGACGGTGTACTCTCGACGGCACGCTCCAGGGCACAACCCAAGTGGTGCCAACCCAGATTTGT
GCATTTCAGGGGCACTTTGATTGGGCAGACATCGAGATCTCCAGATTCTACTGATTCCGCGCCAAGGAGGAGGGACC
ACCCACTCCACGTTTCAAGTAAAAAACCTGGACGGAACCCAGTACGACCTACAGACGAGGTCCCCGCTGTCTCGGA
GCCATCGACTTTAAAGGAAGTGTATTTGGAGTGGCATCCCAAAGGGATGTCTCGGGGACGAGGTGGGAGCTACGA
GAGCACATGAAGTCCACATTAACACCACAGACCCAAGATATACCCAAAAGTGGTCAATTTTAAATGTATTTCGGAA
TCAGACGATTTTGTACAGGTGAGCCCGTGGGTTTACCCGATCGGAATGGGGGACAACGATTGGCACCAGTGGG
AATTGCCCGATTACCTGGACACCTCACCTTGAATATGAATCTGCCCCAGCCGTGCGCGCCCGCTTCCCCGGTGAGC
GGATCCTCTTTTTAGAACATAGTGCCCTCCGAGGTGGGTATGGATCAGGGCAGATTGATTGCCGTGATCCCCAA
GAATGGGTACAGCATTTCTACAGGAAGCAGCCCTAGCCAGTCCGAGTAGCACTGATCAGATATGTTAATCCTGA
TACGGGAAGGAACATCTTGAAGCAAACTGCACCGTGAGGGCTTCATTACCGTCGCCAACAGTGGTAATAACCTT
ATTGTGGTGCTCCTAATGGATACTTCAGGTTTGAGGCATGGGTGAATCAGTTTATACTCTGACTCCCATGGGGAC
AGGCCAGGGGCGACGCCGGGATCAGTGA

Figure 34A

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

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNQVQAPNGEFTVSPRNSPGEVLL
NLSLGPENLPYLAHLRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPVHVIDVRTLEPVLLPLP
DVRNFFHYNQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPPQNGRCALDGELOQTQLLPTAICSFGRINQKVSNGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTDFSGKLFGLVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSALTINMGLAPPVAPTFFGEQJLFFRSHIPLKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 34B

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

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCCGTGGCCGGAGCCTCAATTGCCGCCCCCTCACTGGCCAGAACAACGTGATTGATCCCTGG
ATCAGACTGAACCTTCGTTAGGCTCCTAATGGGGAGTTCACCGTGTCCCCGAGAACTCCCCGGCGAAGTGTTATT
GAATTTGAGCTTAGGACCAGAACTCAACCCCTATCTGGCACATCTGTCTCGGATGTACAACGGCTATGCGGGCGGAG
TGGAGGTGCAAGTTCTTCTCGCTGGAATGCATTCACAGCAGGAAAATTAGTATTTGCAGCGGTTCCACCCCATTTTC
CACTTGAAAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGTG
CTGCTACCCCTGCCGACGTGAGGAACAATTTCTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCGC
CATGCTCTATACTCCTTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTGCGGTGCTCACCCGAC
CTTCCCCAGATTTGACTTCAATTATCTGGTCCCCCCCACGGTAGAGTCCAAAACAAAGCCTTTCACTCTTCAATCCT
TACAATTGGCGAACTGACCAACTCAGCTTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTGT
CGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACCTGTTGCCAACCGCTATA
TGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACACCGTGTGGAACATGCAAGTGACGAATATCG
ACGGGACACCTTTCGATCCAACAGAGGATGTCCAGCGCCTTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCCGGC
GTCCTTTCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTGATTGCCACCAACTCAGCCAAATTCACC
CCAAAACCTGGAGCGATACAGATCGGAACCTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCCC
TGTTGGCCTTTTCGAAAGCGAAGGCTTTAACAGTGGACACTTCCAATTACAGCGGGGCTCTCACTCTTAATATGG

FIGURE 34B (cont)

GACTCGACCAACCGTCGCTCCAACGTTTCCTGGTGAGCAGATTTGTTTTCCGCAGTCATATCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTGAGCACTTGTATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCGATACCGGAAGAGTGTTGTTGAAGCTAACTTCATCGCTCC
GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCGGCAAACGGATACTTTGATTTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

Figure 34C

Amino acid sequence of VP1_GII.12_H510_A90L (SEQ ID NO:90)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNQVQAPNGEFTVSPRNSPGEVLL
NLELGPENPYLLHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPVHVIDVRTLPLEVLLPLP
DVRNFFHYNQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDQELQGTQLLPTAICSFGRINQKVSNGENHVWNMQVTNIDGTPFDPTEDV
PAPLGTDFSGKLFVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTINMGLAPPVAPTFPGEQILFFRSHIPLKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 34D

Nucleic acid sequence of human codon optimized VP1_GII.12_H510_A90L (SEQ ID NO:91)

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCGTGGCCGGAGCCTCAATTGCCGCCCCCTCACTGGCCAGAACAACTGATTGATCCCTGG
ATCAGACTGAACCTTCGTTACAGGCTCCTAATGGGAGTTCACCGTGTCCTCCGAGAACTCCCCGGCGAAGTGTTATT
GAATTTGGAATTAGGACCAGAACTCAACCCCTATCTGCTCCATCTGTCTCGGATGTACAACGGCTATCGGGGCGGAG
TGGAGGTGCAAGTCTTCTCGCTGGTAATGCATTCACAGCAGGAAAATTAGTATTTGCAGCGGTTCCACCCATTTTC
CACTTGAAAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGTG
CTGCTACCCCTGCCGACGTGAGGAACAATTTCTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCGC
CATGCTCTATACTCCTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTCTGGGTGCTCACCCGAC
CTTCCCCAGATTTGACTTCAATTATCTGGTCCCCCAGCGTAGAGTCCAAAACAAAGCCTTTCACTCTTCAATCCT
TACAATTGGCGAACTGACCAACTCAGCTTTCCAGTGCCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTGT
CGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACCTGTTGCCAACCGCTATA
TGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACACGTGTGGAACATGCAAGTGACGAATATCG
ACGGGACACCTTTCGATCCAACAGAGGATGTCCAGCGCCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCCGGC
GTCCTTTCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTATTGCCACCAACTCAGCCAAATTCACC
CCAAAACCTGGAGCGATACAGATCGGAACCTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCCC
TGTTGGCCTTTTCGAAAGCGAAGGCTTTAACAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG
GACTCGACCAACCGTCGCTCCAACGTTTCCTGGTGAGCAGATTTGTTTTCCGCAGTCATATCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTGAGCACTTGTATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCGATACCGGAAGAGTGTTGTTGAAGCTAACTTCATCGCTCC
GGTTACATCACAGTAGCCAACACGGGTTCCAGGCCAATCGTAGTTCGGCAAACGGATACTTTGATTTCGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

Figure 34E

Amino acid sequence of VP1_GII.12_H510_E80S+A90L (SEQ ID NO:92)

MKMASNDAAPSNDGAAGLVPEVNNETMALEPVAGASIAAPLTGQNNVIDPWIRLNFBVQAPNGEFTVSPRNSPGEVLL
NLSLGPENLPYLLHLSRMYNGYAGGVEVQVLLAGNAFTAGKLVFAAVPPHFPLENISPGQITMFPHVVIDVRTLPLEVLLPLP
DVRNFFHYNQNEPRMRLVAMLYTPLRSNGSGDDVFTVSCRVLTRPSPDFDFNYLVPPTVESKTKPFTLPILTIGELTNS
RFPVPIDELYTSPNESLVVQPQNGRCALDGELOQTQLLPTAICSFGRINQKVS GENHVWNMQVTNIDGTPFDPTEDV
PAPLGTPDFSGKLFGLVLSQRDHDNACRSHDAVIATNSAKFTPKLGAIQIGTWEQDDVHINQPTKFTPVGLFESEGFNQW
TLPNYSGALTINMGLAPPVAPTFPGEQILFFRSHIPKGGVADPVIDCLLPQEWIQHLYQESAPSQTDVALIRFTNPDTGRV
LFEAKLHRSGYITVANTGSRPIVVPANGYFRFDSWVNQFYSLAPMGTGNGRRRVQ

Figure 34F

Nucleic acid sequence of human codon optimized VP1_GII.12_H510_E80S+A90L (SEQ ID NO:93)

ATGAAGATGGCGTCTAATGATGCTGCTCCTTCCAATGATGGCGCAGCCGGCCTGGTCCCTGAAGTGAATAACGAGA
CTATGGCTCTCGAACCGTGGCCGGAGCCTCAATTGCCGCCCTCACTGGCCAGAACAACTGATTGATCCCTGG
ATCAGACTGAACTTCGTTCAAGGCTCCTAATGGGGAGTTCACCGTGTCCTCCGAGAACTCCCCGGCGAAGTGTTATT
GAATTTGAGCTTAGGACCAGAACTCAACCCCTATCTGCTCCATCTGTCTCGGATGTACAACGGCTATGCGGGCGGAG
TGGAGGTGCAAGTCTTCTCGCTGGTAATGCATTCACAGCAGGAAATAGTATTTGAGCGGTTCCACCCATTTTC
CACTTGAACATAAGCCCAGGCCAGATCACCATGTTCCCTCACGTGATAATCGACGTGCGGACATTAGAGCCCGTG
CTGCTACCCCTGCCGACGTGAGGAACAATTTCTTCACTACAATCAGCAAAATGAACCAAGAATGCGCCTGGTCGC
CATGCTCTATACTCTTAAGAAGTAATGGCAGTGGGGATGACGTGTTTACTGTTAGCTGTGCGGTGCTCACCCGAC
CTTCCCCAGATTTGACTTCAATTATCTGGTCCCCCCCCACGGTAGAGTCCAAAACAAAGCCTTTCACTCTTCCAATCCT
TACAATTGGCGAACTGACCAACTCAGCTTTCCAGTGCTATTGATGAGCTGTACACAAGTCCAAATGAATCCCTTGT
CGTTCAGCCACAGAATGGGCGCTGCGCGCTTGACGGTGAGCTCCAGGGCACAACACAACCTGTTGCCAACCGCTATA
TGCTCTTTCAGGGGGCGTATTAATCAGAAGGTCTCCGGGGAGAACCACGTGTGGAACATGCAAGTGACGAATATCG
ACGGGACACCTTTCGATCCAACAGAGGATGTCCAGCGCTCTAGGTACCCCTGACTTCTCAGGCAAGTTGTTCCGC
GTCCTTTCCAGCGCGACCATGATAATGCTTGCCGGAGCCACGATGCCGTCATTGCCACCAACTCAGCCAAATTCACC
CCAAACTTGGAGCGATACAGATCGGAACCTTGGGAACAAGACGACGTCCATATCAACCAACCAACAAAGTTTACCCC
TGTTGGCCTTTTCGAAAGCGAAGGCTTTAACAGTGGACACTTCCCAATTACAGCGGGGCTCTCACTCTTAATATGG
GACTCGACCAACCGTCGCTCCAACGTTTCTGGTGAGCAGATTTTGTGTTTCCGCAGTCATATCCACTGAAGGGTG
GAGTTGCTGATCCCGTGATAGACTGCCTCCTCCCTCAGGAATGGATTGAGCACTTGATCAGGAGTCCGCTCCCTCGC
AGACCGATGTGGCCCTGATACGCTTCACAAACCCGATACCGGAAGAGTGTTGTTGAAGCTAACTTCATCGCTCC
GGTTACATCACAGTAGCCAACAGGGTTCCAGGCCAATCGTAGTTCGGGCAAACGGATACTTTGATTGACAGTTG
GGTCAATCAGTTCTACAGCCTGGCTCCAATGGGAACAGGAAATGGGAGGAGGCGTGTGCAGTAA

FIGURE 34G

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

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAPVPTGQNNIIDPWIRTNFBVQAPNGEFTVSPRNS
PGEILLNLELGPDLNLPYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPDPVRNFFHYNNQPNRMRMLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTPDFEFTYLVPP
SVESKTKPFSPLITLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLGELQGTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV

FIGURE 34G (cont)

PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFQWELPDYSGLLTNLMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34H

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

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGTGCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTTCGGACAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGTCTGAAGTGCAGGTCCTCCTGGCCGAAACGCCTTACCGCT
GGCAAAATTCTGTTTGGCGCCGTTCCACCAAACCTTTCCAGTCGAATTCCTCTCTCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAACTCTCGGATGAGACTTGTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTCACTGCCAATCTTAACTCT
CTCCGAAGTACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACCTTAAACGGGACCACCTACGACCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCGCCAATGGGAACCTACCAGATTATTCTGGGCTGCTCACCTCAATATGAACCTCGCCCCACCCGTG
GCCCCAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTACCAGGAAAGTGCGCCCTCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCGGGCT
CAGTAG

FIGURE 34I

Amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:194)

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWITNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPLYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLDVRNTFFHYNNQPNRMRMLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTDFEFTYLVP
SVESKTPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLGELQGTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV

FIGURE 34I (cont)

PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFQWELPDYSGLLTNLMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVPA
NGYFRFDSWVNQFYSLAPMGTGNRRRAQ

FIGURE 34J

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

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGGATTATCACAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGTCTGAAGTGCAGGTCCTCCTGGCCGAAACGCCTTTACCGCT
GGCAAAATTCTGTTTGGCGCCGTTCCACCAAATTTCCAGTCGAATTCCTCTCTCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAACTCTCGGATGAGACTTGTTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAAGTACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACCTTAAACGGGACCACCTACGACCAACCGACGACGTCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTGCGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTCCGCCAATGGGAACCTACCAGATTATTCTGGGCTGCTCACCTCAATATGAACCTCGCCCCACCCGTG
GCCCCAATTTCCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTACCAGGAAAGTGCGCCCTCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCGGGCT
CAGTAG

FIGURE 34K

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

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPYLLHLSRMNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLIV
DVRTLEPIMIPLPDVRNTEFFHYNQPNRMRVLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTDFEFTYLVPPS
VESKTKPFSPLITLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLGELQGTQLLPSGICAFRGRVTAET
DHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFVP

FIGURE 34K (cont)

KLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTNLMNLAPPVAPNFPGEQLLFFRSFV
PCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVPPA
NGYFRFDSWVNQFYSLAPMGTGNRRRAQ

FIGURE 34L

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

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAAT
ATTATAGACCTTGGATTTCGGACAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGCTGCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGTTCGAAGTGAGGTCCTCCTGGCCGAAACGCCTTACCGCT
GGCAAAATTCTGTTTGGCGCCGTTCCACCAAATTTCCAGTCGAATTCCTCTCTCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAACTCTCGGATGAGACTTGTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAAGTACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACCTTAAACGGGACCACCTACGACCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCGCCAATGGGAAGTACCAGATTATTCTGGGCTGCTCACCTCAATATGAACCTCGCCCCACCCGTG
GCCCCAATTTCCCCGGTGAGCAGCTGCTGTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTACCAGGAAAGTGCGCCCTCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

FIGURE 34M

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

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAPVPTGQNNIIDPWIIITNFVQAPNGEFTVSPRNS
PGEILLNLELGPDLNPLYLAHLSRMYNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLI
VDVRTLEPIMIPLDVRNTFFHYNNQPNRMRVLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTDFEFTYLVP
SVESKTPFSLPILTLSELTNSRFPVPIDSLFTAQNNVLQVQCQNGRCTLGELQGTQLLPSGICAFRGRVTAE
TDHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFV

FIGURE 34M (cont)

PKLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTNLMNLAPPVAPNFPGEQLLFFRSF
VPCSGGYNQIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVPA
NGYFRFDSWVNQFYSLAPMGTGNGRRRAQ

FIGURE 34N

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

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGTGCCAGTGACAGGGCAGAATAAT
ATTATAGACCCTTGATTATCACAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTGAGCTCGGCCCTGACCTCAATCCATATCTGGCTCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGTCTGAAGTGCAGGTCCTCCTGGCCGAAACGCCTTACCGCT
GGCAAAATTCTGTTTGGCGCCGTTCCACCAAATTTCCAGTCGAATTCCTCTCTCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTTCCATTATAACAATCAGCCAACTCTCGGATGAGACTTGTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAACCGTTTTCACTGCCAATCTTAACTCT
CTCCGAAGTACTAACAGCCGGTTTCCAGTACCCATAGATTCTCTTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCGTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACCTTAAACGGGACCACCTACGACCAACCGACGACGTCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTTCGCCAATGGGAACCTACCAGATTATTCTGGGCTGCTCACCTCAATATGAACCTCGCCCCACCCGTG
GCCCCAATTTCCCGGTGAGCAGCTGCTGTTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTACCAGGAAAGTGCGCCCTCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTTACTTTAG
GTTTCGATAGTTGGGTCAACCAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCGGGCT
CAGTAG

FIGURE 34O

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

MKMASNDAAPSNDGAAGLVPEGNNETLPLEPVAGAAIAAPVTGQNNIIDPWIRTNFVQAPNGEFTVSPRNS
PGEILLNLSLGPDLNPLYLLHLSRMNGYAGGVEVQVLLAGNAFTAGKILFAAVPPNFPVEFLSPAQITMLPHLIV
DVRTLEPIPIPLDVRNTEFFHYNQPNRMRMLVAMLYTPLRSNGSGDDVFTVSCRVLTRPTDFEFTYLVPPS
VESKTKPFSPLILTSELNTRFPVPIDSLFTAQNNVLQVQCQNGRCTLGELQGTQLLPSGICAFRGRVTAET
DHRDKWHMQLQNLNGTTYDPTDDVPAPLGTPDFKGVVFGVASQRNVGNDAPGSTRAHEAVISTYSPQFVP

FIGURE 34O (cont)

KLGSVNFRSNDNDFQLQPTKFTPVGINDDGDHPFRQWELPDYSGLLTNLMNLAPPVAPNFPGEQLLFFRSFV
PCSGGYNQGIVDCLIPQEWIQHFYQESAPSQSDVALIRYVNPDTGRTLFEAKLHRSGYITVAHSGDYPLVPA
NGYFRFDSWVNQFYSLAPMGTGNRRRAQ

FIGURE 34P

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

ATGAAAATGGCATCTAACGACGCAGCCCCCTCAAACGATGGCGCTGCTGGACTCGTGCCGGAGGGGAAT
AATGAGACACTTCCACTAGAGCCGGTTGCAGGCGCCGCTATAGCTGCCCCAGTGACAGGGCAGAATAAT
ATTATAGACCTTGGATTTCGGACAACTTCGTGCAGGCACCCAACGGCGAGTTTACAGTATCCCCCGGA
ACTCCCCAGGTGAGATACTCCTGAATCTTAGCCTCGGCCCTGACCTCAATCCATATCTGCTGCATCTGAGC
CGCATGTACAATGGTTACGCTGGGGGGTTCGAAGTGAGGTCCTCCTGGCCGGAAACGCCTTACCCT
GGCAAAATTCTGTTGCCGCCGTTCCACCAAACTTTCAGTCGAATTCCTCTCTCCCGCGCAAATAACCAT
GCTGCCACATTTGATCGTTGACGTGCGGACCCTGGAGCCAATAATGATTCCCCTGCCGGATGTGCGTAAC
ACCTTTTCCATTATAACAATCAGCCAACTCTCGGATGAGACTTGTGCTATGCTGTACACCCCCCTGCG
GAGCAACGGCAGTGGCGATGATGTGTTACCGTGAGTTGCAGAGTCCTGACGCGCCCAACCCCGGACTT
CGAGTTCACCTACCTGGTGCCCCCTTCTGTGGAATCTAAGACCAAAACCGTTTCACTGCCAATCTTAACTCT
CTCCGAACTGACTAACAGCCGTTTCCAGTACCCATAGATTCTCTTTTACCGCTCAAAACAACGTACTCC
AAGTCCAGTGCCAGAACGGCCGCTGTACGCTTGATGGTGAGTTGCAGGGGACAACACAGCTACTCCCCA
GTGGCATCTGTGCATTCCGGGGCCGCTGACCGCTGAGACAGACCATCGTGACAAATGGCACATGCAAC
TCCAAAACCTTAAACGGGACCACCTACGACCAACCGACGACGTCCCTGCTCCGCTAGGGACTCCTGACTT
TAAGGGGGTGGTGTTCGGAGTGGCCTCTCAGCGGAATGTTGGGAATGACGCCCCCGGCTCTACCCGAGC
TCACGAGGCCGTTATCTCAACATATAGCCCCCAATTTGTGCCAAGCTCGGATCCGTTAATTTTCGTAGTA
ACGACAACGACTTCCAACCTGCAACCAACGAAGTTTACGCCAGTGGGGATTAATGATGATGGAGACCATC
CTTCCGCCAATGGGAACTACCAGATTATTCTGGGCTGCTCACCTCAATATGAACCTCGCCCCACCCGTG
GCCCCAATTTCCCCGGTGAGCAGCTGCTGTTTTTCGGAGCTTTGTGCCATGCAGTGGCGGATATAATCA
AGGCATCGTAGACTGCTTGATTCCCCAAGAGTGGATACAACATTTTACCAGGAAAGTGCGCCCTCCAG
TCCGATGTGGCCCTGATACGGTACGTTAACCCCGATACCGGAAGAACATTATTCGAAGCGAAATTGCACA
GATCAGGGTACATTACCGTTGCACATTCCGGCGATTATCCCCTGGTGGTTCCCGCCAACGGTACTTTAG
GTTTCGATAGTTGGGTCAACCAAGTTCTATTCACTAGCCCCAATGGGCACCGGTAACGGCAGACGCCGGGCT
CAGTAG

Figure 35A

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

MAQAIIGAIAGTAGSALGAGIQVGGEAALQSQRYYQNLQLQENSFKHDREMIGYQVEASNQLLAKNLATRYSLRAGG
LTSADAARSVAGAPVTRIVDWNGVRVSAPESSATTLR5GGFMSVPIPFASKQKQVQSSGISNPNYSPSSISRTTSWVESQ
N5SRFGNLSPHYAEALNTVWLTTPPGSTASSTLSSVPRGYFNTDRLPLFANNRR

Figure 35B

Nucleic acid sequence of human codon optimized VP.2_GI1_Norwalk (SEQ ID NO:100)

ATGGCTCAGGCCATTATTGGCGCCATCGCTGCAAGTACAGCCGGGAGTGCATTGGGGGCCGGAATACAGGTGGGC
GGGGAAGCTGCATTGCAGAGCCAGCGGTACCAGCAAAACCTGCAGTTACAGGAGAATAGCTTTAAACACGACAGG
GAGATGATTGGATATCAGGTGGAGGCCAGCAATCAGCTGCTCGCCAAAACTTGGCTACTCGATACTCATTACTGCG
CGCCGGGGGTTGACTAGCGCCGACGCCGACGATCTGTGCGAGGCGCCCCGTGACTCGGATCGTAGACTGGAA
CGGGGTACGAGTCTCGGCTCCCGAGTCGCTGCAACCACCTGAGGTGCGGAGGGTTTATGTCCGTGCCCATCCCAT
TCGCTAGCAAACAGAAACAGGTCCAGAGCTCCGGAATCTCCAATCCCAATTACTCCCCTAGCTCTATCTCTCGTACCA
CTTCCTGGGTCGAGAGTCAGAACAGCAGTAGATTTGGCAACCTGAGCCCCCTACCATGCTGAAGCCCTGAACACTGTG
TGGTTGACTCCACCTGGTAGCAGGCCTCCTCAACCCTGAGTTCGGTGCTCGCGGGTACTTCAATACCGACAGACTT
CCTCTGTTGCTAACAACCGCCGCTGA

Figure 36A

Amino acid sequence of VP2_GI.3_Lil08 (SEQ ID NO:94)

MAQAIFGAIAATAAGSAVGAGIQAGTEAALQHQRQQDLTLQSNFKHDKEMLGQVGASTALLQNSLNTRYNMLTD
AGLSSDAARMVVGAPATRVVDWNGTRISAPRSTATTLRSGGFMTIPTLYKGKQQQKAPTEIGLSNPNYGSSVSSRVAD
WVSSQNSSHSLGPYHPYALQTTWVTPPGSSSTSISSVSTVPRYFNTDRLPLFANMRK

Figure 36B

Nucleic acid sequence of human codon optimized VP2_GI.3_Lil08 (SEQ ID NO:95)

ATGGCTCAGGCAATCTTCGGCGCAATCGCTGCCACTGCTGCCGGATCCGCTGTGGGAGCCGGCATAACAGGCCGGAA
CTGAGGCGGCCCTTCAGCATCAGCGTTCCAGCAGGATCTGACATTACAGAGTAACACATTCAAACATGACAAGGA
GATGCTGGGTCTGCAGGTGGGTGCCAGTACTGCCCTGCTCCAAAACTCTCTGAATACCAGATATAACATGTTAACTG
ATGCGGGACTGTCTAGTAGCGACGCAGCTCGCATGGTCGTGGGCGCCCCAGCTACGAGAGTTGTGGACTGGAATG
GCACCCGAATCAGTGCACCAAGGTCTACAGCCACTACCCTCAGAAGTGGCGGCTTATGACCATCCCGACTTTATAC
AAGGGCAAACAACAGCAGAAGGCACCTACTGAAATCGGTCTCTCCAATCCCAACTACGGCAGCAGTGTGTCTCTCG
CGTGGCCGATTGGGTCTCAAGCCAGAACTCCAGTCATAGTTCTCTTGGGCCCTTATCATCCATCAGCCTTCGACACAAC
TTGGGTCACCCACCCGGGTCCAGTAGCACGTCAACCATCAGTTCCGTCTCCACAGTCCCTCGCTATTTTAATACTGA
TAGGCTTCCCCTGTTTCGCAACATGAGGAAGTGA

Figure 37A

Amino acid sequence of VP2_GII6_HS10 (SEQ ID NO:96)

MASAFLAGLAGDVITNGVGSINAGANAVNQKVEYDFNKQLQMASFKHDKEMLSQVLATKQLQQEMMNIRQGVLT
AGGFSPADAARGAVNAPMTKILDWNGTRYWAPNSMKTTSSYGQFSSSPVHKSPAPSQHTALPKSRLQNDFAVSYSFVS
SVSSQSTHSTALSAGTGSRSISPTATPTLSRTSDWVRGQNERLSPFMDGALQTAFTPPSSKASSNGTVSTVPKAVLDS
WTPMFNTHRQPLFAHPRRRGESQV

Figure 37B

Nucleic acid sequence of human codon optimized VP2_Gli6_HS10 (SEQ ID NO:97)

ATGGCCTCCGCATTTCTAGCTGGATTGGCCGGGGACGTGATCACCAACGGCGTAGGATCGCTGATTAATGCAGGCG
CCAATGCTGTTAATCAGAAGGTTGAATACGACTTCAACAAACAAGTGCAGATGGCTTCATTCAAGCACGACAAAGAA
ATGTTGCAGTCACAGGTTCTCGCCACCAAGCAGCTACAACAGGAGATGATGAACATTCGGCAGGGCGTACTGACCG
CTGGAGGATTCAGCCCTGCTGACGCAGCACGGGGGGCCGTGAACGCGCCGATGACCAAGATCCTGGATTGGAACG
GAACTCGGTATTGGGCTCCCAACTCTATGAAAACCACTTCTTACTCTGGTCAGTTCTCCAGCTCGCCAGTCCACAAAA
GTCCGGCCCCCTTACAGCACACAGCACTCCCTAAGTCCAGGCTGCAAAACGACTTTGCCTCCGTGTACTCCTTCCCAT
CCAGCGTGTCTCTCAGAGCACTATTCAACCGCCCTGTCCGCCGGAAGTGGGTCTAGCCGCAGCATTTCCCCAAGC
ACAGCTACTCCAACCTCTGAGCAGGACTAGCGATTGGGTCTAGAGGACAAAAACGAACGACTGTCCCTTTTCTGAGCG
GAGCTCTGCAAAACCGCCTTCGTCACTCCACCTAGCAGCAAGGCCTCGAGCAACGGTACGGTTAGTACCGTGCCAAAG
GCTGTTCTTGACAGCTGGACCCCCATGTTTAACACACACAGGCAGCCATTGTTTGACACCCCCAGGCGACGGGGAGA
ATCACAAGTTTAG

Figure 38A

Cloning vector 1190 from left to right T-DNA (SEQ ID NO:162)

TGGCAGGATATATTGTGGTGTAACAAATTGACGCTTAGACAACCTTAATAACACATTGCGGACGTTTTTAATGTACT
GAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTCAAAAACCATAAAAGTTTAAGTTAGCA
AGTGTGTACATTTTTACTTGAACAAAAATATTCACCTACTACTGTTATAAATCATTATTAACATTAGAGTAAAGAAAT
ATGGATGATAAGAACAAGAGTAGTGATATTTTGACAACAATTTGTTGCAACATTTGAGAAAATTTGTTGTTCTCTC
TTTTATTGGTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGAGA
AAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGCTACACAAATAAGGGT
TAATTGCTGTAAATAAATAAGGATGACGCATTAGAGAGATGTACCATTAGAGAATTTTGGCAAGTCATTAAAAAGA
AAGAATAAATTATTTTTAAAATTAAGTTGAGTCATTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGT
TGGATTAAAGTTGTATTAGTAATTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCTATATATTGCCCCA
TAGAGTCAGTTAACTCATTTTTATATTTATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCCAAAAA
AAACGGTATATTTACTAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCCGTAGGAGGATAACATCCAATCC
AACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCCACGCATCTGTGGCACATCTACATTATCTAATCAC
ACATTTCTCCACACATCTGAGCCACACAAAAACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTG
AGTCTACACTTTGATTCCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATG
GAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCAGGAGGTACC
ACTTCTCCCTTCAAACCTTCTGACGAAAGTCCGAGTTGGACTGAGTGCGGCTACATAACGATGAGACGAATTCGAA
TCAAGATAATCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTATTTAAGAGATATCTCAGATACGACA
GGACGGAAGCTTCACTGCACAGAGTCCTTGGATCTTGGACGGGAGATTCCGGTTAACTATGCAGCATCTCGATTTTT
GGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAAC
TCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAAGTCTACAGCTTGCCCCAATCGAAGTGGAAGTA
ATGTATCAAGAGGATGCCCTGAAGGTACTCAAACCTTCGAAAAAGAAAGCGAGTAAGTTAAATGCTTCTTCGTCTC
CTATTTATAATATGGTTTGTTATTGTTAATTTGTTCTGTAGAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTAT
TTGTATGAGATGAACTGGTGTAAATGTAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCTCCATAACTAAC
TAGACATGAAGACCTGCCGCTACAATTGTCTTATATTTGAACAATAAAATTGAACATCTTTGCCACAACCTTTATA
AGTGGTTAATATAGCTCAAATATATGGTCAAGTTCAATAGATTAATAATGGAAATATCAGTTATCGAAATTCATTAAC
AATCAACTTAACGTTATTAATACTACTAATTTTATATCATCCCTTTGATAAATGATAGTACACCAATTAGGAAGGAGCAT
GCTCGCTAGGAGATTGTCGTTTCCGCTTCAGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAACCGCCTC

FIGURE 38A (cont)

TCCCCGCGCGTTGGGAATTACTAGCGCGTGTGACAAAGCTTGCATGCCGGTCAACATGGTGGAGCACGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATC
CGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCT
ACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACC
CCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAAC
ATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGA
CTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAG
TGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAG
CAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCCTCCTCT
ATATAAGGAAGTTCATTTTATTTGGAGAGGTATTTAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCC
GAACCAAACCTTCTTCTAACTCTCTCTCATCTCTTAAAGCAAACCTTCTCTTGTCTTTCTTGCCTGAGCGATCTTC
AACGTTGTGAGATCGTGCTTCGGCACC CGCGATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTTCTTGT
GTTGGTTCTTCTCAGATCTTCGCTGCAGGCTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCTG
GATCTGCTGCCCAAATACTCCATGGTGACCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTG
ACCTGGAATCTGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTGCAGTCTGACCTCTACACTCTGAGC
AGCTCAGTGACTGTCCCTCCAGCACCTGGCCAGCGAGACCGTCACCTGCAACGTTGCCACCCGGCCAGCAGCAC
CAAGGTGGACAAGAAAATTGTGCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCAGAAAGTATCATCTG
TCTTCATCTTCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCAGTGTGTTGTGGTAGACA
TCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGATAGATGATGTGGAGGTGCACACAGCTCAGACGCAACC
CCGGGAGGAGCAGTTCAACAGCACTTCCGCTCAGTCAGTGAACCTCCCATCATGCACCAGGACTGGCTCAATGGCA
AGGAGCGATCGCTCACCATCACCATCACCATCACCATTAAAGGCCTATTTCTTTAGTTTGAATTTACTGTTA
TTCGGTGTGCATTTCTATGTTTGGTGAGCGTTTTCTGTGCTCAGAGTGTGTTTATTTATGTAATTTAATTTCTTGT
GAGCTCCTGTTTAGCAGGTCGTCCCTCAGCAAGGACACAAAAAGATTTTAAATTTATTAATAAAAAAAAAAAAAAAAAA
GACCGGGAATTCGATATCAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATC
CTGTTGCCGGTCTTGCAGTATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCAT
GACGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATA
GCGCGCAAACCTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCTCTAGAGTCTCAAGCTTGGCGCGC
CCAGTGACTAGTGGCACTGGCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCCAACCTTAATCGC
CTTGACGACATCCCCCTTCGCCAGCTGGCGTAATAGCGAAGAGGGCCCGCACCGATCGCCCTTCCCAACAGTTGCG
CAGCCTGAATGGCAATGCTAGAGCAGCTTGAGCTTGGATCAGATTGTGTTTCCCGCCTTCAAGTTAACTATCAG
TGTTTGACAGGATATATTGGCGGGTAAACCTAAGAGAAAAGAGCGTTTA

Figure 38B

Construct 2724 from 2X35S promoter to NOS terminator (SEQ ID NO:163)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAA
TTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTC
TGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGT
CTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAG
CTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAG
GCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAG
AAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCC

FIGURE 38B (cont)

CACTATCCTTCGCAAGACCCCTTCTCTATATAAGGAAGTTCATTTTCATTTGGAGAGGTATTTAAATCTTAATAGGTTTT
 GATAAAAGCGAACGTGGGGAACCCGAACCAACCTTCTTCTAAACTCTCTCTCATCTCTCTTAAAGCAAACCTTCTCT
 CTTGTCTTTCTTGCCTGAGCGATCTTCAACGTTGTGAGATCGTGCTTCGGCACCAGTACAATGATGATGGCTAGTAAA
 GATGCGACCTCCTCTGTGGATGGTGCGTCAGGGGCGAGGACAACCTCGTACCCGAGGTAAACGCCAGCGACCCCACTTG
 CCATGGACCCCGTTGCCGGAAGTTCCACAGCAGTGGCCACAGCCGGTCAAGTGAATCCAATTGATCCGTGGATTATC
 AACAATTTCTGTCAGGCACCCAGGGCGAGTTCACAATTTACCAAACAATAACCCGGGCGATGTGCTATTCGATCT
 TTCCTTGGGTCCTCACCTTAACCTTTTCTACTCCATCTCTACAGATGTACAATGGTTGGGTAGGAAACATGAGAGT
 CCGGATCATGCTGGCTGGCAATGCCTTTACCGCTGGCAAGATCATCGTCAGTTGTATTCTCCCGGATTGGATCTCA
 TAATCTGACCATTGCTCAAGCGACTCTCTTCCCATGTGTCGCGGACGTTAGGACCCTGGACCCCATCGAGGTGCC
 CCTGGAGGACGTCGGAATGTTTTGTTCCACAACAACGACAGAAACCAGCAGACGATGAGACTTGTCTGTATGCTCT
 ATACCCCACTGCGGACTGGAGGCGGGACTGGAGACTCCTTCGTTGTGGCAGGAAGAGTGATGACATGCCCTCCCC
 CGACTTCAACTTTCTTTTTCTGGTCCCAACCAACCGTTGAGCAGAAGACGCGGCCCTTACACTGCCCAATCTCCCGCTT
 TCAAGTCTGAGTAATTCACGGGCCCCATTGCCGATCTCCTCAATGGGAATCTCCCCGACAACGTCCAAGTCTGTCCAA
 TTCCAAAATGGGAGATGCACACTGGACGGTGCCTGGTGGGAACAACCTCCGGTGTCCCTCTCACATGTCGCCAAAAT
 CCGCGGCACATCAAATGGTACCCTAATCAATCTGACAGAACTTGATGGCACGCCCTTCCATCCCTTTGAAGGACCAG
 CCCCTATTGGATTCTCTGATCTGGGAGGTTGCGACTGGCACATAAACATGACACAGTTTGGCCACTCCAGCCAGACA
 CAGTATGATGTCGATAACAACCCAGATACCTTCGTGCCACACCTGGGATCTATTCAAGCTAACGGTATTGGATCCGG
 CAACTACGTGGGAGTCTTATCTTGGATCTCACCACCATCCACCCCTCAGGATCCAGGTTGACTTGTGGAGATACC
 GAATTATGGATCCTCGATCACTGAAGCCACGCACCTCGACCTTCCGTCTACCCACCAGGTTTTGGAGAAGTCTTGGT
 GTTTTTCATGAGCAAAATGCCCGGCCCTGGAGCCTACAATCTCCCTGCTACTCCCTCAAGAGTATATTAGTCACCT
 CGCATCTGAGCAGGCCCCGACCGTTGGCGAGGCGCCCTGCTGCATTATGTGGATCCGGACACCGGCAGGAACCTG
 GGTGAGTTCAAAGCTTATCTGACGGTTTTCTAACATGTGTACCAATGGCGCTTCCAGCGGCCCTCAACAGCTCCCA
 ATCAATGGCGTGTTCGTTTTGTGAGCTGGTAAGCCGCTTCTACCAGCTGAAGCCCGTGGGGACAGCTTCTTCTGC
 CCGCGGACGCTCGGTCTGCGGAGATAAAGGCCTATTTCTTTAGTTTGAATTTACTGTTATTCGGTGTGCATTTCTA
 TGTTCGGTGAGCGTTTTCTGTGCTCAGAGTGTGTTATTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTTAGCAG
 GTCGTCCTTTCAGCAAGGACACAAAAAGATTTTAAATTTATTAATAAAAAAAAAAAAAAAAAAGACCGGGAATTCGATAT
 CAAGCTTATCGACCTGCAGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCG
 ATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTATGAGAT
 GGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACTAGGAT
 AAATTATCGCGCGCGGTGTCATCTATGTTACTAGAT

Figure 38C

Cloning vector 3677 from left to right T-DNA (SEQ ID NO:164)

TGGCAGGATATATTGTGGTGTAACAAATTGACGCTTAGACAACCTTAATAACACATTGCGGACGTTTTTAATGTACT
 GAATTAACGCCGAATCCCGGGCTGGTATATTTATATGTTGTCAAATAACTCAAAAACCATAAAAGTTTAAGTTAGCA
 AGTGTGTACATTTTACTTGAACAAAAATATTCACCTACTACTGTTATAAATCATTATTAACATTAGAGTAAAGAAAT
 ATGGATGATAAGAACAAGAGTAGTGATTTTTGACAACAATTTTGTGCAACATTTGAGAAAAATTTGTTGTTCTCTC
 TTTTCATTGGTCAAAAACAATAGAGAGAGAAAAAGGAAGAGGGAGAATAAAAACATAATGTGAGTATGAGAGAGA
 AAGTTGTACAAAAGTTGTACCAAAATAGTTGTACAAATATCATTGAGGAATTTGACAAAAGCTACACAAATAAGGGT
 TAATTGCTGTAATAAATAAGGATGACGCATTAGAGAGATGTACCATTAGAGAATTTTGGCAAGTCATTAAAAAGA
 AAGAATAAATTATTTTAAAAATTAAGTTGAGTCATTTGATTAAACATGTGATTATTTAATGAATTGATGAAAGAGT
 TGGATTAAAGTTGATTAGTAATTAGAATTTGGTGTCAAATTTAATTTGACATTTGATCTTTTCTATATATTGCCCA
 TAGAGTCAGTTAACTCATTTTTATATTTATAGATCAAATAAGAGAAATAACGGTATATTAATCCCTCAAAAAAAAAA
 AACGGTATATTTACTAAAAATCTAAGCCACGTAGGAGGATAACAGGATCCCGTAGGAGGATAACATCCAATCC
 AACCAATCACAACAATCCTGATGAGATAACCCACTTTAAGCCACGCATCTGTGGCACATCTACATTATCTAAATCAC
 ACATTTCTCCACACATCTGAGCCACACAAAAACCAATCCACATCTTTATCACCCATTCTATAAAAAATCACACTTTGTG
 AGTCTACACTTTGATTCCCTTCAAACACATACAAAGAGAAGAGACTAATTAATTAATTAATCATCTTGAGAGAAAATG
 GAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCAGGAGGTACC

FIGURE 38C (cont)

ACTTCTCCCTTCAAACCTTCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTACATAACGATGAGACGAATTCGAA
TCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTATTTAAGAGATATCTCAGATACGACA
GGACGGAAGCTTCACTGCACAGAGTCTTGGATCTTGGACGGGAGATTGCGTTAACTATGCAGCATCTCGATTTTTC
GGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAAC
TCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCAATCGAAGTGGAAGTA
ATGTATCAAGAGGATGCCCTGAAGGTAACAACCTTCGAAAAAGAAAGCGAGTAAGTTAAATGCTTCTTCGTCTC
CTATTTATAATATGGTTTGTATTGTTAATTTGTTCTGTAGAAAGAGCTTAATTAATCGTTGTTGTTATGAAATACTAT
TTGTATGAGATGAACCTGGTGAATGTAATTCATTTACATAAGTGGAGTCAGAATCAGAATGTTTCTCCATAACTAAC
TAGACATGAAGACCTGCCGCGTACAATTGTCTTATATTTGAACAACTAAAATTGAACATCTTTTGCCACAACCTTTATA
AGTGGTTAATATAGCTCAAAATATATGGTCAAGTCAATAGATTAATAATGGAAATATCAGTTATCGAAATTCATTAAC
AATCAACTTAACGTTATTAACCTACTAATTTTATATCATCCCTTTGATAAATGATAGTACACCAATTAGGAAGGAGCAT
GCTCGCTAGGAGATTGTGCTTTCCCGCTTCAGTTTGCAAGCTGCTCTAGCCGTGTAGCCAATACGCAAACCGCCTC
TCCCCGCGCGTTGGGAATTACTAGCGCGTGTGACAAGCTTGCATGCCGTCACATGGTGGAGCAGACACACTT
GTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATC
CGGAAACCTCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCT
ACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACC
CCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATAAC
ATGGTGGAGCAGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGA
CTTTTCAACAAAGGGTAATATCCGGAAACCTCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAG
TGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGA
CAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCTTCAAAG
CAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCTTCCTCT
ATATAAGGAAGTTCATTTCAATTTGGAGAGGTATTTAAATCTTAATAGGTTTTGATAAAAGCGAACGTGGGGAAACCC
GAACCAAACCTTCTTCTAACTCTCTCATCTCTTAAAGCAAACCTTCTCTTGTCTTTCTTGGTGAGCGATCTTC
AACGTTGTGAGATCGTGCTTCGGCACCGCGGATGGCGAAAAACGTTGCGATTTTCGGCTTATTGTTTTCTTCTTGT
GTTGGTTCTTCTCAGATCTTCGCCTGCAGGCTCCTCAGCCAAAACGACACCCCCATCTGTCTATCCACTGGCCCTG
GATCTGCTGCCAAACTAACTCCATGGTGACCTGGGATGCCTGGTCAAGGGCTATTTCCCTGAGCCAGTGACAGTG
ACCTGGAACCTCGGATCCCTGTCCAGCGGTGTGCACACCTTCCAGCTGTCTGCAGTCTGACCTCTACACTCTGAGC
AGCTCAGTGACTGTCCCCTCCAGCACCTGGCCAGCGAGACCGTCACCTGCAACGTTGCCACCCGGCCAGCAGCAC
CAAGGTGGACAAGAAAATTGTGCCAGGGATTGTGGTTGTAAGCCTTGCATATGTACAGTCCCAGAAGTATCATCTG
TCTTCATCTTCCCCCAAAGCCCAAGGATGTGCTCACCATTACTCTGACTCCTAAGGTCACGTGTGTTGTGGTAGACA
TCAGCAAGGATGATCCCGAGGTCCAGTTCAGCTGGTTTGTAGATGATGTGGAGGTGCACACAGCTCAGACGCAACC
CCGGGAGGAGCAGTTCAACAGCACTTTCGCTCAGTCAGTGAACCTCCCATCATGCACCAGGACTGGCTCAATGGCA
AGGAGCGATCGCTCACCATCACCATCACCATCACCATTAAAGGCCTATTTCTTTAGTTTGAATTTACTGTTA
TTCGGTGTGCAATTTCTATGTTTGGTGAGCGTTTTCTGTGCTCAGAGTGTGTTATTTTATGTAATTTAATTTCTTTGT
GAGCTCCTGTTTAGCAGGTGTCCTTCAGCAAGGACACAAAAAGATTTAATTTTATTATCGTTCAAACATTTGGCA
ATAAAGTTTCTTAAGATTGAATCCTGTTGCCGCTCTTGCATGATTATCATATAATTTCTGTTGAATTACGTTAAGCAT
GTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTATGATTAGAGTCCCGCAATTATACATTTAA
TACGCGATAGAAAACAAATATAGCGCGCAAACCTAGGATAAATTATCGCGCGGTGTCATCTATGTTACTAGATCT
CTAGGTAATAATCCCAATTATATTTGGTCTAATTTAGTTTGGTATTGAGTAAACAAATTCGAACCAACCAAAATAT
AAATATATAGTTTTATATATATGCCTTAAAGACTTTTTATAGAATTTTCTTTAAAAAATATCTAGAAATATTTGCGACT
CTTCTGGCATGTAATATTTTCGTTAAATATGAAGTGCTCCATTTTTATTAACCTTAAATAATTGGTTGTACGATCACTTC
TTATCAAGTGTTACTAAAATGCGTCAATCTCTTGTCTTCCATATTCATATGTCAAAATCTATCAAAATCTTATATAT
CTTTTTCGAATTTGAAGTGAAATTTGATAATTTAAATTAAGATATCATATTTAGGTATCATATTGATTTTT
ATACTTAATTACTAAATTTGGTTAACTTTGAAAGTGTACATCAACGAAAAATTAGTCAAACGACTAAAATAAATAAT
ATCATGTGTTATTAAGAAAATTTCTCTATAAGAATATTTAATAGATCATATGTTTGTAAAAAAATTAATTTTTACTA
ACACATATATTTACTTATCAAAAATTTGACAAAGTAAGATTAATAATATTCATCTAACAAAAAACCAGAAAA
TGCTGAAAACCCGGCAAAACCGAACCAATCCAAACCGATATAGTTGGTTTGGTTTGATTTTGATATAACCGAACCA
ACTCGGTCCATTTGCACCCCTAATCATAATAGCTTTAATTTCAAGATATTATTAAGTTAACGTTGTCAATATCCTGG
AAATTTTGCAAAATGAATCAAGCCTATATGGCTGTAATATGAATTTAAAGCAGCTCGATGTGGTGGTAATATGTAA

FIGURE 38C (cont)

TTTACTTGATTCTAAAAAATATCCCAAGTATTAATAATTTCTGCTAGGAAGAAGGTTAGCTACGATTTACAGCAAAG
CCAGAATACAAAGAACCATAAAGTGATTGAAGCTCGAAATATACGAAGGAACAAATATTTTTAAAAAATACGCAAT
GACTTGGAAACAAAAGAAAGTGATATATTTTTGTTCTTAAACAAGCATCCCTCTAAAGAATGGCAGTTTTCTTTGC
ATGTAACATTATGCTCCCTTCTTACAAAAATTTGGACTACTATTGGGAACTTCTTCTGAAAATTCTAGAGTCTCAA
GCTTGGCGCGCCACGTGACTAGTGGCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGCGTTACCC
AACTTAATCGCCTTGACGACATCCCCCTTTCGCCAGCTGGCGTAATAGCGAAGAGGCCCGACCGATCGCCCTCCC
AACAGTTGCGCAGCCTGAATGGCGAATGCTAGAGCAGCTTGAGCTTGGATCAGATTGTCGTTTCCGCTTCAGTTT
AAACTATCAGTGTTTGACAGGATATATTGGCGGGTAAACCTAAGAGAAAAGAGCGTTTA

Figure 38D

Construct 4133 from 2X355 promoter to NOS terminator (SEQ ID NO:165)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAA
TTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAAGGCCATCGTTGAAGATGCCTC
TGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACCACGTCT
TCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGT
CTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAG
CTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAAG
GCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAG
AAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCC
CACTATCCTTCGCAAGACCTTCTCTATATAAGGAAGTTCATTTCAATTGGAGAGGTATTTAAATCTTAATAGGTTTT
GATAAAAGCGAACGTGGGGAAACCCGAACCAACCTTCTTCTAACTCTCTCTCATCTCTTAAAGCAAACCTTCTCT
CTTGCTTTTCTGCGTGAGCGATCTTCAACGTTGTCAGATCGTGCTTCGGCACCAGTACAATGAAAATGGCCTCGAGT
GACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTCCTGAGGTTAATAATGAGGTGATGGCCTGGAGCCTG
TGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCGTGGATAACGCAACAATTTGT
CCAAGCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTGGCCAGCTTGGGA
CCCGATCTGAACCCCTATTTGTACATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTGAAAGTGCAGGTGAT
TCTGGCTGGGAACGCGTTCACTGCTGGCAAAGTGATCTTGCAGCGGTGCTCCCACTTCCCACTGAAGGACTGT
CTCCAAGCCAGGTACAATGTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCTGATTCCCCTCCCT
GATGTACGCAATAATTTCTACCACTACAATCAATCAATGATCCGACCATTAACCTCATCGGATGTTGTACACCCCTC
TGCGCGCTAACAAATGCTGGAGACGACGTATTCACCGTGCATGCAGAGTGCTCACCAGACCTTACCAGACTTTGAC
TTTATCTTCTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTGTGTCCTGCTACTCAGAGTGCAGGAGATG
ACAAATAGCCGCTTCCAATCCCCCTTGAGAACTGTTACAGGACCTTCTCGGCATTGCTGGTTACGCCACAGAAC
GGACGCTGCACAACTGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGA
CGTAACCTACATAACTGGCTCACGGAACATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCCAACCG
AAGAGATTCGCGACCTCTTGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCTGACACAAACCACCAGAACCC
GATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAACTGGGTAGAGTGC
AGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTCAGGA
CGGGGGCACCCTCACCAGAACGAGCCGCAACAATGGGTCTGCCCTCTATAGCGGGAGGAATACTCATAATGTG
CATTTGGCTCCTGCAGTGGCTCCACGTTTCCGGGGAACAACCTGCTTTTTTCTGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGCAGTATTTTTATCAAGAGGCCCGACCCAGC
CCAATCCGACGTGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGAGTGCAAATTCACAAAT
CAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCCAACCGGATATTTAGGTTGCACTCC
TGGGTGAATCAGTTTTATACATTAGCCCCCATGGGGAATGGGACTGGCAGACGAGGGCTGTCTGAAGGCCTATTT
TCTTTAGTTTGAATTTACTGTTATTCGGTGTGCTTTCTATGTTTGGTGAGCGTTTTCTGTGCTCAGAGTGTGTTTAT
TTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTAGCAGGTCTGCCCTCAGCAAGGACACAAAAAGATTTAATTTT
ATTATCGTTCAAACATTTGGCAATAAAGTTTCTAAGATTGAATCCTGTTGCCGCTTGGCGATGATTATCATATAATT
TCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTATGATTAG

FIGURE 38D (cont)

AGTCCCGAATTATACATTTAATACGCGATAGAAAACAAATATAGCGCGCAAAGTAGGATAAATTATCGCGCGCGG
TGTCATCTATGTTACTAGAT

Figure 38E

Construct 4135 from 2X35S promoter to NOS terminator (SEQ ID NO:166)

GTCAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAA
TTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGA
AGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTC
TGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAGAAGACGTTCCAACACGTCT
TCAAAGCAAGTGGATTGATGTGATAACATGGTGGAGCACGACACACTTGTCTACTCCAAAAATATCAAAGATACAGT
CTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGAAACCTCCTCGGATTCCATTGCCAG
CTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCTACAAATGCCATCATTGCGATAAAGGAAAG
GCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGATGGACCCCCACCCACGAGGAGCATCGTGGAAAAAG
AAGACGTTCCAACACGTCTTCAAAGCAAGTGGATTGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCC
CACTATCCTTCGCAAGACCTTCTCTATATAAGGAAGTTCATTTCAATTTGGAGAGGTATTTAAATCTTAATAGGTTTT
GATAAAGCGAACGTGGGGAAACCCGAACCAAACCTTCTTCTAACTCTCTCTCATCTCTCTTAAAGCAAACCTTCTCT
CTTGCTTTTCTTGCGTGAGCGATCTTCAACGTTGTGATCGTGCTTCCGACCAAGTACAATGAAAATGGCCCTCGAGT
GACGCTAACCTAGTGACGGCAGCGCCGCAATCTTGTGCCTGAGGTTAATAATGAGGTGATGGCCCTGGAGCCTG
TGGTGGGCGCAGCCATAGCAGCGCCCGTGGCCGGTCAGCAGAATGTGATTGACCCGTGGATACGCAACAATTTTGT
CCAAGCCCCCTGGTGGGGAGTTCACCGTTAGCCCGAGAAATGCGCCAGGAGAAATCCTGTGGTGGGCCAGCTTGGGA
CCCGATCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTACAACGGGTATGCCGGCGGATTTGAAGTGCAGGTGAT
TCTGGCTGGGAACGCGTTCCTGCTGGCAAAGTGATCTTTGACGCGGTGCCTCCCACTTCCCACTGAAGGACTGT
CTCCAAGCCAGGTACAATGTTTCCACACATCGTGGTGGACGTACGGCAGCTAGAGCCTGTCTGATTCCCCTCCCT
GATGTACGCAATAATTTCTACCACTACAATCAATCAATGATCCGACCATTAACCTCATCGCGATGTTGTACACCCCTC
TGCGCGCTAACCAATGCTGGAGACGACGTATTCACCGTGTATGCAGAGTGCTCACCAGACCTTCACCAGACTTTGAC
TTTATCTTCTAGTGCCCCCACTGTTGAGAGCCGAACCAAGCCCTTTAGTGTCCCGTACTCACAGTCGAGGAGATG
ACAAATAGCCGCTTTCGAATCCCCCTTGAGAACTGTTTACAGGACCTTCTCGGCATTCTGTTGTTGACGCCACAGA
GGACGCTGCACAACGACGGCGTGCTGCTCGGAACCAACCCAGCTTAGCCCTGTTAATATCTGTACGTTTAGAGGCGA
CGTAACCTACATAACTGGCTCACGGAACCTATACCATGAATCTGGCATCACAGAATTGGAATGACTACGACCCAACCG
AAGAGATTCGCGACCTCTTGAACCCCCGACTTTGTGGGAAAAATACAGGGCGTCTGACACAAACCACAGAAC
GATGGCTCCACACGGGGACACAAGGCAACCGTCTACACTGGCTCTGCCGATTTTGCCCCGAACTGGGTAGAGTGC
AGTTTGAGACCGACACTGACCGGGACTTTGAAGCCAATCAGAATACTAAGTTCACACCTGTAGGAGTGATTGAGGA
CGGGGGCACCCTCACCGGAACGAGCCGCAACAATGGTCTGCTCTTATAGCGGGAGGAATACTCATAATGTG
CATTTGGCTCCTGCAGTGGCTCCACGTTTCCCGGGGAACAACGCTCTTTTTCGTTCAACCATGCCTGGATGCTCC
GGATATCCCAATATGGATCTCGATTGCTGCTCCACAGGAATGGGTGACGATTTTTATCAAGAGGCCGACCCAGC
CCAATCCGACGTCGCACTTCTGCGGTTCTGTAATCCAGACACAGGCCGCGTGTGTTGAGTGCAAATTCACAAAT
CAGGATACGTTACAGTGGCTCATACTGGACAGCATGACCTGGTGATCCACCCAACGGATATTTAGGTTGCACTCC
TGGGTGAATCAGTTTTATACATTAGCCCCATGGGGAATGGGACTGGCAGACGAGGGCTGTCTGAAGGCCTATTT
TCTTTAGTTTGAATTTACTGTTATTCGGTGTGATTTCTATGTTTGGTGAGCGTTTTCTGTGCTCAGAGTGTGTTTAT
TTTATGTAATTTAATTTCTTTGTGAGCTCCTGTTAGCAGTCTGCTCCCTCAGCAAGGACACAAAAAGATTTAATTTT
ATTATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCATATAATT
TCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTATGATTAG
AGTCCCGAATTATACATTTAATACGCGATAGAAAACAAATATAGCGCGCAAAGTAGGATAAATTATCGCGCGCGG
TGTCATCTATGTTACTAGAT

Figure 39C

Construct 3979 (Wt Gl.3 hCod)

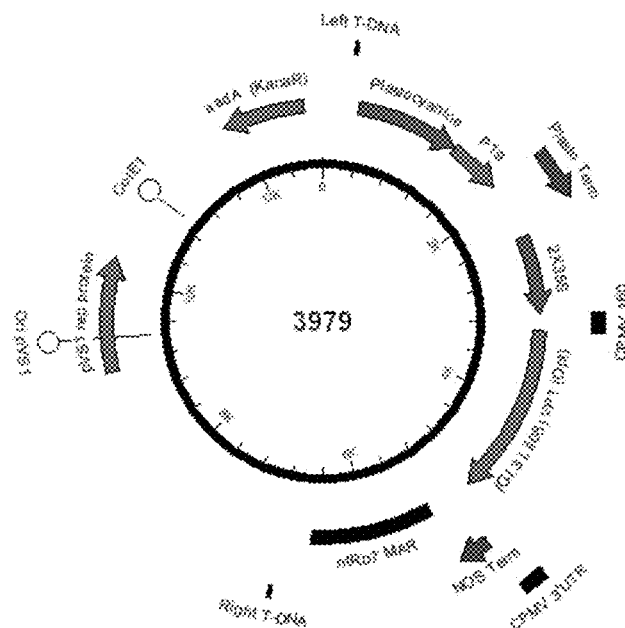


Figure 40A

Construct 4140 (VP1 GL3_Q84S hCod)

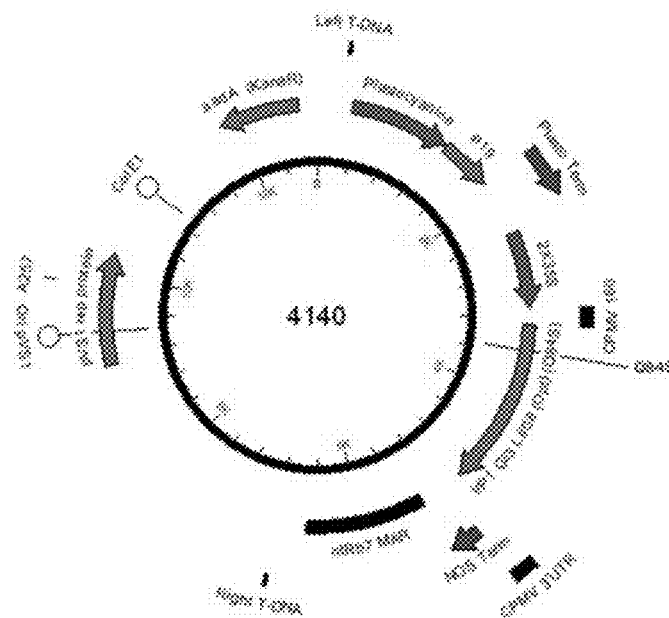


Figure 41D

Construct 4132 (VP1 Gl.5 Q84S+A94L hCod)

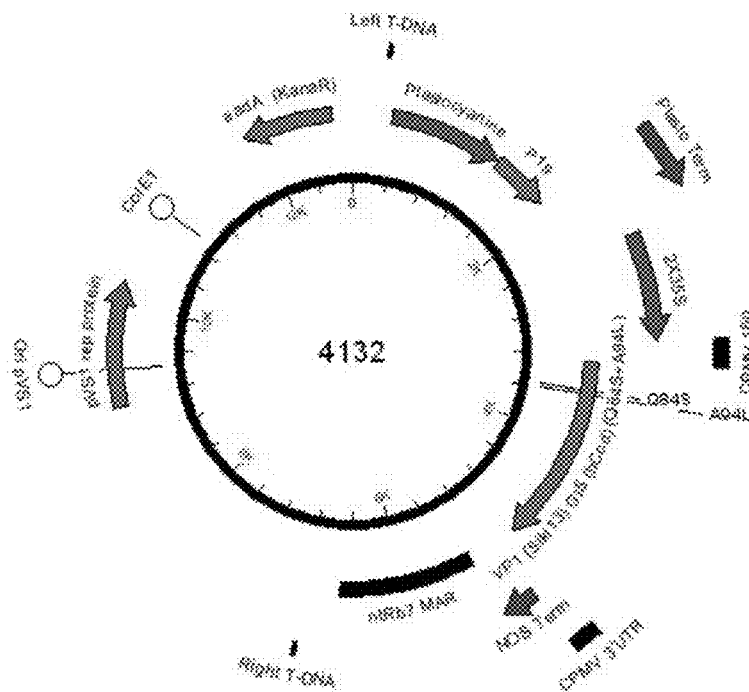


FIGURE 41E

Construct 4210 (VP1 Gl.7_R84S hCod)

