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- (54) **RECOMBINANT MULTIVALENT INFLUENZA VIRUSES**
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CPC *A61K 39/295* (2013.01); *A61K 39/145* (2013.01); *A61K 39/215* (2013.01); *A61P 31/14* (2018.01); *A61P 31/16* (2018.01); *C07K 14/005* (2013.01); *C12N 7/00* (2013.01); *A61K 2039/5254* (2013.01); *A61K 2039/5256* (2013.01); *A61K 2039/55* (2013.01); *A61K 2039/70* (2013.01); *C07K 2319/03* (2013.01); *C12N 2760/16121* (2013.01); *C12N 2760/16122* (2013.01); *C12N 2760/16134* (2013.01); *C12N 2760/16171* (2013.01); *C12N 2770/18021* (2013.01); *C12N 2770/18022* (2013.01); *C12N 2770/18034* (2013.01); *C12N 2770/18071* (2013.01)

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None
See application file for complete search history.

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(57) **ABSTRACT**

The invention provides a composition useful to prepare influenza vaccine viruses, e.g., in the absence of helper virus, which includes internal viral segments from an influenza virus vaccine strain or isolate, e.g., one that is safe in humans, for instance, one that does not result in significant disease, and encodes a heterologous antigen.

16 Claims, 58 Drawing Sheets

Specification includes a Sequence Listing.

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PRB(CAMBRIDGE)

PB2

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GTGAGCATTGACCGGTTCTTGAGAGTCAGGGACCAACGAGGAAATGTACTACTGTCTCCCGAGGAGGTCAGTGAAACACAGGGA
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TTTCAGTCTTTAGTACCTAAGGCCATTAGAGGCCAATACAGTGGGTTTGTAAAGAACTCTGTTCCAACAAATGAGGGATGTGCTT
GGGACATTTGATACCGCACAGATAATAAACTTCTTCCCTTCGCAGCCGCTCCACCAAAGCAAAGTAGAATGCAGTTCTCCTCA
TTTACTGTGAATGTGAGGGGATCAGGAATGAGAATACTTGTAAGGGGCAATTCTCCTGTATTCAACTACAAACAAGGCCACGAAG
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Fig. 1A

(SEQ ID NO:11)

PR8(CAMBRIDGE)

PB1

AGCGAAAGCAGGCAAACCATTTGAATGGATGTCAATCCGACCTTACTTTTCTTAAAAGTGCCAGCACAAAATGCTATAAGCACAACTTTCCCTTATACCGGAGACCCTCCTTACAGCCATGGGACAGGAACAGGATACACCATGGATACTGTCAACAGGACACATCAGTACTCAGAAAAGGGAAGATGGACAACAAACACCGAAAAGTGGAGCACCGCAACTCAACCCGATTGATGGGCCACTGCCAGAAGACAATGAACCAAGTGGTTATGCCCAAACAGATTGTGTATTGGAAGCAATGGCTTTCTTTGAGGAATCCCATCCTGGTATTTTTGAAACTCGTGTATTGAAACGATGGAGGTTGTTGAGCAAACACGAGTAGACAAGCTGACACAAGGCCGACAGACCTATGACTGGACTTTAAATAGAAAACGAGCCTGCTGCAACAGCATTGGCCAAACACAATAGAAGTGTTGAGATCAAATGGCCTCACGGCCAATGAGTCAAGGAAGGCTCATAGACTTCCTTAAGGATGTAATGGAGTCAATGAAAAAGAAAGAAATGGGGATCACAACTCATTTCAGAGAAAGAGACGGGTGAGAGACAATATGACTAAGAAAATGATAACACAGAGAACAAATAGGTAAAAGGAAACAGAGATTGAACAAAAGGGGTATCTAATTAGAGCATTGACCCTGAACACAATGACCAAAGATGCTGAGAGAGGGGAAGCTAAAACGGAGAGCAATTGCAACCCCAAGGATGCAAAATAAGGGGGTTTGTATACTTTGTTGAGACACTGGCAAGGAGTATATGTGAGAACTTGAACAATCAGGGTTGCCAGTTGGAGGCAATGAGAAGAAAGCAAAGTTGGCAAATGTTGTAAGGAAGATGATGACCAATTCTCAGGACACCGAACTTTCTTTCACCATCACTGGAGATAACACCAAATGGAACGAAAATCAGAATCCTCGGATGTTTTTGGCCATGATCACATATATGACCAGAAATCAGCCCGAATGGTTGAGAAATGTTCTAAGTATTGCTCCAATAATGTTCTCAAAACAAAATGGCGAGACTGGGAAAAGGGTATATGTTTGAGAGCAAGAGTATGAAACTTAGAACTCAAATACCTGCAGAAATGCTAGCAAGCATTGATTTGAAATATTTCAATGATTCAACAAGAAAGAAGATTGAAAAAATCCGACCGCTCTTAATAGAGGGGACTGCATCATTGAGCCCTGGAATGATGATGGGCATGTTCAATATGTTAAGCACTGTATTAGGCGTCTCCATCCTGAATCTTGGACAAAAGAGATACACCAAGACTACTTACTGGTGGGATGGTCTTCAATCCTCTGACGATTTTGCTCTGATTGTGAATGCACCCAATCATGAAGGGATTCAAGCCGGAGTCGACAGGTTTTATCGAACCTGTAAGCTACTTGGAATCAATATGAGCAAGAAAAAGTCTTACATAAACAGAACAGGTACATTTGAATTCACAAGTTTTTCTATCGTTATGGGTTTGTGGCAATTTGAGCATGGAGCTTCCAGTTTTGGGGTGTCTGGGATCAACGAGTCAGCGGACATGAGTATTGGAGTTACTGTCAAAAAACAATATGATAAAACAATGATCTTGGTCCAGCAACAGCTCAAATGGCCCTTCAGTTGTTCAACAAGATTACAGGTACACGTACCGATGCCATAGAGGTGACACACAAATACAAACCCGAAGATCATTGAAATAAAGAAACTGTGGGAGCAAACCCGTTCCAAAGCTGGACTGCTGGTCTCCGACGGAGGCCCAAATTTATACAACATTAGAAATCTCCACATTCCTGAAATGCTGCCTAAAATGGGAATTGATGGATGAGGATTACCAGGGGCGTTTATGCAACCCACTGAACCCATTTGTGAGCCATAAAGAAATTGAATCAATGAACAATGCAGTGATGATGCCAGCACATGGTCCAGCCAAAAACATGGAGTATGATGCTGTTGCAACAACACATCCTGGATCCCCAAAAGAAATCGATCCATCTTGAATACAAGTCAAAGAGGAGTACTTGAAGATGAACAAATGTACCAAAGGTGCTGCAATTTATTTGAAAAATTTCTTCCCAGCAGTTCATACAGAAGACCAGTCGGGATATCCAGTATGGTGGAGGCTATGGTTTCCAGAGCCCGAATTGATGCACGGATTGATTTGCAATCTGGAAGGATAAAGAAAGAAAGAGTTCACTGAGATCATGAAGATCTGTTCCACCATGAAGAGCTCAGACGGCAAATAAGTGAATTTAGCTTGTCTTCATGAAAAATGCCTTGTTTCTACT

Fig. 1B

(SEQ ID NO:10)

PR8(CAMBRIDGE)

PA

AGCGAAAGCAGGTA CTGATTCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATGATTGTCGAGCTTGCGGAAAAAACA
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TCAGATTTCCACTTCATCAATGAGCAAGGCGAGTCAATAATCGTAGAACTTGGTGATCCTAATGCACTTTTGAAGCACAGATTT
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TACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAAACCAGGCTATTCAACATAAGACAAGAAATGGCCAGCAGAGGCTCTGG
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CAAAGTCTCCCGCCGAACCTTCTCCAGCCTTGAAAATTTAGAGCCTATGTGGATGGATTGGAACCGAACGGCTACATTGAGGGC
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(SEQ ID NO:12)

Fig. 1C

NP

PR8(CAMBRIDGE)

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCCCAAGGCACCAAAACGGTCTTACGAACAGATG
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(SEQ ID NO:13)

Fig. 1D

PR8(CAMBRIDGE)

M

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(SEQ ID NO:14)

NS

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(SEQ ID NO:15)

Fig. 1E

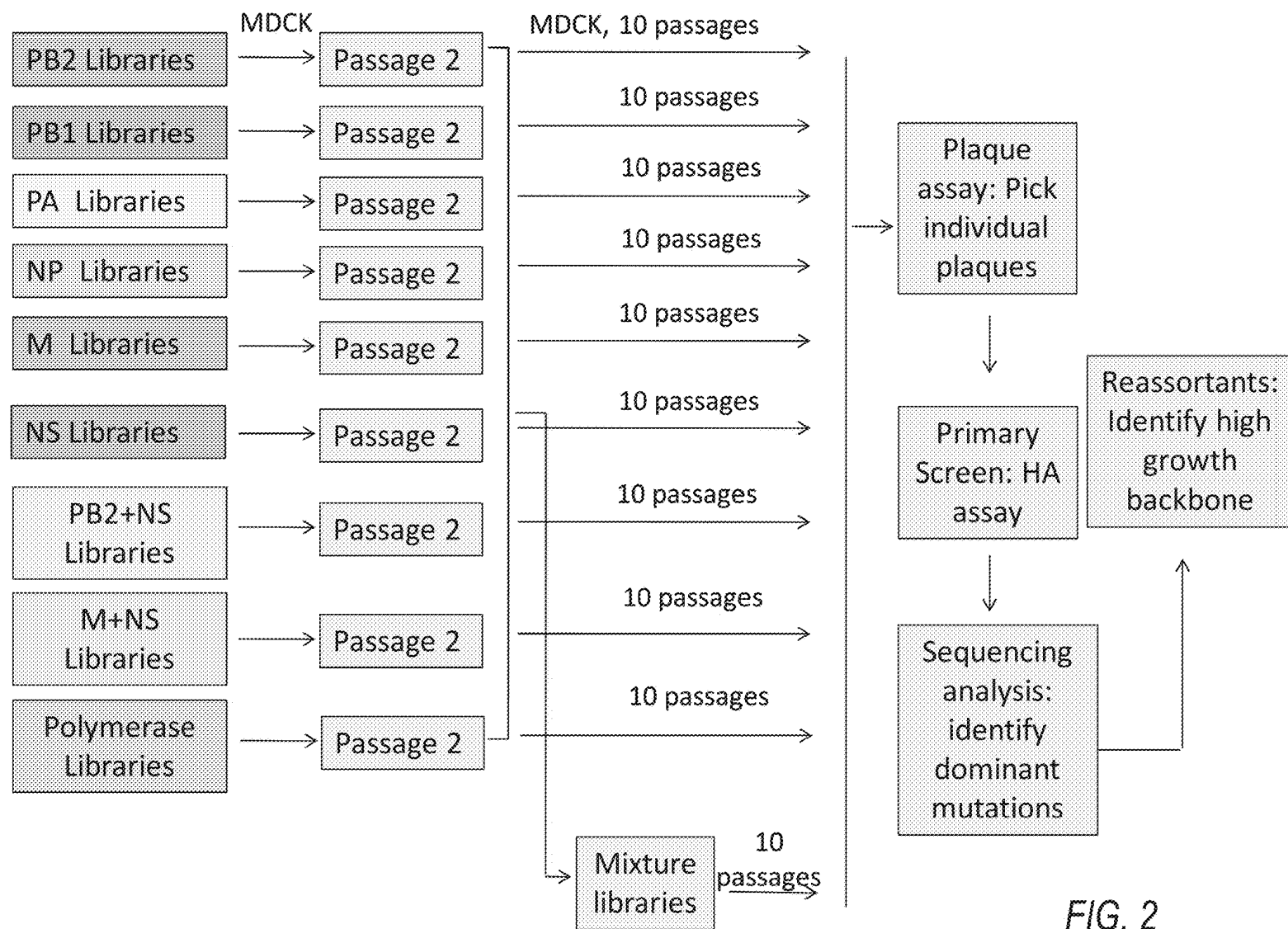


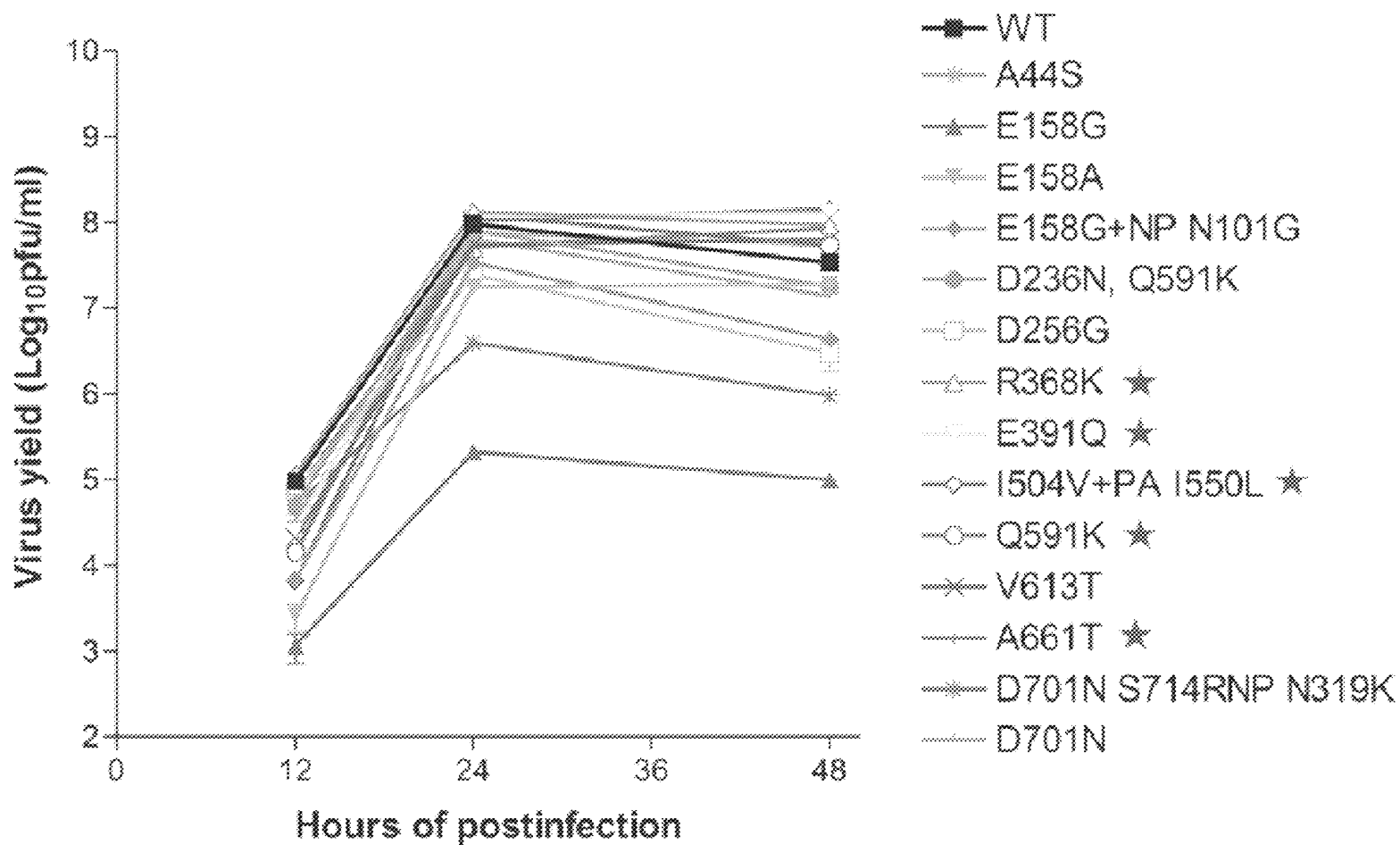
Figure 3 Summary of HA assay of 1434 individual clones

Groups	Numbers of clone	Fold change	%
WT HA titer = 2^7	-	-	-
HA titer = $2^{>9-9.5}$	8	>4	0.6%
HA titer = $2^{>8.5-9}$	23	>2.8 - 4	1.6%
HA titer = $2^{7-8.5}$	748	1 - 2.8	52.2%
HA titer < 2^7	655	<1	45.6%
Total	1434	-	100%

Figure 4 Recombinant viruses generated from dominant mutations

Viruses	Gene backbone								Virus stock titer	
	HA	NA	PB2	PB1	PA	NP	M	NS	2 ⁿ	Pfu/ml
WT	Indo/NC /09 delHA	Indo/NC /09 NA	PR8-wt	PR8-wt	PR8-wt	PR8-wt	PR8-wt	PR8-wt	7	3.0E+07
1			M202L F323L	M507V V644A		I116L		K55E	9~9.5	2.0E+08
2			M202L F323L	Q247H	R401K			T49A	9	1.0E+08
3			I504V	M507V V644A	I550L	R74K N417D		K55E	8~8.5	5.7E+07
4			I505V	E112G	I550L	R74K		S161T	9	1.6E+08
5			M202L F323L	E112G				S161T	8.5	1.3E+08
6			M66R	M40I G180W		R74K		S161T	8~8.5	2.3E+07

Figure 5A Growth curve – PB2 mutants
(MOI=0.001)



5B PB1 Mutants

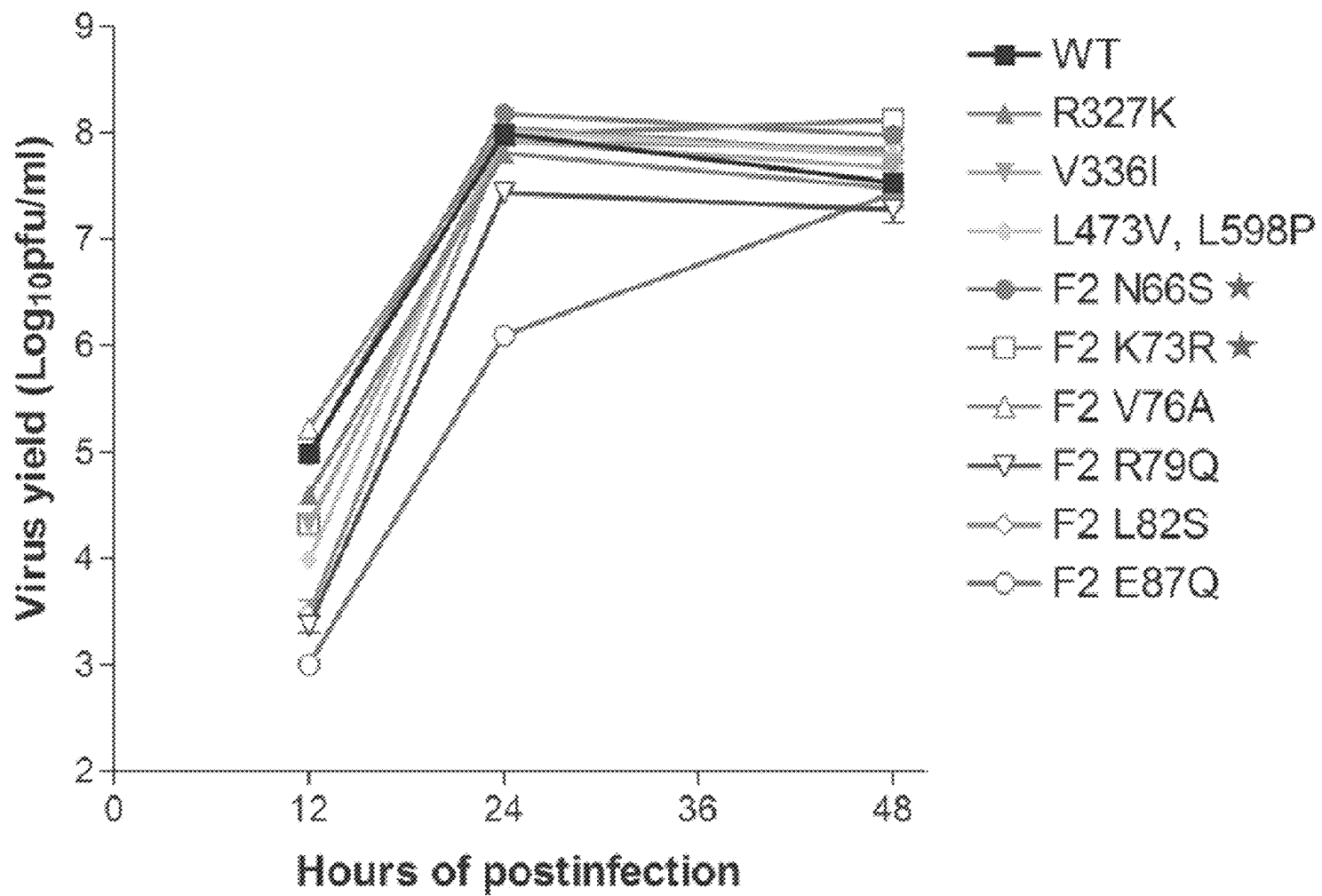
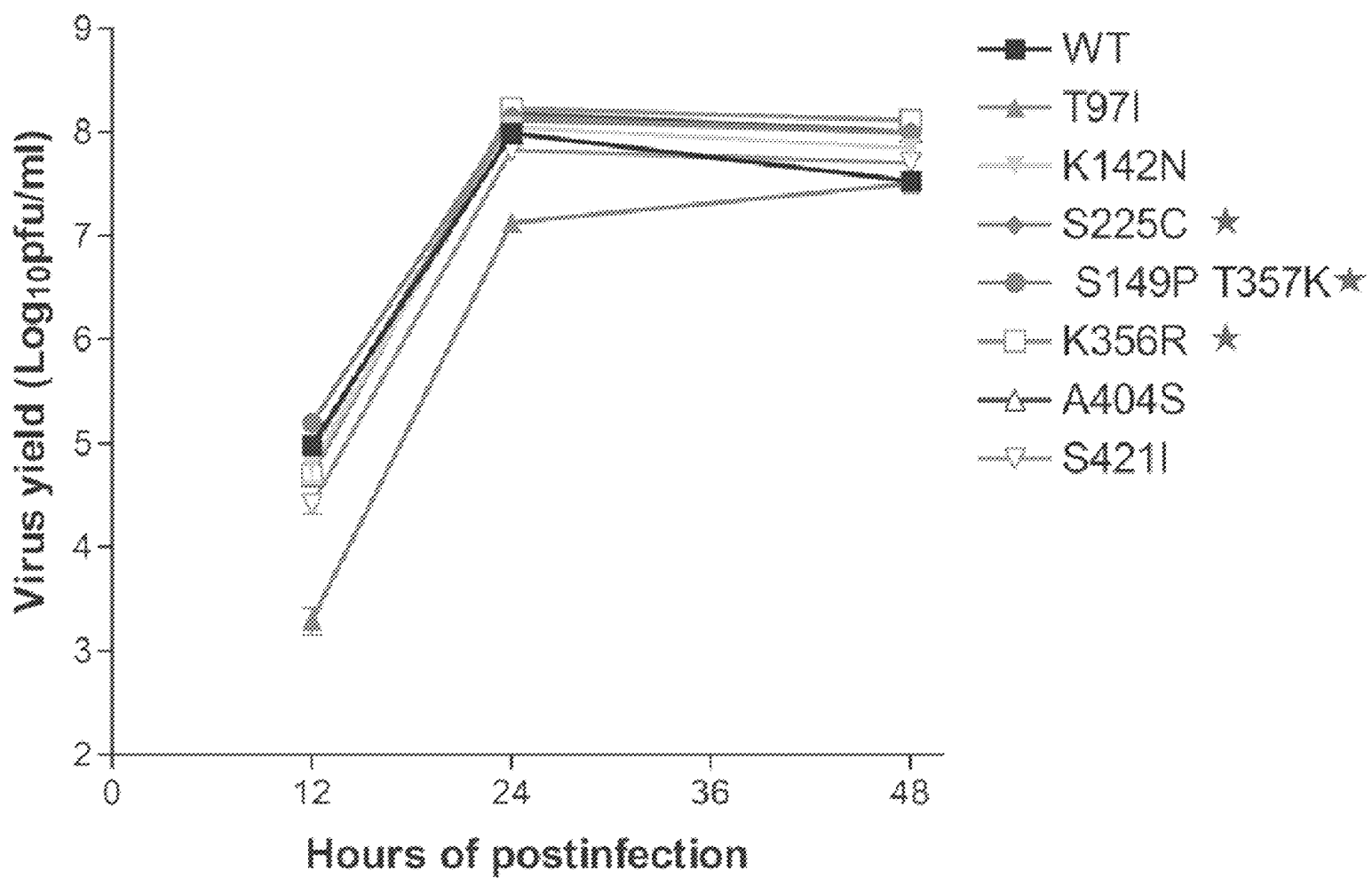


Figure 5C PA Mutants



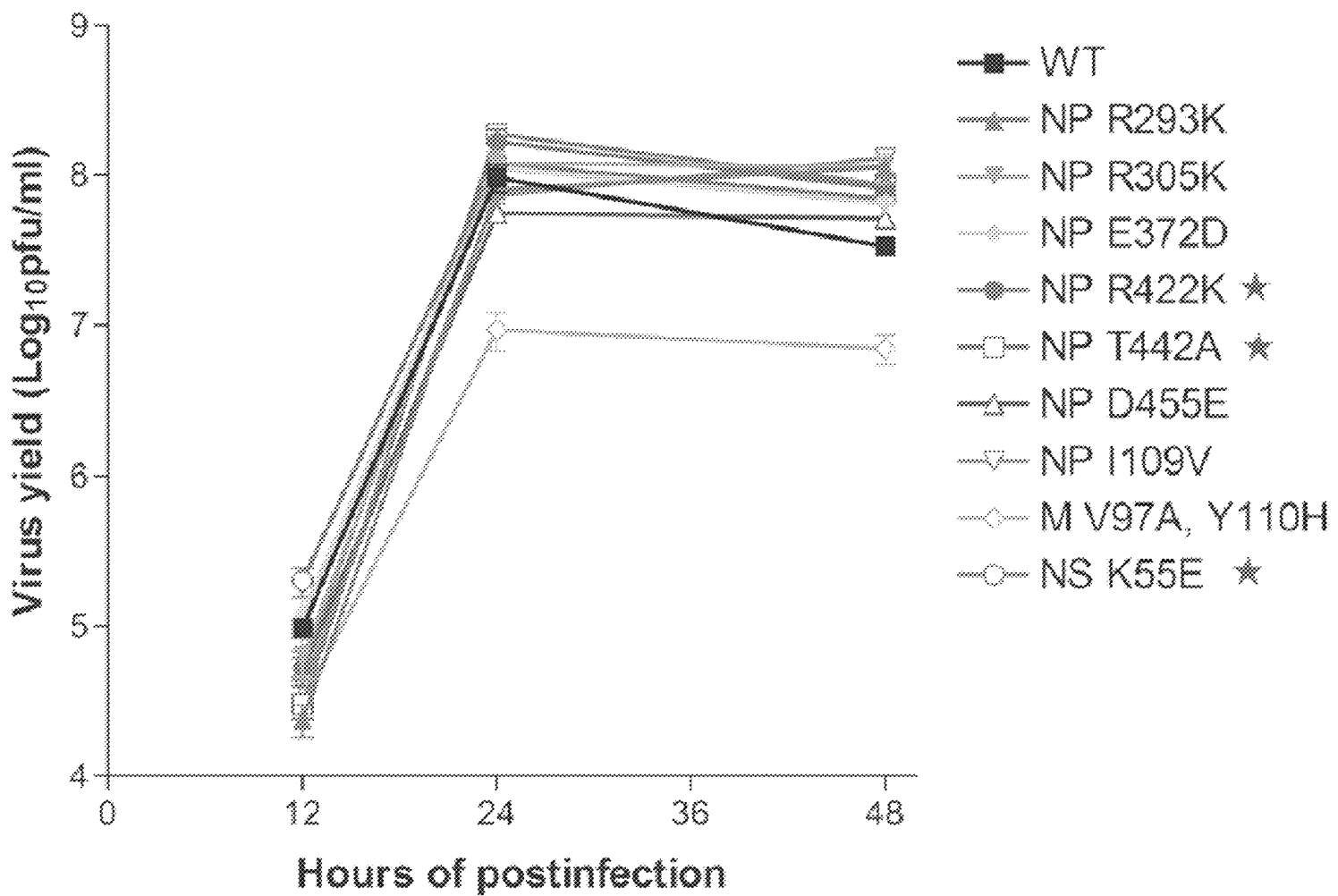


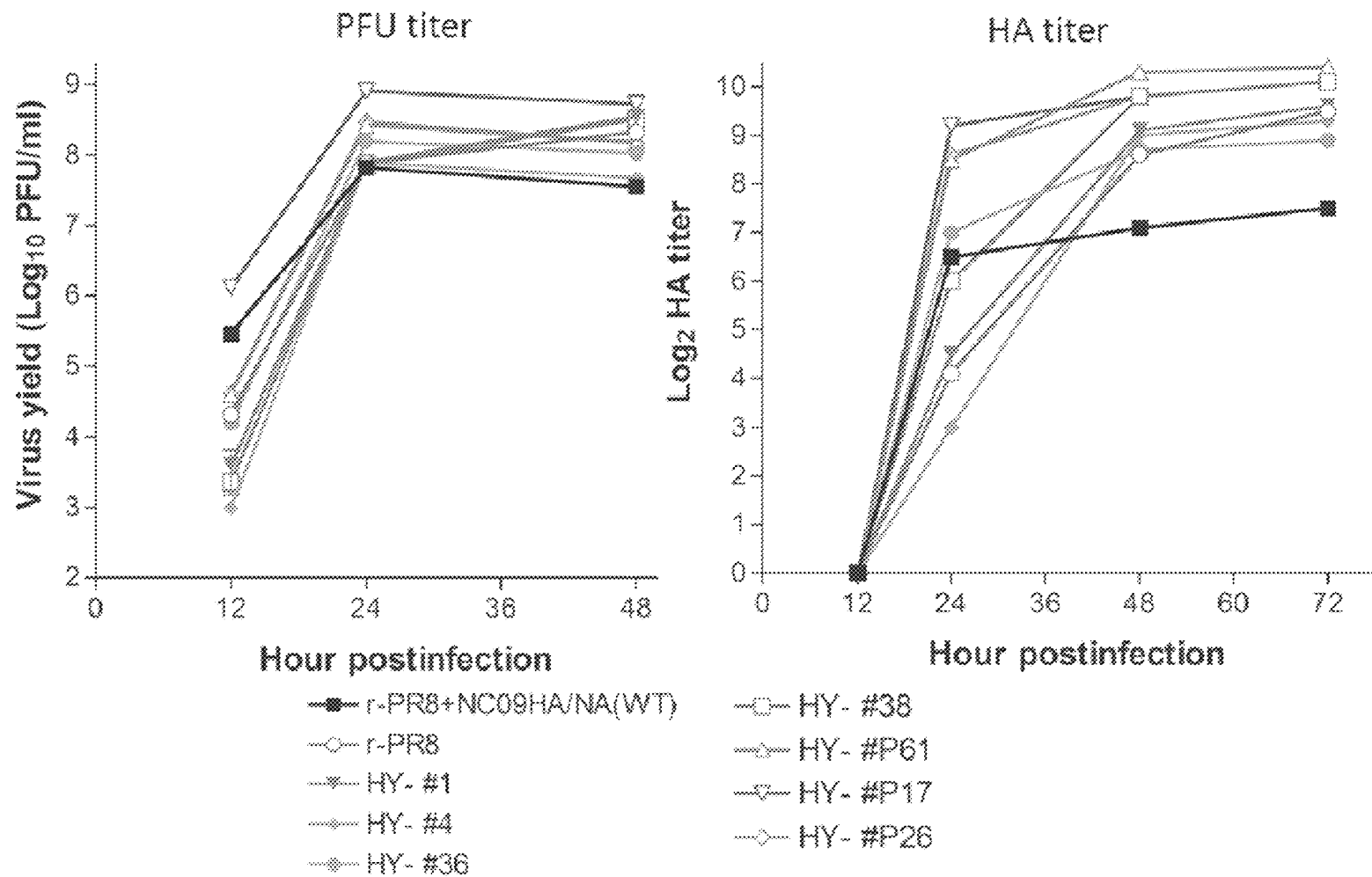
Figure 6 Confirmed high replicative mutations

Gene	Screened from viruses libraries	Described in literature
PB2	<u>M202L F323L, I504V, M66R</u>	A44S, E158G, E158A, D236N, D256G, R368K, E391Q, I504V, Q591K, V613T, <u>A661T</u> , D701N, D701N S714R
PB1	M507V V644A, <u>V644A, R54I, Q247H, E112G, M40I G180W, I667T M714T</u>	R327K, V336I, L473V L598P
PB1 F2	-	<u>N66S, K73R, V76A, R79Q, L82S, E87Q</u>
PA	F105C, R401K	T97I, K142N, <u>S225C, S149PP T357K, K356R, A404S, S421I</u>
NP	R293M, <u>I116L, N224I, R74K, R74K N417D,</u>	R293K, R305K, E372D, <u>R422K, T442A, D455E, I109V, N101G, N319K</u>
M	P90S	V97A, <u>Y100H, V97A Y100H</u>
NS	A30P, T49A, R140Q, <u>S161T, A223E</u>	<u>K55E</u>

Figure 7A Recombinant viruses generated by RGS

Virus #	Gene backbone								Virus stock titer	
	HA	NA	PB2	PB1	PA	NP	M	NS	2 ⁿ	Pfu/ml
wt	Inda/NC/09 delHA	Indo/NC/09 NA	wt	wt	wt	wt	wt	wt	7	3.0E+07
1			M202L F323L	M507V V644A		I116L		K55E	9~9.5	2.0E+08
4			M202L F323L	M507V V644A	K356R	T442A	V97A Y100H	K55E	10~10.5	1.6E+08
36			I504V	E112G	I550L	I112L	Y100H	R140Q	9.5	1.3E+08
38			M202L F323L	M507V V644A		I116L	Y100H	K55E	10~10.5	2.3E+08
HY-#17			I504V	E112G	S225C	R74K N417D	V97A Y100H	K55E	9.5~10	5.8E+08
HY-#61			M202L F323L	Q247H	K142N	R74K	V97A Y100H	K55E	10~10.5	2.0E+08
HY-#26			M202L F323L	M40L G180W	S225C	R422K	V97A Y100H	K55E	10	3.0E+08

Figure 7B Growth characteristics (MOI=0.001)



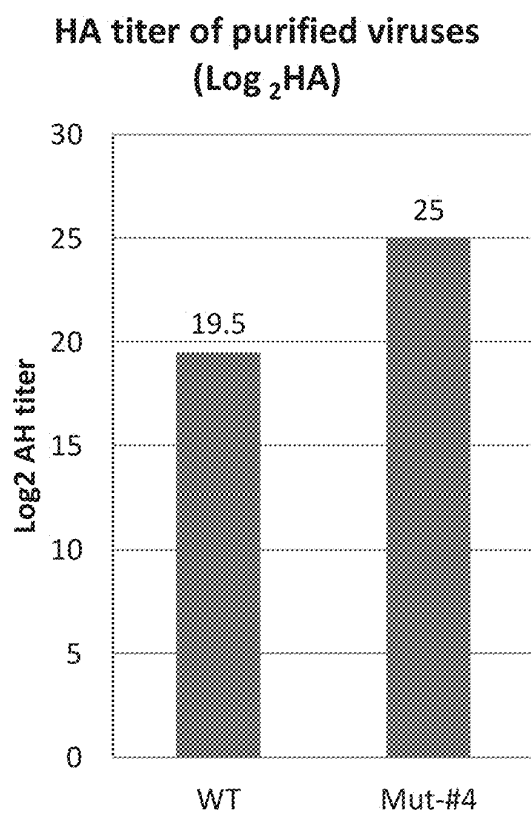


FIG. 8A

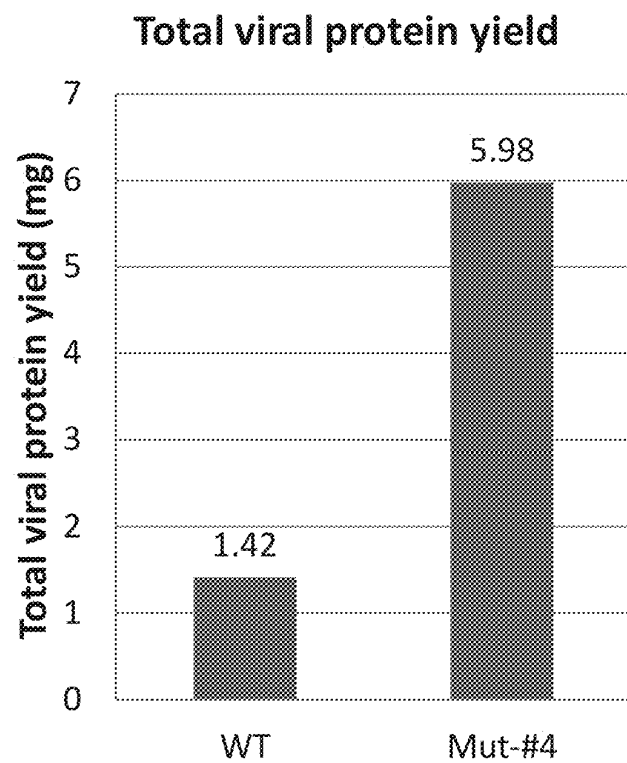
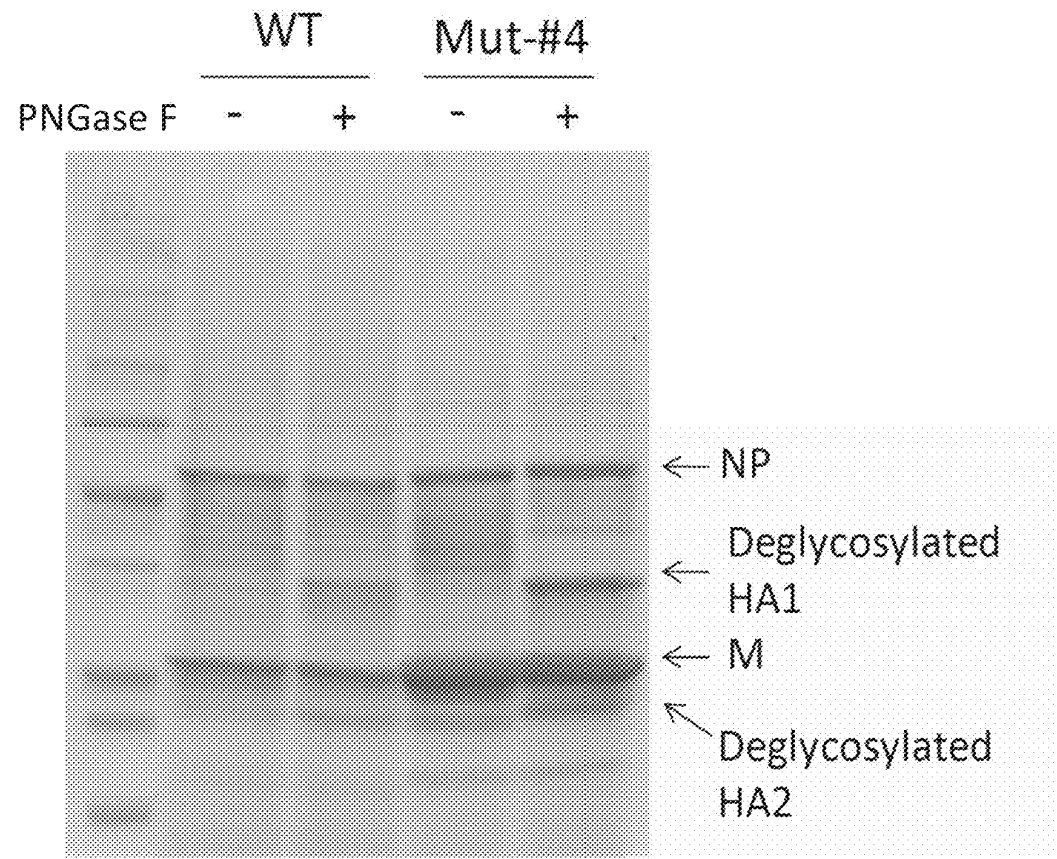


FIG. 8B

Total viral protein yield: 4.2 fold

Figure 8C SDS-PAGE analysis

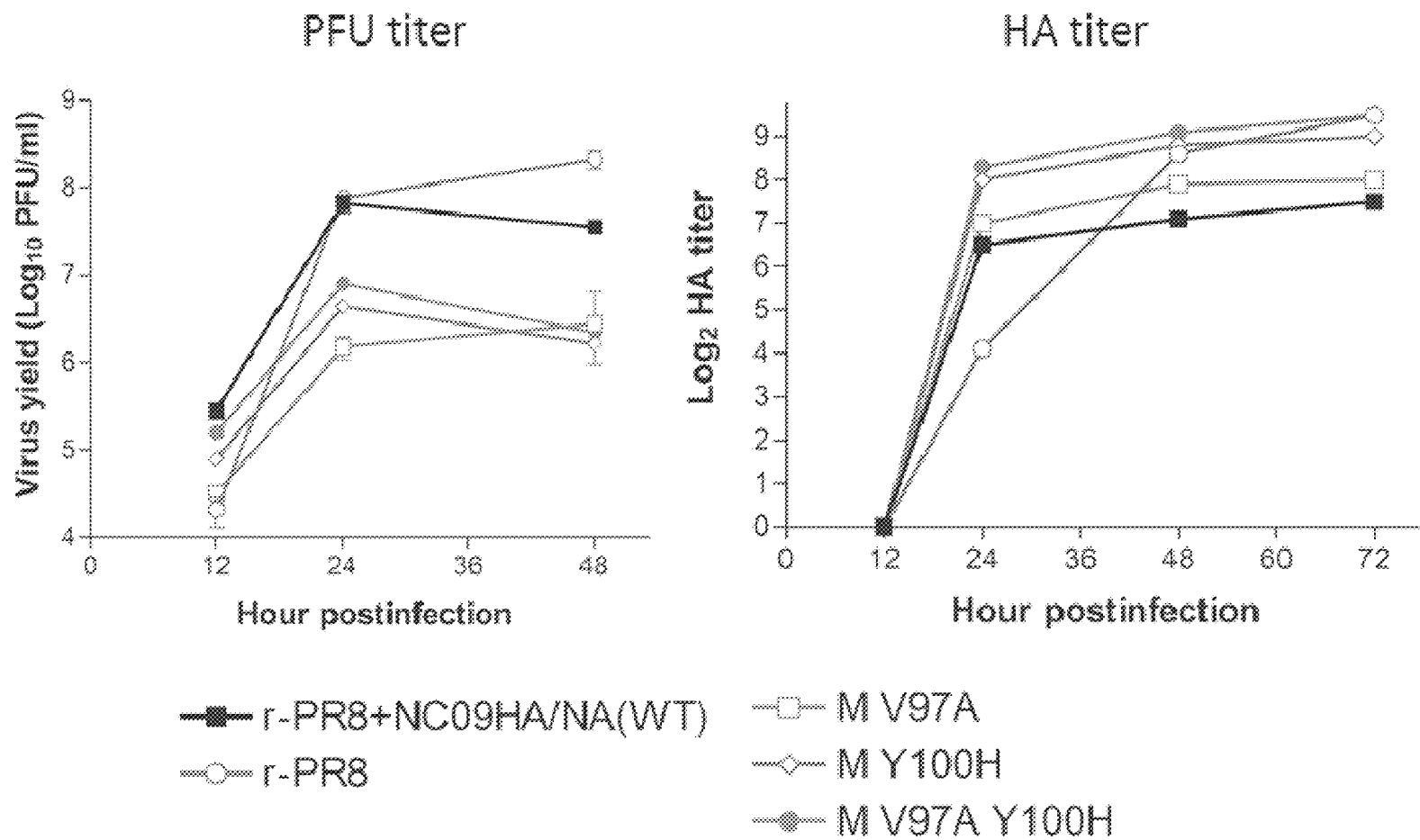


Mutant virus generates much more M1 and HA1 proteins than wild type.

Figure 9A Wild type VS. mutant

#	Gene backbone								Virus stock titer	
	HA	NA	PB2	PB1	PA	NP	M	NS	HA titer (2 ⁿ)	Pfu/ml
WT	Indo/NC/09 delHA	Indo/NC/09 NA	PR8-wt	PR8-wt	PR8-wt	PR8-wt	PR8-wt	PR8-wt	7	3.0E+07
4			M202L F323L	M507V V644A	K356R	T442A	V97A Y100H	K55E	10~10.5	1.6E+08

Figure 9B Growth kinetics (MOI=0.001)



CANIS FAMILIARIS [gbmam]: 1194 CDS's(559501 CODONS)

FIELDS: [TRIPLET] [AMINO ACID] [FRACTION] [FREQUENCY: PER THOUSAND] ([NUMBER])

UUU F 0.41 17.1 (9540)	UCU S 0.18 13.8 (7723)	UAU Y 0.40 11.5 (6456)	UGU C 0.42 10.1 (5665)
UUC F 0.59 24.4 (13671)	UCC S 0.24 18.4 (10299)	UAC Y 0.60 17.5 (9786)	UGC C 0.58 13.8 (7723)
UUA L 0.06 5.8 (3270)	UCA S 0.13 9.8 (5487)	UAA * 0.27 0.6 (325)	UGA * 0.53 1.1 (642)
UUG L 0.12 11.8 (6627)	UCG S 0.06 4.6 (2584)	UAG * 0.21 0.5 (254)	UGG W 1.00 13.8 (7704)
CUU L 0.12 11.7 (6523)	CCU P 0.27 15.6 (8713)	CAU H 0.39 9.0 (5039)	CGU R 0.07 3.9 (2163)
CUC L 0.22 21.8 (12224)	CCC P 0.35 20.4 (11422)	CAC H 0.61 14.1 (7888)	CGC R 0.20 10.6 (5943)
CUA L 0.06 6.5 (3644)	CCA P 0.25 14.6 (8157)	CAA Q 0.25 11.0 (6149)	CGA R 0.11 5.6 (3155)
CUG L 0.43 42.8 (23966)	CCG P 0.12 7.0 (3892)	CAG Q 0.75 32.6 (18244)	CGG R 0.21 11.0 (6132)
AUU I 0.32 15.5 (8662)	ACU T 0.22 12.3 (6886)	AAU N 0.43 16.5 (9253)	AGU S 0.14 10.8 (6029)
AUC I 0.53 25.7 (14391)	ACC T 0.39 21.4 (11979)	AAC N 0.57 21.6 (12104)	AGC S 0.25 18.9 (10595)
AUA I 0.15 7.2 (4017)	ACA T 0.26 14.2 (7972)	AAA K 0.40 22.2 (12410)	AGA R 0.20 10.5 (5847)
AUG M 1.00 22.7 (12717)	ACG T 0.13 7.2 (4005)	AAG K 0.60 33.9 (18967)	AGG R 0.21 11.1 (6228)
GUU V 0.14 9.3 (5189)	GCU A 0.25 17.2 (9609)	GAU D 0.43 19.7 (11012)	GGU G 0.16 11.3 (6298)
GUC V 0.27 17.2 (9607)	GCC A 0.44 30.3 (16927)	GAC D 0.57 26.2 (14655)	GGC G 0.35 24.2 (13513)
GUA V 0.10 6.5 (3660)	GCA A 0.20 13.7 (7651)	GAA E 0.40 26.4 (14776)	GGA G 0.24 16.9 (9465)
GUG V 0.48 31.0 (17366)	GCG A 0.11 7.9 (4431)	GAG E 0.60 40.3 (22552)	GGG G 0.25 17.4 (9718)

CODING GC 53.16% 1ST LETTER GC 55.35% 2ND LETTER GC 41.92% 3RD LETTER GC 62.22%

GENETIC CODE 1: STANDARD

Fig. 10A

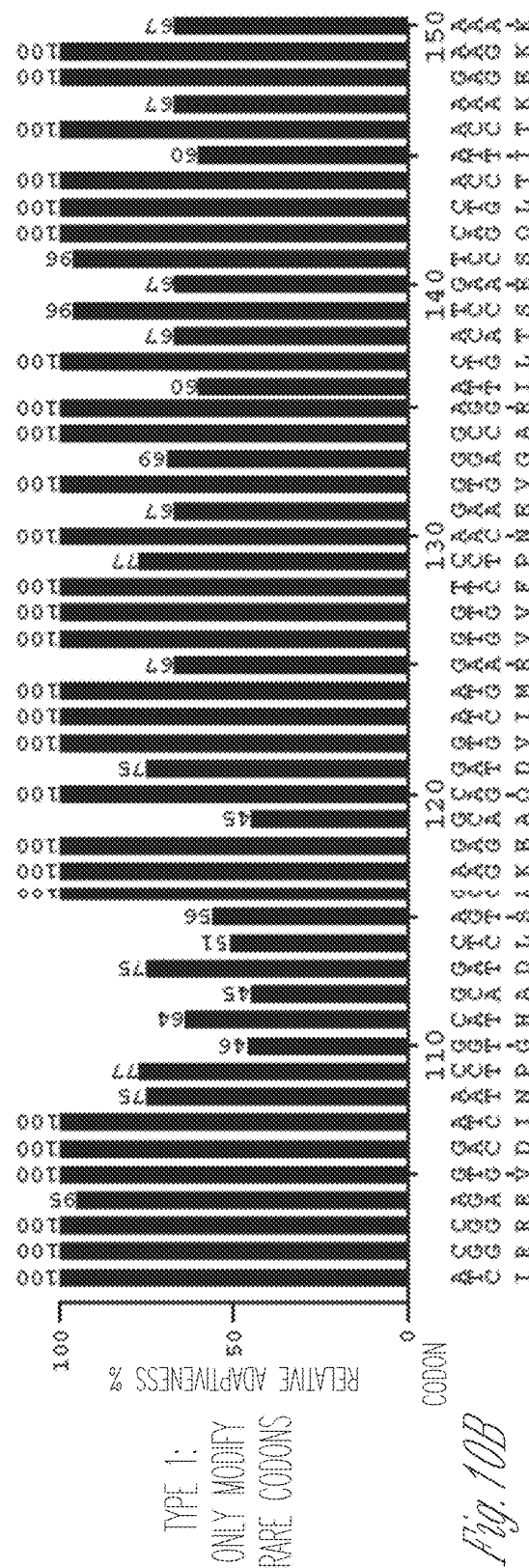
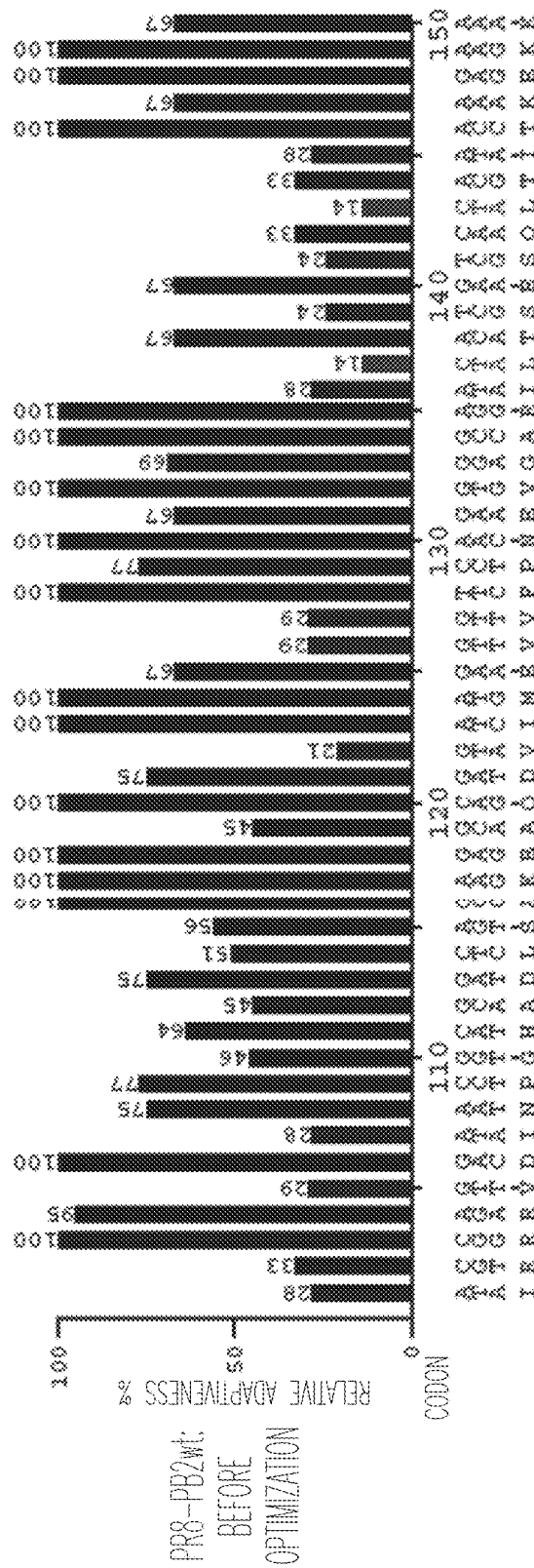


