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(54) **MUTATIONS THAT CONFER GENETIC STABILITY TO GENES IN INFLUENZA VIRUSES**

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(56) **References Cited**

U.S. PATENT DOCUMENTS

4,071,618	A	1/1978	Konobe et al.
4,659,569	A	4/1987	Mitsuhashi et al.
5,166,057	A	11/1992	Palese et al.
5,716,821	A	2/1998	Wertz et al.
5,789,229	A	8/1998	Wertz et al.
5,820,871	A	10/1998	Palese et al.
5,840,520	A	11/1998	Clarke et al.
5,854,037	A	12/1998	Palese et al.
5,948,410	A	9/1999	Van Scharrenburg et al.
5,994,526	A	11/1999	Meulewaeter et al.
6,033,886	A	3/2000	Conzelmann
6,037,348	A	3/2000	Colacino et al.
6,146,642	A	11/2000	Garcia-Sastre et al.
6,169,175	B1	1/2001	Frace et al.
6,194,546	B1	2/2001	Newton et al.
6,455,298	B1	9/2002	Groner et al.
6,544,785	B1	4/2003	Palese et al.
6,656,720	B2	12/2003	Groner et al.
6,825,036	B2	11/2004	Makizumi et al.
6,872,395	B2	3/2005	Kawaoka
6,951,752	B2	10/2005	Reiter et al.
6,951,754	B2	10/2005	Hoffmann
6,974,695	B2	12/2005	Vogels et al.
7,037,707	B2	5/2006	Webster et al.
7,176,021	B2	2/2007	Kawaoka
7,226,774	B2	6/2007	Kawaoka
7,312,064	B2	12/2007	Hoffmann
7,507,411	B2	3/2009	Zhou et al.
7,566,458	B2	7/2009	Yang et al.
7,585,657	B2	9/2009	Kawaoka
7,588,769	B2	9/2009	Kawaoka
7,670,837	B2	3/2010	Schwartz
7,833,788	B2	11/2010	Pau et al.
7,883,844	B2	2/2011	Nouchi et al.
7,955,833	B2	6/2011	Reiter et al.
7,959,930	B2	6/2011	De Wit et al.
7,972,843	B2	7/2011	Hoffmann
7,993,924	B2	8/2011	Billeter et al.
8,012,736	B2	9/2011	Hoffman et al.
8,048,430	B2	11/2011	Yang et al.
8,057,806	B2	11/2011	Kawaoka et al.
8,093,033	B2	1/2012	Kemble et al.
8,114,415	B2	2/2012	Hoffmann et al.
8,119,337	B2	2/2012	Gregersen
8,119,388	B2	2/2012	Schwartz et al.
8,309,099	B2	11/2012	Hoffmann
8,354,114	B2	1/2013	Lu et al.
8,357,376	B2	1/2013	Liu et al.
8,409,843	B2	4/2013	Kemble et al.
8,460,914	B2	6/2013	Gregersen
8,475,806	B2	7/2013	Kawaoka
8,524,497	B2	9/2013	Reiter et al.
8,546,123	B2	10/2013	Lewis

(Continued)

FOREIGN PATENT DOCUMENTS

AU	2012204138 B2	5/2014
AU	2014202470	11/2016

(Continued)

OTHER PUBLICATIONS

"Result 17, NCBI Blast nucleotide search of SEQ ID No. 2, database nr", (Jul. 18, 2006), 3 pgs.

(Continued)

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(57) **ABSTRACT**

The disclosure provides for an isolated recombinant influenza virus having at least one of: a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, and methods of making and using the virus.

20 Claims, 54 Drawing Sheets

Specification includes a Sequence Listing.

(56) **References Cited**

U.S. PATENT DOCUMENTS

8,574,591	B2	11/2013	Hoffmann et al.
8,574,593	B2	11/2013	Yang et al.
8,580,277	B2	11/2013	Yang et al.
8,591,914	B2	11/2013	Yang et al.
9,109,013	B2	8/2015	Kawaoka et al.
9,254,318	B2	2/2016	Kawaoka et al.
9,474,798	B2	10/2016	Watanabe et al.
9,890,363	B2	2/2018	Kawaoka
9,926,535	B2	3/2018	Kawaoka et al.
9,950,057	B2	4/2018	Kawaoka et al.
10,053,671	B2	8/2018	Kawaoka et al.
10,059,925	B2	8/2018	Kawaoka et al.
10,172,934	B2	1/2019	Kawaoka et al.
10,246,686	B2	4/2019	Kawaoka et al.
2002/0164770	A1	11/2002	Hoffmann
2002/0197705	A1	12/2002	Kawaoka
2003/0035814	A1	2/2003	Kawaoka et al.
2003/0044962	A1	3/2003	Makizumi et al.
2003/0073223	A1	4/2003	Groner et al.
2003/0119183	A1	6/2003	Groner
2003/0194694	A1	10/2003	Kawaoka
2004/0002061	A1	1/2004	Kawaoka
2004/0063141	A1	4/2004	Lok
2004/0077086	A1	4/2004	Reiter et al.
2004/0219170	A1	11/2004	Kawaoka
2005/0003349	A1	1/2005	Kawaoka
2005/0037487	A1	2/2005	Kawaoka et al.
2005/0118140	A1	6/2005	Vorlop et al.
2005/0158342	A1	7/2005	Kemble et al.
2005/0186563	A1	8/2005	Hoffmann
2005/0202553	A1	9/2005	Groner et al.
2005/0232950	A1	10/2005	Kawaoka
2005/0266026	A1	12/2005	Hoffmann et al.
2006/0057116	A1	3/2006	Kawaoka et al.
2006/0166321	A1	7/2006	Kawaoka et al.
2006/0188977	A1	8/2006	Schwartz et al.
2006/0246092	A1	11/2006	Neirynck et al.
2007/0231348	A1	10/2007	Kawaoka et al.
2008/0233560	A1	9/2008	Hoffmann
2008/0254067	A1	10/2008	Trepanier et al.
2008/0274141	A1	11/2008	Groner et al.
2008/0311148	A1	12/2008	Hoffmann
2008/0311149	A1	12/2008	Hoffmann
2009/0074812	A1	3/2009	Watanabe et al.
2009/0081252	A1	3/2009	Gregersen
2009/0181446	A1	7/2009	Nouchi et al.
2010/0112000	A1	5/2010	Schwartz
2010/0183671	A1	7/2010	Gregersen et al.
2010/0247572	A1	9/2010	Kawaoka
2011/0027314	A1	2/2011	Broeker
2011/0045022	A1	2/2011	Tsai
2011/0110978	A1	5/2011	Kawaoka et al.
2011/0236417	A1	9/2011	Watanabe et al.
2012/0020997	A1	1/2012	Hoffman et al.
2012/0034600	A1	2/2012	Gregersen
2012/0115206	A1	5/2012	Schwartz et al.
2012/0156241	A1	6/2012	De Wit et al.
2012/0207785	A1	8/2012	Fabry et al.
2013/0095135	A1	4/2013	Collignon et al.
2013/0183741	A1	7/2013	Park et al.
2013/0316434	A1	11/2013	Reiter et al.
2014/0022731	A1	8/2014	Li et al.
2015/0017205	A1	1/2015	Kawaoka et al.
2015/0368621	A1	12/2015	Kawaoka et al.
2016/0024479	A1	1/2016	Kawaoka et al.
2016/0208223	A1	7/2016	Kawaoka et al.
2016/0355790	A1	12/2016	Kawaoka et al.
2017/0067029	A1	3/2017	Kawaoka et al.
2017/0096645	A1	4/2017	Watanabe et al.
2017/0258888	A1	9/2017	Kawaoka
2017/0354730	A1	12/2017	Kawaoka et al.
2018/0245054	A1	8/2018	Kawaoka et al.
2018/0340152	A1	11/2018	Kawaoka et al.
2019/0032023	A1	1/2019	Kawaoka et al.
2019/0048324	A1	2/2019	Kawaoka et al.