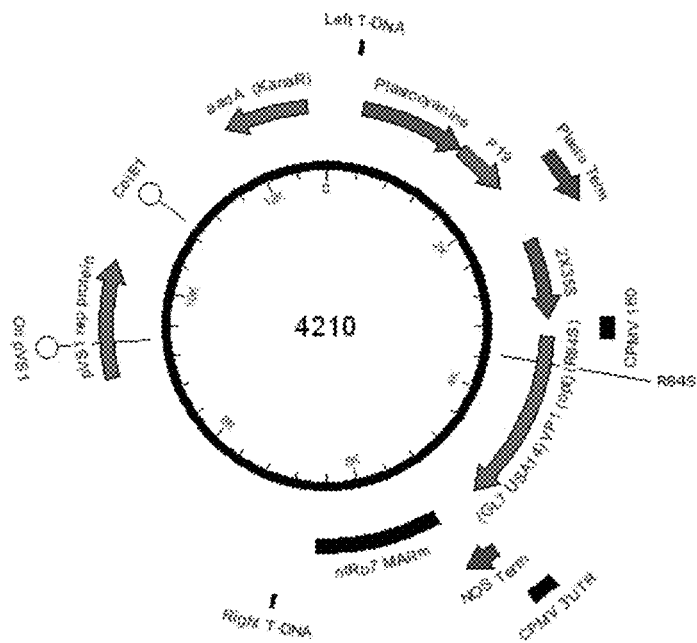


Figure 43B

Construct 4146 (VP1 GII.3_E80S hCod)

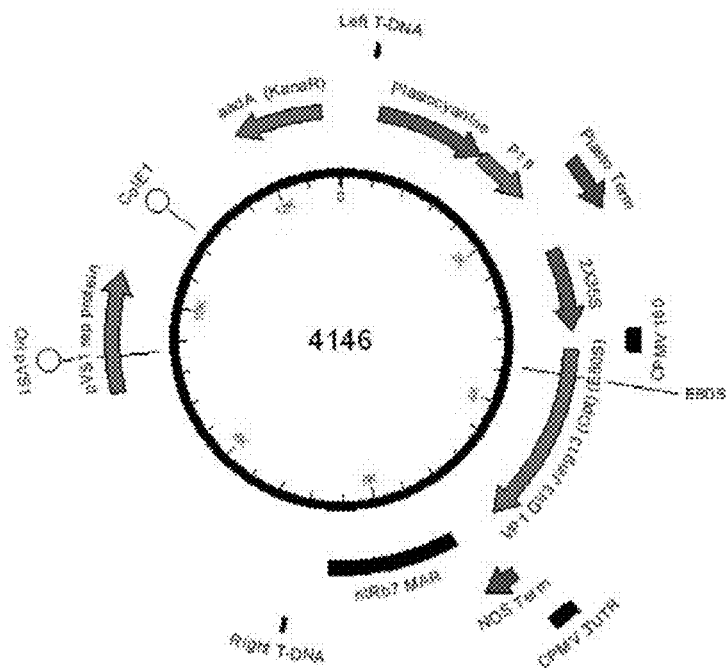


Figure 43C

Construct 4147 (VP1 GII.3_A90L hCod)

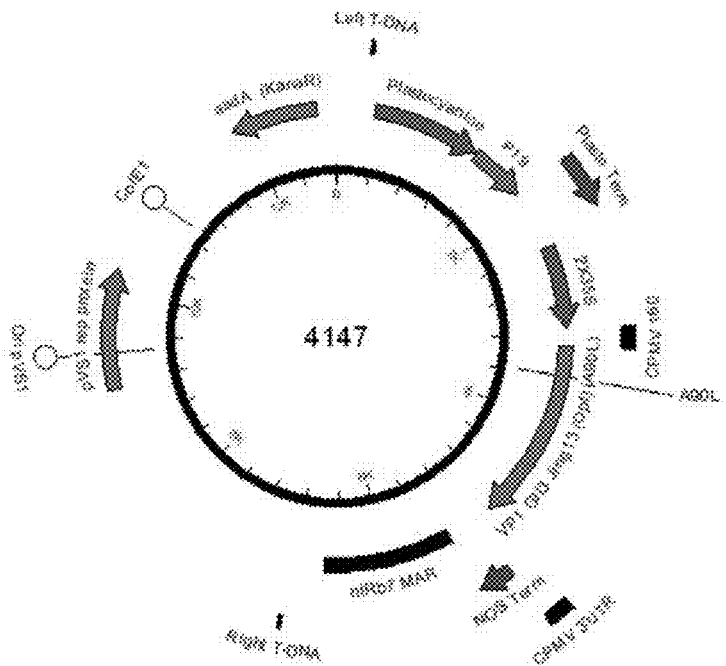


Figure 43D

Construct 4148 (VP1 GII.3_E80S+A90L)

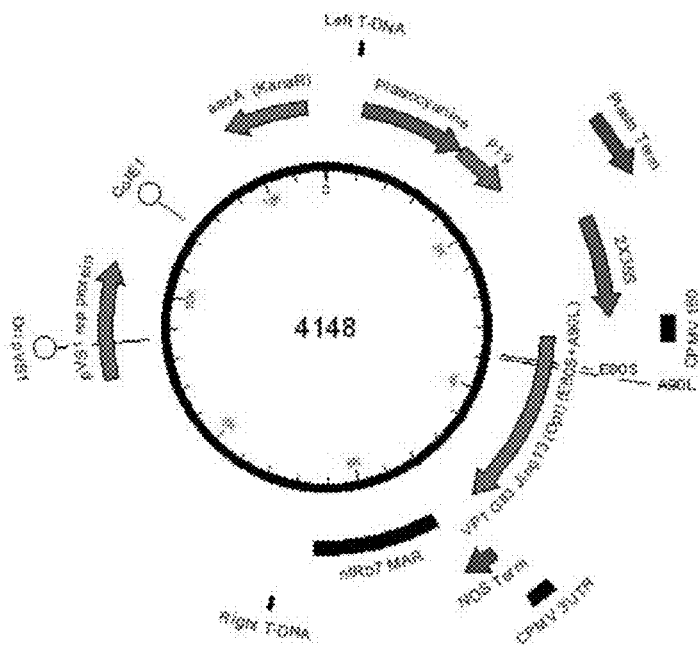


Figure 44A

Construct 3760 (Wt VP1 GII.4 hCod)

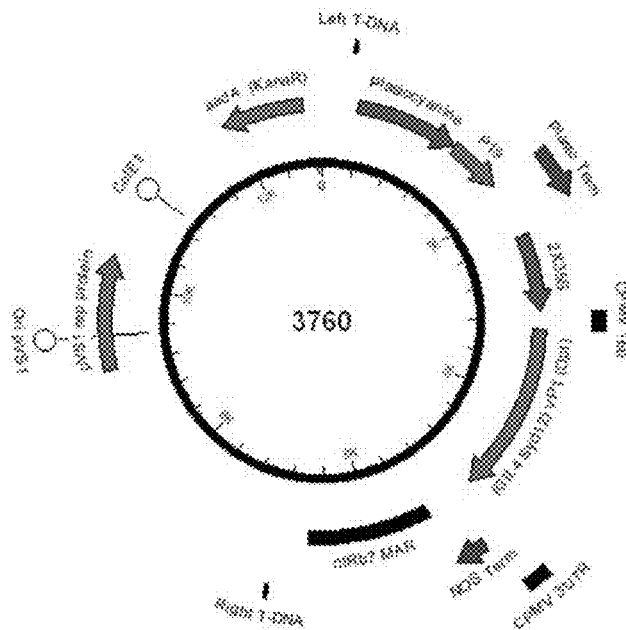


Figure 44L

Construct 4135 (VP1 GII.4_P80S+S90L hCod)

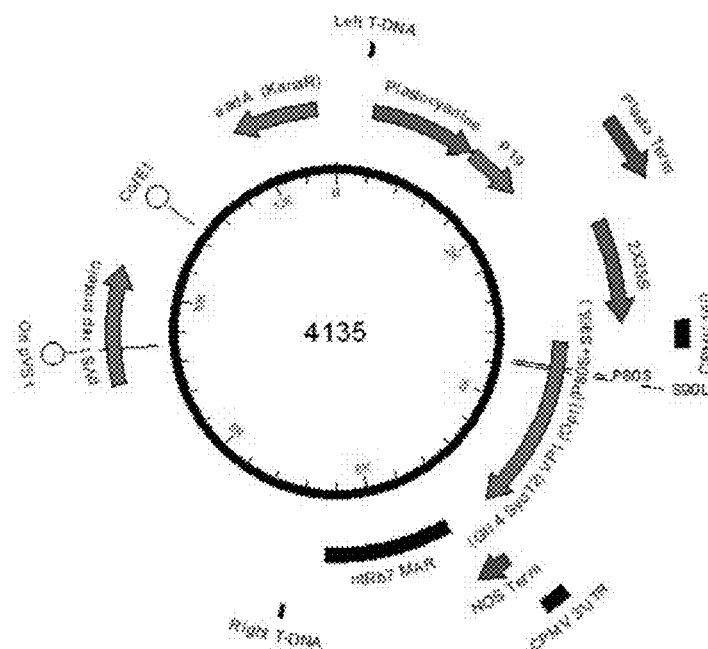


Figure 44M

Construct 4168 (GII.4_P80S+Δ35-42 hCod)

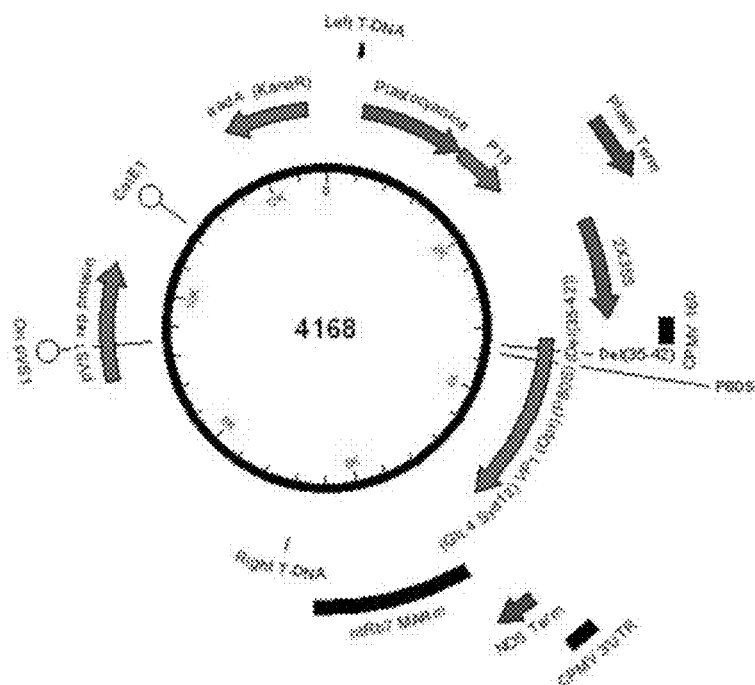


Figure 44N
Construct 4169 (VP1 GII.4_P80S+SSTAVATA hCod)

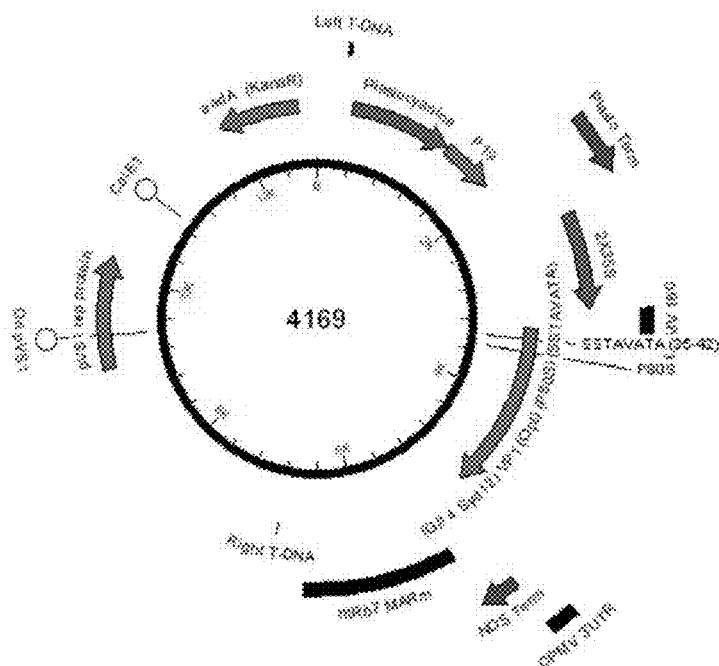


FIGURE 44O

Construct 4185 (VP1 GII.4_A39V+R53I hCod);

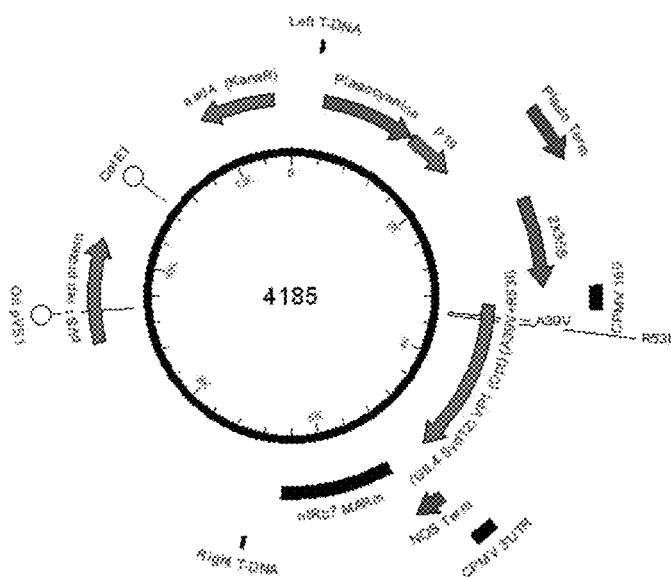


Figure 45B

Construct 4149 (VP1 GII.6_E80S hCod)

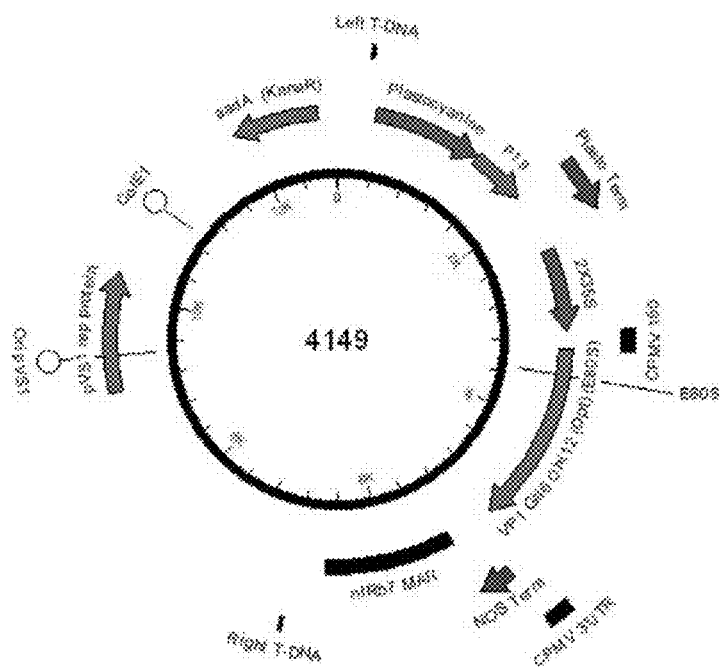


Figure 45C

Construct 4150 (VP1 GII.6_S90L hCod)

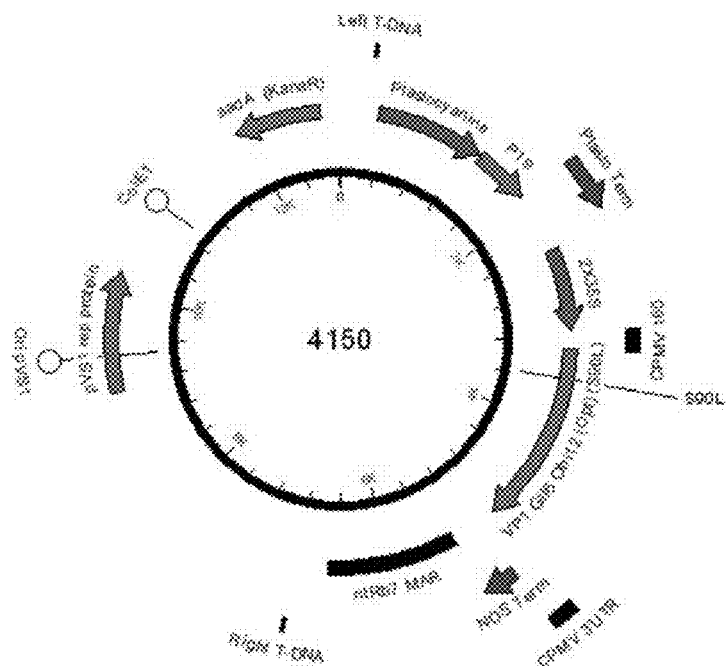


Figure 45D

Construct 4151 (VP1 GII.6 E80S+S90L)

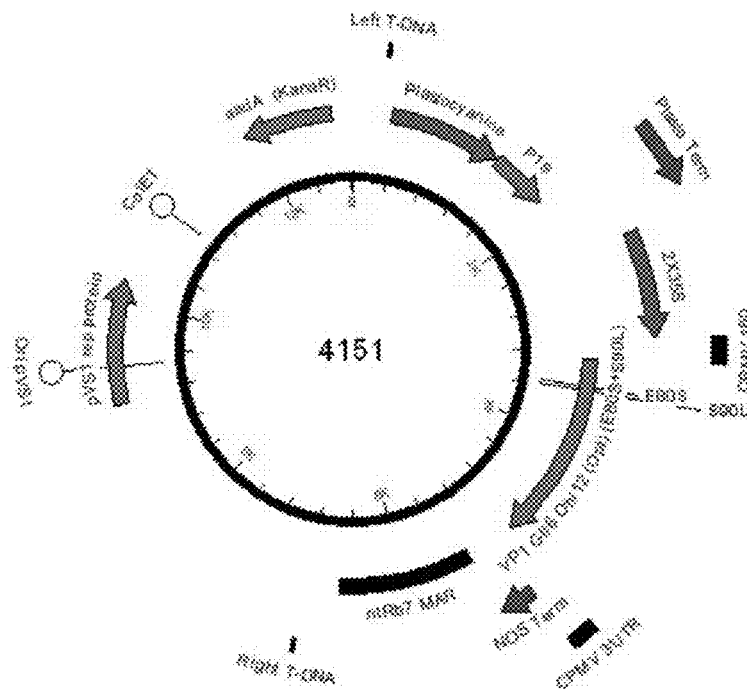


Figure 46A

Construct 3995 (Wt VP1 GII.12 hCod)

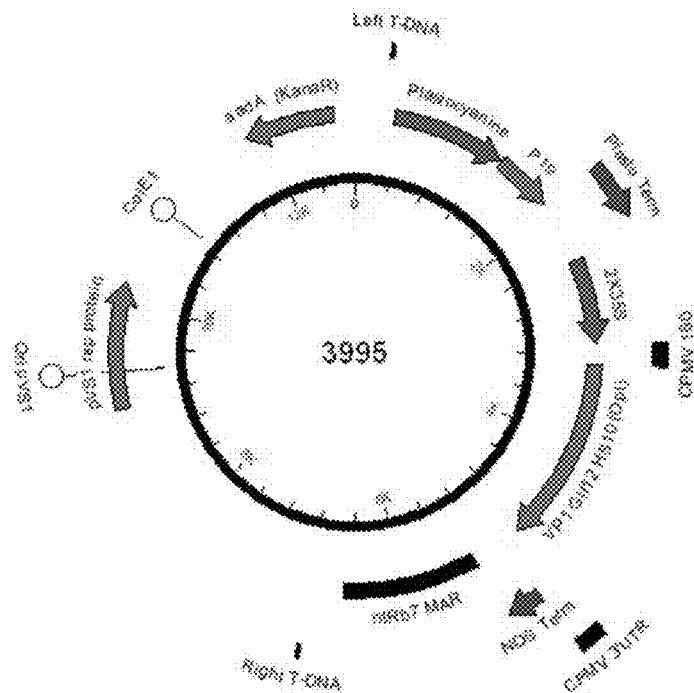


Figure 46B

Construct 4136 (VP1 GII.12_E80S hCod)

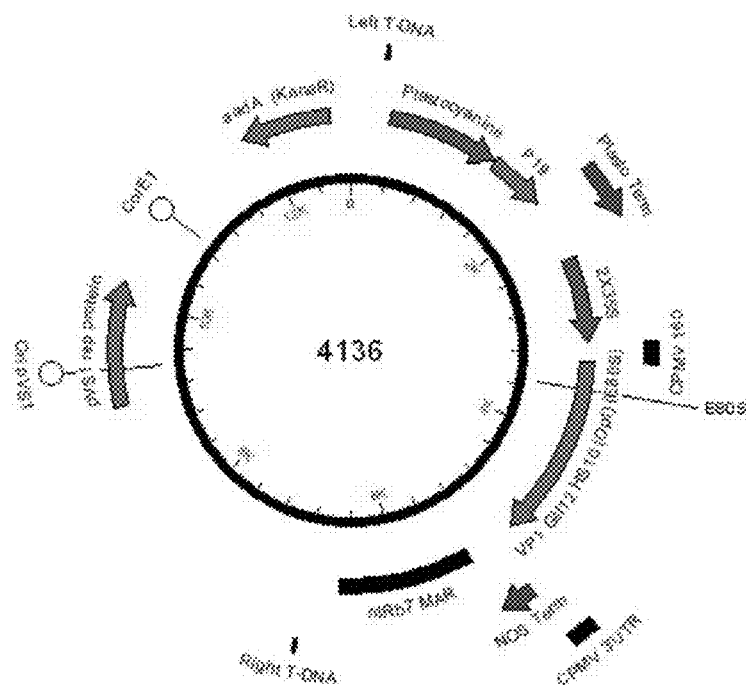


Figure 46C

Construct 4137 (VP1 GII.12_A90L hCod)

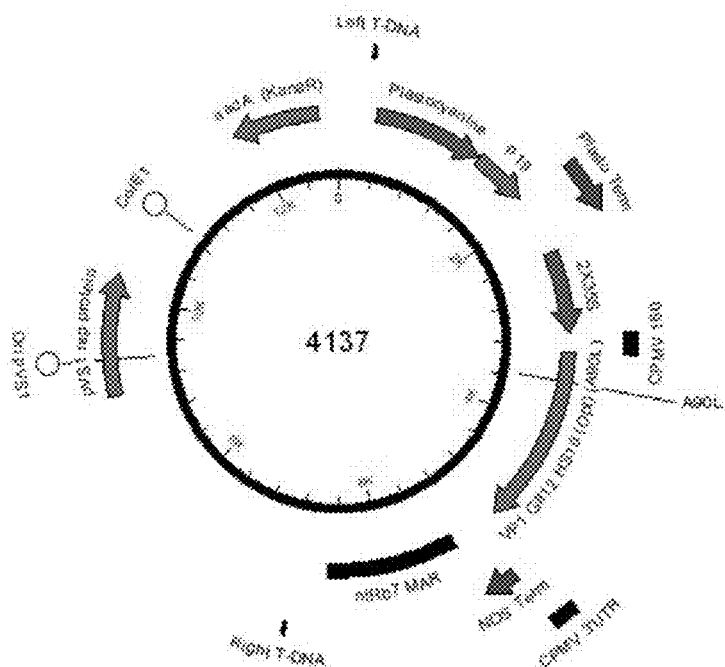


Figure 46D

Construct 4138 (VP1 GII.12_E80S+A90L)

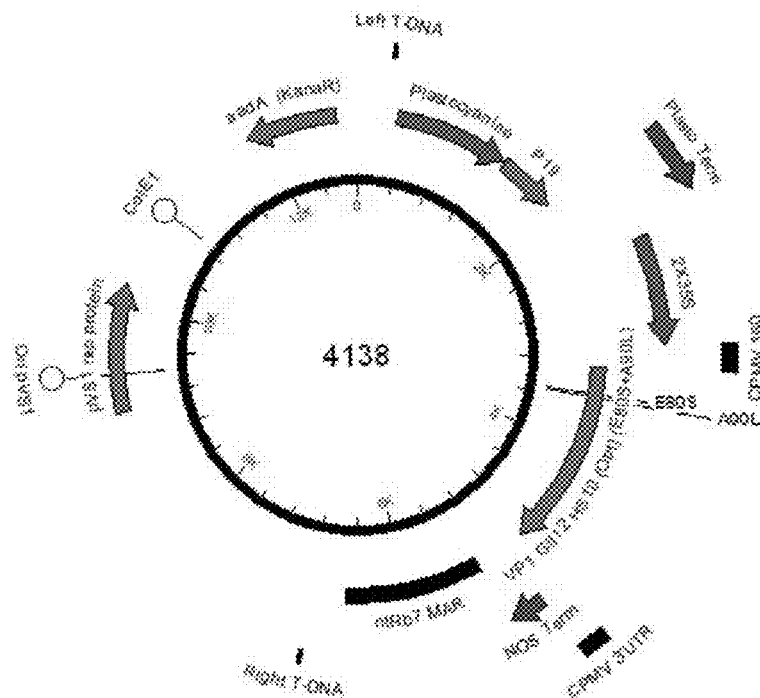


FIGURE 46E

Construct 4234 (VP1 GII.17_A39V hCod)

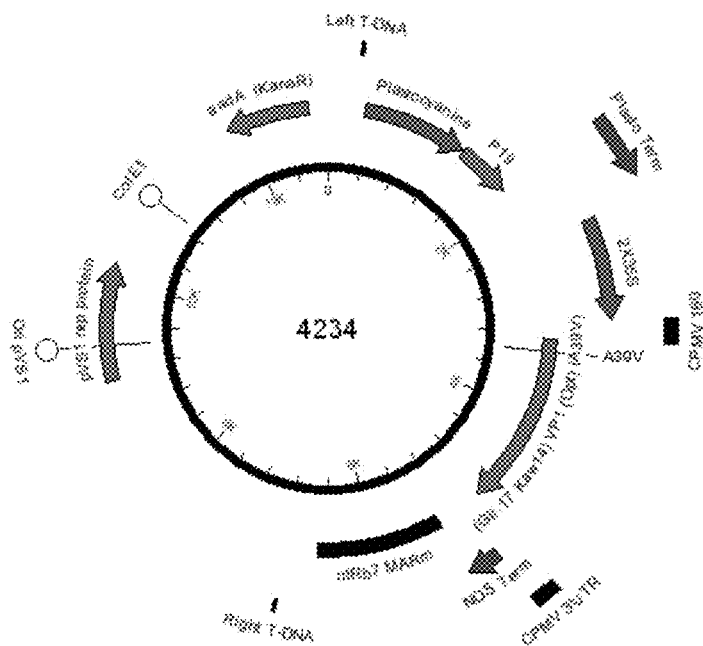


FIGURE 46H

Construct 4236 (VP1 GII.17_A39V+R53I hCod)

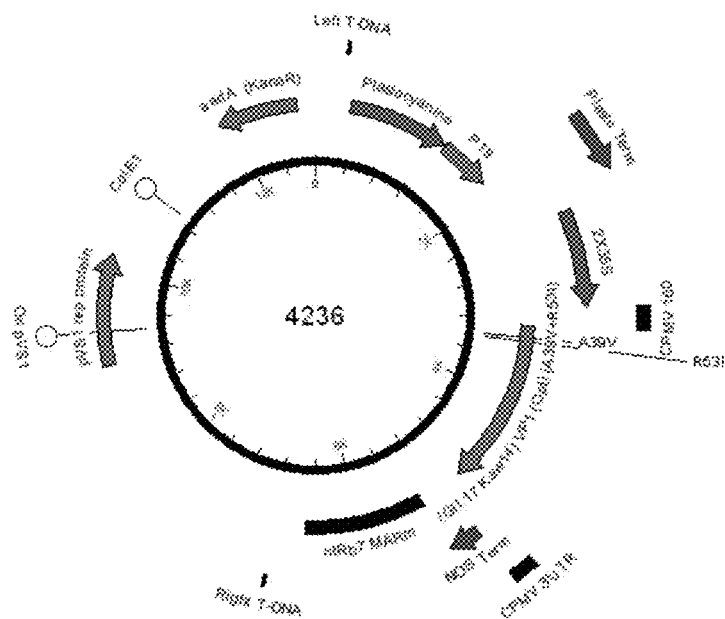


FIGURE 46I

Construct 4233 (VP1 GII.17_E80S+A90L hCod)

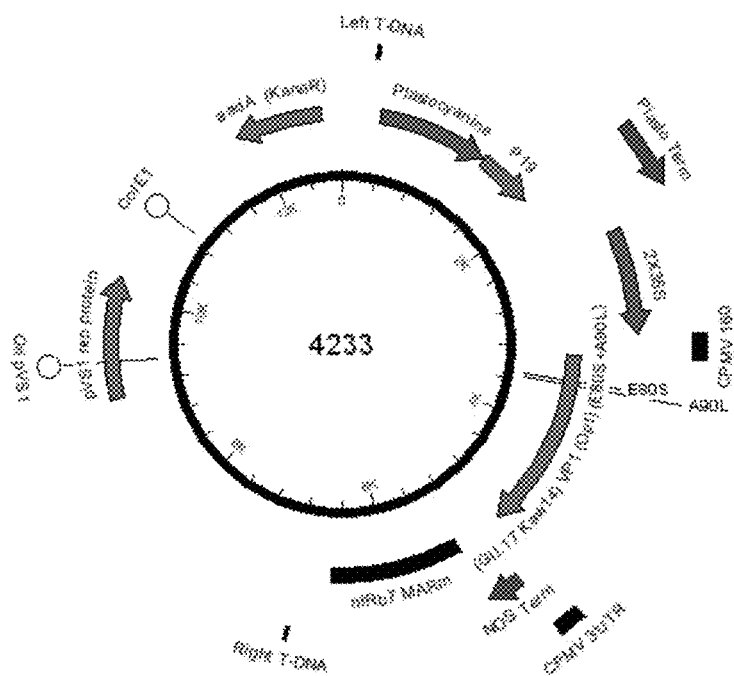


Figure 47C

Construct 3307 (Wt VP2 GII.6)

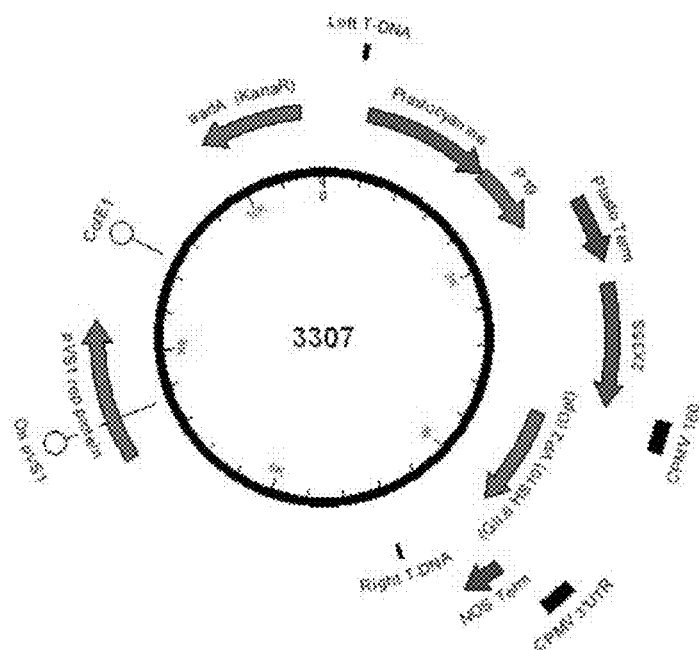


Figure 48

Construct 1190 (Cloning vector 1190)

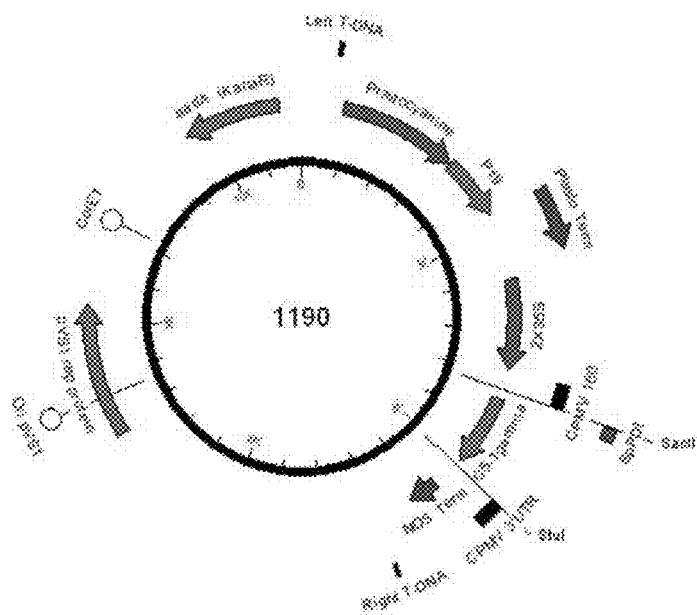


Figure 49

Construct 3677 (Cloning vector 3677)

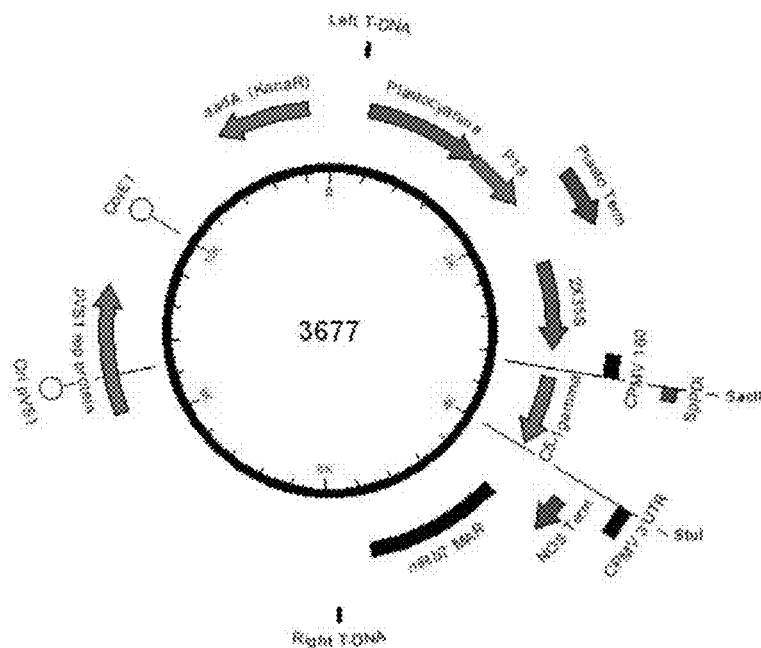


Figure 50A

GII.4 P80X constructs (cloning vectors), wherein X=A (4281); X=N (4285); X=K (4286); X=H (4287)

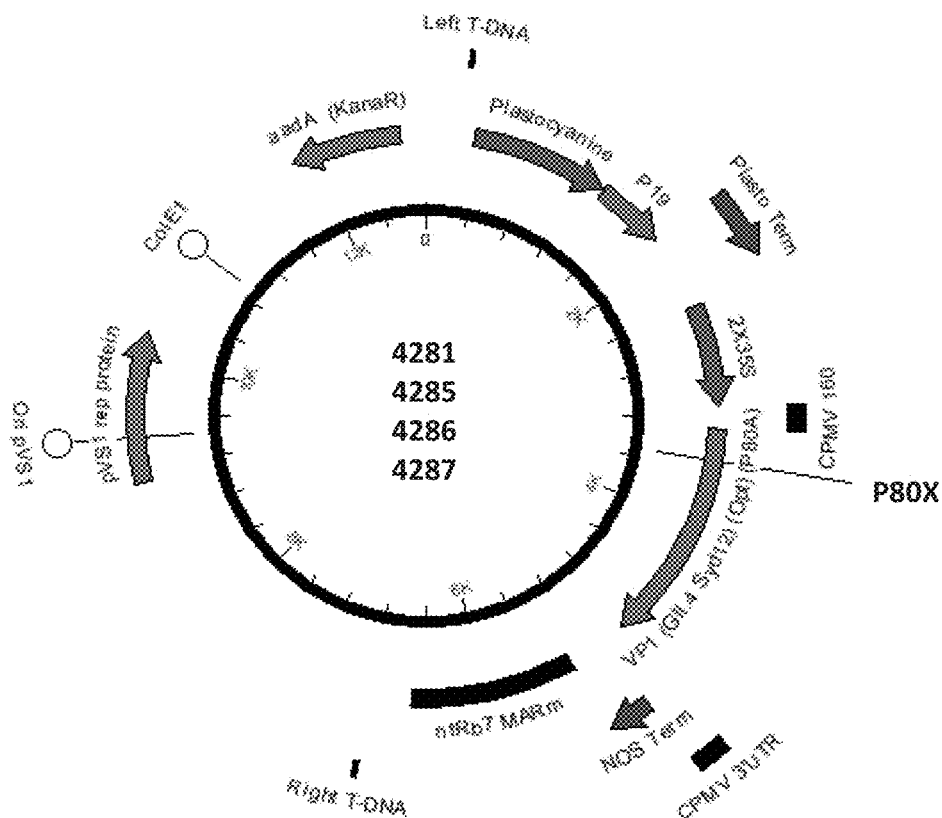


Figure 50B

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)

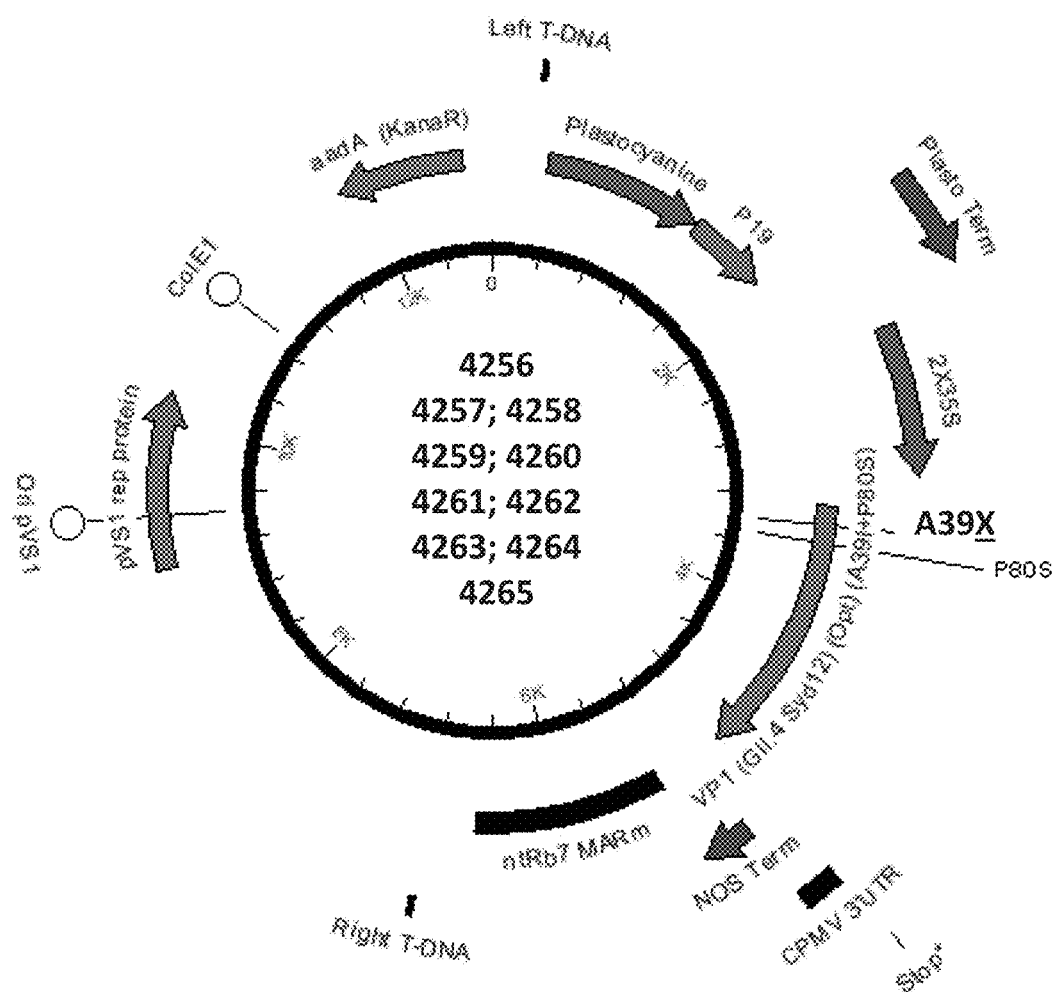


Figure 51

Gl.7 M57X constructs (cloning vectors), wherein X= L 4266; G (4268); S (4269); T (4270; N (4273); Q (4274); K (4275); or H (4276).

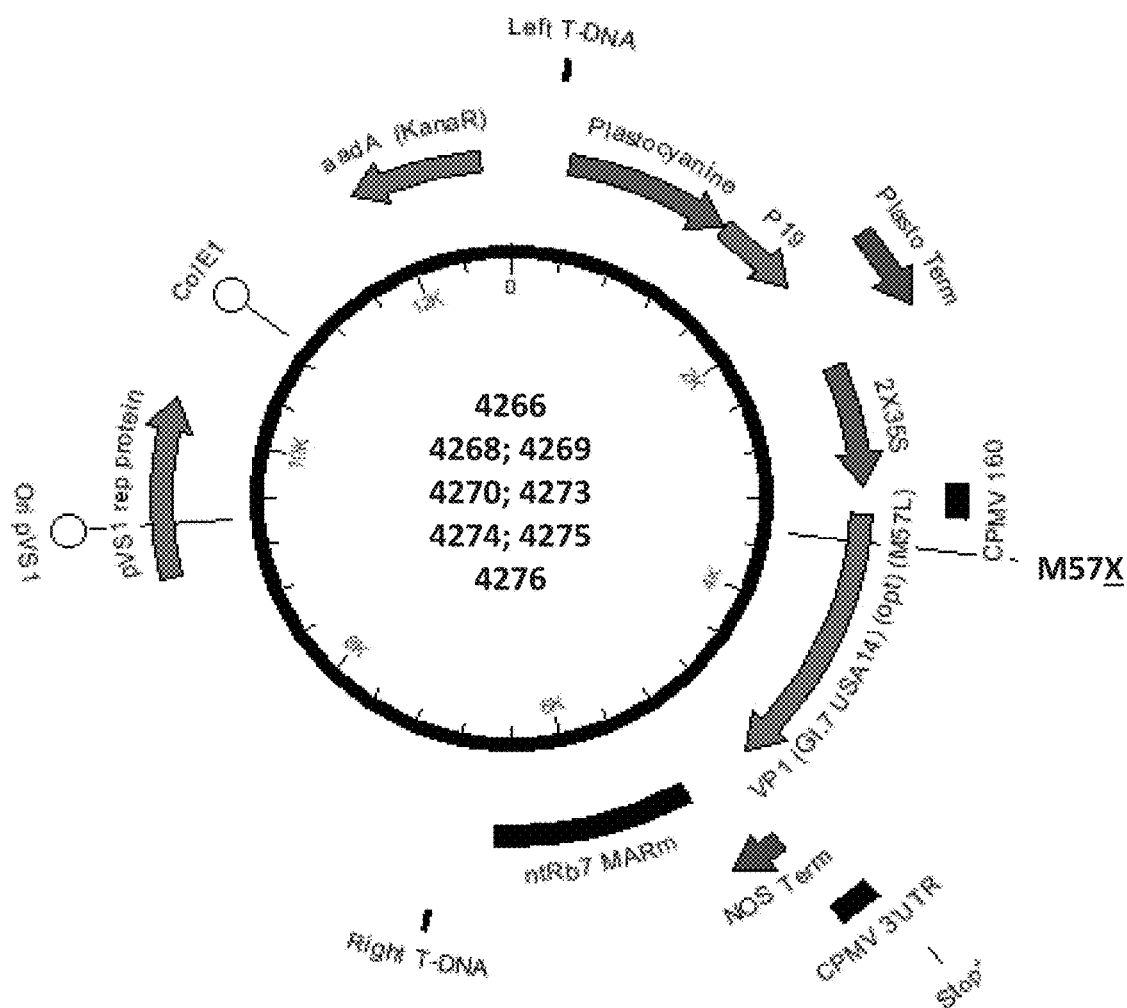
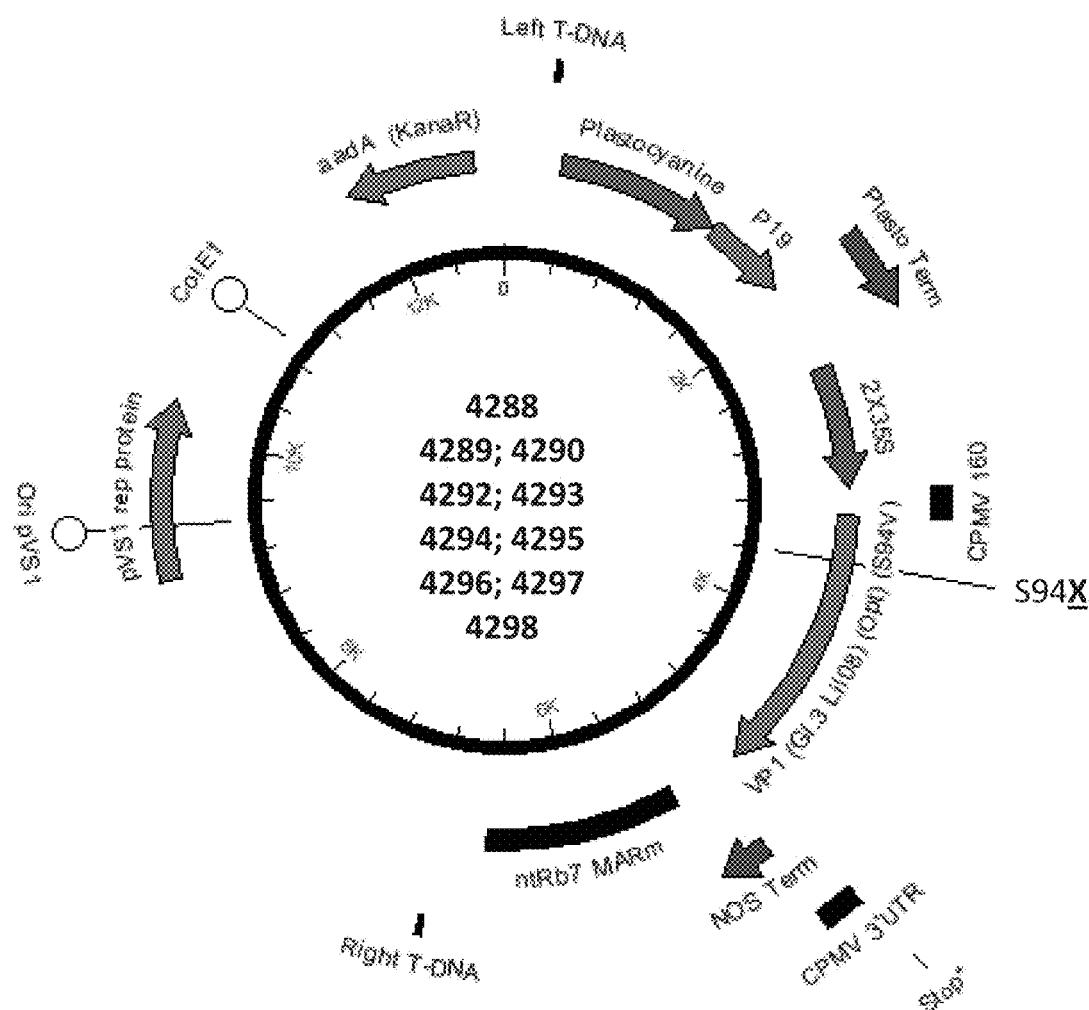


Figure 52

Gl.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).



MODIFIED NOROVIRUS VP1 PROTEINS AND VLPs COMPRISING MODIFIED NOROVIRUS VP1 PROTEINS

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a Continuation application of U.S. application Ser. No. 16/768,524 filed May 29, 2020, which is a National Stage of International Application No. PCT/CA2018/051530 filed Nov. 30, 2018, claiming priority based on U.S. Patent Application No. 62/593,006 filed Nov. 30, 2017 and U.S. Patent Application No. 62/712,744 filed Jul. 31, 2018, the entire contents of which are hereby incorporated by reference.

INCORPORATION BY REFERENCE OF SEQUENCE LISTING

[0002] The content of the electronically submitted sequence listing, file name: Q284770_Substitute_Sequence_Listing.xml; size: 528,965 bytes; and date of creation: Mar. 23, 2023, filed herewith, is incorporated herein by reference in its entirety.

FIELD OF INVENTION

[0003] 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

[0004] 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 food-borne 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.

[0005] 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).

[0006] 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.

[0007] 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 struc-

tures: 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.

[0008] 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.

[0009] 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.

[0010] 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.

[0011] 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.

[0012] 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.

[0013] 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.

[0014] US 2013/0273105 teaches the production of norovirus formulations comprising antigenic peptides, proteins or VLPs derived from genogroup I (GI), genogroup II (GII), or consensus viral sequences. The norovirus antigens may include variants of the capsid proteins expressed in the VLPs.

[0015] 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 from GII, 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.

[0016] 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).

[0017] 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.

SUMMARY OF THE INVENTION

[0018] 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.

[0019] It is an object of the invention to produce modified norovirus proteins, VLPs comprising modified norovirus proteins, and to produce VLPs comprising modified norovirus proteins in plants.

[0020] 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:

[0021] an amino acid selected from positions in sequence alignment with amino acids 43, 57, 84 and 94 of norovirus VP1 genotype GI.1,

[0022] a deletion of a peptide fragment in sequence alignment with amino acids 39-46 of norovirus VP1 genotype GI.1,

[0023] amino acids corresponding to positions 39-46 of norovirus VP1 genotype GI.1, are mutated to the sequence SSTAVATA, or

[0024] a combination thereof, and the nucleotide sequence is not derived from a genotype GI.1 norovirus VP1.

[0025] 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 G1.3/S29/2008/Lilla Edet/Sweden, G1.5/Siklos-HUN5407/2013/HUN, G1.7/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/H5206/2010/USA, and GII.17_Kawa_2014_A0A077KVU6.

[0026] The recombinant polynucleotide described above may comprise specific substitutions, modifications or mutations, independently selected from the following:

[0027] 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;

[0028] 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;

[0029] 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

[0030] 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.

[0031] Any of the recombinant polynucleotides described above may also be optimized for human codon usage, increased GC content, or a combination thereof.

[0032] 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.

[0033] 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 modified 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.

[0034] 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 50 nm. 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).

[0035] 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.

[0036] 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.

[0037] 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.

[0038] The present disclosure also provides a vaccine for inducing an immune response, wherein the vaccine com-

prises 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.

[0039] 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 FIGS. 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 FIGS. 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.

[0040] 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.

[0041] 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.

[0042] This summary of the invention does not necessarily describe all features of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0043] 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:

[0044] FIG. 1A shows a schematic representation of the linear structure of the norovirus genome and the polyprotein and proteins translated therefrom. FIG. 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). FIG. 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).

[0045] FIG. 2A shows Uniprot and NCBI references for several norovirus VP1 (upper panel) and VP2 (lower panel) proteins. FIG. 2B shows NCBI references for several noro-

virus VP1 (upper panel) and VP2 (lower panel) nucleic acid sequences. FIGS. 2C and 2D show 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 GI VP1 sequences and the GI VP1 sequences by 4 amino acids.

[0046] FIG. 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. FIG. 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. FIG. 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)). FIG. 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).

[0047] FIG. 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)). FIG. 4B shows electron micrographs of norovirus VLPs purified from 29-35% iodixanol gradient fractions of VP1.

[0048] FIG. 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. FIG. 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). FIG. 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 FIG. 5B), mut hCod GI.3/S29/2008/Lila Edet/Sweden VP1_S94L (Construct #: 4141, middle panel; fractions F2-F6 of FIG. 5B), or mut hCod GI.3/S29/2008/Lila Edet/Sweden VP1_Q84S+S94L (Construct #: 4142, right panel; fractions F2-F6 of FIG. 5B). 15,000× magnification; scale bar=500 nm. FIG. 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)). FIG. 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); 15,000× magnification; scale bar=500 nm. FIG. 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.

[0049] FIG. 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. FIG. 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). FIG. 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). 15,000× magnification; scale bar=200 nm. FIG. 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 FIG. 6E). FIG. 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 (Construct #4218). 15,000× magnification; scale bar=500 nm. FIG. 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.

[0050] FIG. 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. FIG. 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). FIG. 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)); 15,000× magnification; scale bar=500 nm.

[0051] FIG. 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)). FIG. 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). 15,000× magnification; scale bar=500 nm.

[0052] FIG. 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.14/Sydney/NSW0514/2012/AU_V47P VP1 (Construct #: 4156; SEQ ID NO:56 (nucleotide); SEQ ID NO:55 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_R53I VP1 (Construct #: 4157; SEQ ID NO:58 (nucleotide); SEQ ID NO:57 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133; SEQ ID NO:60 (nucleo-

tide); SEQ ID NO:59 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_S90L VP1 (Construct #: 4134; SEQ ID NO:62 (nucleotide); SEQ ID NO:61 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_Δ35-42 VP1 (Construct #: 4158; SEQ ID NO:64 (nucleotide); SEQ ID NO:63 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_SSTAVATA VP1 (Construct #: 4159; SEQ ID NO:66 (nucleotide); SEQ ID NO:65 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_P80S+A39V (Construct #: 4165; SEQ ID NO:68 (nucleotide); SEQ ID NO:67 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_P80S+V47P VP1 (Construct #: 4166; SEQ ID NO:70 (nucleotide); SEQ ID NO:69 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_P80S+R53I VP1 (Construct #: 4167; SEQ ID NO:72 (nucleotide); SEQ ID NO:71 (amino acid)), mut hCod GII.14/Sydney/NSW0514/2012/AU_P80S+S90L VP1 (Construct #: 4135; SEQ ID NO:74 (nucleotide); SEQ ID NO:73 (amino acid)), mut hCod GII.14/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.14/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. FIG. 9B shows a Coomassie-stained SDS-PAGE analysis (upper panel) and transmission electron micrographs (TEM; lower panel; 15,000× 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.14/Sydney/NSW0514/2012/AU VP1 (Construct #: 3760), mut hCod GII.14/Sydney/NSW0514/2012/AU_P80S VP1 (Construct #: 4133), mut hCod GII.14/Sydney/NSW0514/2012/AU_S90L VP1 (Construct #: 4134), GII.4/Sydney/NSW0514/2012/AU_P80S+S90L VP1 (Construct #: 4135). FIG. 9C shows a Coomassie-stained SDS-PAGE analysis (upper panel) and transmission electron micrographs (TEM; lower panel; 15,000× 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). FIG. 9D shows a Coomassie-stained SDS-PAGE analysis (upper panel) and transmission electron micrographs (TEM; lower panel; 15,000× 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). FIG. 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). FIG. 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). FIG. 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)); 15,000× magnification; scale bar=500 nm. FIG. 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 (P80 set as “Fold Change” of 1; C #: construct number. FIG. 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.

[0053] FIG. 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). FIG. 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). 15,000× magnification; scale bar=200 nm.

[0054] FIG. 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. FIG. 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). FIG. 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). 15,000 $\times$ magnification; scale bar=500 nm. FIG. 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 A0A077KVU6 VP1 (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)); 15,000 $\times$ magnification; scale bar=500 nm.

[0055] FIG. 12A shows the amino acid sequence of VP1 GI.1 United States Norwalk 1968 (SEQ ID NO:1); FIG. 12B shows the nucleic acid sequence of wild type VP1 GI.1 United States Norwalk 1968 (SEQ ID NO:2); FIG. 12C shows the nucleic acid sequence of hCod VP1 GI.1 United States Norwalk 1968 (SEQ ID NO:3).

[0056] FIG. 13A shows the amino acid sequence of VP1 GI.2 Leuven 2003 D2DEL3 (SEQ ID NO:4); FIG. 13B shows the nucleic acid sequence of hCod VP1 GI.2 Leuven 2003 D2DEL3 (SEQ ID NO:5).

[0057] FIG. 14A shows the amino acid sequence of VP1 GI.3 LillaEdet 2008 H2DG70 (SEQ ID NO:6); FIG. 14B

shows the nucleic acid sequence of hCod GI.3 LillaEdet 2008 H2DG70 (SEQ ID NO:7).

[0058] FIG. 15A shows the amino acid sequence of VP1 GI.5 Siklos HUN5407 2013 HUN AHW99832 (SEQ ID NO:12). FIG. 15B shows the nucleic acid sequence of hCod VP1 GI.5 Siklos HUN5407 2013 HUN AHW99832 (SEQ ID NO:33).

[0059] FIG. 16A shows the amino acid sequence of GI.7/GA5043/USA/2014 VP1 (SEQ ID NO:101). FIG. 16B shows the nucleic acid sequence of GI.7/GA5043/USA/2014 VP1 (SEQ ID NO:175). FIG. 16C shows the amino acid sequence of VP1 GII.1 Ascension208 2010 USA AFA55174 (SEQ ID NO:13).

[0060] FIG. 17A shows the amino acid sequence of VP1 GII.2 CGMH47 2011 TW AGT39206 (SEQ ID NO:14). FIG. 17B shows the nucleic acid sequence of hCod VP1 GII.2 CGMH47 2011 TW AGT39206 (SEQ ID NO:40).

[0061] FIG. 18A shows the amino acid sequence of VP1 GII.3 Jingzhou 2013402 CHN AGX01095 (SEQ ID NO:15). FIG. 18B shows the nucleic acid sequence of hCod VP1 GII.3 Jingzhou 2013402 CHN AGX01095 (SEQ ID NO:45).

[0062] FIG. 19A shows the amino acid sequence of VP1 GII.4 Sydney NSW0514 2012 (SEQ ID NO:16). FIG. 19B shows the nucleic acid sequence of hCod VP1 GII.4 Sydney NSW0514 2012 (SEQ ID NO: 52). FIG. 19C shows the amino acid sequence of VP1 US96: GII.4 Dresden174 1997 DE AY741811 (SEQ ID NO:27). FIG. 19D shows the amino acid sequence of VP1 FH02: GII.4 FarmingtonHills 2002 US AY502023 (SEQ ID NO:28). FIG. 19E shows the amino acid sequence of VP1 Hnt04: GII.4 Hunter-NSW504D 2004 AU DQ078814 (SEQ ID NO:29). FIG. 19F shows the amino acid sequence of VP1 2006b: GII.4 Shellharbour-NSW696T 2006 AU EF684915 (SEQ ID NO:30). FIG. 19G shows the amino acid sequence of VP1NO09: GII.4 Orange-NSW001P 2008 AU GQ845367 (SEQ ID NO:31).

[0063] FIG. 20 shows the amino acid sequence of VP1 GII.5 Alberta 2013 CA ALT54485 (SEQ ID NO:17).

[0064] FIG. 21A shows the amino acid sequence of VP1 GII.6 Ohio 2012 M9T020 (SEQ ID NO:20). FIG. 21B shows the nucleic acid sequence of hCod-optimized VP1 GII.6 Ohio 2012 M9T020 (SEQ ID NO:21);

[0065] FIG. 22 shows the amino acid sequence of VP1 GII.7 Musa 2010 AII173774 (SEQ ID NO:18).

[0066] FIG. 23A shows the amino acid sequence of VP1 GII.12_HS206_2010_USA_AEI29586 (SEQ ID NO:19); FIG. 23B shows the nucleic acid sequence of hCod VP1 GII.12_HS206_2010_USA_AEI29586 (SEQ ID NO:87).

[0067] FIG. 24A shows the amino acid sequence of VP1 GII.13 VA173 2010 H9AWU4 (SEQ ID NO:22). FIG. 24B shows the nucleic acid sequence of human codon-optimized VP1 GII.13 VA173 2010 H9AWU4 (SEQ ID NO:23).

[0068] FIG. 25 shows the amino acid sequence of VP1 GII.14 Saga 2008 JPN ADE28701 (SEQ ID NO:32).

[0069] FIG. 26A shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6 (SEQ ID NO:24). FIG. 26B shows the nucleic acid sequence of human codon-optimized VP1 GII.17 Kawa 2014 A0A077KVU6 (SEQ ID NO:25).

[0070] FIG. 27 shows the amino acid sequence of VP1 GII.21 Sali 2011 USA AFC89665 (SEQ ID NO:26).