Fig. 10B

Fig. 10C

Figure 10D Growth kinetics in MDCK cells

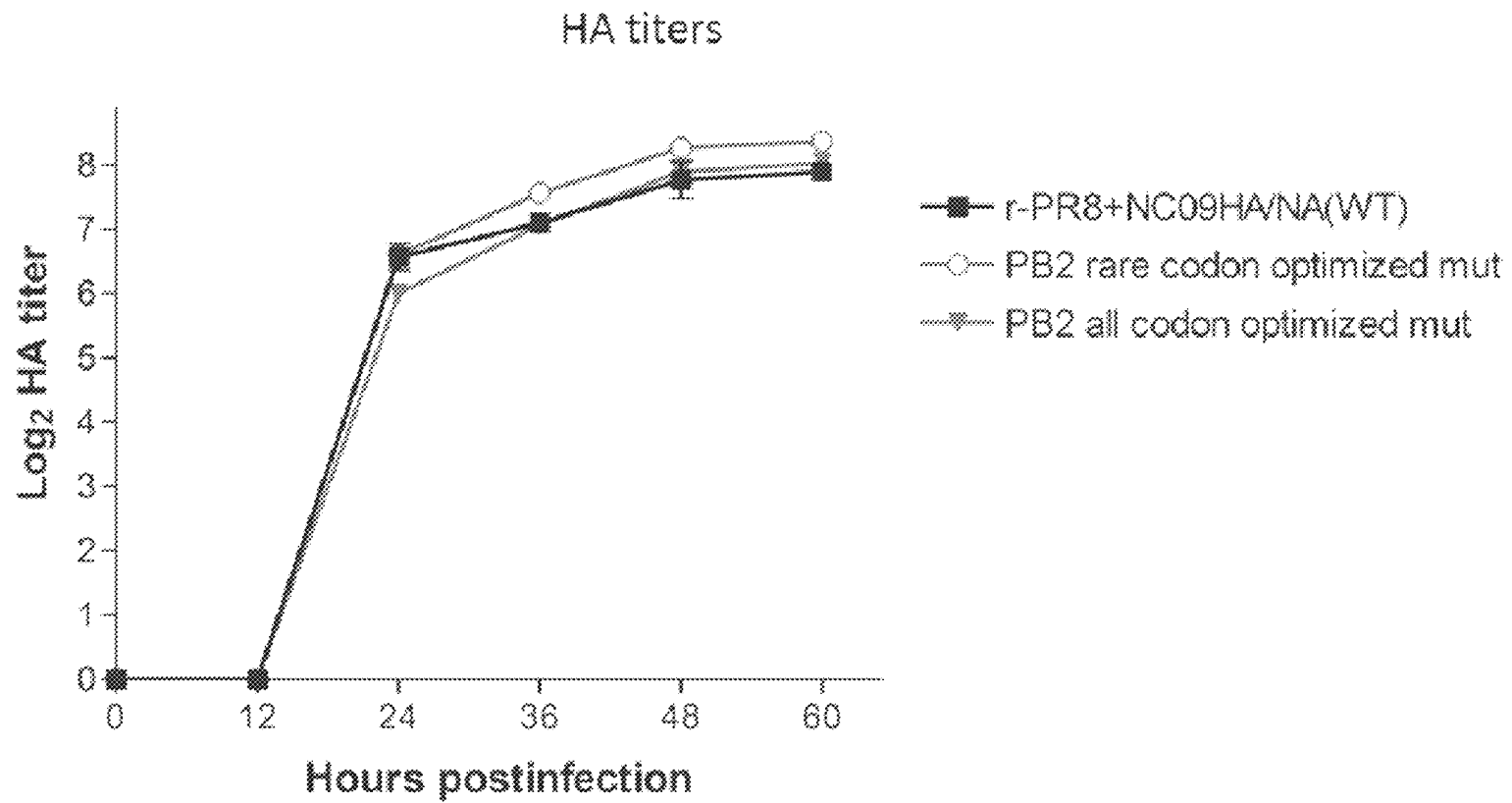
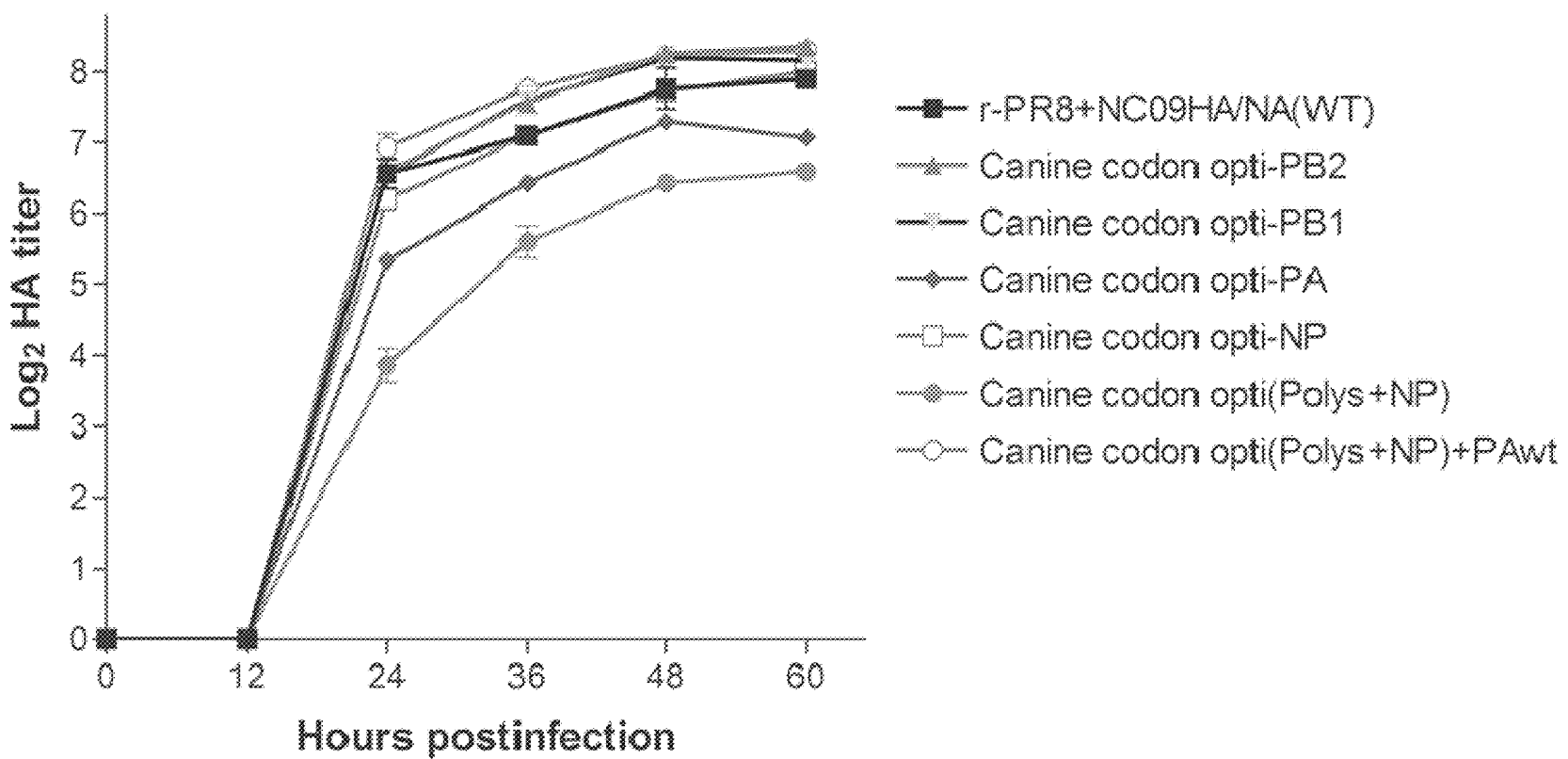


Figure 10E



PR8-UW PB2:

AGCGAAAGCAGGTCAATTATATTCAATATGGAAAGAATAAAAGAACTACGAAATCTAATGTGCGAGTCTCGCACCCGCGA
GATACTCACAAAAACCACCGTGGACCATATGGCCATAATCAAGAAGTACACATCAGGAAGACAGGAGAAGAACCAGCAC
TTAGGATGAAATGGATGATGGCAATGAAATATCCAATTACAGCAGACAAGAGGATAACGGAAATGATTCTGAGAGAAAT
GAGCAAGGACAACTTTATGGAGTAAATGAATGATGCCGGATCAGACCGAGTGATGGTATCACCTCTGGCTGTGACATG
GTGGAATAGGAATGGACCAATAACAAATACAGTTCATTATCCAAAAATCTACAAAACCTATTTTGAAAGAGTCGAAAGGC
TAAAGCATGGAACCTTTGGCCCTGTCCATTTTAGAAACCAAGTCAAAATACGTGCGAGAGTTGACATAAATCTGGTCAT
GCAGATCTCAGTGCCAAGGAGGCACAGGATGTAATCATGGAAGTTGTTTTCCCTAACGAAGTGGGAGCCAGGATACTAAC
ATCGGAATCGCAACTAACGATAACCAAGAGAAGAAAGAAGAACTCCAGGATTGCAAAATTTCTCTTTGATGGTTGCAT
ACATGTTGGAGAGAGAACTGGTCCGCAAAACGAGATTCTCCAGTGCGTGGTGGAAACAAGCAGTGTGTACATTGAAGTG
TTGCATTTGACTCAAGGAACATGCTGGGAACAGATGTATACTCCAGGAGGGGAAGTGAGGAATGATGATGTTGATCAAAG
CTTGATTATTGCTGTAGGAACATAGTGAGAAGAGCTGCAGTATCAGCAGATCCACTAGCATCTTTATTGGAGATGTGCC
ACAGCACACAGATTGGTGGAAATTAGGATGGTAGACATCCTTAGGCAGAACCCAACAGAAGAGCAAGCCGTGGATATATGC
AAGGCTGCAATGGGACTGAGAATTAGCTCATCCTTCAGTTTTGGTGGATTACATTTAAGAGAACAAGCGGATCATCAGT
CAAGAGAGAGGAAGAGGTGCTTACGGGCAATCTTCAAACATTGAAGATAAGAGTGCATGAGGGATATGAAGAGTTCACAA
TGTTTGGGAGAAGAGCAACAGCCATACTCAGAAAAGCAACCAGGAGATTGATTGAGCTGATAGTGAGTGGGAGAGACGAA
CAGTCGATTGCCGAAGCAATAATTGTGGCCATGGTATTTTCAAGAGGATTGTATGATAAAAGCAGTCAGAGGTGATCT
GAATTCGTCATAGGGCGAATCAACGATTGAATCCTATGCATCAACTTTAAGACATTTTCAGAAGGATGCGAAAGTGC
TTTTTCAAATTTGGGGAGTTGAACCTATCGACAATGTGATGGGAATGATTGGGATATTGCCCCACATGACTCCAAGCATC
GAGATGTCAATGAGAGGAGTGAGAATCAGCAAAATGGGTGTAGATGAGTACTCCAGCACGGAGAGGGTAGTGGTGAGCAT
TGACCGTTTTTTGAGAATCCGGGACCAACGAGGAAATGTACTACTGTCTCCGAGGAGGTGAGTGAACACAGGGAACAG
AGAAACTGACAATAACTTACTCATCGTCAATGATGTGGGAGATTAATGGTCTGAATCAGTGTGGTCAATACCTATCAA
TGGATCATCAGAACTGGGAACTGTAAAAATCAGTGGTCCCAGAACCTACAATGCTATACAATAAAATGGAATTTGA
ACCATTTGAGTCTTTAGTACCTAAGGCCATTAGAGGCCAATACAGTGGGTTTGTAAGAACTCTGTTCCAACAAATGAGGG
ATGTGCTTGGGACATTTGATACCGCACAGATAATAAACTTCTTCCCTTCGCAGCCGCTCCACCAAAGCAAAGTAGAATG
CAGTTCTCCTCATTTACTGTGAATGTGAGGGGATCAGGAATGAGAATACTTGAAGGGGCAATTCTCCTGTATTCAACTA
TAACAAGGCCACGAAGAGACTCACAGTTCTCGGAAAGGATGCTGGCACTTTAACTGAAGACCCAGATGAAGGCACAGCTG
GAGTGGAGTCCGCTGTTCTGAGGGGATTCCTCATTCTGGGCAAAGAAGACAAGAGATATGGGCCAGCTAAGCATCAAT
GAACTGAGCAACCTTGGGAAAGGAGAGAAGGCTAATGTGCTAATTGGGCAAGGAGACGTGGTGTGGTAATGAAACGGAA
ACGGGACTCTAGCATACTTACTGACAGCCAGACAGCGACCAAAAGAATTCCGATGGCCATCAATTAGTGTGAATAGTTT
AAAAACGACCTGTTTCTACT (SEQ ID NO:3)

FIG. 10F

Canine codon optimized PR8-PB2:

AGCGAAAGCAGGTCAATTATATTC AATATGGAAGAATAAAAGAACTACGAAATCTAATGTCGCAGTCTCGACCCGCGA
GATACTCACAAAAACCACCGTGGACCATATGGCCATAATCAAGAAGTACACATCAGGAAGACAGGAGAAGAACCAGCAC
TGAGGATGAAATGGATGATGGCAATGAAATATCCAATTACAGCAGACAAGAGGATCACCGAAATGATTCTGAGAGAAAT
GAGCAGGGACAGACTCTGTGGAGTAAATGAATGATGCCGGATCAGACCGAGTGATGGTGTCACCTCTGGCTGTGACATG
GTGGAATAGGAATGGACCAATCACAATACAGTGCATTATCCAAAAATCTACAAAATTATTTTGAAAGAGTCGAAAGGC
TGAAGCATGGAACCTTTGGCCCTGTCCATTTTAGAAACCAGGTCAAAATCCGGCGGAGAGTGGACATCAATCCTGGTCAT
GCAGATCTCAGTGCCAAGGAGGCACAGGATGTGATCATGGAAGTGGTGTCCCTAACGAAGTGGGAGCCAGGATTCTGAC
ATCCGAATCCCAGCTGACCATTTACCAAGAGAAGAAAGAAGAACTCCAGGATTGCAAAATTTCTCTCTGATGGTGGCAT
ACATGCTGGAGAGAGAACTGGTCCGCAAAACAAGATTCCTCCAGTGGCTGGTGGAAACAAGCAGTGTGTACATTGAAGTG
CTGCATCTGACTCAGGGAACATGCTGGGAACAGATGTATACTCCAGGAGGGGAAGTGAGGAATGATGATGTGGATCAGAG
CCTGATTATTGCTGCTAGGAACATTGTGAGAAGAGCTGCAGTGTGAGCAGATCCACTGGCATCTCTGCTGGAGATGTGCC
ACAGCACACAGATTGGTGGAAATTAGGATGGTGGACATCCTGAGGCAGAACCCAACAGAAGAGCAGGCCGTGGATATTTGC
AAGGCTGCAATGGGACTGAGAATTAGCTCATCCTTCAGTTTTGGTGGATTACATTTAAGAGAACAAAGCGGATCATCAGT
CAAGAGAGAGGAAGAGGTGCTGACCGGCAATCTGCAGACACTGAAGATCAGAGTGCATGAGGGATATGAAGAGTTCACAA
TGGTGGGGAGAAGAGCAACAGCCATCCTCAGAAAAGCAACCAGGAGACTGATTGAGCTGATCGTGAGTGGGAGAGACGAA
CAGTCCATTGCCGAAGCAATTATTGTGGCCATGGTGTTCACAGGAGGATTGTATGATTAAAGCAGTCAGAGGTGATCT
GAATTCGTC AATAGGGCCAATCAGCGACTGAATCCTATGCATCAGCTGCTGAGACATTTTCAGAAGGATGCCAAAGTGC
TGTTTCAGAATTGGGGAGTGGAACCTATCGACAATGTGATGGGAATGATTGGGATCCTGCCCACATGACTCCAAGCATC
GAGATGTCAATGAGAGGAGTGAGAATCAGCAAAATGGGTGTGGATGAGTACTCCAGCACCGAGAGGGTCGTGGTGAGCAT
TGACAGATTTCTGAGAATCCGGGACCAGCGAGGAAATGTGCTCCTGTCTCCGAGGAGGTGAGTGAACACAGGGAACAG
AGAAACTGACAATTACTTACTCATCTCAATGATGTGGGAGATTAATGGTCTGAATCAGTGCTGGTCAATACCTATCAG
TGGATCATCAGAACTGGGAACTGTGAAAATTCAGTGGTCCAGAACCTACAATGCTGTACAATAAAATGGAATTTGA
ACCATTTAGTCTCTGGTGCCTAAGGCCATTAGAGGCCAGTACAGTGGGTTTGTGAGAACTCTGTTCCAGCAGATGAGGG
ATGTGCTGGGGACATTTGATACCGCACAGATTATTAAGTGTGCTGCCCTTCGAGCCGCTCCACCAAAGCAGAGTAGAATG
CAGTTCTCCTCATTTACTGTGAATGTGAGGGGATCAGGAATGAGAATCCTGGTGAGGGGCAATTCTCCTGTGTTCAACTA
TAACAAGGCCACCAAGAGACTCACAGTGCTCGGAAAGGATGTCTGGCACTCTGACTGAAGACCCAGATGAAGGCACAGCTG
GAGTGGAGTCCGCTGTGCTGAGGGGATTCCTCATTTCTGGGCAAGAAGACAAGAGATATGGGCCAGCACTGAGCATCAAT
GAACTGAGCAACCTGGCCAAAGGAGAGAAGGCTAATGTGCTAATTGGGCAAGGAGACGTGGTGTGGTAATGAAACGGAA
ACGGGACTCTAGCATACTTACTGACAGCCAGACAGCGACCAAAAGAATTTCGGATGGCCATCAATTAGTGTGCAATAGTTT
AAAAACGACCTGTTTCTACT (SEQ ID NO:16)

FIG. 10G

PR8-UW PB1:

AGCGAAAGCAGGCAAACCATTTGAATGGATGTCAATCCGACCTTACTTTTCTAAAAGTGCCAGCACAAAATGCTATAAG
CACAACTTTCCTTATACTGGAGACCTCCTTACAGCCATGGGACAGGAACAGGATACACCATGGATACTGTCAACAGGA
CACATCAGTACTCAGAAAAGGGAAGATGGACAACAAACCCGAAACTGGAGCACCAGCACTCAACCCGATTGATGGGCCA
CTGCCAGAAGACAATGAACCAAGTGGTTATGCCCAAACAGATTGTGTATTGGAGGCGATGGCTTTCCTTGAGGAATCCCA
TCCTGGTATTTTGAACACTCGTGTATTGAAACGATGGAGGTTGTTCAAGCAACACGAGTAGACAAGCTGACACAAGGCC
GACAGACCTATGACTGGACTCTAAATAGAAACCAACCTGCTGCAACAGCATTGGCCAACACAATAGAAGTGTTCAGATCA
AATGGCCTCACGGCCAATGAGTCTGGAAGGCTCATAGACTTCCTTAAGGATGTAATGGAGTCAATGAACAAAGAAGAAAT
GGGGATCACAACCTCATTTTCAGAGAAAGAGACGGGTGAGAGACAATAGACTAAGAAAATGATAACAGAGAAACAATGG
GTAAAAAGAAGCAGAGATTGAACAAAAGGAGTTATCTAATTAGAGCATTGACCCTGAACACAATGACCAAAGATGCTGAG
AGAGGGAAGCTAAAACGGAGAGCAATTGCAACCCAGGGATGCAATAAGGGGGTTGTATACTTTGTTGAGACACTGGC
AAGGAGTATATGTGAGAACTTGAACAATCAGGGTTGCCAGTTGGAGGCAATGAGAAGAAAGCAAAGTTGGCAAATGTTG
TAAGGAAGATGATGACCAATTCTCAGGACACCGAACTTTCTTTCAACCATCACTGGAGATAACACCAAATGGAACGAAAAT
CAGAATCCTCGGATGTTTTGGCCATGATCACAATATGACCAGAAATCAGCCGAATGGTTCAGAAATGTTCTAAGTAT
TGCTCCAATAATGTTCTCAAACAAAATGGCGAGACTGGGAAAAGGGTATATGTTTGAGAGCAAGAGTATGAACTTAGAA
CTCAATACCTGCAGAAATGCTAGCAAGCATCGATTGAAATATTTCAATGATTCAACAAGAAAGAAGATTGAAAAATC
CGACCGCTCTAATAGAGGGGACTGCATCATTGAGCCCTGGAATGATGATGGGCATGTTCAATATGTTAAGCACTGTATT
AGGCGTCTCCATCCTGAATCTTGACAAAAGAGATACACCAAGACTACTTACTGGTGGGATGGTCTTCAATCCTCTGACG
ATTTTGCTCTGATTGTGAATGCACCCAATCATGAAGGGATTCAAGCCGGAGTCGACAGGTTTTATCGAACCTGTAAGCTA
CTTGAATCAATATGAGCAAGAAAAAGTCTTACATAAACAGAACAGGTACATTTGAATTCACAAGTTTTTCTATCGTTA
TGGGTTTGTGCAATTCAGCATGGAGCTTCCAGTTTTGGGGTGTCTGGGATCAACGAGTCAGCGGACATGAGTATTG
GAGTTACTGTCAAAAAACAATATGATAAACAATGATCTTGGTCCAGCAACAGCTCAAATGGCCCTTCAGTTGTTTCATC
AAAGATTACAGGTACACGTACCGATGCCATATAGGTGACACACAAATACAACCCGAAGATCATTTGAAATAAAGAAACT
GTGGGAGCAAAACCCGTTCCAAAGCTGGACTGCTGGTCTCCGACGGAGGCCAAATTTATACAACATTAGAAATCTCCACA
TTCTGAAGTCTGCCTAAAAATGGGAATTGATGGATGAGGATTACCAGGGGCGTTTATGCAACCCACTGAACCCATTTGTC
AGCCATAAAGAAATGAATCAATGAACAATGCAGTGATGATGCCAGCACATGGTCCAGCCAAAAACATGGAGTATGATGC
TGTTGCAACAACACACTCCTGGATCCCCAAAAGAAATCGATCCATCTTGAATACAAGTCAAAGAGGAGTACTTGAGGATG
AACAAATGTACCAAAGGTGCTGCAATTTATTTGAAAAATTTCTCCCCAGCAGTTCATACAGAAGACCAGTCGGGATATCC
AGTATGGTGGAGGCTATGGTTCCAGAGCCGAATTGATGCACGGATTGATTCGAATCTGGAAGGATAAAGAAAGAAGA
GTTCACTGAGATCATGAAGATCTGTTCCACCATTGAAGAGCTCAGACGGCAAAAATAGTGAATTTAGCTTGTCCTTCATG
AAAAATGCCTTGTCTTACT (SEQ ID NO:2)

FIG. 10H

Canine codon optimized PR8 PB1:

AGCGAAAGCAGGCAAACCATTTGAATGGATGTCAATCCGACCTTACTTTTCTAAAAGTGCCAGCACAAAATGCTATAAG
CACAACTTTCCTTATACTGGAGACCCCTCTTACAGCCATGGGACAGGAACAGGATACACCATGGATACTGTCAACAGGA
CACATCAGTACTCAGAAAAGGGAAGATGGACAACAAACACCGAAACTGGAGCACCGCAACTCAACCCGATTGATGGGCCA
CTGCCAGAAGACAATGAACCAAGTGGTTATGCCCAAACAGATTGTGTATTGGAGGCGATGGCTTTCCTTGAGGAATCCCA
TCCTGGTATTTTTGAAAACGTCGTATTGAAACGATGGAGGTTGTTTCAGCAAACACGAGTGGACAAGCTGACACAGGGCC
GACAGACCTATGACTGGACTCTGAATAGAAAACAGCCTGCTGCAACAGCACTGGCCAACACAATCGAAGTGTTCAGATCA
AATGGCCTCACCGCAATGAGTCTGGAAGGCTCATCGACTTCTGAAGGATGTGATGGAGTCAATGAACAAAGAAGAAAT
GGGGATCACAACTCATTTTCAGAGAAAGAGACGGGTGAGAGACAATATGACTAAGAAAATGATTACACAGAGAACAATGG
GTAAAAAGAAGCAGAGACTGAACAAAAGGAGTTATCTGATTAGAGCACTGACCCTGAACACAATGACCAAAGATGCTGAG
AGAGGGAAGCTGAAACGGAGAGCAATTGCAACCCAGGGATGCAGATTAGGGGGTTTGTGTACTTTGTGGAGACACTGGC
AAGGAGTATTTGTGAGAACTGGAACAGTCAGGGCTGCCAGTGGGAGGCAATGAGAAGAAAGCAAAGCTGGCAAATGTGG
TGAGGAAGATGATGACCAATTCTCAGGACACCGAACTGTCTTTCACCATCACTGGAGATAACACCAAATGGAACGAAAAT
CAGAATCCTCGGATGTTTCTGGCCATGATCACATATATGACCAGAAATCAGCCCGAATGGTTCAGAAATGTGCTGAGTAT
TGCTCCAATTATGTTCTCAAACAAAATGGCCAGACTGGGAAAAGGGTATATGTTTGAGAGCAAGAGTATGAAACTGAGAA
CTCAGATTCTGCAGAAATGCTGGCAAGCATCGATCTGAAATATTTCAATGATTCAACAAGAAAGAAGATTGAAAAATC
CGACCCCTCCTGATTGAGGGGACTGCATCACTGAGCCCTGGAATGATGATGGGCATGTTCAATATGCTGAGCACTGTGCT
GGGCGTCTCCATCTGAATCTGGGACAGAAGAGATACACCAAGACTACTTACTGGTGGGATGGTCTGCAGTCTCTGACG
ATTTTGCTCTGATTGTGAATGCACCCAATCATGAAGGGATTGAGCCGGAGTCGACAGGTTTTATCGAACCTGTAAGCTG
CTGGGAATCAATATGAGCAAGAAAAAGTCTTACATCAACAGAACAGGTACATTTGAATTCACAAGTTTTTCTATCGCTA
TGGGTTTGTGGCAATTTTCAGCATGGAGCTGCCAGTTTTGGGGTGTCTGGGATCAACGAGTCAGCCGACATGAGTATTG
GAGTGAATGTCATCAAAAACAATATGATCAACAATGATCTGGGTCCAGCAACAGCTCAGATGGCCCTGCAGCTGTTTCATC
AAAGATTACAGGTACACCTACCGATGCCATATCGGTGACACACAGATTGAGCCCGAAGATCATTTGAAATCAAGAAACT
GTGGGAGCAGACCCGCTCAAAGCTGGACTGCTGGTCTCCGACGGAGGCCAAATCTGTACAACATTAGAAATCTCCACA
TTCCTGAAGTCTGCCTGAAATGGGAACTGATGGATGAGGATTACCAGGGGCGCTGTGCAACCCACTGAACCCATTTGTC
AGCCATAAAGAAATTGAATCAATGAACAATGCAGTGTGATGCCAGCACATGGTCCAGCCAAAACATGGAGTATGATGC
TGTGGCAACAACACACTCTGGATCCCAAAGAAATCGATCCATCTGAATACAAGTCAGAGAGGAGTGTGGAGGATG
AACAGATGTACCAGAGGTGCTGCAATCTGTTTGAAAAATTCTTCCCAGCAGTTCATACAGAAGACCAGTCGGGATCTCC
AGTATGGTGGAGGCTATGGTGTCCAGAGCCGAATTGATGCACGGATTGATTTGGAATCTGGAAGGATCAAGAAAGAAGA
GTTCACTGAGATCATGAAGATCTGTTCCACCATGAAGAGCTCAGACGGCAAAAATAGTGAATTTAGCTTGCTTCATG
AAAAAATGCCTTGTCTTACT (SEQ ID NO:17)

FIG. 10I

PR8-UW PA:

AGCGAAAGCAGGTA CTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATGATTGTCGAGCTTGCGGAAAA
AACAAATGAAAGAGTATGGGGAGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTGAAGTATGCT
TCATGTATTTCAGATTTTCACTTCATCAATGAGCAAGGCGAGTCAATAATCGTAGAACTTGGTGATCCAAATGCACATTTTG
AAGCACAGATTTGAAATAATCGAGGGAAGAGATCGCACAAATGGCCTGGACAGTAGTAAACAGTATTTGCAACACTACAGG
GGCTGAGAAACCAAGTTTCTACCAGATTTGTATGATTACAAGGAGAATAGATTCAATCGAAATTGGAGTAACAAGGAGAG
AAGTTCACATATACTATCTGGAAGGCCAATAAAATTAATCTGAGAAAACACATCCACATTTTCTCGTTCACTGGG
GAAGAAATGGCCACAAAGGCAGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAACAGACTATTCACCATAAG
ACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCTTTCGTCACTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTG
AAATCACAGGAACAATGCGCAAGCTTGCCGACCAAAGTCTCCCGCCGAACCTTCTCCAGCCTTGAAAATTTAGAGCCTAT
GTGGATGGATTGCAACCGAACGGCTACATTGAGGGCAAGCTGTCTCAAATGTCCAAAGAAGTAAATGCTAGAATTGAACC
TTTTTTGAAAACAACACCACGACCACTTAGACTTCCGAATGGGCCTCCCTGTTCTCAGCGGTCCAAATTCCTGCTGATGG
ATGCCTTAAATTAAGCATTGAGGACCCAAGTCATGAAGGAGAGGGAATACCGCTATATGATGCAATCAAATGCATGAGA
ACATTCTTTGGATGGAAGGAACCAATGTTGTTAAACCACACGAAAAGGGAATAAATCCAAATTATCTTCTGTCATGGAA
GCAAGTACTGGCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCAAAGACTAAAAATATGAAGAAAACAAGTCAGC
TAAAGTGGGCACCTTGGTGAGAACATGGCACCAGAAAAGGTAGACTTTGACGACTGTAAAGATGTAGGTGATTTGAAGCAA
TATGATAGTGATGAACCAGAAATTGAGGTGCTTGAAGTTGGATTGAGAATGAGTTTAACAAGGCATGCGAACTGACAGA
TTCAAGCTGGATAGAGCTCGATGAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATT
TCACATCAGAGGTGTCTCACTGCAGAGCCACAGAATACATAATGAAGGGAGTGACATCAATACTGCCTTGCTTAATGCA
TCTTGTGCAGCAATGGATGATTTCCAATTAATTCCAATGATAAGCAAGTGATAGAACTAAGGAGGGAAGGCGAAAGACCAA
CTTGATGGTTTCATCATAAAAGGAAGATCCCACTTAAGGAATGACACCGACGTGGTAAACTTTGTGAGCATGGAGTTTT
CTCTCACTGACCCAAGACTTGAACCACATAAATGGGAGAAGTACTGTGTTCTTGAGATAGGAGATATGCTTATAAGAAGT
GCCATAGGCCAGGTTTCAAGGCCCATGTTCTGTATGTGAGAACAAATGGAACTCAAAAATTAATGAAATGGGGAAT
GGAGATGAGGCGTTGCTCTCCAGTCACCTTCAACAAATGAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAAG
ACATGACCAAAGAGTTCTTTGAGAACAAATCAGAAACATGGCCATTGGAGAGTCCCCAAAGGAGTGGAGGAAAGTTCC
ATTGGGAAGGTCTGCAGGACTTTATTAGCAAAGTCGGTATTCACAGCTTGATGCATCTCCAACTAGAAGGATTTTC
AGCTGAATCAAGAAAACCTGCTTCTATCGTTCAAGCTCTTAGGGACAACCTGGAACTGGGACCTTTGATCTTGGGGGGC
TATATGAAGCAATTGAGGAGTGCCTGATTAATGATCCCTGGGTTTTGCTTAATGCTTCTTGGTTCAACTCCTTCTTACA
CATGCATTGAGTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAGTACCTTGTCTTACT (SEQ ID NO:1)

FIG. 10J

Canine codon optimized PR8 PA:

AGCGAAAGCAGGTA CTGATCCAAAATGGAAGATTTTGTGCGACAATGCTTCAATCCGATGATTGTCGAGCTTGCGGAAAA
AACAAATGAAAGAGTATGGGGAGGACCTGAAAATCGAAACAAACAAATTTGCAGCAATATGCACTCACTTGGAAGTATGCT
TCATGTATTGAGATTTTCACTTCATCAATGAGCAAGGCGAGTCAATAATCGTAGAACTTGGTGATCCAAATGCATTTTG
AAGCACAGATTTGAAATAATCGAGGGAAGAGATCGCACAAATGGCCTGGACAGTAGTAAACAGTATTTGCAACACTACAGG
GGCTGAGAAACCAAGTTTCTACCAGATTTGTATGATTACAAGGAGAATAGATTCATCGAAATTGGAGTAACAAGGAGAG
AAGTTCACATATACTATCTGGAAAAGGCCAATAAAATTAATCTGAGAAAACACACATCCACATTTTCTCGTTCACTGGG
GAAGAAATGGCCACAAAGGCAGACTACACTCTCGATGAAGAAAGCAGGGCTAGGATCAAAACCAGACTATTACCATAAG
ACAAGAAATGGCCAGCAGAGGCCTCTGGGATTCCTTTCGTCACTCCGAGAGAGGAGAAGAGACAATTGAAGAAAGGTTTG
AAATCACAGGAACAATGCGCAAGCTTGCCGACCAAGTCTCCCGCCGAACCTCTCCAGCCTTGAAAATTTAGAGCCTAT
GTGGATGGATTGGAACCGAACGGCTACATTGAGGGCAAGCTGTCTCAAATGTCCAAAGAAGTAAATGCTAGAATTGAACC
TTTTCTGAAAACAACACCACGACCACTGAGACTGCCCAATGGGCCTCCCTGTTCTCAGCGGTCCAAATTCCTGCTGATGG
ATGCCCTGAAACTGAGCATTGAGGACCCAAGTCATGAAGGAGAGGGAATTCCTGTATGATGCAATCAAATGCATGAGA
ACATTCTTTGGATGGAAGGAACCAATGTGGTGAAACCACAGAAAAGGGAATCAATCCAAATTATCTGCTGTCATGGAA
GCAGGTGCTGGCAGAACTGCAGGACATTGAGAATGAGGAGAAAATTCAAAGACTAAAAATATGAAGAAAACAAGTCAGC
TGAAGTGGGCACTGGGTGAGAACATGGCACCAGAAAAGGTGGACTTTGACGACTGTAAAGATGTGGGTGATCTGAAGCAG
TATGATAGTGATGAACCAGAACTGAGGTCCCTGGCAAGTTGGATTGAGAATGAGTTTAACAAGGCATGCGAACTGACAGA
TTCAAGCTGGATTGAGCTCGATGAGATTGGAGAAGATGTGGCTCCAATTGAACACATTGCAAGCATGAGAAGGAATTATT
TCACATCAGAGGTGTCTACTGCAGAGCCACAGAATACATCATGAAGGGAGGTACATCAATACTGCCCTGCTGAATGCA
TCTTGTCAGCAATGGATGATTTCCAGCTGATTCGAATGATCAGCAAGGTGTAGAACTAAGGAGGGAAGGCGAAAGACCAA
CCTGTATGGTTTCATCATCAAAGGAAGATCCACCTGAGGAATGACCCGACGTGGTGAACCTTTGTGAGCATGGAGTTTT
CTCTCACTGACCCAAGACTGGAACCACATAAATGGGAGAAGTACTGTGTGCTGGAGATTGGAGATATGCTGATCAGAAGT
GCCATTGGCCAGGTGTCAAGGCCATGTTCTGTATGTGAGAACAAATGGAACCTCAAAAATTAATGAAATGGGGAAT
GGAGATGAGGCGCTGCCTCTCCAGTCACTGCAGCAGATTGAGAGTATGATTGAAGCTGAGTCCTCTGTCAAAGAGAAAG
ACATGACCAAAGAGTCTTTGAGAACAAATCAGAAACATGGCCATTGGAGAGTCCCCAAAGGAGTGGAGGAAAGTTCC
ATTGGGAAGGTCTGCAGGACTCTGCTGGCAAAGTCCGTGTTCAACAGCCTGTATGCATCTCCACAGCTGGAAGGATTTTC
AGCTGAATCAAGAAAACCTGCTGCTGATGCTGCAGGCTCTGAGGGACAACCTGGAACCTGGGACCTTTGATCTGGGGGGGC
TGTATGAAGCAATTGAGGAGTGCCTGATTAATGATCCCTGGGTGCTGCTGAATGCTTCTGGTTCAACTCCTTCCTTACA
CATGCATTGAGTTAGTTGTGGCAGTGCTACTATTTGCTATCCATACTGTCCAAAAAGTACCTTGTTTCTACT (SEQ ID NO:18)

FIG. 10K

PR8-UW NP:

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGCACCAAACGATCTTACGAACA
GATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAGCATCCGTCGGAAAAATGATTGGTGGAATTGGACGAT
TCTACATCCAAATGTGCACCGAACTCAAACTCAGTGATTATGAGGGACGTTGATCCAAACAGCTTAACAATAGAGAGA
ATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCAGTGCGGGGAAAGATCCTAAGAAAAC
TGGAGGACCTATATACAGGAGAGTAAACGGAAAGTGGATGAGAGAACTCATCCTTTATGACAAAGAAGAAATAAGGCGAA
TCTGGCGCCAAGCTAATAATGGTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGAT
GCAACTTATCAGAGGACAAGAGCTCTTGTCGACCGGAATGGATCCAGGATGTGCTCTCTGATGCAAGGTTCAACTCT
CCCTAGGAGGTCTGGAGCCGAGGTGCTGCAGTCAAAGGAGTTGGAACAATGGTGATGGAATTGGTCAGAATGATCAAAC
GTGGGATCAATGATCGGAACCTCTGGAGGGGTGAGAATGGACGAAAAACAAGAATTGCTTATGAAAGATGTGCAACATT
CTCAAAGGGAAATTTCAAACCTGCTGCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGCCGGAACCCAGGGAATGCTGA
GTTCAAGATCTCACTTTTCTAGCACGGTCTGCACTCATATTGAGAGGGTCGGTTGCTCACAAGTCTGCTGCCTGCCTGCCT
GTGTGTATGGACCTGCCGTAGCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTCTAGTCGGAATAGACCCTTTCAGA
CTGCTTCAAACAGCCAAGGTGACAGCCTAATCAGACCAATGAGAATCCAGCACACAAGAGTCAACTGGTGTGGATGGC
ATGCCATTCTGCCGATTTGAAGATCTAAGAGTATTAAGCTTCATCAAAGGGACGAAGGTGCTCCAAGAGGGAAGCTTT
CCACTAGAGGAGTTCAAATTGCTTCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAAGTGAAGCAGGTAC
TGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAAATCAGCATACAACCTACGTT
CTCAGTACAGAGAAATCTCCCTTTTGACAGAACAACCATTATGGCAGCATTCATGGGAATACAGAGGGGAGAACATCTG
ACATGAGGACCGAAATCATAAGGATGATGGAAGTGAAGACCAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAG
CTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGATCTTATTTCTTCGGAGACAA
TGCAGAGGAGTACGACAATTAAAGAAAAATACCTTGTTTCTACT (SEQ ID NO:4)

FIG. 10L

Canine codon optimized NP:

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGCACCAAACGATCTTACGAACA
GATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAGCATCCGTCGGAAAAATGATTGGTGAATTGGACGAT
TCTACATCCAGATGTGCACCGAACTCAAACCTCAGTGATTATGAGGGACGGCTGATCCAGAACAGCCTGACAATCGAGAGA
ATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACCTGGAAGAACATCCAGTGCCGGGAAAGATCCTAAGAAAAC
TGGAGGACCTATCTACAGGAGAGTGAACGGAAAGTGGATGAGAGAACTCATCCTGTATGACAAAGAAGAAATCAGGCGAA
TCTGGCGCCAGGCTAATAATGGTGACGATGCAACCGCTGGTCTGACTCACATGATGATCTGGCATTCCAATCTGAATGAT
GCAACTTATCAGAGGACAAGAGCTCTGGTGCGCACCGGAATGGATCCAGGATGTGCTCTCTGATGCAGGGTTCAACTCT
CCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTGGGAACAATGGTGATGGAAGTGGTCAAGATGATCAAAA
GAGGGATCAATGATCGGAACCTTCTGGAGGGGTGAGAATGGACGAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATT
CTCAAAGGGAAATTCAGACTGCTGCACAGAAAGCAATGATGGATCAGGTGAGAGAGAGCCGGAACCCAGGGAATGCTGA
GTTGGAAGATCTCACTTTTCTGGCACGGTCTGCACTCATCCTGAGAGGGTCCGTGGCTCACAAGTCTGCCTGCCTGCCT
GTGTGTATGGACCTGCCGTGGCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTCTGGTCGGAATTGACCTTTTCAGA
CTGCTGCAGAACAGCCAGGTGTACAGCCTGATCAGACCAATGAGAATCCAGCACACAAGAGTCAGCTGGTGTGGATGGC
ATGCCATTCTGCCGATTTGAAGATCTGAGAGTGCTGAGCTTCATCAAAGGGACCAAGGTGCTCCCAAGAGGGAAGCTGT
CCACTAGAGGAGTGCAGATTGCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTGGAAGTGAAGCAGGTAC
TGGGCCATCAGGACCAGAAGTGGAGGAAACACCAATCAGCAGAGGGCATCTGCCGGCCAGATCAGCATTAGCCTACCTT
CTCAGTGCAGAGAAATCTCCCTTTTGACAGAACCAACATTATGGCAGCATTCAATGGGAATACAGAGGGGAGAACATCTG
ACATGAGGACCGAAATCATCAGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTCCAGGGGCGGGGAGTCTTCGAG
CTCTCGGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGATCTTATTTCTTCGGAGACAA
TGCAAGAGGAGTACGACAATTAAAGAAAAATACCTTGTTTCTACT (SEQ ID NO:19)

FIG. 10M

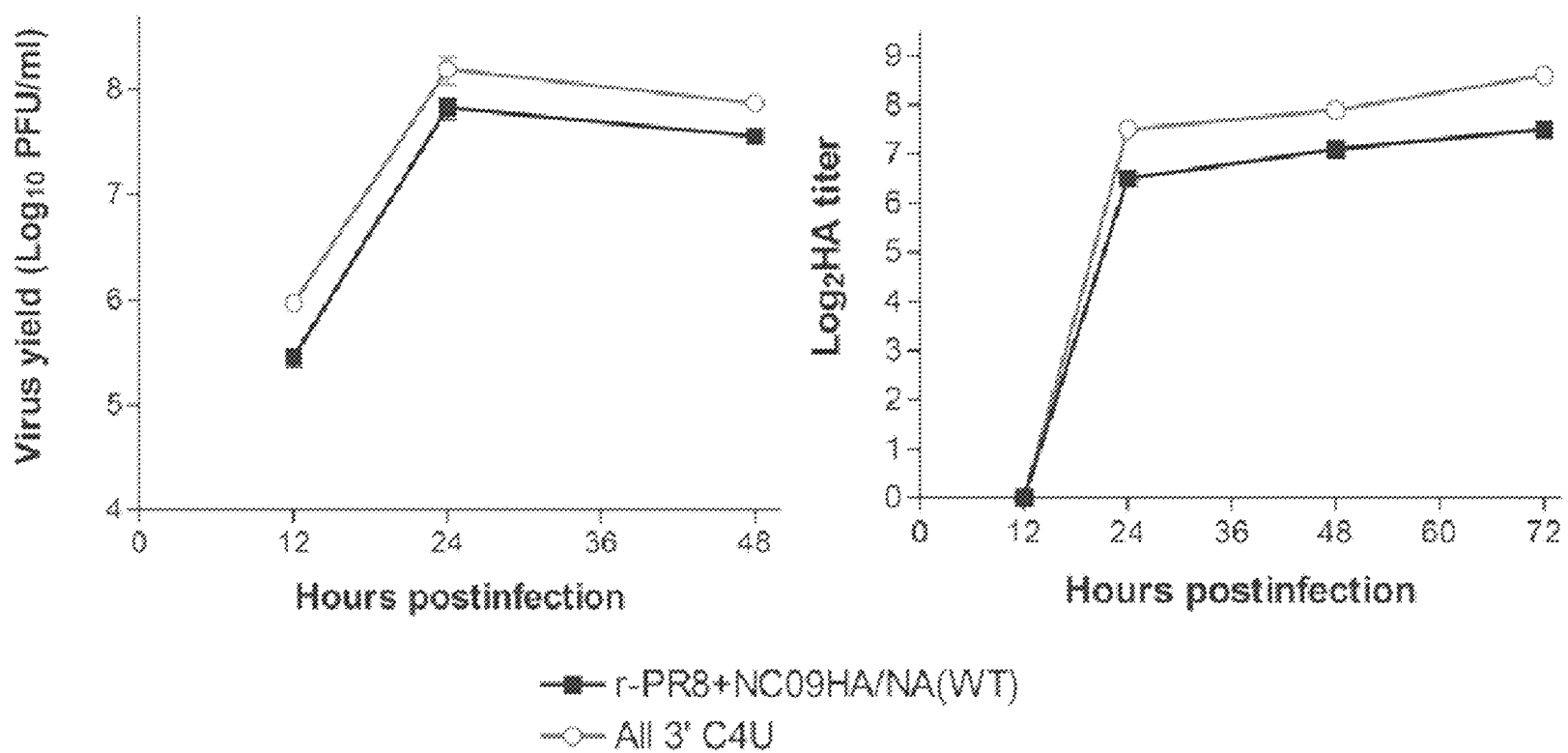
Figure 11 A Nucleotide mutation in position 4 of each gene of PR8 and Indo/NC/09.

Genes	Position 4 of vRNA	
PR8 PB2	C	
PR8 PB1	C	
PR8 PA	C	
PR8 NP		U
PR8 M		U
PR8 NS		U
Indo/NC/09 HA		U
Indo/NC/09 NA		U

Figure 11B All 3'C4U mutant

Genes	Position 4 of vRNA	
PR8 PB2		U
PR8 PB1		U
PR8 PA		U
PR8 NP		U
PR8 M		U
PR8 NS		U
Inda/NC/09 HA		U
Inda/NC/09 NA		U

Figure 11C Growth kinetics of 3' C4U mutant



HA

atgaacactcaaatcctggtattcgtctgattgcatcttccaacaaatgcagacaaaatcgtcctcggacatcatgccgtgtcaaacggaaccaagtaaa
cacattaactgaaagaggagtggaagtcgtcaatgcaactgaaacagtggaacgaacaaacatcccaggatctgctcaaaagggaagacagtgacc
tcggtcaatgtggaactcctggggacaatcactggaccacctaattgtgaccaattcctagaattttcagccgatttaattattgagaggcgagaagggaagtgtg
tctgttatcctgggaaattcgtgaatgaagaagcctgaggcaaatctcagagaatcaggcgggaattgacaaggaagcaatgggattcacatacagtggaat
aagaaactaatggagcaaccagtgcatgtaggagatcaggatcttctctatgcagaaatgaaatggctcctgtcaaacacagataatgtcgtattccgcga
tgactaagtcataataaaatacaagaaaaagcccagctctaatagtatggggatccatcttccgtatcaactgcagagcaaaccaagctatatgggagtg
aaacaaactgggtgacagtggtggttctaattatcaacaactctttgtacggagtcaggagcgagaccacaagttaatggtctatctggaagaattgacttcat
tggctaattgctaaatcccaatgatacagtcactttcagtttcaatggggcttctatagctccagaccgtgcaagcttctgagaggaaaatctatgggaatcag
agtgagtgacaggttgatgccaattgtgaaggggactgctatcatagtgagggaacaataaagtaacttgcatttcagaacatagatagcagggcagtg
gaaaatgtccgagatagttaagcaaaaggagctgctgctagcaacagggaagaagaatgttctgagattccaagggaaggagcctatttggctatagc
gggttcttgaaatggatgggaaggcctaattgagtggttggtatggtttcagaccagaatgcacaggagagggaactgctgcagattacaaagcact
caatcggaattgatacaataacaggaaaattaaaccggcttatagaaaaaaccaaccaaatgtgattgtagacaatgaattcaatgaggtagagaag
caaatcggtaatgtgataaattggaccagagattctataacagaagtgtgtcatacaatgctgaactcttgtagcaatggagaaccagcatacaattgact
ggctgattcagaaatggcaaacgtgacgaacgagtgaaaagacagctgagagagaatgtggaagaagtggaactggttcttgaataattcacaagt
gatgatgactgtatggcagttatagaataacacctatgacacagcaatacagggaaggcaatgcaaaatagaatacagattgaccagctcaacta
agcagcggtacaaagatgtgatacttgggttagcttcggggcatcatgttctactttagccattgtaatgggccttgcctcatatgtgtaagaatggaaa
catcggtgcactattgtatataa (SEQ ID NO:20)

MNTQLLVFAL	IAIIPTNADK	ICLGHHAVSN	GTKVNTLTER	GVEVVNATET	VERTNIPRIC
SKGKRTVDLG	QCGLLGTTTG	PPQCDQFLEF	SADLI IERRE	GSDVCYPGKF	VNEEALRQIL
RESGGIDKEA	MGFTYSGIRT	NGATSACRRS	GSSFYAEMKW	LLSNTDNAAF	PQMTKSYKNT
RKSPALIVWG	IHHSVSTABQ	TKLYGSGNKL	VTVGSSNYQQ	SFVPSFGARP	QVNLGSGRID
FHWLMLNPND	TVTFSFNCAF	IAPDRASFRL	GKSMGIQSGV	QVDANCEGDC	YHSGGTIISN
LPFQONIDSRA	VGKCPRYVKQ	RSLLLATGMK	NVPEIPKGRG	LFGAIAGFTE	NGWEGLIDGW
YGFRRHQAQG	EGTAADYKST	QSAIDQITGK	LNRLIEKTNQ	QFELIDNEFN	EVEKQIGNVI
NWTRDSITEV	WSYNAELLVA	MENQHTIDLA	DSEMDKLYER	VKRQLRENAE	EDGTGCFEIF
HKCDDDCMAS	IRNNTYDHSK	YREEAMQNRI	QIDPVKLSSG	YKDVILWFSF	GASCFILLAI

VMGLVFICVK NGNMRCTICI (SEQ ID NO:21)

NA

atgaatccaaatcagaagattctatgcacttcagccactgctatcataataggcgcaatgcagtagctcattggaatagcaaacctaggattgaacataggact
gcatctaaacgggctgcaattgtctcacactcacaacctgaaacacacacagccaaacaaataataaacactattataatgaacaaacatcacaa
catccaaatggaagagagaacaagcagggaatttcaataacttaactaaaggctctgtactataaattcatggcacatataagggaagacaatgcagtaaga
attggagagagctcggtgttttagtcacaagagaacctatgttctatgagaccagatgaatgcagggttctatgctctcagccaaggaacaacaatcagagg
gaaacactcaaacggaacaatacacgataggtcccagtatcgcgccctgataagctggccactatcatcaccgccacagtgtaaacagcagggtggaatg
cattgggtggtcaagtactagttgccatgtggcaaatccaggatgtcaatgttatatcaggacaaacaacaatgcatctgcagtagtatggtacaacagaa
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catgttacggggaacgaacaggaattacctgcacatgcagggaacattggcagggtcctcaatagaccagtgattcagatagaccagtagcaatgacacaca
ctagtaatatatagcagtcctgttcttacagacaatccccgaccgaatgacccaataataggtgaatgtaatgaccttatccaggttaataataaatggag
tcaagggttctacacctggtatgggctaacacttggctaggggaggacaataagcacagcctcgaggtctggatagagatgttaaaagtccaatgcat
gacagatgatagatcaaacgccattcaaggctagacaattgtattaaacgctgactggagtggttacagtggaatcttctatggactattgggctgaaggggact
gctatcgagcgtgttttatgtggagttgatctggaagaccgaaggagaataaagtgtggaggaccagcaatagtagtatgtagtctgttccagtagacagaat
tcttgggacaatggaactggcctgatggggctaaaatagagtacttctctaa (SEQ ID NO:22)

MNPNQKILCTSATAIHGAI AVLIGIANLGLNIGLHLKPGCNCSHSQPETTNTSQTHINNYNETNITNIQMEERTSRNFNNLTGKL
CTINSWHIYGKDNAVRIGESSDVLVTRPEYVSCDPDECRFYALSQGTTRG KHSNGTIHDSQYRALISWPLSSPPTVYNSRVECI
GWSSTSCHD GKSRSISICISGPNNNASAVVWYNRRPVAEINTWARNILRTQESECVCHNGVCPVVFTDGSATGPADTRIYYFK

FIG. 12A

EGKILKWESLTGTAKHIEECSCYGERTGITCTCRDNWQGSNRPIQIDPVAMTHTSQYICSPVLTNPNRPNPNIGKCNPDYPG
NNNNGVKGSYLDGANTWLGRITISTASRSGYEMLKVPNALTDORSKPIQGQITVLNADWSGYSGSFMDYWAEGDCYRACF
YVELIRGRPKEDKVWWTNSIVSMCSSTFLGQWNWPDGAKIEYFL (SEQ ID NO:23)

HA

atgaacactcaaatcctggtattcgtctgattgcatcattccaacaaatgcagacaaaatctgctcggacatcatgctgtcacaacggaaccaaagtaaa
cacattaactgaaagaggagtggaagtcgtcaatgcaactgaaacagtggaacgaacaaacatcccaggatctgctcaaaagggaaggaacagtgacc
tcggctcaatgtgactcctgggacaaatcactggaccacccaatgtgacaaatctcagaatttcagccgatttaattattgagaggcgagaaggaaagtgtg
tctgttatcctgggaaattcgtgaatgaagaagcctctgaggcaaatctcagagaatcaggcggaattgacaaggaaagcaatgggattcacacagtggaat
aagaactaatggagcaaccagttcatgtaggagatcaggatcttcttctcagagaatgaatggctcctgtcaaacacagataatgctgcatcctccgaga
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aaacaaactggtgacagtgaggagttctaattatcaacaactttgtacagagtcgggagcgagaacacaagttaattggtcaatctggaagaattgacttca
ttggctaatgtcaaatcccaatgatacagtcactttcagtttcaatggggcttcagctccagaccgtgcaagcttcctgagaggaaaatcatgggaatccag
agtgagtagcagggtgatgcccattgtgaaggggactgtattatagtgaggagacaataataagtaacttgccatttcagaaacatagatagcaggggcagttgg
aaaatgtccgagatattgtaagcaaaaggagtcgtctgtagcaacagggaaggaagaatgttctgtagattccaaagggaaggcctaatttgggtctataggg
gggttcattgaaatggatgggaaggcctaattgtatgggtgtaggttcagacaccagaatgcacaggagagggaactgctgtagattacaaaagcactc
aatcggcaattgatcaataacaggaaaattaaaccggcttatagaaaaaaccaaccaaatgtttagttgatagacaatgaattcactgaggtatagaagc
aaatcggtaatgtataaattggaccagagattctataacagaagtgtggtatatacaatgctgaactcttgtagcaatggagaaccagcatcaaatgatctg
gctgattcagaaatggacaaactgtacgaacagtgaaagacagctgagagagaatgctgaagaagatggcactgggtgcttgaatatttcacaagtgtg
atgatgactgtatggccagcattagaataacacatgatcacagcaaatccagggaagaggcaatgcaaaatagaatcacagattgacccagtcacactaa
gcagcggtctacaagatgtgatacttgggttagcttcggggcatcatgttcatactttagccattgcaatgggcctgtctcatatgtgtaaagaatggaaa
c atgcggtgactattgtatataa (SEQ ID NO:24)

MNTQILVFALIAIPTNADKICLGHHAHSVNGTKVNTLTERGVEVVNATETVERTNIPRICSKGKRTVDLGQCGLLGTITGPPQCDQ
FLEFSADLIERREGSDVCYPGKFVNEELRQILRESGGIDKEAMGFTYSGIRTNGATSSCRRSGSSFYAEMKWLLSNTDNAAFP
QMTKSYKNTRKNPALIVWGIHHSSTAEQTKLYSGSNKLVTVGSSNYQQSFVPSPGARTQVNGQSGRIDFWMLNPNNDTV
TFSFNGAIAPDRASFLRGKSMGIQSGVQVDADCEGDCYSSGTTISNLPFQNIIDSRVAGKCPRYVKQRSLLATGMKNVPEIP
KGRGLFGAIAGFIENGWEGLDGWYGFHONGAQEGTAADYKSTQSAIDQITGKLNRLIEKTNQQFELIDNEFEVEKQIGNVI
NWTRDSITEVWSYNAELLVAMENQHTIDLADSEMDKLYERVKRQLRENAEEDGTGCFEIFHKCDDDCMASIRNNTYDHSKY
REEMQNRIQIDPVKLSSGYKDVILWFSFGASCFILLAIAMGLVFCVKNNGNMRTCTICI (SEQ ID NO:25)

NA

atgaatccaaatcagaagattctatgcacttcagccactgctatcataataggcgcaatgcagtagctacttggaatagcaaacctaggattgaacataggact
gcatctaaaccgagctgcaattgctcacactcacaacctgaacaaacaaacaaagccaacaaataataaacaactattataatgaacaaacacaccaa
catccaatggaaagagagaacaagcaggaatttcaataacttaactaaagggtctgtactataaattcatggcacatatatgggaaagacaatgcggtaaag
attggagagagctcggatgttttagtcacaagagaacctatgtttcatgagaccagatgaatgcagggtctatgctctcagccaaggaaacaacatcagagg
aaaacactcaaacgggaacaatacacgataaggtccagatcgcgcctgataagctggccactatcatcacgcccacagtgtaaacagcagggtggaatg
cattgggtggtcaagtactagttgcatgatggcaaatccaggatgtcaaatgtatatcaggaccaaacacaacatgcatctgcagtagtatgtgtaacagaa
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gtctgccactggacctgcagacacaagaatatactatttaagagggggaataattgaatgggagtcctgactggaactgctaagcatattgaagaatgct
catgttacggggaacgaacaggaattacctgcacatgcaaggacaattggcgggctcaaatagaccagtgattcagatagatccagtagcaatgacacaca
ctagtcagtatatatgcagtcctgtttctacagacaatccccgaccgaatgacccaatataggtgaagtgaatgaccttatccaggtaataataacaatggag
tcaagggtattctacactggatggggtacacacttggctaggagggaacaataagcacagcctcagggtctggatagagatgttaaaagtccaatgcat
gacagatgatagatcaaacgccattcaagggtcagacaattgtattaaacgctgactggagtggttacagtggatcttcatggactattgggtgaggggact
gctatcgagcgtgttttatgtggaattgatactggaagacccaaggaggataaagtgtggtggaccagcaatagtagtatcatgatgtgtccagtagcagaat
tcctgggacaatggaaactggcctgatggggctaaaatagagtacttctctaa (SEQ ID NO:26)