FOREIGN PATENT DOCUMENTS

CN	1826407	B	9/2013
EP	0702085	A1	3/1996
EP	1201760	A1	5/2002
EP	2010557	B1	2/2014
EP	1631663	B1	8/2016
IL	171831	A	5/2015
JP	2004-500842	A	1/2004
JP	2004-531232	A	10/2004
JP	2005-523698	A	8/2005
JP	2005-245302	A	9/2005
JP	2005-535288	A	11/2005
JP	2007-518395	A	7/2007
JP	2009-532352	A	9/2009
JP	4927290	B2	5/2012
JP	2013-507990	A	3/2013
JP	2014-039551	A	3/2014
JP	2014-131516	A	7/2014
JP	2016-144463	A	8/2016
JP	2016-524915	A	8/2016
JP	2016-169225	A	9/2016
JP	6352974	B2	6/2018
JP	6375329	B2	7/2018
MX	285206		3/2011
NO	341506		11/2017
WO	WO-9610631	A1	4/1996
WO	WO-9610632	A1	4/1996
WO	WO-9640955	A1	12/1996
WO	WO-9737000	A1	10/1997
WO	WO-9802530	A1	1/1998
WO	WO-9853078	A1	11/1998
WO	WO-9928445	A1	6/1999
WO	WO-0053786	A1	9/2000
WO	WO-0060050	A2	10/2000
WO	WO-2000060050	A2	10/2000
WO	WO-0060050	A3	1/2001
WO	WO-0179273	A2	10/2001
WO	WO-2001079273	A2	10/2001
WO	WO-0183794	A2	11/2001
WO	WO-2001083794	A2	11/2001
WO	WO-02064757	A2	8/2002
WO	WO-03068923	A2	8/2003
WO	WO-2003068923	A2	8/2003
WO	WO-03076462	A1	9/2003
WO	WO-03091401	A2	11/2003
WO	WO-2003091401	A2	11/2003
WO	WO-2004094466	A2	11/2004
WO	WO-2004112831	A2	12/2004
WO	WO-2004112831	A3	12/2004
WO	WO-2005062820	A2	7/2005
WO	WO-2007126810	A2	11/2007
WO	WO-2007126810	A3	11/2007
WO	WO-2008156778	A2	12/2008
WO	WO-2008156778	A3	12/2008
WO	WO-2008157583	A1	12/2008
WO	WO-2008156778	A9	2/2009
WO	WO-2011056591	A1	5/2011
WO	WO-2012177924	A2	12/2012
WO	WO-2013034069	A1	3/2013
WO	WO-2014195920	A2	12/2014
WO	WO-2015009743	A1	1/2015
WO	WO-2015196150	A2	12/2015
WO	WO-2015196150	A3	12/2015
WO	WO-2017007839	A1	1/2017
WO	WO-2017143236	A1	8/2017
WO	WO-2020167432	A2	8/2020
WO	WO-2020167432	A3	12/2020

OTHER PUBLICATIONS

"Result 7, NCBI Blast nucleotide search of SEQ ID: 1, database nr", (Jul. 18, 2006), 3 pgs.

"Result 1, NCBI Blast nucleotide search of SEQ ID No. 3, database "nr"; Result 4, NCBI Blast nucleotide search of SEQ ID No. 4, database nr", (Jul. 22, 2006), 11 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"Result 2, NCBI Blast nucleotide search of SEQ ID No. 5, database "nr"; Result 4, NCBI Blast nucleotide search of SEQ ID No. 6, database nr", (Jul. 22, 2006), 6 pgs.

"Results 1, NCBI Blast nucleotide search of SEQ ID No. 7, database "nr"; Result 1, NCBI Blast nucleotide search of SEQ ID No. 8, database nr", (Jul. 23, 2006), 8 pgs.