[0071] FIG. 28A shows the amino acid sequence of modified VP1 GI.3_Lil08_Q84S (SEQ ID NO:98). FIG. 28B shows the nucleic acid sequence of VP1 GI.3_Lil08_Q84S (SEQ ID NO:167). FIG. 28C shows the amino acid sequence

of VP1 GI.3 Lil08_S94L (SEQ ID NO:8). FIG. 28D shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_S94L (SEQ ID NO:9). FIG. 28E shows the amino acid sequence of VP1 GI.3 Lil08_Q84S+S94L (SEQ ID NO:10). FIG. 28F shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_Q84S+S94L (SEQ ID NO:11). FIG. 28G shows the amino acid sequence of VP1 GI.3 Lil08_A43V+S94L (SEQ ID NO:170). FIG. 28H shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_A43V+S94L (SEQ ID NO:169). FIG. 28I shows the amino acid sequence of VP1 GI.3 Lil08_M57I+S94L (SEQ ID NO:172). FIG. 28J shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_M57I+S94L (SEQ ID NO:171). FIG. 28K shows the amino acid sequence of VP1 GI.3 Lil08_A43V+M57I+S94L (SEQ ID NO:174). FIG. 28L shows the nucleic acid sequence of hCod VP1 GI.3 Lil08_A43V+M57I+S94L (SEQ ID NO:173). FIG. 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. FIG. 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).

[0072] FIG. 29A shows the amino acid sequence of modified VP1 GI.5 Siklos Q84S (SEQ ID NO:34). FIG. 29B shows the nucleic acid sequence of modified VP1 GI.5 Siklos Q84S (SEQ ID NO:35). FIG. 29C shows the amino acid sequence of VP1 GI.5 Siklos A94L (SEQ ID NO:36). FIG. 29D shows the nucleic acid sequence of hCod VP1 GI.5 Siklos A94L (SEQ ID NO:37). FIG. 29E shows the amino acid sequence of VP1 GI.5 Siklos Q84S+A94L (SEQ ID NO:38). FIG. 29F shows the nucleic acid sequence of hCod VP1 GI.5 Siklos Q84S+A94L (SEQ ID NO:39). FIG. 29G shows the amino acid sequence of modified VP1 GI.7/GA5043/USA/2014_R84S (SEQ ID NO:177). FIG. 29H shows the nucleic acid sequence of modified VP1 hCod GI.7/GA5043/USA/2014_R84S (SEQ ID NO:176). FIG. 29I shows the amino acid sequence of modified VP1 GI.7/GA5043/USA/2014_M57I (SEQ ID NO:179). FIG. 29J shows the nucleic acid sequence of modified VP1 hCod GI.7/GA5043/USA/2014_M57I (SEQ ID NO:178). FIG. 29K shows the amino acid sequence of modified VP1 GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:181). FIG. 29L shows the nucleic acid sequence of modified VP1 hCod GI.7/GA5043/USA/2014_M57I+R84S (SEQ ID NO:180). FIG. 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. FIG. 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).

[0073] FIG. 30A shows the amino acid sequence of VP1 GII.2 CGMH47 E80S (SEQ ID NO:85). FIG. 30B shows the nucleic acid sequence of hCod VP1 GII.2 CGMH47 E80S (SEQ ID NO:86). FIG. 30C shows the amino acid sequence of VP1 GII.2 CGMH47 A90L (SEQ ID NO:41); FIG. 30D shows the nucleic acid sequence of hCod VP1 GII.2 CGMH47 A90L (SEQ ID NO:42). FIG. 30E shows the amino acid sequence of VP1_GII.2_CGMH47_E80S+A90L

(SEQ ID NO:43). FIG. 30F shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_E80S+A90L (SEQ ID NO:44). FIG. 30G shows the amino acid sequence of VP1_GII.2_CGMH47_A39V+E80S+A90L (SEQ ID NO:182). FIG. 30H shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_A39V+E80S+A90L (SEQ ID NO:183). FIG. 30I shows the amino acid sequence of VP1_GII.2_CGMH47_R53I+E80S+A90L (SEQ ID NO:184). FIG. 30J shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_R53I+E80S+A90L (SEQ ID NO:185). FIG. 30K shows the amino acid sequence of VP1_GII.2_CGMH47_A39V+R53I+E80S+A90L (SEQ ID NO:186). FIG. 30L shows the nucleic acid sequence of hCod VP1_GII.2_CGMH47_A39V+R53I+E80S+A90L (SEQ ID NO:187).

[0074] FIG. 31A shows the amino acid sequence of VP1 GII.3_Jing_E80S (SEQ ID NO:46). FIG. 31B shows the nucleic acid sequence of hCod VP1 GII.3_Jing_E80S (SEQ ID NO:47). FIG. 31C shows the amino acid sequence of VP1 GII.3_Jing_A90L (SEQ ID NO:48). FIG. 31D shows the nucleic acid sequence of hCod VP1 GII.3_Jing_A90L (SEQ ID NO:49). FIG. 31E shows the amino acid sequence of VP1 GII.3_Jing_E80S+A90L (SEQ ID NO:50). FIG. 31F shows the nucleic acid sequence of hCod VP1 GII.3_Jing_E80S+A90L (SEQ ID NO:51).

[0075] FIG. 32A shows the amino acid sequence of VP1 GII.4_Syd12_A39V (SEQ ID NO:53). FIG. 32B shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_A39V (SEQ ID NO:54). FIG. 32C shows the amino acid sequence of VP1 GII.4_Syd12_V47P (SEQ ID NO:55). FIG. 32D shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_V47P (SEQ ID NO:56). FIG. 32E shows the amino acid sequence of VP1 GII.4_Syd12_R53I (SEQ ID NO:57). FIG. 32F shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_R53I (SEQ ID NO:58). FIG. 32G shows the amino acid sequence of VP1; GII.4_Syd12_P80S (SEQ ID NO:59). FIG. 32H shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S (SEQ ID NO:60). FIG. 32I shows the amino acid sequence of VP1 GII.4_Syd12_S90L (SEQ ID NO:61). FIG. 32J shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_S90L (SEQ ID NO:62). FIG. 32K shows the amino acid sequence of VP1 GII.4_Syd12_Δ35-42 (SEQ ID NO:63). FIG. 32L shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_Δ35-42 (SEQ ID NO:64). FIG. 32M shows the amino acid sequence of VP1 GII.4_Syd12_SSTAVATA (SEQ ID NO:65). FIG. 32N shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_SSTAVATA (SEQ ID NO:66). FIG. 32O shows the amino acid sequence of VP1 GII.4_Syd12_P80S+A39V (SEQ ID NO:67). FIG. 32P shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+A39V (SEQ ID NO:68). FIG. 32Q shows the amino acid sequence of VP1 GII.4_Syd12_P80S+V47P (SEQ ID NO:69). FIG. 32R shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+V47P (SEQ ID NO:70). FIG. 32S shows the amino acid sequence of VP1 GII.4_Syd12_P80S+R53I (SEQ ID NO:71). FIG. 32T shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+R53I (SEQ ID NO:72). FIG. 32U shows the amino acid sequence of VP1 GII.4_Syd12_P80S+S90L (SEQ ID NO:73). FIG. 32V shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+S90L (SEQ ID NO:74). FIG. 32W shows the amino acid sequence of VP1 GII.4_Syd12_P80S+Δ35-42 (SEQ ID NO:75). FIG. 32X shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+Δ35-42 (SEQ ID NO:76). FIG.

32Y shows the amino acid sequence of VP1 GII.4_Syd12_P80S+SSTAVATA (SEQ ID NO:77). **FIG. 32Z** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_P80S+SSTAVATA (SEQ ID NO:78). **FIG. 32AA** shows the amino acid sequence of VP1 GII.4_Syd12_A39V+R53I (SEQ ID NO:188). **FIG. 32BB** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_A39V+R53I (SEQ ID NO:189). **FIG. 32CC** shows the amino acid sequence of VP1 GII.4_Syd12_A39V+R53I+P80S (SEQ ID NO:190). **FIG. 32DD** shows the nucleic acid sequence of hCod VP1 GII.4_Syd12_A39V+R53I+P80S (SEQ ID NO:191). **FIG. 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). **FIG. 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. **FIG. 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). **FIG. 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.

[0076] **FIG. 33A** shows the amino acid sequence of VP1 GII.6_Ohio_E80S (SEQ ID NO:79). **FIG. 33B** shows the nucleic acid sequence of hCod VP1 GII.6_Ohio_E80S (SEQ ID NO:80). **FIG. 33C** shows the amino acid sequence of VP1 GII.6_Ohio_S90L (SEQ ID NO:81). **FIG. 33D** shows the nucleic acid sequence of hCod VP1 GII.6_Ohio_S90L (SEQ ID NO:82). **FIG. 33E** shows the amino acid sequence of VP1 GII.6_Ohio_E80S+S90L (SEQ ID NO:83). **FIG. 33F** shows the nucleic acid sequence of hCod VP1 GII.6_Ohio_E80S+S90L (SEQ ID NO:84).

[0077] **FIG. 34A** shows the amino acid sequence of VP1 GII.12_HS10_E80S (SEQ ID NO:88). **FIG. 34B** shows the nucleic acid sequence of hCod VP1 GII.12_HS10_E80S (SEQ ID NO:89). **FIG. 34C** shows the amino acid sequence of VP1 GII.12_HS10_A90L (SEQ ID NO:90). **FIG. 34D** shows the nucleic acid sequence of hCod VP1 GII.12_HS10_A90L (SEQ ID NO:91). **FIG. 34E** shows the amino acid sequence of VP1 GII.12_HS10_E80S+A90L (SEQ ID NO:92); **FIG. 34F** shows the nucleic acid sequence of hCod VP1 GII.12_HS10_E80S+A90L (SEQ ID NO:93). **FIG. 34G** shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_A39V (SEQ ID NO:192). **FIG. 34H** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V (SEQ ID NO:193). **FIG. 34I** shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:194). **FIG. 34J** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_R53I (SEQ ID NO:195). **FIG. 34K** shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_A90L (SEQ ID NO:196). **FIG. 34L** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A90L (SEQ ID NO:197). **FIG. 34M** shows the amino acid sequence of VP1 GII.17 Kawa 2014 A0A077KVU6_A39V+M53I (SEQ ID NO:198). **FIG. 34N** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_A39V+M53I (SEQ ID NO:199). **FIG. 34O** shows the amino acid sequence of VP1 GII.17 Kawa

2014 A0A077KVU6_E80S+A90L (SEQ ID NO:200). **FIG. 34P** shows the nucleic acid sequence of VP1 hCod GII.17 Kawa 2014 A0A077KVU6_E80S+A90L (SEQ ID NO:201);

[0078] **FIG. 35A** shows the amino acid sequence of VP2_GI.1_Norwalk (SEQ ID NO:99). **FIG. 35B** shows the nucleic acid sequence of human codon optimized VP2_GI.1_Norwalk (SEQ ID NO:100).

[0079] **FIG. 36A** shows the amino acid sequence of VP2_GI.3_Lil08 (SEQ ID NO:94). **FIG. 36B** shows the nucleic acid sequence of human codon optimized VP2_GI.3_Lil08 (SEQ ID NO:95).

[0080] **FIG. 37A** shows the amino acid sequence of VP2_GII.6_HS10 (SEQ ID NO:96). **FIG. 37B** shows the nucleic acid sequence of human codon optimized VP2_GII.6_HS10 (SEQ ID NO:97).

[0081] **FIG. 38A** shows the cloning vector 1190 from left to right T-DNA (SEQ ID NO:162). **FIG. 38B** shows the construct 2724 from 2x355 promoter to NOS terminator (SEQ ID NO:163). **FIG. 38C** shows the cloning vector 3677 from left to right T-DNA (SEQ ID NO:164). **FIG. 38D** shows the construct 4133 from 2x355 promoter to NOS terminator (SEQ ID NO:165). **FIG. 38E** shows the construct 4135 from 2x355 promoter to NOS terminator (SEQ ID NO:166).

[0082] **FIG. 39A** shows a schematic representation of construct 2724 (VP1 Wt GI.1 hCod). **FIG. 39B** shows a schematic representation of construct 3300 (VP1 Wt GI.2 hCod). **FIG. 39C** shows a schematic representation of construct 3979 (VP1 Wt GI.3 hCod).

[0083] **FIG. 40A** shows a schematic representation of construct 4140 (VP1 GI.3_Q84S hCod). **FIG. 40B** shows a schematic representation of construct 4141 (VP1 GI.3_S94L hCod). **FIG. 40C** shows a schematic representation of construct 4142 (VP1 GI.3_P84S+S94L hCod). **FIG. 40D** shows a schematic representation of construct 4179 (VP1 GI.3_A43V+S94L hCod). **FIG. 40E** shows a schematic representation of construct 4180 (VP1 GI.3_M57I+S94L hCod). **FIG. 40F** shows a schematic representation of construct 4181 (VP1 GI.3_A43V+M57I+S94L hCod).

[0084] **FIG. 41A** shows a schematic representation of construct 3980 (VP1 Wt GI.5 hCod (Wt GI.5 hCod)). **FIG. 41B** shows a schematic representation of construct 4130 (VP1 GI.5_Q84S). **FIG. 41C** shows a schematic representation of construct 4131 (VP1 GI.5_A94L hCod). **FIG. 41D** shows a schematic representation of construct 4132 (VP1 GI.5_Q84S+A94L hCod). **FIG. 41E** shows a schematic representation of construct 4210 (VP1 GI.7_R84S hCod). **FIG. 41F** shows a schematic representation of construct 4217 (VP1 GI.7_M57I hCod). **FIG. 41G** shows a schematic representation of construct 4218 (VP1 GI.7_M57I+R84S hCod).

[0085] **FIG. 42A** shows a schematic representation of construct 3982 (Wt VP1 GII.2 hCod). **FIG. 42B** shows a schematic representation of construct 4143 (VP1 GII.2_E80S). **FIG. 42C** shows a schematic representation of construct 4144 (VP1 GII.2_A90L hCod). **FIG. 42D** shows a schematic representation of construct 4145 (VP1 GII.2_E80S+A90L hCod). **FIG. 42E** shows a schematic representation of construct 4182 (VP1 GII.2_A39V+E80S+A90L hCod). **FIG. 42F** shows a schematic representation of construct 4183 (VP1 GII.2_R53I+E80S+A90L hCod). **FIG. 42G** shows a schematic representation of construct 4184 (VP1 GII.2_A39V+R53I+E80S+A90L hCod).

[0086] FIG. 43A shows a schematic representation of construct 3983 (Wt VP1 GII.3 hCod). FIG. 43B shows a schematic representation of construct 4146 (VP1 GII.3_E80S hCod). FIG. 43C shows a schematic representation of construct 4147 (VP1 GII.3_A90L hCod). FIG. 43D shows a schematic representation of construct 4148 (VP1 GII.3_E80S+A90L).

[0087] FIG. 44A shows a schematic representation of construct 3760 (Wt VP1 GII.4 hCod). FIG. 44B shows a schematic representation of construct 4155 (VP1 GII.4_A39V hCod). FIG. 44C shows a schematic representation of construct 4156 (VP1 GII.4_V47P hCod). FIG. 44D shows a schematic representation of construct 4157 (VP1 GII.4_R53I hCod). FIG. 44E shows a schematic representation of construct 4133 (VP1 GII.4_P80S hCod). FIG. 44F shows a schematic representation of construct 4134 (VP1 GII.4_S90L hCod). FIG. 44G shows a schematic representation of construct 4158 (VP1 GII.4_Δ35-42 hCod). FIG. 44H shows a schematic representation of construct 4159 (VP1 GII.4_SSTAVATA hCod). FIG. 44I shows a schematic representation of construct 4165 (VP1 GII.4_A39V+P80S hCod). FIG. 44J shows a schematic representation of construct 4166 (VP1 GII.4_V47P+P80S hCod). FIG. 44K shows a schematic representation of construct 4167 (VP1 GII.4_R53I+P80S hCod). FIG. 44L shows a schematic representation of construct 4135 (VP1 GII.4_P80S+S90L hCod). FIG. 44M shows a schematic representation of construct 4168 (GII.4_P80S+Δ35-42 hCod). FIG. 44N shows a schematic representation of construct 4169 (VP1 GII.4_P80S+SSTAVATA hCod). FIG. 44O shows a schematic representation of construct 4185 (VP1 GII.4_A39V+R53I hCod). FIG. 44P shows a schematic representation of construct 4186 (VP1 GII.4_A39V+R53I+P80S hCod).

[0088] FIG. 45A shows a schematic representation of construct 3993 (Wt VP1 GII.6 hCod). FIG. 45B shows a schematic representation of construct 4149 (VP1 GII.6_E80S hCod). FIG. 45C shows a schematic representation of construct 4150 (VP1 GII.6_S90L hCod). FIG. 45D shows a schematic representation of construct 4151 (VP1 GII.6_E80S+S90L).

[0089] FIG. 46A shows a schematic representation of construct 3995 (Wt VP1 GII.12 hCod). FIG. 46B shows a schematic representation of construct 4136 (VP1 GII.12_E80S hCod). FIG. 46C shows a schematic representation of construct 4137 (VP1 GII.12_A90L hCod). FIG. 46D shows a schematic representation of construct 4138 (VP1 GII.12_E80S+A90L). FIG. 46E shows a schematic representation of construct 4234 (VP1 GII.17_A39V). FIG. 46F shows a schematic representation of construct 4235 (VP1 GII.17_R53I). FIG. 46G shows a schematic representation of construct 4232 (VP1 GII.17_A90L). FIG. 46H shows a schematic representation of construct 4236 (VP1 GII.17_A39V+R53I). FIG. 46I shows a schematic representation of construct 4233 (VP1 GII.17_E80S+A90L).

[0090] FIG. 47A shows a schematic representation of construct 2725 (Wt VP2 GI.1).

[0091] FIG. 47B shows a schematic representation of construct 3303 (Wt VP2 GI.3 hCod).

[0092] FIG. 47C shows a schematic representation of construct 3307 (Wt VP2 GII.6).

[0093] FIG. 48 shows a schematic representation of construct 1190 (Cloning vector 1190).

[0094] FIG. 49 shows a schematic representation of construct 3677 (Cloning vector 3677).

[0095] FIG. 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). FIG. 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).

[0096] FIG. 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).

[0097] FIG. 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).

DETAILED DESCRIPTION

[0098] The following description is of a preferred embodiment.

[0099] 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.”

[0100] 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 expres-

sion 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 batatas*), ginseng, pea, oat, rice, soybean, wheat, barley, sunflower, cotton, corn, rye (*Secale cereale*), sorghum (*Sorghum bicolor*, *Sorghum vulgare*), safflower (*Carthamus tinctorius*).

[0101] 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 suprastructures 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.

[0102] 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.

[0103] 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.

[0104] 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.

[0105] 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; U.S. Pat. No. 4,962,028; which is incorporated herein by reference), the promoter used in regulating plastocyanin expression.

[0106] 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 deter-

minants. Several of these latter elements may be located proximal to the coding region.

[0107] 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.

[0108] 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 U.S. Pat. No. 7,125,978, which is incorporated herein by reference).

[0109] 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).

[0110] 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. Pat. No. 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).

[0111] 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.

[0112] 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).

[0113] 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.

[0114] 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 oligo-

nucleotide 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.

[0115] 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 VP1 and/or VLP include:

- [0116] 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);
 - [0117] 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);
 - [0118] 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);
 - [0119] 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);
 - [0120] 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);
 - [0121] 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
 - [0122] a combination thereof.
- [0123] 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 FIG. 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.

[0124] With reference to the sequences shown in FIG. 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 FIG. 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

[0125] 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.

[0126] 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.

[0127] 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.

[0128] 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 con-

struct). 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. tumefaciens* suspensions permits co-expression of multiple transgenes.

[0129] 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.

[0130] 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 Lomonosoff 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.

[0131] 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 U.S. Provisional Patent Application No. 62/643,053 (Filed Mar. 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 U.S. 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.

[0132] 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.

[0133] 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.

[0134] 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.

[0135] 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.

[0136] 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.

[0137] 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.

[0138] 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 polypeptide 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 FIG. 1A).

[0139] 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 acid sequences), but are not limited to Hu/GI.1/United States/Norwalk/1968 (GI.1; SEQ ID NO:1; FIG. 12A), Hu/GI.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; FIG. 13A), Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; FIG. 14A), Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; FIG. 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; FIG. 16A), Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; FIG. 16B), Hu/GII.2/CGMH47/2011/TW (GII.2; SEQ ID NO: 14; FIG. 17A), Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO: 15; FIG. 18A), Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO: 16; FIG. 19A), US96/GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27; FIG. 19C), FH02/GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28; FIG. 19D), Hnt04: GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29; FIG. 19E), 2006b: GII.14/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30; FIG. 19F), NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31; FIG. 19G), Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID NO:17; FIG. 20), Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; FIG. 21A), GII.7/Musa/2010/A1173774 (GII.7; SEQ ID NO:18; FIG. 22), Hu/GII.12/HS206/2010/USA (GII.2; SEQ ID NO: 19; FIG. 23A), GII.13/VA173/2010/H9AWU4 (GII.13; SEQ ID NO:22; FIG. 24A), GII.14_Saga_2008_JPN_ADE28701 native VP1 (GII.14; SEQ ID NO: 32; FIG. 25), Hu/GII.17/Kawasaki323/2014/JP (0117; SEQ ID NO: 24; FIG. 26A), and Hu/GII.21/Salisbury150/2011/USA (0121; SEQ ID NO:26; FIG. 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 FIGS. 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 FIGS. 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 FIG. 2C.

[0140] 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.).

[0141] 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., (1997, 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/).

[0142] 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 FIG. 1B). The VP1 protein forms a dimer (FIG. 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 FIG. 1B, comprising of a globular S domain (bottom of ribbon structure) and a P domain (top of ribbon structure).

[0143] As shown in FIG. 1C, the VP1 protein dimerizes via P-domain interactions. These interactions stabilize the spontaneous assembly of norovirus capsid molecules.

[0144] 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.

[0145] 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 15 nm to 50 nm 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, 50 nm, 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.

[0146] As shown in the electron micrographs of FIGS. 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

[0147] 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; FIG. 12A), GI.2 (SEQ ID NO:4; FIG. 13A), GI.3 (SEQ ID NO:6; FIG. 14A), GI.5 (SEQ ID NO:12; FIG. 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; FIG. 16A), GII.1 (SEQ ID NO:13; FIG. 16B), GII.2 (SEQ ID NO:14; FIG. 17A), GII.3 (SEQ ID NO:15; FIG. 18A), GII.4/Sydney (SEQ ID NO:16; FIG. 19A), GII.14/Dresden (SEQ ID NO:27; FIG. 19C), GII.14/FarmingtonHills (SEQ ID NO:28; FIG. 19D), GII.4/Hunter (SEQ ID NO:29; FIG. 19E), GII.14/Shellharbour (SEQ ID NO:30; FIG. 19F), GII.14/Orange (SEQ ID NO:31; FIG. 19G), GII.5 (SEQ ID NO:17; FIG. 20), GII.6 (SEQ ID NO:20; FIG. 21A), GII.7 (SEQ ID NO:18; FIG. 22), GII.12 (SEQ ID NO:19; FIG. 23A), GII.13 (SEQ ID NO:22; FIG. 24A), GII.14/Saga (SEQ ID NO:32; FIG. 25), GII.17 (SEQ ID NO:24; FIG.

26A), GII.21 (SEQ ID NO:26; FIG. 27), provided that the VP1 protein is expressed in a plant and it induces immunity to norovirus when administered to a subject.

[0148] 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 FIG. 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.

[0149] As shown in FIG. 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 FIG. 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.

[0150] As previously shown in U.S. provisional application 62/475,660 (filed Mar. 23, 2017; which is incorporated herein by reference) and PCT/CA2018/050352 (filed Mar. 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.

[0151] Furthermore, as described in U.S. provisional application 62/475,660 and PCT/CA2018/050352 (filed Mar. 23, 2017; and Mar. 23, 2018, respectively, both of which are incorporated herein by reference), leaves infil-

trated 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.

[0152] 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.

[0153] 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.

[0154] 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 FIG. 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 (FIG. 3B), and high density VLPs were produced from plants expressing wild type GI.5 VLPs, GII.12 VLPs (FIG. 3C) and GI.2 VLPs, (FIG. 4A). In contrast, wild type GII.4 VP1 was poorly expressed in plants (FIG. 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).

[0155] Furthermore, expression of native VP1 proteins in plants may result in VLPs characterized as comprising a higher proportion of 23 nm VLPs rather than 38 nm VLPs. For example, expression of wild type GI.3 VP1 results in the production of a significant number of 23 nm VLPs (see FIG.

5C, left hand panel). A greater proportion of 23 nm VLPs also results in the VLPs characterized as being less dense following density gradient centrifugation (see FIG. 5B left hand panel).

[0156] 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 wild-type VP1 and/or VLP that does not comprise the one or more than one substitution, modification or mutation.

[0157] Examples of improved characteristics of the modified VP1 and/or VLP include,

[0158] 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;

[0159] 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;

[0160] 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;

[0161] 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;

[0162] 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);

[0163] 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

[0164] a combination of these improved characteristics.

[0165] 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.

[0166] 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 FIGS. 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/GII.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; FIG. 12A), Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; FIG. 14A), Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; FIG. 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; FIG. 16A), Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; FIG. 16B), Hu/GII.2/CGMH47/2011/TW (SEQ ID NO:14; FIG. 17A), Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO: 15; FIG. 18A), Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO: 16; FIG. 19A), US96/GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27; FIG. 19C), FH02/GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28; FIG. 19D), Hnt04: GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29; FIG. 19E), 2006b: GII.4/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30; FIG. 19F), NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31; FIG. 19G), Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; FIG. 20), Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; FIG. 21A), GII.7/Musa/2010/A1173774 (GII.7; SEQ ID NO:18; FIG. 22), Hu/GII.12/HS206/2010/USA (GII.12; SEQ ID NO: 19; FIG. 23A), GII.13/VA173/2010/H9AWU4 (SEQ ID NO:22; FIG. 24A), GII.14_Saga_2008_JPN_ADE28701 native VP1 (SEQ ID NO: 32; FIG. 25), Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO: 24; FIG. 26A), Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; FIG. 27), provided that the VP1 protein induces immunity to norovirus in a subject, when the VP1 protein is administered to the subject.

[0167] 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; FIG. 12A), Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; FIG. 14A), Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; FIG. 15A), Hu/GI.7/USA/2014/GA5043 (GI.7; SEQ ID NO:101; FIG. 16A), Hu/GII.1/Ascension208/2010/USA (GII.1; SEQ ID NO:13; FIG. 16B), Hu/GII.2/CGM1147/2011/TW (SEQ ID NO:14; FIG. 17A), Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO: 15; FIG. 18A), Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO: 16; FIG. 19A), US96/GII.4/Dresden174/1997/DE_AY741811 (SEQ ID NO: 27; FIG. 19C), FH02/GII.4/FarmingtonHills/2002/US_AY502023 (SEQ ID NO: 28; FIG. 19D), Hnt04: GII.4/Hunter-NSW504D/2004/AU_DQ078814 (SEQ ID NO: 29; FIG. 19E), 2006b: GII.14/Shellharbour-NSW696T/2006/AU_EF684915 (SEQ ID NO: 30; FIG. 19F), NO09: GII.14/Orange-NSW001P/2008/AU_GQ845367 (SEQ ID NO: 31; FIG. 19G), Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; FIG. 20), Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; FIG. 21A), GII.7/Musa/2010/A1173774 (GII.7; SEQ ID NO:18; FIG. 22), Hu/GII.12/HS206/2010/USA (GII.12; SEQ ID NO: 19; FIG. 23A), GII.13/VA173/2010/H9AWU4 (SEQ ID NO:22; FIG. 24A), GII.14_Saga_2008_JPN_ADE28701 native VP1 (SEQ ID NO: 32; FIG. 25), Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO: 24; FIG. 26A), Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; FIG. 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.

[0168] 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.

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

TABLE 1-continued

Listing of Norovirus genotypes (strains) and equivalent amino acid locations of GI and GII strains.				
Position (GI.1 numbering)	43	57	84	94
GI.5	A39	R53	E80	A90
GI.6	A39	R53	E80	S90
GI.7	T39	R53	E80	A90
GI.12	A39	R53	E80	A90
GI.13	A39	R53	E80	A90
GI.14	A39	R53	E80	A90
GI.17	A39	R53	E80	A90
GI.21	A39	R53	E80	A90

[0169] As used herein, the term “conserved substitution” or “conservative substitution” refers to the presence of an amino acid residue in the sequence of the GI.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 hydrophathy value of the same sign and generally of similar magnitude as the amino acid that is replacing the corresponding wild type amino acid.

[0170] 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

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).

[0171] Conservative amino acid substitutions are likely to have a similar effect on the activity of the resultant modified GI.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 Sci., 3:240-247, 1994), Hochuli et al. (Bio/Technology, 6:1321-1325, 1988).

[0172] 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.

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

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,

[0173] 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.

[0174] 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 Gil 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 590X, an alanine, i.e. S94X (590X), 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=L, 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=L, 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.

[0175] Examples of VP1 mutant proteins (modified VP1 proteins) include, but are not limited to, the following.

[0176] 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, FIG. 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, FIG. 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; FIGS. 14A, 14B).

[0177] 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, FIG. 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, FIG. 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, FIG. 28C, SEQ ID NO:292; FIG. 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; FIGS. 14A, 14B).

[0178] 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, FIG. 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, FIG. 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+S94 $\bar{x}$ 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; FIGS. 14A, 14B).

[0179] GI.3_M57X+S94 $\bar{x}$ VP1, where X=I, V, A, L, G, S, T, N, Q, K, or H and $\bar{x}$ =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, FIG. 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, FIG. 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+S94 $\bar{x}$ 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; FIGS. 14A, 14B).

[0180] GI.3_Q84X+S94 $\bar{x}$ VP1, where X=S, N, C or T, and $\bar{x}$ =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, FIG. 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, FIG. 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+S94 $\bar{x}$ 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; FIGS. 14A, 14B).

[0181] GI.3_A43X+M57 $\bar{z}$ +S94 $\bar{x}$ VP1, where X=V, L, I or M, $\bar{z}$ =I, V, A, L, G, S, T, N, Q, K, or H, and $\bar{x}$ =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, FIG. 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 (SEQ ID NO:174, FIG. 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+M57 $\bar{z}$ +S94 $\bar{x}$ 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; FIGS. 14A, 14B).

[0182] 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, FIG. 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, FIG. 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; FIG. 15A).

[0183] 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, FIG. 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, FIG. 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; FIG. 15A).

[0184] 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, FIG. 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, FIG. 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; FIG. 15A).

[0185] 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, FIG. 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; FIG. 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, FIG. 29I; SEQ ID NO:290; FIG. 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; FIG. 16A).

[0186] 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, FIG. 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, FIG. 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; FIG. 16A).

[0187] 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, FIG. 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, FIG. 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; FIG. 16A).

[0188] 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, FIG. 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, FIG. 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; FIG. 17A).

[0189] 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, FIG. 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, FIG. 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; FIG. 17A).

[0190] 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, FIG. 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, FIG. 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; FIG. 17A).

[0191] 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, FIG. 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, FIG. 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; FIG. 17A).

[0192] 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, FIG. 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, FIG. 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; FIG. 17A).

[0193] 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, FIG. 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, FIG. 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; FIG. 17A).

[0194] 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, FIG. 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, FIG. 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; FIG. 18A).

[0195] 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, FIG. 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, FIG. 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; FIG. 18A).

[0196] 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, FIG. 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, FIG. 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; FIG. 18A).

[0197] 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, FIG. 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, FIG. 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.14/Sydney/NSW0514/2012/AU (SEQ ID NO:16, amino acid; SEQ ID NO:52, nucleotide; FIGS. 19A and 19B).

[0198] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0199] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0200] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0201] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0202] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0203] 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, FIG. 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, FIG. 32M), provided that the positions corresponding to amino acids 39-46 of norovirus VP1 genotype GI.1 remain the peptide sequence SSTA-VATA, 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; FIGS. 19A and 19B).

[0204] GII.4_A39X+R53 $\bar{x}$ VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, and $\bar{x}$ =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, FIG. 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, FIG. 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+R53 $\bar{x}$ 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;

[0205] FIGS. 19A and 19B).

[0206] GII.4_A39X+P80 $\bar{x}$ VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, and $\bar{x}$ =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, FIG. 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+P80 $\bar{x}$ 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, FIG. 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+P80 $\bar{x}$ 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; FIGS. 19A and 19B).

[0207] GII.4_V47P+P80S VP1 (GII.4_V47X, where X=P or G+P80 $\bar{x}$, where $\bar{x}$ =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, FIG. 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, FIG. 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+P80 $\bar{x}$ 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; FIGS. 19A and 19B).

[0208] GII.4_R53I+P80S VP1 (GII.4_R53X, where X=I, L, V, A or M+P80 $\bar{x}$, where $\bar{x}$ =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, FIG. 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, FIG. 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, histi-

dine, 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; FIGS. 19A and 19B).

[0209] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0210] GII.4_A39X+R53X+P80Z VP1, where X=V, I, L, M, G, S, E, D, N, Q, K, or H, where X=L, I, 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 position 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0211] 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, FIG. 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, FIG. 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; FIGS. 19A and 19B).

[0212] 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, FIG. 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, FIG. 32Y), provided that 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 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; FIGS. 19A and 19B).

[0213] 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, FIG. 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, FIG. 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; FIGS. 21A and 21B).

[0214] 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, FIG. 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, FIG. 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; FIGS. 21A and 21B).

[0215] 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, FIG. 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, FIG. 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; FIGS. 21A and 21B).

[0216] 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, FIG. 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, FIG. 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; FIG. 23A).

[0217] 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, FIG. 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, FIG. 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; FIG. 23A).

[0218] 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, FIG. 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, FIG. 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; FIG. 23A).

[0219] 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, FIG. 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 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_A39V VP1 protein (SEQ ID NO:192, FIG. 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; FIGS. 26A and 26B).

[0220] 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, FIG. 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, FIG. 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; FIGS. 26A and 26B).

[0221] GII.17_A90L VP1 (GII.17_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, FIG. 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, FIG. 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; FIGS. 26A and 26B).

[0222] 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, FIG. 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 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_A39V+R53I VP1 protein (SEQ ID NO:198, FIG. 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; FIGS. 26A and 26B).

[0223] GII.17_E80S+A90L VP1 (GII.17_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, FIG. 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, FIG. 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; FIGS. 26A and 26B).

VLP Yield

[0224] 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 FIG. 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 FIG. 5F), GI.3_M57I+S94L (see FIG. 5D), and GI.3_Q84S+S94L (see FIG. 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 FIG. 6F) in plants resulted in similar or higher VLPs yields as compared to the yield of wildtype GI.7 VP1.

[0225] An analogous improved characteristic of increased VLP yield is shown with reference to FIGS. 9A-9E, and 9H. VLPs comprising norovirus modified VP1 proteins GII.4_R53I (FIG. 9D), GII.4_P80X, where X=S, A, N, K, or H (FIGS. 9B and 9H), GII.4_P80S+R53I (FIG. 9D), GII.4_P80S+A39X, where X=V, I, M, T, E, D, N, Q, K, or H (FIGS. 9C and 9I), GII.4_P80S+S90L (FIG. 9B), GII.4_P80S+Δ35-42 (FIG. 9C), GII.4_P80S+SSTAVATA (FIG. 9F), and GII.4_A39V+R53I P80S (FIG. 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.

[0226] Increased VLP yield, compared to wild type was also observed in plant extracts expressing GII.6_S90L VP1 (FIGS. 10A and 10B).

[0227] 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 FIG. 6B; GII.3_E80S, also see FIG. 8A), or an increased (GI.7_R84S; GI.7_M57I+R84S; also see FIG. 6D; GII.4_P80S also see FIGS. 9B-9F; GII.12_E80S) VLP yield when compared to the yield of VLPs comprising the corresponding wild type (native) VP1 protein.

[0228] 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 (FIGS. 5B and 5F); GI.5_A94L (see FIG. 6B); GII.2_A90L (see FIG. 7B); GII.4_S90L (see FIG. 9B); GII.6_S90L (see FIG. 10A); GII.12_A90L (see FIG. 11B); and GII.17_A90L (see FIG. 11D).

[0229] 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 FIG. 5B; GI.5_Q84S+A94L, also see FIG. 6B; GII.2_E80S+A90L, also see FIGS. 7B and 7C; GII.4_P80S+S90L, also see FIG. 9B; and GII.2_E80S+A90L, also see FIG. 11B).

[0230] Additional modifications were also observed to increase VLP yield. These modifications include GI.3_M57I+S94L (FIG. 5D), GI.7_M57I (FIG. 6D), GI.7_M57I+R84S (FIG. 6D), GII.2_A39V+E80S+A90L (FIG. 7C), GII.2_R53I+E80S+A90L (FIG. 7C), GII.4_R53I (FIG. 9D), GII.4_A39V+P80X, where X=S, A, N, K, or H (FIGS. 9C and 9I); GII.4_R53I+P80S (FIG. 9D); GII.4_V47P+P80S (FIG. 9E); GII.4_Δ35-42+P80S (FIG. 9C), and GII.4_A39V+R53I+P80S (FIG. 9G).

Size, Density, Stability and Quality of VLPs

[0231] As shown in FIG. 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. 23 nm diameter VLPs than wildtype (FIGS. 5C and 5E) as determined using transmission electron microscopy (TEM).

[0232] 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 (FIG. 6B). As shown in FIG. 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.

[0233] 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 (FIG. 6D). As shown in FIG. 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.

[0234] 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 (FIG. 7C). As shown in FIG. 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.

[0235] Expression of GII.3_E80S in plants, resulted in VLPs of 38 nm diameter particles (FIG. 8B). However, yields of VP1 protein (determined via SDS-PAGE) remained low.

[0236] As shown in FIGS. 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 (FIGS. 9B, 9C, 9D and 9E).

[0237] 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 (FIGS. 9B and 9C). VLPs were also produced from GII.4_V47P; GII.4_V47P+P80S, GII.4_SSTAVATA; GII.4_P80S+SSTAVATA (FIGS. 9E and 9F).

[0238] As shown in FIGS. 10A and 10B, expression of modified norovirus VP1 protein GII.6_S90L produced 38 nm diameter VLPs, determined using transmission electron microscopy (TEM).

[0239] 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 (FIG. 11C) as determined using transmission electron microscopy (TEM).

[0240] 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 (FIG. 11D) as determined using transmission electron microscopy (TEM).

Induction of Immunity Against Norovirus Infection

[0241] 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.

[0242] 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.

[0243] 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.

[0244] 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.

[0245] 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 violet fixation/coloration of cells; microscopic observation of cell lysis in in vitro culture; and 2) ELISA and spectrophotometric detection of norovirus.

[0246] The term “epitope” or “epitopes”, as used herein, refers to a structural part of an antigen to which an antibody specifically binds.

[0247] 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; 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_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 FIG. 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.

[0248] 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 Gil 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.

[0249] 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

[0250] 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); Geier 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 Lefebvre, DB Layzell (eds), Addison Wesley, 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 whisks, 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), Neuhaus et al. (1987, *Theor. Appl. Genet.* 75: 30-36), Klein et al. (1987, *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 Lomonosoff (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. No. 08/438,666, filed May 10, 1995, and Ser. No. 07/951,715, filed Sep. 25, 1992, (all of which are hereby incorporated by reference).

[0251] 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 Lomonosoff, 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.

[0252] 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 Guerinéau 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, Vol I, II 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.

[0253] 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.

[0254] 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.

[0255] 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.

[0256] 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.

[0257] A list of the Norovirus strains and constructs is provided in Table 3.

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/GI.2/Leuven/2003/BEL	4	13A	—
Wt GI.2 hCod (na)	Hu/GI.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	—

TABLE 3-continued

Norovirus strains and constructs.				
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	—
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	—
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 (na)	Hu/GII.2/CGMH47/2011/TW	86	30B	4143 42B
Mut GII.2_A90L (aa)	Hu/GII.2/CGMH47/2011/TW	41	30C	—

TABLE 3-continued

Norovirus strains and constructs.				
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
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	—
Mut GII.4_S90L hCod (na)	Hu/GII.4/Sydney/NSW0514/2012/AU	62	32J	4134 44F
Mut GII.4_A35-42 (aa)	Hu/GII.4/Sydney/NSW0514/2012/AU	63	32K	—
Mut GII.4_A35-42 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
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

TABLE 3-continued

Norovirus strains and constructs.				
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)	FH02/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	8	22	—
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	—
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

TABLE 3-continued

Norovirus strains and constructs.				
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	

[0258] The present invention will be further illustrated in the following examples.

Example 1: Norovirus VP1 Constructs

[0259] The candidate sequences for VP1 and VP2 are available in Genbank (see FIGS. 2A and 2B). Non-limiting examples of these sequences are:

- [0260] Hu/GI.2/Leuven/2003/BEL (GI.2; SEQ ID NO:4; FIG. 13A);
- [0261] Hu/GI.3/S29/2008/Lilla Edet/Sweden (GI.3; SEQ ID NO:6; FIG. 14A);
- [0262] Hu/GI.5/Siklos/Hun5407/2013/HUN (GI.5; SEQ ID NO:12; FIG. 15A);
- [0263] Hu/GI.7/USA/2014/GA5043 (GI.7, SEQ ID NO:101, FIG. 16A)
- [0264] Hu/GII.1/Ascension208/2010/USA SEQ ID NO:13; FIG. 16C);
- [0265] Hu/GII.2/CGMH47/2011/TW (GII.2; SEQ ID NO:14; FIG. 17A);
- [0266] Hu/GII.3/Jingzhou/2013402/CHN (GII.3; SEQ ID NO:15; FIG. 18A);
- [0267] Hu/GII.4/Sydney/NSW0514/2012/AU (GII.4; SEQ ID NO:16; FIG. 19A);
- [0268] US96/GII.4/Dresden174/1997/DE_AY741811 (GII.4; SEQ ID NO:27; FIG. 19C);

- [0269] FH02/GII.4/FarmingtonHills/2002/US_AY502023 (GII.4; SEQ ID NO:28; FIG. 19D);
- [0270] Hnt04: GII.4/Hunter-NSW504D/2004/AU_DQ078814 (GII.4; SEQ ID NO:29; FIG. 19E);
- [0271] 2006b: GII.14/Shellharbour-NSW696T/2006/AU_EF684915 (GII.14; SEQ ID NO:30; FIG. 19F);
- [0272] NO09: GII.4/Orange-NSW001P/2008/AU_GQ845367 (GII.4; SEQ ID NO:31; FIG. 19G);
- [0273] GII.14_Saga_2008_JPN_ADE28701 native VP1 (0114; SEQ ID NO:32; FIG. 25);
- [0274] Hu/GII.5/AlbertaEI390/2013/CA (GII.5; SEQ ID No:17; FIG. 20);
- [0275] Hu/GII.6/Ohio/490/2012/USA (GII.6; SEQ ID NO: 20; FIG. 21A);
- [0276] GII.7/Musa/2010/A1173774 (GII.7; SEQ ID NO:18; FIG. 22);
- [0277] Hu/GII.12/HS206/2010/USA (GII.2; SEQ ID NO:19; FIG. 23A);
- [0278] GII.13/VA173/2010/H9AWU4 (GII.13; SEQ ID NO:22; FIG. 24A);
- [0279] Hu/GII.17/Kawasaki323/2014/JP (GII.17; SEQ ID NO:24; FIG. 26A);
- [0280] Hu/GII.21/Salisbury150/2011/USA (GII.21; SEQ ID NO:26; FIG. 27).
- [0281] 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	ACTAAAGAAAATAGGCCTTTATCTCCGCAGACCGAGGCGTCCGCGGCAGAA	103
IF-GI3Lil08VP1.c	TCGTGCTTCGGCACCAGTACAATGATGATGGCTTCCAAGGATGCTCCCA	104
IF-GI3Lil08VP1.r	ACTAAAGAAAATAGGCCTCTAGCTCCGTCTGATCCCAGGCTCCGAAT	105
VP1_GI.3Lil08(S94L).r	CTGAGCCAAGTGGAGCAGAAACGGATTCAAGTGTGGTCCTAGCTGCAGGTCAAACAAGA	106
VP1_GI.3Lil08(S94L).c	AGGACCACACTTGAATCCGTTTCTGCTCCACTTGGCTCAGATGTATAATGGATGGG	107

TABLE 4-continued

primers used to prepare constructs defined herein.		
Primer	Sequence	SEQ ID NO
VP1_GI.3Lil108(Q84S).r	GTGTGGTCCTAGGCTCAGGTCAAACAAGATGTCACC CGGGGTGTTGTTTGGGCTTAT	108
VP1_GI.3Lil108(Q84S).c	GGTGACATCTTGTTTGACCTGAGCCTAGGACCACAC TTGAATCCGTTT	109
IF-GI3Lil108VP2.c	TCGTGCTTCGGCACCAGTACAATGGCTCAGGCAATC TTCGGCGCAATC	110
IF-GI3Lil108VP2.r	ACTAAAGAAAATAGGCCTTCACTTCCTCATGTTTGC GAACAGGGGAAGC	111
IF-(160)GI.5_Sik113_VP1.c	TCGTGCTTCGGCACCAGTACAATGATGATGGCCTCC AAAGACGCTCCT	112
IF-GI.5_Sik113_VP1.r	ACTAAAGAAAATAGGCCTTCAGCGCCGACGCCAAG GCGCCCCCGGCAGATG	113
GI.5 (hCod) (Q84S).r	GATGAGGGCCTAAGCTCAGGTCTGAACAGAATATCCC CTGGTGTGTTGTTAG	114
GI.5 (hCod) (Q84S).c	TATTCTGTTCGACCTGAGCTTAGGCCCTCATCTCAA CCCCTTCTTGCCCA	115
GI.5 (hCod) (A94L).r	ATCTGGCTCAGGTGGAGCAAGAAGGGGTTGAGATGA GGGCCTAACTGCAG	116
GI.5 (hCod) (A94L).c	TCTCAACCCCTTCTTGCTCCACCTGAGCCAGATGTA CAATGGCTGGGTGGG	117
IF-(160)GII.2_CGMH11_VP1.c	TCGTGCTTCGGCACCAGTACAATGAAGATGGCATCC AACGACGCCGCACCCAGC	118
IF-GII.2_CGMH11_VP1.r	ACTAAAGAAAATAGGCCTTTACTGGATCCGTCGGCG ACCGTTCCCTGTGCCCA	119
VP1_GII.2CGMH11(E80S).r	TTCTGGTCCCAGGCTGAGATTGAGGAGCACTTCCCC AGGGCTATTCTAGGGCTGACCG	120
VP1_GII.2CGMH11(E80S).c	GGAAGTGCTCCTCAATCTCAGCCTGGGACCAGAACT TAATCCGTACCT	121
VP1_GII.2CGMH11(A90L).r	TCCGGGCCAGGTGGAGCAGGTACGGATTAAAGTTCTG GTCCCAGCTCGAGATTGAGGAGC	122
VP1_GII.2CGMH11(A90L).c	GGGACCAGAACTTAATCCGTACCTGCTCCACCTGGC CCGATGTACAATGGATATGCAG	123
IF-(160)GII.3_Jing13_VP1.c	TCGTGCTTCGGCACCAGTACAATGAAAATGGCTTCC AACGATGCAGCACCT	124
IF-GII.3_Jing13_VP1.r	ACTAAAGAAAATAGGCCTTTACTGGATCCGCCGTCT GCCATTGCCTGTAC	125
VP1_GII.3Jing13(E80S).r	ATTTAGGGGCCAGGCTCAAATTCAGAGAACCTCC CCGGGGGAGTTTCGAGGAGAGAC	126
VP1_GII.3Jing13(E80S).c	GGAGGTCTCTTGAATTTGAGCCTGGGCCCTGAAAT TAATCCTTATCT	127
VP1_GII.3Jing13(A90L).r	ATTCGGGCTAGATGGAGCAGATAAGGATTAATTTCA GGGCCAGTTCCAAATTCAGAG	128
VP1_GII.3Jing13(A90L).c	GGGCCCTGAAATTAATCCTTATCTGCTCCATCTAGC CCGAATGTACAACGGCTACG	129
IF-GII.4Syd12VP1.c	TCGTGCTTCGGCACCAGTACAATGAAAATGGCCTCG AGTGACGCTAACC	130
IF-GII.4Syd12VP1.r	ACTAAAGAAAATAGGCCTTCAGACAGCCCTGCGTCT GCCAGTCCCAT	131

TABLE 4-continued

primers used to prepare constructs defined herein.		
Primer	Sequence	SEQ ID NO
VP1_GII.4Syd12 (A39V) . r	GACCGGCCACGGGGACTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	132
VP1_GII.4Syd12 (A39V) . c	GGGCGCAGCCATAGCAGTCCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	133
VP1_GII.4Syd12 (V47P) . r	CGTATCCACGGGTCAATGGGATTCTGCTGACCGGCC ACGGGCGCTGCTATG	134
VP1_GII.4Syd12 (V47P) . c	GGCCGGTCAGCAGAATCCCATTTGACCCGTGGATACG CAACAATTTTGTCGAAG	135
VP1_GII.4Syd12 (R53I) . r	TGGACAAAATTTGTTGATTATCCACGGGTCAATCACA TTCTGCTGACCG	136
VP1_GII.4Syd12 (R53I) . c	GATTGACCCGTGGATAATCAACAATTTTGTCGAAGC CCCTGGTGGGAGT	137
GII.4 (P80S) . r	GATCGGGTCCCAAGCTGGCCGACCACAGGATTTCTC CTGGCGCATTTCTC	138
GII.4 (P80S) . c	AATCCTGTGGTCGGCCAGCTTGGGACCCGATCTGAA CCCCTATTTGTCAC	139
GII.4 (S90L) . r	ATCCGAGCGAGATGCAGCAAATAGGGGTTGAGATCG GGTCCCAATGGGGCCGACCA	140
GII.4 (S90L) . c	TCTGAACCCCTATTTGCTGCATCTCGCTCGGATGTA CAACGGGTATGC	141
VP1_GII.4Syd12 (Del (35-42)) . r	CACATTCTGCTGACCGCCACCACAGGCTCCAGGGC CATCACCTCATTAT	142
VP1_GII.4Syd12 (Del (35-42)) . c	GGAGCCTGTGGTGGGCGGTCAGCAGAATGTGATTGA CCCGTGGATACG	143
VP1_GII.4Syd12 (SSTAVATA) . r	CTGACCGGCTGTAGCGACGGCGGTGAGCTGCCCCAC CACAGGCTCCAGGGCCATCACCTC	144
VP1_GII.4Syd12 (SSTAVATA) . c	TGTGGTGGGCGAGCTCCACCGCGTCTGCTACAGCCGG TCAGCAGAATGTGATTGACCCGTG	145
IF-GII.60hi12VP1 . c	TCGTGCTTCGGCACCAGTACAATGAAGATGGCAAGC AACGACGAGCTC	146
IF-GII.60hi12VP1 . r	ACTAAAGAAAATAGGCCTTCACTGATCCCGGCGTCG CCCCTGGCCTGTCCCCAT	147
IF-GII.6HS10VP2 . c	TCGTGCTTCGGCACCAGTACAATGGCCTCCGCATTT CTAGCTGGATTGGCC	148
IF-GII.6HS10VP2 . r	ACTAAAGAAAATAGGCCTTAACTTGTGATTCTCC CCGTCGCTGGGGTGTG	149
VP1_GII.60hi12 (E80S) . r	AGTTCAGGGCCGAGGCTCAGATTGAGCAGCATCTCG CCCGGGGAGTTCCGAGATTGAGCAG	150
VP1_GII.60hi12 (E80S) . c	CGAGATGCTGCTCAATCTGAGCCTCGGCCCTGAACT AAACCCTTATCT	151
VP1_GII.60hi12 (S90L) . r	ATCCGTGAAAGGTGGAGCAGATAAGGGTTTAGTTCA GGGCCGAGTTCCAGATTGAGCAG	152
VP1_GII.60hi12 (S90L) . c	CCCTGAACTAAACCCCTTATCTGCTCCACCTTTACAG GATGTACAATGGCTACGAGGAG	153
IF- (160) GII.12_HS10_VP1 . c	TCGTGCTTCGGCACCAGTACAATGAAGATGGCGTCT AATGATGCTGCTCCTT	154
IF-GII.12_HS10_VP1 . r	ACTAAAGAAAATAGGCCTTACTGCACACGCCCTCCT CCCATTTCCTGTTCCCAT	155

TABLE 4-continued

primers used to prepare constructs defined herein.		
Primer	Sequence	SEQ ID NO
GII.12 (E80S) .r	AGTTCTGGTCCCTAAGCTCAAATCAATAACACTTCG CCGGGGGAGTTT	156
GII.12 (E80S) .	AGTGTTATTGAATTTGAGCTTAGGACCAGAACTCAA CCCCTATCTGGCA	157
GII.12 (A90L) .r	ATCCGAGACAGATGGAGCAGATAGGGGTTGAGTTCT GGTCCTAATTCCAA	158
GII.12 (A90L) .c	ACTCAACCCCTATCTGCTCCATCTGTCTCGGATGTA CAACGGCTATGCGGGCGGAGT	159
IF-NOV (US68) VP2 (ORF3) (hCod) .c	TCGTGCTTCGGCACCAGTACAATGGCTCAGGCCATT ATTGGCGCCAT	160
IF-NOV (US68) VP2 (ORF3) (hCod) .r	ACTAAAGAAAATAGGCCTTCAGCGGCGGTTGTTAGC GAACAGAGGAAGTC	161
GI.3Lil108 (M571) .r	CTGAACGTAATTTGAGATGATCCAGGGGTCGATCAT GTTTACCTGTCTCGGTGGCGG	202
GI.3Lil108 (M571) .c	GTAACATGATCGACCCCTGGATCATCTCAAATTAC GTTTCAGGCTCCACAGGGGGAGTT	203
IF- (GI.7USA14) VP1 .c	TCGTGCTTCGGCACCAGTACAATGATGATGGCCAGC AAGGACGCTCCGAGTA	204
IF- (GI.7USA14) VP1 .r	ACTAAAGAAAATAGGCCTTCACACCCGCTCAGGCC GAGTCGTGCGACG	205
GI.7USA14_VP1 (R84S) .r	AGTGGGGTCCCTAAGCTGAGGTCAAACAGAAATATCCC CTGGGGTGTTAT	206
GI.7USA14_VP1 (R84S) .c	TATTCTGTTTGACCTCAGCTTAGGACCCCACTTGAA CCCCTTCTGCTTC	207
GI.7USA14_VP1 (M571) .r	AACGAAATGTTGATTATCCACGGGTCGATCATATT GACTTGGCCTGCAGT	208
GI.7USA14_VP1 (M571) .c	GATCGACCCGTGGATAATCAACAATTCGTTTCAGGC ACCAGAAGGAGA	209
GII.2CGMH11 (A39V) .r	TTTGTCTGCCCCGGTCACAGGCACTGCGAGGGCAGCC CCTGCAACAGGCTCCAAGGCCATCAC	210
GII.2CGMH11 (A39V) .c	GTTGCAGGGGCTGCCCTCGCAGTGCCTGTGACCGGG CAGACAAATATCATCGATCCTTG	211
GII.2CGMH11 (R531) .r	CACGAAATTAGCGATAATCCAAGGATCGATGATATT TGTCTGCCCGGTACAGGAGCTG	212
GII.2CGMH11 (R531) .c	GGCAGACAAATATCATCGATCCTTGGATTATCGCTA ATTTCTGTCAAGCCCCAATGGG	213
IF-GII17Kaw14VP1 .c	TCGTGCTTCGGCACCAGTACAATGAAAATGGCATCT AACGACGACGCCCCCTC	214
IF-GII17Kaw14VP1 .r	ACTAAAGAAAATAGGCCTCTACTGAGCCCGGCTCT GCCGTTACCGGTGCCCATTTG	215
GII.17Kaw14 (A90L) .r	GCGGCTCAGATGCAGCAGATATGGATTGAGGTCAGG GCCGAGCTCAAGATTCAGGAGTA	216
GII.17Kaw14 (A90L) .c	CCTGACCTCAATCCATATCTGCTGCATCTGAGCCGC ATGTACAATGGTTAC	217
GII.17Kaw14 (A39V) .r	ATTCTGCCCTGTCACTGGCACAGCTATAGCGGCGCC TGCAACCGGCTCTAGTGGAAGTG	218
GII.17Kaw14 (A39V) .c	AGGCGCCGCTATAGCTGTGCCAGTGACAGGGCAGAA TAATATTATAGACCCTTGGATT	219

TABLE 4-continued

primers used to prepare constructs defined herein.		
Primer	Sequence	SEQ ID NO
GII.17Kaw14 (R531) .r	ACGAAGTTTGTGATAATCCAAGGGTCTATAATATTA TTCTGCCCTGTCACTGGGGCAGC	220
GII.17Kaw14 (R531) .c	GGCAGAATAATATTATAGACCCCTTGGATTATCACAA ACTTCGTGCAGGCACCCAACGGC	221
GII.4Syd12 (P80A) .r	ATCGGGTCCCAAGGCGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	222
GII.4Syd12 (P80A) .c	AATCCTGTGGTCGGCCGCTTGGGACCCGATCTGAA CCCTATTTGTCAC	223
GII.4Syd12 (P80N) .r	ATCGGGTCCCAAGTTGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	224
GII.4Syd12 (P80N) .c	AATCCTGTGGTCGGCCAAGTTGGGACCCGATCTGAA CCCTATTTGTCAC	225
GII.4Syd12 (P80K) .r	ATCGGGTCCCAAGTTGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	226
GII.4Syd12 (P80K) .c	AATCCTGTGGTCGGCCAAGTTGGGACCCGATCTGAA CCCTATTTGTCAC	227
GII.4Syd12 (P80H) .r	ATCGGGTCCCAAGTTGGCCGACCACAGGATTTCTCC TGGCGCATTTCTCG	228
GII.4Syd12 (P80H) .c	AATCCTGTGGTCGGCCCAAGTTGGGACCCGATCTGAA CCCTATTTGTCAC	229
GII.4Syd12 (A391) .r	GACCGGCCACGGGGATTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	230
GII.4Syd12 (A391) .c	GGGCGCAGCCATAGCAATCCCCGTGGCCGTCAGCA GAATGTGATTGACCCGTG	231
GII.4Syd12 (A39M) .r	GACCGGCCACGGGCATTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	232
GII.4Syd12 (A39M) .c	GGGCGCAGCCATAGCAATGCCCGTGGCCGTCAGCA GAATGTGATTGACCCGTG	233
GII.4Syd12 (A39G) .r	GACCGGCCACGGGGCTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	234
GII.4Syd12 (A39G) .c	GGGCGCAGCCATAGCAGGCCCCGTGGCCGTCAGCA GAATGTGATTGACCCGTG	235
GII.4Syd12 (A39S) .r	GACCGGCCACGGGGCTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	236
GII.4Syd12 (A39S) .c	GGGCGCAGCCATAGCAAGCCCCGTGGCCGTCAGCA GAATGTGATTGACCCGTG	237
GII.4Syd12 (A39E) .r	GACCGGCCACGGGCTCTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	238
GII.4Syd12 (A39E) .c	GGGCGCAGCCATAGCAGAGCCCGTGGCCGTCAGCA GAATGTGATTGAC	239
GII.4Syd12 (A39D) .r	GACCGGCCACGGGGTCTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	240
GII.4Syd12 (A39D) .c	GGGCGCAGCCATAGCAGACCCCGTGGCCGTCAGCA GAATGTGATTGACCCGTG	241
GII.4Syd12 (A39N) .r	ACCGGCCACGGGGTTTGTATGGCTGCGCCACCAC AGGCTCCAGGGCCATCAC	242
GII.4Syd12 (A39N) .c	GGGCGCAGCCATAGCAAACCCCGTGGCCGTCAGCA GAATGTGATTGACCCGTG	243

TABLE 4-continued

primers used to prepare constructs defined herein.		
Primer	Sequence	SEQ ID NO
GII.4Syd12 (A39Q) .r	GACCGGCCACGGGCTGTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	244
GII.4Syd12 (A39Q) .c	GGGCGCAGCCATAGCACAGCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	245
GII.4Syd12 (A39K) .r	GACCGGCCACGGGCTTTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCATCA	246
GII.4Syd12 (A39K) .c	GGGCGCAGCCATAGCAAAGCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	247
GII.4Syd12 (A39H) .r	GACCGGCCACGGGCTGTGCTATGGCTGCGCCACCA CAGGCTCCAGGGCCA	248
GII.4Syd12 (A39H) .c	GGGCGCAGCCATAGCACACCCCGTGGCCGGTCAGCA GAATGTGATTGACCCGTG	249
GI.7USA14 (M57L) .r	GAACGAAATTGTTTCAGTATCCACGGGTCGATCATAT TGACTTGGCCTGCA	250
GI.7USA14 (M57L) .c	GATCGACCCGTGGATACTGAACAATTCGTTTCAGGC ACCAGAAGGAGA	251
GI.7USA14 (M57G) .r	GAACGAAATTGTTGCCTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	252
GI.7USA14 (M57G) .c	GATCGACCCGTGGATAGGCAACAATTCGTTTCAGGC ACCAGAAGGAGA	253
GI.7USA14 (M57S) .r	GAACGAAATTGTTGCTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	254
GI.7USA14 (M57S) .c	GATCGACCCGTGGATAAGCAACAATTCGTTTCAGGC ACCAGAAGGAGA	255
GI.7USA14 (M57T) .r	GAACGAAATTGTTGGTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	256
GI.7USA14 (M57T) .c	GATCGACCCGTGGATAACCAACAATTCGTTTCAGGC ACCAGAAGGAGA	257
GI.7USA14 (M57N) .r	GAACGAAATTGTTGTTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	258
GI.7USA14 (M57N) .c	GATCGACCCGTGGATAAACAACAATTCGTTTCAGGC ACCAGAAGGAGA	259
GI.7USA14 (M57Q) .r	GAACGAAATTGTTCTGTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	260
GI.7USA14 (M57Q) .c	GATCGACCCGTGGATACAGAACAATTCGTTTCAGGC ACCAGAAGGAGA	261
GI.7USA14 (M57K) .r	GAACGAAATTGTTCTTTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	262
GI.7USA14 (M57K) .c	GATCGACCCGTGGATAAAGAACAATTCGTTTCAGGC ACCAGAAGGAGA	263
GI.7USA14 (M57H) .r	GAACGAAATTGTTGTGTATCCACGGGTCGATCATAT TGACTTGGCCTGCAGT	264
GI.7USA14 (M57H) .c	GATCGACCCGTGGATACACAACAATTCGTTTCAGGC ACCAGAAGGAGA	265
GI.3Lil108 (S94V) .r	TCTGAGCCAAGTGCACCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	266
GI.3Lil108 (S94V) .c	CTTGAATCCGTTTCTGGTGCCTTGGCTCAGATGTA TAATGGATGGTTGGAAA	267

TABLE 4-continued

primers used to prepare constructs defined herein.		
Primer	Sequence	SEQ ID NO
GI.3Lil108 (S941) .r	TCTGAGCCAAGTGGATCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	268
GI.3Lil108 (S941) .c	CTTGAATCCGTTTCTGATCCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	269
GI.3Lil108 (S94M) .r	TCTGAGCCAAGTGCATCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	270
GI.3Lil108 (S94M) .c	CTTGAATCCGTTTCTGATGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	271
GI.3Lil108 (S94T) .r	TCTGAGCCAAGTGGGTCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	272
GI.3Lil108 (S94T) .c	CTTGAATCCGTTTCTGACCCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	273
GI.3Lil108 (S94E) .r	TCTGAGCCAAGTGCTCCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	274
GI.3Lil108 (S94E) .c	CTTGAATCCGTTTCTGGAGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	275
GI.3Lil108 (S94D) .r	TCTGAGCCAAGTGGTCCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	276
GI.3Lil108 (S94D) .c	CTTGAATCCGTTTCTGGACCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	277
GI.3Lil108 (S94N) .r	TCTGAGCCAAGTGGTTCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	278
GI.3Lil108 (S94N) .c	CTTGAATCCGTTTCTGAACCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	279
GI.3Lil108 (S94Q) .r	TCTGAGCCAAGTGCTGCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	280
GI.3Lil108 (S94Q) .c	CTTGAATCCGTTTCTGCAGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	281
GI.3Lil108 (S94K) .r	TCTGAGCCAAGTGCTTCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	282
GI.3Lil108 (S94K) .c	CTTGAATCCGTTTCTGAAGCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	283
GI.3Lil108 (S94H) .r	TCTGAGCCAAGTGGTGCAGAAACGGATTCAAGTGTG GTCCTAGCTGCAGGTCAA	284
GI.3Lil108 (S94H) .c	CTTGAATCCGTTTCTGCACCACTTGGCTCAGATGTA TAATGGATGGGTTGGAAA	285

WT GI.1 Norovirus VP1: A2×35S/CPMV 160/wt VP1
GI.1/NOS (Construct Number 2724)

[0282] A human codon-optimized sequence encoding VP1 from Norovirus strain GI.1/Norwalk/1968/US was cloned into 2×35S/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 opti-

mized for human codon usage, GC content and mRNA structure. The PCR product was cloned in 2×35S/CPMV 160/NOS expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 1190 (SEQ ID NO:162; FIGS. 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 2×35S/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 (FIG. 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 FIG. 39A.