MNPNQKILCTSAIHGAIIVLIGIANLGLNIGLHLKPSNCNSHSPETNTSQTIIINNYNETNITNIOMEERTSRNFNLTGKL
CTINSWHIYGKDNAVRIGESSDVLVTREPYVSCDPDECFYALSQGTITRGKHSNGTIHDSQYRALISWPLSSPPTVYNSRVECI
GWSSTSCHDGKSRMSICSGPNNNASAVVWYNNRPVAEINTWARNILRTQESECVCHNGVCPVVFTDGSATGPADTRIYYFK

FIG. 12B

EGKILKWESLTGTAKHIEECSCYGERTGITCTCKDNWQGSNRPVIQIDPVAMTHTSQYICSPVLTDNPRPNDPNIGKCNDPYPG
NNNNGVKGFSYLDGANTWLGRTISTASRSGYEMLKVPNALTD DRSKPIQGQTIVLNADWSGYSGSFMDYWAEGDCYRACF
Y VELIRGRPKEDKVWWTSNSIVSMCSSTFLGQWNWPDGAKIEYFL (SEQ ID NO:27)

FIG. 12C

Figure 13A Construct chimeric HA &NA to increase virus replication

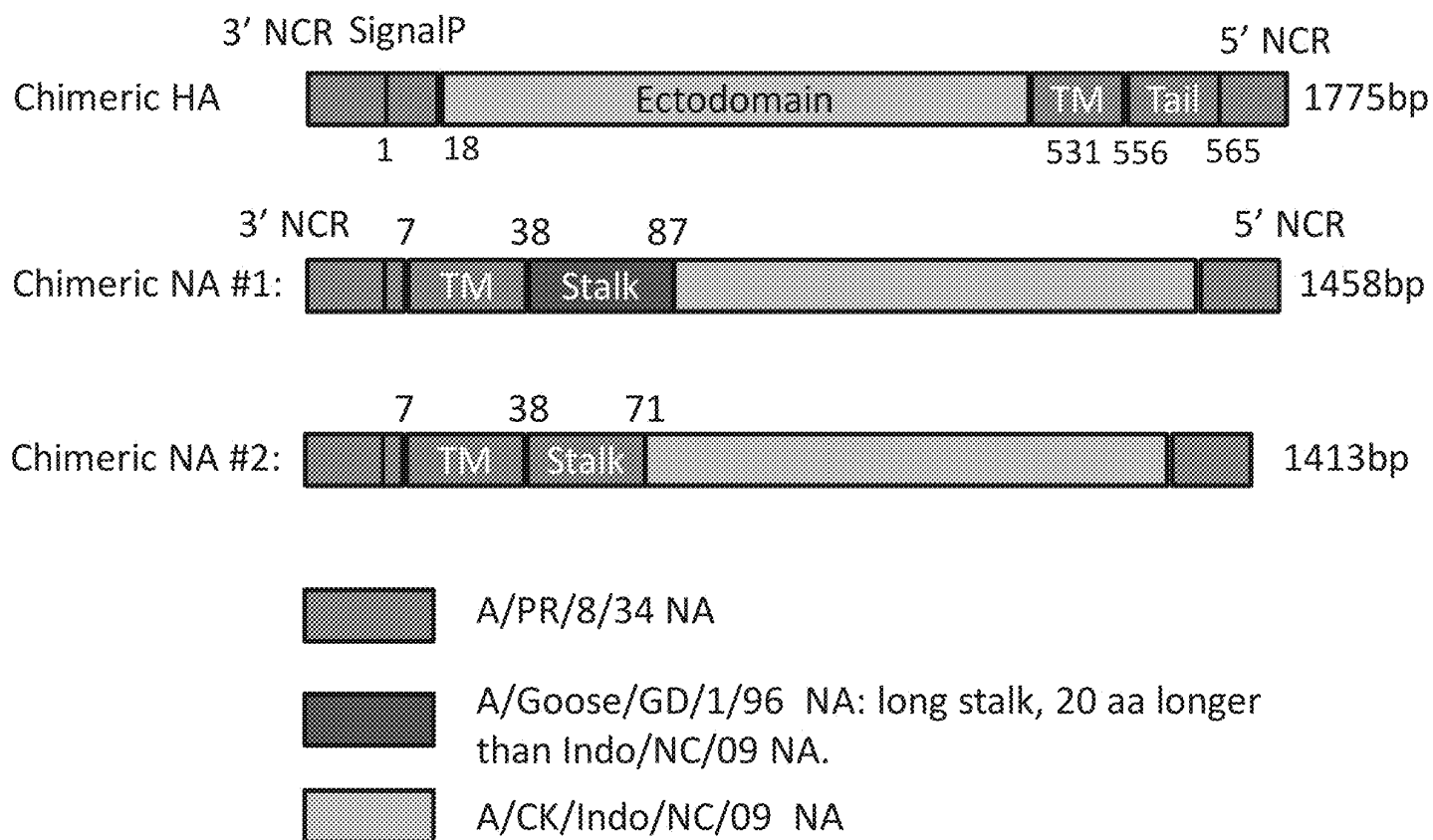


Figure 13B Growth kinetics in MDCK cells

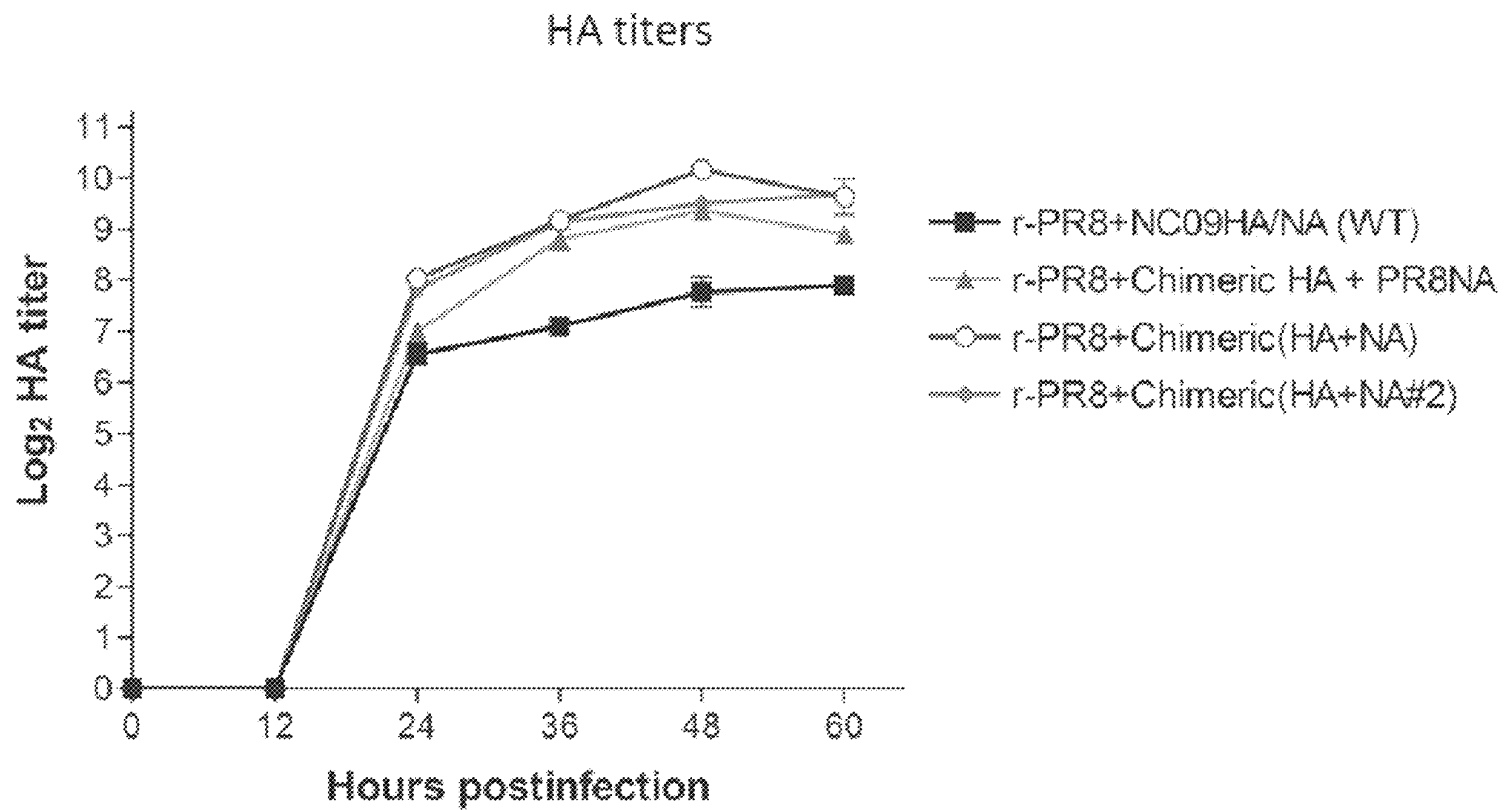
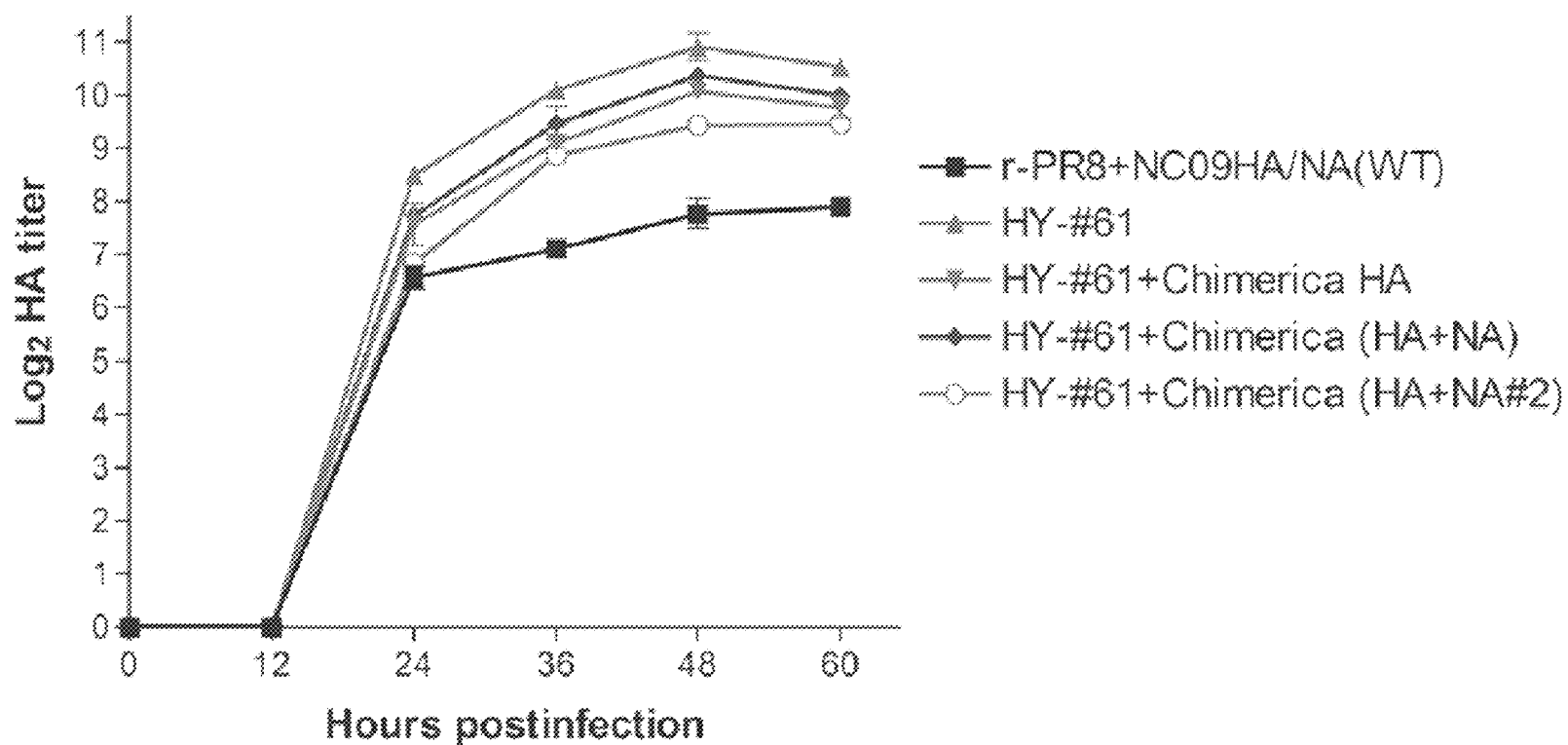
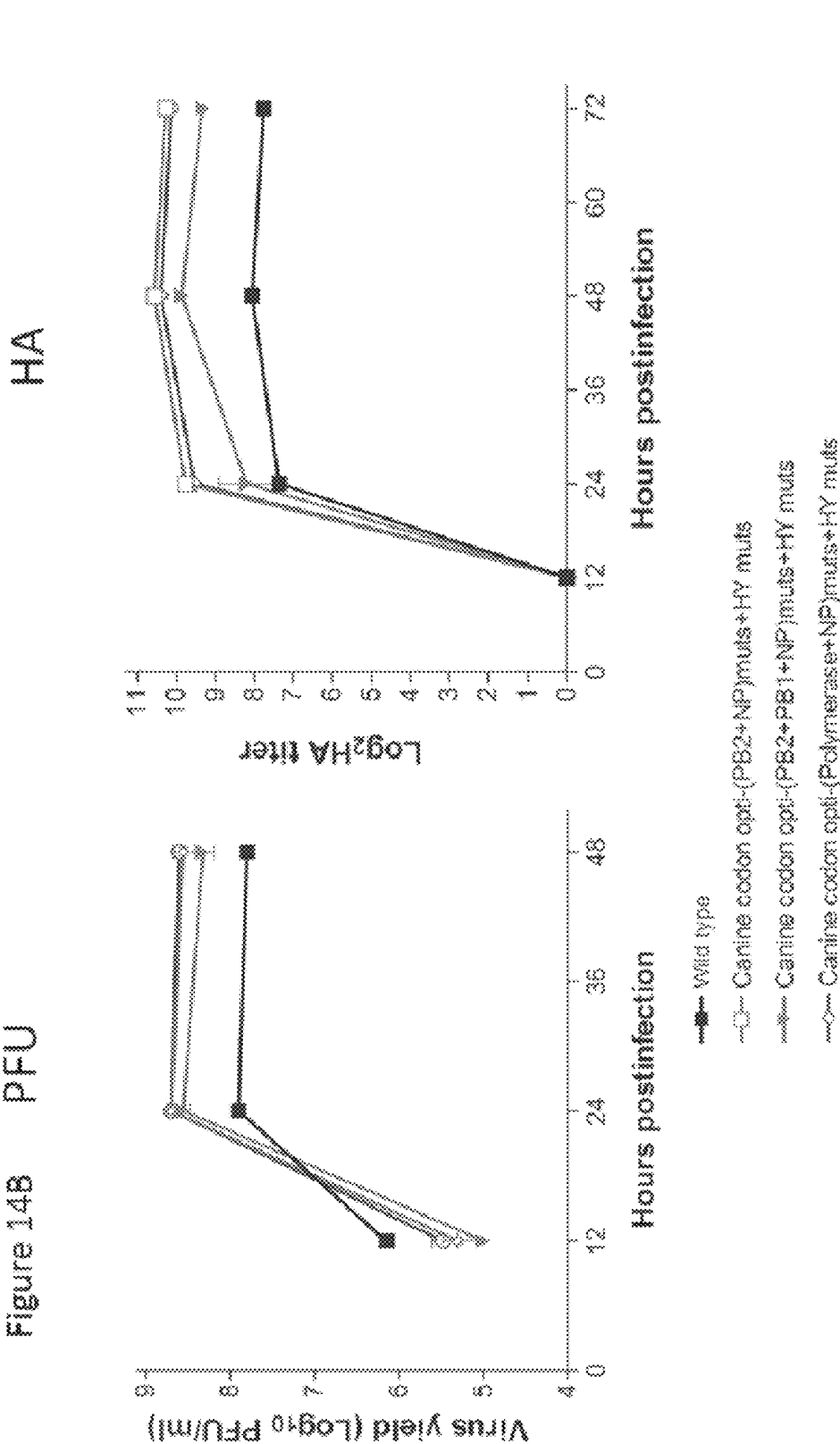


Figure 14A Growth kinetics in MDCK cells



HY-#61 includes PB2: M202L F323L, PB1 Q247H, PA K142N, NP R74K, M V97A Y100H and NS K55E mutations.



HY mutations include PB2: M202L F323L, PB1 Q247H, PA K142N, NP R74K, M V97A Y100H and NS K55E mutations.

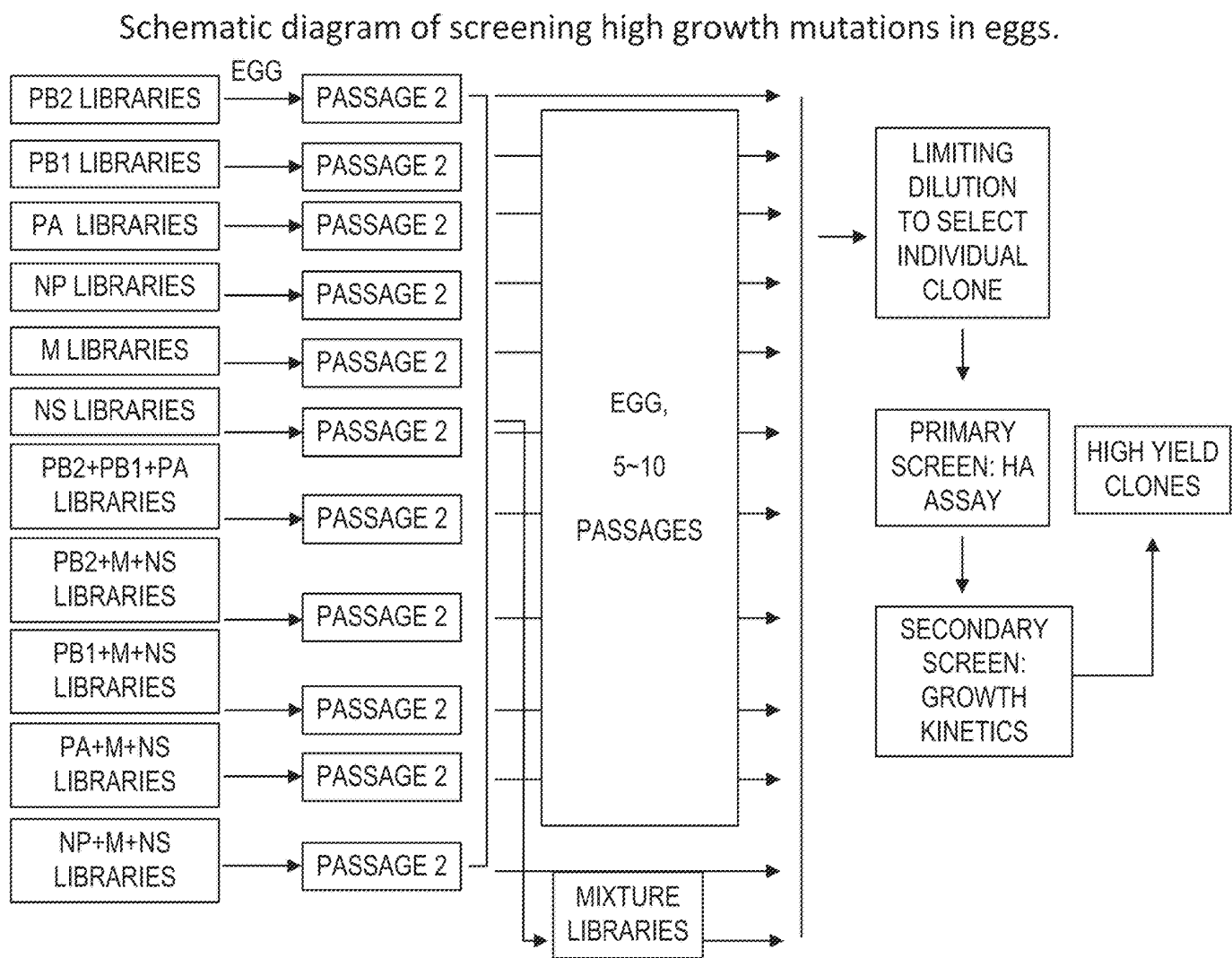


Figure 15

Figure 16 Summary of HA assay of individual clones purified from Vero cells

Groups	Numbers of clone	Fold change	%
WT HA titer = $2^{6.5}$	5	-	2.3%
HA titer = $2^{>9-9.5}$	16	>5.6	7.4%
HA titer = $2^{>8-9}$	91	>2.8 -5.6	42.2%
HA titer = $2^{6.5-8}$	80	1 - 2.8	37.0%
HA titer < $2^{6.5}$	24	<1	11.1%
Total	216	-	100%

Figure 17 Recombinant viruses generated with different PR8 backbone mutants.

#	Del-HA & NA genes	PB2	PB1	PA	NP	M	NS
WT	CK/Indo/NC/09	WT	WT	WT	WT	WT	WT
HY-1		I504V	M40L G180W	R401K	I116L	WT	A30P R118K
HY-2		E391Q		I30T E31K K142N	R74K S377N	WT	S161T
HY-3		I504V		K142N	I116L	V97A Y100H	V136M S161T
HY-4		M202L F323L		K356R	I116L	V97A Y100H	K55E
HY-5				K356R	R422L	WT	K55E

Flow chart of high yield candidate vaccine viruses in MDCK and Vero cells

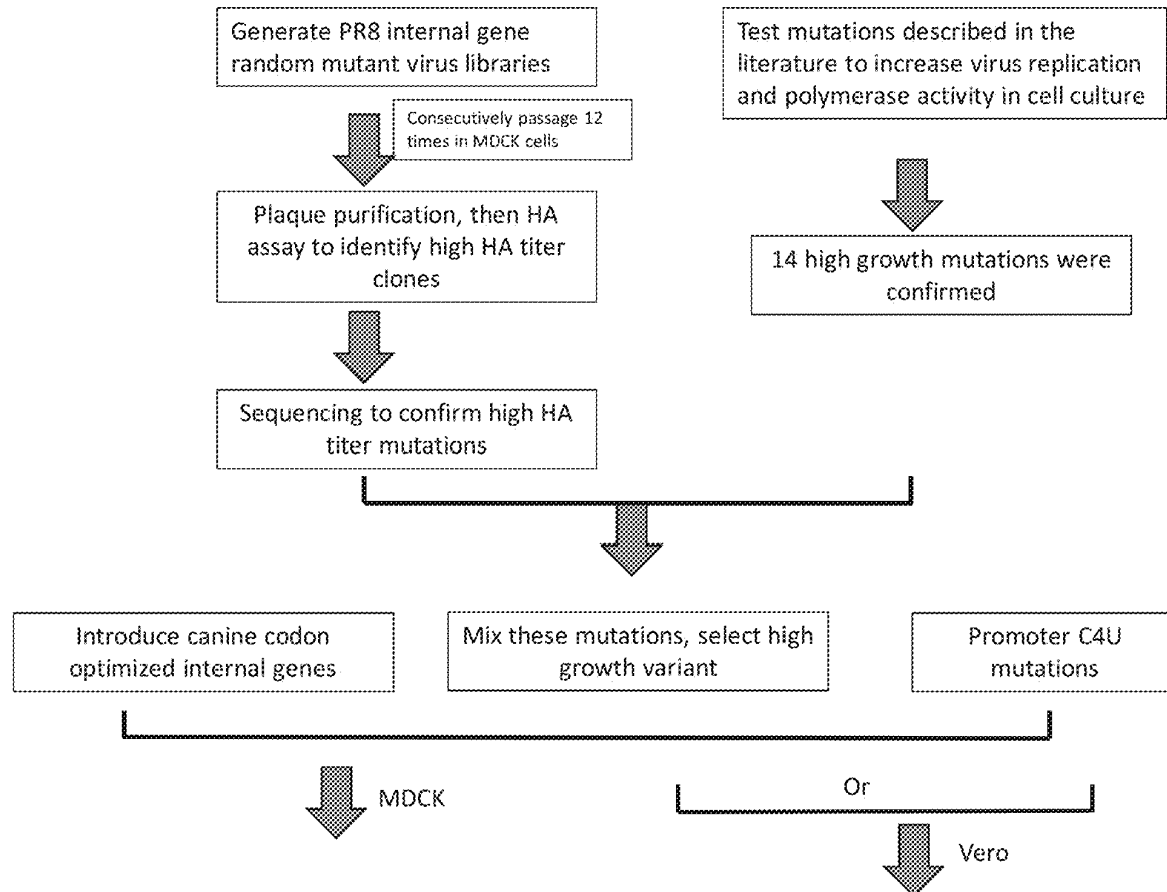


FIG. 18A

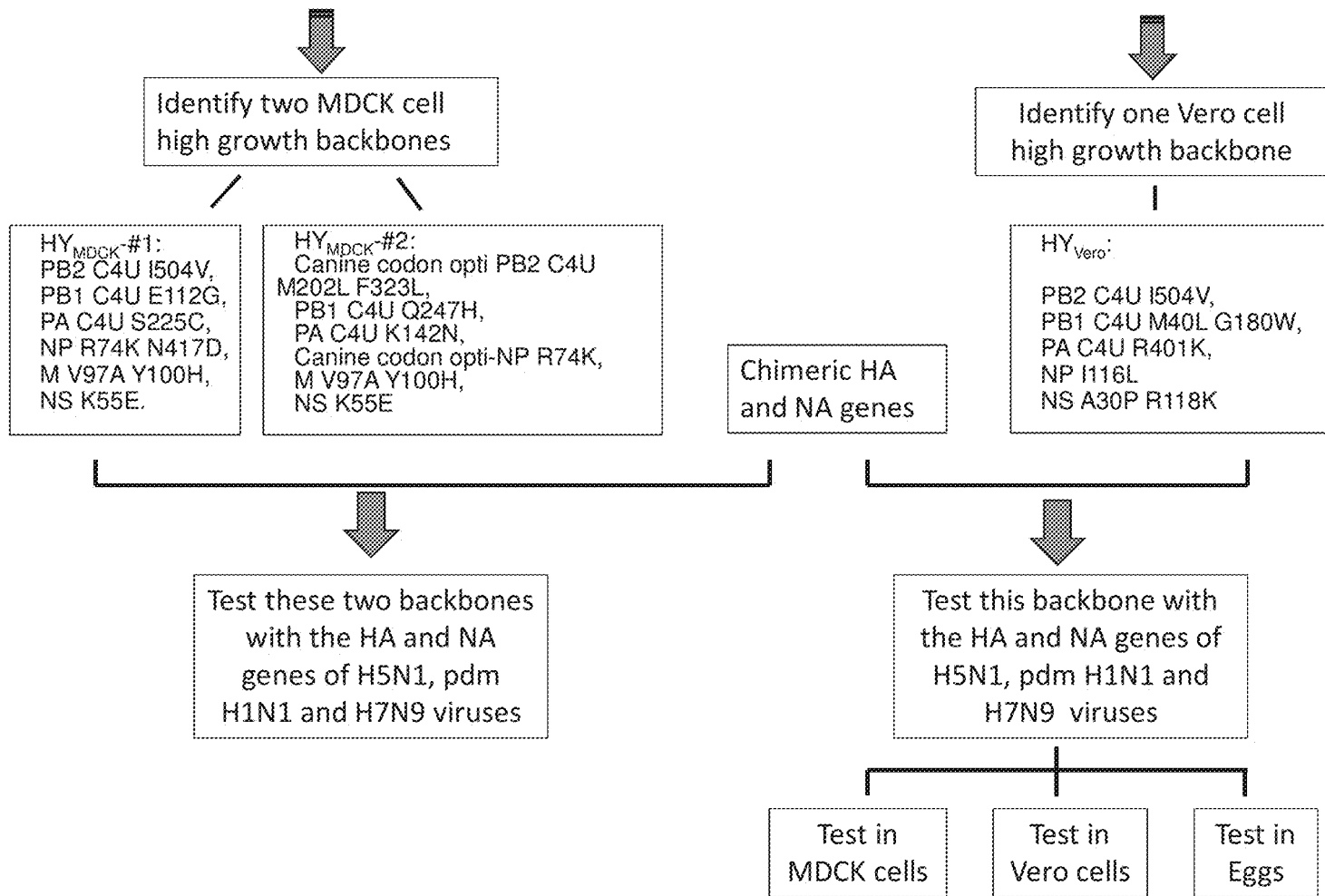


FIG. 18B

Virus number	Surface genes		UW-PR8 internal gene						Growth substrate	Viral titer or HA titer	Fold change
	HA (H3 numbering)	NA	PB2	PB1	PA	NP	M1	NS1			
1	M476I		M202L F323L			R293M			MDCK	HA titer	2.8
2	F252I	L55S	M202L F323L			I116L			MDCK	HA titer	2.8
3			M202L F323L					A223E	MDCK	HA titer	2.8
4	L182V		M202L F323L						MDCK	HA titer	2.8~4
5				E112G (PB1- F2 R81G) ⁵					MDCK	HA titer	2.8
6	E136D/ Q179L/ A194V			R54I					MDCK	HA titer	2.8~4
7	K162E			I667T/M714T					MDCK	HA titer	4
8	L182V					I116L		R140Q	MDCK	HA titer	2.8~4
9	L182V								MDCK	HA titer	2.8~4
10	L182V		M202L F323L						MDCK	HA titer	4
11	L182V		M66R						MDCK	HA titer	2.8~4
12	L182V		M202L F323L						MDCK	HA titer	4
13			M202L F323L	M507V/V644 A					MDCK	HA titer	4
14	L182V		I504V			R74K/ N417D		A30P	MDCK	HA titer	2.8
15	K162E			E112G (PB1- F2-R81G)				S161T	MDCK	HA titer	2.8
16				I667T					MDCK	HA titer	2.8
17	K449E			M40L/G180W					MDCK	HA titer	2.8
18	K162E			E112G (PB1- F2-R81G)/ L624V				S161T	MDCK	HA titer	2.8~4

FIG. 19A

Virus number	Surface genes		UW-PR8 internal gene						Growth substrate	Viral titer or HA titer	Fold change
	HA (H3 numbering)	NA	PB2	PB1	PA	NP	M1	NS1			
19				E112G (PB1-F2-R81G)					MDCK	HA titer	2.8
20				M40L G180W				S161T	MDCK	HA titer	2.8~4
21			M202L F323L M243I	R54I					MDCK	HA titer	4~5.7
22	V184I		M202L F323L		F105C		P90S		MDCK	HA titer	2.8~4
23			M202L F323L	Q247H					MDCK	HA titer	2.8~4
24			M202L F323L			N224I			MDCK	HA titer	2.8~4
25	M476I		I504V			R74K/ N417D			MDCK	HA titer	2.8~4
26	M476I		M202L F323L	V644A	R401K			T49A	MDCK	HA titer	4~5.7
27	F252I		I504V	V644A		M371V			MDCK	HA titer	2.8
28	M476I	A265V	I504V	T59I G62A A63P V644A N694K L695T		R74K/ N417D			MDCK	HA titer	2.8
29	M476I		I504V						MDCK	HA titer	2.8~4
30	F252I		I504V	E75V D76G E78P P79V S80G V644A E697P F699L F700L P701H S702R Y705T		R74K			MDCK	HA titer	2.8~4
31	L182V		I504V			R74K			MDCK	HA titer	2.8~4
32	F252I		M202L F323L	V644A					MDCK	HA titer	4

FIG. 19B

Virus number	Surface genes		UW-PR8 internal gene						Growth substrate	Viral titer or HA titer	Fold change
	HA (H3 numbering)	NA	PB2	PB1	PA	NP	M1	NS1			
33			I57V T58G A59V K61Q E677D D678E P679M	E112G (PB1-F2-R81G) S713C					MDCK	HA titer	2.8
34				M40I G180W				S161T	MDCK	HA titer	2.8
35			R368K						MDCK	Viral titer	2.8
36			E391K						MDCK	Viral titer	3.8
37			I504V		I550L				MDCK	Viral titer	4.3
38				PB1 F2 N66S					MDCK	Viral titer	2.78
39				PB1 F2 K73R					MDCK	Viral titer	3.9
40					K142N				MDCK	Viral titer	2.1
41					K356R				MDCK	Viral titer	3.9
42						R293K			MDCK	Viral titer	3.36
43						R442K			MDCK	Viral titer	2.4
44						T442A			MDCK	Viral titer	2.6
46							V97A		MDCK	HA titer	8
47							Y100H		MDCK	HA titer	9
48							V97A Y100H		MDCK	HA titer	9.5
49								K55E	MDCK	Viral titer	2.1
50			M202L F323L	M507V V644A		I116L		K55E	MDCK	Viral titer	9.9
										HA titer	4.3
51			M202L F323L	M507V V644A	K356R	T442A	V97A Y100H	K55E	MDCK	Viral titer	1.3
										HA titer	3.7
52			I504V	E112G (PB1-F2-R81G)	I550L	I112L	Y100H	R140Q	MDCK	Viral titer	3
										HA titer	3

FIG. 19C

Virus number	Surface genes		UW-PR8 internal gene						Growth substrate	Viral titer or HA titer	Fold change
	HA (H3 numbering)	NA	PB2	PB1	PA	NP	M1	NS1			
53			M202L F323L	M507V V644A		I116L	Y100H	K55E	MDCK	Viral titer	9
										HA titer	6.5
54			M202L F323L	Q247H	K142N	R74K	V97A Y100H	K55E	MDCK	Viral titer	4.3
										HA titer	9.2
55			I504V	E112G (PB1- F2-R81G)	S225C	R74K N417D	V97A Y100H	K55E	MDCK	Viral titer	14.9
										HA titer	6.5
56			M202L F323L	M40L G180W	S225C	R422K	V97A Y100H	K55E	MDCK	Viral titer	4.2
										HA titer	6.5
57			C4U	C4U	C4U				MDCK	Viral titer	3.3
										HA titer	2.1
58	X-181 HA &NA (Derived from A/California/ 07/2009 pdmH1N1)			G180E S261G S361R Q621R N654S					MDCK	Viral titer	3.5
										HA titer	2.1
59	A/Chicken/Indonesia/NC/2009, A/Vietnam/1203/2004, A/Hubei/1/2010, A/Egypt/N03072/2010, A/Indonesia/5/2005, A/Anhui/1/2013, X-181, X-223A		C4U I504V	C4U M40L G180W	C4U R401K	I116L		A30P R118K	Vero	Viral titer	5.1~269
										HA titer	2.2~134
									MDCK	Viral titer	1.8~29
										HA titer	1.3~5.5
									Eggs	Viral titer	4.6~172
HA titer	1.3~17.7										
60	A/Chicken/Indonesia/NC/2009		C4U I504V	C4U M40L G180W	C4U R401K	I116L	G1012C, A1013U, U1014A	A30P R118K	Vero	Viral titer	2.8
										HA titer	1.2
									Egg	Viral titer	1.5
										HA titer	1.6

Note: 1. The HA and NA genes of #1-58 come from A/Chicken/Indonesia/NC/2009 (H5N1) or mutant HA and NA of A/Chicken/Indonesia/NC/2009.

2: All the H5N1 HAs used in this study were mutated to remove multibasic cleavage sites to create lowly pathogenicity mutants.

FIG. 19D

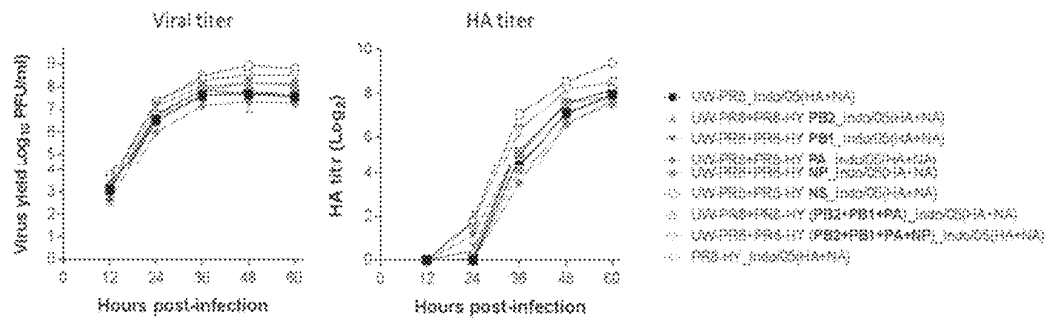


Figure 20

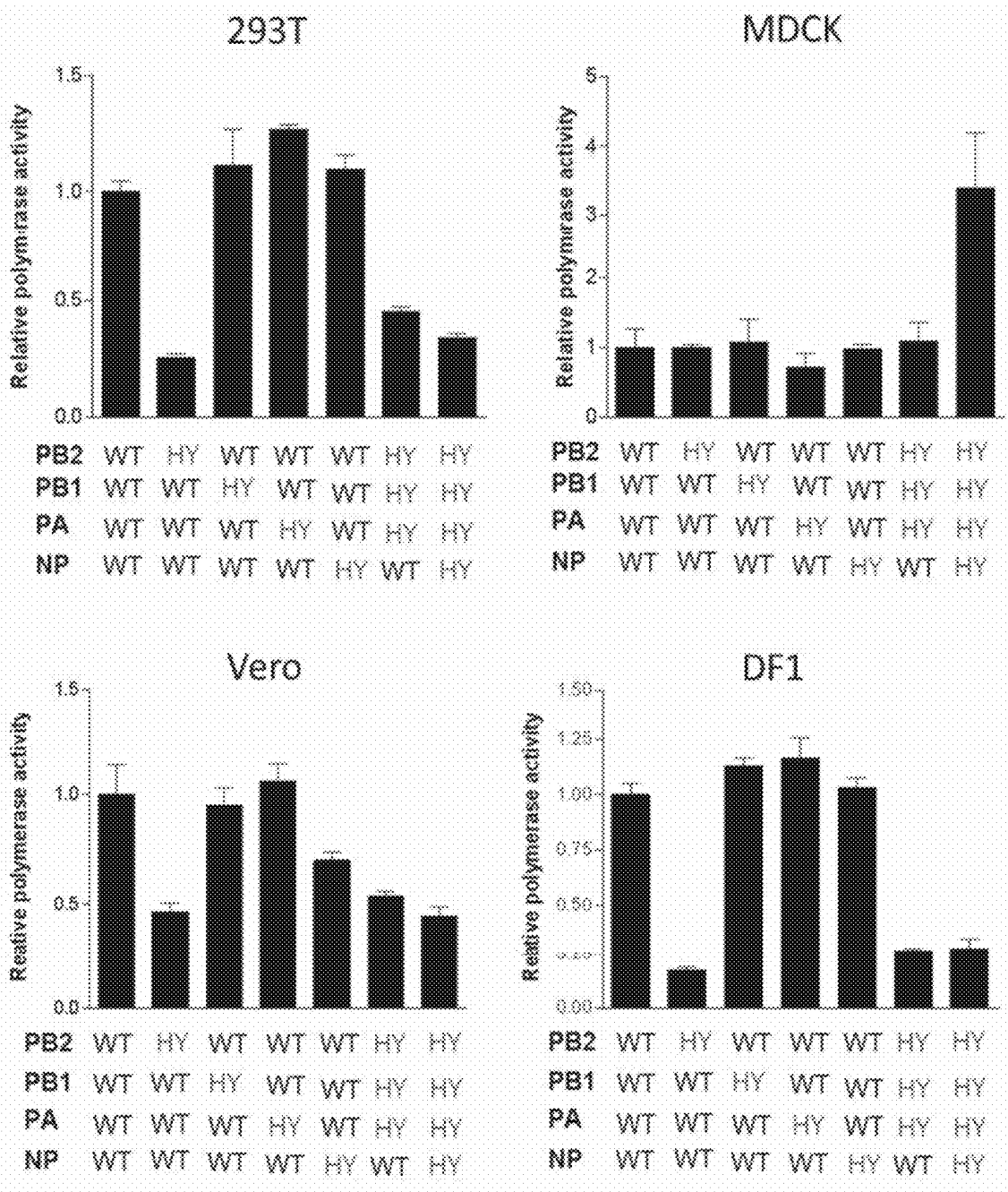


Figure 21

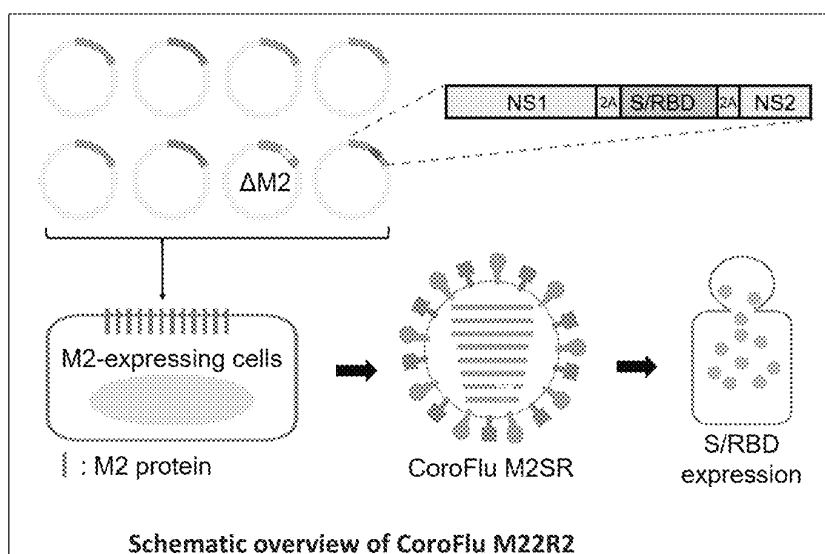


Fig. 22

Figure 23

QIA98554

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  121 nnatnvvikv cefqfcndpf lgvyvhknnk swmesefrvy ssannctfey vsqpfldmle
  181 gkqgnfknlr efvfkndgy fkiyskhtpi nlvrldpqqf saleplvdlp iginitrftq
  241 llalhrsylt pgdsssgwta gaaayyvgyt qprtflilkyn engtitdavid caldplsetk
  301 ctiksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrffasv yawnrkrism
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  481 ngvegfnicyf plqsygfgpt ngvgyqpyrv vvlsfelliha patvcgpkks tnlvknkcnv
  541 fnfngltgtg vltesnkkfl pfqgfgdia dttdavrdpq tleilditpc sfggvsvitp
  601 gtntsnqvav lyqdvncetv pvaihadqit ptwrvystgs nvfqtragcl igaehvnnsy
  661 ecdipigagi casyqtqtns prrarsvasq silaytmslg aensvaysnn siaiptnfti
  721 svtteilpvs mtktsvdctm yicgdstecc nlllqygsfc tqlnraltgi aveqdkntqe
  781 vfaqvqkiyk tppikdfggf nfsqilpdpk kpskrsfied llfnkvtlad agfikqygdc
  841 lgdiaardli caqkfngltv lpplltdemi aqytsallag titsgwtfga gaalqipfam
  901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdsiss tasalgklqd vvnqnaqaln
  961 tlvkqlssnf gaissvlndi lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
 1021 sanlaatkms ecvlgqskrv dfcggkgyhm sfpqsaphgv vflhvtvypa geknfttapa
 1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittndt fvsngcdvvi givnntvydp
 1141 lqpeldsfke eldkyfknhf spdvdldgis ginasvvnig keidrlneva knlneslidl
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BCA87361

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  121 nnatnvvikv cefqfcndpf lgvyvhknnk swmesefrvy ssannctfey vsqpfldmle
  181 gkqgnfknlr efvfkndgy fkiyskhtpi nlvrldpqqf saleplvdlp iginitrftq
  241 llalhrsylt pgdsssgwta gaaayyvgyt qprtflilkyn engtitdavid caldplsetk
  301 ctiksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrffasv yawnrkrism
  361 cvadysvlyn sasfstfkcy gvsptklndi cftnvyadsf virgdevrqi apgqtgkiad
  421 ynyklpddft gcviawnsnn ldskvggyn ylyrlfrksn lkpferdist eiyqagstpc
  481 ngvegfnicyf plqsygfgpt ngvgyqpyrv vvlsfelliha patvcgpkks tnlvknkcnv
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  661 ecdipigagi casyqtqtns prrarsvasq silaytmslg aensvaysnn siaiptnfti
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  901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdsiss tasalgklqd vvnqnaqaln
  961 tlvkqlssnf gaissvlndi lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
 1021 sanlaatkms ecvlgqskrv dfcggkgyhm sfpqsaphgv vflhvtvypa geknfttapa
 1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittndt fvsngcdvvi givnntvydp
 1141 lqpeldsfke eldkyfknhf spdvdldgis ginasvvnig keidrlneva knlneslidl
 1201 qelgkyeyyi kwpyiwlqf iagliaivmv timlccmtsc cscikgccsc gscckfdedd
 1261 sepvikgvkl hyt (SEQ ID NO:27)
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QIK50427

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   61 nvtwfhaihv sgtngtkrfd npvlpfndgv yfasteksni irgwifgttl dsktqsiliv
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Figure 23 (Cont.)

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241 llalhrsylt pgdsssgwta gaaayyvgyt qprtflilkyn engtitdavid caldplsetk
301 ctllksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrfasv yawnrkrisk
361 cvadyssvlyn sasfstfkey gvsptklndi cftnvadysf virgdevrqi apqgtgkiad
421 ynyklpddft gcviawnsnn ldkvgggnyn ylyrlfrksn lkpferdist eiyqagstpc
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541 fnfnlgtgtg vltesnkkfl pfqgfggrdia dttdavrdpq tleilditpc sfggvsvitp
601 gtntsnqvav lyqgvnctev pvaihadqit ptwrvystgs nvfqtragcl igaehvnnsy
661 ecdipigagi casyqtqtns prrarsvasq siiaytmslg aensvaysnn siaiptnfti
721 svtteilpvs mtktsvdctm yicgdsteas nlllqygsfc tqlnraltgi aveqdkntqe
781 vfaqvkiyk tppikdfggf nfsqilpdp kskrsfied llfnkvtlad agfikqygdg
841 lgdiaardli caqkfngltv lpplltdemi aqytsallag titsgwtfga gaalqipfam
901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdsiss tasalgklqd vvnqnaqaln
961 tlvkqlssnf gaissvlnli lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
1021 sanlaatkms ecvlqgskrv dfcgkgyhlm sfpqsaphgv vflhvtvypa qeknfttapa
1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittndt fvsgncdvvi givnntvydp
1141 lqpeldsfke eldkyfknhf spdvdldgis ginasvvnig keidrlneva knlneslidl
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QHU79173

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241 llalhrsylt pgdsssgwta gaaayyvgyt qprtflilkyn engtitdavid caldplsetk
301 ctllksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrfasv yawnrkrisk
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421 ynyklpddft gcviawnsnn ldkvgggnyn ylyrlfrksn lkpferdist eiyqagstpc
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601 gtntsnqvav lyqgvnctev pvaihadqit ptwrvystgs nvfqtragcl igaehvnnsy
661 ecdipigagi casyqtqtns prrarsvasq siiaytmslg aensvaysnn siaiptnfti
721 svtteilpvs mtktsvdctm yicgdsteas nlllqygsfc tqlnraltgi aveqdkntqe
781 vfaqvkiyk tppikdfggf nfsqilpdp kskrsfied llfnkvtlad agfikqygdg
841 lgdiaardli caqkfngltv lpplltdemi aqytsallag titsgwtfga gaalqipfam
901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdsiss tasalgklqd vvnqnaqaln
961 tlvkqlssnf gaissvlnli lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
1021 sanlaatkms ecvlqgskrv dfcgkgyhlm sfpqsaphgv vflhvtvypa qeknfttapa
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YP_009724390

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121 nnatnvvikv cefqfcndpf lgvyvhknnk swmesefrvy ssannctfey vsqpfilmde
181 gkqgnfknlr efvfkndgy fkiyskhtpi nlvrldpqqf saleplvdlp iginitrftq
241 llalhrsylt pgdsssgwta gaaayyvgyt qprtflilkyn engtitdavid caldplsetk
301 ctllksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrfasv yawnrkrisk
361 cvadyssvlyn sasfstfkey gvsptklndi cftnvadysf virgdevrqi apqgtgkiad
421 ynyklpddft gcviawnsnn ldkvgggnyn ylyrlfrksn lkpferdist eiyqagstpc
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```

Figure 23 (Cont.)

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721 svtteilpvs mtktsvdctm yicgdstecs nlllqygsfc tqlnraltgi aveqdkntqe
781 vfaqvkkqiyk tppikdfggf nfsqilpdps kpskrsfied llfnkvtlad agfikqygdc
841 lgdiaardli caqkfngltv lppilt demi aqytsallag titsgwtfga gaalqipfam
901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdslls tasalgklqd vvnqnaqaln
961 tlvkqlssnf gaissvlndi lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
1021 sanlaatkms ecvlqgskrv dfcggkgyhlm sfpqsaphgv vflhvtvypa qeknfttapa
1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittndt fvsngcdvvi givnntvydp
1141 lqpeldsfke eldkyfknhf spdvdldgis ginasvvnig keidrlneva knlneslidl
1201 qelgkyeqyi kwpyiwlqf iagliaivmv timlccmtsc cscikgccsc gsckkfdedd
1261 sepvikgvkl hyt (SEQ ID NO:50)

QII57161

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121 nnatnvvikv cefqfcndpf lgvyvkhknk swmesefrvy ssannctfey vsqpfldle
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301 ctiksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrfasv yawnrkrissn
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421 ynyklpddft gcviawnsnn ldskvgnyn ylyrlfrksn lkpferdist eiyqagstpc
481 ngvegfnicyf plqsygfppt ngvgyqpyrv vlsfellha patvcgpkks tnlvknkcvn
541 fnfnngltgtg vltesnkkfl pfqqfgrdia dttdavrdpq tleilditpc sfggsvvitp
601 gtntsnqvav lyqdvncetv pvaihadqit ptwrvystgs nvfqtragcl igaehvnnsy
661 ecdipigagi casyqtqtns prrarsvasq silaytmslg aensvaysnn siaiptnfti
721 svtteilpvs mtktsvdctm yicgdstecs nlllqygsfc tqlnraltgi aveqdkntqe
781 vfaqvkkqiyk tppikdfggf nfsqilpdps kpskrsfied llfnkvtlad agfikqygdc
841 lgdiaardli caqkfngltv lppilt demi aqytsallag titsgwtfga gaalqipfam
901 qmayrfngig vtqnvlyenq klianqfnsa igkiqdslls tasalgklqd vvnqnaqaln
961 tlvkqlssnf gaissvlndi lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
1021 sanlaatkms ecvlqgskrv dfcggkgyhlm sfpqsaphgv vflhvtvypa qeknfttapa
1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittndt fvsngcdvvi givnntvydp
1141 lqpeldsfke eldkyfknhf spdvdldgis ginasvvnig keidrlneva knlneslidl
1201 qelgkyeqyi kwpyiwlqf iagliaivmv timlccmtsc cscikgccsc gsckkfdedd
1261 sepvikgvkl hyt (SEQ ID NO:51)

QII96493

1 mfvflvllpl vssqcvnlrt rtqlppaytn sftgrgyypd kvfrssvlhs tqdlflpffs
61 nvtwfhaihv sgtngtkrfd npvlpfndgv yfasteksni irgwifgttl dsktqsliliv
121 nnatnvvikv cefqfcndpf lgvyvkhknk swmesefrvy ssannctfey vsqpfldle
181 vkqgnfknlr efvfkndgy fkiyskhtpi nlvrldpqqf saleplvdlp iginitrftq
241 llalhrsylt pgdsssgwta gaaayyvgyt qprtflilkyn engtitdavid caldplsetk
301 ctiksftvek giyqtsnfrv qptesivrfp nitnlcpfge vfnatrfasv yawnrkrissn
361 cvadysvlyn sasfstfkcy gvsptklndi cftnvysadsf virgdevrqi apgqgtkiad
421 ynyklpddft gcviawnsnn ldskvgnyn ylyrlfrksn lkpferdist eiyqagstpc
481 ngvegfnicyf plqsygfppt ngvgyqpyrv vlsfellha patvcgpkks tnlvknkcvn
541 fnfnngltgtg vltesnkkfl pfqqfgrdia dttdavrdpq tleilditpc sfggsvvitp
601 gtntsnqvav lyqdvncetv pvaihadqit ptwrvystgs nvfqtragcl igaehvnnsy
661 ecdipigagi casyqtqtns prrarsvasq silaytmslg aensvaysnn siaiptnfti
721 svtteilpvs mtktsvdctm yicgdstecs nlllqygsfc tqlnraltgi aveqdkntqe

Figure 23 (Cont.)

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781 vfaqvkgiyk tppikdfggf nfsqilpdps kpskrsfied llfnkvttlad agfikqygdc
841 lgdiaardli caqkfngltv lpplltsemi aqytsallag titsgwtfga gaalqipfam
901 qmayrfngig vtqnvlyenq kliangfnsa igkiqdsiss tasalgklqd vvnqnaqaln
961 tlvkqlssnf gaissvindi lsrlckveae vqidrlitgr lqslqtyvtq qliraaeira
1021 sanlaatkms ecvlqgskrv dfcgkgyhlm sfpqsaphgv vflhvtvypa geknfttapa
1081 ichdgkahfp regvfvsngt hwfvtqrnfy epqiittdnt fvsqncdvvi givnntvydp
1141 lqpeldsfke eldkyfknhf spdvdldgis ginasvvniq keidrlneva knlneslidl
1201 qelgkyeqyi kwpyiwlgf iagliaivmv timlccmtsc cscikgcsc gscckfdedd
1261 sepvikgvkl hyt (SEQ ID NO:52)
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RECOMBINANT MULTIVALENT INFLUENZA VIRUSES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of the filing date of U.S. application No. 62/994,738, filed on Mar. 25, 2020, the disclosure of which is incorporated by reference herein.

SUMMARY

In one embodiment, this disclosure provides a coronavirus/influenza virus vaccine. In one embodiment, the vaccine employs a single-replication (SR; a 'single cycle' that results in transcription of vRNAs but no progeny virus production in vivo; that is, a single cycle virus is replication incompetent as a result of not being capable of producing progeny) platform in which the genome of an influenza virus virion lacks at least a portion of a coding region for at least one influenza virus protein, which influenza virus protein is supplied in trans in vitro in cell lines but is restricted to a single round of replication in wild-type cells. In one embodiment, the vaccine employs a M2 Single-Replication (M2SR) platform in which an influenza virus lacking the M2 ion channel protein replicates to high titers in cell lines expressing M2 but is restricted to a single round of replication in wild-type cells. In one embodiment the open reading frame for M2 in M2SR has one or more stop codons, or one or more stop codons and a deletion in M2, rendering the protein non-functional, e.g., the transmembrane domain and/or cytoplasmic domain, or both are not expressed. As described herein, this platform was modified to generate a bivalent coronavirus/influenza virus vaccine (called CoroFlu M2SR) that expresses a secreted version of the spike (S) protein of coronavirus, e.g., SARS-CoV-2.

In one embodiment, a vaccine provides a humoral, mucosal, innate, and/or cell-mediated immune response. In one embodiment, this disclosure provides a replication competent coronavirus/influenza virus vaccine. In one embodiment, the vaccine is inactivated, including chemically inactivated, e.g., with formalin or β -propiolactone.