FLUMISTTM Package Insert Template, [Online]. Retrieved from the Internet: http://www.fda.gov/downloads/BiologicsBioodVaccines!Vaccines/ApprovedProducts/UCM294307.pdf, (Mar. 1, 2012), 26 pgs.

"1.A.32 The Type B Influenza Virus NB Channel (NB-C) Family", Transport Protein Database, (University of California, San Diego, The Sailer Laboratory Bioinformatics Group) [online}. Retrieved from the Internet: URL: http://www.web.archive.org/web/20030131105525 4/http://tcdb.ucsd.edu/tcdb/ tcfamilybrowse.php?tcname=1.A.32>, (Archived Jan. 31, 2003), 1 pg.

"Adaptation of Egg-Grown and Transfectant Influenza Viruses for Growth in Mammalian Cells: Selection of Hemagglutinin Mutants with Elevated pH of Membrane Fusion", Virology, vol. 233, Issue. 2, [Online]. Retrieved from the Internet: <URL: http://www.sciencedirect.com/ science/article/pii/S0042682297986268>, (1997), 402-410.

"Evaluation of Medicines for human Use", EMEA/CPMP/BWP/2289/01, London, The European Agency for the Evaluation of Medicinal Products, Committee for Proprietary Medicinal Products (CPMP), (Feb. 20, 2003), 14 pages.

"FLUZONE® Influenza Virus Vaccine", Sanofi Aventis Pasteur, Swiftwater, (Jul. 2005), 12 pgs.

"Gen Bank Accession AFP82914", matrix protein 1 [Influenza A virus (A/reassortant/IVR-148(Brisbane/59/2007 x Texas/1/1977) (H1N1))], (2012), 2 pgs.

"Gen Bank Accession JX414012", Influenza A virus (A/reassortant/IVR-148(Brisbane/59/2007 x Texas/1/1977)(H1 N1)) segment 7 matrix protein 2 (M2) and matrix protein 1 (M1) genes, complete cds, (2012), 2 pgs.

"Hemagglutinin [Influenza A virus (A/swine/France/WVL13/1995(H1N1))]", GenBank Accession# AC025026, (May 22, 2009), 1 pg.

"Hemagglutinin [Influenza B virus (B/Hong Kong/330/2001)]", GenBank ABL77178.1, (2006), 1 pg.

"Influenza B/lee/40, neuraminidase & nb (seg 6) rna", Database EM_VI E.B.I. Hinxton U.K., (Jun. 13, 1985), 10 pgs.

"Nonstructural protein 1 [influenza B virus (B/Hong Kong/330/2001)]", GenBank AAT69443.1, (2006), 1 pg.

"Polymerase acidic [influenza A virus (A/swine/Shizuoka/120/97(H3N2))]", GenBank AAO15329.1, (2003), 1 pg.

"Polymerase PA [Influenza B virus (B/Hong Kong/330/2001)]", GenBank ABL7718 6.1, (2006), 1 pg.

"Polymerase PB1 [Influenza B virus (B/Hong Kong/330/2001)]", GenBank ABL77187, (2006), 1 pg.

"Polymerase PB2 [Influenza B virus (B/Hong Kong/330/2001)] GenBank ABL77188.1", (2006), 1 pg.

"RecName: Full=Polymerase acidic protein {ECO:0000256|RuleBase;RU361280, ECO: 0000256|SAAS-:SAAS00262764}", XP002744257, retrieved from EBI accession No. UNIPR0T:A3R6C9 Database accession No. A3R6C9 the whole document, (Apr. 3, 2007), 1 pg.

"RecName: Full=Polymerase acidic protein {ECO:0000256|RuleBase;RU361280, ECO: 0000256|SAAS-:SAAS00262764}", XP002744258, retrieved from EBI accession No. UNIPROT:U3S198 Database accession No. U3S198 the whole document, (Dec. 11, 2013), 1 pg.

"The Influenza Virus: Structure and Replication", Rapid Reference to Influenza. Elsevier Ltd, [Online]. Retrieved from the Internet: URL: <http://www. rapidreferenceinfluenza.com/chapter/B978-0-7234-3433-7.50009-8/aim/influenza-virus-structure, (2006), 6 pgs.

"The Integral Membrane Proteins of Influenza A, B, and C Viruses", The Influenza Sequence Database, Retrieved from the Internet: <URL: http://www.flu.lanl.gov/review/fluc.review2.html, (Observed Feb. 26, 2003), 1 pg.

Air, Gillian M., et al., "Antigenic, Sequence, and Crystal Variation in Influenza B Neuraminidase", Virology, 177(2), (1990), 578-587.

Author Unknown, "New Approaches to Influenza Vaccine", Medscape—Infections in Medicine, http://www.medscape.com/viewarticle/417404_3, (Observed Feb. 26, 2003), 4 pgs.

Avetisyan, G, et al., "Cell-mediated immune responses to influenza vaccination in healthy volunteers and allogeneic stem cell transplant recipients", Bone Marrow Transplant, (2005), 411-415.

Avilov, Sergiy V., et al., "Influenza A virus progeny vRNP trafficking in live infected cells studied with the virus-encoded fluorescently tagged PB2 protein", Vaccine, 30, (2012), 7411-7417.

Avilov, Sergiy V., et al., "Replication-Competent Influenza A Virus That Encodes a Split-Green Fluorescent Protein-Tagged PB2 Polymerase Subunit Allows", Journal of Virology, 86, (2012), 1433-1448.

Baez, M., et al., "Complete nucleotide sequence of the influenza A/PR/8/34 virus NS gene and comparison with the NS genes of the A/Udorn/72 and A/FPV/Rostock/34 strains", Nucleic Acids Research, 23(8), (1980), 5845-5858.

Bancroft, C. T, et al., "Evidence for segment-nonspecific packaging of the influenza a virus genome", J Virol., 76(14), (Jul. 2002), 7133-7139.