2×35S/CPMV 160/GII.4_P80S (hCod)/NOS+MAR (Construct Number 4133)

[0283] 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 2×35S/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-01.4Syd12VP1.r (SEQ ID NO:131) as primers. The final PCR product was cloned in 2×35S/CPMV 160/NOS+MAR expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 3677 (SEQ ID NO:164; FIGS. 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 2×35S/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 (FIG. 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 FIG. 44E.

2×35S/CPMV 160/GII.4_P80S+S90L (hCod)/NOS+MAR (Construct Number 4135)

[0284] 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 2×35S/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-01.4Syd12VP1.r (SEQ ID NO:131) as primers. The final PCR product was cloned in 2×35S/CPMV 160/NOS+MAR expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 3677 (SEQ ID NO:164; FIGS. 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 2×35S/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 (FIG. 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 FIG. 44E.

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 2×35S/CPMV 160/NOS+MAR expression system using In-Fusion cloning system (Clontech, Mountain View, CA). Construct number 3677 (SEQ ID NO:164; FIGS. 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 2×35S/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 FIG. 44L.

[0285] 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

[0286] *Agrobacterium tumefaciens* Transfection

[0287] *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 OD₆₀₀ between 0.6 and 1.6. *Agrobacterium* suspensions were centrifuged before use and resuspended in infiltration medium (10 mM MgCl₂ and 10 mM MES pH 5.6).

Preparation of Plant Biomass, Inoculum and Agroinfiltration

[0288] *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

[0289] *Agrobacteria* transfected with each native norovirus VP1, native norovirus VP2, or norovirus VP1 mutant expression vector were grown in a YEB medium supple-

mented with 10 mM 2-(N-morpholino)ethanesulfonic acid (MES), 20 μ M acetosyringone, 50 μ g/ml kanamycin and 25 μ g/ml of carbenicillin pH5.6 until they reached an OD₆₀₀ between 0.6 and 1.6. *Agrobacterium* suspensions were centrifuged before use and resuspended in infiltration medium (10 mM MgCl₂ 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

[0290] 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 μ g/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.

[0291] 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 polyvinylidene difluoride (PVDF) membranes (Roche Diagnostics Corporation, Indianapolis, Ind.) 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

[0292] 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%. Peroxidase-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

[0293] 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

[0294] 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 100000 g. The pellets were re-suspended in 300-1000 μ l of buffer depending of the VP1 quantity.

[0295] 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° C. 20 μ l 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 μ l 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 μ l 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 10,000 $\times$ to 150,000 $\times$.

Example 3: VP1 Protein and VLP Production in Plants

[0296] *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 55-60 kDa 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.

[0297] 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 (FIG.

3A). In contrast, wild type GII.4 VP1 was poorly expressed in plants (FIG. 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

[0298] 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 (FIG. 5F).

[0299] As shown in FIGS. 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).

[0300] 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 (FIGS. 5C and 5E).

GI.5 VLPs and VLPs Comprising Modified GI.5 VP1 Proteins

[0301] 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 (FIG. 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.

[0302] As shown in FIG. 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 iodixanol 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 (FIG. 6C).

GI.7 VLPs and VLPs Comprising Modified GI.7 VP1 Proteins

[0303] 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 (FIG. 6F).

[0304] As shown in FIG. 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 iodixanol 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 (FIG. 6E).

GII.2 VLPs and VLPs Comprising Modified GII.2 VP1 Proteins

[0305] 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 FIG. 7A).

[0306] 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.

[0307] 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 (FIG. 7B). The GII.2 VLP preparations having the E80S+A90L, or A39V+E80S+A90L substitution also comprised the same or fewer damaged viral particles when compared to wildtype GII.2 VLPs (FIG. 7C).

GII.3 VLPs and VLPs Comprising Modified GII.3 VP1 Proteins

[0308] 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.

[0309] 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 (FIG. 8B).

GII.4 VLPs and VLPs Comprising Modified GII.4 VP1 Proteins

[0310] With reference to FIGS. 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=5, 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 (Δ 35-42) in combination with a proline to serine substitution at position 80 (Δ 35-42+P80S), resulted in higher VP1 protein yields following extraction for plants, as compared to VP1 yields using wildtype GII.4.

[0311] 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 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=5, 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_ Δ 35-42+P80S VP1; a 14-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, T, 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.

[0312] Results of VLPs comprising modified GII.4 proteins are shown in FIGS. 9B-9D and 9G. Constructs comprising GII.4 VP1 having: a proline to serine substitution at position 80 (P80S; FIG. 9B, 9C, 9D); a serine to leucine substitution at position 90 (S90L; FIG. 9B); an alanine to valine substitution at position 39 in combination with a proline to serine substitution at position 80 (A39V+P80S; FIG. 9C); an arginine to isoleucine substitution at position 53 in combination with a proline to serine substitution at position 80 (R53I+P80S; FIG. 9D); a proline to serine substitution at position 80 in combination with a serine to leucine substitution at position 90 (P80S+S90L; FIG. 9B); a proline to serine substitution at position 80 in combination with a deletion of positions 35-42 (P80S+ Δ 35-42; FIG. 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; FIG. 9G), resulted in the production of VLPs that reside in higher density iodixanol fractions (29-33%).

[0313] VLPs comprising GII.4 VP1 proteins having: a P80S substitution in combination with an S90L substitution (P80S+S90L; FIG. 9B); an A39V substitution in combination with a P80S substitution (A39V+P80S; FIG. 9C); a P80S substitution in combination with a deletion of positions 35-42 (Δ 35-42+P80S; FIG. 9C); an R53I substitution in combination with a P80S substitution (R53I+P80S; FIG. 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; FIG. 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

[0314] 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

[0315] 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; FIG. 11A).

[0316] 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

[0317] 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).

[0318] 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%).

[0319] 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

[0320] 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.

[0321] 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).

[0322] 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 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.

[0323] 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.

[0324] 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).

[0325] 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 log 10-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 log 10-transformed data.

[0326] 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 FIG. 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 log 10-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 log 10-transformed data. Significant differences were annotated as letters in FIG. 3D (the same letter indicates that no significant difference was detected between treatment groups; p>0.05).

[0327] 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.

[0328] Mouse Immune Response to Norovirus Native VP1 VLPs

[0329] As demonstrated in FIG. 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 μ g and 10 μ g 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 μ g and 10 μ g ($p < 0.05$). 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.

[0330] 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.

[0331] All citations are hereby incorporated by reference.

[0332] 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.

SEQUENCE LISTING

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 organism = unidentified

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 organism = unidentified

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 organism = synthetic construct

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                    mol_type = other DNA
                    organism = synthetic construct

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source           1..1632
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accccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900
ggacaggggc tgaatcttac tgagatcgat ggtacccct accatgcatt cgagtcacct 960
gcacctattg gatttcccgga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020
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gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140
atctgtagcc tagagtggct atctccgcca agcgggtggg cccctaaagt taacctatgg 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 ttgttgcat acgtagacc cgatacccat 1440
agaaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaaactcc 1500
tccggcagtg gccctcaaac ctggccgcatc aacggcggtg tcacgtttat cagctgggtt 1560
tcacggtttt accaaactcaa gcccgctcga acaactgggc cagttcggag gctcgggatc 1620
agacggagct ag                                     1632

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SEQ ID NO: 10      moltype = AA length = 543
FEATURE           Location/Qualifiers
source            1..543
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

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SEQUENCE: 10
MMMASKDAPT NMDGTSGAGQ LVPEVSTAEP ISMEPVAGAA TAAATAGQVN MIDPWIMSNY 60
VQAPQGEFTI SPNNTPGDIL FDLSLGPHLN PFLHLHAQMY NGWVGNMKVR VLLAGNAFTA 120
GKIIISCVPV GFAAQNVISIA QATMFPHVIA DVRVLEPIEV PLEDVRNVLF HNNDSTPTMR 180
LICMLYTPLR ASGSSSGTDP FVIAGRVLTC PSPDFNFLFL VPPNVEQKTK PFSVPLNPLN 240
VLSNSRVPSL IKSNMVQDQH GQMVQFQNGR VTLDGQLQGT TPTSASQLCK IRGTVYHATG 300
GGQLNLTEID GTPYHAFESP APIGFDDLGE CDWHINASPA NAFTDGSIIH RIDVAQDSTF 360
APHLGTIHYT NADYNANVGL ICSLEWLSPP SGGAPKVPNW AIPRYGSTLT EAAQLAPPIY 420
PPGFGEAIVF FMSDFPIANG SDGLSVPCTI PQEFVTHFVN EQAPTRGEAA LLHYVDPDTH 480
RNLGEFKLYP EGFMTCPVNS SSGSPQTLPI NGVFTFISWV SRFYQLKPVG TTGPVRLGI 540
RRS                                     543

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SEQ ID NO: 11      moltype = DNA length = 1632
FEATURE           Location/Qualifiers
misc_feature       1..1632
                  note = Nucleic acid sequence of human codon optimized VP1
                  GI.3 Lil08 Q84S plus sign S94L
source            1..1632
                  mol_type = other DNA
                  organism = synthetic construct

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SEQUENCE: 11
atgatgatgg cttccaagga tgcctccaca aacatggatg gaacaagcgg cgcggggcaa 60
cttgtgcggg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cggcgcgacc 120
actgtctcgg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180
gttcaggctc ccacggggga gtttaccata agcccaaaaa acacccgggg tgacatcttg 240
tttgacctga gcttaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300
aatggatggg ttggaaaacat gaaggtgccc gtgctcctgg cgggcaatgc attcagacc 360
gggaagatta ttactctctg cgtgccacct ggatttgacg ccagaaacgt gtctatcgca 420
caggcaacca tgtttccgca tgtcatcgca gatgtgccc tgctagagcc catcgagggt 480
ccccctgagg acgtgcgcaa cgtcctatcc cataacaatg atagcacccc caccatgcgc 540
ttgatattga tggatatata tccccctccc gccagtgggt ccagctccgg gaccgatcct 600
tttgtgattg ctggcggggt gttgacttgt cctagccctg acttcaactt cttttttctg 660
gtgctcccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gcccttaac 720
gtgctgtcga attcccagagt gccttccctt attaagtgcca tgatgggtatc tcaggatcac 780
gggtcaaatgg tgcagtttca gaacggccga gtgacggttag acgggcagct gcagggcaca 840
accccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900
ggacaggggc tgaatcttac tgagatcgat ggtacccct accatgcatt cgagtcacct 960
gcacctattg gatttcccgga tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020
aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080
gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140
atctgtagcc tagagtggct atctccgcca agcgggtggg cccctaaagt taacctatgg 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 ttgttgcat acgtagacc cgatacccat 1440
agaaaacctgg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaaactcc 1500
tccggcagtg gccctcaaac ctggccgcatc aacggcggtg tcacgtttat cagctgggtt 1560
tcacggtttt accaaactcaa gcccgctcga acaactgggc cagttcggag gctcgggatc 1620
agacggagct ag                                     1632

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SEQ ID NO: 12      moltype = AA length = 543
FEATURE           Location/Qualifiers

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source          1..543
                 mol_type = protein
                 note = Norovirus
                 organism = unidentified

SEQUENCE: 12
MMMASKDAPS SADGANGAGQ LVPEVNNAEP LPLDPVAGAS TALATAGQVN MIDPWIFNNF 60
VQAPQGEFTI SPNNTPGDIL FDLQLGPHLN PFLAHLQMY NGWVGNMVR VILAGNAFTA 120
GKVIICCVPP GFQSRTLSIA QATLFPHIIA DVRTLEPIEI PLEDVRNTLY HTNDNQPTMR 180
LLCMLYTPLR TGGGSGGTD FVVAGRVLTC PSSDFNLFLL VPPTVEQKTR PFSVPNIPLQ 240
LLSNSRVPNL IQSMVLSPDQ AQNVQFQNGR CTTDQQLGT TPVSVSQILK FRGKVSAGSK 300
VINLTELDGS PFLAFEAPAP TGFPDLGTS DWHVEMSLNSN SQSSGNPILL RDIHPNSSEF 360
VPHLGSVCVT AAIEVAGDYT GTIQWTSQPS NVTPVPDVNF WTIPHYGSNL AEASQLAPVV 420
YPPGFGEAIV YFMSPIPGPN TAHKPNLVPC LLPQEFVTHF VSEQAPSMGE AALVHYVDPD 480
TNRNLGEFKL YPEGFITCVP NGTGPQQLPL NGVVFVFSWV SRFYQLKPVG TASSARGRLG 540
VRR 543

SEQ ID NO: 13      moltype = AA length = 535
FEATURE           Location/Qualifiers
source            1..535
                 mol_type = protein
                 note = Norovirus
                 organism = unidentified

SEQUENCE: 13
MKMASNDAAP SNDGAAGLVP EVNNETMALE PVAGASIAAP LTGQNNVIDP WIRMNFVQAP 60
NGEFTVSPRN SPGEVLLNLE LGPELNPFLA HLSRMYNGYA GGVEVQVLLA GNAFTAGKLV 120
FAAIPPHFPL ENLSPGQITM FPHVIDVRT LEPVLLPLPD VRNFFHYNQ QPEPRMRLVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPSPDF DFNLYVPPTV ESKTKPFTLP ILTIGELSNS 240
RFPVPIDELY TSPNEGVMVQ PQNGRSTLDG ELLGTQLVLP SNICALRGRI NAQVPDDHHQ 300
WNLQVTNANG TSPDPTDVP APLGTPDPLA NIYGVTSQRN PDNTRAHDG VLATWSPKFT 360
PKLGSVVLGT WEESDLDLNQ PTRFTPVGLY DTGHFDQWVL PNYSGRLTLN MNLAPSVAPL 420
FPEQILFFR SHIPLKGGTS NGAIIDCLLPQ EWIQHFYQES APSPTDVALI RYTNPDTRGV 480
LFEAKLHRQG FITVANSISR PIVVPPNGYF RFDSWVNQFY SLAPMGTGNG RRRVQ 535

SEQ ID NO: 14      moltype = AA length = 542
FEATURE           Location/Qualifiers
source            1..542
                 mol_type = protein
                 note = Norovirus
                 organism = unidentified

SEQUENCE: 14
MKMASNDAAP STDGAAGLVP ESNNEVMALE PVAGAAALAP VTGQTNIIDP WIRANFVQAP 60
NGEFTVSPRN SPGEVLLNLE LGPELNPFLA HLSRMYNGYA GGMEVQVLLA GNAFTAGKLV 120
FAAVPPHFPV ENLSPQITM FPHVIDVRT LEPVLLPLPD VRNFFHYNQ KDDPKMRIVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPSPDF DFTYLVPPPTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIDQMY TSPNEVISVQ CQNGRCTLDG ELQGTQLQV SGICAFKGEV TAHLHDNDHL 300
YNNITNLNG SPFDPSDIP APLGVDPFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWT DDLTVNQPVK FTPVGLNDTD HFNQWVVPY AGALNLNTNL 420
APSVAPVPPG ERLFFRSYI PLKGGYGTGA IDCLLPQEWV QHFYQEAAPS MSEVALVRYI 480
NPDTEGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWVNQFYSLA PMGTGNGRRR 540
IQ 542

SEQ ID NO: 15      moltype = AA length = 548
FEATURE           Location/Qualifiers
source            1..548
                 mol_type = protein
                 note = Norovirus
                 organism = unidentified

SEQUENCE: 15
MKMASNDAAP SNDGAAGLVP EISSEAMALE PVAGAAIAAP LTGQQNIIDP WIMNMFVQAP 60
GGEFTVSPRN SPGEVLLNLE LGPEINPYLA HLSRMYNGYA GGFEVQVLLA GNAFTAGKII 120
FAAIPPNFPI DNLSAAQITM CPHVIDVRQ LEPVNLPMFD VRNFFHYNQ GSDSRRLRIA 180
MLYTPLRANS SGDDVFTVSC RVLTRPSPDF SFNFLVPPTV ESKTKPFSLP ILTISEMSNS 240
RFPVPIDSLH TSPTEINVQ CQNGRVTLDG ELMGTQLLP SQICAFRGTL TRSTSRASDQ 300
ADTATPRLFN YYWHIQDLN NGTPYDPAED IPAPLGTPDF RGKVFQVQS RNPDATTRAH 360
EAKIDTSSGR FTKPLGSLIE STESGDFDQN QPTRFTPVGI GVDHEPDPQQ WALPDYAGQF 420
THNMNLAPAV APNPPGEQLL FFRSQLPSSG GRSNGILDCL VPQEWVQHFY QESAPSQTQV 480
ALVRVYNPD GRVLFEAKLH KLRFMITAKS GDSPITVPPN GYFRFESWVN PFYTLAPMGT 540
GNRRRIQ 548

SEQ ID NO: 16      moltype = AA length = 540
FEATURE           Location/Qualifiers
source            1..540
                 mol_type = protein
                 note = Norovirus
                 organism = unidentified

SEQUENCE: 16

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MKMASSDANP	SDGSAANLVP	EVNNEVMALE	PVVGAAIAAP	VAGQQNVIDP	WIRNNFVQAP	60
GGFTVSPRN	APGEILWSAP	LGPDLNPYLS	HLARMYNGYA	GGFEVQVILA	GNAFTAGKVI	120
FAAVPPNPFT	EGLSPSQVTM	FPHIVVDVRQ	LEPVLIPLPD	VRNNFYHYNQ	SNDPTIKLIA	180
MLYTPLRANN	AGDDVFTVSC	RVLTRPSPDF	DFIFLVPPTV	ESRTKPFSPV	VLTVEMTNS	240
RFPIPLEKLF	TGPSSAFVVQ	PQNGRCTTDG	VLLGTTQLSP	VNICTFRGDV	THITGSRNYT	300
MNLASQNWND	YDPTTEEIPAP	LGTDPDFVGKI	QGVLTQTTRT	DGSTRGHKAT	VYTGSADFAP	360
KLGRVQFETD	YDRDFEANQN	TKFTPVGVQI	DGGTTHRNEP	QQWVLPSYSG	RNTHNVHLAP	420
AVAPTFPGEQ	LLFFRSTMPG	CSGYPNMDLD	CLLPQEWVQY	FYQEAAPQAS	DVALLRFVNP	480
DTGRVLFPECK	LHKSGYVTVA	HTGQHDLVIP	PNGYFRFDSW	VNQFYTLAPM	GNGTGRRRAV	540

SEQ ID NO: 17 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 17

MKMASNDATP	SNDGAAGLVP	ESNNEAMALE	PVVGASLAAP	VTGQTNIIDP	WIRTNFVQAP	60
NGEFTVSPRN	SPGEILVNLE	LGPDLNPYLA	HLARMYNGYA	GGMEVQVLLA	GNAFTAGKII	120
FAAVPPYFPV	ENLSPSQITM	FPHVIDVVRT	LEPVLLPMPD	VRSTLFHFNQ	KDEPKMRLVA	180
MLYTPLRSNG	SGDDVFTVSC	RILTRPSPEF	DFTYLVPPTV	ESKTKPFTLP	VLTGLGELSNS	240
RFPLSIDEMV	TSPNESIVVQ	PQNGRVTLDG	ELLGTTQLQA	CNICSIRGKV	TGQVPNEQHM	300
WNLEITNLNG	TQFDPTDDVP	APLGVPDFAG	EVFGVLSQRN	RGESNPANRA	HDAVVATYSD	360
KYTPKLGVLQ	IGTWNTNDVE	NQPTKFTPIG	LNEVANGHRF	EQWTLPRYSG	ALTLMNMLAP	420
AVAPLFPGER	LLFFRSYVPL	KGGFGNPAID	CLVPQEWVQH	FYQESAPSLG	DVALVRVYNP	480
DTGRVLFPEAK	LHKGGFLTIVS	STSTGPVVVP	ANGYFRFDSW	VNQFYSLAPM	GTNGRRRRFQ	540

SEQ ID NO: 18 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 18

MKMASNDAAP	SNDGAAGLVP	EINNEVMPL	PVAGASLATP	VVGQQNIIDP	WIRNNFVQAP	60
AGEFTVSPRN	SPGEILLDLE	LGPDLNPYLA	HLARMYNGHA	GGMEVQIVLA	GNAFTAGKII	120
FAAIPPGFPY	ENLSPSQITM	CPHVIIDVRQ	LEPVLLPMPD	IRNNFFHYNQ	GNDPKRLRIA	180
MLYTPLRANN	SGDDVFTVSC	RVLTKPSPDF	EFTFLVPPTV	ESKTKQFTLP	ILKISEMTNS	240
RFPVPVEMMY	TARNENQVVQ	PQNGRVTLDG	ELLGTTPLLA	VNICKFKGEV	IAKNGDVRSY	300
RMDMEITNTD	GTPIDPTEDT	PGPIGSPDFQ	GILFGVASQR	NKNEQNPAIR	AHEANINTGG	360
DQYAPKLAQV	KFFSESQDFE	VHQPTVFPTV	GVAGDTSHPF	RQWVLPYRGG	HLTNNTHLAP	420
AVAPLFPGEQ	ILFFRSQIPS	SGGHELGYMD	CLVPQEWVQH	FYQEAATAQS	EVALIRFINP	480
DTGRVLFPEAK	LHKQGFITVA	HTGDNPIVMP	PNGYFRFEAW	VNQFYSLAPV	GTNGRRRRIQ	540

SEQ ID NO: 19 moltype = AA length = 535
 FEATURE Location/Qualifiers
 source 1..535
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 19

MKMASNDAAP	SNDGAAGLVP	EVNNETMALE	PVAGASIAAP	LTGQNNVIDP	WIRLNFVQAP	60
NGEFTVSPRN	SPGEVLLNLE	LGPDLNPYLA	HLSRMYNGYA	GGVEVQVLLA	GNAFTAGKLV	120
FAAVPPHPPL	ENISPGQITM	FPHVIDVVRT	LEPVLLPLPD	VRNNFFHYNQ	QNEPRMRLVA	180
MLYTPLRSNG	SGDDVFTVSC	RVLTRPSPDF	DFNYLVPPTV	ESKTKPFTLP	ILTIGELTNS	240
RFPVPIDELY	TSPNESLVVQ	PQNGRCALDG	ELQGTQQLLP	TAICSFRGRI	NQKVSGENHV	300
WNMQVTNIDG	TFPDPTEDEV	APLGTDPDFSG	KLFGVLSQRD	HDNACRSHDA	VIAATNSAKFT	360
PKLGAIQGTG	WEQDDVHINQ	PTKFTPVGLF	ESEGFNQWTL	PNYSGALTLN	MGLAPPVAPT	420
FPGEQILFFR	SHIPLKGGVA	DPVIDCLLPQ	EWIQHLYQES	APSQTDVALI	RFTNPDTGRV	480
LFEAKLHRSG	YITVANTGSR	PIVVPANGYF	RFDSWVNQFY	SLAPMGTGNG	RRRVQ	535

SEQ ID NO: 20 moltype = AA length = 547
 FEATURE Location/Qualifiers
 source 1..547
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 20

MKMASNDAAP	SNDGAANLVP	EANNEVMALE	PVVGASIAAP	VVGQQNIIDP	WIRENFVQAP	60
QGEFTVSPRN	SPGEMLLNLE	LGPDLNPYLS	HLSRMYNGYA	GGMQVQVLLA	GNAFTAGKII	120
FAAVPPHPFP	ENINAAQITM	CPHVIVIDVRQ	LEPVLLPLPD	IRNRFFHYNQ	ENTSRMRLVA	180
MLYTPLRANS	GEDVFTVSCR	VLTRPAPDFE	FTFLVPPTVE	SKTKPFSLPI	LTLGELSNSR	240
FPAPIDMLYT	DPNREGIVVQ	QNGRCTLDGT	LQGTTLQVPT	QICAFRGTLI	GQTSRSPDST	300
DSAPRRRDHP	LHVQLKNLDG	TQYDPTDEV	AVLGAIDFKG	TVFGVASQRD	VSGQQVGATR	360
AHEVHINTTD	PRYTPKLGSI	LMYSESDDFV	TGQPVRFPTPI	GMGDNNDHWQ	ELPDYPGHLT	420
LNMNLAPAVA	PAPFGERILF	FRSIVPSAGG	YSGSQIDCLI	PQEWVQHFYQ	EAAPSQSAVA	480

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LIRYVNPDTG RNIFEAKLHR EGFITVANSN NNPIVVPPNG YFRPEAWVNQ FYTLTPMGTG 540
 QGRRRDQ 547

SEQ ID NO: 21 moltype = DNA length = 1644
 FEATURE Location/Qualifiers
 misc_feature 1..1644
 note = Nucleic acid sequence of human codon-optimized VP1
 GII.6 Ohio 2012 M9T020
 source 1..1644
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 21

atgaagatgg	caagcaacga	cgcagctccc	tccaatgatg	gtgccgccaa	cctgggtcccc	60
gaagctaata	atgaggtgat	ggcggttagag	cgggtgggtg	gcgcactctat	tgcagcgcct	120
gtggtcggac	agcagaacat	cattgatccc	tggattcgcg	agaacttcgt	acaagctcca	180
cagggggagt	tcacagcttc	cccccggaac	tccccggcgg	agatgctgct	caatctggaa	240
ctcgccctg	aactaaaccc	ttatctgtca	cacctttcac	ggatgtacaa	tggtctacgca	300
ggaggaatgc	aagttcaggt	ggctcctggcc	ggcaatgctt	tcaccgcggg	caaaatcatc	360
tttgccggcg	ttcctccaca	cttcctgtc	gaaaatatca	acgccgccca	gattactatg	420
tgccccacg	tgattgtgga	tgtgcgacag	ttagagccag	ttctgctgcc	cctgccccgac	480
atcagaaaacc	ggttcttcca	ttacaatcaa	gagaatactt	cacggatgag	acttgttgcg	540
atgctgtaca	cccctcttcg	tgcaaatccc	ggcgaagacg	tgttcaactgt	gtcttgtcga	600
gtacttacc	gacccgcccc	cgatttcgaa	ttcaccttcc	tggttcccc	tactgtggag	660
agcaagacaa	aaccttcag	cctcccaatc	taaactctcg	gggagctgtc	taattcacgc	720
ttccccgcac	ctattgat	gctgtatact	gaccccaacg	aggggatagt	ggtgcagccc	780
caaaatggac	gggtgactct	cgacggcacg	ctccagggca	caacccaact	ggtgccaaacc	840
cagattttgtg	cattcagggg	cactttgatt	gggcagacat	cgagatctcc	agattctact	900
gattccgcgc	caaggaggag	ggaccaccca	ctccacgttc	agttaaaaaa	cctggacgga	960
acccagtaacg	accctacaga	cgaggtcccc	gctgtcctcg	gagccatcga	ctttaaagga	1020
actgtatttg	gagtggtcatc	ccaaagggat	gtctcggggc	agcaggtggg	agctacgaga	1080
gcacatgaag	cccacattaa	caccacagac	ccaagatata	ccccaaaact	agggccaatt	1140
ttaatgtatt	cggaatcaga	cgattttgtt	acaggtcagc	ccgtgcgggt	taccccgatc	1200
ggaatggggg	acaacgattg	gcaccagtg	gaattgcccc	attaccctgg	acacctcacc	1260
ttgaatatga	atctggcccc	cgccgtcgcg	cccgccttcc	ccggtgagcg	gacccctttt	1320
tttagaagca	tagtgccctc	cgcaggtggg	tatggatcag	ggcagattga	ttgcctgac	1380
ccccaaagat	gggtacagca	ttctaccag	gaagcagccc	ctagccagtc	cgcagtagca	1440
ctgatcagat	agttaatcc	tgatacggga	aggaacatct	tcgaagcaaa	actgcaccgt	1500
gagggcttca	ttaccgtcgc	caacagtgg	aataacccta	ttgtgggtgc	tcctaagga	1560
tacttcaggt	ttgaggcatg	ggtgaatcag	ttttatactc	tgactcccat	ggggacaggc	1620
caggggcgac	gcccggatca	gtga				1644

SEQ ID NO: 22 moltype = AA length = 542
 FEATURE Location/Qualifiers
 source 1..542
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 22

MKMASNDAAP	SNDGAASLVP	EAINETMPLE	PVAGASIAAP	VAGQTNIIDP	WIRTNFVQAP	60
NGEFTVSPRN	SPGEILLNLE	LGPLDLNPYLA	HLSRMYNGYA	GGVEVQVLLA	GNAFTAGKIL	120
FAAIPNPFV	DMISPAQITM	LPHLIVDVRT	LEPIMIPLPD	VRNVFYHFNN	QPQPRMRLVA	180
MLYTPLRNSG	SGDDVFTVSC	RVLTRPTPDF	EFIYLVPPSV	ESKTKPFTLP	ILTISELTNS	240
RFPISIEQLY	TAPNENNVVQ	CQNGRCTLDG	ELQGTQQLS	SAVCSYRGRT	VANSQDNWDQ	300
NVLQLTYPSP	ASYDPTDEVP	APLGTQDFSG	ILYGVLTQDN	VRENTGEAKN	AKGVYISTTS	360
GKFTPKIGSI	GLHSITDVR	PNQQRFTPV	GVAQNENTPF	QQWVLPHYAG	ALALNTNLAP	420
AVAPTFPGEQ	LLFPRSFRVPC	VQGLQGQDAF	IDCLLPQEWV	NHFYQEAAPS	QADVALIRYV	480
NPDTGRTLFE	AKLHRSRGRIT	VSHTGAYPLV	VPPNGHFRFD	SWVNFQFYSLA	PMGTGNGRRR	540
VQ						542

SEQ ID NO: 23 moltype = DNA length = 1629
 FEATURE Location/Qualifiers
 misc_feature 1..1629
 note = Nucleic acid sequence of human codon-optimized VP1
 GII.17_Kawa_2014_A0A077KVU6
 source 1..1629
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 23

atgaaaaatgg	cttctaata	tgccgcgccc	agcaatgatg	gtgccgccag	ccttgtgtccc	60
gaagcaatta	acagagacaat	gcccttgagg	ccagtcgccc	gggtctctat	tcgggccccca	120
gttgctggac	agacagatat	catcgatcct	tggatacggg	ctaattttgt	tcaagctcct	180
aacggagagt	tcaactgtctc	cccccgtaat	agtcttgccg	agatcctgtt	gaacctcgag	240
ttggggccag	atctcaatcc	ttacctggct	catctgtcga	gaatgtacaa	cgggtacgcg	300
gggggggttg	aggtgcaggt	cttactggca	ggtaacgcac	tcacagcagg	caagattctg	360
tttgccggcca	tcctctctaa	ttttccagtg	gatatgat	ctccagcaca	gattacaatg	420
ctgccccatt	tgatagtggg	tgtgcgggca	cttgaacctc	tcatgatccc	ttgccccgat	480

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gtccgaaatg tgttttatca tttcaacaac cagccgcgagc caagaatgcg tctcgtcgcg 540
atgctgtaca ccccggttgcg gtccaacggc tctggcgatg atgttttcac agtgcgtgtg 600
cgagtgttaa cccgcccctac cccagatttt gagtttatat atctagtccc ccttctctgtg 660
gaaagcaaga ctaaaccctt tactcttccc attctgacta tatccgagct taccaactcc 720
cgggtccccca tctcaatcga gcaactgtac actgcaccca acgagaacaa cgtagtccag 780
tgccagaaacg ggagatgtac cctggacggg gagctccaa ggaccacgca actgttaagt 840
tcagccggtt gcagttacag aggcaggact gtggcgaact ctggtgataa ctgggatcaa 900
aatgtgttgc agctgactta cccatccggc gcaagctacg atccaacaga tgagggtgcca 960
gcgccccttg gcacacagga tttctcagga attctatacg gggtgcttac tcaggataat 1020
gtgcgagaaa atactggcga ggccaagaat gctaaaggag tgtatataag cacgacaagc 1080
ggtaagttta ccccaaaaat tggcagtatt gggtccaca gcattactga ggacgtccgc 1140
ccaaaccagc agtctcgttt cactcccgtg ggggtggcac agaacgagaa cacacctttc 1200
cagcagtggt tcttgcccca ttatgcaggt gctttggcgc tcaatacaaa tctggcacc 1260
gcgctagcgc cgacatttcc tggggagcaa ttgctgttct ttagaagccg cgtcccggtg 1320
gttcagggtc tgcagggcca ggaacggttc attgattgcc tcttgcccca ggaatgggtc 1380
aaccactttt atcaggagggc agccccctct caagcagatg tggccctgat aagatatgtg 1440
aatcccgaca caggacggac tttgtttgag gcaaaactcc accggtcagg attcattact 1500
gtgagtcaca caggagccta tccccttggt gttccaccta atggccactt cagggttcgac 1560
tcttgggtca atcagtttta ttgcgtggca ccaatgggta ccgggaatgg tcgccgtcgg 1620
gtgcaatga

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SEQ ID NO: 24      moltype = AA length = 538
FEATURE           Location/Qualifiers
source            1..538
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

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SEQUENCE: 24
MKMASNDAAP SNDGAAGLVP EGNNETLPLE PVAGAAIAAP VTGQNNIIDP WIRTNFVQAP 60
NGEFTVSPRN SPGBILNLLE LGPDLNPLYA HLSRMYNGYA GGVEVQVLLA GNAFTAGKIL 120
FAAVPPNFPV EFLSPAQITM LPHLIVDVRT LEPIMIPLEP VRNTFFHYNN QPNRMRMLVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPTPDF EFTYLVPPSV ESKTKPFSLP ILTLSELTNS 240
RFPVPIDSLF TAQNNVLQVQ CQNGRCTLDG ELQGTQQLLP SGICAFRGRV TAETDHRDKW 300
HMQLQNLNGT TYDPTDDVPA PLGTPDFKGV VFGVASQRNV GNDAPGSTRA HEAVISTYSP 360
QFVPKLGSVN FRSNDNDFQL QPTKFTPVGI NDDGDHPFRQ WELPDYSGLL TLNMNLAPPV 420
APNFPGEQLL FFRSFVPCSG GYNQGIVDCL IPQEWIQHFY QESAPSQSDV ALIRYVNPDT 480
GRTLFEAKLH RSGYITVAHS GDYPLVVPAN GYFRFDSWVN QFYSLAPMGT GNGRRRAQ 538

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SEQ ID NO: 25      moltype = DNA length = 1617
FEATURE           Location/Qualifiers
misc_feature       1..1617
                  note = Nucleic acid sequence of human codon-optimized VP1
                  GII.17_Kawa_2014_A0A077KVU6
source            1..1617
                  mol_type = other DNA
                  organism = synthetic construct

```

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SEQUENCE: 25
atgaaaaatgg catctaacga cgcagccccc tcaaacgatg gcgctgctgg actcgtgccg 60
gaggggaata atgagacact tccactagag ccggttgtag gcgcccgtat agtgcgccca 120
gtgacagggc agaataatat tatagacct tggattcgga caaactcgtg gcaggcacc 180
aacggcgagt ttacagtatc ccccccgaac tcccaggtg agatactcct gaatcttgag 240
ctcggccctg acctcaatcc atatctggct catctgagcc gcatgtacaa tggttacgct 300
gggggggtcg aagtgcaggt cctcctggcc ggaaacgctt ttaccgctgg caaaattctg 360
tttgccgcgc ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420
ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgcgggat 480
gtgcgttaaca cctttttcca ttataacaat cagccaaact ctcggatgag acttgttctg 540
atgctgtaca cccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600
agagtcccta cccgcccact cccggacttc gagttcacct acctgggtgc ccttctgtg 660
gaatctaaga ccaaaccggt ttcaactgcca atcttaactc tctccgaact gactaacagc 720
cggtttccag tacccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780
tgccagaaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840
agtggcatct gtgcattccg gggcccgctg accgctgaga cagaccatcg tgacaaatgg 900
cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgagca cgtccctgct 960
ccgctaggga ctccgtactt taaggggggt gtgttcggag tggcctctca gcggaatgtt 1020
gggaatgacg cccccggctc taccgagct caccggcgcg ttatctcaac atatagcccc 1080
caatttgtgc ccaagctcgg atccgttaat ttctgtagta acgacaacga cttccaactg 1140
caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc tttccgcca 1200
tggaactac cagattatc tgggctgctc acctcaata tgaacctcgc cccaccgctg 1260
gcccctaatt tcccgggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320
ggatataatc aaggcatcgt agactcgtt attccccaa agtggatata acatttttac 1380
caggaaagtg gccctcccca gtcgatgtg gccctgatac ggtacgttaa ccccgatacc 1440
ggaagaacat tatcgaagc gaattgcac agatcaggtt acattaccgt tgcacattcc 1500
ggcgattatc ccttggtggt tcccgcacac ggttacttta gggtcgatag ttgggtcaac 1560
cagttctatt cactagcccc aatgggcacc ggtaacggca gacgcggggc tcagtag 1617

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SEQ ID NO: 26      moltype = AA length = 539

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-continued

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FEATURE                               Location/Qualifiers
source                               1..539
                                     mol_type = protein
                                     note = Norovirus
                                     organism = unidentified

SEQUENCE: 26
MKMASNDAAP SDNGATGLVP EINTETLPLE PVAGAAIAAP VTGQNNIIDP WIRNNFVQAP 60
NGEFTVSPRN SPGEILMNL EGPDLNPYLA HLSRMVNGYA GGFEVQVLLA GNAFTAGKIL 120
FAAVPPNFPV DMLSPAQITM LPHLIVDVRT LEPIMIPLPD VRNVFYHFNN QPAPRMRLVA 180
MLYTPLRSNG SGDDVFTVSC RVLTRPTPDF EFTYLVPPSV ESKTKPFTLP ILTIGELTNS 240
RFPAPIDQLY TSPNADVVVQ PQNGRCTLDG ELQGTQQLLT TAICSYRGMT SNPTSDYWD 300
HLLHLVHPNG ATYDPTEDVP APFGTQDFRG ILYGMLTQNP RTSGDEAANS HGIYISSTSE 360
KFTPKLGTIG LHQVQGDIA NQQSKFTPVG IAVNGNTTFR QWELPNYSGA LTLNTNLAPA 420
VGPNPFPGEQI LFFRSNVPSV QGGQPIEIDC LIPQEWVSHF YQESAPSQSD VALVRVNPDP 480
TGRITFEAKL HRQGITITAA TGSNPVVVPP NGYFRFDSWV NQFYALAPMG TGNGRRRVQ 539

SEQ ID NO: 27                       moltype = AA length = 539
FEATURE                               Location/Qualifiers
source                               1..539
                                     mol_type = protein
                                     note = Norovirus
                                     organism = unidentified

SEQUENCE: 27
MKMASNDANP SDGSTANLVP EVNNEVMALE PVVGAIAAP VAGQQNVIDP WIRNNFVQAP 60
GGFTVSPRN APGEILWSAP LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPPT EGLSPSQVTM FPHIIVDVRO LEPVLIPLPD VRNNFYHYNQ SNDSTIKLIA 180
MLYTPLKANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFTVP ILTVEEMSNS 240
RFPIPLEKLY TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSA VNICTFRGDV THIAGSHDYT 300
MNLASQNWNN YDPTTEIPAP LGTPDFVGGI QGMLTQTTRE DGSTRAHKAT VSTGSHVFTP 360
KLGSVQYTTD TNNDFTQGN TKFTPVGVIG DGNHQNNEP QWVLPNYSR TGHNVHLAPA 420
VAPTFPGEQL LFFRSTMPGC SGYPNMNLD LPPQEWVQH YQEAAPQSD VALLRFVNP 480
TGRVLFECKL HKSGYVTVAH TGHDLVIPP NGYFRFDSWV NQFYTLAPMG NGAGRRRAL 539

SEQ ID NO: 28                       moltype = AA length = 540
FEATURE                               Location/Qualifiers
source                               1..540
                                     mol_type = protein
                                     note = Norovirus
                                     organism = unidentified

SEQUENCE: 28
MKMASNDANP SDGSTANLVP EVNNEVMALE PVVGAIAAP VAGQQNVIDP WIRNNFVQAP 60
GGFTVSPRN APGEILWSAP LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKII 120
FAAVPPNFPPT EGLSPSQVTM FPHIIVDVRO LEPVLIPLPD VRNNFYHYNQ LNDPTIKLIA 180
MLYTPLRANN AGEDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFTVP ILTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THIAGTHNYT 300
MNLASQNWNN YDPTTEIPAP LGTPDFVGGI QGMLTQTTRE DGSTRGHKAT VSTGSHVFTP 360
KLGSIQFNTD TNNDFTQGN TKFTPVGVVQ DGNHQNNEP QWVLPNYSR RTGHNVHLAP 420
AVAPTFPGEQ LFFRSTMPG CSYPMNMLD CLLPQEWVQH FYQEAAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTVH HTGQHDVIP PNGYFRFDSW VNQFYTLAPM NGTGRRRAL 540

SEQ ID NO: 29                       moltype = AA length = 540
FEATURE                               Location/Qualifiers
source                               1..540
                                     mol_type = protein
                                     note = Norovirus
                                     organism = unidentified

SEQUENCE: 29
MKMASNDATP SDGSTANLVP EVNNEVMALE PVVGAIAAP VAGQQNVIDP WIRNNFVQAP 60
GGFTVSPRN APGEILWSAP LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKII 120
FAAVPPNFPPT EVLSPSQVTM FPHIIVDVRO LEPVLIPLPD VRNNLYHYNQ SNDPTIRLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFVSP ILTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THIAGTQNYT 300
MNLASQNWNN YDPTTEIPAP LGTPDFVGGI QGVLTQTTRE DGSTRGHKAT VSTGSHVFTP 360
KLGSVQFSTD TSNDFTQGN TRFTPVGVVQ DGSTTHQNEP QWVLPNYSR RDSHNVHLAP 420
AVAPTFPGEQ LFFRSTMPG CSYPMNMLD CLLPQEWVQH FYQESAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTVH HTGQHDVIP PNGYFRFDSW VNQFYTLAPM NGAGRRRAL 540

SEQ ID NO: 30                       moltype = AA length = 540
FEATURE                               Location/Qualifiers
source                               1..540
                                     mol_type = protein
                                     note = Norovirus
                                     organism = unidentified

SEQUENCE: 30
MKMASNDANP SDGSAANLVP EVNNEVMALE PVVGAIAAP VAGQQNVIDP WIRNNFVQAP 60
GGFTVSPRN APGEILWSAP LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKII 120

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FAAVPPNFPT	EGLSPSQVTM	FPHIIVDVRO	LEPVLIPLPD	VRNNFYHYNQ	SNDSTIKLIA	180
MLYTPLRANN	AGEDVFTVSC	RVLTRPSPDF	DFIFLVPPTV	ESRTKPFTVP	ILTVEEMTNS	240
RFPIPLEKLF	TGPGSAFVVQ	PQNGRCTTDG	VLLGTTQLSP	VNICTFRGDV	THIAGSRNYT	300
MNLAASKWKN	YDPTTEIPAP	LGTPDFVGKI	QGVLTQTTKG	DGSTRGHKAT	IYTGSAFPTP	360
KLGSVQFSTD	TENDFETHQN	TKFTPVGVTQ	DGSTTHRNEP	QQWVLPSYSG	RNVHNVHLAP	420
AVAPTFPGEQ	LLFFRSTMPG	CSGYPNMDLD	CLLPQEWVQH	FYQEAAPQS	DVALLRFVNP	480
DTGRVLFECK	LHSGYVTVA	HTGQHDVIP	PNGYFRFDSW	VNQFYTLAPM	GNGTGRRRAL	540

SEQ ID NO: 31 moltype = AA length = 540
FEATURE Location/Qualifiers
source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 31

MKMASSDANP	SDGSTANLVP	EVNNEVMALE	PVVGAAIAP	VAGQQNVIDP	WIRNNFVQAP	60
GGEFTVSPRN	APGEILWSAP	LGPDMNPYLS	HLARMYNGYA	GGFEVQVILA	GNAFTAGKII	120
FAAVPPNFPT	EGLSPSQVTM	FPHIIVDVRO	LEPVLIPLPD	VRNNFYHYNQ	SNDPTIKLIA	180
MLYTPLRANN	AGEDVFTVSC	RVLTRPSPDF	DFIFLVPPTV	ESRTKPFSVP	ILTVEEMTNS	240
RFPIPLEKLF	TGPGSAFVVQ	PQNGRCTTDG	VLLGTTQLSP	VNICTFRGDV	THIAGSRNYT	300
MNLAQNWNNS	YDPTTEIPAP	LGTPDFVGKI	QGVLTQTTTRT	DGSTRGHKAT	VYTGSADFSP	360
KLGRVQFATD	TSRNFEDANQ	TKFTPVGVIQ	DGNTAHRNEP	QQWVLPSYSG	RNTHNVHLAP	420
AVAPTFPGEQ	LLFFRSTMPG	CSGYPNMDLD	CLLPQEWVQY	FYQEAAPQS	DVALLRFVNP	480
DTGRVLFECK	LHSGYVTVA	HTGQHDVIP	PNGYFRFDSW	VNQFYTLAPM	GNGTGRRRAL	540

SEQ ID NO: 32 moltype = AA length = 536
FEATURE Location/Qualifiers
source 1..536
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 32

MKMAENDATP	SDDGAAGLVP	EINNEVMALE	PVAGASIAAP	VVGQQNIIDP	WIRNNFVQAP	60
AGEFTVSPRN	SPGELLLDLE	LGPELNPYLA	HLARMYNGHA	GGMEVQIVLA	GNAFTAGKIL	120
FAAIPSPFPY	ENLSPAQLTM	CPHVIVDVRO	LEPVLLPMPD	IRNVFYHYNQ	NNSPKLRLVA	180
MLYTPLRANN	SGDDVFTVSC	RVLTRPSPDF	QFTFLVPPTV	ESKTKNFTLP	VLRVSEMTNS	240
RFVVLDQMY	TSRNNENIIVQ	PQNGRCTTDG	ELLGTTILQS	VSICNFKGTM	QAKLNEEPY	300
QLQLTNLDGS	PIDPTDDMPA	PLGTPDFQAM	LYGVASQRSS	IDNATRAHDA	QIDTAGDTFA	360
PKIGQVRPKS	SNDPDLHDP	TKFTPIGVNV	DDQHPFRQWS	LPNYGGHLAL	NNHLAPAVTP	420
LFPGEQILFF	RSYIPASAGH	TDGAMDCLLP	QEWVEHFYQE	AAPSQSDIAL	VRFINPDTGR	480
VLFEAKLHKQ	GFLTIAASGD	HPIVMPTNGY	FRFEAWNPNP	YTLAPVGTGS	GRRRIQ	536

SEQ ID NO: 33 moltype = DNA length = 1632
FEATURE Location/Qualifiers
misc_feature 1..1632
 note = Nucleic acid sequence of human codon-optimized VP1
 GI.5 Siklos HUN5407 2013 HUN AHW99832
source 1..1632
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 33

atgatgatgg	ctcccaaaga	cgctcctagc	agtgtctgatg	gcgctaacgg	tgccggccag	60
ctgggtcccg	agggtgaataa	cgccgagcct	ctcccccttg	acccagtagc	cggagcttca	120
acggccctag	ctactgccc	acaggttaat	atgattgacc	cctggatttt	caataatttc	180
gtgcaggccc	ctcaaggcga	gtttactata	agccctaaca	acacaccagg	ggatattctg	240
ttcgacctgc	agttaggccc	tcactctaac	cccttctctg	cccacctgag	ccagatgtac	300
aatggctggg	tgggcaacat	cgcagtgaga	gttatccctc	cagggaacgc	ctttaccgct	360
ggtaagggtga	tcattttgtt	cgtaccacct	ggattccagt	ctaggacatt	aagtatttgc	420
caagctaccc	tccttctctca	tatcatcgcc	gacgtgcgga	cactagagcc	catcgagatc	480
ccactggagg	atgtccggaa	taccctgtac	cataccaacg	ataatcagcc	cactatgagg	540
ttactgtgca	tgtctgtacac	gccactccgg	actggtgggg	gcagtggggg	gaccgatgct	600
ttcgtcgttg	ccggtagggt	gctcacttgc	ccgtcatctg	actttaactt	cctattcctt	660
gtgcccccaa	cggtggaaca	gaaaacgaga	cctttttccg	tacctaaccat	ccctttacag	720
ctccctaagca	atagcagagt	acctaaccct	atccaatcca	tggttcttag	ccctgatcaa	780
gcgcagaaac	tacagtttca	gaacggggcg	tgcaaccacg	atggccagct	gcttggtaca	840
actcccgtct	ccgtgtctca	gatacttaag	tttcgcgcca	aggtctccgc	tgatccaaa	900
gtaatcaacc	tcactgagct	tgatggctct	ccctttctgt	cggttcgagg	gcccgcacca	960
acaggctttc	cagacctggg	aacatccgat	tggcagtctg	agatgagctt	gaatagcaac	1020
tcccagctct	ctggcaatcc	aatactgtc	cgcgatatcc	atcctaattc	tagcagattc	1080
gttcacacac	tgggttctgt	gtgcgtgacg	gctgcaatag	aggtggctgg	cgactacacg	1140
ggtagccattc	agtggaacct	tcagccaagt	aacgtgaccc	ctgtgccaga	cgtaactttt	1200
tggaacaattc	cacactacgg	ctctaacttg	gccgaagcat	cccagcttgc	ccccgttgta	1260
tatccccacg	gctttggcga	agcaatagtt	tattttatgt	ccccaatccc	tggaacctaac	1320
acagcacaca	agccaaacct	cgtcccatgc	ctgtgcctcc	aggagtctcg	gactcatttc	1380
gtttcggaac	aagccccatc	aatgggggag	gccgcccctg	tccactacgt	ggatccagat	1440
accaatcgga	atctggggaga	attcaaaact	taccctgaag	gattcattac	atgtgtgccc	1500

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aatggaacag gaccgcagca gctccactg aacggtgtct ttgtattcgc atcatgggtt 1560
agccggttct atcaacttaa acccgtgggg acagcttcat ctgcccgggg gcgccttgcc 1620
gtgcggcgct ga 1632

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SEQ ID NO: 34      moltype = AA  length = 543
FEATURE           Location/Qualifiers
source            1..543
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

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SEQUENCE: 34
MMASKDAPS SADGANGAGQ LVPEVNNAEP LPLDPVAGAS TALATAGQVN MIDPWIFNNF 60
VQAPQGEFTI SPNNTPGDIL FDLGLGPHLN PFLAHLQMY NGWVGNMRVR VILAGNAFTA 120
GKVIICCVPP GFQSRITLSIA QATLFPPIIA DVRTLEPIEI PLEDVRNTLY HTNDNQPTMR 180
LLCMLYTPLR TGGSGGTDA FVVAGRVLTG PSSDFNLFEL VPPTVEQKTR PFSVPNIPLQ 240
LLNSRVPNL IQSMVLSPDQ AQNVQFQNGR CTTDGQLLGT TPVSVSQILK FRGKVSAGSK 300
VINLTLDGS PFLAFEAPAP TGFDDLGTSD WHVEMSLNSN SQSSGNPILL RDIHPNSSEF 360
VPHLGSVCVT AAIEVAGDYT GTIQWTSQPS NVTVPVDVNF WTIPHYGSNL AEASQLAPVV 420
YPPGFGEAIV YFMSPIPGPN TAHKPNLVPC LLPQEFVTHF VSEQAPSMGE AALVHYVDPD 480
TNRNLGEFPL YPEGFITCVP NGTGPQQLPL NGVVFVFSWV SRFYQLKPVG TASSARGRLG 540
VRR 543

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SEQ ID NO: 35      moltype = DNA  length = 1632
FEATURE           Location/Qualifiers
misc_feature       1..1632
                  note = Nucleic acid sequence of human codon optimized VP1
                  GI.5 Siklos Q84S
source            1..1632
                  mol_type = other DNA
                  organism = synthetic construct

```

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SEQUENCE: 35
atgatgatgg cctccaaaga cgtcctagc agtgctgatg gcgctaacgg tgccggccag 60
ctggcccccg aggtgaataa cgcgcagcct ctcccccttg acccagtagc cggagcttca 120
acggccctag ctactgccgg acagggttaat atgattgacc cctggatttt caataatttc 180
gtgcaggccc ctcaaggcga gtttactata agccctaaca acacaccagg ggatattctg 240
ttcgacctga gcttagggcc tcattctcaac ccttctctgg ccacacctgag ccagatgtac 300
aatggctggg tgggcaaacat gcgagtgaga gttatcctcg cagggaacgc cttacgcgt 360
ggtaagggtga tcatgtgttg cgtaccacct ggattccagt ctaggacatt aagtattgct 420
caagctaccc tcttctctca taccatcgcc gacgtgcgga cactagagcc catcgagatc 480
ccactggagg atgtccggaa taccctgtac cataccaacg ataactcagc cactatgagg 540
ttactgtgca tgtgtgtacac gccactccgg actggtgggg gcagtggggg gaccgatgct 600
ttcgtcgttg ccggtagggt gctcacttgc ccgtcatctg actttaactt cctattcctt 660
gtgcccccaa cgttggaaca gaaaacgaga cctttttccg tacctaactt ccttttacag 720
ctcctaagca atagcagagt acctaaccctg atccaatcca tgggttcttag ccctgatcaa 780
gcgcagaacg tacagtttca gaacggggcg tgcaccacag atggccagct gcttggtaca 840
actccgtct cctgtgtctca gatacttaag ttccgcgcca aggtctccgc tggatccaaa 900
gtaatcaacc tcactgagct tgatggctct ccttttctgg cgttcgaggg gcccgcccca 960
acaggtcttc cagacctggg aactccgat tggcatgtcg agatgagttc gaatagcaac 1020
tccagttctt ctggcaatcc aatactgctc cgcgatatcc atcctaattc tagcgagttc 1080
gttcacacac tgggttctgt gtgcgtgacg gctgcaatag aggtgggtgg cgactacacg 1140
ggatcatttc agtggacctc tcagccaagt aacgtgaccc ctgtgccaga cgttaacttt 1200
tggacaattc cacactacgc ctctaacttg gccgaagcat cccagcttgc ccccgttgta 1260
tatccccag gctttggcga agcaatagtt tattttatgt cccaatccc tggacctaac 1320
acagcacaca agccaaacct cgtcccatgc ctgctgcccc aggagttcgt gactcatttc 1380
gtttcggaac aagccccatc aatgggggag gccgccctgg tccactacgt ggatccagat 1440
accaatcgga atctggggaga attcaaacac taccctgaag gattcattac atgtgtgccc 1500
aatggaacag gaccgcagca gctccactg aacggtgtct ttgtattcgc atcatgggtt 1560
agccggttct atcaacttaa acccgtgggg acagcttcat ctgcccgggg gcgccttgcc 1620
gtgcggcgct ga 1632

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SEQ ID NO: 36      moltype = AA  length = 543
FEATURE           Location/Qualifiers
source            1..543
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

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SEQUENCE: 36
MMASKDAPS SADGANGAGQ LVPEVNNAEP LPLDPVAGAS TALATAGQVN MIDPWIFNNF 60
VQAPQGEFTI SPNNTPGDIL FDLQLGPHLN PFLHLHLSQMY NGWVGNMRVR VILAGNAFTA 120
GKVIICCVPP GFQSRITLSIA QATLFPPIIA DVRTLEPIEI PLEDVRNTLY HTNDNQPTMR 180
LLCMLYTPLR TGGSGGTDA FVVAGRVLTG PSSDFNLFEL VPPTVEQKTR PFSVPNIPLQ 240
LLNSRVPNL IQSMVLSPDQ AQNVQFQNGR CTTDGQLLGT TPVSVSQILK FRGKVSAGSK 300
VINLTLDGS PFLAFEAPAP TGFDDLGTSD WHVEMSLNSN SQSSGNPILL RDIHPNSSEF 360
VPHLGSVCVT AAIEVAGDYT GTIQWTSQPS NVTVPVDVNF WTIPHYGSNL AEASQLAPVV 420
YPPGFGEAIV YFMSPIPGPN TAHKPNLVPC LLPQEFVTHF VSEQAPSMGE AALVHYVDPD 480
TNRNLGEFPL YPEGFITCVP NGTGPQQLPL NGVVFVFSWV SRFYQLKPVG TASSARGRLG 540

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-continued

VRR 543

SEQ ID NO: 37 moltype = DNA length = 1632
 FEATURE Location/Qualifiers
 misc_feature 1..1632
 note = Nucleic acid sequence of human codon optimized VP1
 GI.5 siklos A94L
 source 1..1632
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 37

atgatgatgg	cctccaaaga	cgctcctagc	agtgtctgatg	gcgctaacgg	tgccggccag	60
ctgggtcccg	agggtgaataa	cgccgagcct	ctccccttgg	accagtagc	cggagcttca	120
acggccctag	ctactgcccg	acaggttaat	atgattgacc	cctggatttt	caataatttc	180
gtgcaggccc	ctcaaggcga	gtttactata	agccctaaca	acacaccagg	ggatattctg	240
ttcgacctgc	agttaggccc	tcactcaac	cccttcttgc	tccacctgag	ccagatgtac	300
aatggctggg	tgggcaacat	gcgagtgaga	gttatcctcg	cagggaacgc	ctttaccgct	360
ggtaagggtga	tcattttgttg	cgtaccacct	ggattccagt	ctaggacatt	aagtattgcg	420
caagctaccc	tctttcctca	tatcatcgcc	gacgtgcgga	cactagagcc	catcgagatc	480
ccactggagg	atgtccggaa	taccctgtac	cataccaacg	ataatcagcc	cactatgagg	540
ttactgtgca	tgtgttacac	gccactccgg	actggtgggg	gcagtggggg	gaccgatgct	600
ttcgtcgttg	ccggtagggt	gctcacttgc	ccgtcatctg	actttaactt	cctattcctt	660
gtgcccccaa	cggtggaaca	gaaaaacgaga	cctttttccg	tacctaacat	ccctttacag	720
ctcctaagca	atagcagagt	acctaacctg	atccaatcca	tggttcttag	ccctgatcaa	780
gcgcagaaag	tacagtttca	gaacgggccc	tgacccaacg	atggccagct	gcttggtaca	840
actcccgctc	ccgtgtctca	gatacttaag	tttcgcgcca	aggctctcgc	tggtatccaaa	900
gtaatcaacc	tcactgagct	tgatggctct	ccctttcttg	cggtcgaggg	gcccgcceca	960
acaggctttc	cagactggg	aacatccgat	tggcatgtcg	agatgagttc	gaatagcaac	1020
tcccagttct	tggtcaatcc	aatactgtct	cgcgatatcc	atcctaattc	tagcgagttc	1080
gttcacacac	tggtttctgt	gtcgtgacg	gctgcaatag	agggtggctg	cgactacacg	1140
ggtagccattc	agtggaacct	tcagccaagt	aacgtgaccc	ctgtgccaga	cgtaaacttt	1200
tggacaattc	cactactacg	ctctaacttg	gccgaagcat	cccagcttgc	ccccgttgta	1260
tatccccacg	gccttgccga	agcaatagtt	tattttatgt	ccccaatccc	tggaacctaac	1320
acagcacaca	agccaaacct	cgtcccctgc	ctgctgcccc	aggagttcgt	gactcatttc	1380
gtttcggaac	aagccccatc	aatggggggg	gccgcccttg	tccactacgt	ggatccagat	1440
accaatcgga	atctggggaga	attcaaaact	taccctgaag	gattcattac	atgtgtgccc	1500
aatggaaacg	gaccgcagca	gctcccactg	aacggtgtct	ttgtattcgc	atcatggggt	1560
agccgggtct	atcaacttaa	acccgtgggg	acagcttcat	ctgcccgggg	gcgccttggc	1620
gtgcggcgct	ga					1632