In one embodiment, a coronavirus/influenza virus expresses a full-length spike protein, e.g., but does not express HA and/or NA. In one embodiment, a bivalent coronavirus/influenza virus expresses a truncated version of the spike protein, e.g., including the S1 or receptor-binding (RBD) domain of S, in addition to at least one other antigenic molecule such as influenza HA and/or NA. In vaccinated individuals, the full-length protein or a portion thereof, e.g., a secreted S protein, elicits protective antibodies against SARS-CoV-2 after administration to a vertebrate, e.g., a mammal such as a human. In one embodiment, the vaccine is a bivalent vaccine where the virus also expresses influenza virus HA and/or NA proteins or other microbial proteins. In one embodiment, a bivalent coronavirus/influenza virus expresses a full-length spike protein. In one embodiment, a bivalent coronavirus/influenza virus expresses a truncated version of the spike protein, e.g., including the S1 or RBD domain of S, and influenza HA and NA. In vaccinated individuals, the full-length protein or a portion thereof, e.g., a secreted S protein, elicits protective antibodies against SARS-CoV-2, while the influenza viral HA protein will elicit protective antibodies against influenza virus, after administration to a vertebrate, e.g., a mammal such as a human. In contrast to the majority of influenza and experimental coronavirus vaccines, this vaccine mimics the

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natural infection process and stimulates mucosal, innate, humoral, and/or cell-mediated immune responses.

In one embodiment, an isolated, single cycle recombinant influenza virus having at least seven viral segments selected from PA, PB1, PB2, NP, NS, M, HA or NA (or HEF) viral segments, one of which segments comprises sequences for a heterologous antigen is provided. In one embodiment, the heterologous antigen comprises coronavirus protein sequences. In one embodiment, the coronavirus protein sequences comprise spike protein sequences or a soluble portion thereof. In one embodiment, the portion comprises S1. In one embodiment, the portion comprises the receptor binding domain. In one embodiment, the spike protein sequences or a portion thereof have at least 80% amino acid sequence identity to one of SEQ ID Nos. 25-28 and 50-52 and 50-52. In one embodiment, the spike protein has 1 to 7 proline residues (see Hsieh et al., which is incorporated by reference herein), which in turn stabilize the protein pre-fusion, e.g., proline at position 817, 892, 895, 899, 912, 942, or 946. In one embodiment, the virus comprises eight viral segments. In one embodiment, the virus comprises nine viral segments, where the ninth segment comprises the coronavirus sequences, e.g., on a PB2 or NS segment that does not express PB2 or NS1 or NS2, respectively. In one embodiment, the virus comprises nine viral segments, where the ninth segment comprises the coronavirus sequences, e.g., on a PA, PB1, NA, or M segment that does not express PA, PB1, NA, or M1 or M2, respectively. In one embodiment, the virus is an influenza A virus. In one embodiment, the virus is an influenza B virus. In one embodiment, the virus is an influenza C virus. In one embodiment, the virus is an influenza D virus. In one embodiment, the sequences for a heterologous antigen are inserted into or replace at least some of the coding sequences for one of PA, PB1, PB2, NP, NS1, NS2, M1, M2, HA or NA (or HEF), e.g., at least a portion of the coding sequences for the influenza virus protein are deleted. In one embodiment, sequences for a heterologous antigen are inserted into or replace at least some of the coding sequences for one of PB1, PB2, NA, or M2. In one embodiment, sequences for a heterologous antigen are inserted into or replace at least some of the coding sequences for one of NS1, NS2, HA, or PA. Cell lines employed to prepare such viruses provide one or more influenza proteins in trans so as to complement any non-functional proteins resulting from the deletion. In one embodiment, the sequences for a heterologous antigen are inserted into coding sequences in the viral segment of one of PA, PB1, PB2, NP, NS, M, HA or NA (or HEF) viral segments. In one embodiment, sequences for a heterologous antigen are inserted, e.g., up to 3 to 4 kb into, e.g., expressed as a fusion polypeptide, coding sequences for one of PB1, PB2, NS1, NS2, or M2. Cell lines employed to prepare such viruses may provide one or more influenza proteins in trans so as to complement any non-functional proteins resulting from the insertion. In one embodiment, the virus is a single cycle bivalent virus. In one embodiment, the virus is a single cycle trivalent virus. Multivalent viruses within the scope of this disclosure may express at least two of the following: homologous influenza HA and/or NA, heterologous influenza HA and/or NA, heterologous viral gene products such as coronavirus gene products, or other viral gene products useful to elicit a protective immune response, rhabdovirus GP protein, e.g., VSV-G, a filovirus protein, e.g., Ebolavirus GP, an alphavirus protein, a lentivirus protein, a retrovirus protein, a paramyxovirus protein, a rhinovirus protein, a bunyavirus protein, an arenavirus protein, a flavivirus protein, or a rhabdovirus protein, fungal gene products, or bacterial

gene products. For example, a HA viral segment employed in the virus may replace the HA coding region with VSV-G coding sequences, or other host cell binding sequences, a NA viral segment employed in the virus may replace NA coding sequences with sequences from those from a paramyxovirus, e.g., type 3; heterologous antigenic coding sequences may be added to a viral coding region, e.g., added to the open reading frame for PB2 or NA, or may replace PB2 coding sequences. In one embodiment, the M viral segment is mutated so that upon viral replication the mutant M gene expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and either lacking a transmembrane domain or having a mutated transmembrane domain, wherein the replication of the recombinant virus in vivo is limited to a single cycle (e.g., no progeny viruses are produced) relative to a corresponding influenza virus with a wild-type M viral segment. In one embodiment, the M2 coding region is modified to include one or more stop codons, e.g., at or near the splice site(s), and may also include a deletion of, e.g., downstream, coding sequences so as to result in a truncated M2 protein. In one embodiment, the mutant M2 protein comprises the M2 extracellular domain. In one embodiment, the M2 extracellular domain comprises less than 24 residues. In one embodiment, the M2 extracellular domain comprises at least 9 residues. In one embodiment, the mutation in the transmembrane domain comprises at least one amino acid substitution. In one embodiment, the mutation in the transmembrane domain comprises a deletion in the transmembrane domain. In one embodiment, the deletion in the transmembrane domain includes residues 29 to 31. In one embodiment, the deletion in the transmembrane domain comprises at least 10 residues. In one embodiment, the deletion in the M2 protein deletes the cytoplasmic tail which protein in turn when present in a virus, results in an attenuated virus. In one embodiment, one or more of the PA, PB1, PB2, NP, NS, and M viral segments have selected amino acid residues at positions 30, 31, 105, 142, 149, 225, 356, 357, 401, and/or 550 in PA; positions 40, 54, 59, 62, 63, 75, 76, 78, 79, 80, 112, 180, 247, 327, 507, 624, 644, 667, 694, 695, 697, 699, 700, 701, 702, 705, 713, and/or 714 in PB1; positions 57, 58, 59, 61, 66, 202, 323, 368, 391, 504, 591, 677, 678, and/or 679, in PB2; positions 74, 112, 116, 224, 293, 371, 377, 417, 422 or 442 in NP; positions 90, 97 and/or 100 in M1; or positions 30, 49, 55, 118, 140, 161 and/or 223 in NS1. In one embodiment, the virus is bivalent. In one embodiment, the PB1 viral segment encodes a polypeptide having a residue other than glycine, serine, serine, glutamine or asparagine at position 62, 261, 361, 621, and/or 654 in PB1 or a residue other than arginine at position 81 in F2. In one embodiment, the virus is in a vaccine formulation. In one embodiment, the vaccine comprises influenza A HA, e.g., H1, H3, H5 or H7 HA. In one embodiment, the HA in the recombinant virus is modified at the HA cleavage site. In one embodiment, the vaccine further comprises a different influenza virus. In one embodiment, the vaccine further comprises two different influenza viruses.

For example, in one embodiment, to prepare recombinant virus, vectors for vRNA or cRNA are introduced to host cells expressing M2 in trans. One of vectors has sequences for the M segment and that segment is modified so that functional M2 is not expressed from that segment. In one embodiment, one or two stop codons are introduced, and optionally some M2 coding sequences are deleted. One of the vectors for vRNA or cRNA has the heterologous antigen sequences. For example, the heterologous antigen sequences may be inserted at the end of the coding region for NS1.

In another embodiment, to prepare recombinant virus, vectors for vRNA or cRNA are introduced to host cells expressing PB2 in trans. One of the vectors for vRNA or cRNA has the heterologous antigenic sequences. For example, the heterologous antigen sequences may be inserted at the end of the coding region for NS1 or into the coding sequences for PB2. One of vectors has sequences for the PB2 segment and that segment is modified so that functional PB2 is not expressed from that segment. In one embodiment, at least some PB2 coding sequences are deleted. In one embodiment, the modified PB2 viral gene segment includes 5' and/or 3' PB2 viral non-coding and coding incorporation sequences, optionally flanking a heterologous nucleotide sequence, and does not include contiguous sequences corresponding to sequences encoding a functional PB2. In one embodiment, the heterologous nucleotide sequence is about 30 to about 5,000, e.g., about 100 to about 4,500 or about 500 to about 4,000, nucleotides in length. In one embodiment, the deletion of PB2 coding sequences includes 1 or more contiguous or noncontiguous nucleotides of PB2 and may include a deletion of the entire coding region, e.g., a region encoding 759 amino acids. In one embodiment, the deletion includes at least 10%, 30%, 40%, 50%, 70%, 80%, 85%, 90%, 93%, 95% and up to 99%, or a percent numerical value that is any integer between 10 and 99, but not all, of the PB2 coding region. In one embodiment, the deletion of PB2 coding sequences does not include the deletion of 5' or 3' coding sequences that enhance incorporation of the resulting viral gene segment into virions, e.g., sequences that are contiguous to 3' or 5' non-coding PB2 sequences, relative to a recombinant viral gene segment with only non-coding PB2 incorporation sequences. For instance, if present in the PB2 segment, the heterologous nucleotide sequence may encode coronavirus sequences, and may be flanked by about 3 to about 400 nucleotides of the 5' and/or 3' PB2 coding region adjacent to non-coding sequence. In one embodiment, the 3' PB2 incorporation sequences correspond to nucleotides 3 to 400, nucleotides 3 to 300, nucleotides 3 to 100, nucleotides 3 to 50, or any integer between 3 and 400, of the N-terminal and/or C-terminal PB2 coding region. In one embodiment, the heterologous nucleotide sequence is flanked by about 3 to about 400 nucleotides of the 5' and/or 3' PB2 coding region adjacent to non-coding sequence. In one embodiment, the heterologous nucleotide sequence is flanked by about 100 to about 300, or 120 to about 150 nucleotides of the 5' and/or 3' PB2 terminal sequences which include coding and non-coding sequences. In one embodiment, heterologous sequences, e.g., antigenic sequences for a virus other than influenza virus or for an influenza virus protein from an isolate other than the strain employed to provide the internal viral segments or for the HA and NA viral segments, may be inserted at the end of the coding region for NS1.

In one embodiment, a method to immunize a vertebrate is provided. The method includes administering to the vertebrate the vaccine. In one embodiment, the vertebrate is an avian. In one embodiment, the vertebrate is a mammal. In one embodiment, the vertebrate is a human. In one embodiment, the vaccine is intranasally administered. In one embodiment, the vaccine is intramuscularly administered.

In one embodiment, the internal viral segments (PA, PB1, PB2, NS, M, and NP viral segments) are from a vaccine strain, e.g., the PR8/UW, PR8HY or PR8/Cambridge strain. In one embodiment, the internal viral segments may be modified to enhance replication in host cell used to generate the vaccine. In one embodiment, in addition to the presence of certain amino acid residues in the coding regions of six

internal viral segments, e.g., relative to PR8HY or the PR8/Cambridge strain, mutations in non-coding regions were observed to increase viral titers, including promoter mutations, for instance, C-to-U mutations at position 4 from the 3' end of the PB2, PB1, and/or PA vRNA segments. The resulting sequences may be also codon-usage optimized, e.g., optimized for expression in mammalian cells such as canine cells or primate cells, or avian cells, e.g., chicken embryos. The mutations can be used in various combinations, with results influenced by the cell line (or egg) in use and the desired level of improvement in the replication of the virus.

In one embodiment, the virus is administered intramuscularly while in another embodiment, the virus is administered intranasally. In some dosing protocols, all doses may be administered intramuscularly or intranasally, while in others a combination of intramuscular and intranasal administration is employed. The vaccine may further contain other isolates of influenza virus including recombinant influenza virus, other pathogen(s), additional biological agents or microbial components, e.g., to form a multivalent vaccine. In one embodiment, intranasal vaccination, for instance containing with inactivated influenza virus, and a mucosal adjuvant may induce virus-specific IgA and neutralizing antibody in the nasopharynx as well as serum IgG.

The invention provides isolated recombinant, e.g., reasortant, influenza viruses with, e.g., 7, 8 or 9 viral segments, one of which includes sequences for a microbial pathogen, e.g., sequences for a coronavirus spike protein, or a portion thereof. In one embodiment, the coronavirus sequences replace influenza virus sequences, e.g., replace coding sequences in one of PA, PB1, PB2, NP, M (encoding M1 and M2 proteins), NS (encoding NS1 and NS2 proteins), HA or NA (or HEF) viral segments. In one embodiment, the coronavirus sequences replace influenza virus sequences, e.g., replace coding sequences in one of PA, PB1, PB2, NP, M (encoding M1 and M2 proteins), or NS (encoding NS1 and NS2 proteins). In one embodiment, the coronavirus sequences are inserted into influenza virus sequences, e.g., into coding sequences in one of PA, PB1, PB2, NP, M (encoding M1 and M2 proteins), NS (encoding NS1 and NS2 proteins), HA or NA (or HEF) viral segments in influenza A viral segments. In one embodiment, the coronavirus sequences are inserted into, e.g., fused to, influenza virus coding sequences, e.g., into coding sequences for one of PA, PB1, PB2, NP, M (encoding M1 and M2 proteins), or NS (encoding NS1 and NS2 proteins). In one embodiment, the coronavirus sequences are expressed as a fusion with influenza virus protein sequences, e.g., a fusion with PA, PB1, PB2, NP, M1, M2, NS1, or NS2 proteins. In one embodiment, the coronavirus sequences are inserted into influenza virus coding sequences and the resulting fusion polypeptide is cleaved to release the coronavirus S protein sequences. For example, coronavirus coding sequences flanked by protease recognition sequences, e.g., self-cleaving sites such as those from foot and mouth disease or 2A sequences, for example, T2A (EGRGSLTTCGDVEENPGP; SEQ ID NO:53), P2A (ATNFSLLKQAGDVEENPGP; SEQ ID NO:54), E2A (QCTNYALLKLAGDVESNPGP; SEQ ID NO:55) or F2A (VKQTLNFDLLKAGDVESNPGP; SEQ ID NO:56) sequences, are inserted into the NS viral segment, e.g., between NS1 and NS2 coding sequences. In one embodiment, coronavirus sequences are introduced to a viral segment that, in the recombinant virus, is a ninth viral segment, where the other eight segments are the PA, PB1, PB2, NP, M, NS, HA and NA viral segments. In one embodiment, the M viral segment encodes a truncated M2

protein. In one embodiment, the coronavirus sequences replace coding sequences, e.g., PB1 or PB2 coding sequences. In one embodiment, the coronavirus sequences encode a protein having at least 80%, 82%, 84%, 85%, 87%, 90%, 92%, 94%, 95%, 97%, 98%, 99% or more amino acid sequence identity with one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the coronavirus sequences encode a S1 protein having at least 80%, 82%, 84%, 85%, 87%, 90%, 92%, 94%, 95%, 97%, 98%, 99% or more amino acid sequence identity with S1 in one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the coronavirus sequences encode a RBD having at least 80%, 82%, 84%, 85%, 87%, 90%, 92%, 94%, 95%, 97%, 98%, 99% or more amino acid sequence identity with the RBD in one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the coronavirus sequences encode a protein having at least 80%, 82%, 84%, 85%, 87%, 90%, 92%, 94%, 95%, 97%, 98%, 99% or more amino acid sequence identity with S1 in one of SEQ ID NOS. 25-28 and 50-52. In one embodiment, the coronavirus sequences encode a protein having at least 80%, 82%, 84%, 85%, 87%, 90%, 92%, 94%, 95%, 97%, 98%, 99% or more amino acid sequence identity with the RBD in one of SEQ ID Nos. 25-28 and 50-52.

In one embodiment, the influenza virus is a recombinant influenza virus having a particular amino acid residue at specified positions in one or more of PA, PB1, PB2, NP, M1 and/or NS1 and an amino acid sequence with at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a corresponding polypeptide encoded by one of SEQ ID Nos. 1-6 or 10-15, such as a polypeptide with a residue that is a conservative substitution relative to M202 in PB2, R74 in NP, and/or V97 in M1.

In one embodiment, the influenza virus is a recombinant influenza virus having a particular amino acid residue at specified positions in PA, PB1, PB2, NP, M1 and/or NS1 and an amino acid sequence with at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a corresponding polypeptide encoded by one of SEQ ID Nos. 1-8 or 10-15, e.g., a polypeptide with a residue that is a non-conservative substitution relative to K142 in PA, Q247 in PB1, M202, F323 or I504 in PB2, R74 I112, I116, J442 or N417 in NP, V97 and/or Y100 in M1, and/or K55 or R140 in NS1.

In one embodiment, the influenza virus is a recombinant influenza virus having a particular amino acid residue at specified positions in PA, PB1, PB2, NP, M1 and/or NS1 and an amino acid sequence with at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a corresponding polypeptide encoded by one of SEQ ID Nos. 1-8 or 10-15, e.g., a PB2 viral segment with a residue other than isoleucine and that is a conservative substitution for isoleucine at residue 504; a PB1 viral segment with a non-conservative substitution for E112; a PA viral segment with a substitution for S225; a NP viral segment with a conservative substitution for R74 and N417; a M viral segment with a conservative substitution for V97 and a non-conservative substitution for Y100; and a NS viral segment with a non-conservative substitution for K55.

In one embodiment, the influenza virus is a recombinant influenza virus having a particular amino acid residue at specified positions in PA, PB1, PB2, NP, M1 and/or NS1 and an amino acid sequence with at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a cor-

responding polypeptide encoded by one of SEQ ID Nos. 1-6 or 10-15, e.g., a PB2 viral segment with a non-conservative substitution for M202 and F323; a PB1 viral segment with a non-conservative substitution for Q247; a PA viral segment with a non-conservative substitution for K142; a NP viral segment with a conservative substitution for R74; a M viral segment with a conservative substitution for V97 and a non-conservative substitution for Y100; and a NS viral segment with a conservative substitution for K55E.

In one embodiment, the influenza virus is a recombinant influenza virus having a particular amino acid residue at specified positions in PA, PB1, PB2, NP, M1 and/or NS1 and an amino acid sequence with at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a corresponding polypeptide encoded by one of SEQ ID Nos. 1-6 or 10-15, e.g., a PB2 segment with a conservative substitution for I504; a PB1 segment with a conservative substitution for M40L and a non-conservative substitution for G180; a PA segment with a conservative substitution for R401; a NP segment with a conservative substitution for I116; a NS viral segment with a conservative substitution for A30 or R118.

In one embodiment, the influenza virus is a recombinant influenza virus having a particular amino acid residue at specified positions in one or more of PA, PB1, PB2, NP, M1 and/or NS1 and an amino acid sequence with at least 80%, e.g., 90%, 92%, 95%, 97% or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a corresponding polypeptide encoded by one of SEQ ID Nos. 1-6 or 10-15, such as a polypeptide with a residue that is a non-conservative substitution relative to K142 in PA, Q247 in PB1, F323 in PB2, Y100 in M1, and/or K55 in NS1. In one embodiment, the amino acid residue that is replaced has an aliphatic side chain, amide-containing side chain, basic side chain, or sulfur containing side chain and the replacement of an aromatic side chain or acidic side chain (a nonconservative substitution). In one embodiment, the recombinant influenza virus has a residue that is a neutral or positively charged residue that is replaced with a polar or negatively charged residue.

Viral segments for PA, PB1, PB2, NP, M and/or NS may be combined with a viral segment for HA, e.g., H1, H2, H3, H4, H5, H6, H7, H8, H9, H10, H11, H12, H13, H14, H15, H16, H17, or H18 and a viral segment for NA, e.g., N1, N2, N3, N4, N5, N6, N7, N8, N9, N10, or N11, and any combination of HA and NA, to provide the reassortant vaccine viruses. In one embodiment, the HA is H1, H5 or H7. In one embodiment the NA is N1 or N9. In one embodiment, the HA viral segment in the recombinant or reassortant virus is heterologous to the viral segments for PA, PB1, PB2, NP, M and NS. In one embodiment, the NA viral segment in the recombinant or reassortant virus is heterologous to the viral segments for PA, PB1, PB2, NP, M and NS. In one embodiment, the HA viral segment in the recombinant or reassortant virus has viral segments for PA, PB1, PB2, NP, M and NS from one influenza virus isolate or strain ("parent"), or a variant thereof, e.g., one with viral segments encoding influenza virus proteins with at least 95%, 96%, 97%, 98%, 99%, or 99.5% amino acid sequence identity, or having 1, 2, 5, 10, or 20 substitutions relative, to sequences in a parent influenza virus isolate or strain. In one embodiment, the parent strain has viral segments with sequences corresponding to SEQ ID Nos. 1-6 or 10-15. In one embodiment, the HA viral segment in the recombinant or reassortant virus is a chimeric HA viral segment, e.g., a chimera of heterologous HA ectodomain sequences linked to

HA signal peptide sequences and/or HA transmembrane domain sequences from the HA viral segment of the parent isolate or strain, or variant thereof. In one embodiment, the NA viral segment in the isolated recombinant virus is a chimeric NA viral segment e.g., a chimera of heterologous NA ectodomain sequences linked to NA transmembrane domain sequences from the NA viral segment of the parent isolate or strain, or variant thereof, and/or stalk sequences from the parent isolate or strain, or variant thereof. In one embodiment, the NA viral segment in the isolated recombinant virus is a chimeric NA viral segment e.g., a chimera of heterologous NA ectodomain sequences linked to NA transmembrane domain sequences from the NA viral segment of the parent isolate or strain, or variant thereof, and/or stalk sequences from a second isolate or strain, or variant thereof. In one embodiment, the isolated recombinant virus has a heterologous HA viral segment, a heterologous NA viral segment, a chimeric HA viral segment, a chimeric NA viral segment, or any combination thereof. The nucleic acid sequences employed to prepare vRNA or cRNA may be ones that introduce the residues at the specified positions via recombinant methodology or may be selected as having the residues at the specified positions. Other reassortants with internal genes from other PR8 isolates or other vaccine viruses may be employed in recombinant reassortant viruses.

Vaccine viruses may be grown or passaged in cells in culture, e.g., MDCK or Vero cells or eggs. In one embodiment, the cells are canine or primate, e.g., human or monkey, cells.

The invention provides a plurality of influenza virus vectors, e.g., those useful to prepare reassortant viruses including 6:1:1 reassortants, 6:2 reassortants and 7:1 reassortants. A 6:1:1 reassortant is an influenza virus with 6 internal viral segments from a vaccine virus, a NA viral segment from a different (second) viral isolate, and a HA viral segment from a third isolate; a 6:2 reassortant within the scope of the present invention is an influenza virus with 6 internal viral segments from a vaccine virus, and a NA viral segment and a HA viral segment from a different (second) viral isolate; and a 7:1 reassortant within the scope of the present invention is an influenza virus with 6 internal viral segments and a NA viral segment from a vaccine virus, and a HA viral segment from a different viral source than the vaccine virus, or an influenza virus with 6 internal viral segments and a HA viral segment from the vaccine virus, and a NA viral segment is from a different viral source than the vaccine virus.

In one embodiment, the plurality of vectors includes vectors for vRNA or cRNA production selected from a vector comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector comprising a promoter operably linked to an influenza virus NS DNA linked to a transcription

termination sequence. In one embodiment, the DNAs for vRNA or cRNA production of PB1, PB2, PA, NP, M, and NS, have sequences from an influenza virus that replicates to high titers in cultured mammalian cells such as MDCK cells, e.g., humanized MDCK cells, Vero cells or PER.C6® cells and also optionally embryonated eggs, and/or from a vaccine virus, e.g., one that does not cause significant disease in humans. The DNA for vRNA or cRNA production of NA may be from any NA, e.g., any of N1-N11, and the DNA for vRNA or cRNA production of HA may be from any HA, e.g., H1-H18. In one embodiment, the DNAs for vRNA or cRNA production may be for an influenza B, C or D virus. The DNAs for vRNA or cRNA production of NA and HA may be from different strains or isolates (6:1:1 reassortants) or from the same strain or isolate (6:2 reassortants), or the NA may be from the same strain or isolate as that for the internal genes (7:1 reassortant). The plurality also includes vectors for mRNA production selected from a vector encoding influenza virus PA, a vector encoding influenza virus PB1, a vector encoding influenza virus PB2, and a vector encoding influenza virus NP, and optionally one or more vectors encoding NP, NS, M, e.g., M1 and M2, HA or NA. The vectors encoding viral proteins may further include a transcription termination sequence.

Viruses within the scope of the invention include viruses that have high titers in, for example, MDCK cells, e.g., titers of at least about 10^5 PFU/mL, e.g., at least 10^8 PFU/mL, 10^7 PFU/mL or 10^8 PFU/mL; high titers in embryonated eggs, e.g., titers of at least about 10^7 EID₅₀/mL, e.g., at least 10^8 EID₅₀/mL, 10^9 EID₅₀/mL or 10^{10} EID₅₀/mL; high titers in cells such as MDCK cells, e.g., titers of at least about 10^7 PFU/mL, e.g., at least 10^8 PFU/mL, or high titers in two of more of those host cells.

In one embodiment, the DNAs for the internal genes for PB1, PB2, PA, NP, M, and NS encode proteins with substantially the same activity as a corresponding polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15. As used herein, "substantially the same activity" includes an activity that is about 0.1%, 1%, 10%, 30%, 50%, 90%, e.g., up to 100% or more, or detectable protein level that is about 80%, 90% or more, the activity or protein level, respectively, of the corresponding full-length polypeptide. In one embodiment, the nucleic acid a sequence encoding a polypeptide which is substantially the same as, e.g., having at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to, a polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15. In one embodiment, the isolated and/or purified nucleic acid molecule comprises a nucleotide sequence which is substantially the same as, e.g., having at least 50%, e.g., 60%, 70%, 80% or 90%, including any integer between 50 and 100, or more contiguous nucleic acid sequence identity to one of SEQ ID NOs:1-6 or 10-15 and, in one embodiment, also encodes a polypeptide having at least 80%, e.g., 90%, 92%, 95%, 97%, 98%, or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15. In one embodiment, the influenza virus polypeptide has one or more, for instance, 2, 5, 10, 15, 20 or more, conservative amino acids substitutions, e.g., conservative substitutions of up to 10% or 20% of 2, 5, 10, 15, 20 or more, of a combination of conservative and non-conservative amino acids substitutions, e.g., conservative substitutions of up to 10% or 20% of the residues, or relative to a polypeptide encoded by one of SEQ IS NOs:1-6 or 10-15, and has a characteristic residue in two or more of PA, PB1, PB2, NP, M1, and/or NS1 the residues, relative to

a polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15, and has a characteristic residue in two or more of the viral segments for PA, PB1, PB2, NP, M1, and/or NS1, e.g., there is an asparagine or glutamine at position 142 in PA; a histidine, arginine or lysine at position 247 in PB1; a leucine, alanine, valine, isoleucine, glycine, or serine at position 202 and/or position 323 in PB2; a lysine or a histidine at position 74 in NP; a leucine, isoleucine, alanine, glycine, or serine at position 202 and/or a lysine, arginine, or histidine position 100 in M1; or an asparagine, aspartic acid, glutamic acid or glutamine at position 44 in NS1. In one embodiment, the influenza virus polypeptide has one or more, for instance, 2, 3, 4, 5, 6, 7 or 8 conservative and/or nonconservative amino acid substitutions, relative to a polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15, e.g., those in virus isolates 1, 4, 36, 38, P17, P25 or P61 in Table 4.

The invention thus includes the use of isolated and purified vectors or plasmids, which express or encode influenza virus proteins, or express or encode influenza vRNA or cRNA, both native and recombinant vRNA or cRNA. The vectors comprise influenza cDNA, e.g., influenza A (e.g., any influenza A gene including any of the 18 HA or 11 NA subtypes), B, C or D DNA (see Fields *Virology* (Fields et al. (eds.), 7th edition, Wolter, Kluwer (2020), which is specifically incorporated by reference herein). Any suitable promoter or transcription termination sequence may be employed to express a protein or peptide, e.g., a viral protein or peptide, a protein or peptide of a nonviral pathogen, or a therapeutic protein or peptide.

A composition or plurality of vectors comprises a heterologous gene or open reading frame of interest, e.g., a foreign gene encoding an immunogenic peptide or protein useful as a vaccine. When preparing virus, the vector or plasmid comprising the gene or cDNA of interest may substitute for a vector or plasmid for an influenza viral gene or may be in addition to vectors or plasmids for all influenza viral genes. Thus, another embodiment comprises a composition or plurality of vectors as described above in which one of the vectors is replaced with, or further comprises, 5' influenza virus sequences optionally including 5' influenza virus coding sequences or a portion thereof, linked to a desired nucleic acid sequence, e.g., a desired cDNA, linked to 3' influenza virus sequences optionally including 3' influenza virus coding sequences or a portion thereof. In one embodiment, the desired nucleic acid sequence such as a cDNA is in an antisense (antigenomic) orientation. The introduction of such a vector in conjunction with the other vectors described above to a host cell permissive for influenza virus replication results in recombinant virus comprising vRNA or cRNA corresponding to the heterologous sequences of the vector.

The promoter in a vector for vRNA or cRNA production may be a RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T7 promoter, or a T3 promoter, and optionally the vector comprises a transcription termination sequence such as a RNA polymerase I transcription termination sequence, a RNA polymerase II transcription termination sequence, a RNA polymerase III transcription termination sequence, or a ribozyme. Ribozymes within the scope of the invention include, but are not limited to, tetrahymena ribozymes, RNase P, hammerhead ribozymes, hairpin ribozymes, hepatitis ribozyme, as well as synthetic ribozymes. In one embodiment, the RNA polymerase I promoter is a human RNA polymerase I promoter.

The promoter or transcription termination sequence in a vRNA, cRNA or virus protein expression vector may be the

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same or different relative to the promoter or any other vector. In one embodiment, the vector or plasmid which expresses influenza vRNA or cRNA comprises a promoter suitable for expression in at least one particular host cell, e.g., avian or mammalian host cells such as canine, feline, equine, bovine, ovine, or primate cells including human cells, or for expression in more than one host.

In one embodiment, at least one vector for vRNA or cRNA comprises a RNA polymerase II promoter linked to a ribozyme sequence linked to viral coding sequences linked to another ribozyme sequences, optionally linked to a RNA polymerase II transcription termination sequence. In one embodiment, at least 2, e.g., 3, 4, 5, 6, 7 or 8, vectors for vRNA or cRNA comprise a RNA polymerase II promoter, a first ribozyme sequence, which is 5' to a sequence corresponding to viral sequences including viral coding sequences, which is 5' to a second ribozyme sequence, which is 5' to a transcription termination sequence. Each RNA polymerase II promoter in each vRNA or cRNA vector may be the same or different as the RNA polymerase II promoter in any other vRNA or cRNA vector. Similarly, each ribozyme sequence in each vRNA or cRNA vector may be the same or different as the ribozyme sequences in any other vRNA or cRNA vector. In one embodiment, the ribozyme sequences in a single vector are not the same.

In one embodiment, the invention provides a plurality of influenza virus vectors for a recombinant or reassortant virus comprising a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the DNAs for PB1, PB2, PA, NP, NS, and M are from one or more influenza vaccine seed viruses; and a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector for mRNA production comprising a promoter operably linked to a DNA

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segment encoding influenza virus M2, or a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NS2. In one embodiment, at least one vector comprises sequences corresponding to those encoding PB1, PB2, PA, NP, M, or NS, or a portion thereof, having substantially the same activity as a corresponding polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15, e.g., a sequence encoding a polypeptide with at least 80%, e.g., 85%, 90%, 92%, 95%, 98%, 99% or 100%, including any integer between 80 and 100, amino acid identity to a polypeptide encoded by one of SEQ ID NOs:1-6 or 10-15. Optionally, two vectors may be employed in place of the vector comprising a promoter operably linked to an influenza virus M cDNA linked to a transcription termination sequence, e.g., a vector comprising a promoter operably linked to an influenza virus M1 cDNA linked to a transcription termination sequence and a vector comprising a promoter operably linked to an influenza virus M2 cDNA linked to a transcription termination sequence.

A plurality of the vectors of the invention may be physically linked or each vector may be present on an individual plasmid or other, e.g., linear, nucleic acid delivery vehicle. In one embodiment, each vRNA or cRNA production vector is on a separate plasmid. In one embodiment, each mRNA production vector is on a separate plasmid.

The invention also provides a method to prepare influenza virus. The method comprises contacting a cell with a plurality of the vectors of the invention, e.g., sequentially or simultaneously, in an amount effective to yield infectious influenza virus. The invention also includes isolating virus from a cell contacted with the plurality of vectors. Thus, the invention further provides isolated virus, as well as a host cell contacted with the plurality of vectors or virus of the invention. In another embodiment, the invention includes contacting the cell with one or more vectors, either vRNA, cRNA or protein production vectors, prior to other vectors, either vRNA or protein production vectors. In one embodiment, the promoter for vRNA or cRNA vectors employed in the method is a RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T3 promoter or a T7 promoter. In one embodiment, the RNA polymerase I promoter is a human RNA polymerase I promoter. In one embodiment, each vRNA or cRNA vector employed in the method is on a separate plasmid. In one embodiment, the vRNA or cRNA vectors employed in the method are on one plasmid or on two or three different plasmids. In one embodiment, each mRNA vector employed in the method is on a separate plasmid. In one embodiment, the mRNA vectors for PA, PB1, PB2 and NP employed in the method are on one plasmid or on two or three different plasmids.

The methods of producing virus described herein, which do not require helper virus infection, are useful in viral mutagenesis studies, and in the production of vaccines (e.g., for coronavirus, AIDS, influenza, hepatitis B, hepatitis C, rhinovirus, filoviruses, malaria, herpes, and foot and mouth disease).

The invention also provides isolated viral polypeptides, and methods of preparing and using a recombinant virus of the invention. The methods include administering to a host organism, e.g., a mammal, an effective amount of the influenza virus of the invention, e.g., an inactivated virus preparation, optionally in combination with an adjuvant and/or a carrier, e.g., in an amount effective to prevent or ameliorate infection of an animal such as a mammal by that virus or an antigenically closely related virus. In one embodiment, the virus is administered intramuscularly while

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in another embodiment, the virus is administered intranasally. In some dosing protocols, all doses may be administered intramuscularly or intranasally, while in others a combination of intramuscular and intranasal administration is employed. The vaccine may further contain other isolates of influenza virus including recombinant influenza virus, other pathogen(s), additional biological agents or microbial components, e.g., to form a multivalent vaccine. In one embodiment, intranasal vaccination, for instance containing with live attenuated or single cycle influenza virus, and a mucosal adjuvant may induce virus-specific IgA and neutralizing antibody in the nasopharynx as well as serum IgG.

The influenza virus of the invention may be employed with other anti-virals, e.g., protease inhibitors, for instance, remdesivir, anti-malarials, e.g., chloroquine, amantadine, rimantadine, and/or neuraminidase inhibitors, e.g., may be administered separately in conjunction with those anti-virals, for instance, administered before, during and/or after.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. 1A-1E. Nucleotide sequence for PR8(Cambridge) genes (SEQ ID NOs:10-15).

FIG. 2: Overview of library passages and the identification of high-yield candidates.

FIG. 3. Number of clones with random mutations having specified HA titers.

FIG. 4. Titers of clones having selected mutations.

FIGS. 5A-5D. Growth curves of UW-PR8 viruses possessing previously identified mutations in PB2 (A), PB1 (B), PA (C), and NP, M or NS1 (D).

FIG. 6. Summary of mutations that confer high replicative property in MDCK cells.

FIGS. 7A-7B. A) Virus stocks were tested for HA titers (in 2") and virus titers (in PFU/mL). B) Growth curves in MDCK cells.

FIGS. 8A-8C. A) HA titer of wild type (UW-PR8) and clone #4. B) Viral protein for wild type (UW-PR8) and #4. C) SDS-PAGE analysis of viral proteins of wild type and #4.

FIGS. 9A-9B. A) Comparison of titers of wild type virus (UW-PR8) and high replicative virus with mutations in M1. B) Growth kinetics of wild type virus (UW-PR8) and high replicative virus with mutations in M1.

FIGS. 10A-10M. A) Codon usage table for canines. B) Relative adaptiveness of wild type (UW-PR8) and "rare" codon optimized PB2 viruses. C) Relative adaptiveness of wild type (UW-PR8) and "all" codon optimized PB2 viruses. D) Growth kinetics of PB2 codon optimized viruses. E) Growth kinetics of viruses with codon optimized PB2, PB1, PA, or NP viral segment or combinations of segments. F) Sequence of PB2, PB1, PA and NP viral segments of UW-PR8 and sequence of canine codon-usage optimized PB2, PB1, PA and NP viral segments of UW-PR8 (SEQ ID NOs: 3, 13, 2, 12, 1, 11, 4).

FIGS. 11A-11C. A) Nucleotide position 4 of each gene of PR8 and Indo/NC/09. B) All 3'C4U mutant. C) Growth kinetics of a recombinant UW-PR8 virus encoding 'C' at position 4 of the PB2, PB1, and PA genes (black), and a mutant encoding 'U' at position 4 of all eight segments (red).

FIG. 12A-12C. Nucleotide and amino acid sequences for H7 and N9 which are exemplary sequences for use with the internal viral segment sequences disclosed herein useful to provide high titer influenza viruses for vaccines (SEQ ID NOs: 20-24 and 29-31).

FIGS. 13A-13B. A) Schematic of chimeric HA and NA genes to increase virus titer. B) Growth kinetics of chimeric viruses.

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FIGS. 14A-14B. A) Growth kinetics of viruses with combinations of mutations. B) PFU and HA titers of viruses with combinations of mutations.

FIG. 15. Screening in eggs.

FIG. 16. HA titers of 216 clones isolated from Vero cells.

FIG. 17. Recombinant viruses generated with different PR8 backbone mutations.

FIG. 18A-18B. Overview of generation of viruses with enhanced growth in MDCK cells and Vero cells.

FIGS. 19A-19D. Exemplary high yield substitutions (relative to PR8 (UW)).

FIG. 20. Growth kinetics and HA titers of reassortant viruses possessing one or several vRNAs of PR8-HY virus.

FIG. 21. Viral polymerase activity in mini-replicon assays in 293T, MDCK, Vero, and DF1 cells. The PB2, PB1, PA, and NP proteins were derived from UW-PR8 wild-type (WT) virus or from the high-yield PR8-HY (HY) variant.

FIG. 22. Exemplary method to prepare bivalent viruses.

FIG. 23. Exemplary SARS-CoV-2 spike (S) protein sequences (SEQ ID Nos. 25-28 and 50-52). The S1 portion of S is generally from residues 1 to 681 and the receptor binding domain in S1 is within residues 330 to 521 (see, e.g., Wrapp et al., *Science*, 67:1260 (2020), the disclosure of which is incorporated by reference herein).

DETAILED DESCRIPTION

Definitions

As used herein, the term "isolated" refers to in vitro preparation and/or isolation of a nucleic acid molecule, e.g., vector or plasmid, peptide or polypeptide (protein), or virus of the invention, so that it is not associated with in vivo substances, or is substantially purified from in vitro substances. An isolated virus preparation is generally obtained by in vitro culture and propagation, and/or via passage in eggs, and is substantially free from other infectious agents.

As used herein, "substantially purified" means the object species is the predominant species, e.g., on a molar basis it is more abundant than any other individual species in a composition, and preferably is at least about 80% of the species present, and optionally 90% or greater, e.g., 95%, 98%, 99% or more, of the species present in the composition.

As used herein, "substantially free" means below the level of detection for a particular infectious agent using standard detection methods for that agent.

A "recombinant" virus is one which has been manipulated in vitro, e.g., using recombinant DNA techniques, to introduce changes to the viral genome. Reassortant viruses can be prepared by recombinant or nonrecombinant techniques.

As used herein, the term "recombinant nucleic acid" or "recombinant DNA sequence or segment" refers to a nucleic acid, e.g., to DNA, that has been derived or isolated from a source, that may be subsequently chemically altered in vitro, so that its sequence is not naturally occurring, or corresponds to naturally occurring sequences that are not positioned as they would be positioned in the native genome. An example of DNA "derived" from a source, would be a DNA sequence that is identified as a useful fragment, and which is then chemically synthesized in essentially pure form. An example of such DNA "isolated" from a source would be a useful DNA sequence that is excised or removed from said source by chemical means, e.g., by the use of restriction endonucleases, so that it can be further manipulated, e.g., amplified, for use in the invention, by the methodology of genetic engineering.

As used herein, a "heterologous" influenza virus gene or viral segment is from an influenza virus source that is different than a majority of the other influenza viral genes or viral segments in a recombinant, e.g., reassortant, influenza virus.

The terms "isolated polypeptide", "isolated peptide" or "isolated protein" include a polypeptide, peptide or protein encoded by cDNA or recombinant RNA including one of synthetic origin, or some combination thereof.

The term "recombinant protein" or "recombinant polypeptide" as used herein refers to a protein molecule expressed from a recombinant DNA molecule. In contrast, the term "native protein" is used herein to indicate a protein isolated from a naturally occurring (i.e., a nonrecombinant) source. Molecular biological techniques may be used to produce a recombinant form of a protein with identical properties as compared to the native form of the protein.

Methods of alignment of sequences for comparison are well known in the art. Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm.

Computer implementations of these mathematical algorithms can be utilized for comparison of sequences to determine sequence identity. Alignments using these programs can be performed using the default parameters. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). The algorithm may involve first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold. These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are then extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when the cumulative alignment score falls off by the quantity X from its maximum achieved value, the cumulative score goes to zero or below due to the accumulation of one or more negative-scoring residue alignments, or the end of either sequence is reached.

In addition to calculating percent sequence identity, the BLAST algorithm may also perform a statistical analysis of the similarity between two sequences. One measure of similarity provided by the BLAST algorithm may be the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a test nucleic acid sequence is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid sequence to the reference nucleic acid sequence is less than about 0.1, more preferably less than about 0.01, and most preferably less than about 0.001.

The BLASTN program (for nucleotide sequences) may use as defaults a wordlength (W) of 11, an expectation (E) of 10, a cutoff of 100, M=5, N=-4, and a comparison of both strands. For amino acid sequences, the BLASTP program may use as defaults a wordlength (W) of 3, an expectation

(E) of 10, and the BLOSUM62 scoring matrix. See <http://www.ncbi.nlm.nih.gov>. Alignment may also be performed manually by inspection.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Influenza Virus Structure and Propagation

Influenza A viruses possess a genome of eight single-stranded negative-sense viral RNAs (vRNAs) that encode at least ten proteins. The influenza virus life cycle begins with binding of the hemagglutinin (HA) to sialic acid-containing receptors on the surface of the host cell, followed by receptor-mediated endocytosis. The low pH in late endosomes triggers a conformational shift in the HA, thereby exposing the N-terminus of the HA2 subunit (the so-called fusion peptide). The fusion peptide initiates the fusion of the viral and endosomal membrane, and the matrix protein (M1) and RNP complexes are released into the cytoplasm. RNPs consist of the nucleoprotein (NP), which encapsidates vRNA, and the viral polymerase complex, which is formed by the PA, PB1, and PB2 proteins. RNPs are transported into the nucleus, where transcription and replication take place. The RNA polymerase complex catalyzes three different reactions: synthesis of an mRNA with a 5' cap and 3' polyA structure, of a full-length complementary RNA (cRNA), and of genomic vRNA using the cRNA as a template. Newly synthesized vRNAs, NP, and polymerase proteins are then assembled into RNPs, exported from the nucleus, and transported to the plasma membrane, where budding of progeny virus particles occurs. The neuraminidase (NA) protein plays a crucial role late in infection by removing sialic acid from sialyloligosaccharides, thus releasing newly assembled virions from the cell surface and preventing the self aggregation of virus particles. Although virus assembly involves protein-protein and protein-vRNA interactions, the nature of these interactions is largely unknown.

Although influenza B and C viruses are structurally and functionally similar to influenza A virus, there are some differences. For example, influenza B virus does not have a M2 protein with ion channel activity but has BM2 and has a viral segment with both NA and NB sequences. Influenza C virus and Influenza D virus have only seven viral segments.

Cell Lines that can be Used in the Present Invention

Any cell, e.g., any avian or mammalian cell, such as a human, e.g., 293T or PER.C6@ cells, or canine, e.g., MDCK, e.g., humanized MDCK cells (see U.S. application Ser. No. 16/785,449, filed on Feb. 7, 2020, which is incorporated herein by reference) or M2 expressing cell line (see Itwasuki et al., *J. Virol.*, 80:5233 (2006), the disclosure of which is incorporated by reference herein), bovine, equine, feline, swine, ovine, rodent, for instance mink, e.g., MvLu1 cells, or hamster, e.g., CHO cells, or non-human primate, e.g., Vero cells, including mutant cells, which supports efficient replication of influenza virus can be employed to isolate and/or propagate influenza viruses. Isolated viruses can be used to prepare a reassortant virus. In one embodiment, host cells for vaccine production are continuous mammalian or avian cell lines or cell strains. A complete characterization of the cells to be used, may be conducted so that appropriate tests for purity of the final product can be

included. Data that can be used for the characterization of a cell includes (a) information on its origin, derivation, and passage history; (b) information on its growth and morphological characteristics; (c) results of tests of adventitious agents; (d) distinguishing features, such as biochemical, immunological, and cytogenetic patterns which allow the cells to be clearly recognized among other cell lines; and (e) results of tests for tumorigenicity. In one embodiment, the passage level, or population doubling, of the host cell used is as low as possible.

In one embodiment, the cells are WHO certified, or certifiable, continuous cell lines. The requirements for certifying such cell lines include characterization with respect to at least one of genealogy, growth characteristics, immunological markers, virus susceptibility tumorigenicity and storage conditions, as well as by testing in animals, eggs, and cell culture. Such characterization is used to confirm that the cells are free from detectable adventitious agents. In some countries, karyology may also be required. In addition, tumorigenicity may be tested in cells that are at the same passage level as those used for vaccine production. The virus may be purified by a process that has been shown to give consistent results, before vaccine production (see, e.g., World Health Organization, 1982).

Virus produced by the host cell may be highly purified prior to vaccine or gene therapy formulation. Generally, the purification procedures result in extensive removal of cellular DNA and other cellular components, and adventitious agents. Procedures that extensively degrade or denature DNA may also be used.

Influenza Vaccines

A vaccine of the invention includes an isolated recombinant influenza virus of the invention, and optionally one or more other isolated viruses including other isolated influenza viruses, one or more immunogenic proteins or glycoproteins of one or more isolated influenza viruses or one or more other pathogens, e.g., an immunogenic protein from one or more bacteria, non-influenza viruses, yeast or fungi, or isolated nucleic acid encoding one or more viral proteins (e.g., DNA vaccines) including one or more immunogenic proteins of the isolated influenza virus of the invention. In one embodiment, the influenza viruses of the invention may be vaccine vectors for influenza virus or other pathogens.

A complete virion vaccine may be concentrated by ultrafiltration and then purified by zonal centrifugation or by chromatography. Viruses other than the virus of the invention, such as those included in a multivalent vaccine, may be inactivated before or after purification using formalin or beta-propiolactone, for instance.

A subunit vaccine comprises purified glycoproteins. Such a vaccine may be prepared as follows: using viral suspensions fragmented by treatment with detergent, the surface antigens are purified, by ultracentrifugation for example. The subunit vaccines thus contain mainly HA protein, and also NA. The detergent used may be cationic detergent for example, such as hexadecyl trimethyl ammonium bromide (Bachmeyer, 1975), an anionic detergent such as ammonium deoxycholate (Laver & Webster, 1976); or a nonionic detergent such as that commercialized under the name TRITON X100. The hemagglutinin may also be isolated after treatment of the virions with a protease such as bromelain, and then purified. The subunit vaccine may be combined with a virus of the invention in a multivalent vaccine.

A split vaccine comprises virions which have been subjected to treatment with agents that dissolve lipids. A split vaccine can be prepared as follows: an aqueous suspension of the purified virus obtained as above, inactivated or not, is

treated, under stirring, by lipid solvents such as ethyl ether or chloroform, associated with detergents. The dissolution of the viral envelope lipids results in fragmentation of the viral particles. The aqueous phase is recuperated containing the split vaccine, constituted mainly of hemagglutinin and neuraminidase with their original lipid environment removed, and the core or its degradation products. Then the residual infectious particles are inactivated if this has not already been done. The split vaccine may be combined with a virus of the invention in a multivalent vaccine.

Inactivated Vaccines. Inactivated influenza virus vaccines are provided by inactivating replicated virus using known methods, such as, but not limited to, formalin or β -propiolactone treatment. Inactivated vaccine types that can be used in the invention can include whole-virus (WV) vaccines or subvirion (SV) (split) vaccines. The WV vaccine contains intact, inactivated virus, while the SV vaccine contains purified virus disrupted with detergents that solubilize the lipid-containing viral envelope, followed by chemical inactivation of residual virus.

In addition, vaccines that can be used include those containing the isolated HA and NA surface proteins, which are referred to as surface antigen or subunit vaccines.

Live Attenuated Virus Vaccines. Live, attenuated influenza virus vaccines, can be used for preventing or treating influenza virus infection. In one embodiment, attenuation may be achieved in a single step by transfer of attenuated genes from an attenuated donor virus to a replicated isolate or reassorted virus according to known methods. Since resistance to influenza A virus is mediated primarily by the development of an immune response to the HA and/or NA glycoproteins, the genes coding for these surface antigens come from the reassorted viruses or clinical isolates. The attenuated genes may be derived from an attenuated parent. In this approach, genes that confer attenuation generally do not code for the HA and NA glycoproteins.

Viruses (donor influenza viruses) are available that are capable of reproducibly attenuating influenza viruses, e.g., a cold adapted (ca) donor virus can be used for attenuated vaccine production. Live, attenuated reassortant virus vaccines can be generated by mating the ca donor virus with a virulent replicated virus. Reassortant progeny are then selected at 25° C. (restrictive for replication of virulent virus), in the presence of an appropriate antiserum, which inhibits replication of the viruses bearing the surface antigens of the attenuated ca donor virus. Useful reassortants are: (a) infectious, (b) attenuated for seronegative non-adult mammals and immunologically primed adult mammals, (c) immunogenic and (d) genetically stable. The immunogenicity of the ca reassortants parallels their level of replication. Thus, the acquisition of the six transferable genes of the ca donor virus by new wild-type viruses has reproducibly attenuated these viruses for use in vaccinating susceptible mammals both adults and non-adult.

Other attenuating mutations can be introduced into influenza virus genes by site-directed mutagenesis to rescue infectious viruses bearing these mutant genes. Attenuating mutations can be introduced into non-coding regions of the genome, as well as into coding regions. Such attenuating mutations can also be introduced into genes other than the HA or NA, e.g., the PB2 polymerase gene. Thus, new donor viruses can also be generated bearing attenuating mutations introduced by site-directed mutagenesis, and such new donor viruses can be used in the production of live attenuated reassortants vaccine candidates in a manner analogous to that described above for the ca donor virus. Similarly, other known and suitable attenuated donor strains can be

reassorted with influenza virus to obtain attenuated vaccines suitable for use in the vaccination of mammals.

In one embodiment, such attenuated viruses maintain the genes from the virus that encode antigenic determinants substantially similar to those of the original clinical isolates. This is because the purpose of the attenuated vaccine is to provide substantially the same antigenicity as the original clinical isolate of the virus, while at the same time lacking pathogenicity to the degree that the vaccine causes minimal chance of inducing a serious disease condition in the vaccinated mammal.

The viruses in a multivalent vaccine can thus be attenuated, single cycle (live) or inactivated, formulated and administered, according to known methods, as a vaccine to induce an immune response in an animal, e.g., a mammal. Methods are well-known in the art for determining whether such attenuated, live single cycle or inactivated vaccines have maintained similar antigenicity to that of the clinical isolate or high growth strain derived therefrom. Such known methods include the use of antisera or antibodies to eliminate viruses expressing antigenic determinants of the donor virus; chemical selection (e.g., amantadine or rimantidine); HA and NA activity and inhibition; and nucleic acid screening (such as probe hybridization or PCR) to confirm that donor genes encoding the antigenic determinants (e.g., HA or NA genes) are not present in attenuated viruses.

Pharmaceutical Compositions

Pharmaceutical compositions of the present invention, suitable for inoculation, e.g., nasal, parenteral or oral administration, comprise one or more influenza virus isolates, e.g., one or more attenuated, live single cycle or inactivated influenza viruses, a subunit thereof, isolated protein(s) thereof, and/or isolated nucleic acid encoding one or more proteins thereof, optionally further comprising sterile aqueous or non-aqueous solutions, suspensions, and emulsions. The compositions can further comprise auxiliary agents or excipients, as known in the art. The composition of the invention is generally presented in the form of individual doses (unit doses).

Conventional vaccines generally contain about 0.1 to 200 µg, e.g., 30 to 100 µg, of HA from each of the strains entering into their composition. The vaccine forming the main constituent of the vaccine composition of the invention may comprise a single influenza virus, or a combination of influenza viruses, for example, at least two or three influenza viruses, including one or more reassortant(s).

Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and/or emulsions, which may contain auxiliary agents or excipients known in the art. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers or occlusive dressings can be used to increase skin permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include adjuvants, wetting agents, emulsifying and suspending agents, or sweetening, flavoring, or perfuming agents.

When a composition of the present invention is used for administration to an individual, it can further comprise salts, buffers, adjuvants, or other substances which are desirable for improving the efficacy of the composition. For vaccines, adjuvants, substances which can augment a specific immune

response, can be used. Normally, the adjuvant and the composition are mixed prior to presentation to the immune system, or presented separately, but into the same site of the organism being immunized.

Heterogeneity in a vaccine may be provided by mixing replicated influenza viruses for at least two influenza virus strains, such as 2-20 strains or any range or value therein. Vaccines can be provided for variations in a single strain of an influenza virus, using techniques known in the art.

A pharmaceutical composition according to the present invention may further or additionally comprise at least one chemotherapeutic compound, for example, for gene therapy, immunosuppressants, anti-inflammatory agents or immune enhancers, and for vaccines, chemotherapeutics including, but not limited to, gamma globulin, amantadine, guanidine, hydroxybenzimidazole, interferon-α, interferon-β, interferon-γ, tumor necrosis factor-α, thiosemicarbazones, methisazone, rifampin, ribavirin, a pyrimidine analog, a purine analog, foscarnet, phosphonoacetic acid, acyclovir, dideoxynucleosides, a protease inhibitor, or ganciclovir.

The composition can also contain variable but small quantities of endotoxin-free formaldehyde, and preservatives, which have been found safe and not contributing to undesirable effects in the organism to which the composition is administered.

Pharmaceutical Purposes

The administration of the composition (or the antisera that it elicits) may be for either a "prophylactic" or "therapeutic" purpose. When provided prophylactically, the compositions of the invention which are vaccines are provided before any symptom or clinical sign of a pathogen infection becomes manifest. The prophylactic administration of the composition serves to prevent or attenuate any subsequent infection. When provided prophylactically, the gene therapy compositions of the invention, are provided before any symptom or clinical sign of a disease becomes manifest. The prophylactic administration of the composition serves to prevent or attenuate one or more symptoms or clinical signs associated with the disease.

When provided therapeutically, a viral vaccine is provided upon the detection of a symptom or clinical sign of actual infection. The therapeutic administration of the compound(s) serves to attenuate any actual infection. When provided therapeutically, a gene therapy composition is provided upon the detection of a symptom or clinical sign of the disease. The therapeutic administration of the compound (s) serves to attenuate a symptom or clinical sign of that disease.