Banerjee, A. K., et al., "Gene Expression of Vesicular Stomatitis Virus Genome RNA.", Virology, 188(2), (1992), 417-428.

Baron, M. D., et al., "Rescue of Rinderpest Virus From Cloned cDNA", Journal of Virology, 71(2), (1997), 1265-1271.

Basler, C. F, et al., "Mutation of Neuraminidase Cysteine Residues Yields Temprature-Sensitive Influenza Viruses", Journal of Virology, 73(10), (Jun. 30, 1999), 8095-8103.

Beare, A. S., "Trials in Man With Live Recombinants Made From A/PR/8/34 (H0 N1) and Wild H3 N2 Influenza Viruses", The Lancet, 2(7938), (1975), 729-732.

Betakova, T., et al., "The NB protein is an integral component of the membrane of influenza B virus.", J Gen Virol., 77 (Pt 11), (Nov. 1996), 2689-94.

Biere, Barbara, et al., "Differentiation of Influenza B Virus Lineages Yamagata and Victoria by Real-Time PCR", Journal of Clinical Microbiology, vol. 48, No. 4, (2010), 1425-1427.

Bourmakina, S. V, et al., "Reverse genetics studies on the Filamentous morphology of influenza A Virus", Journal of General Virology (2003) 84,, (2003), 517-527.

Bowie, J. U., et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions", Science, 247(4948), (1990), 1306-1310.

Boyer, J. C., et al., "Infectious transcripts and cDNA clones of RNA viruses", Virology, 198(2), (Feb. 1994), 415-426.

Brassard, D.L., et al., "Influenza B virus NB glycoprotein is a component of the virion", Virol., 220(2), No Document, (1996), 350-360.

Bridgen, A., et al., "Rescue of a Segmented Negative-Strand RNA Virus Entirely From Cloned Complementary DNAs", Proc. Natl. Acad. Sci. USA, 93, (1996), 15400-15404.

Brooke, C B, "Biological activities of 'noninfectious' influenza A virus particles", Future Virol 9(1), (Jan. 2014), 41-51.

Brown, E. G., et al., "Genetic analysis of mouse-adapted influenza A virus identifies roles for the NA, PB1, and PB2 genes in virulence", Virus Research, 61 (1), (May 1999), 63-76.

Buchholz, U. J., et al., "Generation of Bovine Respiratory Syncytial Virus (BRSV) From cDNA: BRSV NS2 is Not Essentiial for Virus Replication in Tissue Culture, and the Human RSV Leader Region Acts as a Functional BRSV Genome Promoter", Journal of Virology, 73(1), (1999), 251-259.

Bukreyev, A., et al., "Recovery of infectious respiratory syncytial virus expressing an additional, foreign gene", Journal of Virology, 70(10), (Oct. 1996), 6634-6641.

Cao, S., et al., "Characterization of the Nucleocytoplasmic Shuttle of the Matrix Protein of Influenza B Virus", Journal of Virology., 88(13), (Jul. 2014), 7464-7473.

(56) **References Cited**

OTHER PUBLICATIONS

Castrucci, Maria R., et al., "Reverse genetics system for generation of an influenza A virus mutant containing a deletion of the carboxyl-terminal residue of M2 protein.", J Virol., 69(5), (May 1995), 2725-2728.

Chan, Winnie, et al., "The cold adapted and temperature sensitive influenza A/Ann Arbor/6/60 virus, the master donor virus for live attenuated influenza vaccines, has multiple defects in replication at the restrictive temperature", Virology, 380(2), (2008), 304-311.

Chen, H, et al., "Generation and evaluation of a high-growth reassortant H9N2 influenza A virus as a pandemic vaccine candidate", Vaccine, 21(17-18), (May 16, 2003), 1974-1979.

Chen, Z., et al., "Influenza A Virus NS1 Protein Targets Poly(A)-Binding Protein II of the Cellular 3'-End Processing Machinery", The EMBO Journal, 18(8), (1999), 2273-2283.

Chevalie, Christophe, et al., "PB1-F2 Influenza A Virus Protein Adopts a B-Sheet Conformation and Forms Amyloid Fibers in Membrane Environments", The of Biological Chemistry, 285(17), (2010), 13233-13243.

Clarke, D. K., et al., "Rescue of Mumps Virus From cDNA", Journal of Virology, 74(10), (2000), 4831-4838.

Collins, P. L., et al., "Chapter 41—Parainfluenza Viruses", In: Fields Virology, edited by Fields, B. N., et al. (3rd Edition, 1996, Lippincott-Raven Publishers, Philadelphia, PA, 1205-1241.

Collins, P. L., et al., "Production of Infectious Human Respiratory Syncytial Virus From Cloned cDNA Confirms an Essential Role for the Transcription Elongation Factor From the 5' Proximal Open Reading Frame of the M2 mRNA in Gene Expression and Provides a Capability for Vaccine D", Proc. Natl. Acad. Sci. USA, 92, (1995), 11563-11567.

Collins, P. L., "Rescue of Synthetic Analogs of Respiratory Syncytial Virus Genomic RNA and Effect of Truncations and Mutations on the Expression of a Foreign Reporter Gene", Proc. Natl. Acad. Sci. USA, 88, (1991), 9663-9667.

Conzelmann, K.-K., "Genetic Engineering of Animal RNA Viruses", Trends in Microbiology, 4(10), (1996), 386-393.

Conzelmann, K.-K., "Genetic manipulation of non-segmented negative-strand RNA viruses", Journal of General Virology, 77(Pt. 3), (Mar. 1996), 381-389.

Conzelmann, K.-K., "Nonsegmented Negative-Strand RNA Viruses: Genetics and Manipulation of Viral Genomes", Annu. Rev. Genet., 32, (1998), 123-162.