SEQ ID NO: 38 moltype = AA length = 543
 FEATURE Location/Qualifiers
 source 1..543
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 38

MMASKDAPS	SADGANGAGQ	LVPEVNNAEP	LPLDPVAGAS	TALATAGQVN	MIDPWIFNNF	60
VQAPQGEFTI	SPNNTPGDIL	FDLSLGPHLN	PFLHLHSQMY	NGWVGNMRVR	VILAGNAFTA	120
GKVIICVPP	GFQSRTLSIA	QATLFPPIIA	DVRTLEPIEI	PLEDVNTLY	HTNDNQPTMR	180
LLCLMYTPLR	TGGSGGTD	FVVAGRVLTC	PSSDFNLF	VPPTVEQKTR	PFSVPNIPLQ	240
LLNSRVRPNL	IQSMVLSPDQ	AQNVQFQNGR	CTTDGQLLGT	TPVSVSQILK	FRGKVSAGSK	300
VINLTDLGS	PFLAFEAPAP	TGFPDLGTS	WHVEMSLNSN	SQSSGNPILL	RDIHPNSSEF	360
VPHLGSVCVT	AAIEVAGDYT	GTIQWTSQPS	NVTPVPDVNF	WTIPHYGSNL	AEASQLAPVV	420
YPPGFGEAIV	YFMSPIPGPN	TAHKPNLVPC	LLPQEFVTHF	VSEQAPSMGE	AALVHYVDPD	480
TNRNLGEFKL	YPEGFITCVP	NGTGPQQLPL	NGVVFVFSWV	SRFYQLKPVG	TASSARGRLG	540
VRR						543

SEQ ID NO: 39 moltype = DNA length = 1632
 FEATURE Location/Qualifiers
 misc_feature 1..1632
 note = Nucleic acid sequence of human codon optimized VP1
 GI.5 siklos Q84S plus sign A94L
 source 1..1632
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 39

atgatgatgg	cctccaaaga	cgctcctagc	agtgtctgatg	gcgctaacgg	tgccggccag	60
ctgggtcccg	agggtgaataa	cgccgagcct	ctccccttgg	accagtagc	cggagcttca	120
acggccctag	ctactgcccg	acaggttaat	atgattgacc	cctggatttt	caataatttc	180
gtgcaggccc	ctcaaggcga	gtttactata	agccctaaca	acacaccagg	ggatattctg	240
ttcgacctga	gcttagggccc	tcactcaac	cccttcttgc	tccacctgag	ccagatgtac	300
aatggctggg	tgggcaacat	gcgagtgaga	gttatcctcg	cagggaacgc	ctttaccgct	360
ggtaagggtga	tcattttgttg	cgtaccacct	ggattccagt	ctaggacatt	aagtattgcg	420
caagctaccc	tctttcctca	tatcatcgcc	gacgtgcgga	cactagagcc	catcgagatc	480
ccactggagg	atgtccggaa	taccctgtac	cataccaacg	ataatcagcc	cactatgagg	540

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ttactgtgca tgcgtgtacac gccactccgg actggtgggg gcaagtgggg gaccgatgct 600
ttcgtcgctg ccggttaggg gctcacttgc cgtcatctg actttaactt cctattcctt 660
gtgcccccaa cgggtggaaca gaaaacgaga cctttttccg tacctaacct ccctttacag 720
ctcctaagca atagcagagt acctaacctg atccaatcca tgggttcttag ccctgatcaa 780
gcgcagaaacg tacagtttca gaacggggcg tgcaccacag atggccagct gcttggtaca 840
actcccgtct ccgtgtctca gatacttaag ttccggcgca aggtctccgc tggatccaaa 900
gtaatcaaac tcactgagct tgatggctct ccctttctgg cggtcgaggc gcccgcccca 960
acaggctttc cagacctggg aacatccgat tggcatgtcg agatgagtc gaatagcaac 1020
tcccagttct ctggcaatcc aatactgctc cgcgatatcc atcctaattc tagcaggttc 1080
gttccacacc tgggttctgt gtgcgtgacg gctgcaatag aggtggctgg cgactacacg 1140
gggtaccattc agtggacctc tcagccaaag aacgtgaccc ctgtgccaga cgttaacttt 1200
tggacaattc cacactacgg ctctaacttg gccgaagcat cccagcttgc ccccgttgta 1260
tatccccag gctttggcga agcaatagtt tattttatgt cccaatccc tggacctaac 1320
acagcacaca agccaaaacct cgtcccagtc ctgtgcccc agggagtcgt gactcatttc 1380
gtttcggaac aagcccattc aatgggggag gccgcccctg tccactacgt ggatccagat 1440
accaatcgga atctgggaga attcaaaact taccctgaag gattcattac atgtgtgcc 1500
aatggaacag gaccgcagca gctcccactg aacggtgtct ttgtattcgc atcatgggtt 1560
agccggttct atcaacttaa acccggtggg acagcttcat ctgcccgggg gcgccttggc 1620
gtgcggcgct ga 1632

SEQ ID NO: 40      moltype = DNA length = 1629
FEATURE          Location/Qualifiers
misc_feature      1..1629
                  note = Nucleic acid sequence of human codon-optimized VP1
                  GII.2 CGMH47 2011 TW AGT39206
source            1..1629
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 40
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgcccg attgggtaccc 60
gagtctaata acgaggtgat ggccctggag cctgttgacg gggctgccct cgcagctcct 120
gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180
aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgtcctt caatctcgag 240
ctgggaccag aacttaatcc gtacctggct cacctggccc ggatgtacaa tggatatgca 300
ggagggatgg aggtgcaggt tatgtggctt ggcaatgcct ttacagcagg caaaactcgtt 360
ttcgagcccg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420
tttccccatg tcatcatcga tgtgcgtacc ctggaaacctg tgcgtttgcc ttaccagac 480
gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540
atgctttata ctccccctgc tagcaatggt agtggggatg acgtttttac agtgagttgt 600
cggtgtactaa ctgcgccctc accagacttc gactttacgt acttgggtgc tcccactgtc 660
gaaagcaaaa ctaagccatt cacacttccc atctccaccc tcggagaact ctcgaaactc 720
cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcac ttctgtgcag 780
tgtcagaaacg gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840
agtgaatttt gcgcctttta gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900
tacaatgtta ctattactaa tctcaatgga agtcccttcg acccctcgga agatattccc 960
gctccactcg gagtacctga ctttcaggga cgctcttcg gcgtgatatc acaacgagat 1020
aagcataaca caccgggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080
acctatacgg ctcagtacac cccaaagctc ggcagagata aaatcgggac ttggcagacc 1140
gatgacctca cgtgtaacga acctgtgaaa ttactccag taggtctgaa tgatacagac 1200
cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260
gccccttcg ttgcacctgt gtttcgggg gagcgggtgc tcttctttag aagctatatt 1320
cctctgaagg gcgggtatgg tactccagca atcgactgcc tgcactccta ggagtgggtt 1380
caacatttct atcaagagcg cgcacctagt atgagcgagg tggctttggt cagatacatc 1440
aatccagaca caggaagagc actgttcgag gccaaagctc acagagccgg ctccatgacc 1500
gtctcatcca atacatccgc acccgtagta gtcccgcaca acgggtactt cagattcgac 1560
agttgggtga atcagtttta ctgctgggcc cccatgggca cagggaacgg tcgccgacgg 1620
atccagtaa 1629

SEQ ID NO: 41      moltype = AA length = 542
FEATURE          Location/Qualifiers
source            1..542
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

SEQUENCE: 41
MKMASNDAAAP STDGAAGLVP ESNNEVMALP PVAGAALAAP VTGQTNIIDP WIRANFVQAP 60
NGEFTVSPRN SPGEVLLNLE LGPELNPYLL HLARMYNGYA GGMEVQVMLA GNAFTAGKLV 120
FAAVPPHPFV ENLSPQQITM FPHVIDVRT LEPVLLPLPD VRNNFFHYNQ KDDPKMRIVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPSPDF DFTYLVPPTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIQMY TSPNEVTSVQ CQNGRCTLDG ELQGTTLQVQ SGICAFKGEV TAHLHDNDHL 300
YNVITITNLNG SPFDPSEDIP APLGVDPDFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWQT DDLTVNQPVK FTPVGLNDTD HFNQWVVPYR AGALNLNLNTL 420
APSVAPVFPF ERLFFRSYI PLKGGYGTPA IDCLLPQEWV QHFYQEAAPS MSEVALVRYI 480
NPDTGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWNQFYSLA PMGTGNRRRR 540
IQ 542

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-continued

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SEQ ID NO: 42      moltype = DNA length = 1629
FEATURE            Location/Qualifiers
misc_feature        1..1629
                    note = Nucleic acid sequence of human codon optimized VP1
                    GII.2 CGMH47 A90L
source              1..1629
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 42
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc 60
gagtcctaata acgaggtgat ggcccttggag cctgttgacg gggctgccct cgcagctcct 120
gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180
aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgtcctt caatctcagc 240
ctgggaccag aacttaatcc gtacctgtct cacctggccc ggatgtacaa tggatatgca 300
ggagggatgg aggtgcaggt tatgtctggt ggcaatgcct ttacagcagg caaactcggt 360
ttcgacgcgg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420
tttcccatg tcatcatcga tgtgcgtacc ctggaacctg tctgtgtgcc 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 atcctcaccg tcggagaact ctcgaaactc 720
cgcttcctcg tttcaattga tcagatgtac acgtctccaa atgaagtcac ttctgtgcag 780
tgtcagaacg gcagggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840
agtggaaatt cgccttttaa gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900
tacaatgtta ctctacttaa tctcaatgga agtcctttcg accctcggga agatattccc 960
gtctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020
aagcataaca caccgggaca taatgagcca gccaatagag cccacgacgc agtcgttcgg 1080
acctatacgg ctcaagtacac ccaaaagctc ggccagatac aaatcgggac ttggcagacc 1140
gatgacctca cttggaatca accctgtgaaa ttcactccag taggtctgaa tgatacagac 1200
cactttaacc agtgggtggt ccttagatac gccggagcct tgaacctaaa cactaacctt 1260
gccctctcgg ttgcacctgt gtttcggggg gagcggttgc tctctcttag aagctatatt 1320
cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtggtt 1380
caacattctc atcaagaggg cgcacctagt atgagcgagg tggctttggt cagatacatc 1440
aatccagaca caggaagagc actggttcgag gccaaagctgc acagagccgg cttcatgacc 1500
gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560
agttgggtga atcagtttta ctgcttgccc cccatgggca cagggaacgg tcgccgacgg 1620
atccagtaa 1629

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SEQ ID NO: 43      moltype = AA length = 542
FEATURE            Location/Qualifiers
source              1..542
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

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SEQUENCE: 43
MKMASNDAAAP STDGAAGLVP ESNNEVMALE PVAGAALAAP VTGQTNIIDP WIRANFVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLL HLARMYNGYA GGMEVQVMLA GNAFTAGKLV 120
FAAVPPHPFV ENLSPQQITM FPHVIDVRT LEPVLLPLPD VRNFFPHYNQ KDDPKMRIVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPSPDF DFTYLVPTTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIQOMY TSPNEVISVQ CQNGRCTLDG ELQGTTLQLV SGICAFKGEV TAHLHDNDHL 300
YNVITITNLNG SPDPSEDIP APLGVPDFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWQT DDLTVNQPVK FTPVGLNDTD HFNQWVVPY AGALNLNTNL 420
APSPVAPVFP ERLFFRSYI PLKGGYGTTPA IDCLLPQEWV QHFYQEAAPS MSEVALVRYI 480
NPDTGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWNVQFYSLA PMGTGNRRR 540
IQ 542

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SEQ ID NO: 44      moltype = DNA length = 1629
FEATURE            Location/Qualifiers
misc_feature        1..1629
                    note = Nucleic acid sequence of human codon optimized VP1
                    GII.2 CGMH47 E80S plus sign A90L
source              1..1629
                    mol_type = other DNA
                    organism = synthetic construct

```

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SEQUENCE: 44
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc 60
gagtcctaata acgaggtgat ggcccttggag cctgttgacg gggctgccct cgcagctcct 120
gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180
aatggggagt ttacggtcag ccctagaaat agccctgggg aagtgtcctt caatctcagc 240
ctgggaccag aacttaatcc gtacctgtct cacctggccc ggatgtacaa tggatatgca 300
ggagggatgg aggtgcaggt tatgtctggt ggcaatgcct ttacagcagg caaactcggt 360
ttcgacgcgg tccctcccca cttcccagtt gaaaatcttt cccctcagca gattaccatg 420
tttcccatg tcatcatcga tgtgcgtacc ctggaacctg tctgtgtgcc tttaccagac 480
gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540
atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600
cgggtactaa ctcgcccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660

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gaaagcaaaa ctaagccatt cacacttccc atcctcacc cgggagaact ctggaactcc 720
cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcac ttctgtgcag 780
tgtcagaacg gcaggtgcac cttagacggg gaactgcagg ggacaacgca gttgcaggtc 840
agtggaaatt gcgcctttaa gggcgaagtg acagctcacc tccacgacaa cgatcatctc 900
tacaatgtta ctattactaa tctcaatgga agtctcttcg acccctcgga agatattccc 960
gtccactcgg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020
aagcataaca caccgggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080
acctatacgg ctccagtacac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140
gatgacctca ctgtgaatca acctgtgaaa ttoactccag taggtctgaa tgatacagac 1200
cactttaacc agtgggtggg ccctagatac gccggagcct tgaacctaaa cactaacctt 1260
gcccccttcg ttgcacctgt gtttcggggg gagegggtgc tcttctttag aagctatatt 1320
cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtggtt 1380
caacatttct atcaagaggc cgcacctagt atgagcgagg tggctttggt cagatacatc 1440
aatccagaca catgaagagc actgttcgag gccaaagctg acagagccgg cttcatgacc 1500
gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560
agttgggtga atcagtttta ctggtggcc cccatgggca cagggaaacg tcgccgacgg 1620
atccagtaa                                     1629

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SEQ ID NO: 45      moltype = DNA length = 1647
FEATURE            Location/Qualifiers
misc_feature       1..1647
                    note = Nucleic acid sequence of human codon-optimized VP1
                    GII.3_Jingzhou_2013402_CHN AGX01095
source             1..1647
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 45
atgaaaaatgg tctccaacga tgcagcacc tctaatgatg gcgctgccgg acttgtgccg 60
gagattagct ctgaggctat ggccctagaa ccagtagccg gggcagccat agctgcccc 120
ctgactggcc agcagaatat cattgacccc tggataatga acaatttcgt gcaggcaccg 180
gggggagaat tcccggtctc tctcgaaac tccccgggg aggttctctt gaatttgaa 240
ctgggcccctg aaattaatcc ttatctggcc catctagccc gaatgtacaa cggtacgcc 300
ggagggttcg aggtccaggt ggtgctcgtt ggtaacgctt tcacagctgg caagatcatt 360
tttgacgcaa tccctccaaa ctccctatc gataatctta gtccgcccc gatcaaatg 420
tgccctcacg ttatcgtaga tgtgaggcag ctggaacctg tcaatctccc aatgccccgac 480
gtgcgcaaca actcttttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540
atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600
cgagtcctga cacgtccatc tccctgactt agcttttaatt tccctcgtgc cccacagtg 660
gaatccaaaa ctaagccatt ctctctgcca attcttacca ttagcgaaat gtcgaatagt 720
agggtcccg tgcctactaga tctactgcat accagtccaa cagaaaacat cgtgtacag 780
tgtcagaacg gacgcgtgat tctcgacggg gagcttatgg gcaactacca gctgctgcc 840
agccagatat gcgccttcg cgccacactg actagaagca cttcgctgac ttctgaccag 900
gcagatacag ctacacactac gctgttcaat tattattggc atatacaact cgataatctg 960
aatggcactc cttatgaccc agccgaggac atccccgcc cacttggcac cccggacttt 1020
agagggaagg tctttggagt ggcttctcaa agaaatcccg acgcaaccac cggggccac 1080
gaggccaaaa tcgatactac atcagggcgt ttcaccctca agttaggcag tctggagata 1140
tctaccgaaa gtggagattt cgatcagaac cagccaaccc gggtttacccc cgtgggaatc 1200
gggggttgacc acgaaccgga ttccagcag tgggctctgc ctgattacgc aggccagttc 1260
acacataaca tgaattctga ccccgtgtg gcccccaact tccggggaga acaactcttg 1320
tttttcagga gccaaactgc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380
gtgccccagg aatgggtgca gcatttttac caggagtcgg cgccctccca gacgcagggt 1440
gctctggtta gatgttcaa tcccgacacc ggcagggtgc tatttgaggc aaagctgcac 1500
aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gcccccaac 1560
ggatacttca gatttgagag ttgggtgaac ccattctata cctcgcccc catgggtaca 1620
ggcaatggca gacggcggat ccagtaa                                     1647

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SEQ ID NO: 46      moltype = AA length = 548
FEATURE            Location/Qualifiers
source             1..548
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

```

```

SEQUENCE: 46
MKMASNDAAAP SNGDAAGLVP EISSEAMALE PVAGAAIAAP LTGQQNIIDP WIMNNFVQAP 60
GGEFTVSPRN SPGEVLNLNL LGPEINPYLA HLARMYNGYA GGFEVQVFLA GNAFTAGKII 120
FAAIPNPFPI DNLGAAQITM CPHVIVDVRO LEPVNLPMPD VRNFFHYNQ GSDSRLRLIA 180
MLYTPLRANM SGDDVFTVSC RVLTRPSPDF SFNFLVPPTV ESKTKPFLSLP ILTISEMSNS 240
RFPVPIDSLH TSPTENIVVQ CQNGRVTLDG ELMGTTQLLP SQICAFRGLT TRSTSRASDQ 300
ADTATPRLFN YYWHIQLDNL NGTPYDPAED IPAPLGTPDF RGKVFVGASQ RNPDATTRAH 360
EAKIDTSSGR FTKPLGSLFI STESGDFDQN QPTRFTPVGI GVDHEPDFQQ WALPDYAGQF 420
THNMNLAPAV APNFPGBQLL FFRSQLPSSG GRSNGILDCL VPQEWVQHFI QESAPSQTQV 480
ALVRYVNPDT GRVLFEAKLH KLRFMTHAKS GDSPITVPPN GYFRFESWVN PFYTLAPMGT 540
GNRRRIQ                                     548

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SEQ ID NO: 47      moltype = DNA length = 1647
FEATURE            Location/Qualifiers

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misc_feature      1..1647
                  note = Nucleic acid sequence of human codon optimized
                  VPI_GII.3_Jing_E80S
source            1..1647
                  mol_type = other DNA
                  organism = synthetic construct

```

SEQUENCE: 47

```

atgaaaaatgg cttccaacga tgcagcacc cttaatgatg gcgctgccgg acttgtgccg 60
gagattagct ctgaggctat gccctagaa ccagtagccg gggcagccat agctgcccc 120
ctgactggcc agcagaatat cattgacccc tggataatga acaatttcgt gcaggcaccg 180
ggggggagaa tcaagggtct tctcgaaac tccccgggg aggtttctct gaatttgagc 240
ctgggcccctg aaattaatcc ttatctggcc catctagccc gaatgtacaa cggctacgcc 300
ggaggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360
tttcagcaaa tccctccaaa ctccctatc gataatctta gtgcgcccc gatcacaatg 420
tgccctcacg ttatcgtaga tbtgaggcag ctggaacctg tcaatctccc aatgccccgac 480
gtgcgcaaca acttctttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540
atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600
cgagtcctga cagctccatc tcttgacttt agctttaatt tcctcgtgcc ccccacagtg 660
gaatccaaaa ctaagccatt ctctctgcca attcttacca ttagcgaaat gtcgaatagt 720
aggttccccg tgcccataga ttactgcat accagtccaa cagaaaaacat cgtcgtacag 780
tgtcagaacg gacgcgtgac tctcgacggg gagcttatgg gcactaccca gctgctgccc 840
agccagatat gcgccttcgg cggcacactg actagaagca cttcgcgtgc ttctgaccag 900
gcagatacac ctacaccaag gctgttcaat tattattggc atatacaact cgataatctg 960
aatggcactc cttatgaccc agccgaggac atccccggcc cacttgccac cccggacttt 1020
agaggggaag tctttggagt ggcttctcaa agaaatcccc acgcaaccac cggggccccc 1080
gagggccaaa tgcataactac atcaggggct ttcaccccta agttaggcag tctggagata 1140
tctaccgaaa gtggagatgt cgtacgaaac cagcccaacc gggttacccc cgtgggaatc 1200
ggggttgacc acgaaccgga ttccagcag tgggctctgc ctgattacgc aggccagttc 1260
acacataaca tgaatcttgc ccccgctgtg gcccccaact tccggggaga acaactctctg 1320
tttttcagga gcccaactgcc ttccagcggc ggccgactca acgggatttt ggactgtctc 1380
gtgccccagg aatgggtgca gcatctttac caggagtcgg cgcctcccca gacgcagggtg 1440
gctctgggta gatattgcaa tcccgacacc ggcagggtgc tatttgaggc aaagctgcac 1500
aagcttcgct ttatgactat cgttaagagc ggtgattcgc ctattacagt gcccccaac 1560
ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620
ggcaatggca gacggcggat ccagtaa 1647

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SEQ ID NO: 48      moltype = AA length = 548
FEATURE            Location/Qualifiers
source             1..548
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

SEQUENCE: 48

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MKMASNDAAP SNDGAAGLVP EISSEAMALE PVAGAAIAAP LTGQQNIIDP WIMNMFVQAP 60
GGFEFTVSPRN SPGEVLLNLE LGPEINPYLL HLRMYNGYA GGFEVQVLA GNAFTAGKII 120
FAAIPNPFPI DNLSAAQITM CPHVIVDVQR LEPVNLPMFD VRNFFPHYNQ GSDSRLRLIA 180
MLYTPLRANN SGDDVFTVSC RVLTRPSPDF SFNFLVPPTV ESKTKPFSLP ILTISEMSNS 240
RFPVPIDSLH TSPTENIVVQ CQNGRVTLDG ELMGTTQLLP SQICAFRGLT TRSTSRASDQ 300
ADTATPRLEFN YYWHIQLDNL NGTPYDPAED IPAPLGTPDF RGKVFVGVSQ RNPDATTRAH 360
EAKIDTTSGR FTPKLGSLEI STESGDFDQN QPTRFTPVGI GVDHEPDFQQ WALPDYAGQF 420
THNMNLAPAV APNFPGEQLL FFRSQLPSSG GRSNGILDCL VPQEWVQHFY QESAPSQTQV 480
ALVRYVNDPT GRVLFEAKLH KLRFMITAKS GDSPI TVPPN GYFRFESWVN PFYTLAPMGT 540
GNRRRIQ 548

```

```

SEQ ID NO: 49      moltype = DNA length = 1647
FEATURE            Location/Qualifiers
misc_feature       1..1647
                  note = Nucleic acid sequence of human codon optimized
                  VPI_GII.3_Jing_A90L
source             1..1647
                  mol_type = other DNA
                  organism = synthetic construct

```

SEQUENCE: 49

```

atgaaaaatgg cttccaacga tgcagcacc cttaatgatg gcgctgccgg acttgtgccg 60
gagattagct ctgaggctat gccctagaa ccagtagccg gggcagccat agctgcccc 120
ctgactggcc agcagaatat cattgacccc tggataatga acaatttcgt gcaggcaccg 180
ggggggagaa tcaagggtct tctcgaaac tccccgggg aggtttctct gaatttgaa 240
ctgggcccctg aaattaatcc ttatctgctc catctagccc gaatgtacaa cggctacgcc 300
ggaggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360
tttcagcaaa tccctccaaa ctccctatc gataatctta gtgcgcccc gatcacaatg 420
tgccctcacg ttatcgtaga tbtgaggcag ctggaacctg tcaatctccc aatgccccgac 480
gtgcgcaaca acttctttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540
atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600
cgagtcctga cagctccatc tcttgacttt agctttaatt tcctcgtgcc ccccacagtg 660
gaatccaaaa ctaagccatt ctctctgcca attcttacca ttagcgaaat gtcgaatagt 720
aggttccccg tgcccataga ttactgcat accagtccaa cagaaaaacat cgtcgtacag 780

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-continued

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tgtcagaacg gacgcgtgac tctcgacggg gagcttatgg gcaactaccca gctgctgccc 840
agccagatat gcgccttcgc cggcacactg actagaagca cttcgcggtgc ttctgaccag 900
gcagatacag ctacaccaag gctgttcaat tattattggc atatacaact cgataatctg 960
aatggcactc cttatgacct agccgaggac atccccgccc cacttgccac cccggacttt 1020
agagggaaagg tctttggagt ggcttctcaa agaaatcccg acgcaaccac cggggcccac 1080
gaggccaaaa tcgatactac atcaggggcg ttcaccccta agttaggcag tctggagata 1140
tctaccgaaa gtggagattt cgatcagaac cagccaaccc gggttaccac cgtgggaatc 1200
gggggttgacc acgaaccgga ttccagcag tgggctctgc ctgattacgc aggccagttc 1260
acacataaca tgaatcttgc ccccgctgtg gcccccaact tcccgggaga acaacttctg 1320
tttttcagga gccaaactgcc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380
gtgccccagg aatgggtgca gcatttttac caggagtcgc cgccctccca gacgcagggtg 1440
gctctgggta gatattgcaa tcccgcaccc ggccagggtgc tatttgaggc aaagctgcac 1500
aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gcccccaac 1560
ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620
ggcaatggca gacggcgcat ccagtaa 1647

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```

SEQ ID NO: 50      moltype = AA  length = 548
FEATURE           Location/Qualifiers
source            1..548
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 50
MKMASNDAAAP SNDGAAGLVP EISSEAMALE PVAGAAIAAP LTGQQNIIDP WIMNNFVQAP 60
GGEFTVSPRN SPGEVLLNLS LGPEINPYLL HLARMYNGYA GGFEVQVLA GNAFTAGKII 120
FAAIPPFPFI DNLSAAQITM CPHVIVDVQR LEPVNLMPMD VRNNFFHYNQ GSDSRLRLIA 180
MLYTPLRANN SGDDVFTVSC RVLTRPSPDF SFNFLVPPTV ESKTKPFSLP ILTISEMSNS 240
RFPVPIDSLH TSPTEIVVQ CQNGRVTLDG ELMGTQLLP SQICAFRGTI TRSTSASDQ 300
ADTATPRLFN YYWHIQLDNL NGTPYDPAED IPAPLGTPDF RGKVFVGASQ RNPDATTRAH 360
EAKIDTTSGR FTPKLGLSLEI STESGDFDQN QPTRFTPVGI GVDHEPDPQQ WALPDYAGQF 420
THNNMLAPAV APNFPGEQLL FFRSQLPSSG GRSNGILDCL VPQEWVQHFY QESAPSQTQV 480
ALVRVYNPDY GRVLFQAKLH KLRFMITAKS GDSPITVPPN GYFRFESWVN PFYTLAPMGT 540
GNRRRIQ 548

```

```

SEQ ID NO: 51      moltype = DNA  length = 1647
FEATURE           Location/Qualifiers
misc_feature       1..1647
                  note = Nucleic acid sequence of human codon optimized
                  VP1_GII.3_Jing_E80S+A90L
source            1..1647
                  mol_type = other DNA
                  organism = synthetic construct

```

```

SEQUENCE: 51
atgaaaaatgg cttccaacga tgcagcaccc tctaattgatg gcgctgcccg acttggtgccg 60
gagattagct ctgaggctat ggccttagaa ccagtagccg gggcagccat agctgccccca 120
ctgactggcc agcagaatat cattgacccc tggataatga acaatttctg gcaggcacccg 180
ggggggagaaat tcacgggtctc tctctgaaac tccccggggg aggttctctt gaatttgagc 240
ctggggccctg aaattaatcc ttatctgtct catctagccc gaattgtacaa cggctacgcc 300
ggagggtttcg aggtccaggt ggtgctcgct ggtaacgcct tcacagctgg caagatcatt 360
tttgacgcaa tccctccaaa ctctccatc gataatctta gtgccgcccc gatcaccaatg 420
tgccctcacg ttatcttaga tgtgaggcag ctggaacctg tcaatctccc aatgccccgac 480
gtgcgcaaca actcttttca ctataaccag ggatctgact cccgccttcg ccttatcgct 540
atgctgtaca cccctctgag ggctaacaat tccggagatg acgttttcac tgtgagttgt 600
cgagtcctga cacgtccatt tcttgacttt agctttaatt tctctgtgcc ccccacagt 660
gaatccaaaaa apaaagccatt ctctctgcca attcttacca ttacgaaat gtcgaatagt 720
aggttccccg tgcccataga ttactgcat accagtccaa cagaaaaacat cgtcgtacag 780
tgtcagaacg gacgcgtgac tctcgacggg gagcttatgg gcaactaccca gctgctgccc 840
agccagatat gcgccttcgc cggcacactg actagaagca cttcgcggtgc ttctgaccag 900
gcagatacag ctacaccaag gctgttcaat tattattggc atatacaact cgataatctg 960
aatggcactc cttatgacct agccgaggac atccccgccc cacttgccac cccggacttt 1020
agagggaaagg tctttggagt ggcttctcaa agaaatcccg acgcaaccac cggggcccac 1080
gaggccaaaa tcgatactac atcaggggcg ttcaccccta agttaggcag tctggagata 1140
tctaccgaaa gtggagattt cgatcagaac cagccaaccc gggttaccac cgtgggaatc 1200
gggggttgacc acgaaccgga ttccagcag tgggctctgc ctgattacgc aggccagttc 1260
acacataaca tgaatcttgc ccccgctgtg gcccccaact tcccgggaga acaacttctg 1320
tttttcagga gccaaactgcc ttccagcggc ggccgatcta acgggatttt ggactgtctc 1380
gtgccccagg aatgggtgca gcatttttac caggagtcgc cgccctccca gacgcagggtg 1440
gctctgggta gatattgcaa tcccgcaccc ggccagggtgc tatttgaggc aaagctgcac 1500
aagcttcgct ttatgactat cgctaagagc ggtgattcgc ctattacagt gcccccaac 1560
ggatacttca gatttgagag ttgggtgaac ccattctata ccctggcccc catgggtaca 1620
ggcaatggca gacggcgcat ccagtaa 1647

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SEQ ID NO: 52      moltype = DNA  length = 1623
FEATURE           Location/Qualifiers
misc_feature       1..1623
                  note = Nucleic acid sequence of human codon-optimized VP1

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source GII.4_Sydney_2012_K4LM89
 1..1623
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 52
 atgaaaatgg cctcgagtga cgtaaccct agtgacggca gcgcgcgcaa tcttggtcct 60
 gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120
 gtggccggtc agcagaatgt gattgaccgg tggatacgca acaattttgt ccaagccccct 180
 ggtggggagt tcaccgttag ccgcagaaat gcgcagagg aaatcctgtg gtcggcccca 240
 ttgggaccgg atctgaacc ctattgtca catctcgctc ggatgtacaa cgggtatgcc 300
 ggcggtattg aatgtagcgt gattctggct gggaacgctg tcaactgtgg caaagtgatc 360
 tttgcagcgg tgccctccaa cttcccccact gaaggactgt ctccaagcca ggtcacaatg 420
 tttccacaca tcgtggtgga cgtacggcag cttagagcctg tccgtattcc cctccctgat 480
 gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540
 atgttgtaca cccctctgcg cgtaacaat gctggagacg acgtattcac cgtgtcatgc 600
 agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
 gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaaatagc 720
 cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggttcag 780
 ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
 gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
 atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgccact 960
 cttggaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
 gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcgca ttttgccccg 1080
 aaactgggta gagtgcagtt tgagaccgac actgaccggg accttgaagc caatcagaat 1140
 actaagttca ccactgtagg agtgattcag gacgggggca ccaactaccg gaacgagccg 1200
 caacaatggg tctcgccctc ttatagcggg aggaataactc ataagtgtca tttggctcct 1260
 gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgacctga 1320
 tgctccggat atcccaatat ggatctcgat tgccctgctc cacaggaatg ggtgcagtat 1380
 ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac tctgcggtt cgtgaatcca 1440
 gacacaggcc gcgtgtgtgt tgagtcaaaa ttgcacaaat caggatacgt tacagtggct 1500
 catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560
 gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggtctgc 1620
 tga 1623

SEQ ID NO: 53 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 53
 MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAIAVP VAGQQNVIDP WIRNNFVQAP 60
 GGEFTVSPRN APGEILWSAP LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
 FAAVPPNPFT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
 MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFVSP VLTVEEMTNS 240
 RPIPLEKLF TGPSSAFVVQ PQNGRCCTDG VLLGTQLSP VNICTFRGDV THITGSRNYT 300
 MNLASQNWND YDPTEEIPAP LGTPDFVVGKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
 KLGRVQFETD TDRDFEANQN TKFTPVGVIG DGGTTHRNEP QQWVLPYSYG RNTHNVHLAP 420
 AVAPTFFPEQ LFFFRSFMGP CSGYPNMDLD CLLPQEWVQY FYQEAAPAQs DVALLRFVNP 480
 DTGRVLFECK LHKSGYVTV AHTGQHDVIP PNGYFRFDWS VNQFYTLAPM NGTGRRRRAV 540

SEQ ID NO: 54 moltype = DNA length = 1623
 FEATURE Location/Qualifiers
 misc_feature 1..1623
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.4_Syd12_A39V
 source 1..1623
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 54
 atgaaaatgg cctcgagtga cgtaaccct agtgacggca gcgcgcgcaa tcttggtcct 60
 gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagtcccc 120
 gtggccggtc agcagaatgt gattgaccgg tggatacgca acaattttgt ccaagccccct 180
 ggtggggagt tcaccgttag ccgcagaaat gcgcagagg aaatcctgtg gtcggcccca 240
 ttgggaccgg atctgaacc ctattgtca catctcgctc ggatgtacaa cgggtatgcc 300
 ggcggtattg aatgtagcgt gattctggct gggaacgctg tcaactgtgg caaagtgatc 360
 tttgcagcgg tgccctccaa cttcccccact gaaggactgt ctccaagcca ggtcacaatg 420
 tttccacaca tcgtggtgga cgtacggcag cttagagcctg tccgtattcc cctccctgat 480
 gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540
 atgttgtaca cccctctgcg cgtaacaat gctggagacg acgtattcac cgtgtcatgc 600
 agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
 gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaaatagc 720
 cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggttcag 780
 ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
 gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
 atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgccact 960

-continued

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cttggaaacc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcga ttttgccccg 1080
aaactgggta gagtgagatt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagtcca cactgttagg agtgattcag gacgggggca ccaactcacc 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 gacgtcgac tctgcgggtt cgtgaatcca 1440
gacacaggcc gcgtgttggt tgagtcaaaa ttgcacaaat caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatt ggggaatggga ctggcagacg cagggctgtc 1620
tga
1623

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SEQ ID NO: 55      moltype = AA  length = 540
FEATURE           Location/Qualifiers
source            1..540
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 55
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAIAAP VAGQONPIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAP LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSPV VLTVEEMTNS 240
RPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTEEIPAP LGTPDFVGGI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVIG DGGTTHRNEP QQWVLPSPYSG RNTHNVHLAP 420
AVAPTFPGEQ LLFFRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTV AHTGQHDVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRRAV 540

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SEQ ID NO: 56      moltype = DNA  length = 1623
FEATURE           Location/Qualifiers
misc_feature       1..1623
                  note = Nucleic acid sequence of human codon optimized
                  VP1_GII.4_Syd12_V47P
source            1..1623
                  mol_type = other DNA
                  organism = synthetic construct

```

```

SEQUENCE: 56
atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcccaa tcttgtgctc 60
gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120
gtggccggtc agcagaatcc cattgaccgg tggatacgca acaattttgt ccaagccccc 180
gggtggggagt tcaccgcttag ccagagaaat gcgccaggag aaatcctgtg gtcggcccca 240
ttgggaccgg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgctg caaagtgatc 360
tttgacggcg tgcctcccaa cttcccaact gaaggactgt ctccaagcca ggtaacaatg 420
tttccacaca tcgtgggtgga cgtacggcag cttagagcctg tcctgattcc cctccctgat 480
gtacgcaata attctacca ctacaatcaa tccaatgac cgaccattaa actcatcgcg 540
atgttgtaca cccctctgag gcctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtctc ccagaccttc accagacttt gactttatct tcttagtgcc cccactgttt 660
gagagccgaa ccaagccctt tagtgtcccc gtaactcacg tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtggttcag 780
ccacagaaag gacgtgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaaatgac tacgacccaa cgaagagat tcccgacct 960
cttggaaacc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcga ttttgccccg 1080
aaactgggta gagtgagatt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagtcca cactgttagg agtgattcag gacgggggca ccaactcacc 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 gacgtcgac tctgcgggtt cgtgaatcca 1440
gacacaggcc gcgtgttggt tgagtcaaaa ttgcacaaat caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatt ggggaatggga ctggcagacg cagggctgtc 1620
tga
1623

```

```

SEQ ID NO: 57      moltype = AA  length = 540
FEATURE           Location/Qualifiers
source            1..540
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

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SEQUENCE: 57
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAIAAP VAGQONVIDP WIINNFFVQAP 60

```

-continued

GGEFTVSPRN	APGEILWSAP	LGPDLNPYLS	HLARMYNGYA	GGFEVQVILA	GNAFTAGKVI	120
FAAVPPNFPT	EGLSPSQVTM	FPHIVVDVRQ	LEPVLIPLPD	VRNNFYHYNQ	SNDPTIKLIA	180
MLYTPLRANN	AGDDVFTVSC	RVLTRPSPDF	DFIFLVPPTV	ESRTKPFSVP	VLTVEEMTNS	240
RFPIPLEKLF	TGPSSAFVVQ	PQNGRCTTDG	VLLGTTQLSP	VNICTFRGDV	THITGSRNYT	300
MNLASQNWND	YDPTTEEIPAP	LGTPDFVVGKI	QGVLTQTTRT	DGSTRGHKAT	VYTGSADFAP	360
KLGRVQFETD	TDRDFEANQN	TKFTPVGVQI	DGGTTHRNEP	QQWVLPYSYG	RNTHNVHLAP	420
AVAPTFPGEQ	LLFFRSTMPG	CSGYPNMDLD	CLLPQEWVQY	FYQEAAPQS	DVALLRFVNP	480
DTGRVLFECK	LHKSQYVTVA	HTGQHDLVIP	PNGYFRFDSW	VNQFYTLAPM	GNGTGRRRRAV	540

SEQ ID NO: 58 moltype = DNA length = 1623
 FEATURE Location/Qualifiers
 misc_feature 1..1623
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.4_Syd12_R53I
 source 1..1623
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 58

atgaaaaatgg	cctcgagtga	cgctaaccct	agtgacggca	gcgcccgc	tcttgtgcct	60
gaggttaata	atgaggtgat	ggccctggag	cctgtggtgg	gcgcagccat	agcagcgccc	120
gtggccggtc	agcagaatgt	gattgaccgc	tggataatca	acaattttgt	ccaagcccct	180
ggtggggagt	tcaccgtag	cccgagaaat	gcgccaggag	aaatcctgtg	gtcggcccca	240
ttgggacccg	atctgaaccc	ctatttgtca	catctcgctc	ggatgtacaa	cggtatgccc	300
ggcggatttg	aagtgcaggt	gattctggct	gggaacgcgt	tcactgctgg	caaagtgtac	360
tttgacagcg	tgcctcccaa	cttcccact	gaaggactgt	ctccaagcca	ggtcacatg	420
tttccacaca	tcgtggtgga	cgtacggcag	ctagagcctg	tcctgattcc	cctccctgat	480
gtacgcaata	atttctacca	ctacaatcaa	tccaatgac	cgaccattaa	actcatcgcg	540
atgttgtaca	cccctctgcg	cgctaacaat	gctggagacg	acgtattcac	cgtgtcatgc	600
agagtgtcca	ccagaccttc	accagacttt	gactttatct	tcttagtgcc	ccccactgtt	660
gagagccgaa	ccaagccctt	tagtgtcccc	gtactcacag	tcgaggagat	gacaaatagc	720
cgctttccaa	tcccccttga	gaaactgttc	acaggacctt	cctcggcatt	cgtgggtcag	780
ccacagaaac	gacgctgcac	aactgacggc	gtgctgctcg	gaaccaccca	gcttagccct	840
gttaatatct	gtacgtttag	agcgacgcta	actcacataa	ctggctcacg	gaactatacc	900
atgaatctgg	catcacagaa	ttggaatgac	tacgacccaa	cgaagagat	tcccgacact	960
cttggaaccc	ccgactttgt	gggaaaaata	cagggcgctc	tgacacaaac	caccagaacc	1020
gatggctcca	cacggggaca	caaggcaacc	gtctacactg	gctctgcgga	ttttgccccg	1080
aaactgggta	gagtgagttg	tgagaccgac	actgaccggg	actttgaagc	caatcagaat	1140
actaaagtca	cacctgtagg	agtgattcag	gacgggggca	ccactcacgc	gaacgagccg	1200
caacaatggg	tcctgccttc	ttatagcggg	aggaatactc	ataatgtgca	tttggtcctc	1260
gcagtggttc	ccacgttttc	cggggaacaa	ctgctctttt	ttcgttcaac	catgcctgga	1320
tgctccggat	atcccaatat	ggatctcgat	tgctctgctc	cacagggaat	ggtgcagtat	1380
ttttatcaag	agggcgaccc	agcccaatcc	gacgtcgcac	ttctgcgggt	cgtgaatcca	1440
gacacaggcc	gcgtgtgtgt	tgagtgcaaa	ttgcacaaat	caggatacgt	tacagtggct	1500
catactggac	agcatgacct	ggtgatccca	cccaacggat	attttagggt	cgactcctgg	1560
gtgaatcagt	tttatacatt	agcccccatg	gggaatggga	ctggcagacg	cagggtctgtc	1620
tga						1623

SEQ ID NO: 59 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 59

MKMASSDANP	SDGSAANLVP	EVNNEVMALE	PVVGAAIAAP	VAGQQNVIDP	WIRNNFVQAP	60
GGEFTVSPRN	APGEILWSAS	LGPDLNPYLS	HLARMYNGYA	GGFEVQVILA	GNAFTAGKVI	120
FAAVPPNFPT	EGLSPSQVTM	FPHIVVDVRQ	LEPVLIPLPD	VRNNFYHYNQ	SNDPTIKLIA	180
MLYTPLRANN	AGDDVFTVSC	RVLTRPSPDF	DFIFLVPPTV	ESRTKPFSVP	VLTVEEMTNS	240
RFPIPLEKLF	TGPSSAFVVQ	PQNGRCTTDG	VLLGTTQLSP	VNICTFRGDV	THITGSRNYT	300
MNLASQNWND	YDPTTEEIPAP	LGTPDFVVGKI	QGVLTQTTRT	DGSTRGHKAT	VYTGSADFAP	360
KLGRVQFETD	TDRDFEANQN	TKFTPVGVQI	DGGTTHRNEP	QQWVLPYSYG	RNTHNVHLAP	420
AVAPTFPGEQ	LLFFRSTMPG	CSGYPNMDLD	CLLPQEWVQY	FYQEAAPQS	DVALLRFVNP	480
DTGRVLFECK	LHKSQYVTVA	HTGQHDLVIP	PNGYFRFDSW	VNQFYTLAPM	GNGTGRRRRAV	540

SEQ ID NO: 60 moltype = DNA length = 1623
 FEATURE Location/Qualifiers
 misc_feature 1..1623
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.4_Syd12_P80S
 source 1..1623
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 60

atgaaaaatgg	cctcgagtga	cgctaaccct	agtgacggca	gcgcccgc	tcttgtgcct	60
gaggttaata	atgaggtgat	ggccctggag	cctgtggtgg	gcgcagccat	agcagcgccc	120
gtggccggtc	agcagaatgt	gattgaccgc	tggatacgcg	acaattttgt	ccaagcccct	180

-continued

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ggtggggagt tcaccgtag cccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240
ttgggaccog atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgttg caaagtgtgc 360
tttgacagcg tgccctccaa ctccccact gaaggactgt ctccaagcca ggtcacaatg 420
tttccacaca tcgtgggtgga cgtacggcag cttagagcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgacg cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggtcag 780
ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctcg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgccact 960
cttggaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cagggggaca caaggcaacc gtctacactg gctctgcgga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagttca cacctgtagg agtgattcag gacgggggca ccaactcacc gaacgagccg 1200
caacaatggg tctcgccctc ttatagcggg aggaatactc ataattgtga tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgccctgctcc cacagggaat ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcgggt cgtgaatcca 1440
gacacaggcc gcgtgtgtgt tgagtgcaca caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttagggt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatg ggggaatggga ctggcagacg cagggtctgtc 1620
tga

```

SEQ ID NO: 61 moltype = AA length = 540

FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 61

```

MKMASSDANP SDGSAANLVP EVNNEVMALP PVVGAIAAP VAGQONVIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAP LGPDLNPYLL HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDVFVTVSC RVLTRPSPDF DFIFLVPTTV ESRTKPSVSP VLTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTTEIPAP LGTPDFVQKI QGVLTQTTRT DGSTRGHKAT VYTGSAFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPYSYG RNTNHNVLAP 420
AVAPTFPGEQ LLFPRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQOS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTV AHTQHDLVIP PNGYFRFDSW VNQFYTLAPM NGTGRRRRAV 540

```

SEQ ID NO: 62 moltype = DNA length = 1623

FEATURE Location/Qualifiers
 misc_feature 1..1623
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.4_Syd12_S90L
 source 1..1623
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 62

```

atgaaaaatg cctcgagtga cgctaaccct agtgacggca gcgccgcca tcttgtgctc 60
gaggttaata atagggatg ggcctctggg cctgtgggtg gcgcagccat agcagcgccc 120
gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagccccc 180
ggtggggagt tcaccgtag cccgagaaat gcgccaggag aaatcctgtg gtcggcccca 240
ttgggaccog atctgaaccc ctatttgtct catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgttg caaagtgtgc 360
tttgacagcg tgccctccaa ctccccact gaaggactgt ctccaagcca ggtcacaatg 420
tttccacaca tcgtgggtgga cgtacggcag cttagagcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgacg cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggtcag 780
ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctcg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgccact 960
cttggaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cagggggaca caaggcaacc gtctacactg gctctgcgga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagttca cacctgtagg agtgattcag gacgggggca ccaactcacc gaacgagccg 1200
caacaatggg tctcgccctc ttatagcggg aggaatactc ataattgtga tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgccctgctc cacaggaaat ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcgggt cgtgaatcca 1440

```

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gacacaggcc gcgtgttggt tgagtgc aaa ttgcacaaa caggatacgt tacagtggct 1500
catactggac agcatgaacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatt gggaatggga ctggcagacg cagggtctgtc 1620
tga 1623

```

```

SEQ ID NO: 63      moltype = AA length = 532
FEATURE           Location/Qualifiers
source            1..532
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 63
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGGQQNVI DPWIRNNFVQ APGGEFTVSP 60
RNAPAGEILWS APLGPDNLNP LSHLARMYNG YAGGFVQVI LAGNAFTAGK VIFAAVPPNF 120
PTEGLSPSQV TMFPHIVVDV RQLEPVLIP L PDVRNNFYHY NQSNPTIKL IAMLYTPLRA 180
NNAGDDVFTV SCRVLTRPSP DFDIFLVPP TVESRTKPFS VPVLTVEEMT NSRFPIPLEK 240
LFTGPSSAFV VQPQNGRCTT DGVLLGTTQL SPVNICTFRG DVTHITGSRN YTMNLASQNW 300
NDYDPTEEIP APLGTPDFVG KIQGVLTQTT RTDGGSTRGHK ATVYTGSAF APKLGRVQFE 360
TDTDRDFEAN QNTKFTPVGV IQDGGTTHRN EPQQWVLPY SGRNTHNVHL APAVAPTFPG 420
EQLLPFRSTM PGCSGYPNMD LDCLLPQEWV QYFYQEAAPA QSDVALLRFV NPDTRGVLF 480
CKLHKSQVVT VAHTGQHDLV IPNGYFRFD SWVNQFYTLA PMNGTGRRR AV 532

```

```

SEQ ID NO: 64      moltype = DNA length = 1599
FEATURE           Location/Qualifiers
misc_feature       1..1599
                  note = Nucleic acid sequence of human codon optimized
                  VPI_GII.4_Syd12_delta 35-42
source            1..1599
                  mol_type = other DNA
                  organism = synthetic construct

```

```

SEQUENCE: 64
atgaaatagg cctcgagtga cgtaaccct agtgacggca ggcgcgcaa tcttgtgct 60
gaggttaata atgaggtgat ggcctcggag cctgtggtgg gcggtcagca gaatgtgatt 120
gaccctggga tacgcaacaa tttgtccaa gcccttggtg gggagttcac cgtagcccg 180
agaaatgcgc caggagaaat cctgtggtcg gcccattgg gaccgatct gaacccctat 240
ttgtcacatc tcgctcggat gtacaacggg tatgcggcg gatttgaagt gcaggtgatt 300
ctggctggga acgcgttcac tgctggcaaa gtgatcttg cagcggtgcc tcccaactc 360
cccactgaag gactgtctcc aagccaggtc acaatgtttc cacacatcgt ggtggacgta 420
cggcagctag agcctgtcct gattccctc cctgatgtac gcaataatct ctaccactac 480
aatcaatcca atgattccga cattaactc atcgcgatgt tgtacacccc tctgcgcgct 540
aacaatgctg gagacgacgt attcaccgtg tcatgcagag tgctcaccag acctcacca 600
gactttgact ttatctcttt agtgccccc actgttgaga gccgaaccaa gccctttagt 660
gtccccgtac tcacactoga ggagatgaca aatagccgct ttccaatccc cttgagaaa 720
ctgttcacag gacctctctc ggcatcgtg gttcagccac agaacggacg ctgcacaaact 780
gacggcgctg tgctcggaac caccagctt agccctgtta atatctgtac gtttagaggg 840
gacgtaaact acataactga ctacgggaac tataccatga atctggcatc acagaattgg 900
aatgactacg acccaaccga agagattccc gcacctcttg gaacccccga ctttgtggga 960
aaaatacagg gcgtcctgac acaaacacc agaaccgat gctccacacg gggacacaa 1020
gcaaccgtct acatcatata tgcgatttt gcccgaaac tgggtagagt gcagtttgag 1080
accgacactg accgggactt tgaagccaat cagaatacta agttcacacc tgtaggagt 1140
attcaggacg ggggcaccac tcaccggaac gagccgcaac aatgggtcct gccctcttat 1200
agcgggagga atactcataa tgtgcatttg gctcctgcag tggctccac gtttccggg 1260
gaacaaactg tcttttttgc ttcaaccatg cctggatgct ccggatattc caatatggat 1320
ctcgattgcc tgcctccaca ggaatgggtg cagtatttt atcaagagcg cgcaccagcc 1380
caatccgacg tcgcacttct gcggttcgtg aatccagaca caggcccgct gttgtttgag 1440
tgcaaatgac acaaatcagg atacgttaca gtggctcata ctggacagca tgacctgggt 1500
atccacacca accgatattt taggttcgac tctgggtga atcagtttta tacattagcc 1560
cccatgggga atgggactgg cagacgcagg gctgtctga 1599

```

```

SEQ ID NO: 65      moltype = AA length = 540
FEATURE           Location/Qualifiers
source            1..540
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

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SEQUENCE: 65
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGSSTAVA TAGQQNVIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAP LGPDNLNPYS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFVSP VLTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTEEIPAP LGTPDFVGKI QGVLTQTTTRT DGSTRGHKAT VYTGSAFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVIG DGGTTHRNEP QQWVLPYSYG RNTHNVHLAP 420
AVAPTFPGEQ LLFPRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQS DVALLRFVNP 480
DTGRVLFPECK LHKSGYVTVA HTGQHDLVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRRAV 540

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SEQ ID NO: 66      moltype = DNA length = 1623
FEATURE            Location/Qualifiers
misc_feature       1..1623
                   note = Nucleic acid sequence of human codon optimized
                   VPI_GII.4_Syd12_SSTAVATA
source             1..1623
                   mol_type = other DNA
                   organism = synthetic construct

```

```

SEQUENCE: 66
atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcgcaa tcttgtgcct 60
gaggttaata atgaggtgat ggccttggag cctgtggtgg gcagctccac cgcgctcgct 120
acagccggtc agcagaatgt gattgaccgg tggatacgca acaattttgt ccaagcccct 180
ggtggggagt tcaccgttag ccgcagaaat gcgccaggag aaatcctgtg gtcggcccca 240
ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgttg caaagtgtgc 360
tttgacagcg tgcttcccaa ctccccact gaaggactgt ctccaagcca ggtcacaatg 420
tttccacaca tcgtgggtgga cgtacggcag cttaggcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgac cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggtcag 780
ccacagaaag gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tccgcacct 960
cttggaaacc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cagggggaca caaggcaacc gtctacactg gctctgcgga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaaagtcca cactgttagg agtgatttcag gacgggggca ccaactcacc gaacgagcgg 1200
caacaatggg tcttcgccctc ttatagcggg aggaatactc ataattgtga tttggctcct 1260
gcagtggctc ccacgttttc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320
tgctccggat atcccaatat ggaatctcat tgctctgctc cacagggaat ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440
gacacaggcc gcgtgttgtt tgagtgcaaa ttgcacaaat caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggtctgc 1620
tga                                                    1623

```

```

SEQ ID NO: 67      moltype = AA length = 540
FEATURE            Location/Qualifiers
source             1..540
                   mol_type = protein
                   note = Norovirus
                   organism = unidentified

```

```

SEQUENCE: 67
MKMASSDANP SDGSAANLVP EVNNEVMALP PVVGAAIAPV VAGQONVIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNPFT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSVP VLTVEEMTNS 240
RPPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTTEIPAP LGTPDFVGKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPYSYG RNTHNHVLAP 420
AVAPTFPGEQ LLFFRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTVA HTGQHDVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRRAV 540

```

```

SEQ ID NO: 68      moltype = DNA length = 1623
FEATURE            Location/Qualifiers
misc_feature       1..1623
                   note = Nucleic acid sequence of human codon optimized
                   VPI_GII.4_Syd12_P80S plus sign A39V
source             1..1623
                   mol_type = other DNA
                   organism = synthetic construct

```

```

SEQUENCE: 68
atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcgcaa tcttgtgcct 60
gaggttaata atgaggtgat ggccttggag cctgtggtgg gcgcagccat agcagtcccc 120
gtggccggtc agcagaatgt gattgaccgg tggatacgca acaattttgt ccaagcccct 180
ggtggggagt tcaccgttag ccgcagaaat gcgccaggag aaatcctgtg gtcggcccagc 240
ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgttg caaagtgtgc 360
tttgacagcg tgcttcccaa ctccccact gaaggactgt ctccaagcca ggtcacaatg 420
tttccacaca tcgtgggtgga cgtacggcag cttaggcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgac cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720

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-continued

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cgctttccaa tcccccttga gaaactgttc acaggacett cctcggcatt cgtgggttcag 780
ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgttttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgacact 960
cttggaaacc cgcactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagttca cactgttagg agtgattcag gacgggggca cactcaccg gaacgagccg 1200
caacaatggg tccctgcctc ttatagcggg aggaatactc ataattgtga tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcgggt cgtgaatcca 1440
gacacaggcc gcgtgtgtgt tgagtgcaaa ttgcacaaat caggatacgt tacagtgggt 1500
catactggac agcatgacct ggtgatccca cccaacggat attttagggt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccattg ggggaatggga ctggcagacg cagggtctgtc 1620
tga

```

```

SEQ ID NO: 69      moltype = AA length = 540
FEATURE           Location/Qualifiers
source            1..540
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 69
MKMASSDANP SDGSAANLVP EVNNEVMALP PVVGAIAAP VAGQONPIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSVP VLTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTTEIPAP LGTPDFVVGKI QGVLTQTTRT DGSTRGHKAT VYTGSAFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPYSYG RNTNHNHLAP 420
AVAPTFPGEQ LLFPRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAPPAQS DVALLRFVNP 480
DTGRVLFCK LHKSGYVTVA HTGQHDLVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRRAV 540

```

```

SEQ ID NO: 70      moltype = DNA length = 1623
FEATURE           Location/Qualifiers
misc_feature       1..1623
                  note = Nucleic acid sequence of human codon optimized
                  VPI_GII.4_Syd12_P80S plus sign V47P
source            1..1623
                  mol_type = other DNA
                  organism = synthetic construct

```

```

SEQUENCE: 70
atgaaaaatg cctcgagtga cgtaaacctt agtgacggca ggcgcgcca tcttgtgctt 60
gaggttaata atgaggtgat ggcctctggg cctgtgggtg gcgcagccat agcagcgccc 120
gtggccgggtc agcagaatcc catgaccccg tggatacgca acaattttgt ccaagccctt 180
gggtggggagt tcaccgttag cccgagaaat ggcgcaggag aaatcctgtg gtgcggccagc 240
ttgggaccgg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgctg caaagtgatc 360
tttgcagcgg tgctctccaa ctctccactt gaaggactgt ctccaagcca ggtcacaaatg 420
tttcacacac tcgtgtggga cgtacggcag ctagagcctg tcttgattcc cctccctgat 480
gtacgcaata atctctacca ctacaatcaa tccaatgata cgaccattaa actcatcgcg 540
atgtgtgata cccctctgct cgtaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc cccactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacett cctcggcatt cgtgggttcag 780
ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgttttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgacact 960
cttggaaacc cgcactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagttca cactgttagg agtgattcag gacgggggca cactcaccg gaacgagccg 1200
caacaatggg tccctgcctc ttatagcggg aggaatactc ataattgtga tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcgggt cgtgaatcca 1440
gacacaggcc gcgtgtgtgt tgagtgcaaa ttgcacaaat caggatacgt tacagtgggt 1500
catactggac agcatgacct ggtgatccca cccaacggat attttagggt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccattg ggggaatggga ctggcagacg cagggtctgtc 1620
tga

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SEQ ID NO: 71      moltype = AA length = 540
FEATURE           Location/Qualifiers
source            1..540
                  mol_type = protein

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note = Norovirus
organism = unidentified

SEQUENCE: 71
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAIAAP VAGQQNVIDP WIINNFBVQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSSVP VLTVEEMTNS 240
RPPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTTEEIPAP LGTPDFVGKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPSSYG RNTHNVHLAP 420
AVAPTFPGEQ LLFRRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAPPAQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTV HTGQHDVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRAV 540

SEQ ID NO: 72      moltype = DNA length = 1623
FEATURE            Location/Qualifiers
misc_feature        1..1623
                    note = Nucleic acid sequence of human codon optimized
                    VPI_GII.4_Syd12_P80S plus sign R53I
source              1..1623
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 72
atgaaaaatgg cctcgagtga cgtaaacct agtgacggca ggcgcgcaa tctgtgctc 60
gaggttaata atgaggtgat ggcctctggag cctgtggtgg ggcagccat agcagcgccc 120
gtggccgggtc agcagaatgt gattgaccgg tggataatca acaattttgt ccaagcccct 180
ggtggggagt tcaccgttag ccagagaaat ggcgcaggag aaatcctgtg gtcggccagc 240
ttgggaccgg atctgaaccc ctattgtgca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcagggt gattctggct gggaacgcgt tcaactgctg caaagtgtac 360
tttgacggcg tgctcccaaa ctcccccaat gaaggactgt tcccaagcca ggtcacaaat 420
tttcacacac tcgtggtgga cgtacggcag cttagagcctg tcctgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgtaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc cccactggtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggttcag 780
ccacagaaac gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtagctttag aggcgacgta actcacataa ctggtcaccg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960
cttggaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca caaggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080
aaactgggta gactgcagtt tgagaccgac actgtgagcg caatcagaat 1140
actaagtcca cactgttagg agtgattcag gacgggggca cactcacccg gaacgagccg 1200
caacaatggg tccctgccctt ttatagcggg aggaataactc ataagtgcga tttggctcct 1260
gcagtggctc ccacgttttc cggggaacaa ctgctctttt ttcgttcaac catgcctgga 1320
tgctccggat atcccaatat ggaatctgat tgctgctccc cacaggaatg ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440
gacacaggcc gcgtgtgtgt tgagtgcata ttgcacaaat caggatagct tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggtctgc 1620
tga
1623

SEQ ID NO: 73      moltype = AA length = 540
FEATURE            Location/Qualifiers
source              1..540
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

SEQUENCE: 73
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAIAAP VAGQQNVIDP WIRNNFBVQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLL HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSSVP VLTVEEMTNS 240
RPPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTTEEIPAP LGTPDFVGKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPSSYG RNTHNVHLAP 420
AVAPTFPGEQ LLFRRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAPPAQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTV HTGQHDVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRAV 540

SEQ ID NO: 74      moltype = DNA length = 1623
FEATURE            Location/Qualifiers
misc_feature        1..1623
                    note = Nucleic acid sequence of human codon optimized
                    VPI_GII.4_Syd12_P80S plus sign S90L
source              1..1623
                    mol_type = other DNA
                    organism = synthetic construct

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SEQUENCE: 74