Thus, a vaccine composition of the present invention may be provided either before the onset of infection (so as to prevent or attenuate an anticipated infection) or after the initiation of an actual infection. Similarly, for gene therapy, the composition may be provided before any symptom or clinical sign of a disorder or disease is manifested or after one or more symptoms are detected.

A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient mammal. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. A composition of the present invention is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient, e.g., enhances at least one primary or secondary humoral or cellular immune response against at least one strain of an infectious influenza virus.

The "protection" provided need not be absolute, i.e., the influenza infection need not be totally prevented or eradicated.

cated, if there is a statistically significant improvement compared with a control population or set of mammals. Protection may be limited to mitigating the severity or rapidity of onset of symptoms or clinical signs of the influenza virus infection.

Pharmaceutical Administration

A composition of the present invention may confer resistance to one or more pathogens, e.g., one or more influenza virus strains, by either passive immunization or active immunization. In active immunization, an attenuated or single cycle live vaccine composition is administered prophylactically to a host (e.g., a mammal), and the host's immune response to the administration protects against infection and/or disease. For passive immunization, the elicited antisera can be recovered and administered to a recipient suspected of having an infection caused by at least one influenza virus strain. A gene therapy composition of the present invention may yield prophylactic or therapeutic levels of the desired gene product by active immunization.

In one embodiment, the vaccine is provided to a mammalian female (at or prior to pregnancy or parturition), under conditions of time and amount sufficient to cause the production of an immune response which serves to protect both the female and the fetus or newborn (via passive incorporation of the antibodies across the placenta or in the mother's milk).

The present invention thus includes methods for preventing or attenuating a disorder or disease, e.g., an infection by at least one strain of pathogen. As used herein, a vaccine is said to prevent or attenuate a disease if its administration results either in the total or partial attenuation (i.e., suppression) of a clinical sign or condition of the disease, or in the total or partial immunity of the individual to the disease. As used herein, a gene therapy composition is said to prevent or attenuate a disease if its administration results either in the total or partial attenuation (i.e., suppression) of a clinical sign or condition of the disease, or in the total or partial immunity of the individual to the disease.

A composition having at least one influenza virus of the present invention, including one which is single cycle, attenuated or inactivated and one or more other isolated viruses, one or more isolated viral proteins thereof, one or more isolated nucleic acid molecules encoding one or more viral proteins thereof, or a combination thereof, may be administered by any means that achieve the intended purposes.

For example, administration of such a composition may be by various parenteral routes such as subcutaneous, intravenous, intradermal, intramuscular, intraperitoneal, intranasal, oral or transdermal routes. Parenteral administration can be accomplished by bolus injection or by gradual perfusion over time.

A typical regimen for preventing, suppressing, or treating an influenza virus related pathology, comprises administration of an effective amount of a vaccine composition as described herein, administered as a single treatment, or repeated as enhancing or booster dosages, over a period up to and including between one week and about 24 months, or any range or value therein.

According to the present invention, an "effective amount" of a composition is one that is sufficient to achieve a desired effect. It is understood that the effective dosage may be dependent upon the species, age, sex, health, and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment, and the nature of the effect wanted. The ranges of effective doses provided below are not intended to limit the invention and represent dose ranges.

The dosage of a live, attenuated or killed virus vaccine for an animal such as a mammalian adult organism may be from about 10^2 – 10^{18} , e.g., 10^3 – 10^{12} , plaque forming units (PFU)/kg, or any range or value therein. The dose of inactivated vaccine may range from about 0.1 to 1000, e.g., 30 to 100 μ g, of HA protein. However, the dosage should be a safe and effective amount as determined by conventional methods, using existing vaccines as a starting point.

The dosage of immunoreactive HA in each dose of replicated virus vaccine may be standardized to contain a suitable amount, e.g., 30 to 100 μ g or any range or value therein, or the amount recommended by government agencies or recognized professional organizations. The quantity of NA can also be standardized, however, this glycoprotein may be labile during purification and storage.

The dosage of immunoreactive HA in each dose of replicated virus vaccine can be standardized to contain a suitable amount, e.g., 1–50 μ g or any range or value therein, or the amount recommended by the U.S. Public Health Service (PHS), which is usually 15 μ g per component for older children (greater than or equal to 3 years of age), and 7.5 μ g per component for children less than 3 years of age. The quantity of NA can also be standardized, however, this glycoprotein can be labile during the processor purification and storage (Kendal et al., 1980; Kerr et al., 1975). Each 0.5-ml dose of vaccine may contain approximately 1–50 billion virus particles, and preferably 10 billion particles.

In one embodiment, the vaccine generally contains about 0.1 to 200 μ g, e.g., 30 to 100 μ g, 0.1 to 2 μ g, 0.5 to 5 μ g, 1 to 10 μ g, 10 μ g to 20 μ g, 15 μ g to 30 μ g, or 10 to 30 μ g, of HA from each of the strains entering into their composition. The vaccine forming the main constituent of the vaccine composition of the invention may comprise a single influenza virus, or a combination of influenza viruses, for example, at least two or three influenza viruses, including one or more reassortant(s).

In one embodiment, the dosage of a live, attenuated or killed virus vaccine for an animal such as a mammalian adult organism may be from about 10^{20} – 10^{20} , e.g., 10^3 – 10^{12} , 10^2 – 10^{10} , 10^5 – 10^{10} , 10^5 – 10^{15} , 10^2 – 10^{10} , or 10^{15} – 10^{20} plaque forming units (PFU)/kg, or any range or value therein. The dose of one viral isolate vaccine, e.g., in an inactivated vaccine, may range from about 0.1 to 1000, e.g., 0.1 to 10 μ g, 1 to 20 μ g, 30 to 100 μ g, 10 to 50 μ g, 50 to 200 μ g, or 150 to 300 μ g, of HA protein. However, the dosage should be a safe and effective amount as determined by conventional methods, using existing vaccines as a starting point.

In one embodiment, the dosage of immunoreactive HA in each dose of replicated virus vaccine may be standardized to contain a suitable amount, e.g., 0.1 μ g to 1 μ g, 0.5 μ g to 5 μ g, 1 μ g to 10 μ g, 10 μ g to 20 μ g, 15 μ g to 30 μ g, or 30 μ g to 100 μ g or any range or value therein, or the amount recommended by government agencies or recognized professional organizations. The quantity of NA can also be standardized, however, this glycoprotein may be labile during purification and storage.

The dosage of immunoreactive HA in each dose of replicated virus vaccine can be standardized to contain a suitable amount, e.g., 1–50 μ g or any range or value therein, or the amount recommended by the U.S. Public Health Service (PHS), which is usually 15 μ g, per component for older children >3 years of age, and 7.5 μ g per component for children <3 years of age. The quantity of NA can also be standardized, however, this glycoprotein can be labile during the processor purification and storage (Kendal et al., 1980; Kerr et al., 1975). Each 0.5-ml dose of vaccine may contain approximately 0.1 to 0.5 billion viral particles, 0.5 to

2 billion viral particles, 1 to 50 billion virus particles, 1 to 10 billion viral particles, 20 to 40 billion viral particles, 1 to 5 billion viral particles, or 40 to 80 billion viral particles. Exemplary Embodiments for High Growth PR8 or Cambridge Variants

In one embodiment, the invention provides an isolated recombinant influenza virus having PA, PB1, PB2, NP, NS, and M viral segments from a first influenza vaccine virus isolate, a heterologous influenza virus NA viral segment, and a heterologous HA viral segment, wherein two or more of the PA, PB1, PB2, NP, NS, and M viral segments have selected amino acid residues at positions 30, 31, 105, 142, 149, 225, 356, 357, 401, and/or 550 in PA; positions 40, 54, 59, 62, 63, 75, 76, 78, 79, 80, 112, 180, 247, 327, 507, 624, 644, 667, 694, 695, 697, 699, 700, 701, 702, 705, 713, and/or 714 in PB1; positions 57, 58, 59, 61, 66, 202, 323, 368, 391, 504, 591, 677, 678, and/or 679, in PB2; positions 74, 112, 116, 224, 293, 371, 377, 417, 422 or 442 in NP; positions 90, 97 and/or 100 in M1; or positions 30, 49, 55, 118, 140, 161 and/or 223 in NS1. In one embodiment, the isolated virus has 142N, 225C, 358R, or 550L in PA; has one or more of 112G, 247H, 507V, or 644A in PB1; has one or more of 202L, 323L or 504V in PB2; has one or more of 74K, 112L, 116L, 417D, or 442A in NP; 97A and/or 100H in M1; and/or 55E and/or 140Q in NS1, or combinations thereof, e.g., has at least one of 202L and/or 323L in PB2, 247H in PB1 or 74K in NP and optionally at least one of 142N in PA1, 55K in NS1 or 97A and/or 100H in M1. In one embodiment, the virus has at least one of 202L and/or 323L in PB2, 247H in PB1 or 74K in NP and optionally at least one of 142N in PA1, 55K in NS1 or 97A and/or 100H in M1. In one embodiment, the virus has at least one of 202L and/or 323L in PB2, 247H in PB1 or 74K in NP and at least one of 142N in PA1, 55K in NS1 or 97A and/or 100H in M1. In one embodiment, the isolated virus has 202L and/or 323L in PB2, and optionally has 247H in PB1 and optionally 74K in NP. In one embodiment, the isolated virus has 247H in PB1 and optionally 74K in NP. In one embodiment, the isolated virus has 401, 40L, 112G, 180W, 247H, 507V, or 644A in PB1 and optionally has 202L and/or 323L in PB2, and optionally has 74K, 112L, 116L, 377N, 417D, or 422L in NP, and optionally has 30P, 118K, 161T or 140Q in NS1, and optionally has 142N, 225C, 356R, 401K, or 550L in PA. In one embodiment, the isolated virus has 401, 40L, 112G, 180W, 247H, 507V, or 644A in PB1. In one embodiment, the isolated virus has 202L and/or 323L in PB2. In one embodiment, the isolated virus has 74K, 112L, 116L, 377N, 417D, or 422L in NP. In one embodiment, the isolated virus has 30P, 118K, 161T or 140Q in NS1. In one embodiment, the isolated virus has 142N, 225C, 356R, 401K, or 550L in PA. In one embodiment, the selected amino acid residues at specified positions in the PA is/are at position(s) 97, 105, 142, 149, 225, 356, 357, 401, 404, and/or 421. In one embodiment, the selected amino acid residues at specified positions in the PB1 is/are at position(s) 12, 40, 54, 59, 62, 63, 66, 75, 76, 78, 79, 80, 180, 247, 507, 624, 644, 694, 695, 697, 699, 700, 701, 705, 713, 714, and/or 762. In one embodiment, the selected amino acid residues at specified positions in the PB2 is/are at position(s) 57, 58, 59, 61, 66, 202, 243, 323, 504, 677, 678, and/or 679. In one embodiment, the selected amino acid residues at specified positions in the NP is/are at position(s) 74, 112, 116, 224, 293, 417, and/or 442. In one embodiment, the selected amino acid residues at specified positions in the M1 is/are at position(s) 90, 97, and/or 100. In one embodiment, the selected amino

acid residues at specified positions in the NS1 is/are at position(s) 49, 30, 55, 161, and/or 223. In one embodiment, the selected amino acid residues at specified positions in the PA is/are at position(s) 97, 105, 142, 149, 225, 356, 357, 401, 404, and/or 421; and optionally the selected amino acid residues at specified positions in the PB1 is/are at position(s) 12, 40, 54, 59, 62, 63, 66, 75, 76, 78, 79, 80, 180, 247, 507, 624, 644, 694, 695, 697, 699, 700, 701, 705, 713, 714, and/or 762, in any combination with the selected residues for PA; and optionally the selected amino acid residues at specified positions in the PB2 is/are at position(s) 57, 58, 59, 61, 66, 202, 243, 323, 504, 677, 678, and/or 679 in any combination with the selected residues for PA and/or PB1; and optionally the selected amino acid residues at specified positions in the NP is/are at position(s) 74, 112, 116, 224, 293, 417, and/or 442 any combination with the selected residues for PA, PB1 and/or PB2; and optionally the selected amino acid residues at specified positions in the M1 is/are at position(s) 90, 97, and/or 100 any combination with the selected residues for PA, PB1, PB2, and/or NP; and optionally the selected amino acid residues at specified positions in the NS1 is/are at position(s) 49, 30, 55, 161, and/or 223, or in any combination with the selected residues for PA, PB1, PB2, NP, and/or M1.

For any of the exemplary viruses disclosed above, in one embodiment, the PA, PB1, PB2, NP, NS, and M viral segments comprise sequences for at least one of the following: a PB1 having the amino acid sequence encoded by SEQ ID NO:2 or PB1 with at least 95% amino acid sequence identity to the PB1 encoded by SEQ ID NO:2; a PB2 having the amino acid sequence encoded by SEQ ID NO:3 or PB2 with at least 95% amino acid sequence identity to the PB2 encoded by SEQ ID NO:3; a PA having the amino acid sequence encoded by SEQ ID NO:1 or PA with at least 95% amino acid sequence identity to the PA encoded by SEQ ID NO:1; a NP having the amino acid sequence encoded by SEQ ID NO:4 or NP with at least 95% amino acid sequence identity to the NP encoded by SEQ ID NO:4; a M having the amino acid sequence encoded by SEQ ID NO:5 or M with at least 95% amino acid sequence identity to the M encoded by SEQ ID NO:5; or a NS having the amino acid sequence encoded by SEQ ID NO:6 or NS with at least 95% amino acid sequence identity to the NS encoded by SEQ ID NO:6, or the PA, PB1, PB2, NP, NS, and M viral segments comprise sequences for at least one of the following: a PB1 having the amino acid sequence encoded by SEQ ID NO:10 or PB1 with at least 95% amino acid sequence identity to the PB1 encoded by SEQ ID NO:10; a PB2 having the amino acid sequence encoded by SEQ ID NO:11 or PB2 with at least 95% amino acid sequence identity to the PB2 encoded by SEQ ID NO:11; a PA having the amino acid sequence encoded by SEQ ID NO:12 or PA with at least 95% amino acid sequence identity to the PA encoded by SEQ ID NO:12; a NP having the amino acid sequence encoded by SEQ ID NO:13 or NP with at least 95% amino acid sequence identity to the NP encoded by SEQ ID NO:13; a M having the amino acid sequence encoded by SEQ ID NO:14 or M with at least 95% amino acid sequence identity to the M encoded by SEQ ID NO:14; or a NS having the amino acid sequence encoded by SEQ ID NO:15 or NS with at least 95% amino acid sequence identity to the NS encoded by SEQ ID NO:15.

For any of the exemplary viruses disclosed above, in one embodiment, at least one of the PA, PB1, PB2, NP, NS, and M viral segments has a C to U promoter mutation.

Any of the isolated viruses disclosed herein may be employed in a vaccine.

In one embodiment, the invention provides a plurality of influenza virus vectors for preparing a reassortant. In one embodiment, the plurality includes a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the PB1, PB2, PA, NP, NS, and M DNAs in the vectors for vRNA or cRNA production are from one or more influenza vaccine virus isolates, wherein the NA DNA in the vector for vRNA production of NA has sequences for a heterologous NA, and wherein the HA DNA in the vector for vRNA or cRNA production of HA has sequences for a heterologous HA, 30, 31, 105, 142, 149, 225, 356, 357, 401, and/or 550 in PA; 40, 54, 59, 62, 63, 75, 76, 78, 79, 80, 112, 180, 247, 327, 507, 624, 644, 667, 694, 695, 697, 699, 700, 701, 702, 705, 713, or 714 and/or 247 in PB1; 57, 58, 59, 61, 66, 202, 323, 368, 391, 504, 591, 677, 678, or 679, 202 and/or 323 in PB2; 74, 112, 116, 224, 293, 371, 377, 417, 422 and/or 442 in NP; 90, 97 and/or 100 in M1; or 30, 49, 55, 118, 140, 161 and/or 223 in NS; and a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NS2. In one embodiment, the PB1, PB2, PA, NP, NS, and M DNAs in the vectors for vRNA or cRNA production have a sequence corresponding to one that encodes a polypeptide having at least 95% amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-6 or 10-15. In one embodiment, the promoter for vRNA or cRNA vectors is a RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T3 promoter or a T7 promoter. In one embodiment, the NA is N9. In one embodiment, the HA

is H7. In one embodiment, the PA, PB1, PB2, NP, NS, and/or M viral segments has/have a promoter C to a mutation.

In one embodiment, the invention provides a method to prepare influenza virus. The method includes contacting a cell with: a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA or cRNA production comprising a promoter operably linked to an influenza virus NS DNA linked to a transcription termination sequence, wherein the PB1, PB2, PA, NP, NS, and M DNAs in the vectors for vRNA or cRNA production are from one or more influenza vaccine virus isolates, wherein the NA DNA in the vector for vRNA or cRNA production of NA has sequences for a heterologous NA, and wherein the HA DNA in the vector for vRNA or cRNA production of HA has sequences for a heterologous HA, 30, 31, 105, 142, 149, 225, 356, 357, 401, and/or 550 in PA; 40, 54, 59, 62, 63, 75, 76, 78, 79, 80, 112, 180, 247, 327, 507, 624, 644, 667, 694, 695, 697, 699, 700, 701, 702, 705, 713, and/or 714 and/or 247 in PB1; 57, 58, 59, 61, 66, 202, 323, 368, 391, 504, 591, 677, 678, and/or 679, 202 and/or 323 in PB2; 74, 112, 116, 224, 293, 371, 377, 417, 422 and/or 442 in NP; 90, 97 and/or 100 in M1; or 30, 49, 55, 118, 140, 161 or 223 in NS; and a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PB1, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus PB2, and a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NP, and optionally a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus HA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NA, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus M1, a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus M2, or a vector for mRNA production comprising a promoter operably linked to a DNA segment encoding influenza virus NS2; in an amount effective to yield infectious influenza virus. In one embodiment, the cell is an avian cell or a mammalian cell, e.g., a Vero cell, a human cell or a MDCK cell. In one embodiment, the PB1, PB2, PA, NP, NS, and M DNAs in the vectors for vRNA productions have a sequence that corresponds to one that encodes a polypeptide having at least 95% amino acid sequence identity to a corresponding polypeptide encoded by SEQ ID NOs:1-6 or 10-15. In one embodiment, the

method includes isolating the virus. In one embodiment, at least one of PA, PB1, or PB2 viral segments has a C to U promoter mutation.

Further provided is a vector for vRNA, cRNA or mRNA expression of influenza virus PA having at least 95% amino acid sequence identity to a polypeptide encoded by SEQ ID NO:1 and having a threonine at position 30, a lysine at position 31, cysteine at position 105 or a lysine at position 401; a vector for vRNA, cRNA or mRNA expression of influenza virus PB1 having at least 95% amino acid sequence identity to a polypeptide encoded by SEQ ID NO:2 and having a leucine at position 40, an alanine or isoleucine at position 54, glycine at position 112, histidine at position 247, valine at position 507, alanine at position 644, or cysteine at position 713; a vector for vRNA, cRNA or mRNA expression of PB2 having at least 95% amino acid sequence identity to a polypeptide encoded by SEQ ID NO:3 and a leucine at position 202 and/or 323; a vector for vRNA, cRNA or mRNA expression of influenza virus NP having at least 95% amino acid sequence identity to a polypeptide encoded by SEQ ID NO:4 and having a lysine at position 74, leucine at position 116, isoleucine at position 224, lysine at position 293, asparagine at position 377, or aspartic acid at position 417; a vector for vRNA, cRNA or mRNA expression of influenza virus NS1 having at least 95% amino acid sequence identity to a NS1 polypeptide encoded by SEQ ID NO:6 and having a proline at position 30, alanine at position 49, lysine at position 118, glutamine at position 140, threonine at position 161, or glutamic acid at position 223; and a vector for vRNA, cRNA or mRNA expression of influenza virus M1 having at least 95% amino acid sequence identity to a M1 polypeptide encoded by SEQ ID NO:5 and having a serine at position 90.

Exemplary M Viral Segments

Wild-type influenza A virus M2 protein consists of three structural domains: a 24-amino-acid extracellular domain, a 19-amino-acid transmembrane domain, and a 54-amino-acid cytoplasmic tail domain. The M2 transmembrane domain has ion channel activity, which functions at an early stage of the viral life cycle between the steps of virus penetration and uncoating. The M2 cytoplasmic tail domain may also have an important role in viral assembly and morphogenesis. M1 protein and M2 protein share N-terminal sequences. The M2 protein is encoded by a spliced transcript and RNAs encoding the M1 protein and the M2 protein share 3' sequences, although the coding sequences for M1 and M2 in those 3' sequences are in different reading frames. The C-terminal residues of M1 and C-terminal portion of the extracellular domain of M2 are encoded by the overlapping 3' coding sequences.

A "functional" M1 protein provides for export of viral nucleic acid from the host cell nucleus, a viral coat, and/or virus assembly and budding. Thus, the M1 protein in the recombinant influenza viruses of the invention has substantially the same function (e.g., at least 10%, 20%, 50% or greater) as a wild-type M1 protein. Thus, any alteration in the M1 coding region in a mutant M viral segment in a recombinant influenza virus does not substantially alter the replication of that virus, e.g., in vitro, for instance, viral titers are not reduced more than about 1 to 2 logs in a host cell that supplies M2 in trans.

In one embodiment, an isolated recombinant influenza virus comprises a mutant M2 protein having a deletion of one or more residues of the cytoplasmic tail of M2, which virus replicates in vitro, e.g., producing titers that are substantially the same or at most 10, 100 or 1,000 fold less than a corresponding wild-type influenza virus, but wherein

the replication of the recombinant virus in vivo is limited to a single cycle (e.g., no progeny viruses are produced). In one embodiment, the deletion includes 2 or more residues and up to 21 residues of the cytoplasmic tail of M2. In one embodiment, the M viral segment for the mutant M2 has one to two stop codons near the splice donor or splice acceptor site for the M2 transcript. In one embodiment, the coding region for the transmembrane and/or cytoplasmic domain of M2 is also deleted.

In one embodiment, the deletion of M2 includes 21 or more residues and up to 54 residues, i.e., the entire cytoplasmic tail, of the cytoplasmic tail of M2. In one embodiment, the mutant M2 protein may also comprise at least one amino acid substitution relative to a corresponding wild-type M2 protein. The substitution(s) in the M2 protein may be in the extracellular domain, the transmembrane (TM) domain, or the cytoplasmic domain, or any combination thereof. For example, substitutions in the TM domain may be at residues 25 to 43 of M2, e.g., positions 27, 30, 31, 34, 38, and/or 41 of the TM domain of M2. In another embodiment, the mutant M2 protein may also comprise a deletion in at least a portion of the extracellular domain and/or the TM domain, e.g., a deletion of residues 29 to 31, relative to a corresponding wild-type M2 protein. In yet another embodiment, the mutant M2 protein further comprises a heterologous protein, e.g., the cytoplasmic domain of a heterologous protein (a non-influenza viral protein), which may have a detectable phenotype, fused to the cytoplasmic tail or extracellular domain of M2, forming a chimeric protein. In one embodiment, a cytoplasmic domain of a heterologous protein is fused to the remaining residues of the cytoplasmic tail of the deleted M2 protein. In one embodiment, the presence of one or more substitutions, deletions, or insertions of heterologous sequences, or any combination thereof, does not substantially alter the properties of the recombinant influenza virus, e.g., the presence of one or more substitutions, deletions, or insertions of heterologous sequences does not result in virus titers in vitro that are more than about 1.5 to 2 logs lower, but allows for a single cycle of replication in vivo (e.g., no progeny viruses are produced) for a recombinant influenza virus comprising a mutant M2 protein having a deletion of one or more residues of the cytoplasmic tail of M2.

In one embodiment, the deletion in the cytoplasmic domain of M2 includes 2, 3, 4, 5 or more, e.g., 11, 12, 13, 14, or 15 residues, but less than 22 residues, of the C-terminus of the cytoplasmic tail of M2. In one embodiment, the deletion is 2 up to 10 residues, including any integer in between. In one embodiment, the deletion is from 1 up to less than 8 residues, including any integer in between. In one embodiment, the deletion is from 5 up to 21 residues, including any integer in between. In one embodiment, the deletion is from 5 up to less than 28 residues, including any integer in between. In one embodiment, the deletion is from 9 up to 15 residues, including any integer in between. In one embodiment, the deletion is from 9 up to 23 residues, including any integer in between.

In one embodiment, the deletion in the cytoplasmic domain of M2 includes 22, 23, 24, 25 or more, e.g., 41, 42, 43, 44, or 45 residues, but less than 54 residues, of the C-terminus of the cytoplasmic tail of M2.

In one embodiment, the deletion is from 22 up to 35 residues, including any integer in between. In one embodiment, the deletion is from 29 up to 35 residues, including any integer in between. In one embodiment, the deletion is from 35 up to 45 residues, including any integer in between.

In one embodiment, the deletion is from 9 to less than 28 residues, including any integer in between.

In one embodiment, an isolated recombinant influenza virus is provided comprising a mutant M viral segment that is mutated so that upon viral replication, the mutant M gene expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and a deletion of at least a portion of the transmembrane domain, e.g., internal or C-terminal deletions, and/or includes one or more substitutions in the transmembrane domain. In one embodiment, the mutant M2 protein has a deletion that includes the entire cytoplasmic tail and transmembrane domain of M2, and has one or more residues of the extracellular domain, e.g., has the first 9 to 15 residues of the extracellular domain. The replication of the recombinant virus is, in one embodiment, a single cycle *in vivo* relative to a corresponding virus without a mutant M viral segment. The recombinant influenza virus replicates *in vitro* in the presence of M2 supplied in trans, e.g., producing titers that are substantially the same or at most 10, 100 or 1,000 fold less than a corresponding wild-type influenza virus.

In one embodiment, a live single cycle or attenuated influenza virus elicits both systemic and mucosal immunity at the primary portal of infection. In one embodiment, the live, single cycle or attenuated influenza virus has reduced replication in lung compared to wild-type influenza virus, e.g., the live, single cycle or attenuated influenza virus has titers in lung that are at least one to two logs less, and in one embodiment, replication in nasal turbinates is not detectable. The live, single cycle or attenuated virus may be employed in a vaccine or immunogenic composition, and so is useful to immunize a vertebrate, e.g., an avian or a mammal, or induce an immune response in a vertebrate, respectively.

In one embodiment, the mutations in the M2 gene result in a mutant M2 protein with a deletion of the entire cytoplasmic tail and deletion or substitution of one or more residues in the transmembrane (TM) domain of M2 and may also comprise at least one amino acid substitution in the extracellular domain, or a combination thereof, relative to a corresponding wild-type M2 protein encoded by a M viral segment. For example, substitutions in the TM domain may include those at residues 25 to 43 of M2, e.g., positions 27, 30, 31, 34, 38, and/or 41 of the TM domain of M2. Substitutions and/or deletions in the TM domain may result in a truncated M2 protein that is not embedded in the viral envelope. For example, a deletion of 10 residues at the C-terminus of the transmembrane domain may result in a truncated M2 protein that is not embedded in the viral envelope. In another embodiment, the mutant M2 protein may also comprise a deletion in at least a portion of the extracellular domain in addition to deletion of the cytoplasmic domain and a deletion in the TM domain. In one embodiment, the mutant M2 protein has a deletion of the entire cytoplasmic tail and the TM domain and at least one residue of the extracellular domain, e.g., 1 to 15 residues, or any integer in between, of the C-terminal portion of the extracellular domain. In yet another embodiment, the mutant M2 protein having at least a portion of the extracellular domain further comprises a heterologous protein, e.g., the cytoplasmic and/or TM domain of a heterologous protein (a non-influenza viral protein), which may have a detectable phenotype, that is fused to the C-terminus of at least the extracellular domain of M2, forming a chimeric protein. In one embodiment, the presence of one or more substitutions, deletions, or insertions of heterologous sequences, or any combination thereof, in the M2 gene does not substantially alter the properties of the recombinant influenza virus, e.g.,

the presence of one or more substitutions, deletions, or insertions of heterologous sequences does not result in virus titers *in vitro* that are more than about 1.5 to 2 logs lower, and/or but allows for a single cycle (e.g., no progeny viruses are produced) of replication *in vivo* for the recombinant influenza virus with a mutant M2 protein gene having a deletion of the cytoplasmic tail and TM domain of M2.

In one embodiment, the deletion in the TM domain of M2 includes 1, 2, 3, 4, 5 or more, e.g., 11, 12, 13, 14, or 15 residues, up to 19 residues. In one embodiment, the deletion is from 2 up to 9 residues, including any integer in between. In one embodiment, the deletion is from 15 up to 19 residues, including any integer in between. In one embodiment, the deletion is from 10 up to 19 residues, including any integer in between. In one embodiment, the deletion is the result of at least one substitution of a codon for an amino acid to a stop codon. In one embodiment, the deletion is the result of deletion of at least one codon for an amino acid. In one embodiment, the TM domain of M2 has one or more substitutions, e.g., includes 1, 2, 3, 4, 5 or more, e.g., 11, 12, 13, 14, or 15 substitutions, up to 19 residues of the TM domain. In one embodiment, the one or more amino acid deletions and/or substitutions in the TM domain in a mutant M2 protein that also lacks the cytoplasmic tail of M2, provides for a mutant M2 protein that lacks M2 activity and/or when expressed in a virus yields a live, single cycle virus.

In one embodiment, a deletion in the extracellular (ectodomain) domain of M2 may include 1, 2, 3, 4 or more, e.g., 5, 10, 15, or 20 residues, up to 24 residues of the extracellular domain. In one embodiment, the deletion in the extracellular domain is from 1 up to 15 residues, including any integer in between. In one embodiment, the deletion is the result of at least one substitution of a codon for an amino acid to a stop codon. In one embodiment, the deletion is the result of deletion of at least codon for an amino acid. In one embodiment, the extracellular domain of M2 may also include one or more substitutions. In one embodiment, the mutations in the M2 gene of a M viral segment that result in deletion(s) or substitution(s) in the extracellular domain of M2 do not substantially alter the function of the protein encoded by the M1 gene.

In one embodiment, fewer than 20%, e.g., 10% or 5%, of the residues in the TM domain or extracellular domain are substituted. In one embodiment, fewer than 60%, e.g., 50%, 40%, 30%, 20%, 10%, or 5% of the residues in the extracellular domain are deleted. In one embodiment, more than 20%, e.g., 30%, 40%, 50%, 80% or more, of the residues in the TM domain are deleted.

Exemplary PR8 Viral Segment Variants

Example A

Methods

Cells and Viruses

293T human embryonic kidney cells are maintained in Dulbecco's modified Eagle's minimal essential medium (DMEM) with 10% fetal calf serum and antibiotics. Madin-Darby canine kidney (MDCK) cells are grown in MEM with 5% newborn calf serum and antibiotics. African green monkey Vero WCB cells, which had been established after biosafety tests for use in human vaccine production (Sugawara et al., 2002), are maintained in serum-free VP-SFM medium (GIBCO-BRL) with antibiotics. Cells are maintained at 37° C. in 5% CO₂. A WHO-recommended vaccine seed virus is NIBRG-14.

Construction of Plasmids and Reverse Genetics

To generate reassortants of influenza A viruses, a plasmid-based reverse genetics (Neumann et al., 1999) is used. The full-length cDNAs were cloned into a plasmid under control of the human polymerase I promoter and the mouse RNA polymerase I terminator (Poll plasmids).

A previously produced series of Poll constructs, derived from A/WSN/33 (H5N1; WSN) or PR8 strains is used, for reverse genetics (Horimoto et al., 2006; Neumann et al., 1999). The World Health Organization (WHO) recommends A/Puerto Rico/8/34 (H1N1; PR8) as a donor virus, because of its safety in humans (Wood & Robertson, 2004; Webby & Webster, 2003).

Plasmids expressing WSN or PR8 NP, PA, PB1, or PB2 under control of the chicken actin, e.g., beta-actin, promoter are used for all reverse genetics experiments (Horimoto et al., 2006; Neumann et al., 1999). Briefly, Poll plasmids and protein expression plasmids are mixed with a transfection reagent, Trans-IT 293T (Panvera), incubated at room temperature for 15 minutes, and then added to 293T cells. Transfected cells are incubated in Opti-MEM 1 (GIBCO-BRL) for 48 hours. For reverse genetics in Vero WCB cells, an electroporator (Amaxa) is used to transfect the plasmid mixtures according to the manufacturer's instructions. Sixteen hours after transfection, freshly prepared Vero WCB cells were added onto the transfected cells and TPCK-trypsin (1 µg/mL) is added to the culture 6 hours later. Transfected cells are incubated in serum-free VP-SFM for a total of 4 days. Supernatants containing infectious viruses are harvested, and may be biologically cloned by limiting dilution.

A recombinant virus having the HA and NA genes from A/Hong Kong/213/2003 (H5N1) and the remainder of the type A influenza virus genes from PR8(UW) was prepared. The titer of the recombinant virus was $10^{10.87}$ EID₅₀/mL, and the HA titer was 1:1600

TABLE 1

Virus possessing PR8 genes together with the following HA and NA genes	HA titer (HAU/mL) in each dilution						
	10-2	10-3	10-4	10-5	10-6	10-7	10-8
WSN-HA NA	160	40	40	320	40	640	<1
HK-HAavir NA	400	800	400	400	400	800	<1

The sequences of PR8 (UVV) genes are as follows:
Exemplary viral sequences for a master vaccine strain (PR8UW)
HA

(SEQ ID NO: 32)
AGCAAAAGCAGGGGAAAATAAAACAACCAAAATGAAGGCAACCTACT
GGCTCTGTTATGTGCACTTGCAGCTGCAGATGCAGACACAATATGTATA
GGCTACCATGCGAACAATTCAACCGACACTGTTGACACAGTACTCGAGA
AGAATGTGACAGTGACACACTCTGTTAACCTGCTCGAAGACAGCCACAA
CGGAAAACATATGTAGATTAAAGGAATAGCCCCACTACAATTGGGGAAA
TGTAACATCGCCGATGGCTCTTGGGAAACCCAGAATGCGACCCACTGC

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TTCCAGTGAGATCATGGTCCTACATTGTAGAAACACCAAACTCTGAGAA
TGGAATATGTTATCCAGGAGATTTCATCGACTATGAGGAGCTGAGGGAG
5 CAATTGAGCTCAGTGTCTATCATTGAAAGATTGAAATATTTCCAAAG
AAAGCTCATGGCCCAACCAACACAAACGAGTAACGGCAGCATGCTC
CCATGAGGGGAAAAGCAGTTTTTACAGAAATTTGCTATGGCTGACGGAG
10 AAGGAGGGCTCATACCCAAAGCTGAAAAATCTTATGTGAACAAAAAG
GGAAAGAAGTCTTGTACTGTGGGTATTTCATCACC CGCTAACAGTAA
GGAAACAACAGAATCTCTATCAGAATGAAATGCTTATGTCTGTAGTG
15 ACTTCAAATTATAACAGGAGATTTACCCCGGAAATAGCAGAAAGACCCA
AAGTAAGAGATCAAGCTGGGAGGATGAACATTA CTGGACCTTGCTAAA
ACCCGGAGACACAATAATATTTGAGGCAATGGAATCTAATAGCACCA
ATGTATGCTTTCGCACTGAGTAGAGGCTTTGGGTCCGGCATCATCACCT
20 CAAACGCATCAATGCATGAGTGAACACGAAGTGTCAACACCCCTGGG
AGCTATAAACAGCAGTCTCCCTTACCAGAAATATACCCAGTCACAATA
GGAGAGTGCCCAAAATACGTGAGGAGTGCCAAATGAGGATGGTTACAG
25 GACTAAGGAACATTCCGTCCATTCAATCCAGAGGTCTATTTGGAGCCAT
TGCCGGTTTTATTGAAGGGGATGGACTGGAATGATAGATGGATGGTAT
GGTTATCATCATCAGAATGAACAGGGATCAGGCTATGCAGCGGATCAAA
30 AAAGCACACAAAATGCCATTACCGGATTACAAACAAGGTGAACACTGT
TATCGAGAAATGAACATTCAATTCAAGCTGTGGGTAAAGAATTCAAC
AAATTAGAAAAAGGATGGAATTTAAATAAAAAGTTGATGATGGAT
35 TTCTGGACATTTGGACATATAATGCAGAAATGTTAGTTCTACTGAAAA
TGAAAGGACTCTGGATTCCATGACTCAATGTGAAGAATCTGTATGAG
AAAGTAAAAAGCCAATTAAAGAATAATGCCAAGAAATCGGAAATGGAT
40 GTTTTGAGTTCTACCAAGTGTGACAATGAATGCATGGAAGGTGAAG
AAATGGGACTTATGATTATCCCAATATTGCAAGAGTCAAAGTTGAAC
AGGGAAAAGGTAGATGGAGTGAATTTGGAATCAATGGGGATCTATCAGA
45 TTCTGGCGATCTACTCACTGTCCAGTTCACTGGTGCTTTTGGTCTC
CCTGGGGCAATCAGTTTCTGGATGTGTTCTAATGGATCTTTGCACTGC
AGAATATGCATCTGAGATTAGAATTTGAGATATGAGGAAAAACACCC
50 TTGTTTCTACT
NA
55 (SEQ ID NO: 33)
AGCAAAAGCAGGGGTTTAAATGAATCCAATCAGAAAAATAAACCAT
TGGAATCAATCTGTCTGGTAGTCGACTAATAGCCTAATATTGCAATA
GGGAATATAATCTCAATATGGATTAGCCATTCAATTCAAATGGAAGTC
60 AAAACCATACTGGAATATGCAACCAAAACATCATTACCTATAAAAAATAG
CACCTGGGTAAAGGACACAACCTCAGTGATATTAACCGCAATTTCATCT
CTTTGTCCCATCCGTGGGTGGGTATATACAGCAAGACAATAGCATAA
65 GAATTGGTTCCAAAGGAGACGTTTTTGTCTAAGAGAGCCCTTTATTTT

33

-continued

ATGTTCTCACTTGAATGCAGGACCTTTTCTGACCCAAGGTGCCTTA
 CTGAATGACAAGCATTCAAGTGGGACTGTTAAGGACAGAAGCCCTTATA
 GGGCCTTAATGAGCTGCCCTGTGCGTGAAGCTCCGTCCCGTACAATTC
 AAGATTTGAATCGGTTGCTTGGTCAGCAAGTGCATGTCATGATGGCATG
 GGCTGGCTAACAATCGGAATTTCAAGTCCAGATAATGGAGCAGTGGCTG
 TATTAATAACAACGGCATAATAACTGAAACCATAAAAGTTGGAGGAA
 GAAAAATATTGAGGACACAAGAGTCTGAATGTGCTGTGTAATGGTTCA
 TGTTTTACTATAATGACTGATGGCCGAGTGTGGGCTGGCCTCGTACA
 AAATTTTCAAGATCGAAAAGGGGAAGTTACTAAATCAATAGAGTTGAA
 TGCACCTAATCTCACTATGAGGAATGTTCTGTACCCTGATACCGGC
 AAAGTGATGTGTGTGTCAGAGACAATTGGCATGGTTCGAACCGGCCAT
 GGGTGTCTTTGATCAAAACCTGGATTATCAAATAGGATACATCTGCAG
 TGGGGTTTTCGGTGACAACCCGCGTCCCGAAGATGGAACAGGCAGCTGT
 GGTCCAGTGTATGTTGATGGAGCAACCGAGTAAAGGGATTTTCATATA
 GGTATGGTAATGGTGTGGATAGGAAGGACAAAAGTCACAGTTCAG
 ACATGGGTTTGAGATGATTGGGATCCTAATGGATGGACAGAGACTGAT
 AGTAAGTTCTCTGTGAGGCAAGATGTTGTGCAATGACTGATTGGTCAG
 GGTATAGCGGAAGTTTCGTTCAACATCCTGAGCTGACAGGGCTAGACTG
 TATGAGGCCGTGCTTCTGGGTGAATTAATCAGGGGACGACCTAAAGAA
 AAAACAATCTGGACTAGTGCAGCAGCATTTCTTTTGTGGCGTGAATA
 GTGATACTGTAGATTGGTCTTGGCCAGACGCTGCTGAGTTGCCATTGAG
 CATTGACAAGTAGTCTGTTCAAAAACTCCTTGTCTACT

PA

(SEQ ID NO: 34)

AGCGAAAGCA GGTACTGATC CAAAATGGAA GATTTGTGC
 GACAATGCTT CAATCCGATG ATTGTCGAGC TTGCGGAAAA
 AACAAAGAAA GAGTATGGGG AGGACCTGAA AATCGAAACA
 AACAAATTTG CAGCAATATG CACTCACTTG GAAGTATGCT
 TCATGTATTC AGATTTTCAC TTCATCAATG AGCAAGGCGA
 GTCAATAATC GTAGAAGTTG GTGATCCAAA TGCACTTTTG
 AAGCACAGAT TTGAATAAT CGAGGGAAGA GATCGACAAA
 TGGCCTGGAC AGTAGTAAAC AGTATTTGCA AACTACAGG
 GGCTGAGAAA CCAAAGTTTC TACCAGATTT GTATGATTAC
 AAGGAGAATA GATTCAATCGA AATTGGAGTA ACAAGGAGAG
 AAGTTCACAT ATACTATCTG GAAAGGCCA ATAAATTA
 ATCTGAGAAA ACACACATCC ACATTTTCTC GTTCACTGGG
 GAAGAAATGG CCACAAAGGC AGACTACACT CTCGATGAAG
 AAAGCAGGGC TAGGATCAAA ACCAGACTAT TCACCATAAG
 ACAAGAAATG GCCAGCAGAG GCCTCTGGGA TTCCTTTCGT
 CAGTCCGAGA GAGGAGAAGA GACAATTGAA GAAAGGTTTG

34

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AAATCACAGG AACAAATGCGC AAGCTTGCCG ACCAAAGTCT
 CCCGCCGAAC TTCTCCAGCC TTGAAAATTT TAGAGCCTAT
 GTGGATGGAT TCGAACCGAA CGGCTACATT GAGGGCAAGC
 TGTCTCAAAT GTCCAAAGAA GTAAATGCTA GAATTGAACC
 TTTTTTGAAA ACAACACCAC GACCACTTAG ACTTCCGAAT
 GGGCCTCCCT GTTCTCAGCG GTCCAAATTC CTGCTGATGG
 ATGCCTTAAA ATTAAGCATT GAGGACCCAA GTCATGAAGG
 AGAGGGAATA CCGCTATATG ATGCAATCAA ATGCATGAGA
 ACATTCTTTG GATGGAAGGA ACCCAATGTT GTTAAACCAC
 ACGAAAAGGG AATAAATCCA AATTATCTTC TGTGATGGAA
 GCAAGTACTG GCAGAACTGC AGGACATTGA GAATGAGGAG
 AAAATTCCAA AGACTAAAAA TATGAAGAAA ACAAGTCAGC
 TAAAGTGGGC ACTTGGTGAG AACATGGCAC CAGAAAAGGT
 AGACTTTGAC GACTGTAAAG ATGTAGGTGA TTTGAAGCAA
 TATGATAGTG ATGAACCAGA ATTGAGGTCG CTTGCAAGTT
 GGATTCAGAA TGAGTTTAAC AAGGCATGCG AACTGACAGA
 TTCAAGCTGG ATAGAGCTCG ATGAGATTGG AGAAGATGTG
 GCTCCAATTG AACACATTGC AAGCATGAGA AGGAATTATT
 TCACATCAGA GGTGTCTCAC TGCAGAGCCA CAGAATACAT
 AATGAAGGGA GTGTACATCA ATACTGCCTT GCTTAATGCA
 TCTTGTGCAG CAATGGATGA TTTCCAATTA ATTCCAATGA
 TAAGCAAGTG TAGAACTAAG GAGGGAAGGC GAAAGACCAA
 CTTGTATGGT TTCATCATAA AAGGAAGATC CCACCTTAAGG
 AATGACACCG ACGTGGTAAA CTTTGTGAGC ATGAGATTTT
 CTCTCACTGA CCCAAGACTT GAACCACATA AATGGGAGAA
 GTACTGTGTT CTTGAGATAG GAGATATGCT TATAAGAAGT
 GCCATAGGCC AGGTTTCAAG GCCCATGTTT TGTATGTGA
 GAACAAATGG AACCTCAAAA ATTAATGA AATGGGGAAT
 GGAGATGAGG CGTTGCCTCC TCCAGTCACT TCAACAAATT
 GAGAGTATGA TTGAAGCTGA GTCCTCTGTC AAAGAGAAAG
 ACATGACCAA AGAGTTCTTT GAGAACAAAT CAGAAACATG
 GCCCATTGGA GAGTCCCCCA AAGGAGTGGA GGAAAGTTCC
 ATTGGGAAGG TCTGCAGGAC TTTATTAGCA AAGTCGGTAT
 TCAACAGCTT GTATGCATCT CCACAAC TAG AAGGATTTTC
 AGCTGAATCA AGAAACTGC TTCTTATCGT TCAGGCTCTT
 AGGGACAACC TGGAACCTGG GACCTTTGAT CTTGGGGGGC
 TATATGAAGC AATTGAGGAG TGCCTGATTA ATGATCCCTG
 GGTTTTGCTT AATGCTTCTT GGTCAACTC CTTCTTACA
 CATGCATTGA GTTAGTTGTG GCAGTGCTAC TATTTGCTAT
 CCATACTGTC CAAAAAGTA CCTTGTCTTCT ACT

35

PB1

(SEQ ID NO: 35)

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 TGGAGACCCCTCTTACGCCATGGGACAGGAACAGGATACACCATTGGAT
 ACTGTCAACAGGACACATCAGTACTCAGAAAAGGGAAGATGGACAACAA
 ACACCGAAACTGGAGCACCGCAACTCAACCCGATTGATGGGCCACTGCC
 AGAAGACAATGAACCAAGTGGTTATGCCCAACAGATTGTGTATTGGAG
 GCGATGGCTTTCCTTGAGGAATCCCATCCTGGTATTTTTGAAAACTCGT
 GTATTGAAACGATGGAGGTGTTCAGCAAAACAGTAGACAAGCTGAC
 ACAAGGCCGACAGACCTATGACTGGACTCTAAATAGAAACCAACCTGCT
 GCAACAGCATTGGCCAACACAATAGAAGTGTTCAGATCAATGGCCTCA
 CGGCCAATGAGTCTGGAAGGCTCATAGACTTCCTTAAGGATGTAATGGA
 GTCAATGAACAAGAAGAAATGGGGATCACAACCTCATTTCAGAGAAAG
 AGACGGGTGAGAGACAATATGACTAAGAAAATGATAACACAGAGAACAA
 TGGGTAAAAGAAGCAGAGATTGAACAAAAGGAGTTATCTAATTAGAGC
 ATTGACCTTGAACACAATGACCAAAGATGTGTGAGAGAGGGAAGCTAAAA
 CGGAGAGCAATTGCAACCCAGGGATGCAATAAGGGGGTTGTATACT
 TTGTTGAGACACTGGCAAGGAGTATATGTGAGAACTTGAACAATCAGG
 GTTGCCAGTTGGAGGCAATGAGAAGAAAGCAAAGTTGGCAAATGTTGTA
 AGGAAGATGATGACCAATTCTCAGGACACCGAACTTTCTTCACCATCA
 CTGGAGATAACACCAATGGAACGAAAATCAGAATCCTCGGATGTTTTT
 GGCCATGATCACATATATGACCAGAAATCAGCCCGAATGGTTCAGAAAT
 GTTCTAAGTATTGCTCCAATAATGTTCTCAAAACAAAATGGCGAGACTGG
 GAAAAGGTATATGTTTGAGAGCAAGAGTATGAACTTAGAACTCAAAT
 ACCTGCAGAAATGCTAGCAAGCATCGATTGAAATATTICAATGATTCA
 ACAAGAAAGAGATTGAAAAATCCGACCGCTCTTAATAGAGGGGACTG
 CATCATTTGAGCCCTGGAATGATGATGGGCATGTTCAATATGTTAAGCAC
 TGTATTAGGCGTCTCCATCCTGAATCTTGGACAAAAGAGATACACCAAG
 ACTACTTACTGGTGGGATGGTCTTCAATCCTCTGACGATTTTGCTCTGA
 TTGTGAATGCACCAATCATGAAGGGATTCAAGCCGGAGTCGACAGGTT
 TTATCGAACCTGTAAGCTACTTGGAATCAATATGAGCAAGAAAAAGTCT
 TACATAAACAGAACAGGTACATTTGAATTCACAAGTTTTTCTATCGTT
 ATGGGTTTGTGGCAATTTGAGCATGGAGCTTCCAGTTTTGGGGTGTC
 TGGGATCAACGAGTCAGCGGACATGAGTATTGGAGTTACTGTATCAAA
 AACAAATATGATAAACATGATCTTGGTCCAGCAACAGCTCAAATGGCCC
 TTCAGTTGTTTCATCAAAGATTACAGGTACACGTACCGATGCCATATAGG
 TGACACACAAATACAAACCCGAGATCATTGAAATAAAGAACTGTGG
 GAGCAAAACCCGTTCCAAAGCTGGACTGTGTCTCCGACGGAGGCCCAA
 ATTTATACAACATTAGAAATCTCCACATTCTGAAGTCTGCCTAAAAATG
 GGAATTGATGGATGAGGATTACCAGGGCGTTTATGCAACCCACTGAAC

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CCATTTGTGTCAGCCATAAAGAAATTGAATCAATGAACAATGCAGTGATGA
 TGCCAGCACATGGTCCAGCCAAAAACATGGAGTATGATGCTGTTGCAAC
 AACACACTCCTGGATCCCCAAAAGAAATCGATCCATCTTGAATACAAGT
 CAAAGAGGAGTACTTGAGGATGAACAAATGTACCAAAGGTGCTGCAATT
 TATTTGAAAAATTCTTCCCAGCAGTTCATACAGAAGACCAGTCGGGAT
 ATCCAGTATGGTGGAGGCTATGGTTTCCAGAGCCCGAATTGATGCACGG
 ATTGATTTGGAATCTGGAAGGATAAAGAAAGAGAGTTCACTGAGATCA
 TGAAGATCTGTTCCACCATTGAAGAGCTCAGACGGCAAAAATAGTGAAT
 TTAGCTTGTCTTCATGAAAAAATGCCTTGTTTCTACT

PB2

(SEQ ID NO: 36)

AGCGAAAGCA GGTCAATTAT ATTCAATATG GAAAGAATAA
 AAGAACTACG AAATCTAATG TCGCAGTCTC GCACCCGCGA
 GATACTCACA AAAACACCG TGGACCATAT GGCCATAATC
 AAGAAGTACA CATCAGGAAG ACAGGAGAAG AACCCAGCAC
 TTAGGATGAA ATGGATGATG GCAATGAAAT ATCCAATTAC
 AGCAGACAAG AGGATAACGG AAATGATTCC TGAGAGAAAT
 GAGCAAGGAC AAACTTTATG GAGTAAATG AATGATGCCG
 GATCAGACCG AGTGATGGTA TCACCTCTGG CTGTGACATG
 GTGGAATAGG AATGGACCAA TAACAAATAC AGTTCATTAT
 CCAAAAATCT ACAAACCTTA TTTTGAAAGA GTCGAAAGGC
 TAAAGCATGG AACCTTTGGC CCTGTCCATT TTAGAAACCA
 AGTCAAATA CGTCGGAGAG TTGACATAAA TCCTGGTCAT
 GCAGATCTCA GTGCCAAGGA GGCACAGGAT GTAATCATGG
 AAGTTGTTTT CCCTAACGAA GTGGGAGCCA GGATACTAAC
 ATCGGAATCG CAACTAACGA TAACCAAAGA GAAGAAAGAA
 GAACTCCAGG ATTGCAAAAT TTCTCCTTTG ATGGTTGCAT
 ACATGTTGGA GAGAGAACTG GTCGCAAAA CGAGATTCTT
 CCCAGTGGCT GGTGGAACAA GCAGTGTGTA CATTGAAGTG
 TTGCATTGTA CTCAAGGAAC ATGCTGGGAA CAGATGTATA
 CTCCAGGAGG GGAAGTGAGG AATGATGATG TTGATCAAAG
 CTTGATTATT GCTGCTAGGA ACATAGTGAG AAGAGCTGCA
 GTATCAGCAG ATCCACTAGC ATCTTTATTG GAGATGTGCC
 ACAGCACACA GATTGGTGGA ATTAGGATGG TAGACATCCT
 TAGGCAGAAC CCAACAGAAG AGCAAGCCGT GGATATATGC
 AAGGCTGCAA TGGGACTGAG AATTAGCTCA TCCTTCAGTT
 TTGGTGGATT CACATTTAAG AGAACAAGCG GATCATCAGT
 CAAGAGAGAG GAAGAGGTGC TTACGGGCAA TCTTCAAACA
 TTGAAGATAA GAGTGCATGA GGGATATGAA GAGTTCACAA
 TGGTTGGGAG AAGAGCAACA GCCATACTCA GAAAAGCAAC

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CAGGAGATTG ATTCAGCTGA TAGTGAGTGG GAGAGACGAA
 CAGTCGATTG CCGAAGCAAT AATTGTGGCC ATGGTATTTT
 CACAAGAGGA TTGTATGATA AAAGCAGTCA GAGGTGATCT
 GAATTCGTGC AATAGGGCGA ATCAACGATT GAATCCTATG
 CATCAACTTT TAAGACATTT TCAGAAGGAT GCGAAAGTGC
 TTTTTCAAAA TTGGGAGATT GAACCTATCG ACAATGTGAT
 GGGAAATGATT GGGATATTGC CCGACATGAC TCCAAGCATC
 GAGATGTCAA TGAGAGGAGT GAGAATCAGC AAAATGGGTG
 TAGATGAGTA CTCGAGCAGC GAGAGGGTAG TGGTGAGCAT
 TGACCGTTTT TTGAGAATCC GGGACCAACG AGGAAATGTA
 CTACTGTCTC CCGAGGAGGT CAGTGAAACA CAGGGAACAG
 AGAACTGAC AATAACTTAC TCATCGTCAA TGATGTGGGA
 GATTAATGGT CCTGAATCAG TGTTGGTCAA TACCTATCAA
 TGGATCATCA GAAACTGGGA AACTGTATAA ATTCAGTGGT
 CCCAGAAGCC TACAATGCTA TACAATAAAA TGGAATTTGA
 ACCATTTTCAG TCTTTAGTAC CTAAGGCCAT TAGAGGCCAA
 TACAGTGGGT TTGTAAGAAC TCTGTTCCAA CAAATGAGGG
 ATGTGCTTGG GACATTTGAT ACCGCACAGA TAATAAACT
 TCTTCCCTTC GCAGCCGCTC CACCAAAGCA AAGTAGAATG
 CAGTTCTCCT CATTTACTGT GAATGTGAGG GGATCAGGAA
 TGAGAATACT TGTAAGGGGC AATTCTCCTG TATTCAACTA
 TAACAAGGCC ACGAAGAGAC TCACAGTTCT CGGAAAGGAT
 GCTGGCACTT TAACTGAAGA CCCAGATGAA GGCACAGCTG
 GAGTGGAGTC CGTGTTCTG AGGGGATTCC TCATTCTGGG
 CAAAGAAGAC AAGAGATATG GGCCAGCACT AAGCATCAAT
 GAACTGAGCA ACCTTGCGAA AGGAGAGAAG GCTAATGTGC
 TAATTGGGCA AGGAGACGTG GTGTTGGTAA TGAAACGGAA
 ACGGGACTCT AGCATACTTA CTGACAGCCA GACAGCGACC
 AAAAGAATTC GGATGGCCAT CAATTAGTGT CGAATAGTTT
 AAAACGACC TTGTTTCTAC T

NP

(SEQ ID NO: 37)