Conzelmann, K.-K., "Rescue of Synthetic Genomic RNA Analogs of Rabies Virus by Plasmid-Encoded Proteins", Journal of Virology, 68(2), (1994), 713-719.

De, B. P., et al., "Requirements and Functions of Vesicular Stomatitis Virus L and NS Proteins in the Transcription Process in Vitro", Biochemical and Biophysical Research Communications, 126(1), (1985), 40-49.

De, B. P., et al., "Rescue of synthetic analogs of genome RNA of human parainfluenza virus type 3", Virology, 196(1), (Sep. 1993), 344-348.

De, B. P., et al., "Reverse Genetics of Negative Strand RNA Viruses", Indian Journal of Biochemistry & Biophysics, 31, (1994), 367-375.

De Filette, Marina, et al., "An influenza A vaccine based on tetrameric ectodomain of matrix protein 2", J Biol Chem. 2008 ; 283 (17):, (Feb. 5, 2008), 11382-7.

De La Luna, S., et al., "Influenza virus naked RNA can be expressed upon transfection into cells co-expressing the three subunits of the polymerase and the nucleoprotein from simian virus 40 recombinant viruses", Journal of General Virology, 74(pt. 3), (Mar. 1993), 535-539.

De La Luna, S., et al., "Influenza Virus NS1 Protein Enhances the Rate of Translation Initiation of Viral mRNAs", Journal of Virology, 69(4), (1995), 2427-2435.

Desheva, J. A, et al., "Characterization of an influenza A H5N2 reassortant as a candidate for live-attenuated and inactivated vaccines against highly pathogenic H5N1 viruses with pandemic potential", Vaccine, 24, (2006), 6859-6866.

Dimmock, Nigel J, et al., "In vivo antiviral activity: defective interfering virus protects better against virulent Influenza A virus than avirulent virus", Journal of General Virology 87, (Jan. 8, 2006), 1259-1265.

Dimock, K., et al., "Rescue of Synthetic Analogs of Genomic RNA and Replicative-Intermediate RNA of Human Parainfluenza Virus Type 3", Journal of Virology, 67(5), (1993), 2772-2778.

Dos Santos Afonso, Emmanuel, et al., "The generation of recombinant influenza A viruses expressing a PB2 fusion protein requires the conservation of a packaging signal overlapping the coding and noncoding regions at the 5V end of the PB2 segment", Virology, 341, (2005), 34-46.

Dreher, T. W., et al., "Mutational Analysis of the Sequence and Structural Requirements in Brome Mosaic Virus RNA for Minus Strand Promoter Activity", Journal of Molecular Biology, 201(1), (1988), 31-40.

Duff, K. C., et al., "The secondary structure of influenza A M2 transmembrane domain", FEBS Letters, 311 (3), (Oct. 1992), 256-258.

Duff, K. C., et al., "The Transmembrane Domain of Influenza A M2 Protein Forms Amantadine-Sensitive Proton Channels in Planar Lipid Bilayers", Vilology, 190(1), (Sep. 1992), pp. 485-489.

Dunham, Eleca J., et al., "Different Evolutionary Trajectories of European Avian-Like and Classical Swine H1N1 Influenza A Viruses", Journal of Virology, 83(11), (Jun. 2009), 5485-5494.

Dunn, E. F., et al., "Transcription of a recombinant bunyavirus RNA template by transiently expressed bunyavirus proteins", Virology, 211(1), (1995), 133-143.

Durbin, A. P., et al., "Recovery of infectious human parainfluenza virus type 3 from cDNA", Virology, 235(2), (Sep. 1, 1997), 323-332.

Elhefnawi, M, et al., "Identification of novel conserved functional motifs across most Influenza A viral strains", Virology Journal, 8:44, (2011), 10 pages.

Elliott, R. M., et al., "Rescue of Infectious Bunyavirus Entirely From Cloned cDNA", 10th International Conference on Negative Strand Virus, (Abstract No. 96), (1997), 1 pg.

Elliott, R. M., et al., "Some Highlights of Virus Research in 1990", Journal of General Virology, 72(Part 8), (1991), 1761-1779.

Emerson, S. U., et al., "Both NS and L Proteins Are Required for In Vitro RNA Synthesis by Vesicular Stomatitis Virus", Journal of Virology, 15(6), (1975), 1348-1356.

Enami, M., "An Influenza Virus Containing Nine Different RNA Segments", Virology, 185(1), (1991), 291-298.

Enami, M., et al., "High-Efficiency Formation of Influenza Virus Transfectants", Journal of Virology, 65(5), (1991), 2711-2713.

Enami, M., et al., "Introduction of Site-Specific Mutations Into the Genome of Influenza Virus", Proc. Natl. Acad. Sci. USA, 87, (1990), 3802-3805.

Fahey, J. L., et al., "Status of Immune-Based Therapies in HIV Infection and Aids", Clinincal and Experimental Immunology, 88(1), (1992), 1-5.

Fan, J, et al., "Preclinical study of influenza virus A M2 peptide conjugate vaccines in mice, ferrets, and rhesus monkeys", Vaccine, 22, (2004), 2993-3003.

Fischer, W. B, et al., "Viral ion channels: structure and function.", Biochim Biophys Acta., 1561(1), (Mar. 19, 2002), 27-45.

Fleming, D. M, et al., "Comparison of the efficacy and safety of live attenuated cold-adapted influenza vaccine, trivalent, with trivalent inactivated influenza virus vaccine in children and adolescents with asthma", Pediatr Infect Dis J., 25(10), (2006), 860-869.

Fodor, E., et al., "Rescue of Influenza A Virus from Recombinant DNA", Journal of Virology, 73(11), XP002151487; ISSN:0022-538X, (Nov. 1999), 9679-9682.

Forbes, Nicole E, et al., "Multifunctional Adaptive NS1 Mutations Are Selected upon Human Influenza Virus Evolution in the Mouse", Plos One, vol. 7, No. 2, (Feb. 21, 2012), 20 pgs.