```

atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcgcaa tcttgtgcct 60
gaggttaata atgaggtgat ggccctggag cctgtggtgg gcgcagccat agcagcgccc 120
gtggccgggtc agcagaatgt gattgaccog tggatagcca acaattttgt ccaagccct 180
gggtggggagt tcaccgttag ccgagaaat gcgcagagg aaatcctgtg gtcggccagc 240
ttgggaccog atctgaaccc ctatttctgt catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgtgg caaagtgtac 360
tttgacggg tgccctccaa ctccccact gaaggactgt ctccaagcca ggtcacatg 420
tttcacacaca tctgtggtgga cgtacggcag cttagagcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgac cgaccattaa actcctcgcg 540
atgttgtaga cccctctgcg cgtaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc cccactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtggttcag 780
ccacagaacg gacgctgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgaagta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960
cttggaaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca ccaagggaac caaggcaacc gtctacactg gctctgccga ttttgccccg 1080
aaactgggta gactgcaagt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagtcca cactgttagg agtgattcag gacgggggca ccaactaccg gaacgagccg 1200
caacaatggg tccctgcctc ttatagcggg aggaataact ataagtgcga tttggctcct 1260
gcagtggctc ccactgtttc cggggaaacaa ctgctctttt tctgttcaac catgcctgga 1320
tgctccggat atcccaatat ggaatctgat tgcctgctcc cacaggaatg ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgac ttctgcggtt cgtgaatcca 1440
gacacagggc cgtgtgtgtt tgagtcaaaa ttgcacaaat caggatacag tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggtt cgaactcctg 1560
gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggtgtgc 1620
tga

```

SEQ ID NO: 75 moltype = AA length = 532

FEATURE Location/Qualifiers

```

source 1..532
        mol_type = protein
        note = Norovirus
        organism = unidentified

```

SEQUENCE: 75

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MKMASSDANP SDGSAANLVP EVNNEVMALP PVVGGQONVI DPWIRNNFVQ APGGEFTVSP 60
RNAPGEILWS ASLGPDLNPN LSHLARMYNG YAGGFVEVQVI LAGNAFTAGK VIFAAVPPNF 120
PTEGLSPSQV TMFPHIVVDV RQLEPVLIP L PDVRNNFYHY NQSNPTIKL IAMLVTPLR 180
NNAGDDVFTV SCRVLTRPSP DFDIFLVPV TVESRTKPFS VPVLTVEEMT NSRFPIPLEK 240
LFTGPSSAFV VQPQNGRCTT DGVLLGTTQL SPVNICTFRG DVTHITGSRN YTMNLASQNW 300
NDYDPTTEIP APLGTPDFVG KIQGVLTQTT RTDGSSTRGHK ATVTYGSADF APKLGRVQFE 360
TDTDRDFEAN QNTKFTPVGV IQDGGTTHRN EPQQWVLPST SGRNTHNVHL APAVAPTFPG 420
BQLLFRRSTM PGCSGYPNMD LDCLLPQEWV QYFYQEAAPA QSDVALLRFV NPDTRVRLFE 480
CKLHKSQVVT VAHTGQHDLV IPNNGYFRFD SWVNQFYTLA PMNGTGRRR AV 532

```

SEQ ID NO: 76 moltype = DNA length = 1599

FEATURE Location/Qualifiers

```

misc_feature 1..1599
        note = Nucleic acid sequence of human codon optimized
              VP1_GII.4_Syd12_P80Splus sign delta 35-42
source 1..1599
        mol_type = other DNA
        organism = synthetic construct

```

SEQUENCE: 76

```

atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcgcaa tcttgtgcct 60
gaggttaata atgaggtgat ggccctggag cctgtggtgg gcggtcagca gaatgtgatt 120
gaccctgtgga tacgcaacaa tttgtccaa gccctgtgtg gggagttcac cgttagcccc 180
agaaatgcgc caggagaaat cctgtggtcg gccagcttgg gaccgatctc gaaccctcat 240
ttgtcacatc tgcctcggat gtacaacggg tatgcggcgc gatttgaagt gcagggtatt 300
ctggctggga acgcgttcac tgtctggcaa gtgatctttg cagcgggtgc tcccaacttc 360
cccactgaag gactgtctcc aagccaggtc acaatgtttc cacacatcgt ggtggacgta 420
cggcagctag agcctgtctc gattccccct cctgatgtac gcaataattt ctaccactac 480
aatcaatcca atgacgcgac cattaaactc atcgcgatgt tgtacacccc tctgcgcgct 540
aacaatgctg gagacgacgt attcacogtg tcatgcagag tgctcaccag accttcacca 600
gactttgact ttatctctct agtgcccccc actgttgaga gccgaaccaa gccctttagt 660
gtccccgtac tcacagtoga ggagatgaca aatagccgct ttccaatccc ccttgagaaa 720
ctgttcacag gaccttcctc ggcatctgtg gttcagccac agaacggacg ctgcacaaact 780
gacggcgctg tgctcgggaa cccccagctt agccctgtta atatctgtac gtttagagggc 840
gacgtaactc acataactgg ctacacggaac tataccatga atctggcattc acagaattgg 900
aatgactacg acccaacoga agagattccc gcacctcttg gaacccccga ctttgtggga 960
aaaatacagg gcgtcctgac acaaacaccc 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

```

-continued

```

agcgggagga atactcataa tgtgcatttg gctcctgcag ttggtccccc gtttccccgg 1260
gaacaactgc tcttttttcg ttcaaccatg cctggatgct ccggatatcc caatatggat 1320
ctcgattgccc tgctcccaca ggaatgggtg cagtattttt atcaagaggg cgcaccagcc 1380
caatccgacg tcgcacttct gcggttcgtg aatccagaca caggcccgct gttgtttgag 1440
tgcaaatgac acaaatcagg atacgttaca gtggctcata ctggacagca tgacctgggtg 1500
atcccaccca acggatatatt taggttcgac tcttgggtga atcagtttta tacattagcc 1560
cccatgggga atgggactgg cagacgcagg gctgtctga 1599

```

SEQ ID NO: 77 moltype = AA length = 540

FEATURE Location/Qualifiers

source 1..540

mol_type = protein

note = Norovirus

organism = unidentified

SEQUENCE: 77

```

MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGSSTAVA TAGQQNVIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPTV ESRTKPFSVP VLTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTEEIPAP LGTPDFVGGI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPYSYG RNTHNVLHAP 420
AVAPTFPGEQ LLFPRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTV AHTGQDLVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRRAV 540

```

SEQ ID NO: 78 moltype = DNA length = 1623

FEATURE Location/Qualifiers

misc_feature 1..1623

note = Nucleic acid sequence of human codon optimized

VP1_GII.4_Syd12_P80S plus sign SSTAVATA

source 1..1623

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 78

```

atgaaaaatgg cctcgagtga cgtaaacct agtgacggca gcgcccgc aa tcttgtgcct 60
gaggttaata atgaggtgat ggcctcggag cctgtgtggg gcagctccac cgcctgcgt 120
acagccgggc acgcaaatgt cctgacccg tggatacgca acaattttgt ccaagccct 180
ggtggggagt tcaccgttag ccagagaaat gcgccaggag aaatcctgtg gtcggccagc 240
ttgggaccgc atctgaaccc ctatttgc ca ctctgcgc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcagg gattctggct gggaacgcgt tcaactgctg caaagtgtatc 360
tttcagcggg tgctcccaa ctccccact gaaggactgt tccaagcca ggtcacaaatg 420
tttcacaca tcgtgtggga cgtacggcag cttagcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgatc cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgtaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccctc accagacttt gactttatct tcttagtgcc cccactggt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcggeatt cgtggttcag 780
ccacagaacg gacgtgcac aactgacggc gtgtgctgct gaaccaccca gcttagccct 840
gttaatatct gtaagttag agggacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgcacct 960
cttggaaacc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca caggggaca caaggcaacc gtctacactg gctctgccga ttttgccccg 1080
aaactgggta gactgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagttca cactgttagg agtgattcag gacgggggca ccaactaccc gaacgagccg 1200
caacaatggg tcttgccttc ttatagcggg aggaataactc ataagtgc a tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt ttctgtcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgcctgtccc cacaggaatg ggtgcagtat 1380
ttttatcaag agggccgacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440
gacacaggcc gcgtgttgtt tgagtgc aaa ttgcacaaat caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca ccaaacggat attttaggtt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatt gggaaatggga ctggcagacg cagggctgtc 1620
tga 1623

```

SEQ ID NO: 79 moltype = AA length = 547

FEATURE Location/Qualifiers

source 1..547

mol_type = protein

note = Norovirus

organism = unidentified

SEQUENCE: 79

```

MKMASNDAAP SNDGAANLVP EANNEVMALE PVVGASIAAP VVGQQNIIDP WIRENFVQAP 60
QGEFTVSPRN SPGEMLLNL LGEPLNPYLS HLSRMNGYA GGMQVQVLA GNAFTAGKII 120
FAAVPPHFPV ENINAAQITM CPHIVVDVRQ LEPVLLPLPD IRNRFHYNQ ENTSRMLVA 180
MLYTPLRANS GEDVFTVSCR VLTRPAPDFE FTFLVPPTVE SKTKPFSLPI LTLGELNSNR 240
FPAPIDMLYT DPNBGIVVQP QNGRCTL DGT LQGTQLVPT QICAFRGTLI GQTSRSPDST 300
DSAPRRRDHP LHVQLKNLDG TQYDPTDEVP AVLGAIDFKG TVFGVASQRD VSGQQVGATR 360

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AHEVHINTTD	PRYTPKLGSI	LMYSESDDFV	TGQPVRFPTPI	GMGDNDWHQW	ELPDYPGHLT	420
LNMNLAPAVA	PAPFGERILF	FRSIVPSAGG	YSGGQIDCLI	PQEWVQHIFYQ	EAAPSQSAVA	480
LIRYVNPDTG	RNIFEAKLHR	EGFITVANS	NNPIVVPNG	YFRFEAWVNQ	FYTLTPMGTG	540
QGRRRDQ						547

SEQ ID NO: 80 moltype = DNA length = 1644
 FEATURE Location/Qualifiers
 misc_feature 1..1644
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.6_Ohio_E80S
 source 1..1644
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 80

atgaagatgg	caagcaacga	cgcagctccc	tccaatgatg	gtgccgcca	cctgggtccc	60
gaagctaata	atgaggtgat	ggcggttagag	ccggtggttg	gcgcattctat	tgcagcgcct	120
gtggtcggac	agcagaacat	cattgatccc	tggattcgcg	agaacttcgt	acaagctcca	180
cagggggag	tcacagctct	cccccggaac	tccccgggcg	agatgctgct	caatctgagc	240
ctcgccctg	aactaaaccc	ttatctgtca	cacctttcac	ggatgtacaa	tggtacgca	300
ggaggaatgc	aagttcaggt	ggctcctggcc	ggcaatgctt	tcaccgcggg	caaaatcatc	360
tttgcggcgc	ttctccaca	cttccctgtc	gaaaatatca	acgcccacca	gattactatg	420
tgccccacg	tgattgtgga	tgtgcgacag	ttagagccag	ttctgtgccc	cctgcccagc	480
atcagaaacc	ggttcttcca	ttacaatcaa	gagaatactt	cacggatgag	acttgttgcg	540
atgctgtaca	cccctcttgc	tgcaaatccc	ggcgaagacg	tgttcactgt	gtcttgctga	600
gtacttacc	gacccgcccc	cgatttcgaa	ttcaccttcc	tggttcccc	tactgtggag	660
agcaagacaa	aacccttcag	cctcccaatc	ttaacactcg	gggagctgtc	taattcacgc	720
ttccccgcac	ctattgatat	gctgtatact	gaccccaacg	aggggatagt	ggtgcagccc	780
caaaatggac	ggtgtactct	cgacggcacg	ctccaggcca	caaccacaact	ggtgcccaacc	840
cagattttgtg	cattcacgggg	cactttgatt	gggcagacat	cgagatctcc	agattctact	900
gattccgcgc	caaggaggag	ggaccaccca	ctccacgttc	agttaaaaaa	cctggacgga	960
acccagtagc	accctacaga	cgaagtcctc	gctgtcctcg	gagccatcga	ctttaaagga	1020
actgtatttg	gagtgggcatc	ccaaagggat	gtctcggggc	agcaggtggg	agctacgaga	1080
gcacatgaag	cccacattaa	caccacagac	ccaagatata	ccccaaaact	agggtcaatt	1140
ttaatgtatt	ggaatcaga	cgattttgtt	acaggtcagc	ccgtgcggtt	taccocgac	1200
ggaatggggg	acaacgattg	gcaccagtgg	gaattgccc	attaccctgg	acacctcacc	1260
ttgaatatga	atctggcccc	agccgtcgcg	cccgccttcc	ccggtgagcg	gatcctcttt	1320
tttagaagca	tgtgctcctc	cgacgtggg	tatggatcag	ggcagattga	ttgcctgac	1380
cccccaagaat	gggtacagca	ttctaccag	gaagcagccc	ctagccagtc	cgcagtagca	1440
ctgacagat	atgttaatcc	tgatacggga	aggaacatct	tcgaagcaaa	actgcaccgt	1500
gagggcttca	ttaccgtcgc	caacagtggg	aataacccta	ttgtggtgcc	tcctaattgga	1560
tacttcaggt	ttgaggcatc	ggtgaatcag	ttttatactc	tgactcccat	ggggacaggc	1620
cagggggcag	gccgggatca	gtga				1644

SEQ ID NO: 81 moltype = AA length = 547
 FEATURE Location/Qualifiers
 source 1..547
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 81

MKMASNDAA	P	SNDAANLVP	EANNEVMALE	PVVGASIAAP	VVGQONIIDP	WIRENFVQAP	60
QGEFTVSPRN	P	SPGEMLLNLE	LGPELNPYLL	HLSRMYNGYA	GGMQVQVLA	GNAFTAGKII	120
FAAVPPHPFV	P	ENINAAQITM	CPHVIDVVRQ	LEPVLLPLPD	IRNRFPHYNQ	ENTSRMLVA	180
MLYTPLRANS	P	GEDVFTVSCR	VLTRPAPDPE	FTFLVPPTVE	SKTKPFSLPI	LTLGELSISR	240
FPAPIDMLYT	P	DPNEGIVVQP	QNGRCTLDGT	LQGTTLQVPT	QICAFRGTLI	GQTSRSPDST	300
DSAPRRRDHP	P	LHVQLKNLDG	TQYDPTDEVP	AVLGAIDFKG	TVFVGASQRD	VSGQVVGATR	360
AHEVHINTTD	P	PRYTPKLGSI	LMYSESDDFV	TGQPVRFPTPI	GMGDNDWHQW	ELPDYPGHLT	420
LNMNLAPAVA	P	PAPFGERILF	FRSIVPSAGG	YSGGQIDCLI	PQEWVQHIFYQ	EAAPSQSAVA	480
LIRYVNPDTG	P	RNIFEAKLHR	EGFITVANS	NNPIVVPNG	YFRFEAWVNQ	FYTLTPMGTG	540
QGRRRDQ							547

SEQ ID NO: 82 moltype = DNA length = 1644
 FEATURE Location/Qualifiers
 misc_feature 1..1644
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.6_Ohio_S90L
 source 1..1644
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 82

atgaagatgg	caagcaacga	cgcagctccc	tccaatgatg	gtgccgcca	cctgggtccc	60
gaagctaata	atgaggtgat	ggcggttagag	ccggtggttg	gcgcattctat	tgcagcgcct	120
gtggtcggac	agcagaacat	cattgatccc	tggattcgcg	agaacttcgt	acaagctcca	180
cagggggag	tcacagctct	cccccggaac	tccccgggcg	agatgctgct	caatctggaa	240
ctcgccctg	aactaaaccc	ttatctgtct	cacctttcac	ggatgtacaa	tggtacgca	300
ggaggaatgc	aagttcaggt	ggctcctggcc	ggcaatgctt	tcaccgcggg	caaaatcatc	360

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tttgcggcgc ttcctccaca ctteccctgtc gaaaatatca acgcccgcga gattactatg 420
tgccccacag tgatttgtga tgtgcgacag ttagagccag ttctgctgcc cctgcccagc 480
atcagaaaacc ggttcttcca ttacaatcaa gagaatactt cacggatgag acttggtgcg 540
atgctgtaca cccctcttcg tgcaaatcc ggcaagacg tgttcaactgt gtcttgtcga 600
gtacttaccc gaccgcgccc cgatttcgaa ttcaccttcc tggttccccc tactgtggag 660
agcaagacaa aacccttcag cctcccaatc ttaacactcg gggagctgtc taattcacgc 720
ttccccgcac ctattgatat gctgtatact gaccccaacg aggggatagt ggtgcagccc 780
caaaatggac ggtgtactct cgacggcacg ctccagggca caacccaact ggtgcccaacc 840
cagattttgtg cattcagggg cacttttgatt gggcagacat cgagatctcc agattctact 900
gattccgcgc caaggaggag ggaccacca ctccacgttc agttaaaaaa cctggacgga 960
acccagtagc accctacaga cgaggtcccc gctgtcctcg gagccatcga ctttaaagga 1020
actgtatttg gattggcatc ccaaagggat gtctcggggc agcaggtggg agctacgaga 1080
gcacatgaag tccacattaa caccacagac ccaagatata ccccaaaact aggggtcaatt 1140
ttaatgtatt cggaatcaga cgattttgtt acaggtcagc ccgtgcggtt taccocgatc 1200
ggaatggggg acaacgattg gcaccagtgg gaattgcccc attaccctgg acacctcacc 1260
ttgaatatga atctggcccc agccgtcgcg cccgccttcc ccggtgagcg gatcctcttt 1320
tttagaagca tagtgccctc cgaggtggg tatggatcag ggcagattga ttgcctgatc 1380
ccccagaat gggtagacga ttctaccag gaagcagccc ctagccagtc cgcagtagca 1440
ctgacagat atgttaatcc tgatacggga aggaacatct tcgaagcaaa actgcaccgt 1500
gagggcttca ttaccgtcgc caacagtggg aataacccta ttgtggtgcc tcctaagga 1560
tacttcaggt ttgaggcatg ggtgaatcag ttttatactc tgactcccat ggggacagcg 1620
cagggcgac gccgggatca gtga 1644

```

SEQ ID NO: 83 moltype = AA length = 547

FEATURE Location/Qualifiers

source 1..547

mol_type = protein

note = Norovirus

organism = unidentified

SEQUENCE: 83

```

MKMASNDAAP SNDGAANLVP EANNEVMALP PVVGASIAAP VVGQONIIDP WIRENFVQAP 60
QGEFTVSPRN SPGEMLLNLS LGPELNPLYL HLSRMVNGYA GGMQVQVFLA GNAFTAGKII 120
FAAVPPHPV ENINAAQITM CPHVIVDVRQ LEPVLLPLPD IRNRFFHYNQ ENTSRMLVA 180
MLYTPLRANS GEDVFTVSCR VLTRPADDFE FTFLVPPTVE SKTKPFLPI LTLGELSNSR 240
FPAPIDMLYT DPNEGIVVQP QNGRCTLDTG LQGTTLQVPT QICAFRGTLI GQTSRSPDST 300
DSAPRRRDHP LHVQLKNLDG TQYDPTDEVP AVLGAIDFKG TVFVVASQRD VSGQVQVATR 360
AHEVHINTD PRYTPKLGSI LMYSESDDFV TGQPVRFPTI GMGDNDWHQW ELPDYPGHLT 420
LNMNLAPAVA PAFPGERILF FRSIVPSAGG YGSGQIDCLI PQEWVQHFIYQ EAAPSQSAVA 480
LIRYVNPDTG RNIPEAKLHR EGFITVANSQ NNPIVVPNG YFRFEAWVNO FYTLTPMGTG 540
QRRRDQ 547

```

SEQ ID NO: 84 moltype = DNA length = 1644

FEATURE Location/Qualifiers

misc_feature 1..1644

note = Nucleic acid sequence of human codon optimized

VP1_GII.6_Ohio_E80S plus sign S90L

source 1..1644

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 84

```

atgaagatgg caagcaacga cgcagctccc tccaatgatg gtgcccgcga cctgggtcccc 60
gaagctaata ataggttgat ggcgttagag ccggtgggtg gcgcactat tgacgagcct 120
gtggctcgac agcagaacat catgtatccc tggattcgcg agaacttcgt acaagctcca 180
cagggggaggt tcacagtcct cccccggaac tccccgggag agatgctgct caatctgagc 240
ctcggccctg aactaaaccc ttatctgctc cacctttcac ggatgtacaa tggctaacga 300
ggagggaatgc aagttcaggt ggtcctggcc ggcaatgctt tcaccgcggg caaaatcacc 360
tttgcggcgc ttcctccaca ctteccctgtc gaaaatatca acgcccgcga gattactatg 420
tgccccacag tgatttgtga tgtgcgacag ttagagccag ttctgctgcc cctgcccagc 480
atcagaaaacc ggttcttcca ttacaatcaa gagaatactt cacggatgag acttggtgcg 540
atgctgtaca cccctcttcg tgcaaatcc ggcaagacg tgttcaactgt gtcttgtcga 600
gtacttaccc gaccgcgccc cgatttcgaa ttcaccttcc tggttccccc tactgtggag 660
agcaagacaa aacccttcag cctcccaatc ttaacactcg gggagctgtc taattcacgc 720
ttccccgcac ctattgatat gctgtatact gaccccaacg aggggatagt ggtgcagccc 780
caaaatggac ggtgtactct cgacggcacg ctccagggca caacccaact ggtgcccaacc 840
cagattttgtg cattcagggg cacttttgatt gggcagacat cgagatctcc agattctact 900
gattccgcgc caaggaggag ggaccacca ctccacgttc agttaaaaaa cctggacgga 960
acccagtagc accctacaga cgaggtcccc gctgtcctcg gagccatcga ctttaaagga 1020
actgtatttg gattggcatc ccaaagggat gtctcggggc agcaggtggg agctacgaga 1080
gcacatgaag tccacattaa caccacagac ccaagatata ccccaaaact aggggtcaatt 1140
ttaatgtatt cggaatcaga cgattttgtt acaggtcagc ccgtgcggtt taccocgatc 1200
ggaatggggg acaacgattg gcaccagtgg gaattgcccc attaccctgg acacctcacc 1260
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tttagaagca tagtgccctc cgaggtggg tatggatcag ggcagattga ttgcctgatc 1380
ccccagaat gggtagacga ttctaccag gaagcagccc ctagccagtc cgcagtagca 1440
ctgacagat atgttaatcc tgatacggga aggaacatct tcgaagcaaa actgcaccgt 1500
gagggcttca ttaccgtcgc caacagtggg aataacccta ttgtggtgcc tcctaagga 1560

```

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```
tacttcaggt ttgaggcagtg ggtgaatcag ttttatactc tgactcccat ggggacaggc 1620
cagggcgac gccgggatca gtga 1644
```

```
SEQ ID NO: 85      moltype = AA length = 542
FEATURE           Location/Qualifiers
source            1..542
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified
```

```
SEQUENCE: 85
MKMASNDAAP STDGAAGLVP ESNNEVMALE PVAGAALAAP VTGQTNIIDP WIRANFVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLA HLARMYNGYA GGMEVQVMLA GNAFTAGKLV 120
FAAVPPHPFV ENLSPQQITM FPHVIIDVRT LEPVLLPLPD VRNFFHYNQ KDDPKMRIVA 180
MLYTPPLRSNG SGDDVFTVSC RVLTRPSPDF DFTYLVPPTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIQDMY TSPNEVISVQ CQNGRCTLDG ELQGTQLQV SGICAFKGEV TAHLHDNDHL 300
YNVTTITNLNG SPFDPSDIP APLGVPDFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWQT DDLTVNQPVK FTPVGLNDTD HFNQWVVPY AGALNLNTNL 420
APSVAPVFPF ERLFFRSYI PLKGGYGTGA IDCLLPQEWV QHFYQEAAPS MSEVALVRYI 480
NPDTEGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWVNQFYSLA PMGTGNGRRR 540
IQ 542
```

```
SEQ ID NO: 86      moltype = DNA length = 1629
FEATURE           Location/Qualifiers
misc_feature       1..1629
                  note = Nucleic acid sequence of human codon optimized
                  VP1_GII.2_CGMH47_E80S_
source            1..1629
                  mol_type = other DNA
                  organism = synthetic construct
```

```
SEQUENCE: 86
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgccgg attggtaccc 60
gagtcataa acgaggtgat ggccctggag cctgttcag gggctgccct cgcagctcct 120
gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180
aatggggagt ttacgggtcag ccttagaaat agccctgggg aagtgcctct caatctcagc 240
ctgggaccag aacttaatcc gtacctggct cacctggccc ggaatgtaca tggatatgca 300
ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360
ttcgacggcg tccctcccca ctcccagtt gaaaatcttt cccctcagca gattaccatg 420
tttccccatg tcatcatoga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480
gtgcggaata atttcttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540
atgctttata ctcccctgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600
cgggtactaa ctgcctcttc accagacttc gactttacgt acttggtgcc tcccactgtc 660
gaaagcaaaa ctaagccatt cacacttccc atcctcacc ctcgagaact ctcgaaactc 720
cgcttcctcg tttcaattga tcagatgtac acgtctccaa atgaagtc atctgtgcag 780
tgtcagaaag gcaggtgcac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840
agtggaattt gcgcctttaa gggcgaagt acagctcacc tccacgaca cgatcatctc 900
tacaatgtta ctattactaa ttcgaatgga agtcctttcg accctcggga agatattccc 960
gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020
aagcataaca caccgggaca taatgagcca gccaatagag cccacgacgc agtcgttcgg 1080
acctatacgg ctccagtacac cccaagctc ggccagatag aaatcgggac ttggcagacc 1140
gatgacctca ctgtgaatca acctgtgaaa ttcaactcag taggtctgaa tgatacagac 1200
caacttaacc agtgggtgggt ccttagatac gccggagcct tgaacctaaa cactaacctt 1260
gccccttcgg ttgacactgt gtttcggggg gagcggttgc tcttctttag aagctatatt 1320
cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtggtt 1380
caacatttct atcaagaggg cgcacctagt atgagcgagg tggctttggg cagatacatc 1440
aatccagaca caggaagagc actgttcgag gccaaagctgc acagagccgg ctcatgacc 1500
gtctcatcca atacatccgc acccgtagta gtccccgcca acgggtactt cagattcgac 1560
agttgggtga atcagtttta ctgctggccc cccatgggca cagggaacgg tcgccagcgg 1620
atccagtaa 1629
```

```
SEQ ID NO: 87      moltype = DNA length = 1608
FEATURE           Location/Qualifiers
misc_feature       1..1608
                  note = Nucleic acid sequence of human codon-optimized VP1
                  GII.12_HS206_2010_USA_
source            1..1608
                  mol_type = other DNA
                  organism = synthetic construct
```

```
SEQUENCE: 87
atgaagatgg cgtctaata tgctgctcct tccaatgatg gcgcagccgg cctgggtccct 60
gaagtgaata acgagactat ggctctcgaa cccgtggcgg gagcctcaat tgccgcccc 120
ctactggccc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180
aatggggagt tcaccgtgtc cccagaaaac tccccggcgg aagtgttatt gaatttgaa 240
ttaggaccag aactcaaccc ctatctggca catctgtctc ggatgtacaa cggctatgcg 300
ggcggagtgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360
tttcagcggg ttccacccca ttttccactt gaaaacataa gccaggcca gatcaccatg 420
ttccctcagc tgataatcga cgtgcgggca ttagagcccg tgctgctacc cctgccccgac 480
```


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```

gtgaggaaca atttctttca ctacaatcag caaaatgaac caagaatgcg cctgggtcgcc 540
atgctctata ctccctttaag aagtaatggc agtgggggatg acgtgtttac tgttagctgt 600
cggtgtgctca cccgaccttc cccagatttc gacttcaatt atctgggtccc ccccacggta 660
gagtccaaaa caaagccttt cactcttcca atccttaca ttggcgaaact gaccaactca 720
cgctttccag tgccatttga tgagctgtac acaagtccaa atgaatccct tgtcgttcag 780
ccacagaatg ggcgctgcgc gcttgacggg gagtccagg gcacaacaca actgttgcca 840
accgctatat gctctttcag ggggcgtatt aatcagaagg tctccgggga gaaccacgtg 900
tggaacatgc aagtgcagaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960
gcgctcttag gtacccctga cttctcaggc aagttgttcg gcgtcccttc ccagcgcgac 1020
catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaattcacc 1080
ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140
ccaacaaagt ttaccctctg tggccttttc gaaagcgaa gctttaacca gtggacactt 1200
cccaattaca gcggggctct cactcttaat atgggactcg caccaccctg cgctccaacg 1260
tttctcgtg agcagatttt gtttttccgc agtcataatc cactgaaggg tggagttgct 1320
gatcccgtag tagactgcct cctccctcag gaatggattc agcacttgta tcaggagtcc 1380
gctccctcgc agaccgatgt ggccttgata cgcttcacaa accccgatac cggaagagtg 1440
tgttttgaag ctaaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500
ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560
agcctggctc caatgggaac aggaatggg aggagcgctg tgcagtaa 1608

```

SEQ ID NO: 88 moltype = AA length = 535

FEATURE Location/Qualifiers

source

1..535

mol_type = protein

note = Norovirus

organism = unidentified

SEQUENCE: 88

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MKMASNDAAP SNDGAAGLVP EVNNETMALE PVAGASIAAP LTGQNNVIDP WIRLNQVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLA HLSRMVNGYA GGVEVQVLLA GNAFTAGKLV 120
FAAVPPHPL ENISPGQITM FPHVIDVRT LEPVLLPLPD VRNFFHYNQ QNEPRMRLVA 180
MLYTPLRNNG SGDDVFTVSC RVLTRPSPDF DFNYLVPTTV ESKTKPFTLP ILTIGELTNS 240
RFPVPIDELY TSPNESLVVQ PQNGRCALDG ELQGTQLLP TAICSFGRRI NQKVSGENHV 300
WNMQVTNIDG TPDPPTEDVP APLGTPDFSG KLFGLVSLQRD HDNACRSHDA VIATNSAKFT 360
PKLGAIQGT WQDDVHINQ PTKFTPVGLF ESEGFNQWTL PNYSGALTLN MGLAPPVAPT 420
FPGEQILFFR SHIPLKGGVA DPVIDCLLPQ EWIQHLYQES APSQTDVALI RFTNPDTGRV 480
LFEAKLHRSG YITVANTGSR PIVVPANGYF RFDSWVNQFY SLAPMGTGNG RRRVQ 535

```

SEQ ID NO: 89 moltype = DNA length = 1608

FEATURE Location/Qualifiers

misc_feature

1..1608

note = Nucleic acid sequence of human codon optimized

VP1_GII.12_HS10_E80S

source

1..1608

mol_type = other DNA

organism = synthetic construct

SEQUENCE: 89

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atgaagatgg cgtctaata tgcgtctcct tccaatgatg ggcagccgg cctgggtccct 60
gaagtgaata acgagactat ggctctcgaa cccgtggccg gagcctcaat tgcgcccccc 120
ctcactggcc agaacaacgt gatgatccc tggatcagac tgaacttctg tcagggtcct 180
aatggggagt tcaccgtgtc ccagagaaac tcccccgccg aagtgttatt gaatttgagc 240
ttaggaccag aactcaaccc ctatctggca catctgtctc ggatgtacaa cggtatgcg 300
ggcggagtgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360
tttgcagcgg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420
ttccctcacg tgataatcga cgtgcggaca ttagagcccg tgctgtacc cctgcccgcg 480
gtgaggaaca atttctttca ctacaatcag caaaatgaac caagaatgcg cctgggtcgcc 540
atgctctata ctccctttaag aagtaatggc agtgggggatg acgtgtttac tgttagctgt 600
cggtgtgctca cccgaccttc cccagatttc gacttcaatt atctgggtccc ccccacggta 660
gagtccaaaa caaagccttt cactcttcca atccttaca ttggcgaaact gaccaactca 720
cgctttccag tgccatttga tgagctgtac acaagtccaa atgaatccct tgtcgttcag 780
ccacagaatg ggcgctgcgc gcttgacggg gagtccagg gcacaacaca actgttgcca 840
accgctatat gctctttcag ggggcgtatt aatcagaagg tctccgggga gaaccacgtg 900
tggaacatgc aagtgcagaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960
gcgctcttag gtacccctga cttctcaggc aagttgttcg gcgtcccttc ccagcgcgac 1020
catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaattcacc 1080
ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140
ccaacaaagt ttaccctctg tggccttttc gaaagcgaa gctttaacca gtggacactt 1200
cccaattaca gcggggctct cactcttaat atgggactcg caccaccctg cgctccaacg 1260
tttctcgtg agcagatttt gtttttccgc agtcataatc cactgaaggg tggagttgct 1320
gatcccgtag tagactgcct cctccctcag gaatggattc agcacttgta tcaggagtcc 1380
gctccctcgc agaccgatgt ggccttgata cgcttcacaa accccgatac cggaagagtg 1440
tgttttgaag ctaaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500
ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560
agcctggctc caatgggaac aggaatggg aggagcgctg tgcagtaa 1608

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SEQ ID NO: 90 moltype = AA length = 535

FEATURE Location/Qualifiers

-continued

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source          1..535
                 mol_type = protein
                 note = Norovirus
                 organism = unidentified

SEQUENCE: 90
MKMASNDAAP SNDGAAGLVP EVNNETMALE PVAGASIAAP LTGQNNVIDP WIRLNFVQAP 60
NGEFTVSPRN SPGEVLLNLE LGPELNPYLL HLSRMYNGYA GGVEVQVLLA GNAFTAGKLV 120
FAAVPPHFPL ENISPGQITM FPHVIDVRT LEPVLLPLPD VRNFFHYNQ QNEPRMRLVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPSPDF DFNLYVPPTV ESKTKPFTLP ILTIGELTNS 240
RFPVPIDELY TSPNESLVVQ PQNGRCALDG ELQGTQQLP TAICSFGRRI NQKVSGENHV 300
WNMQVTNIDG TPPDPTDVP APLGTPDFSG KLFGLVLSQRD HDNACRSHDA VIATNSAKFT 360
PKLGAIQIGT WEQDDVHINQ PTKFTPVGLF ESEGFNQWTL PNYSGALTLN MGLAPPVAPT 420
FPGEQILFFR SHIPLKGGVA DPVIDCLLPQ EWIQHLYQES APSQTDVALI RFTNPDTGRV 480
LFEAKLHRSG YITVANTGSR PIVVPANGYF RFDSWVNQFY SLAPMGTGNG RRRVQ 535

SEQ ID NO: 91      moltype = DNA length = 1608
FEATURE            Location/Qualifiers
misc_feature        1..1608
                    note = Nucleic acid sequence of human codon optimized
                    VPI_GII.12_HS10_A90L

source              1..1608
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 91
atgaagatgg cgtctaata tgcgtctcct tccaatgatg gcgcagccgg cctggtcctc 60
gaagtgaata acgagactat ggctctcgaa cccgtggcgg gagcctcaat tgcgcgcccc 120
ctcactggcc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180
aatggggagt tcaccgtgtc cccagagaaac tccccggcg aagtgttatt gaatttgga 240
ttaggaccag aactcaaccc ctatctgctc catctgtctc ggatgtacaa cggctatgcg 300
ggcggagatg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360
tttgacagcg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420
ttccctcacg tgataatcga cgtgcggaca ttagagcccg tgctgctacc cctgccccgac 480
gtgaggaaca atttctttca ctacaatcag caaatgaac caagaatgcg cctggtcgcc 540
atgctctata ctcttttaag aagtaatggc agtggggatg acgtgtttac tgttagctgt 600
cgggtgtctc cccgaccttc cccagatttc gacttcaatt atctggctcc ccccaaggta 660
gagtcacaaa caaagccttt cactcttcca atccttaca ttggcgaact gaccaactca 720
cgctttccag tgcctattga tgagctgtac acaagtccaa atgaatccct tgcgttcag 780
ccacagaatg ggcgctgcgc gcttgacggt gagctccagg gcacaacaca actgttgcca 840
accgctatat gctcttccag gggcgctatt aatcagaagg tctccgggga gaaccacgtg 900
tggaacatgc aatgacgaa gatcgacggg acacctttcg atccaacaga ggatgtccca 960
gcgcctctag gtacccctga cttctcaggc aagtgtgtcg gcgtccttc ccagcgcgac 1020
catgataatg cttgccggag ccacgatgcc gtcattgcca ccaactcagc caaatccacc 1080
ccaaaacttg cagccttata gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140
ccaacaaagt ttaccctgtg tggccttttc gaaagcgaag gctttaacca gtggacactt 1200
cccaattaca gcggggctct cactcttaat atgggactcg caccaccgt cgctcccaacg 1260
tttctgtgtg agcagatttt gtttttcggc agtcatattc cactgaaggg tggagttgct 1320
gatcccggtg tagactgcct cttccctcag gaatggattc agcacttgta tcaggagtcc 1380
gctccctcgc agaccgatgt ggcctcgata cgcttcacaa accccgatac cggaagagt 1440
ttgtttgaag ctaaaacttc tgcgtccggt tacatcacag tagccaacac ggtttccagg 1500
ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560
agcctggctc caatgggaac aggaaatggg aggaggcggtg tgcagtaa 1608

SEQ ID NO: 92      moltype = AA length = 535
FEATURE            Location/Qualifiers
source              1..535
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

SEQUENCE: 92
MKMASNDAAP SNDGAAGLVP EVNNETMALE PVAGASIAAP LTGQNNVIDP WIRLNFVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLL HLSRMYNGYA GGVEVQVLLA GNAFTAGKLV 120
FAAVPPHFPL ENISPGQITM FPHVIDVRT LEPVLLPLPD VRNFFHYNQ QNEPRMRLVA 180
MLYTPLRNSG SGDDVFTVSC RVLTRPSPDF DFNLYVPPTV ESKTKPFTLP ILTIGELTNS 240
RFPVPIDELY TSPNESLVVQ PQNGRCALDG ELQGTQQLP TAICSFGRRI NQKVSGENHV 300
WNMQVTNIDG TPPDPTDVP APLGTPDFSG KLFGLVLSQRD HDNACRSHDA VIATNSAKFT 360
PKLGAIQIGT WEQDDVHINQ PTKFTPVGLF ESEGFNQWTL PNYSGALTLN MGLAPPVAPT 420
FPGEQILFFR SHIPLKGGVA DPVIDCLLPQ EWIQHLYQES APSQTDVALI RFTNPDTGRV 480
LFEAKLHRSG YITVANTGSR PIVVPANGYF RFDSWVNQFY SLAPMGTGNG RRRVQ 535

SEQ ID NO: 93      moltype = DNA length = 1608
FEATURE            Location/Qualifiers
misc_feature        1..1608
                    note = Nucleic acid sequence of human codon optimized
                    VPI_GII.12_HS10_E80S plus sign A90L

source              1..1608
                    mol_type = other DNA

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organism = synthetic construct

SEQUENCE: 93
atgaagatgg cgtctaata tgcgtgctct tccaatgatg ggcgagccgg cctgggtccct 60
gaagtgaata acgagactat ggctctcgaa cccgtggccg gagcctcaat tgccgcccc 120
ctcactggcc agaacaacgt gattgatccc tggatcagac tgaacttcgt tcaggctcct 180
aatggggagt tcaccgtgtc ccgcagaaac tccccggcg aagtgttatt gaatttgagc 240
ttaggaccag aactcaaccc ctatctgtct catctgtctc ggatgtacaa cggtatgagc 300
ggcgagatgg aggtgcaagt tcttctcgct ggtaatgcat tcacagcagg aaaattagta 360
tttgagcagg ttccacccca ttttccactt gaaaacataa gcccaggcca gatcaccatg 420
ttccctcacg tgataatcga ctgctgggac ttagagcccg tgcgtgtacc cctgcccagc 480
gtgagggaaca atttctttca ctacaatcag caaaatgaac caagaatgag cctgggtcgcc 540
atgctctata ctcttttaag aagtaatggc agtggggatg acgtgtttac tgttagctgt 600
cgggtgtctc cccgaccttc cccagatttc gacttcaatt atctgggtccc ccccacggta 660
gagtcacaaa caaagccttt cactcttcca atccttcaaa ttggcggaat gaccaactca 720
cgctttccag tgcctattga tgagctgtac acaagtccaa atgaatccct tgcgtgtcag 780
ccacagaatg ggcgtgctgc gcttgacggg gagctccagg gcacaacaca actgttgcca 840
accgctatat gctctttcag gggcggtatt aatcagaagg tctccgggga gaaccacgtg 900
tggaacatgc aagtgcagaa tatcgacggg acacctttcg atccaacaga ggatgtccca 960
gcgcctctag gtaccctgga ctctcaggc aagttgttcg gcgtcctttc ccagcgcgac 1020
catgataatg tctcccgagg ccacgatgac gtcattgcca ccaactcagc caaattcacc 1080
ccaaaacttg gagcgataca gatcggaact tgggaacaag acgacgtcca tatcaaccaa 1140
ccaaacaaag ttaccctgtt tggccttttc gaaagcgaag gctttaacca gtggacactt 1200
cccaattaca ggggggctct cactcttaat atgggactcg caccacccgt cgctccaaag 1260
tttcttggtg agcagatttt gtttttcgcg agtcatattc cactgaaggg tggagttgct 1320
gatcccgtag tagactgect cctccctcag gaatggattc agcacttgta tcaggagtcc 1380
gctccctcgc agaccgatgt ggcctcgata cgcttcacaa accccgatac cggaagagtg 1440
ttgtttgaag ctaaacttca tcgctccggt tacatcacag tagccaacac gggttccagg 1500
ccaatcgtag ttccggcaaa cggatacttt cgattcgaca gttgggtcaa tcagttctac 1560
agcctggctc caatgggaac aggaaatggg agggagcggtg tgcagtaa 1608

SEQ ID NO: 94      moltype = AA  length = 215
FEATURE            Location/Qualifiers
source              1..215
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

SEQUENCE: 94
MAQAIFGAIA ATAAGSAVGA GIQAGTEAAL QHQRQQDLT LQSNTPFKHDK EMLGLQVGAS 60
TALLQNSLNT RYNMLTDAGL SSSDAARMVY GAPATRVVDW NGTRISAPRS TATTLRSGGF 120
MTIPTLYKKG QQQKAPTEIG LSNPNYGVSS SSRVADWVSS QNSSHSLSLP YHPSALQTTW 180
VTPPGSSSTS TISSVSTVPR YFNTDRLPLF ANMRK 215

SEQ ID NO: 95      moltype = DNA  length = 648
FEATURE            Location/Qualifiers
misc_feature        1..648
                    note = Nucleic acid sequence of human codon optimized
                    VP2_GI.3_L1108
source              1..648
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 95
atggctcagg caatcttcgg cgcaatcgct gccactgctg ccggatccgc tgtgggagcc 60
ggcatacagg ccggaactga ggcggccctt cagcatcagc ggttcacaga ggatctgaca 120
ttacagagta acacattcaa acatgacaag gagatgctgg gtctgcagggt ggggtgccagt 180
actgccctgc tccaaaactc tctgaatacc agatataaca tgttaactga tgcgggactg 240
tctagtagcg acgcagctcg catggctgtg ggcgccccag ctacgagagt tgtggactgg 300
aatggcaccg gaatcagtgcc accaagggtc acagccacta ccctcagaag tggcggtctt 360
atgaccatcc cgactttata caagggcaaa caacagcaga aggcacctac tgaatcgggt 420
ctctccaatc ccaactacgg cagcagtggt tcttctcgcg tggccgattg ggtctcaagc 480
cagaactcca gtcatagttc tcttgggcct tatcatccat cagccttgca gacaacttgg 540
gtcaccaccac ccgggtccag tagcacgtca accatcagtt ccgtctccac agtccctcgc 600
tattttaata ctgataggct tcccctgttc gcaaacatga ggaagtga 648

SEQ ID NO: 96      moltype = AA  length = 259
FEATURE            Location/Qualifiers
source              1..259
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

SEQUENCE: 96
MASAFLAGLA GDVITNGVGS LINAGANAVN QKVEYDFNKQ LQMASFKHDK EMLQSQVLAT 60
KQLQQEMMNI RQGVLTAGGF SPADAARGAV NAPMTKILDW NGTRYWAPNS MKTTSYSGQF 120
SSSPVHKSPA PSQHTALPKS RLQNDFAVSY SFPSSVSSQS THSTALSAGT GSSRSISPST 180
ATPTLSRTSD WVRQNERLS PFMDGALQTA FVTPPSSKAS SNGTVSTVPK AVLDSTWTPMF 240
NTHRQPLFAH PRRRGESQV 259

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SEQ ID NO: 97 moltype = DNA length = 780
 FEATURE Location/Qualifiers
 misc_feature 1..780
 note = Nucleic acid sequence of human codon optimized
 VP2_GII6_HS10
 source 1..780
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 97

atggcctcgc	catttctagc	tggattggcc	ggggacgtga	tcaccaacgg	cgtaggatcg	60
ctgattaatg	caggcgccaa	tgctgttaat	cagaagggtg	aatacgactt	caacaaacaa	120
ctgcagatgg	cttcattcaa	gcacgacaaa	gaaatgttgc	agtcacaggt	tctcgccacc	180
aagcagctac	aacaggagat	gatgaacatt	cggcaggggc	tactgaccgc	tggaggattc	240
agccctgctg	acgcagcacg	ggggggccgtg	aacgcgcgca	tgaccaagat	cctggattgg	300
aacggaaactc	ggtattgggc	tcccaactct	atgaaaacca	cttcttactc	tggtcagttc	360
tccagctcgc	cagtcacaaa	aagtccggcc	ccttcacagc	acacagcact	ccctaagtcc	420
aggctgcaaa	acgactttgc	ctccgtgtac	tccttcccat	ccagcgtgtc	atctcagagc	480
actcattcaa	ccgccctgtc	cgccggaaat	gggtctagcc	cgagcatttc	cccaagcaca	540
gctactccaa	ctctgagcag	gactagcgat	tgggtcagag	gacaaaacga	acgactgtcc	600
cctttcatgg	acggagctct	gcaaacccgc	tctgtcactc	cacctagcag	caaggcctcg	660
agcaacggta	cggtttagtac	cgtgcccagg	gctgttcttg	acagctggac	ccccatgttt	720
aacacacaca	ggcagccatt	gtttgcacac	cccaggcgac	ggggagaatc	acaagtttag	780

SEQ ID NO: 98 moltype = AA length = 543
 FEATURE Location/Qualifiers
 source 1..543
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 98

MMASKDAPT	NMDGTSGAGQ	LVPEVSTAEP	ISMPEVAGAA	TAAATAGQVN	MIDPWIMSNY	60
VQAPQGEFTI	SPNNTPGDIL	FDSLGLPHLN	PFLSHLAQMY	NGWVGNMKVR	VLLAGNAFTA	120
GKIIISCVPP	GFAAQNVISIA	QATMFPFHIA	DVRVLEPIEV	PLEDVNRNLF	HNNDSTPTMR	180
LICMLYTPLR	ASGSSSGTDP	FVIAGRVLTC	PSPDFNFLFL	VPPNVEQTK	PFSVPNLPLN	240
VLSNSRVPSL	IKSMMVSQDH	GQMVQFQNGR	VTLDGQLQGT	TPTSASQLCK	IRGTVYHATG	300
GQGLNLTEID	GTPYHAFESP	APIGFDDLGE	CDWHINASPA	NAFTDGSIIH	RIDVAQDSTF	360
APHLGTIHYT	NADYNANVGL	ICSLEWLSPP	SGGAPKVNFW	AIPRYGSTLT	EAAQLAPPIY	420
PPGFGEAIVF	FMSDFPIANG	SDGLSVPCTI	PQEFVTHFVN	EQAPTRGEAA	LLHYVDPDTH	480
RNLGEFKLYP	EGFMTCVPNS	SGSGPQTLPI	NGVFTFISWV	SRFYQLKPVG	TTGPVRRLLGI	540
RRS						543

SEQ ID NO: 99 moltype = AA length = 212
 FEATURE Location/Qualifiers
 source 1..212
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 99

MAQAIIGAIA	ASTAGSALGA	GIQVGGEAAL	QSQRVQNNLQ	LQENSFKHDR	EMIGYQVEAS	60
NQLLAKNLAT	RYSLLRAGGL	TSADAARSA	GAPVTRIVDW	NGVRVSAPES	SATTLRSGGF	120
MSVPIPFASK	KQVQSSGIS	NPNYSPSSIS	RTTSWVESQN	SSRFGNLSPY	HAEALNTVWL	180
TPPGSTASST	LSSVPRGYFN	TDRLPLFANN	RR			212

SEQ ID NO: 100 moltype = DNA length = 639
 FEATURE Location/Qualifiers
 misc_feature 1..639
 note = Nucleic acid sequence of human codon optimized
 VP.2_GII_Norwalk
 source 1..639
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 100

atggctcagg	ccattattgg	cgccatcgct	gcaagtacag	ccgggagatgc	attggggggcc	60
ggaatacagg	tggggcggga	agctgcattg	cagagccagc	ggtaccagca	aaacctgcag	120
ttacaggaga	atagctttaa	acacgacagg	gagatgattg	gatatacagg	ggaggccagc	180
aatcagctgc	tgcacaaaaa	cttggtactc	cgatactcat	tactgcgcgc	cgggggggtg	240
actagcgcgc	acgcgcgacg	atctgtcgca	ggcgccccgc	tgactcggat	cgtagactgg	300
aacgggggtac	gagtcctggc	tcccagatcg	tctgcaacca	ccctgagggtc	gggagggttt	360
atgtccgtgc	ccatcccatt	cgctagcaaa	cagaaacagg	tccagagctc	cggaatctcc	420
aatcccaatt	actcccctag	ctctatctct	cgtaccactt	cctgggtcga	gagtcagaac	480
agcagtagat	tctggcaact	gagccctcac	catgctgaag	ccctgaacac	tgtgtggttg	540
actccacctg	gtagcacggc	ctectcaacc	ctgagttccg	tgcctcgccg	gtacttcaat	600
accgacagac	ttcctctggt	cgctaacaac	cgccgctga			639

SEQ ID NO: 101 moltype = AA length = 538
 FEATURE Location/Qualifiers

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source          1..538
                mol_type = protein
                note = Norovirus
                organism = unidentified

SEQUENCE: 101
MMMASKDAPS NMDGTSGAGQ LVPEVNAAEP LPLEPVVGAA TAVATAGQVN MIDPWIMNNF 60
VQAPGEFTI SPNNTPGDIL FDLRLGPHLN PFLHLSQLMY NGWVGNNMRVR VMLAGNAFSA 120
GKIIICCVPP GFESQNISIG QATMFPHVIA DVRVLEPIEV PLDDVRNVLF HTNENRPTMR 180
LLCMLYTPLR AGGASSGTD FVIAGRVLTC PAPDFNLFLL VPPSVEQKTR QLTIPNIPLN 240
NLANSRVPAM INKMTVSADQ NQVVQFQNGR CTLEGQLLGT TPVSANQVAR IRGKVSTNS 300
GTGLNLTEVD GTPYHAFESP APLGFDPDIGN CDWHVYAFKV NQNTGDPMYR LDITQGNFSA 360
PHLGSIEFSS ENHPSGDQLG TLTWISPLNN ASRVDPWKIP TYGSTLTEST NLAPPIFPPG 420
FGEAIVYFMS DFPIVSGNTA QIPCTLPQEF VSSFVEQQAP IRGEAALLHY VDPDTHRNLG 480
EPKLYPDGFI TCVPNTGGGP QNLPSNGVFV FSSWVSRYQ LKPVGTTGPV RRLGVRRV 538

SEQ ID NO: 102      moltype = DNA length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49
                    note = Primer IF-NoV(US68) VP1(ORF1) (hCod) .c
source              1..49
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 102
tcgtgcttcg gcaccagtag aatgatgatg gctagtaaag atgcgacct 49

SEQ ID NO: 103      moltype = DNA length = 52
FEATURE            Location/Qualifiers
misc_feature        1..52
                    note = Primer IF-NoV(US68) VP1(ORF1) (hCod) .r
source              1..52
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 103
actaaagaaa ataggccttt atctccgcag accgaggcgt ccgcgggcag aa 52

SEQ ID NO: 104      moltype = DNA length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49
                    note = Primer IF-GI3Lil108VP1.c
source              1..49
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 104
tcgtgcttcg gcaccagtag aatgatgatg gcttccaagg atgctccca 49

SEQ ID NO: 105      moltype = DNA length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49
                    note = Primer IF-GI3Lil108VP1.r
source              1..49
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 105
actaaagaaa ataggcctct agctccgtct gatcccgagc ctccgaact 49

SEQ ID NO: 106      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer VP1_GI.3Lil108(S94L) .r
source              1..59
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 106
ctgagccaag tggagcagaa acggattcaa gtgtggctct agctgcaggt caaacaaga 59

SEQ ID NO: 107      moltype = DNA length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer VP1_GI.3Lil108(S94L) .c
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 107
aggaccacac ttgaatccgt ttctgctcca cttggctcag atgtataatg gatggg 56

SEQ ID NO: 108      moltype = DNA length = 57

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FEATURE	Location/Qualifiers	
misc_feature	1..57	
	note = Primer VP1_GI.3Lil108(Q84S).r	
source	1..57	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 108		
gtgtggtcct aggtcaggt caaacaagat gtcacccggg gtgtgtttg ggettat		57
SEQ ID NO: 109	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer VP1_GI.3Lil108(Q84S).c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 109		
ggtgacatct tgtttgacct gagcctagga ccacactga atccgttt		48
SEQ ID NO: 110	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer IF-GI3Lil108VP2.c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 110		
tcgtgcttcg gcaccagtac aatggctcag gcaatcttcg gcgcaatc		48
SEQ ID NO: 111	moltype = DNA length = 49	
FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer IF-GI3Lil108VP2.r	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 111		
actaaagaaa ataggccttc acttcctcat gtttgcgaaac aggggaagc		49
SEQ ID NO: 112	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer IF-(160)GI.5_Sik113_VP1.c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 112		
tcgtgcttcg gcaccagtac aatgatgatg gcctccaaag acgctcct		48
SEQ ID NO: 113	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer IF-GI.5_Sik113_VP1.r	
source	1..53	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 113		
actaaagaaa ataggccttc agcgccgcac gccaaaggcgc ccccgggcag atg		53
SEQ ID NO: 114	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer GI.5(hCod) (Q84S).r	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 114		
gatgagggcc taagctcagg tcgaacagaa tatccctcgg tgtgttgta g		51
SEQ ID NO: 115	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer GI.5(hCod) (Q84S).c	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 115
tattctgttc gacctgagct taggcctca tctcaacccc ttcttgccc a 51

SEQ ID NO: 116 moltype = DNA length = 50
FEATURE Location/Qualifiers
misc_feature 1..50
 note = Primer GI.5(hCod) (A94L) .r
source 1..50
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 116
atctggctca ggtggagcaa gaaggggttg agatgagggc ctaactgcag 50

SEQ ID NO: 117 moltype = DNA length = 51
FEATURE Location/Qualifiers
misc_feature 1..51
 note = Primer GI.5(hCod) (A94L) .c
source 1..51
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 117
tctcaacccc ttcttgctcc acctgagcca gatgtacaat ggctgggtgg g 51

SEQ ID NO: 118 moltype = DNA length = 54
FEATURE Location/Qualifiers
misc_feature 1..54
 note = Primer IF-(160)GII.2_CGMH11_VP1.c
source 1..54
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 118
tcgtgcttcg gcaccagtac aatgaagatg gcacccaacg acgccgcacc cagc 54

SEQ ID NO: 119 moltype = DNA length = 53
FEATURE Location/Qualifiers
misc_feature 1..53
 note = Primer IF-GII.2_CGMH11_VP1.r
source 1..53
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 119
actaaagaaa ataggccttt actggatccg tcggcgaccg ttccctgtgc cca 53

SEQ ID NO: 120 moltype = DNA length = 59
FEATURE Location/Qualifiers
misc_feature 1..59
 note = Primer VP1_GII.2CGMH11(E80S) .r
source 1..59
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 120
ttctgggtccc aggctgagat tgaggagcac ttccccaggg ctatttctag ggctgaccg 59

SEQ ID NO: 121 moltype = DNA length = 48
FEATURE Location/Qualifiers
misc_feature 1..48
 note = Primer VP1_GII.2CGMH11(E80S) .c
source 1..48
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 121
ggaagtgtc ctcaatctca gctctgggacc agaacttaac ccgtacct 48

SEQ ID NO: 122 moltype = DNA length = 59
FEATURE Location/Qualifiers
misc_feature 1..59
 note = Primer VP1_GII.2CGMH11(A90L) .r
source 1..59
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 122
tccgggccag gtggagcagg tacggattaa gttctggtcc cagctcgaga ttgaggagc 59

SEQ ID NO: 123 moltype = DNA length = 59
FEATURE Location/Qualifiers
misc_feature 1..59

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source          note = Primer VP1_GII.2CGMH11(A90L).c
                1..59
                mol_type = other DNA
                organism = synthetic construct

SEQUENCE: 123
gggaccagaa cttaatccgt acctgctcca cctggcccgg atgtacaatg gatatgcag   59

SEQ ID NO: 124      moltype = DNA length = 52
FEATURE            Location/Qualifiers
misc_feature        1..52
                    note = Primer IF-(160)GII.3_Jing13_VP1.c
source              1..52
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 124
tcgtgcttcg gcaccagtac aatgaaaatg gcttccaacg atgcagcacc ct         52

SEQ ID NO: 125      moltype = DNA length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer IF-GII.3_Jing13_VP1.r
source              1..50
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 125
actaaagaaa ataggccttt actggatccg ccgtctgccca ttgcctgtac          50

SEQ ID NO: 126      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer VP1_GII.3Jing13(E80S).r
source              1..59
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 126
attcagggc ccaggctcaa attcaagaga acctccccgg gggagtcttcg aggagagac   59

SEQ ID NO: 127      moltype = DNA length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer VP1_GII.3Jing13(E80S).c
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 127
ggaggttctc ttgaatttga gcctggggccc tgaaattaat cttatct          48

SEQ ID NO: 128      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer VP1_GII.3Jing13(A90L).r
source              1..59
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 128
attcgggcta gatggagcag ataaggatta atttcagggc ccagttccaa attcaagag   59

SEQ ID NO: 129      moltype = DNA length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer VP1_GII.3Jing13(A90L).c
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 129
gggcctgaa attaatcctt atctgctcca tctagcccg atgtacaacg gctacg      56

SEQ ID NO: 130      moltype = DNA length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49
                    note = Primer IF-GII.4Syd12VP1.c
source              1..49
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 130
tcgtgcttcg gcaccagtac aatgaaaatg gcctcgagt acgctaacc            49

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SEQ ID NO: 131      moltype = DNA  length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer IF-GII.4Syd12VP1.r
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 131
actaaagaaa ataggccttc agacagccct gcgtctgccca gtcccatt      48

SEQ ID NO: 132      moltype = DNA  length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                    note = Primer VP1_GII.4Syd12 (A39V).r
source              1..54
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 132
gaccggccac ggggactgct atggtgctgcgc ccaccacagg ctccagggcc atca      54

SEQ ID NO: 133      moltype = DNA  length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                    note = Primer VP1_GII.4Syd12 (A39V).c
source              1..54
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 133
ggcgcgacgcc atagcagtc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 134      moltype = DNA  length = 51
FEATURE            Location/Qualifiers
misc_feature        1..51
                    note = Primer VP1_GII.4Syd12 (V47P).r
source              1..51
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 134
cgtatccacg ggtcaatggg attctgctga ccggccacgg gcgctgctat g      51

SEQ ID NO: 135      moltype = DNA  length = 53
FEATURE            Location/Qualifiers
misc_feature        1..53
                    note = Primer VP1_GII.4Syd12 (V47P).c
source              1..53
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 135
ggccggctcag cagaatccca ttgaccctg gatacgcaac aattttgtcc aag      53

SEQ ID NO: 136      moltype = DNA  length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer VP1_GII.4Syd12 (R53I).r
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 136
tggacaaaat tgttgattat ccacgggtca atcacattct gctgaccg      48

SEQ ID NO: 137      moltype = DNA  length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer VP1_GII.4Syd12 (R53I).c
source              1..50
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 137
gattgaccgg tggataatca acaattttgt ccaagcccct ggtggggagt      50

SEQ ID NO: 138      moltype = DNA  length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer GII.4 (P80S).r
source              1..50

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mol_type = other DNA
organism = synthetic construct
SEQUENCE: 138
gatcgggtcc caagctggcc gaccacagga tttctcctgg cgcatttctc 50

SEQ ID NO: 139      moltype = DNA length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer GII.4(P80S).c
source              1..50
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 139
aatcctgtgg tcggccagct tgggacccga tctgaacccc tatttgtaac 50

SEQ ID NO: 140      moltype = DNA length = 56
FEATURE            Location/Qualifiers
misc_feature        1..56
                    note = Primer GII.4(S90L).r
source              1..56
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 140
atccgagcga gatgcagcaa ataggggttc agatcgggtc ccaatggggc cgacca 56

SEQ ID NO: 141      moltype = DNA length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer GII.4(S90L).c
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 141
tctgaacccc tatttgctgc atctcgtcgc gatgtacaac gggtatgc 48

SEQ ID NO: 142      moltype = DNA length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer VP1_GII.4Syd12(Del(35-42)).r
source              1..50
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 142
cacattctgc tgaccgcccc ccacaggtc caggggccatc acctcattat 50

SEQ ID NO: 143      moltype = DNA length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer VP1_GII.4Syd12(Del(35-42)).c
source              1..48
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 143
ggagcctgtg gtgggcggtc agcagaatgt gattgacccg tggatacg 48

SEQ ID NO: 144      moltype = DNA length = 60
FEATURE            Location/Qualifiers
misc_feature        1..60
                    note = Primer VP1_GII.4Syd12(SSTAVATA).r
source              1..60
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 144
ctgaccggct gtagcgacgg cggtaggagct gccaccaca ggctccaggg ccatcacctc 60

SEQ ID NO: 145      moltype = DNA length = 60
FEATURE            Location/Qualifiers
misc_feature        1..60
                    note = Primer VP1_GII.4Syd12(SSTAVATA).c
source              1..60
                    mol_type = other DNA
                    organism = synthetic construct
SEQUENCE: 145
tgtgtggggc agctccaccg ccgtcgctac agccggtcag cagaatgtga ttgacccgtg 60

SEQ ID NO: 146      moltype = DNA length = 49

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FEATURE	Location/Qualifiers	
misc_feature	1..49	
	note = Primer IF-GII.60hi12VP1.c	
source	1..49	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 146		
tcgtgcttcg gcaccagtac aatgaagatg gcaagcaacg acgcagctc		49
SEQ ID NO: 147	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer IF-GII.60hi12VP1.r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 147		
actaaagaaa ataggccttc actgatcccg gcgtcgcccc tggcctgtcc ccat		54
SEQ ID NO: 148	moltype = DNA length = 51	
FEATURE	Location/Qualifiers	
misc_feature	1..51	
	note = Primer IF-GII.6HS10VP2.c	
source	1..51	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 148		
tcgtgcttcg gcaccagtac aatggcctcc gcatttctag ctggattggc c		51
SEQ ID NO: 149	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
misc_feature	1..53	
	note = Primer IF-GII.6HS10VP2.r	
source	1..53	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 149		
actaaagaaa ataggcctct aaacttgatg ttctccccgt cgctgggggt gtg		53
SEQ ID NO: 150	moltype = DNA length = 59	
FEATURE	Location/Qualifiers	
misc_feature	1..59	
	note = Primer VP1_GII.60hi12(E80S).r	
source	1..59	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 150		
agttcagggc cgaggctcag attgagcagc atctcgcccc gggagttccg gggggagac		59
SEQ ID NO: 151	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer VP1_GII.60hi12(E80S).c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 151		
cgagatgctg ctcaatctga gcctcggccc tgaactaac ctttatct		48
SEQ ID NO: 152	moltype = DNA length = 59	
FEATURE	Location/Qualifiers	
misc_feature	1..59	
	note = Primer VP1_GII.60hi12(S90L).c	
source	1..59	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 152		
ccctgaacta aacccttatc tgctccacct ttcacggatg tacaatggct acgcaggag		59
SEQ ID NO: 153	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer IF-(160)GII.12_HS10_VP1.c	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	

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SEQUENCE: 153
tcgtgcttcg gcaccagtag aatgaagatg gcgtctaattg atgctgctcc tt 52

SEQ ID NO: 154 moltype = DNA length = 54
FEATURE Location/Qualifiers
misc_feature 1..54
 note = Primer IF-GII.12_HS10_VP1.r
source 1..54
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 154
actaaagaaa ataggccttt actgcacacg cctcctccca ttctctgttc ccat 54

SEQ ID NO: 155 moltype = DNA length = 48
FEATURE Location/Qualifiers
misc_feature 1..48
 note = Primer GII.12(E80S).r
source 1..48
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 155
agttctggtc ctaagctcaa attcaataac acttcgcccgg gggagttt 48

SEQ ID NO: 156 moltype = DNA length = 49
FEATURE Location/Qualifiers
misc_feature 1..49
 note = Primer GII.12(E80S).c
source 1..49
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 156
agtgttattg aatttgagct taggaccaga actcaacccc tatctggca 49

SEQ ID NO: 157 moltype = DNA length = 50
FEATURE Location/Qualifiers
misc_feature 1..50
 note = Primer GII.12(A90L).r
source 1..50
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 157
atccgagaca gatggagcag atagggggtg agttctggtc ctaattccaa 50

SEQ ID NO: 158 moltype = DNA length = 57
FEATURE Location/Qualifiers
misc_feature 1..57
 note = Primer GII.12(A90L).c
source 1..57
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 158
actcaacccc tatctgctcc atctgtctcg gatgtacaac ggctatgcgg gcggagt 57

SEQ ID NO: 159 moltype = DNA length = 47
FEATURE Location/Qualifiers
misc_feature 1..47
 note = Primer IF-NoV(US68)VP2(ORF3)(hCod).c
source 1..47
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 159
tcgtgcttcg gcaccagtag aatggctcag gccattattg gcgccat 47

SEQ ID NO: 160 moltype = DNA length = 47
FEATURE Location/Qualifiers
misc_feature 1..47
 note = Primer IF-NoV(US68)VP2(ORF3)(hCod).c
source 1..47
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 160
tcgtgcttcg gcaccagtag aatggctcag gccattattg gcgccat 47

SEQ ID NO: 161 moltype = DNA length = 50
FEATURE Location/Qualifiers
misc_feature 1..50

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source          note = Primer IF-NoV(US68) VP2 (ORF3) (hCod) .r
                1..50
                mol_type = other DNA
                organism = synthetic construct

SEQUENCE: 161
actaagaaa ataggccttc agcggcggtt gttagcgaac agaggaagtc      50

SEQ ID NO: 162      moltype = DNA length = 4540
FEATURE            Location/Qualifiers
misc_feature        1..4540
                    note = Cloning vector 1190 from left to right T-DNA
source              1..4540
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 162
tggcaggata tattgtgggtg taaacaaatt gacgcttaga caacttaata acacattgcg 60
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SEQ ID NO: 163 moltype = DNA length = 2976
 FEATURE Location/Qualifiers
 misc_feature 1..2976
 note = Construct 2724 from 2X35S promoter to NOS terminator
 source 1..2976
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 163

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SEQ ID NO: 164 moltype = DNA length = 5652

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FEATURE	Location/Qualifiers
misc_feature	1..5652
	note = Cloning vector 3677 from left to right T-DNA
source	1..5652
	mol_type = other DNA
	organism = synthetic construct

SEQUENCE: 164

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SEQ ID NO: 165 moltype = DNA length = 2952
 FEATURE Location/Qualifiers
 misc_feature 1..2952
 note = Construct 4133 from 2X35S promoter to NOS terminator
 source 1..2952
 mol_type = other DNA
 organism = synthetic construct

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atgttactag at                                     2952

SEQ ID NO: 166      moltype = DNA length = 2952
FEATURE            Location/Qualifiers
misc_feature        1..2952
                    note = Construct 4135 from 2X35S promoter to NOS terminator
source              1..2952
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 166
gtcaacatgg tggagcagca cacacttgtc tactccaaaa atatcaaaaga tacagtctca 60
gaagaccaaa gggcaattga gactttttcaa caaagggtaa tatccggaaa ctcctcgcga 120
ttccattgcc cagctatctg tcactttatt gtgaagatag tggaaaagga aggtggctcc 180
tacaattgcc atcattgcga taaaggaaag gccatcggtg aagatgcctc tgccgacagt 240
ggtcccaaaag atggaccccc acccacgagg agcatcggtg aaaaagaaga cgttccaacc 300
acgtcttcaa agcaagtggg ttgatgtgat aacatgggtg agcacgcacac acttgtctac 360
tccaaaaata tcaaaagatac agtctcagaa gaccaaaggg caattgagac ttttcaacaa 420
agggtaatat ccgaaaaacct cctcggaattc cattgcccag ctatctgtca ctttattgtg 480
aagatagtagg aaaagggaagg tggctcctac aaatgccatc attgcgataa aggaaaggcc 540
atcggtgaag atgcctctgc gcacagtggg cccaagatg gaccccacc cacgaggagc 600
atcggtgaaa aagaagacgt tccaaaccag tcttcaaaag aagtggattg atgtgatgc 660
tccactgacg taagggatga cgcacaatcc cactatcctt cgcaagaccc ttctctata 720
taagggaagt catttcattt ggagaggtat taaaatctta atagggtttg ataaaagcga 780
acgtggggaa acccgaacca aaccttcttc taaactctct ctcatctctc ttaaaagcaaa 840
cttctctctt gtctttcttg cgtgagcgat cttcaacggt gtcagatcgt gcttcggcac 900
cagtacaatg aaaaatggct cgagtgcgcg taacctagt gacggcagcg ccgccaatct 960
tgtgcctgag gttaataaat aggtgatggc cctggagcct gtgggtggcg cagccatagc 1020
agcgcctcgt gccggtcagc agaattgtat tgaccctggt atacgcaaca attttgtcca 1080
agccctcgtt ggggagtcca ccgttagccc gagaaatgcg ccaggagaaa tctgtggtc 1140
ggccagcttg ggaaccgatc tgaacccta tttgtgcat ctgcctcgga tgtacaacgg 1200
gtatgccggc ggatttgaag tgcaggatg tctggtcggg aacgcgttca ctgctggcaa 1260
agtgatcttt ccagcgggtgc ctcccactt ccccactgaa ggactgtctc caagccaggt 1320
cacaatgttt ccacacatcg ttgtggacgt acggcagcta gagcctgttc tgattccct 1380
ccctgatgta cgcataatct tctaccacta caatcaatcc aatgatccga ccattaaact 1440
catcgcgatg ttgtacaccc cctctgcgcg taacaatgct ggagacgacg tattcacctg 1500
gtcatgcaga gtgtcaccca gaccttcacc agactttgac tttatctctt tagtgcccc 1560
cactgttgag agccgaacca agccctttag tgtccccgta ctacagatcg aggagatgac 1620
aaaatagcgc tttccaatcc cccttgagaa actgttcaca ggaccttctt cggcattcgt 1680
ggttcagcca cagaacggac gctgcacaa tgacggcggt ctgctcggaa ccaccagct 1740
tagccctggt aatctctgta cgtttagagg cgacgtaact cacataactg gctcacggaa 1800
ctataccatg aatctggcat cacagaattg gaatgactac gacccaaccg aagagattcc 1860
cgcaacctctt ggaacccccc actttgtggg aaaaatacag ggctcctga cacaacccac 1920
cagaaccgat ggctccacac ggggacacaa ggcaaccgtc tacactggct ctgccgattt 1980
tgccccgaaa ctgggtagag tgcagtttga gaccgacact gaccgggact ttgaagccaa 2040
tcagaatact aagttcacac ctgtaggagt gattcaggac ggggggcacca ctacccggaa 2100
cgagccgcaa caatgggttc tgccctctta tagcgggagg aatactcata atgtgcattt 2160
ggctcctgca tgggtcccca cgtttcccgg ggaacaactg ctcttttttc gttcaacct 2220
gcctggatgc tccggatata ccaatatgga tctcgattgc ctgctccac aggaatgggt 2280
gcagtatttt tatcaagagg ccgcaccagc ccaatccgac gtccgacttc tgcggttcgt 2340
gaatccagac acaggccgcg tgtgttttga gtgcaaatg cacaatcag gatcgttac 2400
agtggctcat actggacagc atgacctggt gatccacccc aacggatatt ttaggttcga 2460
ctcctgggtg aatcagtttt atacattagc ccccatgggg aatgggactg gcagacgcag 2520
ggctgtctga aggcctattt tctttagttt gaatttactg ttattcggtg tgcatttcta 2580
tgtttggtga gcggtttttct gtgctcagag tgtgtttatt ttatgtaatt taatttcttt 2640
gtgagctcct gtttagcagg tcgtcccttc agcaaggaca caaaaagatt ttaattttat 2700
tatcgttcaa acattttggca ataaagtttc ttaagattga atcctgttgc cggctcttgcg 2760
atgattatca tataatttct gttgaattac gttaagcatg taataattaa catgtaatgc 2820
atgacgttat ttatgagatg ggtttttatg attagagtcc cgcaattata catttaatac 2880
gcgatagaaa acaaaatata gcgcgcgcaac taggataaat tatcgcgcgcg ggtgtcatct 2940
atgttactag at                                     2952

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SEQ ID NO: 167      moltype = DNA length = 1632
FEATURE            Location/Qualifiers
misc_feature        1..1632
                    note = Nucleic acid sequence of human codon optimized
                    VP1_GI.3_Lil08_Q84S
source              1..1632
                    mol_type = other DNA