AGCAAAAGCA GGGTAGATAA TCACTCACTG AGTGACATCA
 AAATCATGGC GTCTCAAGGC ACCAAACGAT CTTACGAACA
 GATGGAGACT GATGGAGAAC GCCAGAATGC CACTGAAATC
 AGAGCATCCG TCGGAAAAAT GATTGGTGA ATTGGACGAT
 TCTACATCCA AATGTGCACC GAACTCAAAC TCAGTGATTA
 TGAGGGACGG TTGATCCAAA ACAGCTTAAC AATAGAGAGA
 ATGGTGCTCT CTGCTTTTGA CGAAAGGAGA AATAAATACC
 TTGAAGAACA TCCAGTGC GGGAAAGATC CTAAGAAAAC

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TGGAGGACCT ATATACAGGA GAGTAAACGG AAAGTGGATG
 AGAGAACTCA TCCTTTATGA CAAAGAAGAA ATAAGGCGAA
 TCTGGCGCCA AGCTAATAAT GGTGACGATG CAACGGCTGG
 TCTGACTCAC ATGATGATCT GGCATTCCAA TTTGAATGAT
 GCAACTTATC AGAGGACAAG AGCTCTTGTT CGCACC GGAA
 TGGATCCCAG GATGTGCTCT CTGATGCAAG GTTCAACTCT
 CCCTAGGAGG TCTGGAGCCG CAGGTGCTGC AGTCAAAGGA
 GTTGAACAA TGGTGATGGA ATTGGTCAGA ATGATCAAAC
 GTGGGATCAA TGATCGGAAC TTCTGGAGGG GTGAGAATGG
 ACGAAAAACA AGAATTGCTT ATGAAAGAAT GTGCAACATT
 CTCAAAGGGA AATTTCAAAC TGCTGCACAA AAAGCAATGA
 TGGATCAAGT GAGAGAGAGC CGGAACCCAG GGAATGCTGA
 GTTCGAAGAT CTCACCTTTC TAGCACGGTC TGCACTCATA
 TTGAGAGGGT CGGTTGCTCA CAAGTCTTGC CTGCCTGCCT
 GTGTGTATGG ACCTGCCGTA GCCAGTGGGT ACGACTTTGA
 AAGGGAGGGA TACTCTCTAG TCGGAATAGA CCCTTTCAGA
 CTGCTTCAA ACAGCCAAGT GTACAGCCTA ATCAGACCAA
 ATGAGAATCC AGCACACAAG AGTCAACTGG TGTGGATGGC
 ATGCCATTCT GCCGCATTG AAGATCTAAG AGTATTAAGC
 TTCATCAAAG GGACGAAGGT GCTCCCAAGA GGAAGCTTT
 CCACTAGAGG AGTTCAAAT GCTTCCAATG AAAATATGGA
 GACTATGGAA TCAAGTACAC TTGAAGTGA AAGCAGGTAC
 TGGGCCATAA GGACCAGAAG TGAGAGGAAAC ACCAATCAAC
 AGAGGGCATC TGCGGGCCAA ATCAGCATAC AACCTACGTT
 CTCAGTACAG AGAAATCTCC CTTTGTACAG AACCAACATT
 ATGGCAGCAT TCAATGGGAA TACAGAGGGG AGAACATCTG
 ACATGAGGAC CGAAATCATA AGGATGATGG AAAGTGCAAG
 ACCAGAAGAT GTGTCTTTCC AGGGGCGGGG AGTCTTCGAG
 CTCTCGGACG AAAAGGCAGC GAGCCCGATC GTGCCTTCCT
 TTGACATGAG TAATGAAGGA TCTTATTCT TCGGAGACAA
 TGCAGAGGAG TACGACAATT AAAGAAAAAT ACCCTTGTTT
 CTACT

55 M

(SEQ ID NO: 38)

AGCAAAAGCA GGTAGATATT GAAAGATGAG TCTTCTAACC
 GAGGTGAAA CGTACGTACT CTCTATCATC CCGTCAGGCC
 CCCTCAAAGC CGAGATCGCA CAGAGACTTG AAGATGTCTT
 TGCAGGGAAG AACACCGATC TTGAGTTCT CATGGAATGG
 CTAAAGACAA GACCAATCCT GTCACCTCTG ACTAAGGGGA
 TTTTAGGATT TGTGTTACG CTCACCGTGC CCAGTGAGCG

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AGGACTGCAG CGTAGACGCT TTGTCCAAA TGCCCTTAAT
 GGAACGGGG ATCCAATAA CATGGACAAA GCAGTTAAAC
 TGTATAGGAA GCTCAAGAGG GAGATAACAT TCCATGGGGC
 CAAAGAAATC TCACTCAGTT ATTCTGCTGG TGCACCTGCC
 AGTTGTATGG GCCTCATATA CAACAGGATG GGGGCTGTGA
 CCACTGAAGT GGCATTGGC CTGGTATGTG CAACCTGTGA
 ACAGATTGCT GACTOCCAGC ATCGGTCTCA TAGGCAAATG
 GTGACAACAA CCAATCCACT AATCAGACAT GAGAACAGAA
 TGGTTTTAGC CAGCACTACA GCTAAGGCTA TGGAGCAAAT
 GGCTGGATCG AGTGAGCAAG CAGCAGAGGC CATGGAGGTT
 GCTAGTCAGG CTAGACAAAT GGTGCAAGCG ATGAGAACCA
 TTGGGACTCA TCCTAGCTCC AGTGCTGGTC TGAATAATGA
 TCTTCTTGAA AATTTGCAGG CCTATCAGAA ACGAATGGGG
 GTGCAGATGC AACGGTTCAA GTGATCCTCT CACTATTGCC
 GCAAATATCA TTGGGATCTT GCACCTGACA TTGTGGATTC
 TTGATCGTCT TTTTTTCAA TGCATTTACC GTCGCTTTAA
 ATACGGACTG AAAGGAGGGC CTTCTACGGA AGGAGTGCCA
 AAGTCTATGA GGAAGAATA TCGAAAGGAA CAGCAGAGTG
 CTGTGGATGC TGACGATGGT CATTTGTCA GCATAGAGCT
 GGAGTAAAA ACTACCTTGT TTCTACT

NS

(SEQ ID NO: 39)

AGCAAAAGCA GGGTGACAAA AACATAATGG ATCCAACAC
 TGTGTCAAGC TTTCAGGTAG ATTGCTTTCT TTGGCATGTC
 CGCAAACGAG TTGCAGACCA AGAACTAGGC GATGCCCCAT
 TCCTTGATCG GCTTCGCCGA GATCAGAAAT CCCTAAGAGG
 AAGGGGCAGT ACTCTCGGTC TGGACATCAA GACAGCCACA
 CGTGTGGAA AGCAGATAGT GGAGCGGATT CTGAAAGAAG
 AATCCGATGA GGCACTTAAA ATGACCATGG CCTCTGTACC
 TCGTTCGCGT TACCTAACTG ACATGACTCT TGAGGAAATG
 TCAAGGGACT GGTCCATGCT CATACCCAAG CAGAAAGTGG
 CAGGCCCTCT TTGTATCAGA ATGGACCAGG CGATCATGGA
 TAAGAATATC ATACTGAAAG CGAACTTCAG TGTGATTTT
 GACCGGCTGG AGACTCTAAT ATTGCTAAGG GCTTTCACCG
 AAGAGGGAGC AATTGTTGGC GAAATTTTAC CATTCGCTTC
 TCTTCCAGGA CATACTGCTG AGGATGTCAA AAATGCAGTT
 GGAGTCCTCA TCGGAGGACT TGAATGGAAT GATAACACAG
 TTCGAGTCTC TGAAACTCTA CAGAGATTCT CTTGGAGAAG
 CAGTAATGAG AATGGGAGAC CTCCTACTAC TCCAAACAG
 AAACGAGAAA TGGCGGAAC AATTAGGTCA GAAGTTTGAA

40

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GAAATAAGAT GGTGATTGA AGAAGTGAGA CACAACTGA
 AGATAACAGA GAATAGTTT GAGCAAATAA CATTATGCA
 AGCCTTACAT CTATTGCTTG AAGTGGAGCA AGAGATAAGA
 ACTTTCTCGT TTCAGCTTAT TTAGTACTAA AAAACACCCCT
 TGTTCCTACT

High-titer A/PR/8/34 (H1N1, PR8(UW)) virus grows 10 times better than other NAPR/8/34 PR8 strains 45 in eggs (10^{10} EID₅₀/mL; HA titer:1:8.000). Thus, replacement of the HA and NA genes of PR8(UW) with those of a currently circulating strain of influenza virus results in a vaccine strain that can be safely produced, and validates the use of PR8 (UW) as a master vaccine strain.

Genes that contribute to different growth properties between PR8(UW) and PR8 (Cambridge), which provides the non-HA and -NA genes of the NIBRG-14 vaccine strain (FIG. 1), were determined. Higher titers in eggs were obtained when the majority of internal genes were from PR8(UW). Highest titers were with the M viral segment of PR8(UW) and the NS gene of PR8 (Cambridge). The NS gene in PR8(UW) has a K (lysine) at residue 55 while the NS gene in PR8(Cam) has a E (glutamic acid). The polymerase subunit (PA, PB1, and PB2) and NP genes of PR8(UW) enhanced the growth of an H5N1 vaccine seed virus in chicken embryonated eggs, and the NS gene of PR8(Cambridge) enhanced the growth of an H5N1 vaccine seed virus in chicken embryonated eggs. A tyrosine (Y) at position 360 in PB2 of PR8(UW) likely contributes to the high growth rate of that virus in MDCK cells.

Example B

To develop a high-yield A/PR/8/34 (H1N1; PR8) virus backbone for growth of vaccine virus in specific host cells, random mutagenesis of the internal genes of PR8(HG) (PRBUW) was conducted. Random mutations were introduced into the UW-PR8 (Example 1) internal genes by error-prone PCR after which plasmid libraries were prepared that possessed the random mutations in an individual UW-PR8 internal gene. Then virus libraries (PR8H5N) were generated that possessed random mutations in an individual UW-PR8 internal gene, along with the other wild type internal genes and the NA and 'detoxified' HA genes of A/chicken/Indonesia/NC/09 (H5N) virus (Table 1), to generate "6+2" recombinant viruses. Consecutive passages of the virus in MDCK cells were employed to select for variants with high-growth properties.

TABLE 1

Virus libraries generated				
Internal genes			Titer of virus	
Number	Gene library	Other internal genes	HA + NA	library (pfu/ml)
Control		PR8 wild type	NC/09/H5N1	3×10^6
1	PB2	5 UW-PR8 genes	NC/09/H5N1	2.1×10^2
2	PB1	5 UW-PR8 genes	NC/09/H5N1	1.6×10^5
3	PA	5 UW-PR8 genes	NC/09/H5N1	7×10^3
4	NP	5 UW-PR8 genes	NC/09/H5N1	1.5×10^3

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TABLE 1-continued

Virus libraries generated				
Number	Gene library	Internal genes	HA + NA	Titer of virus library (pfu/ml)
		Other internal genes		
5	M	5 UW-PR8 genes	NC/09/H5N1	1×10^6
6	NS	5 UW-PR8 genes	NC/09/H5N1	1.8×10^6
7	PB2 + PB1 + PA	3UW-PR8 genes	NC/09/H5N1	75
8	PB2 + PB1 + PA + NP	2UW-PR8 genes	NC/09/H5N1	33
9	PB2 + NS	4UW-PR8 genes	NC/09/H5N1	2×10^2
10	M + NS	4UW-PR8 genes	NC/09/H5N1	5.7×10^5

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Virus libraries were passaged 12 times in MDCK cells or, after 2 passages, the libraries were mixed and 10 more passages were carried out (FIG. 2).

5 After 10 to about 12 consecutive passages in MDCK cells, plaque assays were performed and over 1,400 individual plaques were picked. FIG. 3 shows the numbers of clones with various HA titers. Growth enhancing mutations included: PB2: M202L, F323L, I504V, PB1: E1112G, V644A, NP: R74K, N417D, I116L, and NS: S161T. FIG. 4 provides the titers of recombinant viruses generated from selected mutations.

38 viruses with the highest HA titers from the random mutagenesis libraries were sequenced (Table 2)

TABLE 2

Sequences of viruses with the highest HA titers									
Clone #	Library	HA titer (2 ⁿ)	PB2	PB1	PA	HA (H3 numbering)	NP	NA	M NS
WT		7							
329	Mix	9	M202L			L182V			
			F323L						
154	Mix	8.5~9	M202L			L182V			
			F323L						
347	Mix	9	M202L			L182V			
			F323L						
94	Mix	8.5	M202L			F252I	I116L	L55S	
			F323L						
1045	Mix	9	M202L	V644A		F252I			
			F323L						
965	Mix	8.5~9	M202L		F105C	V184I			P90S
			F323L						
50	Mix	8.5	M202L			M148I (HA2)	R293M		
			F323L						
1005	Mix	9~9.5	M202L	V644A	R401K	M148I (HA2)			T49A
			F323L						
134	Mix	8.5	M202L						A223E
			F323L						
387	Mix	9	M202L	M507V					
			F323L	V644A					
852	Mix	9~9.5	M202L	R54I					
			F323L						
			M243I						
981	Mix	8.5~9	M202L	Q247H					
			F323L						
993	Mix	8.5~9	M202L				N224I		
			F323L						
1043	Mix	8.5~9	I504V			L182V	R74K		
398	Mix	8.5	I504V			L182V	R74K, N417D		A30P
1007	Mix	8.5	I504V	V644A		F252I	M371V		
1042	Mix	8.5~9	I504V	E75V		F252I	R74K		
			D76G						
			E78P						
			P79V						
			S80G						
			V644A						
			E697P						
			F699L						
			F700L						
			P701H						
			S702R						
			Y705T						
999	Mix	8.5~9	I504V			M148I (HA2)	R74K, N417D		
1014	Mix	8.5	I504V	T59I		M148I (HA2)	R74K, N417D	A265V	
			G62X						
			A63P						
			V644A						
			N694K						
			L695T						

TABLE 2-continued

Sequences of viruses with the highest HA titers									
Clone #	Library	HA titer (2 ^o)	PB2	PB1	PA	HA (H3 numbering)	NP	NA	M NS
1016	Mix	8.5~9	I504V			M148I (HA2)			
540	PB1	8.5		E112G		K162E			S161T
548	PB1	8.5~9		E112G		K162E			S161T
				L624V					
191	PB1	8~8.5		E112G					
571	PB1	9~9.5		E112G					
572	PB1	8.5		E112G					
573	PB1	8.5		E112G					
1404	PB1	8.5	I57V	E112G					
			T58G	S713C					
			A59V						
			K61Q						
			E677D						
			D678E						
			P679M						
1408	PB1	8.5		M40I					S161T
				G180W					
582	PB1	8.5~9		M40L,					S161T
				G180W					
545	PB1	8.5		M40L,		K121E (HA2)			
				G180W					
543	PB1	8.5		I667T					
219	PB1	9		I667T,		K162E			
				M714T					
344	Mix	8.5~9	M66R			L182V			
312	Mix	8.5~9				L182V	I116L		R140Q
320	Mix	8.5				L182V			
209	PB1	8.5~9		R54I		E136D, Q179L, A194V			

In a second approach, potentially growth-enhancing mutations described in the literature were introduced into the background of UW-PR8 virus (see Table 3 for virus stock titers) and tested for replicative ability. FIGS. 5A-D show growth curves for various viruses.

TABLE 3

UW-PR8 viruses possessing mutation(s) identified in the literature		
Gene	Mutation(s)	Virus stock titer (Pfu/ml)
WT	—	2×10^7
PB2	A44S	4.5×10^7
	E158G	3.2×10^4
	E158G + NP N101G	7.5×10^4
	E158A	8.3×10^6
	D253N + Q591K	8.3×10^6
	D256G	2.8×10^7
	R368K	3.1×10^7
	E391Q	1.4×10^8
	I504V + PA I550L	1.1×10^8
	Q591K	4.4×10^7
	V613T	1.8×10^7
	A661T	2.2×10^7
	D701N + S714R + NP N319K	1×10^6
	D701N	2.1×10^7
PB1	R327K	1.3×10^7
	V336I	2.3×10^7
	L473V + L598P	3.9×10^6
PB1F2	F2 N66S	1.6×10^8
	F2 K73R	1.1×10^8
	F2 V76A	4.4×10^7

TABLE 3-continued

UW-PR8 viruses possessing mutation(s) identified in the literature		
Gene	Mutation(s)	Virus stock titer (Pfu/ml)
	F2 R79Q	6.2×10^6
	F2 L82S	2.7×10^7
	F2 E87Q	1.5×10^6
PA	T97I	1.6×10^7
	K142N	3.3×10^7
	S225C	6.7×10^7
	S149P + T357K	3.4×10^8
	K356R	8.5×10^7
	A404S	5.2×10^7
	S421I	2.7×10^7
NP	R293K	4.7×10^7
	R305K	7.2×10^7
	E372D	2.2×10^7
	R422K	1.3×10^3
	T442A	5×10^7
	D455E	2.2×10^7
	I109V	3.9×10^7
M	V97A + Y100H	1.4×10^7
NS1	K55E	1.6×10^7

In a third approach, candidates from approaches 1 and 2 were combined and HA titers and PFU/mL determined (Table 4).

TABLE 4

High-growth candidates identified in approaches 1 and 2 were tested in various combinations										
#	HA	Gene origin							Virus stock titer	
		NA	PB2	PB1	PA	NP	M	NS	HA (2 ⁿ)	Pfu/ml
WT	Indo/NC/09 (detoxified)	Indo/NC/09	UW-PR8	UW-PR8	UW-PR8	UW-PR8	UW-PR8	UW-PR8	7	3.00E+07
1			M202L F323L	M507V V644A		I116L		K55E	9~9.5	2.00E+08
2			M202L F323L	R54I		N224I		K55E	5	1.00E+05
3			M202L F323L	Q247H	R401K			T49A	9	1.00E+08
4			M202L F323L	M507V V644A	K356R	T442A	V97A Y100H	K55E	10~10.5	1.60E+08
5			I504V	M507V V644A	I550L	R74K N417D		K55E	8~8.5	5.70E+07
6			I504V	M507V V644A	I550L	R74K N417D	V97A Y100H	K55E	9~9.5	4.40E+07
7			I505V	E112G	I550L	R74K		S161T	9	1.60E+08
8			M202L F323L	I667T M714T		I116L		R140Q	<1	<1E3
9			M202L F323L	E112G				S161T	8.5	1.30E+08
10			M66R	M40I G180W		R74K		S161T	8~8.5	2.30E+07
12			R368K	PB1 F2 N66S	K356R	R422K		K55E	5.5	9.00E+02
13			E391Q	R327K	S149P T357K	R293K			3	1.60E+06
14			Q591K	PB1 F2 K73R	S225C	R422K		K55E	7.5	2.00E+07
23							V97A		8.5~9	1.50E+07
24							Y100H		9~9.5	2.90E+07
25	NOR 15-19 nt mut ¹	Indo/NC/09	M202L F323L	M507V V644A	K356R	R422K	V97A Y100H	K55E	9.5~10	7.50E+07
26	Indo/NC/09 (detoxified)	Indo/NC/09						A30P	6.5~7	1.00E+07
27								T49A	6.5~7	2.00E+07
28								R140Q	8	4.00E+07
29								S161T	7~7.5	1.40E+07
30								A223E	7.5	1.00E+07
31				I667T M714T					3.5	4.00E+05
32	NCR 15-19 nt mut	UW-PR8	M202L F323L	V644A	K356R	T442A	Y100H	K55E	7~7.5	4.30E+06
33	Indo/NC/09 (detoxified)	Indo/NC/09	M202L F323L	E112G	K356R	R74K	Y100H	K55E	9~9.5	7.00E+07
34	NCR 15-19 nt mut	UW-PR8	I504V	M507V V644A			V97A Y100H	K55E	7	2.00E+05
35	Indo/NC/09 (detoxified)	Indo/NC/09	M202L F323L	M507V V644A	R401K	T442A	Y100H	R140Q	9	3.20E+07
36			I504V	E112G	I550L	I112L	Y100H	R140Q	9.5	1.30E+08
37			M202L F323L	E112G	S149P T357K	T442A	Y100H	K55E	0	0.00E+00
38			M202L F323L	M507V V644A		I116L	Y100H	K55E	10.1	2.30E+08
39			M202L F323L	M507V V644A	K356R	T442A	Y100H	K55E	9.8	1.00E+08
40			I504V	M507V V644A	I550L	T442A	Y100H	K55E	9.2	6.00E+07
41			I504V	I112G	I550L	R74K	Y100H	K55E	9.2	7.50E+07
P17			I504V	E112G	S225C	R74K N417D	V97A Y100H	K55E	9.5~10	5.80E+08
P26			M202L F323L	M40L G180W	S225C	R422K	V97A Y100H	K55E	10	3.00E+08
P61		Indo/NC/09 NA P263T ²	M202L F323L	Q247H	K142N	R74K	V97A Y100H	K55E	10~10.5	2.00E+08

¹Mutation in the HA gene noncoding region;²A P263T mutation was detected in the NA protein of this virus clone

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As shown in Table 4, several recombinant viruses were identified that replicated better than wild type, such as #1, #4, #36, #38, P17, P16, and P61. To identify the growth characteristics of these viruses, growth kinetics in MDCK cells were determined (FIG. 7). For one candidate, virus was purified on sucrose gradients and HA content and viral total protein evaluated. FIG. 8A shows HA titer of wild type (UW-PR8) and #4, FIG. 8B shows viral protein for wild type (UW-PR8) and #4, and FIG. 8BC is a SDS-PAGE analysis of viral proteins of wild type (UW-PR8) and #4. Further analysis demonstrated that viruses possessing the V97ANY100H mutations in M1 yielded higher HA titers than the parental virus, although the virus titer was lower (see FIGS. 9A-B). The V97A/Y100H mutations in M1 may result in particles with a larger surface into which more HA protein can be incorporated. Since inactivated influenza viruses are dosed based on their HA content, variants with high HA content are attractive vaccine candidates.

To identify mutations in the influenza promoter region that provide for enhanced replication, viruses possessing a 'U' at position 4 at the 3' end of all eight vRNA segments were prepared in the UW-PR8 PA, PB1 and PB2 internal genes (the UW-PR8 PB2, PB1, and PA segments possess a 'C' at position 4). The growth curves of the resulting viruses are shown in FIG. 11C.

Viruses possessing combinations of promoter mutations and amino acid changes were prepared and titers determined (Table 5).

TABLE 5

Virus titers of high-growth candidates.									
Viruses	Gene backbone								Virus stock titer
	HA	NA	PB2	PB1	PA	NP	M	NS	HA (2 ⁿ) pfu/ml
Control	WT	WT	WT	WT	WT	WT	WT	WT	7 3.0E+07
1	WT	WT	3'C4U	3'C4U	3'C4U	R74K	V97A	K55E	10.5 2.2E+09
2	3' G3A U5C C8U & 5' U3C A8G		M202L F323L	Q247H	K142N		Y100H		8.5~9 5.6E+07
3	NCR 15-19 nt mut								9~9.5 1.4E+09
4	3' G3A U5C C8U & 5' U3C A8G & NCR 15-19 nt mut								7 7.0E+07

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Codon usage optimization was also conducted. Alteration of codons may increase protein expression but could also alter

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reflect the codon usage in canine cells (since MOCK cells are of canine origin) (FIG. 10A), while leaving the packaging signals (located at the 5' and 3' ends of the vRNA) unaltered. In one approach, codon optimization was performed for all codons in the 'internal' region of the PB2 gene (FIG. 10C) and in another approach, codon optimization was performed for so-called 'rare' codons (FIG. 10B) (used at significantly lower frequency compared to the codon used most frequently for a given amino acid) (see SEQ ID NO:25 in FIG. 10F). Analyses were carried out using the "Graphical Codon Usage Analyser" (www.gcua.de). The titers of those viruses are shown in Table 6 (see also FIGS. 10B-C).

TABLE 6

Titers of viruses encoding codon-optimized PB2 genes.									
Virus	Gene backbone								Virus stock titer
	HA	NA	PB2	PB1	PA	NP	M	NS	HA (2 ⁿ) pfu/ml
Wild type	WT	WT	WT	WT	WT	WT	WT	WT	7~7.5 3.5E+07
PB2 codon optimization-1	WT	WT	Rare codon optimized PB2	WT	WT	WT	WT	WT	9 2.1E+08
PB2 codon optimization-2	WT	WT	All Codon optimized PB2	WT	WT	WT	WT	WT	3 9.0E+05

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RNA structure and stability. For example, codon usage optimization of the PB2 gene segment was performed to

Optimization of rare codons in PB2 resulted in increased titers compared to wild type virus (UW-PR8) (see FIG.

10D). Other gene segments were codon optimized and titers of viruses with those segments or combinations of optimized segments were determined (FIG. 10E).

In another approach to increase virus titer in MDCK cells, chimeric HA and NA genes were prepared (FIG. 13A) and titers of viruses having those genes were determined (FIG. 13B).

Viruses with combinations of the above-mentioned mutations (high growth backbone mutations, promoter mutations, chimeric HA and NA genes and canine codon optimization) were prepared and growth kinetics, PFU and HA titers of those viruses were determined (see FIG. 14).

An exemplary set of backbone mutations are canine codon opti-PB2+C4U+M202L, F323L; PB1: C4U+Q247H; PA: C4U+K142N; NP: Canine codon opti-NP+R74K; M: V97A, Y100H; and NS: K55E.

Any of the mutations described herein, or any combination thereof, may be combined with, for instance, seasonal H1N1 and H3N2, H3N2 Variant, PdmH1N1, H5N1, H7N9 or H9N2, or other clades or candidate vaccine strains. For example, HA and NA genes from A/California/04/2009(pdm H1N1) were combined with the six internal genes of UW-PR/8 to generate “6+2” recombinant viruses. Eleven virus libraries were generated and passaged 10 times in eggs. Three rounds of limiting dilution were performed to screen for high growth mutants (FIG. 15). In one embodiment, a variant with high growth properties in MDCK cells has a PB2 gene segment with a promoter mutation (C4U) and a mutation that results in I504V (relative to the parental virus); a PB1 gene segment with a promoter mutation (C4U) and a mutation that results in E112G; a PA gene segment with a promoter mutation (C4U) and a mutation that results in S225C; a NP gene segment with mutations that result in R74K and N417D; a M gene segment with mutations that result in V97A and Y100H; and a NS gene segment with a mutation that results in K55E, where optionally the sequence of one or more gene segments, e.g., the NP gene segment, is modified to include canine codon optimized codons. In one embodiment, a variant with high growth properties in MDCK cells has a canine codon optimized PB2 gene segment with a promoter mutation (C4U) and mutations that result in M202L and F323L; a PB1 gene segment with a promoter mutation (C4U) and a mutation that results in Q247H; a PA gene segment with a promoter mutation (C4U) and a mutation that results in K142N; a canine codon optimized NP gene segment with a mutation that results in R74K; a M gene segment with mutations that result in V97A Y100H; and a NS gene segment with a mutation that results in K55E.

Similar experiments were conducted in Vero cells, e.g., after about 3 to 5 passages in Vero cells, using clones with high replicative properties in MDCK cells (see FIG. 16). FIG. 17 shows 5 viruses likely to have high replicative properties in Vero cells. In one embodiment, a PR8(UW) variant with high-growth properties in Vero cells has the following mutations that may be used in various combinations to increase the replicative ability of PR8(UW) virus: PB2 segment: C4U (promoter mutation), I504V (amino acid change); PB1 segment: C4U (promoter mutation); M40L (amino acid change), G180W (amino acid change); PA segment: C4U (promoter mutation), R401K (amino acid change); NP segment: I116L (amino acid change); NS segment: A30P (amino acid change in NS1), or R118K (amino acid change in NS1).

In one embodiment, a PR8(UW) variant with high-growth properties has the following residues that may be used in various combinations with each other and/or other residues,

e.g., those that enhance virus replication, to increase the replicative ability of reassortants having PR8(UW) based viral segment(s): a HA segment with one or more of 136D, 162E, 179L, 182V, 184I, 252I, 449E, and/or 476I; a NA segment with 55S and/or 265V; a NS segment with NS1 having 118K; F2 with 81G; a PB1 segment with 62A, 261G, 361R, 621R, and/or 654S, and/or viral segment promoters with the growth-enhancing nucleotides described herein. e.g., having one or more of the nucleotide changes G1012C, A1013U, or U1014A in the M viral segment.

Example C

To assess the contribution of individual viral RNA (vRNA) segments to high-yield properties, a series of reassortant viruses was generated that possessed one or several vRNA segments of a high-yield PR8 (PR8-HY) variant in the background of the parental virus [UW-PR8_Indo/05 (HA+NA)]. Vero cells were infected in triplicate with the indicated viruses at a MOI of 0.005 and incubated at 37° C. in the presence of trypsin. At the indicated time points, virus titers and HA titers were determined by performing plaque or HA assays, respectively. The results are shown in FIG. 20. These data indicated that several vRNA segments contribute to the properties of PR8-HY virus. In particular, the PB2+PB1+PA+NP vRNAs of PR8-HY virus conferred an appreciable increase in virus and HA titers, evidencing the enhanced replicative ability of this virus.

To further assess which component of the viral replication complex that provides for high-yield properties, wild-type or high-yield PB2, PB1, PA, and NP proteins were tested in various combinations in minireplicon assays in human 293T, canine MDCK, African green monkey Vero, and avian DF1 cells. The results are shown in FIG. 21. Interestingly, the PB2, PB1, PA, and NP proteins of PR8-HY virus attenuated the viral replicative ability in 293T, Vero, and DF1 cells; this effect was primarily conferred by the PB2 protein. In contrast, the combination of PB2+PB1+PA+NP proteins derived from PR8-HY virus conferred a substantial increase in replicated ability in canine MDCK cells, which were used for the selection of PR8-HY virus. The findings suggested host-dependent mechanisms underlying the high yield of PR8-HY virus. For example, the combination of PB1+PA+NP proteins, or a subset thereof, derived from PR8-HY may confer enhanced viral replicative ability in 293T, Vero, and DF1 cells.

Exemplary Embodiments

An isolated, single cycle recombinant influenza virus is provided having at least seven viral segments selected from PA, PB1, PB2, NP, NS, M, HA or NA viral segments, or having at least six viral segments selected from PA, PB1, PB2, NP, NS, M, or HEF viral segments, one of which segments comprises coding sequences for an antigenic coronavirus protein or an antigenic portion thereof. In one embodiment, the antigenic coronavirus protein comprises coronavirus S (spike) sequences. In one embodiment, the antigenic coronavirus protein comprises S1 sequences. In one embodiment, the antigenic coronavirus protein comprises a soluble protein. In one embodiment, the antigenic portion comprises the receptor binding domain. In one embodiment, the antigenic coronavirus protein sequences or the portion thereof have at least 80% amino acid sequence identity to one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the virus comprises eight viral segments. In one embodiment, the virus comprises nine viral segments. In

one embodiment, the virus is an influenza A or B virus. In one embodiment, the virus is an influenza C or D virus. In one embodiment, coding sequences for the antigenic coronavirus protein sequences or the portion thereof replace at least a portion of the coding sequences for one of PA, PB1, PB2, NP, NS1, NS2, M1, M2, HA, or NA. In one embodiment, coding sequences for the antigenic coronavirus protein sequences or the portion thereof are inserted into coding sequences in the viral segment of one of PA, PB1, PB2, NP, NS, M, HA or NA viral segments. In one embodiment, the virus is bivalent or trivalent. In one embodiment, the M viral segment is mutated so that upon viral replication the mutant M gene expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and either lacking a transmembrane domain or having a mutated transmembrane domain. In one embodiment, the mutant M2 protein comprises the M2 extracellular domain. In one embodiment, the M2 extracellular domain comprises less than 24 residues. In one embodiment, the M2 extracellular domain comprises at least 9 residues. In one embodiment, the mutation in the transmembrane domain comprises at least one amino acid substitution. In one embodiment, the transmembrane domain is deleted. In one embodiment, the deletion in the transmembrane domain includes residues 29 to 31. In one embodiment, the deletion in the transmembrane domain comprises at least 10 residues. In one embodiment, two or more of the PA, PB1, PB2, NP, NS, and M viral segments have selected amino acid residues at positions 30, 31, 105, 142, 149, 225, 356, 357, 401, and/or 550 in PA; positions 40, 54, 59, 62, 63, 75, 76, 78, 79, 80, 112, 180, 247, 327, 507, 624, 644, 667, 694, 695, 697, 699, 700, 701, 702, 705, 713, and/or 714 in PB1; positions 57, 58, 59, 61, 66, 202, 323, 368, 391, 504, 591, 677, 678, and/or 679, in PB2; positions 74, 112, 116, 224, 293, 371, 377, 417, 422 or 442 in NP; positions 90, 97 and/or 100 in M1; or positions 30, 49, 55, 118, 140, 161 and/or 223 in NS1. In one embodiment, at least of the viral segments has a C to U promoter mutation. In one embodiment, at least one of PA, PB1, or PB2 viral segments has a C to U promoter mutation. In one embodiment, the PB2 segment has a C4U promoter mutation or 504V; the PB1 segment has one or more of C4U, 40L or 180W; the PA segment has C4U or 401K; the NP segment has 116L; or the NS segment has 30P in NS1 or 118K in NS1.

An isolated, single cycle recombinant influenza virus is provided having PA, PB1, PB2, NP, NS, M, HA or NA viral segments, or having PA, PB1, PB2, NP, NS, M, or HEF viral segments, wherein the NS or PB2 segment comprises coding sequences for an antigenic coronavirus protein or an antigenic portion thereof, and optionally the M viral segment is mutated so that upon viral replication the mutant M gene expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and either lacking a transmembrane domain or having a mutated transmembrane domain. In one embodiment, the antigenic coronavirus protein comprises coronavirus S (spike) sequences. In one embodiment, the antigenic coronavirus protein comprises coronavirus S (spike) RBD sequences.

An isolated, single cycle recombinant influenza virus is provided having PA, PB1, PB2, NP, NS, M, HA or NA viral segments, or having PA, PB1, PB2, NP, NS, M, or HEF viral segments, wherein the NS segment comprises coding sequences for an antigenic coronavirus protein or an antigenic portion thereof, and optionally the M viral segment is mutated so that upon viral replication the mutant M gene expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and either lacking a

transmembrane domain or having a mutated transmembrane domain. In one embodiment, the antigenic coronavirus protein comprises coronavirus S (spike) sequences. In one embodiment, the antigenic coronavirus protein comprises coronavirus S (spike) RBD sequences.

Also provided is an isolated influenza virus having at least seven viral segments selected from PA, PB1, PB2, NP, NS, M, HA or NA viral segments, or having at least six viral segments selected from PA, PB1, PB2, NP, NS, M, or HEF viral segments, one of which segments comprises coding sequences for an antigenic coronavirus protein or an antigenic portion thereof. In one embodiment, the antigenic coronavirus protein comprises S1 sequences. In one embodiment, the antigenic portion comprises the receptor binding domain. In one embodiment, the antigenic coronavirus protein sequences or the portion thereof have at least 80% amino acid sequence identity to one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the virus comprises eight or nine viral segments. In one embodiment, the virus is an influenza A or B virus. In one embodiment, coding sequences for the antigenic coronavirus protein sequences or the portion thereof replace at least a portion of the coding sequences for one of PA, PB1, PB2, NP, NS1, NS2, M1, M2, HA, or NA. In one embodiment, coding sequences for the antigenic coronavirus protein sequences or the portion thereof are inserted into coding sequences in the viral segment of one of PA, PB1, PB2, NP, NS, M, HA or NA viral segments. In one embodiment, the virus is bivalent or trivalent. In one embodiment, the M viral segment is mutated so that upon viral replication the mutant M gene expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and either lacking a transmembrane domain or having a mutated transmembrane domain, wherein the replication of the recombinant virus is abrogated or attenuated in vivo relative to a corresponding influenza virus with a wild-type M viral segment. In one embodiment, the mutant M2 protein comprises the M2 extracellular domain. In one embodiment, the M2 extracellular domain comprises at least 9 or 10 residues. In one embodiment, the mutation in the transmembrane domain comprises a deletion in the transmembrane domain. In one embodiment, two or more of the PA, PB1, PB2, NP, NS, and M viral segments have selected amino acid residues at positions 30, 31, 105, 142, 149, 225, 356, 357, 401, and/or 550 in PA; positions 40, 54, 59, 62, 63, 75, 76, 78, 79, 80, 112, 180, 247, 327, 507, 624, 644, 667, 694, 695, 697, 699, 700, 701, 702, 705, 713, and/or 714 in PB1; positions 57, 58, 59, 61, 66, 202, 323, 368, 391, 504, 591, 677, 678, and/or 679, in PB2; positions 74, 112, 116, 224, 293, 371, 377, 417, 422 or 442 in NP; positions 90, 97 and/or 100 in M1; or positions 30, 49, 55, 118, 140, 161 and/or 223 in NS1. In one embodiment, at least of the viral segments has a C to U promoter mutation. In one embodiment, at least one of PA, PB1, or PB2 viral segments has a C to U promoter mutation. In one embodiment, the PB2 segment has a C4U promoter mutation or 504V; the PB1 segment has one or more of C4U, 40L or 180W; the PA segment has C4U or 401K; the NP segment has 116L; or the NS segment has 30P in NS1 or 118K in NS1.

In one embodiment, a vaccine comprising an effective amount of the virus is provided. In one embodiment, the vaccine is formulated for intranasal delivery. In one embodiment, the virus is bivalent. In one embodiment, the recombinant virus comprises influenza A HA. In one embodiment, the virus comprises H1, H3, H5 or H7 HA. In one embodiment, the vaccine which further comprises a different influenza virus. In one embodiment, the vaccine further com-

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prises at least two different influenza viruses. In one embodiment, the virus is inactivated.

Further provided is a method to immunize a vertebrate, comprising: administering to the vertebrate the vaccine disclosed herein. In one embodiment, the vertebrate is an avian. In one embodiment, the vertebrate is a mammal. In one embodiment, the vertebrate is a human. In one embodiment, the vaccine is intranasally administered. In one embodiment, the vaccine is intramuscularly administered. In one embodiment, more than one dose is administered.

The invention will be described by the following nonlimiting examples.

Example 1

In one embodiment, an eight segment single cycle recombinant influenza A virus is prepared. One of the viral RNA segments (for example, the NS segment) is modified to also express SARS-CoV-2 S (or portions thereof), e.g., a fusion of NS1 and SARS-CoV-2 S protein or a portion thereof. For fusion protein between the flu and SARS proteins, proteases that autocatalytically cleave are employed to generate functional flu and SARS proteins. The addition of heterologous protein sequences does not result in the need for a helper cell to express a protein in trans. However, if influenza virus coding sequences on one or more the viral segments are deleted (either a portion thereof or in their entirety), the corresponding influenza virus protein(s) are supplied in trans. For example, the viral M segment is modified by inserting two stop codons into M2 (downstream of the splice acceptor site), and by deleting the coding region for the transmembrane domain of M2, referred to as M2SR, which undergoes only one round of replication and requires a helper cell line for propagation That is in contrast to live-attenuated viruses which undergo several rounds of slow replication). In one embodiment, one or more of the internal viral segments are from PR8HY. In one embodiment, the HA and NA viral segments are from a heterologous strain. The M2SR having coronavirus sequences (CoroFlu M2SR) is intranasally administered. In other embodiments, inactivated coronavirus/influenza viruses may be intramuscularly administered.

In one embodiment, a nine-segment virus is generated with eight segments expressing the flu proteins (with M2 modified as described above), and a ninth viral segment in which (part of) the flu coding region is replaced with SARS-CoV-2 S (or portions thereof).

In one embodiment, an attenuated virus is generated, e.g., one having M2 mutations that result in attenuation, e.g., M2del29-31 or M2 cytoplasmic tail deletions (see, e.g., del11 or del 22 etc. in Iwatsuki-Horimoto et al. (2006) and Watanabe et al. (2008).

Other alterations in M2 include two stop codons to prevent expression of the transmembrane domain and cytoplasmic tails and two stop codons and deletion of the coding region of the transmembrane domain (see Watanabe et al. (2009) and Sarawar et al. (2016), which are incorporated by reference herein)

Example 2

An influenza vaccine that includes coronavirus sequences and is limited to a single round of replication in vaccinated individuals, but stimulates mucosal, innate, humoral, and/or cell-mediated immune responses, was prepared. Phase I and Phase IIa clinical studies with the vaccine virus (without coronavirus sequences) have demonstrated its safety (no

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serious adverse events; no virus shedding) and the ability to elicit neutralizing immune responses to homologous and antigenically mismatched influenza virus strains. Importantly, this vaccine mimics the natural infection process and stimulates mucosal, innate, humoral, and cell-mediated immune responses. Thus, this platform may be employed to generate a single-cycle bivalent influenza vaccine expressing a soluble portion of the spike protein (the major antigen) of a coronavirus, e.g., the new 2019 coronavirus. The immunogenicity and protective efficacy of this vaccine is likely to be superior to that of inactivated vaccines, which stimulate B cell responses, but fail to induce other immune responses.

Generate a Bivalent Coronavirus/Influenza Virus Vaccine Candidate and Test its Protective Efficacy in Animal Models

To generate the novel bivalent coronavirus/influenza virus vaccine based on the M2SR platform (called CoroFlu M2SR, FIG. 22), cells were transfected with plasmids for influenza virus generation. One plasmid possesses a deletion of the influenza viral M2 coding region. In another plasmid, the coding region for the receptor-binding domain (RBD) of the 2019-nCoV spike (S) protein is inserted between the influenza viral NS1 and NS2 coding regions, separated by foot-and-mouth virus protease 2A autoproteolytic cleavage sites (2A). In cells expressing the M2 protein, CoroFlu M2SR vaccine virus is generated.

In one embodiment, the coronavirus S amino acid sequence, or a portion thereof, has at least 80%, e.g., 90%, 92%, 95%, 97% or 99%, including any integer between 80 and 99, contiguous amino acid sequence identity to a polypeptide having one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the S polypeptide or a portion thereof has one or more, for instance, 2, 5, 10, 15, 20 or more, conservative amino acids substitutions, e.g., conservative substitutions of up to 10% or 20% of the residues, relative to a polypeptide having one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, a S polypeptide or a portion thereof has one or more, for instance, 2, 5, 10, 15, 20 or more, conservative amino acids substitutions, e.g., conservative substitutions of up to 10% or 20% of 2, 5, 10, 15, 20 or more, of a combination of conservative and non-conservative amino acids substitutions, e.g., conservative substitutions of up to 10% or 20% of the residues, or relative to a polypeptide with one of the sequences disclosed herein. In one embodiment, the coronavirus sequence in the influenza virus has 1, 2, 3, 4 or 5 substitutions relative to one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the coronavirus S1 sequence in the influenza virus has 1, 2, 3, 4 or 5 substitutions relative to the S1 sequence in one of SEQ ID Nos. 25-28 and 50-52. In one embodiment, the coronavirus RBD sequence in the influenza virus has 1, 2, 3, 4 or 5 substitutions relative to the RBD sequence in one of SEQ ID Nos. 25-28 and 50-52.

For example, the amino acid(s) can be any amino acid within these positions such as any of the amino acids listed in the table below.

Original Residue	Exemplary Substitutions	Alternative Substitutions
Ala (A)	val; leu; ile	Val
Arg (R)	lys; gln; asn	Lys
Asn (N)	gln; his; lys; arg	Gln
Asp (D)	Glu, Asn	Glu, Asn
Cys (C)	Ser	Ser
Gln (Q)	Asn	Asn
Glu (E)	Asp	Asp
Gly (G)	Pro	Pro

-continued

Original Residue	Exemplary Substitutions	Alternative Substitutions
His (H)	asn; gln; lys; arg; gln;	Arg; Gln
Ile (I)	leu; val; met; ala; phe norleucine	Leu
Leu (L)	norleucine; ile; val; met; ala; phe	Ile
Lys (K)	arg; gln; asn	Arg
Met (M)	leu; phe; ile	Leu
Phe (F)	leu; val; ile; ala	Leu
Pro (P)	Gly	Gly
Ser (S)	Thr	Thr
Thr (T)	Ser, Ala	Ser, Als
Trp (W)	Tyr	Tyr
Tyr (Y)	trp; phe; thr; ser	Phe
Val (V)	ile; leu; met; phe; ala; norleucine	Leu

Conservative amino acid substitutions refer to the interchangeability of residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine and tryptophan; a group of amino acids having basic side chains is lysine, arginine and histidine; and a group of amino acids having sulfur-containing side chain is cysteine and methionine. In one embodiment, conservative amino acid substitution groups are: threonine-valine-leucine-isoleucine-alanine; phenylalanine-tyrosine; lysine-arginine; alanine-valine; glutamic-aspartic; and asparagine-glutamine.

The basic characterization of CoroFlu M2SR includes assessment of virus titers in the Vero M2 production cell line; the virus is passaged 10 consecutive times (followed by sequence analysis) in Vero M2-expressing cells to assess the genomic stability of CoroFlu M2SR.

Animal studies are carried out in Syrian hamsters (in which SARS-CoV replicates efficiently), in ferrets (an animal model that has been used for SARS-CoV research) and in transgenic mice expressing the human angiotensin-converting enzyme-2 (ACE-2) receptor, the SARS-CoV receptor to which 2019-nCoV also binds. Animals are intranasally administered with different amounts of CoroFlu M2SR (e.g., 10^5 to 10^7 PFU). Control animals are administered with M2SR vaccine (expressing the same HA and NA genes as CoroFlu M2SR, but not expressing S/RDB). Another control group is mock-treated. On days 1, 3, 5, and 7 after vaccination, nasal swab samples are collected to confirm the lack of virus shedding. Three weeks post-vaccination, serum samples are collected and tested for antibodies to SARS-CoV2 S/RBD and influenza HA; if the titers are low, animals are boosted.

Animals are vaccinated and challenged with live SARS-CoV2 or influenza virus three weeks after the last immunization. Control groups are mock-vaccinated, followed by live virus challenge with SARS-CoV2 and influenza virus. Groups of animals are euthanized on days 3, 6, and 9 post-infection to titrate the amounts of virus in the nasal turbinates and lungs. Other groups of animals are observed for weight changes and clinical symptoms. Nasal swabs are collected every other day (starting on day 1 post-challenge) to determine the virus load in the challenged animals.

Assess Whether the Vaccine Candidates Cause Antibody-Dependent Enhancement (ADE) of Virulence

ADE (i.e., antibody-dependent enhancement of infectivity and disease severity) is a potential concern with the development of vaccines to a variety of viruses, including coronaviruses (Halsted, 2014; Huisman et al, 2009; Smatti et al., 2018; Wan et al., 2019; Wang et al., 2014; Yip et al., 2014; Takada et al., 2001; Takada et al., 2003; and Takada et al., 2007). Since ADE is most likely caused by non-neutralizing antibodies directed at sub-dominant epitopes, the use of S/RDB (instead of full-length S) may reduce the likelihood of ADE. To test this, animals are vaccinated with CoroFlu M2SR, M2SR, or mock-vaccinated, and sera will be collected three weeks later.

To assess ADE in vitro, the SARS-Cov2 is mixed with different dilutions of serum (obtained from vaccinated or control animals; see previous paragraph) and added to cells to determine virus titers. To assess ADE in vivo, two sets of experiments are carried out: In the first set of experiments, animals are administered different serum dilutions and subsequently infected with the SARS-Cov2. Control groups are treated with serum obtained from mock-vaccinated. In the other set of experiments, animals are vaccinated with CoroFlu M2SR, M2SR, or mock-vaccinated, and three weeks later infected with live SARS-Cov2. At different times post-infection, animals are euthanized to collect organs for virus titration and histopathological analysis, and sera are collected to determine antibody titers. The finding that sera obtained from CoroFlu M2SR-vaccinated animals and vaccination with CoroFlu M2SR do not increase virus titers, disease symptoms, or histopathology compared with the controls establishes the absence of ADE for CoroFlu M2SR vaccine.

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 World Health Organization TSR No. 673 (1982).

World Health Organization. Confirmed human cases of avian influenza A (H5N1). http://www.who.int/csr/disease/avian_influenza/country/en/index.html

Yip et al., *Virol. J.*, 11:82 (2014).