Fortes, P., et al., "Influenza Virus NS1 Protein Inhibits Pre-mRNA Splicing and Blocks mRNA Nucleocytoplasmic Transport", The EMBO Journal, 13(3), (1994), 704-712.

(56) **References Cited**

OTHER PUBLICATIONS

Fujii, Ken, et al., "Importance of both the Coding and the Segment-Specific Noncoding Regions of the Influenza A Virus NS Segment for Its Ef?cient", Journal of Virology, 79(6), (Mar. 2005), 3766-3774.
Gao, Qinshan, et al., "A Nine-Segment In?uenza A Virus Carrying Subtype H1 and H3 Hemagglutinins†", Journal of Virology, 84(16), (Aug. 2010), 8062-8071.
Gao, Qinshan, et al., "The In?uenza A Virus PB2, PA, NP, and M Segments Play a Pivotal Role during Genome Packaging", Journal of Virology, 86(13), Chou, (Jul. 2011),7 043-7051.
Garcia-Sastre, A., et al., "Genetic Manipulation of Negative-Strand RNA Virus Genomes", Annu. Rev. Microbiol., 47, (1993), 765-790.
Garcin, D., et al., "A Highly Recombinogenic System for the Recovery of Infectious Sendai Paramyxovirus From cDNA: Generation of a Novel Copy-Back Nondefective Interfering Virus", The EMBO Journal, 14(24), (1995), 6087-6094.
Giddings, A M, et al., "The matrix protein of HIV-1 is not sufficient for assembly and release of virus-like particles", Virology, 248(1), (1998), 108-16.
Gorman, O T, et al., "Evolution of influenza A virus PB2 genes: implications for evolution of the ribonucleoprotein complex and origin of human influenza A virus", J. Virol., 64(10), (Oct. 1990), 4893-4902.
Gotea, V, et al., "The functional relevance of somatic synonymous mutations in melanoma and other cancers", Pigment Cell & Melanoma Research, 28 issue 6, (Nov. 1, 2015), 673-686.
Goto, H., "Mutations Affecting the Sensitivity of the Influenza Virus Neuraminidase to 4-Guanidino-2, 4-dideoxy 2, 3-dehydro-N-acetylneuraminic Acid", Virology, 238, (1997), 265-272.
Govorkova, E A, et al., "Replication of Influenza A Viruses in a Green Monkey Kidney Continuous Cell Line (Vero)", J. Infect. Dis. 172(1), (1995), 250-253.
Grambas, S., et al., "Influence of amantadine resistance mutations on the pH regulatory function of the M2 protein of influenza A viruses", Virology, 191(2), (Dec. 1992), 541-549.
Grosfeld, H., et al., "RNA Replication by Respiratory Syncytial Virus (RSV) Is Directed by the N, P, and L Proteins; Transcription Also Occurs Under These Conditions but Requires RSV Superinfection for Efficient Synthesis of Full-Length mRNA", Journal of Virology, 69(9), (1995), 5677-5686.
Hai, Rong, et al., "Influenza B Virus NS1-Truncated Mutants: Live-Attenuated Vaccine Approach", Journal of Virology, 82(21), (2008), 10580-10590.
Harty, Ronald N, "A Proline-Rich Motif within the Matrix Protein of Vesicular Stomatitis Virus and Rabies Virus Interacts with WW Domains of Cellular Proteins: Implications for Viral Budding", Journal of Virology, 73 (4), (1999), 2921-2929.
Hatada, E., et al., "Binding of Influenza A Virus NS1 Protein to dsRNA in vitro", Journal of General Virology, 73, (1992), 3325-3329.
Hatta, M., et al., "The NB protein of influenza B virus is not necessary for virus replication in vitro", Journal of Virology, 77(10), (May 2003), 6050-6054.
Hay, A. J., et al., "The role of the M2 protein in influenza A virus infection", Proceedings of the International Conference on Options for the Control of Influenza, Courchevel, (1992), 281-288.
He, B., et al., "Recovery of infectious SV5 from cloned DNA and expression of a foreign gene", Virology, 237(2), (1997), 249-260.
Helenius, A., "Unpacking the Incoming Influenza Virus", Cell, 69, (May 1992), pp. 577-578.
Hevey, Michael, et al., "Marburg virus vaccines based upon alphavirus replicons protect guinea pigs and nonhuman primates", Virology, 251(1), (Nov. 10, 1998), 28-37.
Hickman, Danielle, et al., "An avian live attenuated master backbone for potential use in epidemic and pandemic influenza vaccines", Journal of General Virology, 89(Part 11), (2008), 2682-2690.
Hiromoto, Y., et al., "Phylogenetic Analysis of the Three Polymerase Genes (PB1, PB2 and PA) of Influenza B Virus", Journal of General Virology, 81, (Apr. 2000), 929-937.
Hoffman, Lucas R, et al., "Structure-Based Identification of an Inducer of the Low-pH Conformational Change in the Influenza Virus Hemagglutinin: Irreversible Inhibition of Infectivity", Journal of Virology , vol. 71, No. 11, (Nov. 1997), 8808-8820.
Hoffman, M. A., et al., "An Infectious Clone of Human Parainfluenza Virus Type 3", Journal of Virology, 71(6), (1997), 4272-4277.
Hoffmann, E., et al., "A DNA transfection system for generation of influenza A virus from eight plasmids", Proc Natl Acad Sci U S A., 97(11), (May 23, 2000), 6108-13.
Hoffmann, E., et al., "Ambisense Approach for the Generation of Influenza A Virus: vRNA and mRNA Synthesis from One Template", Virology, 267, (2000), 310-317.
Hoffmann, E., et al., "Eight-plasmid System for Rapid Generation of Influenza Virus Vaccines", Vaccine, Butterworth Scientific Guildford, 20(25-56), (Aug. 19, 2002), 3165-3170.
Hoffmann, E., et al., "Rescue of Influenza B Virus from Eight Plasmids", Proceedings of the National Academy of Sciences of USA, National Academy of Science, 99(17), (Aug. 20, 2002), 11411-11416.
Holmes, E. C, et al., "Whole-Genome Analysis of Human Influenza A Virus Reveals Multiple Persistent Lineages and Reassortment Among Recent H3N2 Viruses", PLoS Biology, 3(9), (2005), 1579-1589.
Holsinger, L. J., et al., "Influenza A Virus M_2 Ion Channel Protein: a Structure-Function Analysis", Journal of Virology, 68 (3), (1994), 1551-1563.
Honda, Ayae, et al., "Differential Roles of Viral RNA and cRNA in Functional Modulation of the Influenza Virus RNA Polymerase", The Journal of Biological Chemistry, 276(33), (2001), 31179-31185.
Horimoto, "Designing Vaccines for Pandemic Influenza", Current Topics Microbiol Immunol 333, (2009), 165-176.
Horimoto, T., et al., "Enhanced growth of seed viruses for H5N1 influenza vaccines", Virology, 366(1), (Sep. 15, 2007), 23-27.
Horimoto, T., et al., "Generation of Influenza A Viruses with Chimeric (Type A/B) Hemagglutinins", Journal of Virology, 77(14), (2003), 8031-8038.
Horimoto, T., et al., "The Development and Characterization of H5 Influenza Virus Vaccines Derived from a 2003 Human Isolate", Vaccine, 24(17), (2006), 3669-3676.
Huang, T.-S., et al., "Determination of Influenza Virus Proteins Required for Genome Replication", Journal of Virology, 64(11), (1990), 5669-5673.
Hunt, R., "Virology—Chapter Eight—Vaccines: Past Successes and Future Prospects", Microbiology and Immunology On-Line, http://www.med.sc.edu:85/lecture/vaccines.htm, (Observed Feb. 26, 2003), 15 pgs.
Isakova-Sivak, Irina, et al., "Characterization of Reverse Genetics-Derived Cold-Adapted Master Donor Virus A/Leningrad/134/17/57 (H2N2) and Reassortants with H5N1 Surface Genes in a Mouse Model", Clinical and Vaccine Immunology, 21(5), (May 2014), 722-731.
Ives, J. A., et al., "The H274Y mutation in the influenza A/H1N1 neuraminidase active site following oseltamivir phosphate treatment leave virus severely compromised both in vitro and in vivo.", Antiviral Research, 55(2), (2002), 307-317.
Iwatsuki-Horimoto, K., et al., "The cytoplasmic tail of the influenza A virus M2 protein plays a role in viral assembly.", J Virol., 80(11), (Jun. 2006), 5233-40.
Jackson, D., et al., "A reverse genetics approach for recovery of recombinant influenza B viruses entirely from cDNA.", J Virol., 76(22), (Nov. 2002), 11744-7.
Jang, S.-W., et al., "Deoxygedunin, a Natural Product with Potent Neurotrophic Activity in Mice", PLoS ONE 5(7): e11528, (2010), 1-15.
Jasenosky, Luke D, et al., "Ebola Virus VP40-Induced Particle Formation and Association with the Lipid Bilayer", Journal of Virology, 75 (110, (Jun. 2001), 5205-5214.
Jiang, H, et al., "Influenza virus genome C4 promoter/origin attenuates its transcription and replication activity by the low polymerase recognition activity", Virology, 408(2), (2010), 190-196.
Kaplan, G., et al., "In vitro Synthesis of Infectious Poliovirus RNA", Proc. Natl. Acad. Sci. USA, 82, (1985), 8824-8428.