```

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organism = synthetic construct

SEQUENCE: 167
atgatgatgg cttccaagga tgctcccaca aacatggatg gaacaagcgg cgcggggcaa 60
cttggtgcgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cgcgcgagcc 120
actgctgcgg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180
gttcaggctc cacaggggga gtttaccata agcccaaaaca acaccccggg tgacatcttg 240
tttgacctga gcctaggacc acacttgaat ccgtttctga gtcacttggc tcagatgtat 300
aatggatggg ttggaatacat gaaggtgctc gtgctcctgg cgggcaatgc attcacagcc 360
gggaagatta ttatctcttg cgtgccacct ggatttgcag ccagaaacgt gtctatcgca 420
caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgagggtg 480
ccccttgagg acgtgcgcaa cgtcctatcc cataacaatg atagcaccac caccatgcgc 540
ttgatattga tgttatatac tcccctccgc gccagtggtt ccagctccgg gaccgatcct 600
tttggtattg ctgggcgggt gttgacttgt cctagccctg acttcaactt cctttttctg 660
gtgctcccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720
gtgctgtcga attcccaggt gccctccctt attaagtcca tgatggtatc tcaggatcac 780
ggtaaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840
acccaaccca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900
ggacaggggc tgaatcttac tgagatcgat ggtacccctt accatgcatt cgagtcacct 960
gcacctattg gatttccgca tcttggggag tgtgattggc atatcaatgc ttacactgcc 1020
aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080
gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140
atctgtagcc tagagtggct atctccgcca agcgggtggg cccctaaagt taacctatgg 1200
gctattcctc ggtacgggtc tacgctgact gaggcgcgtc agctggcacc ccccatatat 1260
ccaccaggat tcgggggaagc catgtgtttc tttatgtccg attttccgat agccaacggt 1320
tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380
gagcaggctc ctactcgggg cgaggctgcc ttgttgcaat acgtagaccc cgatacccat 1440
agaaaacctg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaaactc 1500
tccggcagtg gccctcaaac cttgccgcat aacggcgtgt tcacgtttat cagctgggtt 1560
tcacgggtttt aacactcaaa gccctcgga acaactgggc cagttcggag gctcggggtc 1620
agacggagct ag                                     1632

SEQ ID NO: 168      moltype = AA  length = 8
FEATURE             Location/Qualifiers
REGION              1..8
                    note = Mutation of SEQ ID NO:1 at positions 39-46
source              1..8
                    mol_type = protein
                    organism = synthetic construct

SEQUENCE: 168
SSTAVATA                                     8

SEQ ID NO: 169      moltype = DNA  length = 1632
FEATURE             Location/Qualifiers
misc_feature         1..1632
                    note = Nucleic acid sequence of human codon optimized
                    VPI_GI.3_Lil08_A43V plus sign
source              1..1632
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 169
atgatgatgg cttccaagga tgctcccaca aacatggatg gaacaagcgg cgcggggcaa 60
cttggtgcgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cgcgcgagcc 120
actgctgcgg ccaccgcagg acaggtaaac atgatcgacc cctggatcat gtcaaattac 180
gttcaggctc cacaggggga gtttaccata agcccaaaaca acaccccggg tgacatcttg 240
tttgacctga agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300
aatggatggg ttggaatacat gaaggtgctc gtgctcctgg cgggcaatgc attcacagcc 360
gggaagatta ttatctcttg cgtgccacct ggatttgcag ccagaaacgt gtctatcgca 420
caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgagggtg 480
ccccttgagg acgtgcgcaa cgtcctatcc cataacaatg atagcaccac caccatgcgc 540
ttgatattga tgttatatac tcccctccgc gccagtggtt ccagctccgg gaccgatcct 600
tttggtattg ctgggcgggt gttgacttgt cctagccctg acttcaactt cctttttctg 660
gtgctcccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gccccttaac 720
gtgctgtcga attcccaggt gccctccctt attaagtcca tgatggtatc tcaggatcac 780
ggtaaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840
acccaaccca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900
ggacaggggc tgaatcttac tgagatcgat ggtacccctt accatgcatt cgagtcacct 960
gcacctattg gatttccgca tcttggggag tgtgattggc atatcaatgc ttacactgcc 1020
aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080
gccccgcacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140
atctgtagcc tagagtggct atctccgcca agcgggtggg cccctaaagt taacctatgg 1200
gctattcctc ggtacgggtc tacgctgact gaggcgcgtc agctggcacc ccccatatat 1260
ccaccaggat tcgggggaagc catgtgtttc tttatgtccg attttccgat agccaacggt 1320
tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380
gagcaggctc ctactcgggg cgaggctgcc ttgttgcaat acgtagaccc cgatacccat 1440
agaaaacctg gcgaattcaa actctaccct gaaggtttca tgacctgcgt acctaaactc 1500
tccggcagtg gccctcaaac cttgccgcat aacggcgtgt tcacgtttat cagctgggtt 1560

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tcacgggttt accaactcaa gcccgctcgga acaactgggc cagttcggag gctcgggatc 1620
agacggagct ag 1632

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SEQ ID NO: 170      moltype = AA length = 543
FEATURE            Location/Qualifiers
source              1..543
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

```

```

SEQUENCE: 170
MMASKDAPT NMDGTSGAGQ LVPEVSTAEP ISMEPVAGAA TAVATAGQVN MIDPWIMSNY 60
VQAPQGEFTI SPNNTPGDIL FDLQLGPHLN PFLHLHAQMY NGWVGNMKVR VLLAGNAFTA 120
GKIIISCVPV GFAAQNVISIA QATMFPHVIA DVRVLEPIEV PLEDVRNVLF HNNDSTPTMR 180
LICMLYTPLR ASGSSSGTDP FVIAGRVLTC PSPDFNLFLL VPPNVEQKTK PFSVPNLPLN 240
VLSNSRVPSL IKSMVVSQDH GQMVQFQNGR VTLDGQLQGT TPTSASQLCK IRGTVYHATG 300
GQGLNLTEID GTPYHAFESP APIGFPDLGE CDWHINASPA NAFTDGSIIH RIDVAQDSTF 360
APHLGTIHYT NADYNANVGL ICSLEWLSPP SGGAPKVNFW AIPRYGSTLT EAAQLAPPIY 420
PPGFGEAIVF FMSDFPIANG SDGLSVPCIT PQEFVTHFVN EQAPTRGEAA LLHYVDPDTH 480
RNLGEFKLYP EGFMTCPVNS SSGSPQTLPI NGVFTFISWV SRFYQLKPVG TTGPVRRLLGI 540
RRS 543

```

```

SEQ ID NO: 171      moltype = DNA length = 1632
FEATURE            Location/Qualifiers
misc_feature        1..1632
                    note = Nucleic acid sequence of human codon optimized
                    VP1_GI.3_Lil08_M57I plus sign S94L
source              1..1632
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 171
atgatgatgg cttccaagga tgctcccaca aacatgggatg gaacaagcgg cgcggggcaa 60
cttgtgccgg aggtgtccac ggccgaaccc atttccatgg aacctgtggc cggcgcagcc 120
actgctgcgc ccaccgcagg acaggtaaac atgatcgacc cctggatcat ctcaaattac 180
gttcagggtc caccggggga gtttaccata agcccaaaaca acaccgggg tgacatcttg 240
tttgacctgc agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300
aatggatggg ttggaaacat gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360
gggaagatta ttatctcttg cgtgccacct ggatttgca cccagaacgt gtctatcgca 420
caggcaacca tgtttccgca tgtcatcgca gatgtgcgc tgctagagcc catcgaggtg 480
ccccttgagg acgtgcgcaa cgtcctatcc cataacaatg atagcacccc caccatgcgc 540
ttgatattga tttatataac tcccctccgc gccagtggtt ccagctccgg gaccgatcct 600
tttgtgattg ctgggcgggt gttgacttgt cctagccctg acttcaactt cctttttctg 660
gtgctcccaa atgtagaaca gaaaacaaag ccatcagcg tgccaaacct gcccttaac 720
gtgctgtcga attcccgagt gccttccctt attaagtcga tgatggatc tcaggatcac 780
gggtcaaatg tgcagtttca gacgggccga gtgacgttag acgggcagct gcagggcaca 840
accccaacca gttccagtcg gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900
ggacaggggc tgaatcttac tgagatcgat ggtacccctc accatgcatt cgagtcacct 960
gcacctattg gatttccgca tcttggggag tgtgattggc atatcaatgc ttacactgcc 1020
aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080
gcccgcacc tgggtgacac cactatacgc aacgcagatt acaacgcaaa cgtgggtctt 1140
atctgtagcc ttaggtggct atctccgcca agcgggtggg cccctaaagt taacctatgg 1200
gctattccct ggtacgggtc tacgtgact gaggccgctc agctggcacc ccccatatat 1260
ccaccaggat tcggggagc cattgttttc ttatgtccg attttccgat agccaaaggc 1320
tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca cttcgtaaac 1380
gagcaggctc ctactcgggg cgaggctgcc ttgtgcatt acgtagacc cgatacccat 1440
agaaacctgg gcgaattcaa actctacct gaaggtttca tgacctgcgt acctaacctc 1500
tccggcagtg gccctcaaac cttgccgac aacggcgtgt tcacgtttat cagctgggtt 1560
tcacgggttt accaactcaa gcccgctcgga acaactgggc cagttcggag gctcgggatc 1620
agacggagct ag 1632

```

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SEQ ID NO: 172      moltype = AA length = 543
FEATURE            Location/Qualifiers
source              1..543
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

```

```

SEQUENCE: 172
MMASKDAPT NMDGTSGAGQ LVPEVSTAEP ISMEPVAGAA TAAATAGQVN MIDPWIISNY 60
VQAPQGEFTI SPNNTPGDIL FDLQLGPHLN PFLHLHAQMY NGWVGNMKVR VLLAGNAFTA 120
GKIIISCVPV GFAAQNVISIA QATMFPHVIA DVRVLEPIEV PLEDVRNVLF HNNDSTPTMR 180
LICMLYTPLR ASGSSSGTDP FVIAGRVLTC PSPDFNLFLL VPPNVEQKTK PFSVPNLPLN 240
VLSNSRVPSL IKSMVVSQDH GQMVQFQNGR VTLDGQLQGT TPTSASQLCK IRGTVYHATG 300
GQGLNLTEID GTPYHAFESP APIGFPDLGE CDWHINASPA NAFTDGSIIH RIDVAQDSTF 360
APHLGTIHYT NADYNANVGL ICSLEWLSPP SGGAPKVNFW AIPRYGSTLT EAAQLAPPIY 420
PPGFGEAIVF FMSDFPIANG SDGLSVPCIT PQEFVTHFVN EQAPTRGEAA LLHYVDPDTH 480
RNLGEFKLYP EGFMTCPVNS SSGSPQTLPI NGVFTFISWV SRFYQLKPVG TTGPVRRLLGI 540
RRS 543

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-continued

SEQ ID NO: 173 moltype = DNA length = 1632
 FEATURE Location/Qualifiers
 misc_feature 1..1632
 note = Nucleic acid sequence of human codon optimized
 VP1_GI.3_Lil08_A43Vplus sign M57Iplus sign S94L
 source 1..1632
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 173
 atgatgatgg cttccaagga tgcctccaca aacatggatg gaacaagcgg cgcgggggcaa 60
 cttgtgccgg aggtgtccac ggcggaaccc atttccatgg aacctgtggc cgcgcgagcc 120
 actgctgtgg ccaccgcagg acaggtaaac atgatcgacc cctggatcat ctcaaattac 180
 gttcaggctc cacaggggga gtttaccata agcccaaaaca acacccggg tgacatcttg 240
 tttgacctgc agctaggacc acacttgaat ccgtttctgc tccacttggc tcagatgtat 300
 aatggatggg ttggaacatc gaaggtgcgc gtgctcctgg cgggcaatgc attcacagcc 360
 gggaagatta ttatctcttg cgtgccacct ggatttgca cccagaacgt gtctatcgca 420
 caggcaacca tgtttccgca tgtcatcgca gatgtgcgcg tgctagagcc catcgagggtg 480
 ccccttgagg acgtgcgcaa cgtcctattc cataacaatg atagcaccac caccatgcgc 540
 ttgatattga tgttatatac tcccctccgc gccagtgggt ccagctccgg gaccgatcct 600
 tttgtgattg ctgggcgggg gttgacttgt cctagccctg acttcaactt cctttttctg 660
 gtgcctccaa atgtagaaca gaaaacaaag ccattcagcg tgccaaacct gcccttaac 720
 gtgctgtcga attcccgagt gccttccctt attaagtcca tgatggatc tcaggatcac 780
 ggtcaaatgg tgcagtttca gaacggccga gtgacgttag acgggcagct gcagggcaca 840
 acccaacca gtgccagtca gctgtgtaag atcagaggca ccgtctacca cgcaactggc 900
 ggacaggggc tgaattctac tgagatcgat ggtacccctt accatgcatt cgagtcacct 960
 gcacattatg gatttccgca tcttggggag tgtgattggc atatcaatgc ttcacctgcc 1020
 aacgctttca cagacgggtc tattattcat cgcattgacg tagcacagga tagcacattt 1080
 gcccgcgacc tgggtaccat ccactatacg aacgcagatt acaacgcaaa cgtgggtctt 1140
 atctgtagcc tagagtggct atctccgcca agcgggtggg cccctaaagt taacctatgg 1200
 gctattcctc ggtacgggtc tacgctgact gaggccgctc agctggcacc ccccatatat 1260
 ccaccaggat tcggggaagc catgttttct tttatgtccg attttccgat agccaacggt 1320
 tcagatggcc ttagtgtccc ttgcacgatt ccacaggaat ttgtgacaca ctctgtaaac 1380
 gagcaggctc ctactcgggg cgaggctgcc ttgttgcatc acgtagacc cgatacccat 1440
 agaaacctgg gcgaattcaa actctacctt gaaggtttca tgacctgcgt acctaaactc 1500
 tccggcagtg gccctcaaac ctgcccgcgc aacggcgtgt tcacgtttat cagctgggtt 1560
 tcacgggttt accaactcaa gcccgctcga acaactgggc cagttcggag gctcgggatc 1620
 agacggagct ag 1632

SEQ ID NO: 174 moltype = AA length = 543
 FEATURE Location/Qualifiers
 source 1..543
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 174
 MMMASKDAPT NMDGTSGAGQ LVPEVSTAEP ISMEPVAGAA TAVATAGQVN MIDPWIISNY 60
 VQAPQGEFTI SPNNTPGDIL FDLQLGPHLN PFLHLAQMY NGWVGNMKVR VLLAGNAFTA 120
 GKIIISCVPP GFAAQNVISA QATMFPHVIA DVRVLEPIEV PLEDVRNVLF HNNDSTPTMR 180
 LICMLYTPLR ASGSSSGTDP FVIAGRVLTC PSPDFNLFLL VPPNVEQKTK PFSVPLPLN 240
 VLSNSRVPSL IKSMMVQDGH GQMVFQNGR VTLDGQLQGT TPTSASQLCK IRGTVYHATG 300
 GQGLNLTEID GTPYHAFESP APIGFPDLGE CDWHINASPA NAFTDGSIIH RIDVAQDSTF 360
 APHLGTIHYT NADYNANVGL ICSLEWLSPP SGGAPKVNWP AIPRYGSTLT EAAQLAPPIY 420
 PPGFGEAIVF FMSDFPIANG SDGLSVPCTI PQEFVTHFVN EQAPTRGEAA LLHYVDPDTH 480
 RNLGEFKLYP EGFMTCPVNS SSGSPQTLPI NGVFTFISWV SRFYQLKFPVG TTGPVRLGI 540
 RRS 543

SEQ ID NO: 175 moltype = DNA length = 1617
 FEATURE Location/Qualifiers
 source 1..1617
 mol_type = genomic DNA
 note = Norovirus
 organism = unidentified

SEQUENCE: 175
 atgatgatgg ccagcaagga cgtcccgagt aacatggacg gcacttcggg cgcgggggcag 60
 ctggtgcccg aggtcaatgc cgagaaacca cttcctcttg agcccgctcg tggcgccgcc 120
 acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat gaacaatttc 180
 gttcaggcac cagaaggaga attcaccatc tcccccaata acacccagg ggatattctg 240
 tttgacctca ggttaggacc ccacttgaac ccctttctgc ttcactcttc acaaatgtat 300
 aatggctggg tcgggaatat gcgcgtgcgg gtgatgctag ccggcaatgc tttttctgca 360
 ggcaagatta cctattgtcg cgttcctcct ggattcgaat ctcaaatat cagcattggg 420
 caagcaacca tgtttccaca tgtgatcgct gatgttcgcg tcctggaacc cattgaagtt 480
 cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540
 cttctgtgta tgcctacac ccattaaga gccgggggag catcctcagg tactgaccca 600
 tttgtgattg cggggcggtt gctcacatgc ccggtccag actttaactt ccttttcttg 660
 gtgccaccca gtgtgaaca gaaaaccaga cagctcacca tcccaaatat cccattgaac 720

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aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780
aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840
accccagctc ccgcgaacca ggtggccccga atccggggta aagtcttcag tacaaaactcc 900
ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960
gccccctctg gctttccoga tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020
aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080
ccacacttgg gtatcatcga gttcagttca gagaaccatc cgagtgggtg tcagctaggc 1140
acattgacgt ggatcagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200
acctatgggt ccactctgac agagagcaca aatttggctc cgcccatttt cccacccgga 1260
ttcggcgagg ccatagtgtg ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320
cagattcctt gcacactgcc acaagaatc gtctcatcct ttgtagagca gcaggcacct 1380
attcgaggtg aggcgcctct cttgcaactac gtggaccctg acaccaccg caatcttggc 1440
gagtttaagc tgtacctga cgggtttatt acctgtgtac ccaacaccgg cggcgcccca 1500
caaaatttgc ccagcaatgg cgtgtttgtc ttttctctt ggggtgtctc atactaccag 1560
cttaaacctg tcggaactac gggccccgtg cgacgactcg gcgtgaggcg ggtgtga 1617

SEQ ID NO: 176      moltype = DNA length = 1617
FEATURE            Location/Qualifiers
misc_feature       1..1617
                   note = Nucleic acid sequence of human codon optimized VP1_
                   GI.7/GA5043/USA/2014_R84S
source             1..1617
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 176
atgatgatgg ccagcaagga cgtcccgagt aacatggacg gcacttcggg cgcggggcag 60
ctggtgcccc aggtcaatgc ccgagaacca cttcctcttg agcccgctg tggcgccgcc 120
acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat gaacaatttc 180
gttcaggcac cagaaggaga attcaccatc tcccccaata acaccaccag ggataattctg 240
tttgacctca gcttaggacc ccacttgaac cctttctcgc ttcattcttc acaaatgtat 300
aatggctggg tcgggaatat gcgcgtgcgg gtgatgctag ccggcaatgc tttttctgca 360
ggcaagatta tcatttctgt cgttctctct ggattcgaat ctcaaaatat cagcatttgt 420
caagcaacca tgtttccaca tgtgatcgct gatgttcgcg tcctggaacc cattgaagtt 480
cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540
cttctgtgta tgcctcacac cccattaaga gccgggggag catcctcagg tactgaccca 600
tttgtgatgg ccggcggggt gctcacatgc ccggtccag actttaactt ccttttcttg 660
gtgccacca gtgttgaaac gaaaaccaga cagctcacca tcccaaatat cccattgaac 720
aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780
aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840
accccagctc ccgcgaacca ggtggccccga atccggggta aagtcttcag tacaaaactcc 900
ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960
gccccctctg gctttccoga tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020
aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080
ccacacttgg gtatcatcga gttcagttca gagaaccatc cgagtgggtg tcagctaggc 1140
acattgacgt ggatcagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200
acctatgggt ccactctgac agagagcaca aatttggctc cgcccatttt cccacccgga 1260
ttcggcgagg ccatagtgtg ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320
cagattcctt gcacactgcc acaagaatc gtctcatcct ttgtagagca gcaggcacct 1380
attcgaggtg aggcgcctct cttgcaactac gtggaccctg acaccaccg caatcttggc 1440
gagtttaagc tgtacctga cgggtttatt acctgtgtac ccaacaccgg cggcgcccca 1500
caaaatttgc ccagcaatgg cgtgtttgtc ttttctctt ggggtgtctc atactaccag 1560
cttaaacctg tcggaactac gggccccgtg cgacgactcg gcgtgaggcg ggtgtga 1617

SEQ ID NO: 177      moltype = AA length = 538
FEATURE            Location/Qualifiers
source             1..538
                   mol_type = protein
                   note = Norovirus
                   organism = unidentified

SEQUENCE: 177
MMASKDAPS  NMDGTSGAGQ  LVPEVNAAEP  LPLEPVVGAA  TAVATAGQVN  MIDPWIMNMF  60
VQAPEGEFTI SPNNTPGDIL  FDLSLGPHLN  PFLHLHSQMY  NGWVGNMVRV  VMLAGNAFSA  120
GKIIICCVPP GFESQNTSIG  QATMFPFHVA  DVRVLEPIEV  PLDDVRNVLF  HTNENRPTMR  180
LLCMLYTPLR AGGASSGTD  FVIAGRVLTC  PAPDFNFLFL  VPPSVEQKTR  QLTIPNIPLN  240
NLANSRVFAM INKMTVSADQ  NQVVQFQNGR  CTLEGQLLGT  TPVSANQVAR  IRGKVFSTNS  300
GTGLNLTEVD GTPYHAFESP  APLGFDPDIGN  CDWHVYAFKV  NQNTGDPMYR  LDITQGNSFA  360
PHLGSIEFSS ENHPSGDQLG  TLTWISPLNN  ASRVDPWKIP  TYGSTLTST  NLAPPFIFPPG  420
FGEATVYFMS DFPVVSNGTA  QIPCTLPQEF  VSSFVEQQAP  IRGEAALLHY  VDPDTHRNLG  480
EFKLYPDGFI TCVPTNGGGP  QNLPSNGVFV  FSSWVSRYQ  LKPVGTTGVP  RRLGVRRV  538

SEQ ID NO: 178      moltype = DNA length = 1617
FEATURE            Location/Qualifiers
misc_feature       1..1617
                   note = Nucleic acid sequence of human codon optimized VP1_
                   GI.7/GA5043/USA/2014_M57I
source             1..1617

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```

mol_type = other DNA
organism = synthetic construct

SEQUENCE: 178
atgatgatgg ccagcaagga cgtcccgagt aacatggacg gcacttcggg cgcggggagc 60
ctgggtgccg aggtcaatgc cgcagaacca ctctctcttg agcccgctcg tggcgccgcc 120
acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat caacaatttc 180
gttcaggcac cagaaggaga attcaccatc tcccccaata acacccagg ggatattctg 240
tttgacctca ggttaggacc ccacttgaac cctttctgc ttcactcttc acaaatgtat 300
aatggctggg tcgggaatat gcgcgtgctg gtgatgctag ccggcaatgc tttttctgca 360
ggcaagatta tcatttgcgt cgttctctct ggattcgaat ctcaaaatat cagcattggg 420
caagcaacca tgtttccaca tgtgatcgct gatgttcgct tcctggaacc cattgaagtt 480
cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540
cttctgtgta tgcctctacac cccattaaga gccgggggag catcctcagg tactgacca 600
tttggattgg cggggcggtt gctcacatgc ccggtccag actttaactt ccttttcttg 660
gtgccaccca gtgttgaaac gaaaaccaga cagctcacca tcccaaatat cccattgaac 720
aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780
aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840
accccgctct ccgcaacca ggtggcccca atccgggcta aagtcttcag tacaactcc 900
ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960
gccccctctg gctttcccca tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020
aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080
ccacacttgg gtagcatcga gttcagttca gagaaccatc cgagtggtag tcagctaggc 1140
acattgacgt ggcacagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200
acctatgggt ccactctgac agagagcaca aatttggctc cgcccatatt cccacccgga 1260
ttcggcgagg ccatagtgtg ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320
cagattcctt gcacactgcc acaagaattc gtctcatcct ttgtagagca gcaggcacct 1380
attcgaggtg aggcgcctct ctgacactac gtggaccctg acacccaccg caatcttggc 1440
gagtttaagc tgtaccctga cgggtttatt acctgtgtac ccaacaccgg cgcgcgccca 1500
caaaatttgc ccagcaatgg cgtgtttgtc tttctctctt gggtgtctcg atactaccag 1560
cttaaacctg tcggaactac gggccccctg cgacgactcg gcgtgaggcg ggtgtgta 1617

SEQ ID NO: 179      moltype = AA  length = 538
FEATURE            Location/Qualifiers
source              1..538
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

SEQUENCE: 179
MMASKDAPS NMDGTSGAGQ LVPEVNAAEP LPLEPVVGAA TAVATAGQVN MIDPWIINN 60
VQAPGEFTI SPNNTPGDIL FDLRLGPHLN PFLHLHSQMY NGWVGNMVRV VMLAGNAFSA 120
GKIIICVPP GFESQNISIG QATMFPHVIA DVRVLEPIEV PLDDVRNVLF HTNENRPTMR 180
LLCMLYTPLR AGGASSGTD FVIAGRVLTC PAPDFNLFLE VPPSVEQKTR QLTIPNIPLN 240
NLANSRVPAM INKMTVSADQ NQVVQFQNGR CTLEGQLLGT TPVSANQVAR IRGKVFSTNS 300
GTGLNLTEVD GTPYHAFESP APLGFPDIGN CDWHVYAFKV NQNTGDPMYR LDITQGNSPA 360
PHLSIEFSS ENHPSGQQLG TLTWISPLNN ASRVPWKIP TYGSTLTST NLAPPFPPG 420
FGEAIVYFMS DFPITVSNTA QIPCTLPQEF VSSFVEQQAP IRGEAALLHY VDPDTHRNLG 480
EPKLYPDGFI TCVPTNGGGP QNLPSNGVFV FSSWVSRYQ LKPVGTGTGPV RRLGVRRV 538

SEQ ID NO: 180      moltype = DNA  length = 1617
FEATURE            Location/Qualifiers
misc_feature        1..1617
                    note = Nucleic acid sequence of human codon optimized VP1_
                    GI.7/GA5043/USA/2014_M57I plus sign R84S
source              1..1617
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 180
atgatgatgg ccagcaagga cgtcccgagt aacatggacg gcacttcggg cgcggggagc 60
ctgggtgccg aggtcaatgc cgcagaacca ctctctcttg agcccgctcg tggcgccgcc 120
acagctgtcg caactgcagg ccaagtcaat atgatcgacc cgtggataat caacaatttc 180
gttcaggcac cagaaggaga attcaccatc tcccccaata acacccagg ggatattctg 240
tttgacctca gcttaggacc ccacttgaac cctttctgc ttcactcttc acaaatgtat 300
aatggctggg tcgggaatat gcgcgtgctg gtgatgctag ccggcaatgc tttttctgca 360
ggcaagatta tcatttgcgt cgttctctct ggattcgaat ctcaaaatat cagcattggg 420
caagcaacca tgtttccaca tgtgatcgct gatgttcgct tcctggaacc cattgaagtt 480
cctctcgacg acgtgagaaa tgttctcttc cacaccaacg agaataggcc gactatgaga 540
cttctgtgta tgcctctacac cccattaaga gccgggggag catcctcagg tactgacca 600
tttggattgg cggggcggtt gctcacatgc ccggtccag actttaactt ccttttcttg 660
gtgccaccca gtgttgaaac gaaaaccaga cagctcacca tcccaaatat cccattgaac 720
aatctcgcca acagcagggt gccagcaatg ataaacaaaa tgacagtcag tgctgaccag 780
aaccaggtag tccagtttca gaacggcaga tgcacgcttg agggccaact gcttgggacg 840
accccgctct ccgcaacca ggtggcccca atccgggcta aagtcttcag tacaactcc 900
ggcactggcc ttaacctcac agaggttgac ggcactccct atcatgcttt tgagtctcca 960
gccccctctg gctttcccca tataggcaac tgtgactggc acgtttatgc gtttaaagta 1020
aaccagaaca ccggcgatcc tatgtatagg ttggatataa cacaaggtaa ttcattcgcc 1080
ccacacttgg gtagcatcga gttcagttca gagaaccatc cgagtggtag tcagctaggc 1140

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acattgacgt ggatcagccc tctgaataac gcatcaagag tggatccctg gaagatccct 1200
acctatgggt ccactctgac agagagcaca aatttggctc cgcccathtt cccaccgga 1260
ttcggcgagg ccatagtgtg ctttatgtct gactttccta tcgtcagcgg gaatacagcc 1320
cagattcctt gcacactgcc acaagaattc gtctcatcct ttgtagagca gcaggcacct 1380
attcgaggtg aggcgcgcct ctgacactac gtggaccctg acaccacccg caatcttggc 1440
gagtttaagc tgtaccctga cgggtttatt acctgtgtac ccaacaccgg cggcgggcca 1500
caaaatttgc ccagcaatgg cgtgtttgtc ttttcctctt gggtgtctcg atactaccag 1560
cttaaacctg tcggaactac gggccccctg cgacgactcg gcgtgaggcg ggtgtga 1617

```

```

SEQ ID NO: 181      moltype = AA length = 538
FEATURE            Location/Qualifiers
source             1..538
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 181
MMASKDAPS NMDGTSGAGQ LVPEVNAAEP LPLEPVVGAA TAVATAGQVN MIDPWIINN 60
VQAPGEFTI SPNNTPGDIL FDLSLGPHLN PFLHLHLSQMY NGWVGNMRVR VMLAGNAFSA 120
GKIIICCVPP GFESQNISIG QATMFPHVIA DVRVLEPIEV PLDDVRNVLF HTNENRPTMR 180
LLCMLYTPLR AGGASSGTD FVIAGRVLTC PAPDFNLFEL VPPSVEQKTR QLTIPNIPLN 240
NLANSRVPAM INKMTVSADQ NQVVQFQNGR CTLEGQLLGT TPVSANQVAR IRGKVFSTNS 300
GTGLNLTEVD GTPYHAFESP APLGFDPDIGN CDWHVYAPKV NQNTGDPMYR LDITQGNSFA 360
PHLGSIEFSS ENHPSGDQLG TLTWISPLNN ASRVDPWKIP TYGSTLTST NLAPPIFPPG 420
FGEAIVYFMS DFPIVSGNTA QIPCTLPQEF VSSFVEQQAP IRGEAALLHY VDPDTHRNLG 480
EFKLYPDGFI TCVPNTGGGP QNLPSNGVFV FSSWVSRYQ LKPVGTGTGPV RRLGVRRV 538

```

```

SEQ ID NO: 182      moltype = AA length = 542
FEATURE            Location/Qualifiers
source             1..542
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 182
MKMASNDAAP STDGAAGLVP ESNNEVMALE PVAGAALAVP VTGQTNIIDP WIRANFVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLL HLARMYNGYA GGMEVQVMLA GNAFTAGKLV 120
FAAVPPHPFV ENLSPQQITM FPHVIDVRT LEPVLLPLPD VRNNFFHYNQ KDDPKMRIVA 180
MLYTPLRSNG SGDDVFTVSC RVLTRPSPDF DFTYLVPPTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIQOMY TSPNEVISVQ CQNGRCTLDG ELQGTTLQVQ SGICAFKGEV TAHLHDNDHL 300
YNVITITNLNG SPFDPSEDIP APLGVPDFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWQT DDLTVNQPVK FTPVGLNDTD HFNQWVVPYR AGALNLNTNL 420
APSPAPVFPF ERLFFRSYI PLKGGYGTTP IDCLLPQEWV QHFVQEAAPS MSEVALVRYI 480
NPDTGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWVNIQFSLA PMGTGNRRR 540
IQ                                                    542

```

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SEQ ID NO: 183      moltype = DNA length = 1629
FEATURE            Location/Qualifiers
misc_feature       1..1629
                  note = Nucleic acid sequence of human codon optimized
                  VPI_GII.2_CGMH47_A39V plus sign E80S plus sign A90L
source            1..1629
                  mol_type = other DNA
                  organism = synthetic construct

```

```

SEQUENCE: 183
atgaagatgg catccaacga cgccgcaccc agcacagacg gagctgcccg attggtaacc 60
gagtctaata acgaggtgat ggccttggag cctgttgacg gggctgccct cgcagtgcc 120
gtgaccgggc agacaaatat catcgatcct tggattagag ctaatttcgt gcaagcccca 180
aatggggagt ttaccggtcag ccttagaaat agccctgggg aagtgtcctt caatctcagc 240
ctgggaccag aacttaatcc gtacctgctc cacctggccc ggatgtacaa tggatatgca 300
ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcggt 360
ttcgagcccg tccctcccca ctcccagtt gaaaatcttt cccctcagca gattaccatg 420
tttcccatg tcatcatcga tgtgcgtacc ctggaacctg tgcgtgtgcc ttaccagac 480
gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540
atgctttata ctccctcgcg tagcaatggt agtggggatg acgtttttac agtgagttgt 600
cgggtactaa ctgcgctctc accagacttc gactttacgt acttggtgcc tcccactgtc 660
gaaagcaaaa ctaagccatt cacacttccc atctcaccct tcggagaact ctggaactcc 720
cgcttccctg tttcaattga tcagatgtac acgtctccaa atgaagtcac ttctgtgcag 780
tgtcagaacg gcaggtgcac cttagacggg gaactgcagg ggacaacgca gttgcaggtc 840
agtggaattt gcgcctttaa gggcgaagt acagctcacc tccacgacaa cgaatcatct 900
tacaatgtta ctattactaa tctcaatgga agtcctttcg acccctcgga agatattccc 960
gtccactcag gactactcga ctttcaggga cgcgtcttcg gcgtgatata acaacgagat 1020
aagcataaca caccgggaca ttaatgagca gccaatagag cccacgacgc agtcgttccg 1080
acctatacgg ctcagtagac cccaaagctc ggccagatac aaatcgggac ttggcagacc 1140
gatgacctca ctgtgaatca acctgtgaaa ttcactccag taggtctgaa tgatacagac 1200
cactttaacc agtgggtggt ccctagatac gccggagcct tgaacctaaa cactaacctt 1260
gcccttcctg ttgcacctgt gtttcgggg gagcgggtgc tcttcttag aagctatatt 1320
cctctgaagg gcgggtatgg tactccagca atcgactgcc tgctacctca ggagtgggtt 1380

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caacatttct atcaagagggc cgcacctagt atgagcggagg tggctttggt cagatacatc 1440
aatccagaca caggaagagc actgttcgag gccaaagctgc acagagccgg ctccatgacc 1500
gtctcatcca atacatccgc acccgtagta gtccccgccca acgggtactt cagattcgac 1560
agttgggtga atcagtttta ctcggtggcc cccatgggca caggggaacgg tcgccgacgg 1620
atccagtaa                                     1629

```

```

SEQ ID NO: 184      moltype = AA length = 542
FEATURE            Location/Qualifiers
source             1..542
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 184
MKMASNDAAP STDGAAGLVP ESNNEVMALE PVAGAALAAP VTGQTNIIDP WIIANFVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLL HLARMYNGYA GGMEVQVMLA GNAFTAGKLV 120
FAAVPPHPFV ENLSPQQITM FPHVIDVVRT LEPVLLPLPD VRNFFPHYNQ KDDPKMRIVA 180
MLYTPLRSNG SGDDVFTVSC RVLTRPSPDF DFTYLVPPTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIDQMY TSPNEVISVQ CQNGRCTLDG ELQGTTLQV SGICAFKGEV TAHLHDNDHL 300
YNVITITNLNG SPFDPSDIP APLGVPDFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWQT DDLTVNQPVK FTPVGLNDTD HFNQWVVPY AGALNLNTNL 420
APSVAPVFPF ERLLFRRSYI PLKGGYGTGA IDCLLPQEWV QHFYQEAAPS MSEVALVRYI 480
NPDTEGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWVNQFYSLA PMGTGNGRRR 540
IQ                                                    542

```

```

SEQ ID NO: 185      moltype = DNA length = 1629
FEATURE            Location/Qualifiers
misc_feature        1..1629
                  note = Nucleic acid sequence of human codon optimized
                  VP1_GII.2_CGMH47_ R53I plus sign E80S plus sign A90L
source              1..1629
                  mol_type = other DNA
                  organism = synthetic construct

```

```

SEQUENCE: 185
atgaagatgg catcaacga cgcgcgaccc agcacagacg gagctgccgg attggtaccc 60
gagtctaata acgaggtgat ggccctggag cctgttgacg gggctgccct cgcagctcct 120
gtgaccgggc agacaaatat catcgatcct tggattatcg ctaatttcgt gcaagcccca 180
aatggggagt ttacgggtcag cccatgaaat agccctgggg aagtgcctct caatctcagc 240
ctgggaccag aacttaatcc gtacctgctc cacctggccc ggaatgtacaa tggatatgca 300
ggagggatgg aggtgcaggt tatgctggct ggcaatgcct ttacagcagg caaactcgtt 360
ttcgacggcg tccctcccca ctcccagtt gaaaatcttt cccctcagca gattaccatg 420
tttcccatg tcacatcgga tgtgcgtacc ctggaacctg tgctgttgcc tttaccagac 480
gtgcggaata atttctttca ctataatcag aaggatgacc caaaaatgcg gatcgttgcg 540
atgctttata ctccccctgc tagcaatggt agtggggatg acgtttttac agtgagttgt 600
cgggtactaa ctgcaccttc accagacttc gactttacgt acttggtgcc tcccactgtc 660
gaaagcaaaa ctaagccatt cacacttccc atcctcacc cggagaact ctcgaaactc 720
cgcttcctg tttcaattga tcagatgtag acgtctccaa atgaagtc tctgtgagc 780
tgtagaagc gcagggtgac cttagacggt gaactgcagg ggacaacgca gttgcaggtc 840
agtggaattt gcgcctttaa gggcgaagt acagctcacc tccacgacaa cgatcatctc 900
tacaatgcta ctattactga tctcaatgga agtcctttcg acccctcgga agatattccc 960
gctccactcg gagtacctga ctttcaggga cgcgtcttcg gcgtgatatc acaacgagat 1020
aagcataaca caccgggaca taatgagcca gccaatagag cccacgacgc agtcgttccg 1080
acctatacgg ctccagtacac cccaaagctc ggccagatag aaatcgggac ttggcagacc 1140
gatgacctca ctgtgaatca acctgtgaaa ttcaactcag taggtctgaa tgatacagac 1200
cactttaacc agtgggtggt cccatgatac gccggagcct tgaacctaaa cactaacctt 1260
gccccttcg ttgcacctgt gtttcgggg gagcgggtgc tcttctttag aagctatatt 1320
cctctgaagg gggggtatgg tactccagca atcgactgcc tgctacctca ggagtggtt 1380
caacatttct atcaagaggc cgcacctagt atgagcggag tggctttggt cagatacatc 1440
aatccagaca caggaagagc actgttcgag gccaaagctc acagagccgg ctccatgacc 1500
gtctcatcca atacatccgc acccgtagta gtccccgccca acgggtactt cagattcgac 1560
agttgggtga atcagtttta ctcggtggcc cccatgggca caggggaacgg tcgccgacgg 1620
atccagtaa                                     1629

```

```

SEQ ID NO: 186      moltype = AA length = 542
FEATURE            Location/Qualifiers
source             1..542
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

```

```

SEQUENCE: 186
MKMASNDAAP STDGAAGLVP ESNNEVMALE PVAGAALAVP VTGQTNIIDP WIIANFVQAP 60
NGEFTVSPRN SPGEVLLNLS LGPELNPYLL HLARMYNGYA GGMEVQVMLA GNAFTAGKLV 120
FAAVPPHPFV ENLSPQQITM FPHVIDVVRT LEPVLLPLPD VRNFFPHYNQ KDDPKMRIVA 180
MLYTPLRSNG SGDDVFTVSC RVLTRPSPDF DFTYLVPPTV ESKTKPFTLP ILTLGELSNS 240
RFPVSIDQMY TSPNEVISVQ CQNGRCTLDG ELQGTTLQV SGICAFKGEV TAHLHDNDHL 300
YNVITITNLNG SPFDPSDIP APLGVPDFQG RVFGVISQRD KHNTPGHNEP ANRAHDAVVP 360
TYTAQYTPKL GQIQIGTWQT DDLTVNQPVK FTPVGLNDTD HFNQWVVPY AGALNLNTNL 420

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APSVAPVFPF ERLLFRRSYI PLKGGYGTTPA IDCLLPQEWV QHFYQEAAPS MSEVALVRYI 480
 NPDTGRALFE AKLHRAGFMT VSSNTSAPVV VPANGYFRFD SWVNQFYSLA PMGTGNRRR 540
 IQ 542

SEQ ID NO: 187 moltype = DNA length = 1629
 FEATURE Location/Qualifiers
 misc_feature 1..1629
 note = Nucleic acid sequence of human codon optimized
 VP1_GII.2_CGMH47_A39Vplus sign R53I plus sign E80S plus
 sign A90L
 source 1..1629
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 187

atgaagatgg	catccaacga	cgccgcaccc	agcacagacg	gagctgcccg	attggtaccc	60
gagtcctaata	acgaggtgat	ggccttggag	cctgttgacg	gggctgccct	cgcagtgcct	120
gtgaccgggc	agacaaatat	catcgatcct	tggattatcg	ctaatttcgt	gcaagcccca	180
aatggggag	ttacgggtcag	ccctagaaat	agccctgggg	aagtgtccct	caatctcagc	240
ctgggaccag	aacttaatcc	gtacctgctc	cacctggccc	ggatgtacaa	tggatatgca	300
ggagggatgg	agggtgcaggt	tatgctggct	ggcaatgcct	ttacagcagg	caaactcggt	360
ttcgagccg	tcctccccc	cttcccagtt	gaaaatcttt	cccctcagca	gattaccatg	420
tttccccatg	tcatactgca	tgctgcgtacc	ctggaacctg	tgctgttgcc	ttaccagac	480
gtgcggaata	atttctttca	ctataatcag	aaggatgacc	caaaaatgcg	gacgtttgcg	540
atgctttata	ctcccctgcg	tagcaatggt	agtggggatg	acgtttttac	agtgagttgt	600
cgggtactaa	ctcgcccttc	accagacttc	gactttacgt	acttgggtgc	tcccactgtc	660
gaaagcaaaa	ctaagccatt	cacacttccc	atcctcaccc	tcggagaact	ctcgaactcc	720
cgcttccctg	tttcaattga	tcagatgtac	acgtctccaa	atgaagtc	ttctgtgcag	780
tgctcagaacg	gcaggtgcac	cttagacggg	gaactgcagg	ggacaacgca	gttgacggtc	840
agtgaatttt	gcgcctttta	gggcgaagtg	acagctcacc	tccacgacaa	cgatcatctc	900
tacaatgtta	ctattactaa	tctcaatgga	agtcccttcg	accctcggga	agatattccc	960
gctccactcg	gagtcactga	ctttcaggga	cgcgtcttcg	gcgtgatatc	acaacgagat	1020
aagcataaca	caccgggaca	taataagcca	gccaatagag	cccacgacgc	agtcgttccg	1080
acctatacgg	ctcagtagac	cccaagctc	ggccagatag	aaatcgggac	ttggcagacc	1140
gatgacctca	ctgtgcaatca	acctgtgaaa	ttcactccag	taggtctgaa	tgatacagac	1200
cactttaacc	agtggtgggt	ccctagatag	gcccggagcct	tgaacctaaa	cactaacctt	1260
gccccttcg	ttgcacctgt	gtttccgggg	gagcggttgc	tcttcttag	aagctatatt	1320
cctctgaagg	gcggtgatgg	tactccagca	atcgactgcc	tgctacctca	ggagtgggtt	1380
caacatttct	atcaagaggg	cgcacctagt	atgagcggag	tggtcttggg	cagatacatc	1440
aatccagaca	caggaagagc	actgttcgag	gccaagctgc	acagagccgg	cttcgatgac	1500
gtctcatcca	atacatccg	accctagtag	gtccccgcca	acgggtactt	cagattcgac	1560
agttgggtga	atcagtttta	ctcgttggcc	cccattggga	caggggaacg	tcgccgacgg	1620
atccagtaa						1629

SEQ ID NO: 188 moltype = AA length = 540
 FEATURE Location/Qualifiers
 source 1..540
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 188

MKMASSDANP	SDGSAANLVP	EVNNEVMALE	PVVGAAIAPV	VAGQONVIDP	WIINNFBVQAP	60
GGEFTVSPRN	APGEILWSAP	LGPDLNPYLS	HLARMYNGYA	GGFEVQVILA	GNAFTAGKVI	120
FAAVPPNFPT	EGLSPSQVTM	FPHIVVDVRQ	LEPVLIPLPD	VRNNFYHYNQ	SNDPTIKLIA	180
MLYTPLRANN	AGDDVFTVSC	RVLTRPSPDF	DFIFLVPPTV	ESRTKPFSPV	VLTVEEMTNS	240
RFPIPLEKLF	TGPSSAFVQ	PQNGRCCTDG	VLLGTQLSP	VNICTFRGDV	THITGSRNYT	300
MNLASQNWND	YDPTTEIPAP	LGTPDFVFGKI	QGVLTQTTRT	DGSTRGHKAT	VYTGSADFAP	360
KLGRVQFETD	TDRDFEANQN	TKFTPVGVIG	DGGTTHRNEP	QQWVLPYSYG	RNTHNVHLAP	420
AVAPTFFGEQ	LLFFRSTMPG	CSGYPNMDLD	CLLPQEWVQY	FYQEAAPQAS	DVALLRFVNP	480
DTGRVLFECK	LHKSGYVTVA	HTGQHDLVIP	PNGYFRFDSW	VNQFYTLAPM	GNGTGRRRRAV	540

SEQ ID NO: 189 moltype = DNA length = 1623
 FEATURE Location/Qualifiers
 misc_feature 1..1623
 note = Nucleic acid sequence of human codon optimized VP1
 GII.4_Syd12_A39V plus sign R53I
 source 1..1623
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 189

atgaaaaatgg	cctcgagtga	cgctaaccct	agtgacggca	gcgccgcca	tcttgtgcct	60
gaggttaata	atgaggtgat	ggccctggag	cctgtggtgg	gcgcagccat	agcagtcctc	120
gtggccgggtc	agcagaatgt	gattgacccg	tggataatca	acaattttgt	ccaagccctc	180
ggtggggag	tcaccgttag	cccgagaaat	gcgccaggag	aaatcctgtg	gtcggcccca	240
ttgggacccg	atctgaaccc	ctatttgtca	catctcgctc	ggatgtacaa	cgggtatgcc	300
ggcggtattg	aagtgcaggt	gattctggct	gggaacgcgt	tcactgctgg	caaagtgatc	360
tttgacgcgg	tgccctccaa	cttcccact	gaaggactgt	ctccaagcca	ggtcaccaatg	420

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tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgac cgaccattaa actcatcgcg 540
atgttggtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcga ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggttcag 780
ccacagaacg gacgtgcgac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgccact 960
cttggaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcoga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagtcca cctctgtagg agtgattcag gacgggggca ccaactcacc gaacgagccg 1200
caacaatggg tctctgccctc ttatagcggg aggaatactc ataagtgcga tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt tctgttcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380
ttttatcaag aggccgcacc agcccaatcc gacgtgcgac tcttgccggt cgtgaatcca 1440
gacacaggcc gcgtgtgtgt tgagtcaaaa ttgcacaaat caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620
tga 1623

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SEQ ID NO: 190      moltype = AA length = 540
FEATURE            Location/Qualifiers
source              1..540
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

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SEQUENCE: 190
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAIAVP VAGQQNVIDP WIINNFBQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNPFT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSPV VLTVEEMTNS 240
RPIPLEKLF TGPSSAFVVQ PQNGRCCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTEEIPAP LGTPDFVVGKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVIG DGGTTHRNEP QQWVLPYSYG RNTHNVHLAP 420
AVAPTFFGEQ LLFFRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYTVVA HTGQHDLVIP PNGYFRFDSW VNQFYTLAPM NGNGTGRRAV 540