- 5 All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be
- 10 apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 56

<210> SEQ ID NO 1

<211> LENGTH: 2233

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 1

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tcttgtgcag caatggatga tttccaatta attccaatga taagcaagtg tagaactaag     1500
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<211> LENGTH: 2340
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 2

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<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 3

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 <211> LENGTH: 1565
 <212> TYPE: DNA
 <213> ORGANISM: Influenza virus

<400> SEQUENCE: 4

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<400> SEQUENCE: 9

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<210> SEQ ID NO 10

<211> LENGTH: 2342

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 10

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<211> LENGTH: 2341

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 11

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gagagggtag tgggtgacat tgaccgggtc ttgagagtca gggaccaacg aggaaatgta	1560
ctactgtctc ccgaggaggt cagtgaacaa cagggaacag agaaactgac aataacttac	1620
tcacgtccta tgatgtggga gattaatggt cctgaatcag tgttggtcaa tacctatcaa	1680
tggatcatca gaaactggga aactgttaaa attcagtggg ccagagaacc tacaatgcta	1740
tacaataaaa tggaatttga accatttcag tctttagtag ctaaggccat tagaggccaa	1800
tacagtgggt ttgtaagaac tctgttccaa caaatgaggg atgtgcttgg gacatttgat	1860
accgcacaga taataaaact tcttccttc gcagccgctc caccaaagca aagtagaatg	1920
cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatact tgtaaggggc	1980
aattctcctg tattcaacta caacaaggcc acgaagagac tcacagttct cggaaggat	2040
gctggcactt taaccgaaga ccagatgaa ggcacagctg gagtggagtc cgctgttctg	2100
aggggattcc tcattctggg caaagaagac aggagatatg ggccagcatt aagcatcaat	2160
gaactgagca accttgcgaa aggagagaag gctaattgtc taattgggca aggagacgtg	2220
gtgttggtaa tgaaacgaaa acgggactct agcatactta ctgacagcca gacagcgacc	2280
aaaagaattc ggtgggcat caattagtgt cgaatagttt aaaaacgacc ttgtttctac	2340
t	2341

<210> SEQ ID NO 12

<211> LENGTH: 2234

-continued

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 12

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agcgaagca ggtactgatt caaatggaa gattttgtgc gacaatgctt caatccgatg    60
attgtcgagc ttgcggaaaa acaatgaaa gagtatgggg aggacctgaa aatcgaaaca    120
aacaatttg cagcaatatg cactcacttg gaagtatgct tcatgtattc agatttcac    180
ttcatcaatg agcaaggcga gtcaataatc gtagaacttg gtgacctaag tgcacttttg    240
aagcacagat ttgaaataat cgagggaaga gatcgacaaa tggcctggac agtagtaaac    300
agtatttgca acactacagg ggctgagaaa ccaaagtttc taccagattt gtatgattac    360
aagggaaaata gattcatcga aattggagta acaaggagag aagttcacat atactatctg    420
gaaaaggcca ataaaattaa atctgagaaa acacacatcc acattttctc gttcactggg    480
gaagaaatgg ccacaagggc cgactacact ctcatgaag aaagcagggc taggatcaaa    540
accaggctat tcaccataag acaagaaatg gccagcagag gcctctggga ttctttctgt    600
cagtcggaga gaggagaaga gacaattgaa gaaagggttg aaatcacagg aacaatgcgc    660
aagcttgccg accaaagtct ccgcgcgaac ttctccagcc ttgaaaattt tagagcctat    720
gtggatggat tcgaaccgaa cggctacatt gagggcaagc tgtctcaaat gtccaagaa    780
gtaaatgcta gaattgaacc ttttttgaaa acaacaccac gaccacttag acttccgaat    840
gggcctccct gttctcagcg gtccaaatc ctgctgatgg atgccttaaa attaagcatt    900
gaggacccaa gtcatgaagg agagggaata ccgctatatg atgcaatcaa atgcatgaga    960
acattctttg gatggaagga acccaatgtt gttaaaccac acgaaaaggg aataaatcca   1020
aattatcttc tgtcatgaa gcaagtactg gcagaactgc aggacattga gaatgaggag   1080
aaaattccaa agactaaaaa tatgaaaaa acaagtcagc taaagtgggc acttggtgag   1140
aacatggcac cagaaaagggt agactttgac gactgtaaag atgtagggtga tttgaagcaa   1200
tatgatagtg atgaaccaga attgagggtc cttgcaagtt ggattcagaa tgagttcaac   1260
aaggcatgcg aactgacaga ttcaagctgg atagagcttg atgagattgg agaagatgtg   1320
gtccaattg aacacattgc aagcatgaga aggaattatt tcacatcaga ggtgtctcac   1380
tgcagagcca cagaatacat aatgaagggg gtgtacatca atactgcctt acttaatgca   1440
tcttgtgcag caatggatga ttccaatta attccaatga taagcaagtg tagaactaag   1500
gagggaaggc gaaagaccaa cttgatgtgt ttcatacataa aaggaagatc ccacttaagg   1560
aatgacaccg acgtgggtaa ctttgtgagc atggagtttt ctctcactga cccaagactt   1620
gaaccacaca aatgggagaa gtactgtgtt cttgagatag gagatatgct tctaagaagt   1680
gccataggcc aggttttcaag gcccatgttc ttgtatgtga ggacaaatgg aacctcaaaa   1740
attaaatga aatggggaat ggagatgagg cgttgtctcc tccagtcact tcaacaaatt   1800
gagagtatga ttgaagctga gtctctgtc aaagagaaaag acatgaccaa agagttcttt   1860
gagaacaaat cagaaacatg gccatttga gagtctccca aaggagtggg ggaaagtctc   1920
attggggaag gtctgcagga ctttattagc aaagtcggta tttaacagct tgtatgcac   1980
tcacaaacta gaaggatttt cagctgaatc aagaaaactg cttcttatcg ttcaggctct   2040
tagggacaat ctggaacctg ggacctttga tcttgggggg ctatatgaag caattgagga   2100
gtgcctaatt aatgatccct gggttttgct taatgcttct tggttcaact ccttccttac   2160
acatgcattg agttagttgt ggcagtgtc ctatttgcta tccatactgt ccaaaaaagt   2220

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accttgtttc tact 2234

<210> SEQ ID NO 13
 <211> LENGTH: 1565
 <212> TYPE: DNA
 <213> ORGANISM: Influenza virus

<400> SEQUENCE: 13

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agcaaaagca gggtagataa tcaactactg agtgacatca aaatcatggc gtcccaaggc    60
accaaaccgt cttacgaaca gatggagact gatggagaac gccagaatgc cactgaaatc    120
agagcatccg tcggaaaaat gattggtgga attggacgat tctacatcca aatgtgcaca    180
gaacttaaac tcagtgatta tgagggacgg ttgatccaaa acagcttaac aatagagaga    240
atggtgctct ctgcttttga cgaaggaga aataaatacc tggaagaaca tcccagtgcg    300
gggaaagatc ctaagaaaac tggaggacct atatacagaa gagtaaacgg aaagtggatg    360
agagaactca tcctttatga caaagaagaa ataaggcgaa tctggcgcca agctaataat    420
ggtgacgatg caacggctgg tctgactcac atgatgatct ggcattccaa tttgaatgat    480
gcaacttata agaggacaag ggctcttggt cgcaccggaa tggatcccag gatgtgctct    540
ctgatgcaag gttcaactct ccctaggagg tctggagccg caggtgctgc agtcaaagga    600
gttggacaaa tgggtgatga attggtcagg atgatcaaac gtgggatcaa tgatcggaac    660
ttctggaggg gtgagaatgg acgaaaaaca agaattgctt atgaaagaat gtgcaacatt    720
ctcaaaggga aatttcaaac tgctgcacaa aaagcaatga tggatcaagt gagagagagc    780
cggaaaccag ggaatgctga gttcgaagat ctcaactttc tagcacggtc tgcactcata    840
ttgagagggt cggttgctca caagtcctgc ctgcctgcct gtgtgtatgg acctgccgta    900
gccagtgggt acgactttga aagagaggga tactctctag tcggaataga ccctttcaga    960
ctgcttcaaa acagccaagt gtacagccta atcagaccaa atgagaatcc agcacacaag   1020
agtcaactgg tgtggatggc atgccattct gccgcatttg aagatctaag agtattgagc   1080
ttcatcaaa ggacgaaggt ggtcccaaga ggggaagctt ccactagagg agttcaaat   1140
gcttccaatg aaaatatgga gactatggaa tcaagtacac ttgaactgag aagcaggtag   1200
tgggcccata ggaccagaag tggaggaaac accaatcaac agagggcatc tgcgggccaa   1260
atcagcatac aacctacgtt ctcagtacag agaaatctcc cttttgacag aacaaccgtt   1320
atggcagcat tcactgggaa tacagagggg agaacatctg acatgaggac cgaatcata   1380
aggatgatgg aaagtgcagg accagaagat gtgtctttcc aggggcgggg agtcttcgag   1440
ctctcggacg aaaaggcagc gagcccgcgc gtgccttcct ttgacatgag taatgaagga   1500
tcttatttct tcggagacaa tgcagaggag tacgacaatt aaagaaaaat accttggttt   1560
ctact                                             1565

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<210> SEQ ID NO 14
 <211> LENGTH: 1027
 <212> TYPE: DNA
 <213> ORGANISM: Influenza virus

<400> SEQUENCE: 14

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agcaaaagca ggtagatatt gaaagatgag tcttctaacc gaggtcgaaa cgtacgttct    60
ctctatcatc ccgtcaggcc ccctcaaacg cgagatcgca cagagacttg aagatgtctt    120
tgcagggaag aacaccgacg ttgaggttct catggaatgg ctaaagacaa gaccaatcct    180
gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg    240

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aggactgcag cgtagacgct ttgtccaaaa tgcctttaat gggaacgggg atccaaataa 300
catggacaaa gcagttaaac tgtataggaa gctcaagagg gagataacat tccatggggc 360
caaagaaatc tcaactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata 420
caacaggatg ggggctgtga ccactgaagt ggcatTTggc ctggtatgtg caacctgtga 480
acagattgct gactcccagc atcgggtctca taggcaaatg gtgacaacaa ccaaccact 540
aatcagacat gagaacagaa tggTTTTagc cagcactaca gctaaggcta tggagcaaat 600
ggctggatcg agtgagcaag cagcagaggc catggagggt gctagttagg ctaggcaaat 660
ggtgcaagcg atgagaacca ttgggactca tcctagctcc agtgcTggc tgaaaaatga 720
tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa 780
gtgatectct cgctattgcc gcaaatatca ttgggatctt gcacttgata ttgtggattc 840
ttgatcgtct ttttttcaaa tgcatttacc gtcgctttaa atacggactg aaaggagggc 900
cttctacgga aggagtcca aagtctatga gggaagaata tcgaaaggaa cagcagagtg 960
ctgtggatgc tgacgatggt cattttgtca gcatagagct ggagtaaaaa actaccttgt 1020
ttctact 1027

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<210> SEQ ID NO 15
<211> LENGTH: 890
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

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<400> SEQUENCE: 15

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agcaaaagca gggtgacaaa gacataatgg atccaaacac tgtgtcaagc tttcaggtag 60
attgctttct ttggcatgct cgcaaacgag ttgcagacca agaactagggt gatgccccat 120
tccttgatcg gcttcgccga gatcagaaat ccctaagagg aaggggcagc actcttggtc 180
tggacatcga gacagccaca cgtgctggaa agcagatagt ggagcggatt ctgaaagaag 240
aatccgatga ggcacttaaa atgaccatgg cctctgtacc tgcgtcgcgt tacctaaccg 300
acatgactct tgaggaaatg tcaagggaat ggtccatgct catacccaag cagaaagtgg 360
caggccctct ttgtatcaga atggaccagg cgatcatgga taaaacatc atactgaaag 420
cgaacttcag tgtgattttt gaccggctgg agactctaatt attgctaagg gctttcacccg 480
aagagggagc aattgttggc gaaatttcac cattgccttc tcttcaggga catactgctg 540
aggatgtcaa aaatgcagtt ggagtcctca tcggaggact tgaatggaat gataacacag 600
ttcagagtct tgaaactcta cagagattcg cttggagaag cagtaatgag aatgggagac 660
ctccactcac tccaaaacag aaacgagaaa tggcgggaac aattaggta gaagtttgaa 720
gaaataagat ggttgattga agaagtgaga cacaactga aggtaacaga gaatagtttt 780
gagcaataa catttatgca agccttacat ctattgcttg aagtggagca agagataaga 840
actttctcat ttcagcttat ttaataataa aaaacaccct tgtttctact 890

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<210> SEQ ID NO 16
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

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<400> SEQUENCE: 16

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agcgaaagca ggtcaattat attcaatatg gaaagaataa aagaactacg aaatctaattg 60
tcgcagtctc gcaccgcga gatactcaca aaaaccaccg tggaccatat ggccataatc 120

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aagaagtaca catcaggaag acaggagaag aaccagcac tgaggatgaa atggatgatg	180
gcaatgaaat atccaattac agcagacaag aggatcacccg aaatgattcc tgagagaaat	240
gagcaggagac agactctgtg gagtaaaatg aatgatgccg gatcagaccg agtgatgggtg	300
tcacctctgg ctgtgacatg gtggaatagg aatggacca tcaaaaatac agtgcattat	360
ccaaaaatct acaaaactta ttttgaaaga gtcgaaaggc tgaagcatgg aacctttggc	420
cctgtccatt ttagaaacca ggtcaaaatc cggcggagag tggacatcaa tcctgggtcat	480
gcagatctca gtgccaagga ggcacaggat gtgatcatgg aagtgggtgt ccctaacgaa	540
gtgggagcca ggattctgac atccgaatcc cagctgacca ttaccaaaga gaagaaagaa	600
gaactccagg attgcaaaat ttctctctg atgggtggcat acatgctgga gagagaactg	660
gtccgcaaaa caagattcct ccagtggtg ggtggaacaa gcagtgtgta cattgaagtg	720
ctgcatctga ctacagggaac atgctgggaa cagatgtata ctccaggagg ggaagtgagg	780
aatgatgatg tggatcagag cctgattatt gctgctagga acattgtgag aagagctgca	840
gtgtcagcag atccactggc atctctgctg gagatgtgcc acagcacaca gattgggtgga	900
attaggatgg tggacatcct gaggcagaac ccaacagaag agcaggccgt ggatatttgc	960
aaggctgcaa tgggactgag aattagctca tccttcagtt ttggtggatt cacatttaag	1020
agaacaagcg gatcatcagt caagagagag gaagaggtgc tgaccggcaa tctgcagaca	1080
ctgaagatca gagtgcata gggatatgaa gagttcaca tgggtgggag aagagcaaca	1140
gccatctca gaaaagcaac caggagactg attcagctga tctgtagtgg gagagacgaa	1200
cagtcattg ccgaagcaat tattgtggcc atggtgtttt cacaggagga ttgtatgatt	1260
aaagcagtc gaggtgatct gaatttcgtc aataggcca atcagcgact gaatcctatg	1320
catcagctgc tgagacattt tcagaaggat gccaaagtgc tgtttcagaa ttggggagtg	1380
gaacctatcg acaatgtgat gggaatgatt gggatcctgc ccgacatgac tccaagcatc	1440
gagatgtcaa tgagaggagt gagaatcagc aaaatgggtg tggatgagta ctccagcacc	1500
gagagggtcg tggtagcat tgacagattt ctgagaatcc gggaccagcg aggaaatgtg	1560
ctctgtctc ccgaggaggt cagtgaaca cagggaacag agaaactgac aattacttac	1620
tcatectcaa tgatgtggga gattaatggt cctgaatcag tctgtgtcaa tacctatcag	1680
tggatcatca gaaactggga aactgtgaaa attcagtggg ccagagaacc tacaatgctg	1740
tacaataaaa tggaatttga accatttcag tctctggtgc ctaaggccat tagaggccag	1800
tacagtgggt ttgtgagaac tctgttccag cagatgaggg atgtgctggg gacatttgat	1860
accgcacaga ttattaaact gctgcccttc gcagccgctc caccaaagca gagtagaatg	1920
cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatcct ggtgaggggc	1980
aattctcctg tgttcaacta taacaaggcc accaagagac tcacagtgtc cggaaaggat	2040
gctggcactc tgactgaaga ccagatgaa ggcacagctg gagtggagtc cgctgtgctg	2100
aggggattcc tcattctggg caaagaagac aagagatatg ggcagcact gagcatcaat	2160
gaactgagca acctggccaa aggagagaag gctaattgtc taattgggca aggagacgtg	2220
gtgttggtaa tgaaacggaa acgggactct agcatactta ctgacagcca gacagcgacc	2280
aaaagaattc ggatggccat caattagtgt cgaatagttt aaaaacgacc ttgtttctac	2340
t	2341

<210> SEQ ID NO 17

<211> LENGTH: 2341

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<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 17

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agcgaagca ggcaaacat ttgaatggat gtcaatccga ccttactttt cttaaaagtg    60
ccagcacaaa atgctataag cacaactttc ccttatactg gagaccctcc ttacagccat   120
gggacaggaa caggatacac catggatact gtcaacagga cacatcagta ctcagaaaag   180
ggaagatgga caacaaacac cgaaactgga gcaccgcaac tcaaccgat tgatgggcca   240
ctgccagaag acaatgaacc aagtgggtat gcccaaacag attgtgtatt ggaggcgatg   300
gctttccttg aggaatccca tcttggtatt ttgaaaact cgtgtattga aacgatggag   360
gttggttcagc aaacacgagt ggacaagctg acacagggcc gacagaccta tgactggact   420
ctgaatagaa accgcctgc tgcaacagca ctggccaaca caatcgaagt gttcagatca   480
aatggcctca ccgccaatga gtctggaagg ctcatcgact tctgaagga tgtgatggag   540
tcaatgaaca aagaagaaat ggggatcaca actcattttc agagaaagag acgggtgaga   600
gacaatatga ctaagaaaaa gattacacag agaacaatgg gtaaaaagaa gcagagactg   660
aacaaaagga gttatctgat tagagcactg accctgaaca caatgaccaa agatgctgag   720
agaggggaagc tgaacggag agcaattgca accccaggga tgcagattag ggggtttgtg   780
tactttgtgg agacactggc aaggagtatt tgtgagaaac tggaaacagc agggctgcca   840
gtggggaggca atgagaagaa agcaaagctg gcaaatgtgg tgaggaagat gatgaccaat   900
tctcaggaca ccgaactgtc ttccaccatc actggagata acaccaaag gaacgaaaat   960
cagaatcttc ggtatgtttc ggccatgac acatatatga ccagaaatca gcccgaaatg  1020
ttcagaaatg tgctgagtat tgctccaatt atgttctcaa acaaaatggc cagactggga  1080
aaaggggata tgtttgagag caagagtatg aaactgagaa ctcagattcc tgcagaaatg  1140
ctggcaagca tcgatctgaa atatttcaat gattcaacaa gaaagaagat tgaaaaaatc  1200
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acaagttttt tctatcgcta tgggtttgtg gccaatcca gcatggagct gccagttttt  1560
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aatatgatca acaatgatct gggccagca acagctcaga tggccctgca gctgttcac  1680
aaagattaca ggtacacctc ccgatgccat atcggtgaca cacagattca gaccggaaga  1740
tcatttgaaa tcaagaaact gtgggagcag acccgctcca aagctggact gctggtctcc  1800
gacggaggcc caaatctgta caacattaga aatctccaca ttcctgaagt ctgcctgaaa  1860
tgggaactga tggatgagga ttaccagggg cgctgtgca acccactgaa cccatttgtc  1920
agccataaag aaattgaatc aatgaacaat gcagtgtatg tgccagcaca tggccagacc  1980
aaaaacatgg agtatgatgc tgtggcaaca acacactcct ggatcccaa aagaaatcga  2040
tccatctgta atacaagtcg gagaggagtg ctggaggatg aacagatgta ccagaggtgc  2100
tgcaatctgt ttgaaaaatt ctccccagc agttcatata gaagaccagt cgggatctcc  2160
agtatggtgg aggctatggt gtccagagcc cgaattgatg cacggattga tttcgaatct  2220

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ggaaggatca agaaagaaga gttcactgag atcatgaaga tctgttccac cattgaagag	2280
ctcagacggc aaaaatagtg aatttagctt gtccttcacg aaaaaatgcc ttgtttctac	2340
t	2341

<210> SEQ ID NO 18
 <211> LENGTH: 2233
 <212> TYPE: DNA
 <213> ORGANISM: Influenza virus

<400> SEQUENCE: 18

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attgtcgagc ttgcggaaaa aacaatgaaa gattatgggg aggacctgaa aatcgaaaca	120
aacaaatttg cagcaatatg cactcacttg gaagtatgct tcatgtattc agattttcac	180
ttcatcaatg agcaaggcga gtcaataatc gtagaacttg gtgatccaaa tgcacttttg	240
aagcacagat ttgaataaat cgagggaaga gatcgacaaa tggcctggac agtagtaaac	300
agtatttgca acactacagg ggctgagaaa ccaaagtttc taccagattt gtatgattac	360
aaggagaata gattcatcga aattggagta acaaggagag aagttcacat atactatctg	420
gaaaaggcca ataaaaattaa atctgagaaa acacacatcc acattttctc gttcactggg	480
gaagaaatgg ccacaaaggc agactacact ctcgatgaag aaagcagggc taggatcaaa	540
accagactat tcaccataag acaagaaatg gccagcagag gcctctggga ttctttctgt	600
cagtccgaga gaggagaaga gacaattgaa gaaaggtttg aaatcacagg aacaatgcgc	660
aagcttgccg accaaagtct cccgccgaac ttctccagcc ttgaaaattt tagagcctat	720
gtggatggat tcgaaccgaa cggctacatt gagggcaagc tgtctcaaat gtccaaagaa	780
gtaaatgcta gaattgaacc ttttctgaaa acaacaccac gacctgag actgccaat	840
gggcctccct gttctcagcg gtccaaatc ctgctgatgg atgcctgaa actgagcatt	900
gaggacccaa gtcataagg agagggaatt cccctgtatg atgcaatcaa atgcatgaga	960
acattctttg gatggaagga acccaatgtg gtgaaaccac acgaaaaggg aatcaatcca	1020
aattatctgc tgtcatgaa gcaggtgctg gcagaactgc aggacattga gaatgaggag	1080
aaaattccaa agactaaaaa tatgaagaaa acaagtcagc tgaagtgggc actgggtgag	1140
aacatggcac cagaaaagg ggactttgac gactgtaaa atgtgggtga tctgaagcag	1200
tatgatagtg atgaaccaga actgaggtcc ctggcaagtt ggattcagaa tgagttaaac	1260
aaggcatgcg aactgacaga ttcaagctgg attgagctcg atgagattgg agaagatgtg	1320
gtccaattg aacacattgc aagcatgaga aggaattatt tcacatcaga ggtgtctcac	1380
tgcagagcca cagaatacat catgaaggga gtgtacatca atactgccct gctgaatgca	1440
tcttggtcag caatggatga ttccagctg attccaatga tcagcaagt tagaactaag	1500
gagggaaggc gaaagaccaa cctgtatggt ttcatcatca aaggaagatc ccacctgagg	1560
aatgacaccg acgtggtgaa ctttgtagc atggagtgtt ctctcactga cccaagactg	1620
gaaccacata aatgggagaa gtactgtgtg ctggagattg gagatatgct gatcagaagt	1680
gccattggcc aggtgtcaag gcccatgttc ctgtatgtga gaacaaatgg aacctcaaaa	1740
attaaaatga aatggggaat ggagatgagg cgctgcctcc tccagtcact gcagcagatt	1800
gagagtatga ttgaagctga gtcctctgtc aaagagaaag acatgaccaa agagttcttt	1860
gagaacaaat cagaacatg gcccatgtga gattccccca aaggagtggg ggaaagtcc	1920
attgggaagg tctgcaggac tctgctggca aagtcctgtg tcaacagcct gtatgcattc	1980

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ccacagctgg aaggattttc agctgaatca agaaaactgc tgctgacgt gcaggctctg 2040
agggacaacc tggaaacctgg gacctttgat ctgggggggc tgtatgaagc aattgaggag 2100
tgccatgatta atgatccctg ggtgctgctg aatgcttctt ggttcaactc cttccttaca 2160
catgcattga gttagttgtg gcagtgctac tatttgctat ccatactgtc caaaaaagta 2220
ccttgtttct act 2233

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<210> SEQ ID NO 19
<211> LENGTH: 1565
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

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<400> SEQUENCE: 19

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agcaaaagca gggtagataa tcaactcactg agtgacatca aaatcatggc gtctcaaggc 60
accaaagcat cttacgaaca gatggagact gatggagaac gccagaatgc cactgaaatc 120
agagcatccg tcggaaaaat gattggtgga attggacgat tctacatcca gatgtgcacc 180
gaactcaaac tcagtgatta tgagggacgg ctgatccaga acagcctgac aatcgagaga 240
atggtgctct ctgcttttga cgaaggaga aataaatacc tggagaaca tcccagtgcc 300
gggaaagatc ctaagaaaaa tggaggacct atctacagga gagtgaacgg aaagtggatg 360
agagaactca tcctgtatga caaagaagaa atcaggcgaa tctggcgcca ggctaataat 420
ggtgacgatg caaccgctgg tctgactcac atgatgatct ggcatccaa tctgaatgat 480
gcaacttacc agaggacaag agctctgggtg cgcaccggaa tggatcccag gatgtgctct 540
ctgatgcagg gttcaactct ccctaggagg tctggagccg caggtgctgc agtcaaagga 600
gtgggaacaa tgggtgatga actggtcaga atgatcaaaa gagggatcaa tgatcggaac 660
ttctggaggg gtgagaatgg acgaaaaaca agaattgctt atgaaagaat gtgcaacatt 720
ctcaaaggga aatttcagac tgctgcacag aaagcaatga tggatcaggt gagagagagc 780
cggaaccagg ggaatgctga gttcgaagat ctcacttttc tggcacggtc tgcaactc 840
ctgagagggg cctgggctca caagtcctgc ctgcctgcct gtgtgtatgg acctgccgtg 900
gccagtgggt acgactttga aaggaggagg tactctctgg tcggaattga ccttttcaga 960
ctgctgcaga acagccaggt gtacagcctg atcagaccaa atgagaatcc agcacacaag 1020
agtcagctgg tgtggatggc atgccattct gccgcatttg aagatctgag agtgctgagc 1080
ttcatcaaag ggaccaaggt gctcccaaga gggagctgt ccactagagg agtgcagatt 1140
gcttccaatg aaaatatgga gactatggaa tcaagtacac tggaaactgag aagcaggtac 1200
tgggccatca ggaccagaag tggaggaaac accaatcagc agagggcatc tgccggccag 1260
atcagcattc agcctacctt ctcatgtcag agaaatctcc cttttgacag aacaaccatt 1320
atggcagcat tcaatgggaa tacagagggg agaacatctg acatgaggac cgaaatcatc 1380
aggatgatgg aaagtgcagg accagaagat gtgtctttcc aggggcgggg agtcttcgag 1440
ctctcggagc aaaaggcagc gagcccgatc gtgccttcct ttgacatgag taatgaagga 1500
tcttatttct tcggagacaa tgcagaggag tacgacaatt aaagaaaaat acccttgttt 1560
ctact 1565

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<210> SEQ ID NO 20
<211> LENGTH: 1684
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

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<400> SEQUENCE: 20

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atgaacactc aaatcctcgt attcgcctcg attgcgatca ttccaacaaa tgcagacaaa    60
atctgcctcg gacatcatgc cgtgtcaaac ggaaccaaag taaacacatt aactgaaaga    120
ggagtggaag tcgtcaatgc aactgaaaca gtggaacgaa caaacatccc caggatctgc    180
tcaaaaggga aaaggacagt tgacctcggc caatgtggac tcttggggac aatcactgga    240
ccacctcaat gtgaccaatt cctagaattt tcagccgatt taattattga gaggcgagaa    300
ggaagtgatg tctgttatcc tgggaaatto gtgaatgaag aagctctgag gcaaattctc    360
agagaatcag gcggaattga caaggaagca atgggattca catacagtgg aataagaact    420
aatggagcaa ccagtgcgat taggagatca ggatcttcat tctatgcaga aatgaaatgg    480
ctcctgtcaa acacagataa tgctgcattc ccgccagatg actaagtcac ataaaaatac    540
aagaaaaagc ccagctctaa tagtatgggg gatccatcat tccgtatcaa ctgcagagca    600
aaccaagcta tatgggagtg gaacaaaact ggtgacagtt gggagttcta attatcaaca    660
atcttttgta ccgagtcacg gagcgagacc acaagttaat ggtctatctg gaagaattga    720
ctttcattgg ctaatgctaa atcccaatga tacagtcact ttcagtttca atggggcttt    780
catagctcca gaccgtgcaa gcttctcgag aggaaaatct atgggaatcc agagtggagt    840
acaggttgat gccaatgtg aaggggactg ctatcatagt ggagggacaa taataagtaa    900
cttgccattt cagaacatag atagcagggc agttggaaaa tgtccgagat atgttaagca    960
aaggagtctg ctgctagcaa cagggatgaa gaatgttcct gagattccaa agggaagagg   1020
cctatttggt gctatagcgg gtttcattga aaatggatgg gaaggcctaa ttgatggttg   1080
gtatggtttc agacaccaga atgcacaggg agagggaact gctgcagatt acaaaagcac   1140
tcaatcggca attgatcaaa taacaggaaa attaaaccgg cttatagaaa aaaccaacca   1200
acaatttgag ttgatagaca atgaattcaa tgaggtagag aagcaaatcg gtaatgtgat   1260
aaattggacc agagattcta taacagaagt gtggtcatac aatgctgaac tcttggtagc   1320
aatggagaac cagcatacaa ttgatctggc tgattcagaa atggacaaac tgtacgaacg   1380
agtgaaaaga cagctgagag agaattgctga agaagatggc actggttgct ttgaaatatt   1440
tcacaagtgt gatgatgact gtatggccag tattagaaat aacacctatg atcacagcaa   1500
atacagggaa gaggcaatgc aaaatagaat acagattgac ccagtcaaac taagcagcgg   1560
ctacaaagat gtgatacttt ggttttagctt cggggcatca tgtttcatac ttctagccat   1620
tgtaaatggc cttgtcttca tatgtgtaaa gaatggaaac atgcggtgca ctatttgat   1680
ataa                                         1684

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<210> SEQ ID NO 21

<211> LENGTH: 560

<212> TYPE: PRT

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 21

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Met Asn Thr Gln Ile Leu Val Phe Ala Leu Ser Lys Gly Lys Arg Thr
1           5           10          15

Val Asp Leu Gly Ile Ala Ile Ile Pro Thr Asn Ala Asp Lys Gln Cys
          20          25          30

Gly Leu Leu Gly Thr Ile Thr Gly Ile Cys Leu Gly His His Ala Val
          35          40          45

Ser Asn Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Gly Thr Lys Val
          50          55          60

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Asn	Thr	Leu	Thr	Glu	Arg	Ser	Ala	Asp	Leu	Ile	Ile	Glu	Arg	Arg	Glu	65	70	75	80
Gly	Val	Glu	Val	Val	Asn	Ala	Thr	Glu	Thr	Gly	Ser	Asp	Val	Cys	Tyr	85	90	95	
Pro	Gly	Lys	Phe	Val	Glu	Arg	Thr	Asn	Ile	Pro	Arg	Ile	Cys	Val	Asn	100	105	110	
Glu	Glu	Ala	Leu	Arg	Gln	Ile	Leu	Arg	Glu	Ser	Gly	Gly	Ile	Asp	Lys	115	120	125	
Glu	Ala	Met	Gly	Phe	Thr	Tyr	Ser	Gly	Ile	Arg	Thr	Asn	Gly	Ala	Thr	130	135	140	
Ser	Ala	Cys	Arg	Arg	Ser	Gly	Ser	Ser	Phe	Tyr	Ala	Glu	Met	Lys	Trp	145	150	155	160
Leu	Leu	Ser	Asn	Thr	Asp	Asn	Ala	Ala	Phe	Pro	Gln	Met	Thr	Lys	Ser	165	170	175	
Tyr	Lys	Asn	Thr	Arg	Lys	Ser	Pro	Ala	Leu	Ile	Val	Trp	Gly	Ile	His	180	185	190	
His	Ser	Val	Ser	Thr	Ala	Glu	Gln	Thr	Lys	Leu	Tyr	Gly	Ser	Gly	Asn	195	200	205	
Lys	Leu	Val	Thr	Val	Gly	Ser	Ser	Asn	Tyr	Gln	Gln	Ser	Phe	Val	Pro	210	215	220	
Ser	Pro	Gly	Ala	Arg	Pro	Gln	Val	Asn	Gly	Leu	Ser	Gly	Arg	Ile	Asp	225	230	235	240
Phe	His	Trp	Leu	Met	Leu	Asn	Pro	Asn	Asp	Thr	Val	Thr	Phe	Ser	Phe	245	250	255	
Asn	Gly	Ala	Phe	Ile	Ala	Pro	Asp	Arg	Ala	Ser	Phe	Leu	Arg	Gly	Lys	260	265	270	
Ser	Met	Gly	Ile	Gln	Ser	Gly	Val	Gln	Val	Asp	Ala	Asn	Cys	Glu	Gly	275	280	285	
Asp	Cys	Tyr	His	Ser	Gly	Gly	Thr	Ile	Ile	Ser	Asn	Leu	Pro	Phe	Gln	290	295	300	
Asn	Ile	Asp	Ser	Arg	Ala	Val	Gly	Lys	Cys	Pro	Arg	Tyr	Val	Lys	Gln	305	310	315	320
Arg	Ser	Leu	Leu	Leu	Ala	Thr	Gly	Met	Lys	Asn	Val	Pro	Glu	Ile	Pro	325	330	335	
Lys	Gly	Arg	Gly	Leu	Phe	Gly	Ala	Ile	Ala	Gly	Phe	Ile	Glu	Asn	Gly	340	345	350	
Trp	Glu	Gly	Leu	Ile	Asp	Gly	Trp	Tyr	Gly	Phe	Arg	His	Gln	Asn	Ala	355	360	365	
Gln	Gly	Glu	Gly	Thr	Ala	Ala	Asp	Tyr	Lys	Ser	Thr	Gln	Ser	Ala	Ile	370	375	380	
Asp	Gln	Ile	Thr	Gly	Lys	Leu	Asn	Arg	Leu	Ile	Glu	Lys	Thr	Asn	Gln	385	390	395	400
Gln	Phe	Glu	Leu	Ile	Asp	Asn	Glu	Phe	Asn	Glu	Val	Glu	Lys	Gln	Ile	405	410	415	
Gly	Asn	Val	Ile	Asn	Trp	Thr	Arg	Asp	Ser	Ile	Thr	Glu	Val	Trp	Ser	420	425	430	
Tyr	Asn	Ala	Glu	Leu	Leu	Val	Ala	Met	Glu	Asn	Gln	His	Thr	Ile	Asp	435	440	445	
Leu	Ala	Asp	Ser	Glu	Met	Asp	Lys	Leu	Tyr	Glu	Arg	Val	Lys	Arg	Gln	450	455	460	
Leu	Arg	Glu	Asn	Ala	Glu	Glu	Asp	Gly	Thr	Gly	Cys	Phe	Glu	Ile	Phe	465	470	475	480

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His	Lys	Cys	Asp	Asp	Asp	Cys	Met	Ala	Ser	Ile	Arg	Asn	Asn	Thr	Tyr
			485						490					495	
Asp	His	Ser	Lys	Tyr	Arg	Glu	Glu	Ala	Met	Gln	Asn	Arg	Ile	Gln	Ile
			500					505					510		
Asp	Pro	Val	Lys	Leu	Ser	Ser	Gly	Tyr	Lys	Asp	Val	Ile	Leu	Trp	Phe
			515				520					525			
Ser	Phe	Gly	Ala	Ser	Cys	Phe	Ile	Leu	Leu	Ala	Ile	Val	Met	Gly	Leu
			530			535					540				
Val	Phe	Ile	Cys	Val	Lys	Asn	Gly	Asn	Met	Arg	Cys	Thr	Ile	Cys	Ile
545					550					555					560

<210> SEQ ID NO 22

<211> LENGTH: 1398

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 22

atgaatccaa atcagaagat tctatgcact tcagccactg ctatcataat aggcgcaatc	60
gcagtactca ttggaatagc aaacctagga ttgaacatag gactgcatct aaaaccgggc	120
tgcaattgct cacactcaca acctgaaaca accaacacaa gccaaacaat aataaacaac	180
tattataatg aaacaaacat caccaacatc caaatggaag agagaacaag caggaatttc	240
aataacttaa ctaaagggct ctgtactata aattcatggc acatatatgg gaaagacaat	300
gcagtaagaa ttggagagag ctcggtatgt ttagtcacaa gagaacccta tgtttcatgc	360
gaccagatg aatgcagggt ctatgctctc agccaaggaa caacaatcag agggaaacac	420
tcaaacggaa caatacacga taggtcccag tatcgcgccc tgataagctg gccactatca	480
tcaccgcccc cagtgtacaa cagcaggggt gaatgcattg ggtggtcaag tactagtgtc	540
catgatggca aatccaggat gtcaatatgt atatcaggac caaacaacaa tgcactgtca	600
gtagtatggt acaacagaag gcctgttgca gaaattaaca catgggcccc aaacatacta	660
agaacacagg aatctgaatg tgtatgccac aacggcgatg gccagtagt gttcaccgat	720
gggtctgcca ctggacctgc agacacaaga atatactatt ttaaagaggg gaaaatattg	780
aaatgggagt ctctgactgg aactgctaag catattgaag aatgctcatg ttacggggaa	840
cgaacaggaa ttacctgcac atgcagggac aattggcagg gctcaaatac accagtgatt	900
cagatagacc cagtagcaat gacacacact agtcaatata tatgcagtcc tgttcttaca	960
gacaatcccc gaccgaatga cccaaatata ggtaagtgt atgaccctta tccaggtaat	1020
aataacaatg gagtcaaggg attctcatac ctggatgggg ctaacacttg gctagggagg	1080
acaataagca cagcctcgag gtctggatac gagatgttaa aagtgccaaa tgcattgaca	1140
gatgatagat caaagcccat tcaaggtcag acaattgtat taaacgctga ctggagtggg	1200
tacagtggat ctttcatgga ctattgggct gaaggggact gctatcgagc gtgtttttat	1260
gtggagtga tacgtggaag acccaaggaa gataaagtgt ggtggaccag caatagtata	1320
gtatcgatgt gttccagtac agaattcctg ggacaatgga actggcctga tggggctaaa	1380
atagagtact tcctctaa	1398

<210> SEQ ID NO 23

<211> LENGTH: 464

<212> TYPE: PRT

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 23

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Met	Asn	Pro	Asn	Gln	Lys	Ile	Leu	Cys	Thr	Ser	Ala	Thr	Ala	Ile	Ile	1	5	10	15
Ile	Gly	Ala	Ile	Ala	Val	Leu	Ile	Gly	Ile	Ala	Asn	Leu	Gly	Leu	Asn	20	25	30	
Ile	Gly	Leu	His	Leu	Lys	Pro	Gly	Cys	Asn	Cys	Ser	His	Ser	Gln	Pro	35	40	45	
Glu	Thr	Thr	Asn	Thr	Ser	Gln	Thr	Ile	Ile	Asn	Asn	Tyr	Tyr	Asn	Glu	50	55	60	
Thr	Asn	Ile	Thr	Asn	Ile	Gln	Met	Glu	Glu	Arg	Thr	Ser	Arg	Asn	Phe	65	70	75	80
Asn	Asn	Leu	Thr	Lys	Gly	Leu	Cys	Thr	Ile	Asn	Ser	Trp	His	Ile	Tyr	85	90	95	
Gly	Lys	Asp	Asn	Ala	Val	Arg	Ile	Gly	Glu	Ser	Ser	Asp	Val	Leu	Val	100	105	110	
Thr	Arg	Glu	Pro	Tyr	Val	Ser	Cys	Asp	Pro	Asp	Glu	Cys	Arg	Phe	Tyr	115	120	125	
Ala	Leu	Ser	Gln	Gly	Thr	Ile	Ile	Arg	Gly	Lys	His	Ser	Asn	Gly	Thr	130	135	140	
Ile	His	Asp	Arg	Ser	Gln	Tyr	Arg	Ala	Leu	Ile	Ser	Trp	Pro	Leu	Ser	145	150	155	160
Ser	Pro	Pro	Thr	Val	Tyr	Asn	Ser	Arg	Val	Glu	Cys	Ile	Gly	Trp	Ser	165	170	175	
Ser	Thr	Ser	Cys	His	Asp	Gly	Lys	Ser	Arg	Met	Ser	Ile	Cys	Ile	Ser	180	185	190	
Gly	Pro	Asn	Asn	Asn	Ala	Ser	Ala	Val	Val	Trp	Tyr	Asn	Arg	Arg	Pro	195	200	205	
Val	Ala	Glu	Ile	Asn	Thr	Trp	Ala	Arg	Asn	Ile	Leu	Arg	Thr	Gln	Glu	210	215	220	
Ser	Glu	Cys	Val	Cys	His	Asn	Gly	Val	Cys	Pro	Val	Val	Phe	Thr	Asp	225	230	235	240
Gly	Ser	Ala	Thr	Gly	Pro	Ala	Asp	Thr	Arg	Ile	Tyr	Phe	Lys	Glu	Gly	245	250	255	
Lys	Ile	Leu	Lys	Trp	Glu	Ser	Leu	Thr	Gly	Thr	Ala	Lys	His	Ile	Glu	260	265	270	
Glu	Cys	Ser	Cys	Tyr	Gly	Glu	Arg	Thr	Gly	Ile	Thr	Cys	Thr	Cys	Arg	275	280	285	
Asp	Asn	Trp	Gln	Gly	Ser	Asn	Arg	Pro	Val	Ile	Gln	Ile	Asp	Pro	Val	290	295	300	
Ala	Met	Thr	His	Thr	Ser	Gln	Tyr	Ile	Cys	Ser	Pro	Val	Leu	Thr	Asp	305	310	315	320
Asn	Pro	Arg	Pro	Asn	Asp	Pro	Asn	Ile	Gly	Lys	Cys	Asn	Asp	Pro	Tyr	325	330	335	
Pro	Gly	Asn	Asn	Asn	Asn	Gly	Val	Lys	Gly	Phe	Ser	Tyr	Leu	Asp	Gly	340	345	350	
Ala	Asn	Thr	Trp	Leu	Gly	Arg	Thr	Ile	Ser	Thr	Ala	Ser	Arg	Ser	Gly	355	360	365	
Tyr	Glu	Met	Leu	Lys	Val	Pro	Asn	Ala	Leu	Thr	Asp	Asp	Arg	Ser	Lys	370	375	380	
Pro	Ile	Gln	Gly	Gln	Thr	Ile	Val	Leu	Asn	Ala	Asp	Trp	Ser	Gly	Tyr	385	390	395	400
Ser	Gly	Ser	Phe	Met	Asp	Tyr	Trp	Ala	Glu	Gly	Asp	Cys	Tyr	Arg	Ala	405	410	415	
Cys	Phe	Tyr	Val	Glu	Leu	Ile	Arg	Gly	Arg	Pro	Lys	Glu	Asp	Lys	Val				

	420								425							430					
Trp	Trp	Thr	Ser	Asn	Ser	Ile	Val	Ser	Met	Cys	Ser	Ser	Thr	Glu	Phe						
		435					440						445								
Leu	Gly	Gln	Trp	Asn	Trp	Pro	Asp	Gly	Ala	Lys	Ile	Glu	Tyr	Phe	Leu						
	450					455					460										
<210>	SEQ ID NO 24																				
<211>	LENGTH: 1683																				
<212>	TYPE: DNA																				
<213>	ORGANISM: Influenza virus																				
<400>	SEQUENCE: 24																				
atgaacactc aaatcctggt attcgctctg attgcgatca ttccaacaaa tgcagacaaa															60						
atctgcctcg gacatcatgc tgtgtcaaac ggaaccaaag taaacacatt aactgaaaga															120						
ggagtgggaag tcgtcaatgc aactgaaaca gtggaacgaa caaacatccc caggatctgc															180						
tcaaaaggga aaaggcacgt tgacctcggg caatgtggac tcctggggac aactactgga															240						
ccacctcaat gtgaccaatt cctagaattt tcagccgatt taattattga gaggcgagaa															300						
ggaagtgatg tctgttatcc tgggaaaattc gtgaatgaag aagctctgag gcaaatcttc															360						
agagaatcag gcggaattga caaggaagca atgggattca catacagtgg aataagaact															420						
aatggagcaa ccagttcatg taggagatca ggatcttcat tctatgcaga aatgaaatgg															480						
ctcctgtcaa acacagataa tgctgcattc ccgcagatga ctaagtcata taaaaataca															540						
agaaaaaacc cagctctaata agtatggggg atccatcatt ccggatcaac tgcagagcaa															600						
accaagctat atgggagtggt aaacaaaactg gtgacagttg ggagttctaa ttatcaacia															660						
tcttttgtac cgagtcggg agcgagaaca caagttaatg gtcaatctgg aagaattgac															720						
tttcattggc taatgctaaa tccaatgat acagtcactt tcagtttcaa tggggctttc															780						
atagetccag accgtgcaag ctctctgaga ggaaaatcta tgggaatcca gagtggagta															840						
caggttgtag ccgattgtga aggggactgc tattatatgtg gagggacaat aataagtaac															900						
ttgccatttc agaacataga tagcagggca gttggaaaat gtccgagata tghtaagcaa															960						
aggagtctgc tgctagcaac agggatgaag aatgttctctg agattccaaa gggaagagggc															1020						
ctatttggtg ctatagcggg tttcattgaa aatggatggg aaggcctaata tgatggttgg															1080						
tatggttttc gaccaccгаа тгсасаggга gagggaactg ctgcagatta caaaagcact															1140						
caatcgcaa ttgatcaaat aacaggaaaa ttaaaccggc ttatagaaaa aaccaaccaa															1200						
caatttgagt tgatagacaa tgaattcact gaggtagaga агсааатсgg таатgtgата															1260						
aattggacca gagattctat aacagaagtг tggtcataca атgctgaact сttggtagca															1320						
atggagaacc агсатасаат tgatctgggt gatтсagaaa тggacaaact гtacgaacga															1380						
gtgaaaagac агсtgagaga gaatgctgaa gaagatggca ctgggtgctt tgaaatattt															1440						
cacaagtgtg atgatgactg tatggccagc attagaaata асасстатга тсасаgсааа															1500						
tacagggaag aggcaatgca aaatagaata сagattgacc сagtcaaaсt ааgсagсggс															1560						
tacaaagatg tgatactttg gtttagcttc ggggcatcat gtttcatact tctagccatt															1620						
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taa															1683						
<210>	SEQ ID NO 25																				
<211>	LENGTH: 1273																				
<212>	TYPE: PRT																				
<213>	ORGANISM: Influenza virus																				

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<400> SEQUENCE: 25

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1 5 10 15
 Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
 20 25 30
 Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
 35 40 45
 Tyr Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 50 55 60
 Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
 65 70 75 80
 Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 85 90 95
 Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 100 105 110
 Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 115 120 125
 Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 130 135 140
 Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
 145 150 155 160
 Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
 165 170 175
 Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
 180 185 190
 Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
 195 200 205
 Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
 210 215 220
 Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
 225 230 235 240
 Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
 245 250 255
 Gly Trp Thr Ala Gly Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
 260 265 270
 Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
 275 280 285
 Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
 290 295 300
 Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
 305 310 315 320
 Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
 325 330 335
 Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
 340 345 350
 Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 355 360 365
 Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 370 375 380
 Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 385 390 395 400
 Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly

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405							410							415						
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys					
			420							425				430						
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn					
			435							440				445						
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe					
			450							455				460						
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys					
			465										475							
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly					
															485					
															490					
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val					
															500					
															505					
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys					
															515					
															520					
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn					
															535					
															540					
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu					
															545					
															550					
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val					
															565					
															570					
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe					
															580					
															585					
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val					
															595					
															600					
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile					
															610					
															615					
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser					
															625					
															630					
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val					
															645					
															650					
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala					
															660					
															665					
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala					
															675					
															680					
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser					
															695					
															700					
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile					
															705					
															710					
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val					
															725					
															730					
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu					
															740					
															745					
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr					
															755					
															760					
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln					
															770					
															775					
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe					
															785					
															790					
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser					
															805					
															810					
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly					
															820					
															825					

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Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp
 835 840 845
 Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu
 850 855 860
 Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly
 865 870 875 880
 Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile
 885 890 895
 Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr
 900 905 910
 Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn
 915 920 925
 Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala
 930 935 940
 Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn
 945 950 955 960
 Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val
 965 970 975
 Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln
 980 985 990
 Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
 995 1000 1005
 Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 1010 1015 1020
 Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val
 1025 1030 1035 1040
 Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala
 1045 1050 1055
 Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu
 1060 1065 1070
 Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His
 1075 1080 1085
 Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val
 1090 1095 1100
 Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr
 1105 1110 1115 1120
 Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr
 1125 1130 1135
 Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu
 1140 1145 1150
 Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
 1155 1160 1165
 Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp
 1170 1175 1180
 Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu
 1185 1190 1195 1200
 Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
 1205 1210 1215
 Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
 1220 1225 1230
 Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
 1235 1240 1245

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Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
1250 1255 1260

Leu Lys Gly Val Lys Leu His Tyr Thr
1265 1270

<210> SEQ ID NO 26
<211> LENGTH: 1273
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 26

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65 70 75 80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
210 215 220

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr
225 230 235 240

Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser
245 250 255

Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro
260 265 270

Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala
275 280 285

Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys
290 295 300

Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val
305 310 315 320

Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys
325 330 335

Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala
340 345 350

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Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu
 355 360 365
 Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro
 370 375 380
 Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe
 385 390 395 400
 Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly
 405 410 415
 Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys
 420 425 430
 Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn
 435 440 445
 Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe
 450 455 460
 Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys
 465 470 475 480
 Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly
 485 490 495
 Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val
 500 505 510
 Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys
 515 520 525
 Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn
 530 535 540
 Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu
 545 550 555 560
 Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val
 565 570 575
 Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe
 580 585 590
 Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val
 595 600 605
 Ala Val Leu Tyr Gln Gly Val Asn Cys Thr Glu Val Pro Val Ala Ile
 610 615 620
 His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser
 625 630 635 640
 Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val
 645 650 655
 Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala
 660 665 670
 Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala
 675 680 685
 Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser
 690 695 700
 Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile
 705 710 715 720
 Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val
 725 730 735
 Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu
 740 745 750
 Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr
 755 760 765

Gly 770	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln
Val 785	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe 800
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser 815
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly 830
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp 845
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu 860
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly 880
Thr	Ile	Thr	Ser	Gly	Trp	Thr	Phe	Gly	Ala	Gly	Ala	Ala	Leu	Gln	Ile 895
Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Val	Thr 910
Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Leu	Ile	Ala	Asn	Gln	Phe	Asn 925
Ser	Ala	Ile	Gly	Lys	Ile	Gln	Asp	Ser	Leu	Ser	Ser	Thr	Ala	Ser	Ala 940
Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	Ala	Gln	Ala	Leu	Asn 960
Thr	Leu	Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	Ala	Ile	Ser	Ser	Val 975
Leu	Asn	Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	Glu	Ala	Glu	Val	Gln 990
Ile	Asp	Arg	Leu	Ile	Thr	Gly	Arg	Leu	Gln	Ser	Leu	Gln	Thr	Tyr	Val 1005
Thr	Gln	Gln	Leu	Ile	Arg	Ala	Ala	Glu	Ile	Arg	Ala	Ser	Ala	Asn	Leu 1020
Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys	Arg	Val 1040
Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln	Ser	Ala 1055
Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro	Ala	Gln	Glu 1070
Lys	Asn	Phe	Thr	Thr	Ala	Pro	Ala	Ile	Cys	His	Asp	Gly	Lys	Ala	His 1085
Phe	Pro	Arg	Glu	Gly	Val	Phe	Val	Ser	Asn	Gly	Thr	His	Trp	Phe	Val 1100
Thr	Gln	Arg	Asn	Phe	Tyr	Glu	Pro	Gln	Ile	Ile	Thr	Thr	Asp	Asn	Thr 1120
Phe	Val	Ser	Gly	Asn	Cys	Asp	Val	Val	Ile	Gly	Ile	Val	Asn	Asn	Thr 1135
Val	Tyr	Asp	Pro	Leu	Gln	Pro	Glu	Leu	Asp	Ser	Phe	Lys	Glu	Glu	Leu 1150
Asp	Lys	Tyr	Phe	Lys	Asn	His	Thr	Ser	Pro	Asp	Val	Asp	Leu	Gly	Asp 1165
Ile	Ser	Gly	Ile	Asn	Ala	Ser	Val	Val	Asn	Ile	Gln	Lys	Glu	Ile	Asp 1180
Arg	Leu	Asn	Glu	Val	Ala	Lys	Asn	Leu	Asn	Glu	Ser	Leu	Ile	Asp	Leu 1195

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1185	1190	1195	1200
Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile	1205	1210	1215
Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile	1220	1225	1230
Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys	1235	1240	1245
Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val	1250	1255	1260
Leu Lys Gly Val Lys Leu His Tyr Thr	1265	1270	

<210> SEQ ID NO 27
 <211> LENGTH: 1273
 <212> TYPE: PRT
 <213> ORGANISM: Influenza virus

<400> SEQUENCE: 27

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val	1	5	10	15
Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe	20	25	30	
Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu	35	40	45	
His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp	50	55	60	
Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp	65	70	75	80
Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu	85	90	95	
Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser	100	105	110	
Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile	115	120	125	
Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr	130	135	140	
Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr	145	150	155	160
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu	165	170	175	
Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe	180	185	190	
Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr	195	200	205	
Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu	210	215	220	
Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr	225	230	235	240
Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser	245	250	255	
Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro	260	265	270	
Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala	275	280	285	

Val 290	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys
Ser 305	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val 320
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys 335
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala 350
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu 365
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro 380
Thr 385	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe 400
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly 415
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys 430
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn 445
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe 460
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys 480
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly 495
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val 510
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys 525
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn 540
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu 560
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val 575
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe 590
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val 605
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile 620
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser 640
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val 655
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala 670
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala 685
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser 700
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile

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705	710	715	720
Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val			
725		730	735
Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu			
740		745	750
Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr			
755		760	765
Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln			
770		775	780
Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe			
785		790	795
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser			
805		810	815
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly			
820		825	830
Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp			
835		840	845
Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu			
850		855	860
Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly			
865		870	875
Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile			
885		890	895
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr			
900		905	910
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn			
915		920	925
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala			
930		935	940
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn			
945		950	955
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val			
965		970	975
Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln			
980		985	990
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val			
995		1000	1005
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu			
1010		1015	1020
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val			
1025		1030	1035
Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala			
1045		1050	1055
Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu			
1060		1065	1070
Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His			
1075		1080	1085
Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val			
1090		1095	1100
Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr			
1105		1110	1115
Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr			
1125		1130	1135

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Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu
      1140              1145              1150

Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
      1155              1160              1165

Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp
      1170              1175              1180

Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu
      1185              1190              1195              1200

Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
      1205              1210              1215

Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
      1220              1225              1230

Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
      1235              1240              1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
      1250              1255              1260

Leu Lys Gly Val Lys Leu His Tyr Thr
      1265              1270

<210> SEQ ID NO 28
<211> LENGTH: 1273
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 28

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1      5              10              15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
      20              25              30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
      35              40              45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
      50              55              60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
      65              70              75              80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
      85              90              95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
      100              105              110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
      115              120              125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
      130              135              140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
      145              150              155              160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
      165              170              175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
      180              185              190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
      195              200              205

Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu
      210              215              220

Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr

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225	230	235	240
Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser	245	250	255
Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro	260	265	270
Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala	275	280	285
Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys	290	295	300
Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val	305	310	315
Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys	325	330	335
Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala	340	345	350
Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu	355	360	365
Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro	370	375	380
Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe	385	390	395
Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly	405	410	415
Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys	420	425	430
Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn	435	440	445
Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe	450	455	460
Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys	465	470	475
Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly	485	490	495
Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val	500	505	510
Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys	515	520	525
Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn	530	535	540
Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu	545	550	555
Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val	565	570	575
Arg Asp Pro Gln Thr Leu Glu Ile Leu Asp Ile Thr Pro Cys Ser Phe	580	585	590
Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Thr Ser Asn Gln Val	595	600	605
Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Glu Val Pro Val Ala Ile	610	615	620
His Ala Asp Gln Leu Thr Pro Thr Trp Arg Val Tyr Ser Thr Gly Ser	625	630	635
Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val	645	650	655

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Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala	660	665	670
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala	675	680	685
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser	690	695	700
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile	705	710	715
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val	725	730	735
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu	740	745	750
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr	755	760	765
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln	770	775	780
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe	785	790	795
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser	805	810	815
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly	820	825	830
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp	835	840	845
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu	850	855	860
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly	865	870	875
Thr	Ile	Thr	Ser	Gly	Trp	Thr	Phe	Gly	Ala	Gly	Ala	Ala	Leu	Gln	Ile	885	890	895
Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Val	Thr	900	905	910
Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Leu	Ile	Ala	Asn	Gln	Phe	Asn	915	920	925
Ser	Ala	Ile	Gly	Lys	Ile	Gln	Asp	Ser	Leu	Ser	Ser	Thr	Ala	Ser	Ala	930	935	940
Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	Ala	Gln	Ala	Leu	Asn	945	950	955
Thr	Leu	Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	Ala	Ile	Ser	Ser	Val	965	970	975
Leu	Asn	Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	Glu	Ala	Glu	Val	Gln	980	985	990
Ile	Asp	Arg	Leu	Ile	Thr	Gly	Arg	Leu	Gln	Ser	Leu	Gln	Thr	Tyr	Val	995	1000	1005
Thr	Gln	Gln	Leu	Ile	Arg	Ala	Ala	Glu	Ile	Arg	Ala	Ser	Ala	Asn	Leu	1010	1015	1020
Ala	Ala	Thr	Lys	Met	Ser	Glu	Cys	Val	Leu	Gly	Gln	Ser	Lys	Arg	Val	1025	1030	1035
Asp	Phe	Cys	Gly	Lys	Gly	Tyr	His	Leu	Met	Ser	Phe	Pro	Gln	Ser	Ala	1045	1050	1055
Pro	His	Gly	Val	Val	Phe	Leu	His	Val	Thr	Tyr	Val	Pro	Ala	Gln	Glu	1060	1065	1070

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Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His
 1075 1080 1085
 Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val
 1090 1095 1100
 Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr
 1105 1110 1115 1120
 Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr
 1125 1130 1135
 Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu
 1140 1145 1150
 Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
 1155 1160 1165
 Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp
 1170 1175 1180
 Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu
 1185 1190 1195 1200
 Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
 1205 1210 1215
 Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
 1220 1225 1230
 Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
 1235 1240 1245
 Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
 1250 1255 1260
 Leu Lys Gly Val Lys Leu His Tyr Thr
 1265 1270

<210> SEQ ID NO 29

<211> LENGTH: 560

<212> TYPE: PRT

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 29

Met Asn Thr Gln Ile Leu Val Phe Ala Leu Ile Ala Ile Ile Pro Thr
 1 5 10 15
 Asn Ala Asp Lys Ile Cys Leu Gly His His Ala Val Ser Asn Gly Thr
 20 25 30
 Lys Val Asn Thr Leu Thr Glu Arg Gly Val Glu Val Val Asn Ala Thr
 35 40 45
 Glu Thr Val Glu Arg Thr Asn Ile Pro Arg Ile Cys Ser Lys Gly Lys
 50 55 60
 Arg Thr Val Asp Leu Gly Gln Cys Gly Leu Leu Gly Thr Ile Thr Gly
 65 70 75 80
 Pro Pro Gln Cys Asp Gln Phe Leu Glu Phe Ser Ala Asp Leu Ile Ile
 85 90 95
 Glu Arg Arg Glu Gly Ser Asp Val Cys Tyr Pro Gly Lys Phe Val Asn
 100 105 110
 Glu Glu Ala Leu Arg Gln Ile Leu Arg Glu Ser Gly Gly Ile Asp Lys
 115 120 125
 Glu Ala Met Gly Phe Thr Tyr Ser Gly Ile Arg Thr Asn Gly Ala Thr
 130 135 140
 Ser Ser Cys Arg Arg Ser Gly Ser Ser Phe Tyr Ala Glu Met Lys Trp
 145 150 155 160
 Leu Leu Ser Asn Thr Asp Asn Ala Ala Phe Pro Gln Met Thr Lys Ser
 165 170 175

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Tyr Lys Asn Thr Arg Lys Asn Pro Ala Leu Ile Val Trp Gly Ile His
      180                      185                      190

His Ser Gly Ser Thr Ala Glu Gln Thr Lys Leu Tyr Gly Ser Gly Asn
      195                      200                      205

Lys Leu Val Thr Val Gly Ser Ser Asn Tyr Gln Gln Ser Phe Val Pro
      210                      215                      220

Ser Pro Gly Ala Arg Thr Gln Val Asn Gly Gln Ser Gly Arg Ile Asp
      225                      230                      235                      240

Phe His Trp Leu Met Leu Asn Pro Asn Asp Thr Val Thr Phe Ser Phe
      245                      250                      255

Asn Gly Ala Phe Ile Ala Pro Asp Arg Ala Ser Phe Leu Arg Gly Lys
      260                      265                      270

Ser Met Gly Ile Gln Ser Gly Val Gln Val Asp Ala Asp Cys Glu Gly
      275                      280                      285

Asp Cys Tyr Tyr Ser Gly Gly Thr Ile Ile Ser Asn Leu Pro Phe Gln
      290                      295                      300

Asn Ile Asp Ser Arg Ala Val Gly Lys Cys Pro Arg Tyr Val Lys Gln
      305                      310                      315                      320

Arg Ser Leu Leu Leu Ala Thr Gly Met Lys Asn Val Pro Glu Ile Pro
      325                      330                      335

Lys Gly Arg Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly
      340                      345                      350

Trp Glu Gly Leu Ile Asp Gly Trp Tyr Gly Phe Arg His Gln Asn Ala
      355                      360                      365

Gln Gly Glu Gly Thr Ala Ala Asp Val Lys Ser Thr Gln Ser Ala Ile
      370                      375                      380

Asp Gln Ile Thr Gly Lys Leu Asn Arg Leu Ile Glu Lys Thr Asn Gln
      385                      390                      395                      400

Gln Phe Glu Leu Ile Asp Asn Glu Phe Thr Glu Val Glu Lys Gln Ile
      405                      410                      415

Gly Asn Val Ile Asn Trp Thr Arg Asp Ser Ile Thr Glu Val Trp Ser
      420                      425                      430

Tyr Asn Ala Glu Leu Leu Val Ala Met Glu Asn Gln His Thr Ile Asp
      435                      440                      445

Leu Ala Asp Ser Glu Met Asp Lys Leu Tyr Glu Arg Val Lys Arg Gln
      450                      455                      460

Leu Arg Glu Asn Ala Glu Glu Asp Gly Thr Gly Cys Phe Glu Ile Phe
      465                      470                      475                      480

His Lys Cys Asp Asp Asp Cys Met Ala Ser Ile Arg Asn Asn Thr Tyr
      485                      490                      495

Asp His Ser Lys Tyr Arg Glu Glu Ala Met Gln Asn Arg Ile Gln Ile
      500                      505                      510