(56) **References Cited**

OTHER PUBLICATIONS

Katinger, D., et al., "Attenuated Influenza Viruses as a Vector for Mucosal Immunization Against HIV-1", Vaccines, 97, Cold Spring Harbor, (1997), 315-319.

Kato, A., et al., "Initiation of Sendai Virus Multiplication From Transfected cDNA or RNA With Negative or Positive Sense", Genes to Cells, 1, (1996), 569-579.

Kawaoka, Y, et al., "Sequence requirements for cleavage activation of influenza virus hemagglutinin expressed in mammalian cells", Proc Natl Acad Sci., 85(2), (1988), 324-328.

Kawaoka, Y., "Mutant Cells With Altered Sialic Acid", U.S. Appl. No. 11/644,179, filed Dec. 22, 2006, 51 pgs.

Kilbourne, E. D, et al., "Related studies of a recombinant influenza-virus vaccine. I. Derivation and characterization of virus and vaccine", J Infect Dis., 124(5), (Nov. 1971), 449-62.

Kim, H., et al., "Cold adaptation generates mutations associated with the growth of influenza B vaccine viruses", Vaccine, 33(43), (2015), 5786-5793.

Kimura, N., et al., "An In Vivo Study of the Replication Origin in the Influenza Virus Complementary RNA", The Journal of Biochemistry, 113(1), (1993), 88-92.

Kimura, N., et al., "Transcription of a Recombinant Influenza Virus RNA in Cells That Can Express the Influenza Virus RNA Polymerase and Nucleoprotein Genes", Journal of General Virology, 73, (1992), 1321-1328.

Kiseleva, I., et al., "Role of individual genes of the A-Leningrad/134/17/57 (H2N2) cold-adapted donor strain in manifestation of the temperature-sensitive phenotype of reassortant influenza A viruses", International Congress Series, vol. 1263, (2004), 547-550.

Kiseleva, Irina V, et al., "PB2 and PA genes control the expression of the temperature-sensitive phenotype of cold-adapted B/USSR/60/69 influenza master donor virus", Journal of General Virology, 91(4), (2010), 931-937.

Kistner, Otfried, et al., "Cell culture (Vero) derived whole virus (H5N1) vaccine based on wild-type virus strain induces cross-protective immune responses", Vaccine, 25(32), (2007), 6028-6036.