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SEQ ID NO: 191      moltype = DNA length = 1623
FEATURE            Location/Qualifiers
misc_feature        1..1623
                    note = Nucleic acid sequence of human codon optimized VP1
                    GII.4_Syd12_A39V plus sign R53I plus sign P80S
source              1..1623
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 191
atgaaaaatgg cctcgagtga cgtaaacct agtgacggca gcgcccgaac tcttgctcct 60
gaggttaata atgaggtgat ggcctgggag cctgtggtgg gcgcagccat agcagtcctc 120
gtggccggtc agcagaatgt gattgaccgg tggataatca acaattttgt ccaagccctc 180
gggtgggagt tcaccgttag ccgagaaat gcgccaggag aaatcctgtg gtcggccagc 240
ttgggacccg atctgaaccc ctatttgtca catctcgctc ggatgtacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct ggggaacgct tcaactgtgg caaagtgatc 360
tttgacggcg tgctctccaa ctccccact gaaggactgt ctccaagcca ggtcacaatg 420
tttccacaca tcgtggtgga cgtacggcag ctagagcctg tcttgattcc cctccctgat 480
gtacgcaata atttctacca ctacaatcaa tccaatgac cgaccattaa actcatcgcg 540
atgttggtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcga ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgtt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtgggttcag 780
ccacagaacg gacgtgcgac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag aggcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgccact 960
cttggaaccc ccgactttgt gggaaaaata cagggcgctc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcoga ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgaccggg actttgaagc caatcagaat 1140
actaagtcca cactgttagg agtgattcag gacgggggca ccaactcacc gaacgagccg 1200
caacaatggg tctctgccctc ttatagcggg aggaatactc ataagtgcga tttggctcct 1260
gcagtggctc ccacgtttcc cggggaacaa ctgctctttt tctgttcaac catgcctgga 1320
tgctccggat atcccaatat ggatctcgat tgcctgctcc cacaggaatg ggtgcagtat 1380
ttttatcaag aggccgcacc agcccaatcc gacgtgcgac tcttgccggt cgtgaatcca 1440
gacacaggcc gcgtgtgtgt tgagtcaaaa ttgcacaaat caggatacgt tacagtggct 1500
catactggac agcatgacct ggtgatccca cccaacggat attttaggt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggctgtc 1620
tga 1623

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SEQ ID NO: 192 moltype = AA length = 538
 FEATURE Location/Qualifiers
 source 1..538
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 192

MKMASNDAAAP	SNDGAAGLVP	EGNNETLPLE	PVAGAAIAVP	VTGQNNIIDP	WIRTNFVQAP	60
NGEFTVSPRN	SPGEILLNLE	LGPDLNPYLA	HLSRMYNGYA	GGVEVQVLLA	GNAFTAGKIL	120
FAAVPPNFPV	EFLSPAQITM	LPHLIVDVRT	LEPIMIPLPD	VRNTFFHYNN	QPNRMRMLVA	180
MLYTPLRSNG	SGDDVFTVSC	RVLTRPTPDF	EFTYLVPPSV	ESKTKPFSLP	ILTLSELTNS	240
RFPVPIDSLF	TAQNNVLQVQ	CQNGRCTLDG	ELQGTQQLP	SGICAFRGRV	TAETDHRDKW	300
HMQLQNLNGT	TYDPTDDVPA	PLGTPDFKGV	VFGVASQRNV	GNDAPGSTR	HEAVISTYSP	360
QFVPKLGSVN	FRSNDNDFQL	QPTKFTPVGI	NDDGDHPFRQ	WELPDYSGLL	TLNMNLAPPV	420
APNFPGEQLL	FFRSFVPCSG	GYNQGIVDCL	IPQEWIQHFY	QESAPSQSDV	ALIRYVNPDT	480
GRTLFEAKLH	RSGYITVAHS	GDYPLVVPAN	GYFRFDSWVN	QFYSLAPMGT	GNGRRRAQ	538

SEQ ID NO: 193 moltype = DNA length = 1617
 FEATURE Location/Qualifiers
 misc_feature 1..1617
 note = Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014
 A0A077KVU6_A39V
 source 1..1617
 mol_type = other DNA
 organism = synthetic construct

SEQUENCE: 193

atgaaaaatgg	catctaacga	cgcagccccc	tcaaacgatg	gcgctgctgg	actcgtgccg	60
gaggggaata	catgacacact	tccactagag	cgggttgacg	gcgcgcgtat	agctgtgccca	120
gtgacagggc	agaataatat	tatagaccct	tggattcggga	caaacctcgt	gcaggcacccc	180
aacggcgagtg	ttacagtatc	cccccggaac	tcccaggtg	agatactcct	gaatcttgag	240
ctcggccctg	acctcaatcc	atatctggct	catctgagcc	gcatgtacaa	tggttacgct	300
gggggggctg	aagtgcaggt	cctcctggcc	ggaaacgcct	ttaccgctgg	caaaattctg	360
tttgccgcgg	ttccaccaaa	ctttccagtc	gaattcctct	ctccgcgcga	aataaccatg	420
ctgccacatt	tgatcgttga	cgtgcggacc	ctggagccaa	taatgattcc	cctgcgggat	480
gtgcgttaaca	cctttttcca	ttataacaat	cagccaaact	ctcggatgag	acttgttgct	540
atgctgtata	ccccctcgcg	gagcaacggc	agtggcggatg	atgtgtttac	cgtgagttgc	600
agagtccctga	cgcgcccac	cccggacttc	gagttcacct	acctgggtgc	cccttctgtg	660
gaatctaaga	ccaaaccgtt	ttcactgcca	atcttaactc	tctccgaact	gactaacagc	720
cgggtttccag	taccatagat	ttctcttttt	accgctcaaa	acaacgtact	ccaagtccag	780
tgccagaaacg	gccgctgtat	gcttgatggg	gagttgcagg	ggacaacaca	gctactcccc	840
agtggcatct	gtgcattccg	gggcccgcgtg	accgctgaga	cagaccatcg	tgacaaatgg	900
cacatgcac	ttccaaaactt	aaacgggacc	acctacgacc	caaccgacga	cgctccctgct	960
ccgctaggga	ctcctgactt	taagggggtg	gtgttcggag	tggcctctca	gcggaatggt	1020
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gccctaatt	tcccgggtga	gcagctgctg	tttttcggga	gctttgtgcc	atgcagtggc	1320
ggatataatc	aaggcatcgt	agaactgctg	attccccaa	agtggataca	acatttttac	1380
caggaaagt	cgccctccca	gtccgatgtg	gccctgatac	ggtagcgtta	ccccgatacc	1440
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ggcgattatc	ccctgggtgt	tcccgcacac	ggttacttta	ggttcgatag	ttgggtcaac	1560
cagttctatt	cactagcccc	aatgggcacc	ggtaacggca	gacgccgggc	tcagtag	1617

SEQ ID NO: 194 moltype = AA length = 538
 FEATURE Location/Qualifiers
 source 1..538
 mol_type = protein
 note = Norovirus
 organism = unidentified

SEQUENCE: 194

MKMASNDAAAP	SNDGAAGLVP	EGNNETLPLE	PVAGAAIAAP	VTGQNNIIDP	WIITNFVQAP	60
NGEFTVSPRN	SPGEILLNLE	LGPDLNPYLA	HLSRMYNGYA	GGVEVQVLLA	GNAFTAGKIL	120
FAAVPPNFPV	EFLSPAQITM	LPHLIVDVRT	LEPIMIPLPD	VRNTFFHYNN	QPNRMRMLVA	180
MLYTPLRSNG	SGDDVFTVSC	RVLTRPTPDF	EFTYLVPPSV	ESKTKPFSLP	ILTLSELTNS	240
RFPVPIDSLF	TAQNNVLQVQ	CQNGRCTLDG	ELQGTQQLP	SGICAFRGRV	TAETDHRDKW	300
HMQLQNLNGT	TYDPTDDVPA	PLGTPDFKGV	VFGVASQRNV	GNDAPGSTR	HEAVISTYSP	360
QFVPKLGSVN	FRSNDNDFQL	QPTKFTPVGI	NDDGDHPFRQ	WELPDYSGLL	TLNMNLAPPV	420
APNFPGEQLL	FFRSFVPCSG	GYNQGIVDCL	IPQEWIQHFY	QESAPSQSDV	ALIRYVNPDT	480
GRTLFEAKLH	RSGYITVAHS	GDYPLVVPAN	GYFRFDSWVN	QFYSLAPMGT	GNGRRRAQ	538

SEQ ID NO: 195 moltype = DNA length = 1617
 FEATURE Location/Qualifiers
 misc_feature 1..1617
 note = Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014

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source          A0A077KVU6_R53I
                1..1617
                mol_type = other DNA
                organism = synthetic construct

SEQUENCE: 195
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gaggggaata atgagacact tccactagag ccggttgacg gcgcgcgtat agctgcccc 120
gtgacagggc agaataatat tatagaccct tggattatca caaacctcgt gcaggcacc 180
aacggcgagt ttacagatct cccccggaac tcccaggtg agataactct gaactcttgag 240
ctcggccctg acctcaatcc atactgtgct catctgagcc gcatgtacaa tggttacgct 300
ggggggggtc aagtgacagt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360
tttccgcgcg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420
ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgcgggat 480
gtgcgtaaca cctttttcca ttataacaat cagccaaact ctcggtatgag acttggttgc 540
atgctgtaca cccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600
agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660
gaatctaaga ccaaacccgtt ttcaactgca atcttaactc tctccgaact gactaacagc 720
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tgccagaaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840
agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaaatgg 900
cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960
ccgctaggga ctctgactt taaggggggtg gtgttcggag tggcctctca gcggaatggt 1020
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caatttgtgc ccaagctcgg atccgttaat ttctgtagta acgacaacga ctccaactg 1140
caaccacaga agtttacgac agtggggatt aatgatgatg gagaccatcc ttccgcgcaa 1200
tgggaactac cagattattc accctcaata tgaacctcgc cccaccctg 1260
gccccataat tccccggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320
ggatataatc aaggcatcgt agactgcttg attcccaag agtggatata acatttttac 1380
caggaaagtg cgcctcccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440
gggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500
ggcgattatc cctcgggtg tcccgcacac ggttacttta ggttcgatag ttgggtcaac 1560
cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

SEQ ID NO: 196      moltype = AA length = 538
FEATURE             Location/Qualifiers
source              1..538
                   mol_type = protein
                   note = Norovirus
                   organism = unidentified

SEQUENCE: 196
MKMASNDAAP SNDGAAGLVP EGNNETLPLE PVAGAAIAAP VTGQNNIIDP WIRTNFVQAP 60
NGEFTVSPRN SPGEILLNLE LGPDLNPLYL HLSRMYNGYA GGVEVQVLLA GNAFTAGKIL 120
FAAVPPNFPV EFLSPAQITM LPHLIVDVRT LEPIMILPD VRNTFFHYNN QPNSRMRLVA 180
MLYTPLRSNG SGDDVFTVSC RVLTRPTPDF EFTYLVPPSV ESKTKPFSLP ILTLSELTNS 240
RFPVPIDSLF TAQNNVLQVQ CQNGRCTLDG ELQGTQLLLP SGICAFRGRV TAETDHRDKW 300
HMQLQNLNGT TYDPTDDVPA PLGTPDFKGV VFGVASQRNV GNDAPGSTRA HEAVISTYSP 360
QFVPKLGSVN FRSNDNDFQL QPTKFTPVGI NDDGDHPPRQ WELPDYSGLL TLNMNLAPPV 420
APNFPGEQLL FFRSFVPCSG GYNQGIVDCL IPQEWIQHFY QESAPSQSDV ALIRYVNPDT 480
GRTLFEAKLH RSGYITVAHS GDYPLVVPAN GYFRFDSWVN QFYSLAPMGT GNGRRRAQ 538

SEQ ID NO: 197      moltype = DNA length = 1617
FEATURE             Location/Qualifiers
misc_feature        1..1617
                   note = Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014
                   A0A077KVU6_A90L
source              1..1617
                   mol_type = other DNA
                   organism = synthetic construct

SEQUENCE: 197
atgaaaaatgg catctaacga cgcagccccc tcaaacgatg gcgctgctgg actcgtgccc 60
gaggggaata atgagacact tccactagag ccggttgacg gcgcgcgtat agctgcccc 120
gtgacagggc agaataatat tatagaccct tggattcgga caaacctcgt gcaggcacc 180
aacggcgagt ttacagatct cccccggaac tcccaggtg agataactct gaactcttgag 240
ctcggccctg acctcaatcc atactgtgct catctgagcc gcatgtacaa tggttacgct 300
ggggggggtc aagtgacagt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360
tttccgcgcg ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420
ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgcgggat 480
gtgcgtaaca cctttttcca ttataacaat cagccaaact ctcggtatgag acttggttgc 540
atgctgtaca cccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600
agagtcctga cgcgcccaac cccggacttc gagttcacct acctggtgcc cccttctgtg 660
gaatctaaga ccaaacccgtt ttcaactgca atcttaactc tctccgaact gactaacagc 720
cgggtttccag taccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780
tgccagaaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840
agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaaatgg 900
cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960
ccgctaggga ctctgactt taaggggggtg gtgttcggag tggcctctca gcggaatggt 1020

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gggaatgaacg cccccggctc taccgagct cagcaggccg ttatctcaac atatagcccc 1080
caatttgtgc ccaagctcgg atccgtaaat ttctgtagta acgacaacga cttccaactg 1140
caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc ttcccgccaa 1200
tgggaactac cagattatc tgggctgctc accctcaata tgaacctcgc cccaccctg 1260
gccccataat tccccggtag gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320
ggatataatc aaggcatcgt agactgcttg attccccaag agtggatata acatttttac 1380
caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440
ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500
ggcgattatc ccttggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560
cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

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SEQ ID NO: 198      moltype = AA length = 538
FEATURE
source             Location/Qualifiers
                   1..538
                   mol_type = protein
                   note = Norovirus
                   organism = unidentified

```

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SEQUENCE: 198
MKMASNDAAP  SNDGAAGLVP  EGNNETLPLE  PVAGAAIAPV  VTGQNNIIDP  WIITNFVQAP  60
NGEFTVSPRN  SPGEILLNLE  LGPDLNPYLA  HLSRMYNGYA  GGVEVQVLLA  GNAFTAGKIL  120
FAAVPPNPFV  EFLSPAQITM  LPHLIVDVRT  LEPIMIPDP  VRNTFFHYNN  QPNRMRRLVA  180
MLYTPLRNSG  SGDDVFTVSC  RVLTRPTPDF  EFTYLVPPSV  ESKTKPFSLP  ILTLSELTN  240
RFPVPIDSLF  TAQNNVLQVQ  CQNGRCTLDG  ELQGTQQLP  SGICAFRGRV  TAETDHRDKW  300
HMQQLQNLGT  TYDPTDDVPA  PLGTPDFKGV  VFGVASQRNV  GNDAPGSTR  HEAVISTYSP  360
QFVPKLGSVN  FRSNDNDFQL  QPTKFTPVGI  NDDGDHPRQ  WELPDYSGLL  TLMNMLAPPV  420
APNPFGEQLL  FFRSFVPCSG  GYNQGIIVDCL  IPQEWIQHPY  QESAPSQSDV  ALIRYVNPDT  480
GRTLFEAKLH  RSGYITVAHS  GDYPLVVPAN  GYFRFDSWVN  QFYSLAPMGT  GNGRRRAQ  538

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SEQ ID NO: 199      moltype = DNA length = 1617
FEATURE
misc_feature       Location/Qualifiers
                   1..1617
                   note = Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014
                   A0A077KVU6_A39V+M53I
source             1..1617
                   mol_type = other DNA
                   organism = synthetic construct

```

```

SEQUENCE: 199
atgaaaaatgg catctaacga cgcagccccc tcaaacgatg gcgctgctgg actcgtgccg 60
gaggggaata atgagacact tccactagag ccggttgtag gcgcgcgtat agctgtgcc 120
gtgacagggc agaataatat tatagacctt tggattatca caaacttcgt gcaggcaccc 180
aacggcgagt ttacagtatc cccccggaac tccccagggt agatactcct gaatcttgag 240
ctcgccctcg acctcaatcc atatctggct catctgagcc gcattgtaca ttggttacgt 300
ggggggggtg cctctgggcc cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360
tttgccgcgc ttccaccaaa ctttccagtc gaattcctct ctcccgcgca aataaccatg 420
ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480
gtgcgtaaca cttttttcca ttataacaat cagccaaact ctcggtatgag acttggttgc 540
atgctgtaca cccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagtgc 600
agagtcctga cgcgccaac cccggaactc gagtccacct acctggtgcc ccttctgtg 660
gaatctaaga ccaaaccgtt ttcaactgca atcttaactc tctccgaact gactaacagc 720
cggttttcag taccataga ttctctttt accgctcaaa acaactgact ccaagtcag 780
tgccagaacg gccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840
agtggcatct gtgcattccg gggcccgctg accgctgaga cagaccatcg tgacaatagg 900
cacatgcaac tccaaaactt aaacggggacc acctacgacc caaccgacga cgtccctgct 960
ccgctaggga ctctgactt taaggggggt gtgttcggag tggcctctca gcggaatgtt 1020
gggaatgaac cccccggctc taccgagct cagcaggccg ttatctcaac atatagcccc 1080
caatttgtgc ccaagctcgg atccgtaaat ttctgtagta acgacaacga cttccaactg 1140
caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc ttcccgccaa 1200
tgggaactac cagattatc tgggctgctc accctcaata tgaacctcgc cccaccctg 1260
gccccataat tccccggtag gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320
ggatataatc aaggcatcgt agactgcttg attccccaag agtggatata acatttttac 1380
caggaaagtg cgccctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440
ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500
ggcgattatc ccttggtggt tcccgccaac ggttacttta ggttcgatag ttgggtcaac 1560
cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

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SEQ ID NO: 200      moltype = AA length = 538
FEATURE
source             Location/Qualifiers
                   1..538
                   mol_type = protein
                   note = Norovirus
                   organism = unidentified

```

```

SEQUENCE: 200
MKMASNDAAP  SNDGAAGLVP  EGNNETLPLE  PVAGAAIAPV  VTGQNNIIDP  WIRTNFVQAP  60
NGEFTVSPRN  SPGEILLNLS  LGPDLNPYLL  HLSRMYNGYA  GGVEVQVLLA  GNAFTAGKIL  120
FAAVPPNPFV  EFLSPAQITM  LPHLIVDVRT  LEPIMIPDP  VRNTFFHYNN  QPNRMRRLVA  180
MLYTPLRNSG  SGDDVFTVSC  RVLTRPTPDF  EFTYLVPPSV  ESKTKPFSLP  ILTLSELTN  240

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RFPVPIDSLF TAQNNVLQVQ CQNGRCTLDG ELQGTQQLP SGICAFGRV TAETDHRDKW 300
HMQLQNLNGT TYDPTDDVPA PLGTPDFKGV VFGVASQRNV GNDAPGSTR HEAVISTYSP 360
QFVPKLGSVN FRSNDNDFQL QPTKFTPVGI NDDGDHPFRQ WELPDYSGLL TLNMNLAPPV 420
APNFPGEQLL FFRSFVPCSG GYNQGIVDCL IPQEWIQHFY QESAPSQSDV ALIRYVNPDT 480
GRTLFEAKLH RSGYITVAHS GDYPLVVPAN GYFRFDSWN QFYSLAPMGT GNGRRRAQ 538

```

```

SEQ ID NO: 201      moltype = DNA length = 1617
FEATURE            Location/Qualifiers
misc_feature        1..1617
                    note = Nucleic acid sequence of VP1 hCod GII.17 Kawa 2014
                    A0A077KVU6_E80S plus sign A90L
source              1..1617
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 201
atgaaaaatgg catctaacga cgcagccccc tcaaacgatg gcgctgctgg actcgtgccg 60
gaggggaata atgagacact tccactagag cgggttgag gcgcccgtat agctgcccc 120
gtgacagggc agaataatat tatagaccct tggattcgga caaacctcgt gcaggcacc 180
aacgcgagtg ttacagtatc ccccgggaac tcccaggtg agatactcct gaattcttagc 240
ctcgccctg acctcaatcc atatctgctg catctgagcc gcatgtacaa tggttacgct 300
gggggggtcg aagtgcaggt cctcctggcc ggaaacgcct ttaccgctgg caaaattctg 360
tttgccgcg ttccaccaaa ctttcagtc gaattcctct ctccgcgcga aataaccatg 420
ctgccacatt tgatcgttga cgtgcggacc ctggagccaa taatgattcc cctgccggat 480
gtgctgaaca cctttttcca ttataacaat cagccaaact ctcggtagag acttgttgct 540
atgctgtaca ccccctgcg gagcaacggc agtggcgatg atgtgtttac cgtgagttgc 600
agagtcctga cgcgcccac cccggacttc gagttcacct acctgggtgc ccttctgtg 660
gaatctaaga ccaaacgggt ttcaactgca atcttaactc tctccgaact gactaacagc 720
cgggtttccag taccataga ttctcttttt accgctcaaa acaacgtact ccaagtccag 780
tgccagaacg gcccgctgtac gcttgatggt gagttgcagg ggacaacaca gctactcccc 840
agtggcatct gtgcattccg gggccgcgtg accgctgaga cagaccatcg tgacaatagg 900
cacatgcaac tccaaaactt aaacgggacc acctacgacc caaccgacga cgtccctgct 960
ccgctaggga ctctgactt taaggggggt gtgttcggag tggcctctca gcggaatgtt 1020
gggaatgacg ccccggctg taccccgagct cagaggccg ttatctcaac atatagcccc 1080
caatttgtgc ccaagctcgg atccgttaat ttctgtagta acgacaacga cttccaaactg 1140
caaccaacga agtttacgcc agtggggatt aatgatgatg gagaccatcc ttccgcgcaa 1200
tggaactac cagattatc tgggtgctc accctcaata tgaacctcgc cccaccctg 1260
gccctaatt tcccgggtga gcagctgctg ttttttcgga gctttgtgcc atgcagtggc 1320
ggatataatc aaggcatcgt agaactgctg attccccaa agtggataca acatttttac 1380
caggaaagtg cgcctccca gtccgatgtg gccctgatac ggtacgttaa ccccgatacc 1440
ggaagaacat tattcgaagc gaaattgcac agatcagggt acattaccgt tgcacattcc 1500
ggcgattatc ccttggtggt tcccgcacac ggttacttta ggttcgatag ttgggtcaac 1560
cagttctatt cactagcccc aatgggcacc ggtaacggca gacgccgggc tcagtag 1617

```

```

SEQ ID NO: 202      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer GI.3Lil108(M57I).r
source              1..59
                    mol_type = other DNA
                    organism = synthetic construct

```

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SEQUENCE: 202
ctgaacgtaa ttgagatga tccaggggtc gatcatgttt acctgtcctg cggtggcgg 59

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```

SEQ ID NO: 203      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer GI.3Lil108(M57I).c
source              1..59
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 203
gtaaacatga tcgacccctg gatcatctca aattacgttc aggtccaca gggggagtt 59

```

```

SEQ ID NO: 204      moltype = DNA length = 52
FEATURE            Location/Qualifiers
misc_feature        1..52
                    note = Primer IF-(GI.7USA14)VP1.c
source              1..52
                    mol_type = other DNA
                    organism = synthetic construct

```

```

SEQUENCE: 204
tcgtgcttcg gcaccagtac aatgatgatg gccagcaagg acgtccgag ta 52

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```

SEQ ID NO: 205      moltype = DNA length = 49
FEATURE            Location/Qualifiers
misc_feature        1..49

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source          note = Primer IF-(GI.7USA14)VP1.r
                1..49
                mol_type = other DNA
                organism = synthetic construct

SEQUENCE: 205
actaaagaaa ataggccttc acaccgcct cagccgagt cgtcgcacg      49

SEQ ID NO: 206      moltype = DNA length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer GI.7USA14_VP1(R84S).r
source             1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 206
agtggggtcc taagctgagg tcaaacagaa tatccctcgg ggtgttat      48

SEQ ID NO: 207      moltype = DNA length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                    note = Primer GI.7USA14_VP1(R84S).c
source             1..50
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 207
tattctgttt gacctcagct taggacccca ctggaacccc tttctgcttc      50

SEQ ID NO: 208      moltype = DNA length = 51
FEATURE            Location/Qualifiers
misc_feature        1..51
                    note = Primer GI.7USA14_VP1(M57I).r
source             1..51
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 208
aacgaaattg ttgattatcc acgggtcgat catattgact tggcctgcag t      51

SEQ ID NO: 209      moltype = DNA length = 48
FEATURE            Location/Qualifiers
misc_feature        1..48
                    note = Primer GI.7USA14_VP1(M57I).c
source             1..48
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 209
gatcgaccgg tggataatca acaatttcgt tcaggcacca gaaggaga      48

SEQ ID NO: 210      moltype = DNA length = 62
FEATURE            Location/Qualifiers
misc_feature        1..62
                    note = Primer GII.2CGMH11(A39V).r
source             1..62
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 210
tttgtctgcc cggtcacagg cactgcgagg gcagcccctg caacaggctc caaggccatc 60
ac                                                  62

SEQ ID NO: 211      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer GII.2CGMH11(A39V).c
source             1..59
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 211
gttgaggggg ctgccctgcg agtgccctgtg accgggcaga caaatatcat cgatccttg 59

SEQ ID NO: 212      moltype = DNA length = 59
FEATURE            Location/Qualifiers
misc_feature        1..59
                    note = Primer GII.2CGMH11(R53I).r
source             1..59
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 212

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cacgaaatta gcgataatcc aagatccgat gatattgtgc tgcccgggtca caggagctg	59
SEQ ID NO: 213	moltype = DNA length = 59
FEATURE	Location/Qualifiers
misc_feature	1..59
source	note = Primer GII.2CGMH11(R53I).c 1..59 mol_type = other DNA organism = synthetic construct
SEQUENCE: 213	
ggcgagacaaa tatcatcgat ccttgaggata tcgctaattt cgtgcaagcc ccaaatggg	59
SEQ ID NO: 214	moltype = DNA length = 53
FEATURE	Location/Qualifiers
misc_feature	1..53
source	note = Primer IF-GII17Kaw14VP1.c 1..53 mol_type = other DNA organism = synthetic construct
SEQUENCE: 214	
tcgtgcttcg gcaccagtac aatgaaatg gcattctaacg acgcagcccc ctc	53
SEQ ID NO: 215	moltype = DNA length = 56
FEATURE	Location/Qualifiers
misc_feature	1..56
source	note = Primer IF-GII17Kaw14VP1.r 1..56 mol_type = other DNA organism = synthetic construct
SEQUENCE: 215	
actaaagaaa ataggcctct actgagcccg gcgtctgccg ttaccgggtgc ccattg	56
SEQ ID NO: 216	moltype = DNA length = 59
FEATURE	Location/Qualifiers
misc_feature	1..59
source	note = Primer GII.17Kaw14(A90L).r 1..59 mol_type = other DNA organism = synthetic construct
SEQUENCE: 216	
gcggctcaga tgcagcagat atggattgag gtcagggccg agctcaagat tcaggagta	59
SEQ ID NO: 217	moltype = DNA length = 51
FEATURE	Location/Qualifiers
misc_feature	1..51
source	note = Primer GII.17Kaw14(A90L).c 1..51 mol_type = other DNA organism = synthetic construct
SEQUENCE: 217	
cctgacctca atccatatct gctgcactcg agccgcatgt acaatggtta c	51
SEQ ID NO: 218	moltype = DNA length = 59
FEATURE	Location/Qualifiers
misc_feature	1..59
source	note = Primer GII.17Kaw14(A39V).r 1..59 mol_type = other DNA organism = synthetic construct
SEQUENCE: 218	
attctgcctt gtcactggca cagctatagc ggcgctcgca accggctcta gtggaagtg	59
SEQ ID NO: 219	moltype = DNA length = 58
FEATURE	Location/Qualifiers
misc_feature	1..58
source	note = Primer GII.17Kaw14(A39V).c 1..58 mol_type = other DNA organism = synthetic construct
SEQUENCE: 219	
aggcgccgct atagctgtgc cagtgcacgg gcagaataat attatagacc cttggatt	58
SEQ ID NO: 220	moltype = DNA length = 59
FEATURE	Location/Qualifiers
misc_feature	1..59
	note = Primer GII.17Kaw14(R53I).r

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source                1..59
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 220
acgaagtttg tgataatcca aggggtctata atattattct gccctgtcac tggggcagc   59

SEQ ID NO: 221        moltype = DNA length = 59
FEATURE              Location/Qualifiers
misc_feature          1..59
                      note = Primer GII.17Kaw14(R53I).c
source                1..59
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 221
ggcagaataa tattatagac ccttggatta tcacaaactt cgtgcaggca cccaacggc   59

SEQ ID NO: 222        moltype = DNA length = 50
FEATURE              Location/Qualifiers
misc_feature          1..50
                      note = Primer GII.4Syd12(P80A).r
source                1..50
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 222
atcgggtccc aaggcggccg accacaggat ttctcctggc gcatttctcg           50

SEQ ID NO: 223        moltype = DNA length = 50
FEATURE              Location/Qualifiers
misc_feature          1..50
                      note = Primer GII.4Syd12(P80A).c
source                1..50
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 223
aatcctgtgg tcggccgctt tgggaccgga tctgaacccc tatttgtcac           50

SEQ ID NO: 224        moltype = DNA length = 50
FEATURE              Location/Qualifiers
misc_feature          1..50
                      note = Primer GII.4Syd12(P80N).r
source                1..50
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 224
atcgggtccc aagttggccg accacaggat ttctcctggc gcatttctcg           50

SEQ ID NO: 225        moltype = DNA length = 50
FEATURE              Location/Qualifiers
misc_feature          1..50
                      note = Primer GII.4Syd12(P80N).c
source                1..50
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 225
aatcctgtgg tcggccaact tgggaccgga tctgaacccc tatttgtcac           50

SEQ ID NO: 226        moltype = DNA length = 50
FEATURE              Location/Qualifiers
misc_feature          1..50
                      note = Primer GII.4Syd12(P80K).r
source                1..50
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 226
atcgggtccc aacttgccg accacaggat ttctcctggc gcatttctcg           50

SEQ ID NO: 227        moltype = DNA length = 50
FEATURE              Location/Qualifiers
misc_feature          1..50
                      note = Primer GII.4Syd12(P80K).c
source                1..50
                      mol_type = other DNA
                      organism = synthetic construct

SEQUENCE: 227
aatcctgtgg tcggccaagt tgggaccgga tctgaacccc tatttgtcac           50

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SEQ ID NO: 228	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer GII.4Syd12 (P80H) .r	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 228		
atcgggtccc aagtgggccc accacaggat ttctcctggc gcattttctcg		50
SEQ ID NO: 229	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
misc_feature	1..50	
	note = Primer GII.4Syd12 (P80H) .c	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 229		
aatcctgtgg tcggcccact tgggacccga tctgaacccc tatttgtcac		50
SEQ ID NO: 230	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GII.4Syd12 (A39I) .r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 230		
gaccggccac ggggattgct atggctgcgc ccaccacagg ctccagggcc atca		54
SEQ ID NO: 231	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GII.4Syd12 (A39I) .c	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 231		
gggcgcagcc atagcaatcc cctgggccgg tcagcagaat gtgattgacc cgtg		54
SEQ ID NO: 232	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GII.4Syd12 (A39M) .r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 232		
gaccggccac gggcattgct atggctgcgc ccaccacagg ctccagggcc atca		54
SEQ ID NO: 233	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GII.4Syd12 (A39M) .c	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 233		
gggcgcagcc atagcaatgc cctgggccgg tcagcagaat gtgattgacc cgtg		54
SEQ ID NO: 234	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GII.4Syd12 (A39G) .r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 234		
gaccggccac ggggcctgct atggctgcgc ccaccacagg ctccagggcc atca		54
SEQ ID NO: 235	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GII.4Syd12 (A39G) .c	
source	1..54	
	mol_type = other DNA	

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                                organism = synthetic construct
SEQUENCE: 235
gggcgcagcc atagcaggcc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 236                moltype = DNA length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GII.4Syd12 (A39S) .r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 236
gaccggccac ggggcttgct atggctgccc ccaccacagg ctccagggcc atca      54

SEQ ID NO: 237                moltype = DNA length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GII.4Syd12 (A39S) .c
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 237
gggcgcagcc atagcaagcc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 238                moltype = DNA length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GII.4Syd12 (A39E) .r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 238
gaccggccac gggctctgct atggctgccc ccaccacagg ctccagggcc atca      54

SEQ ID NO: 239                moltype = DNA length = 49
FEATURE                      Location/Qualifiers
misc_feature                  1..49
                                note = Primer GII.4Syd12 (A39E) .c
source                        1..49
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 239
gggcgcagcc atagcagagc ccgtggccgg tcagcagaat gtgattgac          49

SEQ ID NO: 240                moltype = DNA length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GII.4Syd12 (A39D) .r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 240
gaccggccac ggggtctgct atggctgccc ccaccacagg ctccagggcc atca      54

SEQ ID NO: 241                moltype = DNA length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GII.4Syd12 (A39D) .c
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 241
gggcgcagcc atagcagacc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 242                moltype = DNA length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GII.4Syd12 (A39N) .r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 242
accggccacg gggtttgcta tggctgccc caccacaggc tccagggcca tcac      54

SEQ ID NO: 243                moltype = DNA length = 54
FEATURE                      Location/Qualifiers

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misc_feature      1..54
                  note = Primer GII.4Syd12 (A39N) .c
source            1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 243
gggcgcagcc atagcaaacc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 244      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GII.4Syd12 (A39Q) .r
source              1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 244
gaccggccac gggctgtgct atggctgcgc ccaccacagg ctccagggcc atca      54

SEQ ID NO: 245      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GII.4Syd12 (A39Q) .c
source              1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 245
gggcgcagcc atagcacagc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 246      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GII.4Syd12 (A39K) .r
source              1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 246
gaccggccac gggctttgct atggctgcgc ccaccacagg ctccagggcc atca      54

SEQ ID NO: 247      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GII.4Syd12 (A39K) .c
source              1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 247
gggcgcagcc atagcaaagc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 248      moltype = DNA length = 51
FEATURE            Location/Qualifiers
misc_feature        1..51
                  note = Primer GII.4Syd12 (A39H) .r
source              1..51
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 248
gaccggccac ggggtgtgct atggctgcgc ccaccacagg ctccagggcc a      51

SEQ ID NO: 249      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GII.4Syd12 (A39H) .c
source              1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 249
gggcgcagcc atagcacacc ccgtggccgg tcagcagaat gtgattgacc cgtg      54

SEQ ID NO: 250      moltype = DNA length = 50
FEATURE            Location/Qualifiers
misc_feature        1..50
                  note = Primer GI.7USA14_VP1 (M57L) .r
source              1..50
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 250

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gaacgaaatt gttcagtatc cacgggtcga tcatattgac ttggcctgca	50
SEQ ID NO: 251	moltype = DNA length = 48
FEATURE	Location/Qualifiers
misc_feature	1..48
	note = Primer GI.7USA14_VP1(M57L).c
source	1..48
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 251	
gatcgaccgcg tggatactga acaatttcgt tcaggcacca gaaggaga	48
SEQ ID NO: 252	moltype = DNA length = 52
FEATURE	Location/Qualifiers
misc_feature	1..52
	note = Primer GI.7USA14_VP1(M57G).r
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 252	
gaacgaaatt gttgcctatc cacgggtcga tcatattgac ttggcctgca gt	52
SEQ ID NO: 253	moltype = DNA length = 48
FEATURE	Location/Qualifiers
misc_feature	1..48
	note = Primer GI.7USA14_VP1(M57G).c
source	1..48
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 253	
gatcgaccgcg tggataggca acaatttcgt tcaggcacca gaaggaga	48
SEQ ID NO: 254	moltype = DNA length = 52
FEATURE	Location/Qualifiers
misc_feature	1..52
	note = Primer GI.7USA14_VP1(M57S).r
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 254	
gaacgaaatt gttgcttatac cacgggtcga tcatattgac ttggcctgca gt	52
SEQ ID NO: 255	moltype = DNA length = 48
FEATURE	Location/Qualifiers
misc_feature	1..48
	note = Primer GI.7USA14_VP1(M57S).c
source	1..48
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 255	
gatcgaccgcg tggataagca acaatttcgt tcaggcacca gaaggaga	48
SEQ ID NO: 256	moltype = DNA length = 52
FEATURE	Location/Qualifiers
misc_feature	1..52
	note = Primer GI.7USA14_VP1(M57T).r
source	1..52
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 256	
gaacgaaatt gttggttatc cacgggtcga tcatattgac ttggcctgca gt	52
SEQ ID NO: 257	moltype = DNA length = 48
FEATURE	Location/Qualifiers
misc_feature	1..48
	note = Primer GI.7USA14_VP1(M57T).c
source	1..48
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 257	
gatcgaccgcg tggataacca acaatttcgt tcaggcacca gaaggaga	48
SEQ ID NO: 258	moltype = DNA length = 52
FEATURE	Location/Qualifiers
misc_feature	1..52
	note = Primer GI.7USA14_VP1(M57N).r

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source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 258		
gaacgaaatt gttgtttatc cacgggtcga tcatattgac ttggcctgca gt		52
SEQ ID NO: 259	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer GI.7USA14_VP1(M57N) .c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 259		
gatcgaccgg tggataaaca acaatttcgt tcaggcacca gaaggaga		48
SEQ ID NO: 260	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer GI.7USA14_VP1(M57Q) .r	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 260		
gaacgaaatt gttctgtatc cacgggtcga tcatattgac ttggcctgca gt		52
SEQ ID NO: 261	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer GI.7USA14_VP1(M57Q) .c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 261		
gatcgaccgg tggatacaga acaatttcgt tcaggcacca gaaggaga		48
SEQ ID NO: 262	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer GI.7USA14_VP1(M57K) .r	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 262		
gaacgaaatt gttctttatc cacgggtcga tcatattgac ttggcctgca gt		52
SEQ ID NO: 263	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer GI.7USA14_VP1(M57K) .c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 263		
gatcgaccgg tggataaaga acaatttcgt tcaggcacca gaaggaga		48
SEQ ID NO: 264	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
misc_feature	1..52	
	note = Primer GI.7USA14_VP1(M57H) .r	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 264		
gaacgaaatt gttgtgtatc cacgggtcga tcatattgac ttggcctgca gt		52
SEQ ID NO: 265	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
misc_feature	1..48	
	note = Primer GI.7USA14_VP1(M57H) .c	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 265		
gatcgaccgg tggatacaca acaatttcgt tcaggcacca gaaggaga		48

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SEQ ID NO: 266	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94V).r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 266		
tctgagccaa gtgcaccaga aacggattca agtgtggtcc tagctgcagg tcaa		54
SEQ ID NO: 267	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94V).c	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 267		
cttgaatccg tttctggtgc acttggtcga gatgtataat ggatgggttg gaaa		54
SEQ ID NO: 268	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94I).r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 268		
tctgagccaa gtggatcaga aacggattca agtgtggtcc tagctgcagg tcaa		54
SEQ ID NO: 269	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94I).c	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 269		
cttgaatccg tttctgatcc acttggtcga gatgtataat ggatgggttg gaaa		54
SEQ ID NO: 270	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94M).r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 270		
tctgagccaa gtgcatcaga aacggattca agtgtggtcc tagctgcagg tcaa		54
SEQ ID NO: 271	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94M).c	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 271		
cttgaatccg tttctgatgc acttggtcga gatgtataat ggatgggttg gaaa		54
SEQ ID NO: 272	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94T).r	
source	1..54	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 272		
tctgagccaa gtgggtcaga aacggattca agtgtggtcc tagctgcagg tcaa		54
SEQ ID NO: 273	moltype = DNA length = 54	
FEATURE	Location/Qualifiers	
misc_feature	1..54	
	note = Primer GI.3Lil08(S94T).c	
source	1..54	
	mol_type = other DNA	

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                                organism = synthetic construct
SEQUENCE: 273
cttgaatccg tttctgaccc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 274                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94E).r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 274
tctgagccaa gtgctccaga aacggattca agtgtggtcc tagctgcagg tcaa      54

SEQ ID NO: 275                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94E).c
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 275
cttgaatccg tttctggagc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 276                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94D).r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 276
tctgagccaa gtggtccaga aacggattca agtgtggtcc tagctgcagg tcaa      54

SEQ ID NO: 277                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94D).c
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 277
cttgaatccg tttctggacc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 278                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94N).r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 278
tctgagccaa gtggttcaga aacggattca agtgtggtcc tagctgcagg tcaa      54

SEQ ID NO: 279                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94N).c
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 279
cttgaatccg tttctgaacc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 280                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers
misc_feature                  1..54
                                note = Primer GI.3Lil08(S94Q).r
source                        1..54
                                mol_type = other DNA
                                organism = synthetic construct
SEQUENCE: 280
tctgagccaa gtgctgcaga aacggattca agtgtggtcc tagctgcagg tcaa      54

SEQ ID NO: 281                moltype = DNA  length = 54
FEATURE                      Location/Qualifiers

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misc_feature      1..54
                  note = Primer GI.3Lil108(S94Q).c
source            1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 281
cttgaatccg tttctgcagc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 282      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GI.3Lil108(S94K).r
source            1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 282
tctgagccaa gtgcttcaga aacggattca agtgtggtcc tagctgcagg tcaa      54

SEQ ID NO: 283      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GI.3Lil108(S94K).c
source            1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 283
cttgaatccg tttctgaagc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 284      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GI.3Lil108(S94H).r
source            1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 284
tctgagccaa gtggtgcaga aacggattca agtgtggtcc tagctgcagg tcaa      54

SEQ ID NO: 285      moltype = DNA length = 54
FEATURE            Location/Qualifiers
misc_feature        1..54
                  note = Primer GI.3Lil108(S94H).c
source            1..54
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 285
cttgaatccg tttctgcacc acttggtcga gatgtataat ggatgggttg gaaa      54

SEQ ID NO: 286      moltype = AA length = 540
FEATURE            Location/Qualifiers
VARIANT            80
                  note = X may be Ala, Asn, Lys or His
source            1..540
                  mol_type = protein
                  note = Norovirus
                  organism = unidentified

SEQUENCE: 286
MKMASSDANP SDGSAANLVP EVNNEVMALE PVVGAAIAAP VAGQQNVIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAX LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNPPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSPV VLTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTEEIPAP LGTPDFVGKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPYSYG RNTHNVHLAP 420
AVAPTFFGEQ LLFFRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAPPAQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTVA HTGQHDLVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRAV 540

SEQ ID NO: 287      moltype = DNA length = 1623
FEATURE            Location/Qualifiers
misc_feature        1..1623
                  note = Nucleic acid sequence of human codon optimized VP1
                  GII.4_Syd12_P80X
source            1..1623
                  mol_type = other DNA
                  organism = synthetic construct

SEQUENCE: 287

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atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcgcaa tcttgtgcct 60
gaggttaata atgaggtgat ggccttggag cctgtggtgg gcgcagccat agcagcgccc 120
gtggccggtc agcagaatgt gattgacccg tggatacgca acaattttgt ccaagcccct 180
ggtggggagt tcaccgttat cccgagaaat gcgccaggag aaatcctgtg gtcggccvms 240
ttgggacccg atctgaaccc ctatttgtca catctcgctc gtagtgacaa cgggtatgcc 300
ggcggatttg aagtgcaggt gattctggct gggaacgcgt tcaactgtcg caaagtgtac 360
tttgacagcg tgcctcccaa ctccccact gaaggactgt ctccaagcca ggtcacatg 420
tttcacacac tcgtgggtgga cgtacggcag cttagagcctg tcttgattcc cctccctgat 480
gtacgcaata atttotacca ctacaataca tccaatgata cgaccattaa actcatcgcg 540
atgttgtaca cccctctgcg cgctaacaat gctggagacg acgtattcac cgtgtcatgc 600
agagtgtcca ccagaccttc accagacttt gactttatct tcttagtgcc ccccaactgt 660
gagagccgaa ccaagccctt tagtgtcccc gtactcacag tcgaggagat gacaaatagc 720
cgctttccaa tcccccttga gaaactgttc acaggacctt cctcgccatt cgtggttcag 780
ccacagaacg gacgtgcac aactgacggc gtgctgctcg gaaccaccca gcttagccct 840
gttaatatct gtacgtttag agcgacgta actcacataa ctggctcacg gaactatacc 900
atgaatctgg catcacagaa ttggaatgac tacgacccaa ccgaagagat tcccgacct 960
cttggaaacc ccgactttgt gggaaaaata caggcgctcc tgacacaaac caccagaacc 1020
gatggctcca cacggggaca caaggcaacc gtctacactg gctctgcgca ttttgccccg 1080
aaactgggta gagtgcagtt tgagaccgac actgacccgg actttgaagc caatcagaat 1140
actaagttca cacctgtagg agtgattcag gacgggggca ccaactcacg gaacgagccg 1200
caacaatggg tccctgcctc ttatagcggg aggaatactc ataattgtca tttggtcct 1260
gcagtggttc ccaactttcc cggggaacaa ctgctctttt ttcgttcaac catgctgga 1320
tgctccggat atcccaatat ggatctcgat tgcctgtctc cacagggaat ggtgcagtat 1380
ttttatcaag aggcgcgacc agcccaatcc gacgtcgcac ttctgcggtt cgtgaatcca 1440
gacacaggcc gcgtgttgtt tgagtgcaca caggatacgt tacagtggct 1500
catactggac ggtgatccca cccaacggat attttagggt cgactcctgg 1560
gtgaatcagt tttatacatt agcccccatg gggaatggga ctggcagacg cagggtctgc 1620
tga
1623

SEQ ID NO: 288      moltype = AA  length = 540
FEATURE            Location/Qualifiers
VARIANT            39
                    note = X may be Ile, Met, Gly, Ser, Glu, Asp, Asn, Gln, Lys
                    or His
source              1..540
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

SEQUENCE: 288
MKMASSDANP SDGSAANLVP EVNNEVMALP PVVGAAIAXP VAGQONVIDP WIRNNFVQAP 60
GGEFTVSPRN APGEILWSAS LGPDLNPYLS HLARMYNGYA GGFEVQVILA GNAFTAGKVI 120
FAAVPPNFPT EGLSPSQVTM FPHIVVDVRQ LEPVLIPLPD VRNNFYHYNQ SNDPTIKLIA 180
MLYTPLRANN AGDDVFTVSC RVLTRPSPDF DFIFLVPPTV ESRTKPFSPV VLTVEEMTNS 240
RFPIPLEKLF TGPSSAFVVQ PQNGRCTTDG VLLGTTQLSP VNICTFRGDV THITGSRNYT 300
MNLASQNWND YDPTEEIPAP LGTPDFVVKI QGVLTQTTRT DGSTRGHKAT VYTGSADFAP 360
KLGRVQFETD TDRDFEANQN TKFTPVGVQI DGGTTHRNEP QQWVLPYSYG RNTHNHVLAP 420
AVAPTFPGEQ LLFFRSTMPG CSGYPNMDLD CLLPQEWVQY FYQEAAPQS DVALLRFVNP 480
DTGRVLFECK LHKSGYVTVA HTQHDLVIP PNGYFRFDSW VNQFYTLAPM GNGTGRRRRAV 540

SEQ ID NO: 289      moltype = DNA  length = 1620
FEATURE            Location/Qualifiers
misc_feature        1..1620
                    note = hCod optimize sequence of VP1 GII.4_Syd12_P80S+A39X
source              1..1620
                    mol_type = other DNA
                    organism = synthetic construct

SEQUENCE: 289
atgaaaaatgg cctcgagtga cgctaaccct agtgacggca gcgcgcgcaa tcttgtgcct 60
gaggttaata atgaggtgat ggccttggag cctgtggtgg gcgcagccat agcavdsgtg 120
gccggtcagc agaattgtgat tgaccctgtg atacgcaaca attttgtcca agcccctggt 180
ggggagttca ccgttagccc ccaggagaaa tctgtgtggt gccagctgtg 240
ggaccccgatc tgaaccccta tttgtcacat ctgcctcgga tgtacaacgg gtatgccggc 300
ggatttgaag tgcaggtgat tctggctggg aacgcgttca ctgtggcaca agtgatcttt 360
gcagcgggtgc cctcccaact ccccaactgaa ggactgtctc caagccaggt cacaatgttt 420
ccacacatcg tgggtggacgt accgcagcta gagcctgtcc tgattcccc ccttgatgta 480
cgcaataatt tctaccacta caatcaatcc aatgatccga ccattaaact catcgcgatg 540
ttgtacaccc ctctgcgcgc taacaatgct ggagacgacg tattcacctg gtcattgcaga 600
gtgctcaccg gaccttcacc agactttgac ttatcttct tagtgcccc cactgttgag 660
agccgaacca agcccttttag tgtccccgta ctacacgtcg aggagatgac aaatagccgc 720
tttccaatcc cctttagaaa actgttccaa ggaccttctc cggcattcgt ggttcagcca 780
cagaacggac cgtgcacaa ctgacggcgtg ctgctcgga ccaccagct tagccctgtt 840
aatatctgta cgttttagag cgacgtaact cacataactg gctcacggaa ctataccatg 900
aatctggcat cacagaattg gaatgactac gacccaaccc aagagattcc cgcacctctt 960
ggaacccccg actttgtggg aaaaatacag ggcgtcctga cacaacccac cagaaccgat 1020
ggctccacac agggacacaa ggcaaccgtc tacactggct ctgcccattt tgccccgaaa 1080
ctgggttagag tgcagtttga gaccgacact gaccgggact ttgaagccaa tcagaatact 1140

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aagttcacac ctgtaggagt gattcaggag gggggcacca ctcaccggaa cgagccgcaa 1200
caatgggtcc tgccctctta tagcgggagg aatactcata atgtgcattt ggctcctgca 1260
gtggctccca cgtttcccg ggaacaactg ctcttttttc gttcaacccat gcctggatgc 1320
tccggatata ccaatatgga tctcgattgc ctgctcccac aggaatgggt gcagtatttt 1380
tatcaagagg ccgcaccagc ccaatccgac gtcgcacttc tgcggttcgt gaatccagac 1440
acaggcccgcg tgttggttga gtgcaaatg cacaatcag gatacgttac agtggctcat 1500
actggacagc atgacctggg gatccacccc aacggatatt ttaggttcga ctctgggtg 1560
aatcagtttt atacattagc ccccatgggg aatgggactg gcagacgcag ggctgtctga 1620

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SEQ ID NO: 290      moltype = AA length = 538
FEATURE            Location/Qualifiers
VARIANT            57
                    note = X may be Leu, Gly, Ser, Thr, Asn, Gln, Lys or His
source             1..538
                    mol_type = protein
                    note = Norovirus
                    organism = unidentified

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SEQUENCE: 290
MMASKDAPS NMDGTSGAGQ LVPEVNAAEP LPLEPVVGAA TAVATAGQVN MIDPWIXNNF 60
VQAPEGEFTI SPNNTPGDIL FDLRLGPHLN PFLHLHSQMY NGWVGNMVRV VMLAGNAFSA 120
GKIIICCVPP GFESQNISIG QATMFPHVIA DVRVLEPIEV PLDDVRNVLF HTNENRPTMR 180
LLCMLYTPLR AGGASSGTD PVIAGRVLTC PAPDFNFLFL VPPSVEQKTR QLTIPNIPLN 240
NLANSRVPAM INKMTVSADQ NQVVQFQNGR CTLEGQLLGT TPVSANQVAR IRGKVFSTNS 300
GTGLNLTEVD GTPYHAFESP APLGFDPDIGN CDWHVYAFKV NQNTGDPMYR LDITQGNBSFA 360
PHLGSIEFSS ENHPSGQDLG TLTWISPLNN ASRVDPWKIP TYGSTLTEST NLAPPIFPPG 420
FGEAIVYFMS DPFIVSGNTA QIPCTLPQEF VSSFVEQQAP IRGEAALLHY VDPDTHRNLG 480
EFKLYPDGFI TCVPTNGGGP QNLPSNGVFV FSSWVSRYQ LKPVGTTGPV RRLGVRRV 538

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SEQ ID NO: 291      moltype = DNA length = 1614
FEATURE            Location/Qualifiers
misc_feature        1..1614
                    note = Human codon optimized VP1_GI.7/GA5043/USA/2014_M57x
source              1..1614
                    mol_type = other DNA
                    organism = synthetic construct
variation           170
                    note = a, g, c or t

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SEQUENCE: 291
atgatgatgg ccagcaagga cgctccgagt aacatggagc gcacttcggg cgcggggcag 60
ctgggtcccg aggtcaatgc ccagaaacca ctctctcttg agcccgctgt tggcgccgcc 120
acagctgtcg ccaactgcagg ccaagtcaat atgatcgacc cgtggatavn saatttcgtt 180
caggcaccag aaggagaatt caccatctcc cccaataaca cccaggggga tattctgttt 240
gacctcaggt taggacccca ctggaacccc ttctgtcttc atctctcaca aatgtataat 300
ggctgggtcg ggaatatgag cgtgcgggtg atgctagccg gcaatgcttt ttctgcaggc 360
aagattatca tttgctcggt tcctctctga ttgcaatctc aaaatatcag cattgtgtca 420
gcaaccatgt ttccacatgt gatcgctgat gttcgcgtcc tggaaacccat tgaagttcct 480
ctcgacgacg tgagaaatgt tctcttcacc accaacgaga ataggccgac tatgagactt 540
ctgtgtatgc tctacacccc attaagagcc gggggagcat cctcaggtag tgaccatttt 600
gtgatttcgg ggcgggtgct cacatgcccg gctccagact ttaacttcct ttctttggtg 660
ccaccacagt ttgaacagaa aaccagacag ctcaccatcc caaatatccc attgaacaat 720
ctcgccaaca gcagggtgcc agcaatgata aacaaaatga cagtcagtag tgaccagaac 780
caggtatgtc agtttcagaa cggcagatgc acgcttgagg gccaaactgct tgggacgacc 840
ccagttctcg cgaaccaggt ggcgccgaat cgggggtaaa tcttcagtag aaactccggc 900
actggcctta acctcacaga ggttgacggc actccctatc atgcttttga gtctccagcc 960
cctcttggtc ttcccgatat agtcaactgt gactggcacg tttatgcgtt taaagtaaac 1020
cagaacaccc ggcatactat gtataggttg gatataaac aaggtaatte attcgcccca 1080
cacttgggta gcatcgaggt cagttcagag aaccatccga gtggtgatca gctaggcaca 1140
ttgacgtgga tcagccctct caataacgca tcaagagtgg atccctggaa gatccctacc 1200
tatgggtcca ctctgacaga gacacaaaat ttggtccgag ccattttccc acccggtatt 1260
ggcgaggcca tagtgtactt tatgtctgac ttctctatcg tcagcgggaa tacagcccag 1320
attccttgca cactgccaca agaattcgct tcatcctttg tagagcagca ggcacctatt 1380
cgaggtgagg ccgccctctt gcactacgtg gacctgaca cccaccgcaa tcttgccgag 1440
tttaagctgt acctgacagg gtttattacc tgtgtaccca acaccggcgg cggccccaca 1500
aatgtgcca gcaatggcgt gtttgtcttt tcctcttggt tgtctcgata ctaccagctt 1560
aaactgtcgc gaactacggg ccccgtcgca cgactcggcg tgaggcgggt gtga 1614

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SEQ ID NO: 292      moltype = AA length = 543
FEATURE            Location/Qualifiers
VARIANT            94
                    note = X may be Val, Ile, Met, Thr, Glu, Asp, Asn, Gln, Lys
                    or His
source             1..543
                    mol_type = protein
                    organism = unidentified

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SEQUENCE: 292
MMASKDAPT NMDGTSGAGQ LVPEVSTAEP ISMEPVAGAA TAAATAGQVN MIDPWIMSNY 60

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VQAPQGEFTI	SPNNTPGDIL	FDLQLGPHLN	PFLXHLAQMY	NGWVGNMKVR	VLLAGNAFTA	120
GKIIISCVPP	GFAAQNVSIA	QATMFPHVIA	DVRVLEPIEV	PLEDVNRNLF	HNNDSTPTMR	180
LICMLYTPLR	ASGSSSGTDP	FVIAGRVLTC	PSPDFNLFLE	VPPNVEQKTK	PFSVPNLPLN	240
VLSNSRVPSL	IKSMMVSDH	QMVQFQNGR	VTLDGQLQGT	TPTSASQLCK	IRGTVYHATG	300
GQGLNLTEID	GTPYHAFESP	APIGFPDLGE	CDWHINASPA	NAFTDGSIIH	RIDVAQDSTF	360
APHLGTIHYT	NADYNANVGL	ICSLEWLSPP	SGGAPKVNFW	AIPRYGSTLT	EAAQLAPPIY	420
PPGFGEAIVF	FMSDFPIANG	SDGLSVPCIT	PQEFVTHFVN	EQAPTRGEAA	LLHYVDPDTH	480
RNLGEFKLYP	EGFMTCPVNS	SGSGPQTLPI	NGVFTFISWV	SRFYQLKPVG	TTGPVRRLLGI	540
RRS						543

SEQ ID NO: 293	moltype = DNA	length = 1632
FEATURE	Location/Qualifiers	
misc_feature	1..1632	
	note = hCod optimized VP1_GI.3_Lil08_S94x	
source	1..1632	
	mol_type = other DNA	
	organism = synthetic construct	

SEQUENCE: 293	
atgatgatgg	cttccaagga
cttgtgccgg	aggtgtccac
actgctgccg	ccaccgcagg
gttcaaggctc	cacaggggga
tttgacctgc	agctaggacc
aatggatggg	tttgaaacat
gggaagatta	ttatctcttg
caggcaacca	tgtttccgca
ccccctgagg	acgtgcgcaa
ttgatatgta	tggtatatac
tttgtgattg	gtggcggggt
gtgctcccaa	atgtagaaca
gtgctgtcga	attcccgagt
gggtcaaatgg	tgacagtttc
accccaacca	gtgccagtcg
ggacaggggc	tgaaatctac
gcacctattg	gatttccgga
aacgctttca	cagacgggtc
gcccgcaacc	tggtatcacg
atctgtagcc	ttagatgggt
gctattccct	ggtagcggtc
ccaccaggat	tcggggaagc
tcagatggcc	ttagtgtccc
gagcaggctc	ctactcgggg
agaaacctgg	gcgaattcaa
tcgggcagtg	gccctcaaac
tcacgggttt	accaaactca
agacggagct	ag

1. A norovirus VP1 protein comprising one or more than one amino acid substitution at a position in sequence alignment with amino acids 43, 57, 84 and 94 of reference sequence SEQ ID NO:1, wherein:

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

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

the 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

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

2. The norovirus VP1 protein of claim 1, wherein the 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.

3. The norovirus VP1 protein of claim 1,

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

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

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

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

4. A recombinant polynucleotide encoding the norovirus VP1 protein of claim 1.

5. A virus-like particle (VLP) comprising the norovirus VP1 of claim 1.

6. The VLP of claim 5, further comprising a norovirus VP2 protein.

7. A method of producing a norovirus VP1 protein, or a VLP comprising the norovirus VP1 protein, in a plant, portion of a plant or a plant cell, the method comprising: introducing the recombinant polynucleotide of claim 4; and

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

8. The method of claim 7, wherein the method further comprises a step of harvesting the plant, portion of the plant, or the plant cell.

9. The method of claim 7, 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.

10. The method of claim 8, wherein the method further comprises a step of:

extracting, purifying, or both extracting and purifying the norovirus VP 1 protein, or

extracting, purifying, or both extracting and purifying the virus-like particle (VLP) from the plant, the portion of the plant or the plant cell, wherein the VLP comprises the norovirus VP1 protein.

11. A norovirus virus like particle (VLP) produced by the method of claim 7.

12. A method of producing an antibody or antibody fragment comprising, administering the norovirus VP1 protein of claim 1 to a subject, or a host animal, thereby producing the antibody or the antibody fragment.

13. A method of producing an antibody or an antibody fragment comprising, administering the VLP of claim 5 to a subject, or a host animal, thereby producing the antibody or the antibody fragment.

14. A plant, portion of the plant, or plant cell comprising the norovirus VP1 protein of claim 1.

15. A plant, portion of the plant, or plant cell comprising the VLP of claim 5.

16. A plant, portion of the plant, or plant cell comprising the recombinant polynucleotide of claim 4.

17. A composition for inducing an immune response comprising, an effective dose of the norovirus VP1 protein of claim 1, and a pharmaceutically acceptable carrier, adjuvant, vehicle or excipient.

18. A composition for inducing an immune response comprising, an effective dose of the VLP of claim 6, and a pharmaceutically acceptable carrier, adjuvant, vehicle or excipient.

19. A vaccine comprising an effective dose of the norovirus VP1 protein of claim 1, for inducing an immune response.

20. An antibody or antibody fragment prepared by administering the norovirus VP1 protein of claim 1 to a subject, or host animal.

21. An antibody or antibody fragment prepared by administering the VLP claim 5 to a subject, or host animal.

22. A method for inducing immunity to a norovirus infection in a subject, the method comprising administering the VLP of claim 5 to the subject.

23. The method of claim 22, wherein the VLP is administered to the subject orally intranasally, intramuscularly, intraperitoneally, intravenously, subcutaneously, rectally, or intravaginally.

24. A vaccine comprising an effective dose of the VLP of claim 5, for inducing an immune response.

25. 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 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.

* * * * *