Asp Pro Val Lys Leu Ser Ser Gly Tyr Lys Asp Val Ile Leu Trp Phe
      515                      520                      525

Ser Phe Gly Ala Ser Cys Phe Ile Leu Leu Ala Ile Ala Met Gly Leu
      530                      535                      540

Val Phe Ile Cys Val Lys Asn Gly Asn Met Arg Cys Thr Ile Cys Ile
      545                      550                      555                      560

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<210> SEQ ID NO 30

<211> LENGTH: 1398

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

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<400> SEQUENCE: 30

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atgaatccaa atcagaagat tctatgcact tcagccactg ctatcataat aggcgcaatc   60
gcagtactca ttggaatagc aaacctagga ttgaacatag gactgcatct aaaaccgagc   120
tgcaattgct cacactcaca acctgaaaca accaacacaa gccaaacaat aataaacaac   180
tattataatg aaacaacat caccaacatc caaatggaag agagaacaag caggaatttc   240
aataacttaa ctaaagggtc ctgtactata aattcatggc acatatatgg gaaagacaat   300
gcggtagaa ttggagagag ctcgatggtt ttagtcacaa gagaacccta tgtttcatgc   360
gaccagatg aatgcagggt ctatgctctc agccaaggaa caacaatcag aggaaaacac   420
tcaaacggaa caatacacga taggtcccag tatcgcgccc tgataagctg gccactatca   480
tcaccgcccc cagtgtacaa cagcagggtg gaatgcattg ggtggtcaag tactagttgc   540
catgatggca aatccaggat gtcaatatgt atatcaggac caaacaacaa tgcactcgca   600
gtagtatggt acaacagaag gcctgttgca gaaattaaca catgggcccc aaacatacta   660
agaacacagg aatctgaatg tgtatgccac aacggcgatg gcccagtagt gttcaccgat   720
gggtctgcc actgacctgc agacacaaga atatactatt ttaaagaggg gaaaatattg   780
aaatgggagt ctctgactgg aactgctaag catattgaag aatgctcatg ttacggggaa   840
cgaacaggaa ttacctgcac atgcaaggac aattggcagg gctcaaatag accagtgatt   900
cagatagatc cagtagcaat gacacacact agtcagtata tatgcagtcc tgttcttaca   960
gacaatcccc gaccgaatga cccaaatata ggtaagtgtg atgacctta tccaggtaat  1020
aataacaatg gagtcaaggg attctcatac ctggatgggg ctaacacttg gctaggaggg  1080
acaataagca cagcctcgag gtctggatac gagatgttaa aagtgccaaa tgcattgaca  1140
gatgatagat caaagcccat tcaaggtcag acaattgtat taaacgctga ctggagtggg  1200
tacagtggat ctttcatgga ctattgggct gagggggact gctatcgagc gtgtttttat  1260
gtggaattga tacgtggaag acccaaggag gataaagtgt ggtggaccag caatagtata  1320
gtatcgatgt gttccagtag agaattcctg ggacaatgga actggcctga tggggctaaa  1380
atagagtact tcctctaa                                     1398

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<210> SEQ ID NO 31

<211> LENGTH: 462

<212> TYPE: PRT

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 31

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Met Asn Pro Asn Gln Lys Ile Leu Cys Thr Ser Ala Thr Ala Ile Ile
1      5      10      15
Ile Gly Ala Ile Ala Val Leu Ile Gly Ile Ala Asn Leu Gly Leu Asn
20     25     30
Ile Gly Leu His Leu Lys Pro Ser Cys Asn Cys Ser His Ser Gln Pro
35     40     45
Glu Thr Ile Asn Thr Ser Gln Thr Ile Ile Asn Asn Tyr Tyr Asn Glu
50     55     60
Thr Asn Ile Thr Asn Ile Gln Met Glu Glu Arg Thr Ser Arg Asn Phe
65     70     75     80
Asn Asn Leu Thr Lys Gly Leu Cys Thr Ile Asn Ser Trp His Ile Tyr
85     90     95
Gly Lys Asp Asn Ala Val Arg Ile Gly Glu Ser Ser Asp Val Leu Val
100    105    110

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Thr Arg Glu Pro Tyr Val Ser Cys Asp Pro Asp Glu Cys Arg Phe Tyr
 115 120 125
 Ala Leu Ser Gln Gly Thr Ile Ile Arg Gly Lys His Ser Asn Gly Thr
 130 135 140
 Ile His Asp Arg Ser Gln Tyr Arg Ala Leu Ile Ser Trp Pro Leu Ser
 145 150 155 160
 Ser Pro Pro Thr Val Tyr Asn Ser Arg Val Glu Cys Ile Gly Trp Ser
 165 170 175
 Ser Thr Ser Cys His Asp Gly Lys Ser Arg Met Ser Ile Cys Ile Ser
 180 185 190
 Gly Pro Asn Asn Asn Ala Ser Ala Trp Trp Tyr Asn Arg Arg Pro Val
 195 200 205
 Ala Glu Ile Asn Thr Trp Ala Arg Asn Ile Leu Arg Thr Gln Glu Ser
 210 215 220
 Glu Cys Val Cys His Asn Gly Val Cys Pro Trp Phe Thr Asp Gly Ser
 225 230 235 240
 Ala Thr Gly Pro Ala Asp Thr Arg Ile Tyr Tyr Phe Lys Glu Gly Lys
 245 250 255
 Leu Lys Trp Glu Ser Leu Thr Gly Thr Ala Lys His Ile Glu Glu Cys
 260 265 270
 Ser Cys Tyr Gly Glu Arg Thr Gly Ile Thr Cys Thr Cys Lys Asp Asn
 275 280 285
 Trp Gln Gly Ser Asn Arg Pro Val Ile Gln Ile Asp Pro Val Ala Met
 290 295 300
 Thr His Thr Ser Gln Tyr Ile Cys Ser Pro Val Leu Thr Asp Asn Pro
 305 310 315 320
 Arg Pro Asn Asp Pro Asn Ile Gly Lys Cys Asn Asp Pro Tyr Pro Gly
 325 330 335
 Asn Asn Asn Asn Gly Val Lys Gly Phe Ser Tyr Leu Asp Gly Ala Asn
 340 345 350
 Thr Trp Leu Gly Arg Thr Ile Ser Thr Ala Ser Arg Ser Gly Tyr Glu
 355 360 365
 Met Leu Lys Val Pro Asn Ala Leu Thr Asp Asp Arg Ser Lys Pro Ile
 370 375 380
 Gln Gly Gln Thr Ile Val Leu Asn Ala Asp Trp Ser Gly Tyr Ser Gly
 385 390 395 400
 Ser Phe Met Asp Tyr Trp Ala Glu Gly Asp Cys Tyr Arg Ala Cys Phe
 405 410 415
 Tyr Val Glu Leu Ile Arg Gly Arg Pro Lys Glu Asp Lys Val Trp Trp
 420 425 430
 Thr Ser Asn Ser Ile Val Ser Met Cys Ser Ser Thr Glu Phe Leu Gly
 435 440 445
 Gln Trp Asn Trp Pro Asp Gly Ala Lys Ile Glu Tyr Phe Leu
 450 455 460

<210> SEQ ID NO 32

<211> LENGTH: 1775

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 32

agcaaaagca ggggaaaata aaaacaacca aaatgaaggc aaacctactg gtcctgttat 60

gtgcattgac agctgcagat gcagacacaa tatgtatagg ctaccatgac aacaattcaa 120

ccgacactgt tgacacagta ctcgagaaga atgtgacagt gacacactct gttaacctgc 180

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tcgaagacag ccacaacgga aaactatgta gattaaaagg aatagcccca ctacaattgg	240
ggaaatgtaa catcgccgga tggtctttgg gaaaccacaga atgcgaccca ctgcttccag	300
tgagatcatg gtctctacatt gtagaaacac caaactctga gaatggaata tgttatccag	360
gagatttcat cgactatgag gagctgaggg agcaattgag ctcaagtgtca tcattcgaaa	420
gattcgaaat atttcccaaa gaaagctcat ggcccaacca caacacaaac ggagtaacgg	480
cagcatgctc ccatgagggg aaaagcagtt ttacagaaa ttgctatgg ctgacggaga	540
aggagggctc ataccctaaag ctgaaaaatt cttatgtgaa caaaaaaggg aaagaagtcc	600
ttgtactgtg ggggtattcat caccgccta acagtaagga acaacagaat ctctatcaga	660
atgaaaatgc ttatgtctct gtagtgactt caaattataa caggagattt accccggaaa	720
tagcagaaag acccaagta agagatcaag ctgggaggat gaactattac tggacctgac	780
taaaaccggg agacacaata atatttgagg caaatggaaa tctaatagca ccaatgtatg	840
ctttcgact gagtagaggc ttgggtccg gcacatcac ctcaaacgca tcaatgcatg	900
agtgtaacac gaagtgtcaa acaccctgg gagctataaa cagcagctc ccttaccaga	960
atatacccc agtcacaata ggagagtgc caaatacgt caggagtgc aaattgagga	1020
tggttacagg actaaggaac attccgtcca ttcaatccag aggtctattt ggagccattg	1080
ccggttttat tgaaggggga tggactggaa tgatagatgg atggtatggt tatcatcatc	1140
agaatgaaca gggatcaggc tatgcagcgg atcaaaaaag cacacaaaat gccattaacg	1200
ggattacaaa caaggtgaac actgttatcg agaaaatgaa cattcaattc acagctgtgg	1260
gtaagaatt caacaaatta gaaaaagga tggaaaattt aaataaaaaa gttgatgatg	1320
gatttctgga catttgaca tataatgcag aattgttagt tctactgaa aatgaaagga	1380
ctctggattt ccatgatca aatgtgaaga atctgtatga gaaagtaaaa agccaattaa	1440
agaataatgc caaagaaatc ggaaatggat gttttgagtt ctaccacaag tgtgacaatg	1500
aatgcatgga aagtgaaga aatgggactt atgattatcc caaatattca gaagagtcaa	1560
agttgaacag gaaaaagga gatggagtga aattggaatc aatggggatc tatcagattc	1620
tggcgatcta ctcaactgac gccagttcac tgggtctttt ggtctcctg ggggcaatca	1680
gtttctggat gtgttctaataa ggatctttgc agtgcagaat atgcatctga gattagaatt	1740
tcagagatat gaggaaaaac accctgttt ctact	1775

<210> SEQ ID NO 33

<211> LENGTH: 1413

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 33

agcaaaagca ggggtttaaa atgaatccaa atcagaaaat aataaccatt ggatcaatct	60
gtctggtagt cggactaatt agcctaatat tgcaaatagg gaatataatc tcaatatgga	120
ttagccattc aattcaaaact ggaagtcaaa accatactgg aatatgcaac caaaacatca	180
ttacctataa aaatagcacc tgggtaaaagg acacaacttc agtgatatta accggcaatt	240
catctctttg tcccatccgt ggggtgggcta tatacagcaa agacaatagc ataagaattg	300
gttccaaagg agacgttttt gtcataagag agccctttat ttcattgttct cacttggaat	360
gcaggacctt ttttctgacc caaggtgcct tactgaatga caagcattca agtgggactg	420
ttaaggacag aagcccttat agggccttaa tgagctgccc tgtcggtgaa gctccgtccc	480

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cgtacaattc aagatttgaa tcggttgctt ggtcagcaag tgcatgtcat gatggcatgg	540
gctggctaac aatcggaatt tcaggtccag ataatggagc agtggctgta ttaaaataca	600
acggcataat aactgaaacc ataaaaagt ttgaggaagaa aatattgagg acacaagagt	660
ctgaatgtgc ctgtgtaaat ggttcattgt ttactataat gactgatggc ccgagtgtatg	720
ggctggcctc gtacaaaatt ttcaagatcg aaaaggggaa ggttactaaa tcaatagagt	780
tgaatgcacc taattctcac tatgaggaat gttcctgtta ccttgatacc ggcaaatga	840
tgtgtgtgtg cagagacaat tggcatgggt cgaaccggcc atgggtgtct ttcgatcaaa	900
acctggatta tcaaatagga tacatctgca gtgggggttt cggtgacaac ccgcgtcccg	960
aagatggaac aggcagctgt ggtccagtgt atgttgatgg agcaaacgga gtaagggat	1020
tttcatatag gtatggtaat ggtgtttgga taggaaggac caaaagtcac agttccagac	1080
atgggtttga gatgatttgg gatcctaatt gatggacaga gactgatagt aagttctctg	1140
tgaggcaaga tgttgtgga atgactgatt ggtcagggta tagcggaagt ttcgttcaac	1200
atcctgagct gacagggtta gactgtatga ggccgtgctt ctgggttgaa ttaatcaggg	1260
gacgacctaa agaaaaaca atctggacta gtgcgagcag catttctttt tgtggcgtga	1320
atagtgtac ttagatttgg tcttgccag acggtgctga gttgccattc agcattgaca	1380
agtagtctgt tcaaaaaact ccttgtttct act	1413

<210> SEQ ID NO 34

<211> LENGTH: 2233

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 34

agcgaagca ggtactgatc caaatggaa gattttgtgc gacaatgctt caatccgatg	60
attgtcgagc ttgcggaaaa aacaatgaaa gagtatgggg aggacctgaa aatcgaaaca	120
aacaaatttg cagcaatatg cactcacttg gaagtatgct tcatgtattc agattttcac	180
ttcatcaatg agcaaggcga gtcaataatc gtagaacttg gtgatccaaa tgcacttttg	240
aagcacagat ttgaaataat cgagggaaga gatcgacaaa tggcctggac agtagtaaac	300
agtatttgca acactacagg ggctgagaaa ccaaagtctt taccagattt gtatgattac	360
aaggagaata gattcatcga aattggagta acaaggagag aagttcacat atactatctg	420
gaaaaggcca ataaaaattaa atctgagaaa acacacatcc acattttctc gttcactggg	480
gaagaaatgg ccacaaaggc agactacact ctcgatgaag aaagcagggc taggatcaaa	540
accagactat tcaccataag acaagaaatg gccagcagag gcctctggga ttctttctgt	600
cagtcgaga gaggagaaga gacaattgaa gaaagggttg aaatcacagg aacaatgcgc	660
aagcttgccg accaaagtct ccgcggaac ttctccagcc ttgaaaaatt tagagcctat	720
gtggatggat tcgaaccgaa cggctacatt gagggcaagc tgtctcaaat gtccaaagaa	780
gtaaatgcta gaattgaacc ttttttgaaa acaacaccac gaccacttag acttccgaat	840
gggcctccct gttctcagcg gtccaaatc ctgctgatgg atgccttaa attaaagcatt	900
gaggacccaa gtcatgaagg agagggaata ccgctatatg atgcaatcaa atgcatgaga	960
acattctttg gatggaagga acccaatggt gttaaaccac acgaaaaggg aataaatcca	1020
aattatcttc tgtcatggaa gcaagtactg gcagaactgc aggacattga gaatgaggag	1080
aaaattccaa agactaaaaa tatgaagaaa acaagtcagc taaagtgggc acttggtgag	1140
aacatggcac cagaaaaggg agactttgac gactgtaaag atgtagggtga tttgaagcaa	1200

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tatgatatgt atgaaccaga attgaggtcg cttgcaagtt ggattcagaa tgagtttaac	1260
aaggcatgcg aactgacaga ttcaagctgg atagagctcg atgagattgg agaagatgtg	1320
gtccaattg aacacattgc aagcatgaga aggaattatt tcacatcaga ggtgtctcac	1380
tgcatagcca cagaatacat aatgaaggga gtgtacatca atactgcctt gcttaatgca	1440
tcttgtgcag caatggatga ttccaatta attccaatga taagcaagt tagaactaag	1500
gaggggaaggc gaaagaccaa cttgtatggt ttcatacataa aaggaagatc ccacttaagg	1560
aatgacaccg acgtggtaaa ctttgtgagc atggagtttt ctctcactga cccaagactt	1620
gaaccacata aatgggagaa gtactgtgtt cttgagatag gagatatgct tataagaagt	1680
gccataggcc aggtttcaag gcccatgttc ttgtatgtga gaacaaatgg aacctcaaaa	1740
attaaaatga aatggggaat ggagatgagg cggtgcctcc tccagtcact tcaacaaatt	1800
gagagtatga ttgaagctga gtcctctgtc aaagagaaag acatgaccaa agagttcttt	1860
gagaacaaat cagaacatg gccatttga gagtccccca aaggagtggg ggaagttcc	1920
attgggaagg tctgcaggac ttattatgca aagtcggtat tcaacagctt gtatgcatct	1980
ccacaactag aaggatttcc agctgaatca agaaaactgc ttcttatcgt tcaggctctt	2040
agggacaacc tggaacctgg gacctttgat cttggggggc tatatgaagc aattgaggag	2100
tgcttgatta atgaccctgg ggttttgctt aatgcttctt ggttcaactc cttccttaca	2160
catgcattga gttagtgttg gcagtgtctac tatttgctat ccatactgtc caaaaaagta	2220
ccttgtttct act	2233

<210> SEQ ID NO 35

<211> LENGTH: 2341

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 35

agcgaaagca ggcaaacat ttgaatggat gtcaatccga ccttactttt cttaaaagt	60
ccagcacaaa atgctataag cacaacttcc ccttatactg gagaccctcc ttacagccat	120
gggacaggaa caggatacac catggatact gtcaacagga cacatcagta ctcagaaaag	180
ggaagatgga caacaaacac cgaaactgga gcaccgcaac tcaacccgat tgatgggcca	240
ctgccagaag acaatgaacc aagtggttat gcccaaacag attgtgtatt ggaggcgatg	300
gctttccttg aggaatccca tcttggtatt ttgaaaact cgtgtattga aacgatggag	360
gttgttcagc aaacacgagt agacaagctg acacaaggcc gacagaccta tgactggact	420
ctaaatagaa accaacctgc tgcaacagca ttggccaaca caatagaagt gttcagatca	480
aatggcctca cggccaatga gtctggaagg ctcatagact tccttaagga tgtaatggag	540
tcaatgaaca aagaagaaat ggggatcaca actcatttcc agagaaagag acgggtgaga	600
gacaatatga ctaagaaaat gataacacag agaacaatgg gtaaaaagaa gcagagattg	660
aacaaaagga gttatctaat tagagcattg accctgaaca caatgaccaa agatgctgag	720
agaggggaagc taaaacggag agcaattgca accccaggga tgcaataaag ggggtttgta	780
tactttgttg agacactggc aaggagtata tgtgagaaac ttgaacaatc aggggttgcca	840
gttgagggca atgagaagaa agcaaagttg gcaaatgttg taagggaagat gatgaccaat	900
tctcaggaca ccgaacttcc ttccaccatc actggagata acaccaaag gaacgaaaat	960
cagaatcctc ggaatgtttt ggccatgac acatatatga ccagaaatca gcccgaaatg	1020

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ttcagaaatg ttctaagtat tgctccaata atgttctcaa acaaaatggc gagactggga	1080
aaaggggtata tggttgagag caagagtatg aaacttagaa ctcaaatacc tgcagaaatg	1140
ctagcaagca tcgatttgaa atatttcaat gattcaacaa gaaagaagat tgaaaaaatc	1200
cgaccgctct taatagaggg gactgcatca ttgagccctg gaatgatgat gggcatgttc	1260
aatatgttaa gcactgtatt aggcgtctcc atcctgaatc ttggacaaaa gagatacacc	1320
aagactactt actggtggga tggctctcaa tcctctgacg attttgctct gattgtgaat	1380
gcaccaatc atgaagggat tcaagccgga gtcgacaggt tttatcgaac ctgtaagcta	1440
cttggaatca atatgagcaa gaaaaagtct tacataaaca gaacaggtac atttgaattc	1500
acaagttttt tctatcgta tgggtttgtt gccaatcca gcatggagct tcccagtttt	1560
ggggtgtctg ggatcaacga gtcagcggac atgagtattg gagttactgt catcaaaaac	1620
aatatgataa acaatgatct tgggtccagca acagctcaaa tggcccttca gttgttcac	1680
aaagattaca ggtacacgta ccgatgccat ataggtgaca cacaaataca aacccgaaga	1740
tcatttgaaa taaagaaact gtgggagcaa acccgttcca aagctggact gctggtctcc	1800
gacggaggcc caaatttata caacattaga aatctccaca ttcctgaagt ctgcctaaaa	1860
tgggaattga tggatgagga ttaccagggg cgtttatgca acccactgaa cccatttgtc	1920
agccataaag aaattgaatc aatgaacaat gcagtgatga tgccagcaca tgggtccagcc	1980
aaaaacatgg agtatgatgc tgttgcaaca acacactcct ggatcccaa aagaaatcga	2040
tccatcttga atacaagta aagaggagta cttgaggatg aacaaatgta ccaaggtgc	2100
tgcaatttat ttgaaaaatt ctccccagc agttcatata gaagaccagt cgggatatcc	2160
agtatggtg aggctatggt ttccagagcc cgaattgatg cacgattga ttccgaatct	2220
ggaaggataa agaaagaaga gtccactgag atcatgaaga tctgttccac cattgaagag	2280
ctcagacggc aaaaatagtg aatttagctt gtccttcacg aaaaaatgcc ttgtttctac	2340
t	2341

<210> SEQ ID NO 36

<211> LENGTH: 2341

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 36

agcgaagca ggtcaattat attcaatatg gaaagaataa aagaactacg aaatctaattg	60
tcgcagcttc gaccccgga gatactcaca aaaaccaccg tggaccatat ggccataatc	120
aagaagtaca catcaggaag acaggagaag aaccagcac ttaggatgaa atggatgatg	180
gcaatgaaat atccaattac agcagacaag aggataacgg aaatgattcc tgagagaaat	240
gagcaaggac aaactttatg gagtaaaatg aatgatgccg gatcagaccg agtgatggta	300
tcacctctgg ctgtgacatg gtggaatagg aatggacca taacaaatac agttcattat	360
ccaaaaatct acaaaaacta ttttgaaaga gtcgaaaggc taaagcatgg aacctttggc	420
cctgtccatt ttgaaacca agtcaaaata cgtcggagag ttgacataaa tcctggtcat	480
gcagatctca gtgccaggga ggcacaggat gtaatcatgg aagttgtttt ccctaacgaa	540
gtgggagcca ggataactac atcggaatcg caactaacga taaccaaaga gaagaagaa	600
gaactccagg attgcaaaat ttctccttg atggttgcat acatgttga gagagaactg	660
gtccgcaaaa cgagattcct ccagtggtt ggtggaacaa gcagtgtgta cattgaagtg	720
ttgcatttga ctcaaggaac atgctgggaa cagatgtata ctccaggagg ggaagtgagg	780

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aatgatgatg ttgatcaaag cttgattatt gctgctagga acatagttag aagagctgca	840
gtatcagcag atccactagc atctttattg gagatgtgcc acagcacaca gattggtgga	900
attaggatgg tagacatcct taggcagaac ccaacagaag agcaagccgt ggatatatgc	960
aaggctgcaa tgggactgag aattagctca tccttcagtt ttggtggatt cacatttaag	1020
agaacaagcg gatcatcagt caagagagag gaagaggtgc ttacgggcaa tcttcaaaca	1080
ttgaagataa gagtgcataa gggatatgaa gagttcaca ttggtgggag aagagcaaca	1140
gccatactca gaaaagcaac caggagattg attcagctga tagtgagtgg gagagacgaa	1200
cagtcgattg ccgaagcaat aattgtggcc atggtatttt cacaagagga ttgtatgata	1260
aaagcagtcg gaggtgatct gaatttcgtc aatagggcga atcaacgatt gaatcctatg	1320
catcaacttt taagacattt tcagaaggat gcgaaagtgc tttttcaaaa ttggggagtt	1380
gaacctatcg acaatgtgat gggaatgatt gggatattgc ccgacatgac tccaagcatc	1440
gagatgtcaa tgagaggagt gagaatcagc aaaatgggtg tagatgagta ctccagcagc	1500
gagagggtag tggtagcatg tgaccgtttt ttgagaatcc gggaccaacg aggaaatgta	1560
ctactgtctc ccgaggaggt cagtgaaca cagggaacag agaaactgac aataacttac	1620
tcactgtcaa tgatgtggga gattaatggt cctgaatcag tgttggtcaa tacctatcaa	1680
tggatcatca gaaactggga aactgttaaa attcagtggt ccagaaacc tacaatgcta	1740
tacaataaaa tggaaattga accatttcag tcttttagtac ctaaggccat tagaggccaa	1800
tacagtgggt ttgtaagaac tctgttccaa caaatgaggg atgtgcttgg gacatttgat	1860
accgcacaga taataaaact tcttccttc gcagccgctc caccaaagca aagtagaatg	1920
cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatact tgtaaggggc	1980
aattctcctg tattcaacta taacaaggcc acgaagagac tcacagttct cggaaaggat	2040
gctggcactt taactgaaga ccagatgaa ggcacagctg gagtggagtc cgctgttctg	2100
aggggattcc tcattctggg caaagaagac aagagatatg ggcagcact aagcatcaat	2160
gaactgagca accttgcga aggagagaag gctaattgtc taattgggca aggagacgtg	2220
gtgttggtaa tgaaacggaa acgggactct agcactacta ctgacagcca gacagcgacc	2280
aaaagaattc ggatggccat caattagtgt cgaatagttt aaaaacgacc ttgtttctac	2340
t	2341

<210> SEQ ID NO 37

<211> LENGTH: 1565

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 37

agcaaaagca gggtagataa tcactcactg agtgacatca aaatcatggc gtctcaaggc	60
accaaacgat cttacgaaca gatggagact gatggagaac gccagaatgc cactgaaatc	120
agagcatccg tcggaataat gattggtgga attggacgat tctacatcca aatgtgcacc	180
gaactcaaac tcagtgatta tgaggagcgg ttgatccaaa acagcttaac aatagagaga	240
atggtgctct ctgcttttga cgaaaggaga aataaatacc ttgaagaaca tccagtgctg	300
gggaaagatc ctaagaaaaa tggaggacct atatacagga gagtaaacgg aaagtggatg	360
agagaactca tcctttatga caaagaagaa ataaggcgaa tctggcgcca agctaataat	420
ggtgacgatg caacggctgg tctgactcac atgatgatct ggcattccaa ttgtaatgat	480

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gcaacttatc agaggacaag agctcttgtt cgcaccggaa tggatcccag gatgtgctct	540
ctgatgcaag gttcaactct ccttaggagg tctggagccg caggtgctgc agtcaaagga	600
gttggaaaca tggatgatga attggtcaga atgatcaaac gtgggatcaa tgatcggaac	660
ttctggaggg gtgagaatgg acgaaaaaca agaattgctt atgaaagaat gtgcaacatt	720
ctcaaaggga aatttcaaac tgctgcacaa aaagcaatga tggatcaagt gagagagagc	780
cggaaccag ggaatgctga gttcgaagat ctcacttttc tagcacggtc tgcactcata	840
ttgagagggt cggttgtctc caagtctctc ctgcctgcct gtgtgtatgg acctgccgta	900
gccagtgggt acgactttga aagggaggga tactctctag tcggaataga ccttttcaga	960
ctgcttcaaa acagccaagt gtacagccta atcagaccaa atgagaatcc agcacacaag	1020
agtcaactgg tgtggatggc atgccattct gccgcatttg aagatctaag agtattaagc	1080
ttcatcaaag ggacgaaggt gctcccaaga gggagcttt cactagagg agttcaaatt	1140
gcttccaatg aaaatatgga gactatggaa tcaagtacac ttgaactgag aagcaggtag	1200
tgggccataa ggaccagaag tggaggaaac accaatcaac agagggcatc tgcgggccaa	1260
atcagcatac aacctacgtt ctcatgacag agaaatctcc cttttgacag aacaaccatt	1320
atggcagcat tcaatgggaa tacagagggg agaacatctg acatgaggac cgaatcata	1380
aggatgatgg aaagtgaag accagaagat gtgtctttcc agggcggggg agtcttcgag	1440
ctctcgagcg aaaaggcagc gagcccgatc gtgccttcct ttgacatgag taatgaagga	1500
tcttatttct tcggagacaa tgacagaggg tacgacaatt aaagaaaaat acccttggtt	1560
ctact	1565

<210> SEQ ID NO 38

<211> LENGTH: 1027

<212> TYPE: DNA

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 38

agcaaaagca ggtagatatt gaaagatgag tcttctaacc gaggtcgaaa cgtacgtact	60
ctctatcatc ccgtcaggcc cctcaaaagc cgagatcgca cagagacttg aagatgtctt	120
tgcagggaag aacaccgacg ttgaggttct catggaatgg ctaaagacaa gaccaatcct	180
gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgaagc	240
aggactgcag cgtagacgct ttgtccaaaa tgcccttaat gggaacgggg atccaaataa	300
catggacaaa gcagtttaaac tgtataggaa gctcaagagg gagataacat tccatggggc	360
caaagaaatc tcaactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata	420
caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga	480
acagattgct gactccagc atcgggtctc taggcaaatg gtgacaacaa ccaatccact	540
aatcagacat gagaacagaa tggtttttagc cagcactaca gctaaggcta tggagcaaat	600
ggctggatcg agtgagcaag cagcagaggc catggagggt gctagtccag ctagacaaat	660
ggtgcaagcg atgagaacca ttgggactca tcctagctcc agtgctggtc tgaaaaatga	720
tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacgggtcaa	780
gtgatcctct cactattgoc gcaaatatca ttgggatctt gcacttgaca ttgtggattc	840
ttgatcgtct ttttttcaaa tgcatttacc gtcgctttaa atacggactg aaaggagggc	900
cttctacgga aggagtgcc aagtctatga ggaagaata tcgaaaggaa cagcagagtg	960
ctgtggatgc tgacgatggt cattttgtca gcatagagct ggagtaaaaa actaccttgt	1020

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ttctact 1027

<210> SEQ ID NO 39
<211> LENGTH: 890
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 39

agcaaaagca ggggtgacaaa aacataatgg atccaaacac tgtgtcaagc tttcaggtag 60
attgctttct ttggcatgtc cgcaaacgag ttgcagacca agaactaggc gatgccccat 120
tccttgatcg gcttcgcca gatcagaaat ccctaagagg aaggggcagt actctcggtc 180
tggacatcaa gacagccaca cgtgctggaa agcagatagt ggagcggatt ctgaaagaag 240
aatccgatga ggcacttaaa atgaccatgg cctctgtacc tgcgtcgcgt tacctaactg 300
acatgactct tgaggaaatg tcaagggact ggtccatgct cataccaag cagaaagtgg 360
caggccctct ttgtatcaga atggaccagg cgatcatgga taagaacatc atactgaaag 420
cgaacttcag tgtgattttt gaccggtgg agactctaatt attgctaagg gctttcaccg 480
aagagggagc aattgttggc gaaatttcac cattgccttc tcttcagga catactgctg 540
aggatgtcaa aaatgcagtt ggagtcctca tcggaggact tgaatggaat gataacacag 600
ttcagagtctc tgaactcta cagagattcg cttggagaag cagtaatgag aatgggagac 660
ctccactcac tccaaaacag aaacgagaaa tggcgggaac aattaggtea gaagtttgaa 720
gaaataagat ggttgattga agaagtgaga cactaaactga agataacaga gaatagtttt 780
gagcaataa catttatgca agccttacat ctattgcttg aagtggagca agagataaga 840
actttctcgt ttcagcttat ttagtactaa aaaacaccct tgtttctact 890

<210> SEQ ID NO 40

<400> SEQUENCE: 40

000

<210> SEQ ID NO 41

<400> SEQUENCE: 41

000

<210> SEQ ID NO 42

<400> SEQUENCE: 42

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<210> SEQ ID NO 43

<400> SEQUENCE: 43

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<210> SEQ ID NO 44

<400> SEQUENCE: 44

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<210> SEQ ID NO 45

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<400> SEQUENCE: 45

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<210> SEQ ID NO 46

<400> SEQUENCE: 46

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<210> SEQ ID NO 47

<400> SEQUENCE: 47

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<210> SEQ ID NO 48

<400> SEQUENCE: 48

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<210> SEQ ID NO 49

<400> SEQUENCE: 49

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<210> SEQ ID NO 50

<211> LENGTH: 1273

<212> TYPE: PRT

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 50

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
1 5 10 15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
20 25 30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
35 40 45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
50 55 60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
65 70 75 80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
85 90 95

Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
100 105 110

Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
115 120 125

Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
130 135 140

Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr
145 150 155 160

Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu
165 170 175

Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe
180 185 190

Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr
195 200 205

Pro 210	Ile	Asn	Leu	Val	Arg	Asp	Leu	Pro	Gln	Gly	Phe	Ser	Ala	Leu	Glu
Pro 225	Leu	Val	Asp	Leu	Pro	Ile	Gly	Ile	Asn	Ile	Thr	Arg	Phe	Gln	Thr
Leu	Leu	Ala	Leu	His	Arg	Ser	Tyr	Leu	Thr	Pro	Gly	Asp	Ser	Ser	Ser
Gly	Trp	Thr	Ala	Gly	Ala	Ala	Ala	Tyr	Tyr	Val	Gly	Tyr	Leu	Gln	Pro
Arg	Thr	Phe	Leu	Leu	Lys	Tyr	Asn	Glu	Asn	Gly	Thr	Ile	Thr	Asp	Ala
Val	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys
Ser 305	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro
Thr 385	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly
Phe	Gln	Pro	Thr	Asn	Gly	Val	Gly	Tyr	Gln	Pro	Tyr	Arg	Val	Val	Val
Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser

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625	630	635	640
Asn Val Phe Gln Thr Arg Ala Gly Cys Leu Ile Gly Ala Glu His Val			
645		650	655
Asn Asn Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala			
660		665	670
Ser Tyr Gln Thr Gln Thr Asn Ser Pro Arg Arg Ala Arg Ser Val Ala			
675		680	685
Ser Gln Ser Ile Ile Ala Tyr Thr Met Ser Leu Gly Ala Glu Asn Ser			
690		695	700
Val Ala Tyr Ser Asn Asn Ser Ile Ala Ile Pro Thr Asn Phe Thr Ile			
705		710	715
Ser Val Thr Thr Glu Ile Leu Pro Val Ser Met Thr Lys Thr Ser Val			
725		730	735
Asp Cys Thr Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ser Asn Leu			
740		745	750
Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Thr			
755		760	765
Gly Ile Ala Val Glu Gln Asp Lys Asn Thr Gln Glu Val Phe Ala Gln			
770		775	780
Val Lys Gln Ile Tyr Lys Thr Pro Pro Ile Lys Asp Phe Gly Gly Phe			
785		790	795
Asn Phe Ser Gln Ile Leu Pro Asp Pro Ser Lys Pro Ser Lys Arg Ser			
805		810	815
Phe Ile Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly			
820		825	830
Phe Ile Lys Gln Tyr Gly Asp Cys Leu Gly Asp Ile Ala Ala Arg Asp			
835		840	845
Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu			
850		855	860
Leu Thr Asp Glu Met Ile Ala Gln Tyr Thr Ser Ala Leu Leu Ala Gly			
865		870	875
Thr Ile Thr Ser Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile			
885		890	895
Pro Phe Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr			
900		905	910
Gln Asn Val Leu Tyr Glu Asn Gln Lys Leu Ile Ala Asn Gln Phe Asn			
915		920	925
Ser Ala Ile Gly Lys Ile Gln Asp Ser Leu Ser Ser Thr Ala Ser Ala			
930		935	940
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn			
945		950	955
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val			
965		970	975
Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln			
980		985	990
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val			
995		1000	1005
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu			
1010		1015	1020
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val			
1025		1030	1035
Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala			
1045		1050	1055

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Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu
 1060 1065 1070
 Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His
 1075 1080 1085
 Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val
 1090 1095 1100
 Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr
 1105 1110 1115 1120
 Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr
 1125 1130 1135
 Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu
 1140 1145 1150
 Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
 1155 1160 1165
 Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp
 1170 1175 1180
 Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu
 1185 1190 1195 1200
 Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
 1205 1210 1215
 Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
 1220 1225 1230
 Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
 1235 1240 1245
 Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
 1250 1255 1260
 Leu Lys Gly Val Lys Leu His Tyr Thr
 1265 1270

<210> SEQ ID NO 51
 <211> LENGTH: 1273
 <212> TYPE: PRT
 <213> ORGANISM: Influenza virus

<400> SEQUENCE: 51

Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1 5 10 15
 Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
 20 25 30
 Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
 35 40 45
 His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
 50 55 60
 Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
 65 70 75 80
 Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
 85 90 95
 Lys Ser Asn Ile Ile Arg Gly Trp Ile Phe Gly Thr Thr Leu Asp Ser
 100 105 110
 Lys Thr Gln Ser Leu Leu Ile Val Asn Asn Ala Thr Asn Val Val Ile
 115 120 125
 Lys Val Cys Glu Phe Gln Phe Cys Asn Asp Pro Phe Leu Gly Val Tyr
 130 135 140
 Tyr His Lys Asn Asn Lys Ser Trp Met Glu Ser Glu Phe Arg Val Tyr

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145	150	155	160
Ser Ser Ala Asn Asn Cys Thr Phe Glu Tyr Val Ser Gln Pro Phe Leu	165	170	175
Met Asp Leu Glu Gly Lys Gln Gly Asn Phe Lys Asn Leu Arg Glu Phe	180	185	190
Val Phe Lys Asn Ile Asp Gly Tyr Phe Lys Ile Tyr Ser Lys His Thr	195	200	205
Pro Ile Asn Leu Val Arg Asp Leu Pro Gln Gly Phe Ser Ala Leu Glu	210	215	220
Pro Leu Val Asp Leu Pro Ile Gly Ile Asn Ile Thr Arg Phe Gln Thr	225	230	235
Leu Leu Ala Leu His Arg Ser Tyr Leu Thr Pro Gly Asp Ser Ser Ser	245	250	255
Gly Trp Thr Ala Gly Ala Ala Ala Tyr Tyr Val Gly Tyr Leu Gln Pro	260	265	270
Arg Thr Phe Leu Leu Lys Tyr Asn Glu Asn Gly Thr Ile Thr Asp Ala	275	280	285
Val Asp Cys Ala Leu Asp Pro Leu Ser Glu Thr Lys Cys Thr Leu Lys	290	295	300
Ser Phe Thr Val Glu Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val	305	310	315
Gln Pro Thr Glu Ser Ile Val Arg Phe Pro Asn Ile Thr Asn Leu Cys	325	330	335
Pro Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala	340	345	350
Trp Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu	355	360	365
Tyr Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro	370	375	380
Thr Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe	385	390	395
Val Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly	405	410	415
Lys Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys	420	425	430
Val Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn	435	440	445
Tyr Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe	450	455	460
Glu Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys	465	470	475
Asn Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly	485	490	495
Phe Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val	500	505	510
Leu Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys	515	520	525
Lys Ser Thr Asn Leu Val Lys Asn Lys Cys Val Asn Phe Asn Phe Asn	530	535	540
Gly Leu Thr Gly Thr Gly Val Leu Thr Glu Ser Asn Lys Lys Phe Leu	545	550	555
Pro Phe Gln Gln Phe Gly Arg Asp Ile Ala Asp Thr Thr Asp Ala Val	565	570	575

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Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe	580	585	590	
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val	595	600	605	
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile	610	615	620	
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser	625	630	635	640
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val	645	650	655	
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala	660	665	670	
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala	675	680	685	
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser	690	695	700	
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile	705	710	715	720
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val	725	730	735	
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu	740	745	750	
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr	755	760	765	
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln	770	775	780	
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe	785	790	795	800
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser	805	810	815	
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly	820	825	830	
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp	835	840	845	
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu	850	855	860	
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly	865	870	875	880
Thr	Ile	Thr	Ser	Gly	Trp	Thr	Phe	Gly	Ala	Gly	Ala	Ala	Leu	Gln	Ile	885	890	895	
Pro	Phe	Ala	Met	Gln	Met	Ala	Tyr	Arg	Phe	Asn	Gly	Ile	Gly	Val	Thr	900	905	910	
Gln	Asn	Val	Leu	Tyr	Glu	Asn	Gln	Lys	Leu	Ile	Ala	Asn	Gln	Phe	Asn	915	920	925	
Ser	Ala	Ile	Gly	Lys	Ile	Gln	Asp	Ser	Leu	Ser	Ser	Thr	Ala	Ser	Ala	930	935	940	
Leu	Gly	Lys	Leu	Gln	Asp	Val	Val	Asn	Gln	Asn	Ala	Gln	Ala	Leu	Asn	945	950	955	960
Thr	Leu	Val	Lys	Gln	Leu	Ser	Ser	Asn	Phe	Gly	Ala	Ile	Ser	Ser	Val	965	970	975	
Leu	Asn	Asp	Ile	Leu	Ser	Arg	Leu	Asp	Lys	Val	Glu	Ala	Glu	Val	Gln	980	985	990	

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Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val
  995                      1000                      1005

Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu
 1010                      1015                      1020

Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val
 1025                      1030                      1035                      1040

Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala
 1045                      1050                      1055

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu
 1060                      1065                      1070

Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His
 1075                      1080                      1085

Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val
 1090                      1095                      1100

Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr
 1105                      1110                      1115                      1120

Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr
 1125                      1130                      1135

Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu
 1140                      1145                      1150

Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
 1155                      1160                      1165

Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp
 1170                      1175                      1180

Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu
 1185                      1190                      1195                      1200

Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
 1205                      1210                      1215

Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
 1220                      1225                      1230

Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
 1235                      1240                      1245

Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val
 1250                      1255                      1260

Leu Lys Gly Val Lys Leu His Tyr Thr
 1265                      1270

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<210> SEQ ID NO 52

<211> LENGTH: 1273

<212> TYPE: PRT

<213> ORGANISM: Influenza virus

<400> SEQUENCE: 52

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Met Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val
 1      5                      10                      15

Asn Leu Thr Thr Arg Thr Gln Leu Pro Pro Ala Tyr Thr Asn Ser Phe
      20                      25                      30

Thr Arg Gly Val Tyr Tyr Pro Asp Lys Val Phe Arg Ser Ser Val Leu
      35                      40                      45

His Ser Thr Gln Asp Leu Phe Leu Pro Phe Phe Ser Asn Val Thr Trp
      50                      55                      60

Phe His Ala Ile His Val Ser Gly Thr Asn Gly Thr Lys Arg Phe Asp
      65                      70                      75                      80

Asn Pro Val Leu Pro Phe Asn Asp Gly Val Tyr Phe Ala Ser Thr Glu
      85                      90                      95

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Lys	Ser	Asn	Ile	Ile	Arg	Gly	Trp	Ile	Phe	Gly	Thr	Thr	Leu	Asp	Ser	
			100					105					110			
Lys	Thr	Gln	Ser	Leu	Leu	Ile	Val	Asn	Asn	Ala	Thr	Asn	Val	Val	Ile	
			115					120					125			
Lys	Val	Cys	Glu	Phe	Gln	Phe	Cys	Asn	Asp	Pro	Phe	Leu	Gly	Val	Tyr	
			130					135					140			
Tyr	His	Lys	Asn	Asn	Lys	Ser	Trp	Met	Glu	Ser	Glu	Phe	Arg	Val	Tyr	
			145					150					155			
Ser	Ser	Ala	Asn	Asn	Cys	Thr	Phe	Glu	Tyr	Val	Ser	Gln	Pro	Phe	Leu	
			165					170						175		
Met	Asp	Leu	Glu	Val	Lys	Gln	Gly	Asn	Phe	Lys	Asn	Leu	Arg	Glu	Phe	
			180					185					190			
Val	Phe	Lys	Asn	Ile	Asp	Gly	Tyr	Phe	Lys	Ile	Tyr	Ser	Lys	His	Thr	
			195					200					205			
Pro	Ile	Asn	Leu	Val	Arg	Asp	Leu	Pro	Gln	Gly	Phe	Ser	Ala	Leu	Glu	
			210					215					220			
Pro	Leu	Val	Asp	Leu	Pro	Ile	Gly	Ile	Asn	Ile	Thr	Arg	Phe	Gln	Thr	
			225					230						235		
Leu	Leu	Ala	Leu	His	Arg	Ser	Tyr	Leu	Thr	Pro	Gly	Asp	Ser	Ser	Ser	
			245					250						255		
Gly	Trp	Thr	Ala	Gly	Ala	Ala	Ala	Tyr	Tyr	Val	Gly	Tyr	Leu	Gln	Pro	
			260					265					270			
Arg	Thr	Phe	Leu	Leu	Lys	Tyr	Asn	Glu	Asn	Gly	Thr	Ile	Thr	Asp	Ala	
			275					280					285			
Val	Asp	Cys	Ala	Leu	Asp	Pro	Leu	Ser	Glu	Thr	Lys	Cys	Thr	Leu	Lys	
			290					295					300			
Ser	Phe	Thr	Val	Glu	Lys	Gly	Ile	Tyr	Gln	Thr	Ser	Asn	Phe	Arg	Val	
			305					310						315		
Gln	Pro	Thr	Glu	Ser	Ile	Val	Arg	Phe	Pro	Asn	Ile	Thr	Asn	Leu	Cys	
			325					330						335		
Pro	Phe	Gly	Glu	Val	Phe	Asn	Ala	Thr	Arg	Phe	Ala	Ser	Val	Tyr	Ala	
			340					345						350		
Trp	Asn	Arg	Lys	Arg	Ile	Ser	Asn	Cys	Val	Ala	Asp	Tyr	Ser	Val	Leu	
			355					360					365			
Tyr	Asn	Ser	Ala	Ser	Phe	Ser	Thr	Phe	Lys	Cys	Tyr	Gly	Val	Ser	Pro	
			370					375					380			
Thr	Lys	Leu	Asn	Asp	Leu	Cys	Phe	Thr	Asn	Val	Tyr	Ala	Asp	Ser	Phe	
			385					390						395		
Val	Ile	Arg	Gly	Asp	Glu	Val	Arg	Gln	Ile	Ala	Pro	Gly	Gln	Thr	Gly	
			405					410						415		
Lys	Ile	Ala	Asp	Tyr	Asn	Tyr	Lys	Leu	Pro	Asp	Asp	Phe	Thr	Gly	Cys	
			420					425					430			
Val	Ile	Ala	Trp	Asn	Ser	Asn	Asn	Leu	Asp	Ser	Lys	Val	Gly	Gly	Asn	
			435					440					445			
Tyr	Asn	Tyr	Leu	Tyr	Arg	Leu	Phe	Arg	Lys	Ser	Asn	Leu	Lys	Pro	Phe	
			450					455					460			
Glu	Arg	Asp	Ile	Ser	Thr	Glu	Ile	Tyr	Gln	Ala	Gly	Ser	Thr	Pro	Cys	
			465					470					475			
Asn	Gly	Val	Glu	Gly	Phe	Asn	Cys	Tyr	Phe	Pro	Leu	Gln	Ser	Tyr	Gly	
			485					490						495		
Phe	Gln	Pro	Thr	Asn												

Leu	Ser	Phe	Glu	Leu	Leu	His	Ala	Pro	Ala	Thr	Val	Cys	Gly	Pro	Lys
515							520					525			
Lys	Ser	Thr	Asn	Leu	Val	Lys	Asn	Lys	Cys	Val	Asn	Phe	Asn	Phe	Asn
530						535					540				
Gly	Leu	Thr	Gly	Thr	Gly	Val	Leu	Thr	Glu	Ser	Asn	Lys	Lys	Phe	Leu
545					550					555					560
Pro	Phe	Gln	Gln	Phe	Gly	Arg	Asp	Ile	Ala	Asp	Thr	Thr	Asp	Ala	Val
				565					570						
Arg	Asp	Pro	Gln	Thr	Leu	Glu	Ile	Leu	Asp	Ile	Thr	Pro	Cys	Ser	Phe
				580				585					590		
Gly	Gly	Val	Ser	Val	Ile	Thr	Pro	Gly	Thr	Asn	Thr	Ser	Asn	Gln	Val
				595			600					605			
Ala	Val	Leu	Tyr	Gln	Asp	Val	Asn	Cys	Thr	Glu	Val	Pro	Val	Ala	Ile
						615					620				
His	Ala	Asp	Gln	Leu	Thr	Pro	Thr	Trp	Arg	Val	Tyr	Ser	Thr	Gly	Ser
625					630					635					640
Asn	Val	Phe	Gln	Thr	Arg	Ala	Gly	Cys	Leu	Ile	Gly	Ala	Glu	His	Val
				645					650					655	
Asn	Asn	Ser	Tyr	Glu	Cys	Asp	Ile	Pro	Ile	Gly	Ala	Gly	Ile	Cys	Ala
				660				665					670		
Ser	Tyr	Gln	Thr	Gln	Thr	Asn	Ser	Pro	Arg	Arg	Ala	Arg	Ser	Val	Ala
				675			680					685			
Ser	Gln	Ser	Ile	Ile	Ala	Tyr	Thr	Met	Ser	Leu	Gly	Ala	Glu	Asn	Ser
					695						700				
Val	Ala	Tyr	Ser	Asn	Asn	Ser	Ile	Ala	Ile	Pro	Thr	Asn	Phe	Thr	Ile
705					710					715					720
Ser	Val	Thr	Thr	Glu	Ile	Leu	Pro	Val	Ser	Met	Thr	Lys	Thr	Ser	Val
				725				730						735	
Asp	Cys	Thr	Met	Tyr	Ile	Cys	Gly	Asp	Ser	Thr	Glu	Cys	Ser	Asn	Leu
				740				745					750		
Leu	Leu	Gln	Tyr	Gly	Ser	Phe	Cys	Thr	Gln	Leu	Asn	Arg	Ala	Leu	Thr
				755			760					765			
Gly	Ile	Ala	Val	Glu	Gln	Asp	Lys	Asn	Thr	Gln	Glu	Val	Phe	Ala	Gln
					775						780				
Val	Lys	Gln	Ile	Tyr	Lys	Thr	Pro	Pro	Ile	Lys	Asp	Phe	Gly	Gly	Phe
785					790					795					800
Asn	Phe	Ser	Gln	Ile	Leu	Pro	Asp	Pro	Ser	Lys	Pro	Ser	Lys	Arg	Ser
				805					810					815	
Phe	Ile	Glu	Asp	Leu	Leu	Phe	Asn	Lys	Val	Thr	Leu	Ala	Asp	Ala	Gly
				820				825					830		
Phe	Ile	Lys	Gln	Tyr	Gly	Asp	Cys	Leu	Gly	Asp	Ile	Ala	Ala	Arg	Asp
				835			840					845			
Leu	Ile	Cys	Ala	Gln	Lys	Phe	Asn	Gly	Leu	Thr	Val	Leu	Pro	Pro	Leu
					855						860				
Leu	Thr	Asp	Glu	Met	Ile	Ala	Gln	Tyr	Thr	Ser	Ala	Leu	Leu	Ala	Gly
					870					875					

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930	935	940
Leu Gly Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn 945 950 955 960		
Thr Leu Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val 965 970 975		
Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln 980 985 990		
Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val 995 1000 1005		
Thr Gln Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu 1010 1015 1020		
Ala Ala Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val 1025 1030 1035 1040		
Asp Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ser Ala 1045 1050 1055		
Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ala Gln Glu 1060 1065 1070		
Lys Asn Phe Thr Thr Ala Pro Ala Ile Cys His Asp Gly Lys Ala His 1075 1080 1085		
Phe Pro Arg Glu Gly Val Phe Val Ser Asn Gly Thr His Trp Phe Val 1090 1095 1100		
Thr Gln Arg Asn Phe Tyr Glu Pro Gln Ile Ile Thr Thr Asp Asn Thr 1105 1110 1115 1120		
Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly Ile Val Asn Asn Thr 1125 1130 1135		
Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu 1140 1145 1150		
Asp Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp 1155 1160 1165		
Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile Asp 1170 1175 1180		
Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile Asp Leu 1185 1190 1195 1200		
Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile 1205 1210 1215		
Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile 1220 1225 1230		
Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys 1235 1240 1245		
Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val 1250 1255 1260		
Leu Lys Gly Val Lys Leu His Tyr Thr 1265 1270		

<210> SEQ ID NO 53

<211> LENGTH: 18

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: A synthetic sequence

<400> SEQUENCE: 53

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro 1 5 10 15
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Gly Pro

-continued

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<210> SEQ ID NO 54
<211> LENGTH: 19
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic sequence

<400> SEQUENCE: 54

Ala Thr Asn Phe Ser Leu Leu Lys Gln Ala Gly Asp Val Glu Glu Asn
1           5           10           15

Pro Gly Pro

<210> SEQ ID NO 55
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic sequence

<400> SEQUENCE: 55

Gln Cys Thr Asn Tyr Ala Leu Leu Lys Leu Ala Gly Asp Val Glu Ser
1           5           10           15

Asn Pro Gly Pro
20

<210> SEQ ID NO 56
<211> LENGTH: 21
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic sequence

<400> SEQUENCE: 56

Val Lys Gln Thr Leu Asn Phe Asp Leu Leu Lys Ala Gly Asp Val Glu
1           5           10           15

Ser Asn Pro Gly Pro
20

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What is claimed is:

1. A composition for intranasal delivery comprising an amount of an isolated, single cycle, multivalent recombinant influenza virus having at least seven viral segments selected from influenza virus PA, PB1, PB2, NP, NS, M, HA or NA viral segments, or having at least six viral segments selected from PA, PB1, PB2, NP, NS, M, or HEF viral segments, wherein the NS viral segment comprises coding sequences for an antigenic coronavirus protein, or an antigenic portion thereof, flanked by protease recognition sites, wherein the coding sequences include a receptor binding domain of the coronavirus S protein, wherein the M viral segment comprises a mutant M gene that expresses a functional M1 protein and a mutant M2 protein with a deletion of the cytoplasmic tail and either lacking a transmembrane domain or having a mutated transmembrane domain, wherein the amount is effective to induce a mucosal immune response.
2. The composition of claim 1 wherein the antigenic coronavirus protein comprises S1 sequences.
3. The composition of claim 1 wherein antigenic coronavirus protein comprises a soluble protein.
4. The composition of claim 1 wherein the antigenic coronavirus protein sequences or the portion thereof have at least 80% amino acid sequence identity to one of SEQ ID Nos. 25-28 and 50-52.
5. The composition of claim 1 wherein the virus comprises eight or nine viral segments.
6. The composition of claim 1 wherein the virus is an influenza A or B virus.
7. The composition of claim 1 wherein the virus is bivalent or trivalent.
8. The composition of claim 1 wherein the M2 lacks the transmembrane domain.
9. The composition of claim 1 wherein at least one of PA, PB1, or PB2 viral segments has a C to U promoter mutation.
10. The composition of claim 1 wherein the PB2 segment has one or more of a C4U promoter mutation, 202L/323L or 504V; the PB1 segment has one or more of C4U, 40L, 112G, 180W or 247H; the PA segment has one or more of C4U, 142N, 225C or 401K; the NP segment has 74K or 116L; or the NS segment has 30P in NS1 or 118K in NS1, wherein the numbering is relative to a PB2 encoded by SEQ ID NO:3, a PB1 encoded by SEQ ID NO:2, a PA encoded by SEQ ID NO:1, a NP encoded by SEQ ID NO:4 or a NS1 encoded by SEQ ID NO:6.
11. A vaccine comprising the virus of claim 1.
12. The vaccine of claim 11 wherein the recombinant virus comprises influenza A HA.
13. A method to immunize a vertebrate, comprising: administering to the vertebrate the vaccine of claim 11.

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14. The method of claim **13** wherein the vertebrate is a human.

15. The composition of claim **1** wherein the NS viral segment encodes protease recognition sites comprising T2A (EGRGSLTTCGDVEENPGP; SEQ ID NO:53), P2A (ATNFSLKQAGDVEENPGP; SEQ ID NO:54), E2A (QCTNYALLKLAGDVESNPGP; SEQ ID NO: 55) or F2A (VKQTLNFDLLKAGDVESNPGP; SEQ ID NO:56).

16. The composition of claim **1** wherein the protease recognition sequences are autocatalytically cleaved.

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