Kittel, Christian, et al., "Generation of an In?uenza A Virus Vector Expressing Biologically Active Human Interleukin-2 from the NS Gene Segment", Journal of Virology, 79(16), (Aug. 2005), 10672-10677.

Kobayashi, M., et al., "Reconstitution of Influenza Virus RNA Polymerase From Three Subunits Expressed Using Recombinant Baculovirus System", Virus Research, 22, (1992), 235-245.

Kochendoerfer, G. G, et al., "Total Chemical Synthesis of the Integral Membrane Protein Influenza A Virus M2: Role of its C-Terminal Domain in Tetramer Assembly", Biochemistry 38, (1999), 11905-11913.

Konarska, M. M., et al., "Structure of RNAs Replicated by the DNA-Dependent T7 RNA Polymerase", Cell, 63(2), (1990), 609-618.

Kovacova, A., et al., "Sequence similarities and evolutionary relationships of influenza virus A hemagglutinins.", Virus Genes, 24(1), (2002), 57-63.

Kovacova, Andrea, et al., "Sequence Similarities and Evolutionary Relationships of Influenza Vrus A Hemagglutinins", Virus Genes, 24(1), (2002), 57-63.

Krystal, M., et al., "Expression of the Three Influenza Virus Polymerase Proteins in a Single Cell Allows Growth Complementation of Viral Mutants", Proc. Natl. Acad. Sci. USA, 83, (1986), 2709-2713.

Krystal, M., "Influenza B/Lee/40, hemagglutinin (seg 4), complete segment.", Database EM_VI E.B.I. Hinxton U.K., (Apr. 25, 1990), 1 page.

Kunkel, T. A., "Rapid and Efficient Site-Specific Mutagenesis Without Phenotypic Selection", Proc. Natl. Acad. Sci. USA, 82, (1985), 488-492.

Lamb, Robert A., et al., "Chapter 20—Paramyxoviridae: The Viruses and Their Replication", In: Fundamental Virology, Fields, B. N., et al., editors, Lippincott-Raven (2nd Edition), (1996), 577-647.

Lawson, N. D., "Recombinant Vesicular Stomatitis Viruses From DNA", Proc. Natl. Acad. Sci. USA, 92(10), (1995), 4477-4481.

Lazarovits, Janette, et al., "Endocytosis of Chimeric Influenza Virus Hemaggulutinin Proteins That Lack a Cytoplasmic Recognition Feature for Coated Pits", The Journal of Cell Biology, vol. 134, No. 2, (1996), 339-348.

Lee, C. W, et al., "Generation of reassortant influenza vaccines by reverse genetics that allows utilization of a DIVA (Differentiating Infected from Vaccinated Animals) strategy for the control of avian influenza", Vaccine, vol. 22, (2004), 3175-3181.

Lee, Dong-Hun, et al., "Progress and hurdles in development of influenza virus-like particle vaccines for veterinary use", Korean Vaccine Society, (2014), 133-139.

Lee, Jong-Soo, et al., "The Highly Conserved HA2 Protein of the Influenza A Virus Induces a Cross Protective Immune Response", Journal of Virological Methods, 194(1-2), (2013), 280-288.

Lee, M. S, et al., "Genetic and pathogenic characterization of H6NI avian influenza viruses isolated in Taiwan between 1972 and 2005", Avian Diseases, 50(4), (Dec. 2006), 561-571.

Levis, R., et al., "Deletion Mapping of Sindbis Virus DI RNAs Derived From cDNAs Defines the Sequences Essential for Replication and Packaging", Cell, 44, (1986), 137-145.

Li, K. S., et al., "Genesis of a highly pathogenic and potentially pandemic H5N1 influenza virus in eastern Asia", Nature, vol. 430, (2004), 209-213 pgs.

Li, K. S, et al., "Genesis of a highly pathogenic and potentially pandemic H5NI influenza virus in eastern Asia", Nature, 430(6996), (Jul. 8, 2004), 209-213.

Li, Y, et al., "Viral liposomes released from insect cells infected with recombinant baculovirus expressing the matrix protein of vesicular stomatitis virus", Journal of Virology, 67(7), (1993), 4415-4420.

Lin, Y P, et al., "Adaptation of egg-grown and transfectant influenza viruses for growth in mammalian cells: selection of hemagglutinin mutants with elevated pH of membrane fusion", Virology, vol. 233, No. 2, (1997), 402-410.

Liu, BO, et al., "[Comparison of three methods in construction fusion gene of influenza A virus Nucleoprotein].", (English Abstract), Zhonghua Shi Yan He Lin Chuang Bing Du Xue Za Zhi, 26(1), 70-74, (Feb. 2012), 1 page.

Lu, Xiuhua, et al., "Cross-protective immunity in mice induced by live-attenuated or inactivated vaccines against highly pathogenic influenza A (H5N1) viruses", Vaccine, 24(44-46), (2006), 6588-6593.

Lugovtsev, V. Y., et al., "Genetic Composition and Mutational Pattern of Influenza B Viruses Adapted to Replication in Embryonated Eggs", GenBank: AAT69446.1, (2005), 1 page.

Luo, M., "Inhibitors of Influenza Virus Neuraminidase", Abstract No. WO296, from a paper presented at the Annual Meeting of the American Crystallographic Association, http://www.hwi.buffalo.edu/ACA/ACA98/abstracts/text/WO296.html, (Observed Feb. 27, 2003), 1 page.

Luytjes, W., "Amplification, Expression, and Packaging of a Foreign Gene by Influenza Virus", Cell, 59(6), (1989), 1107-1113.

Ma, Y.-J., et al., "Cellular micro RNA let-7c inhibits M1 protein expression of the H1N1 influenza A virus in infected human lung epithelial cells", J. Cell. Mol. Med., 16(10), (2012), 2539-2546.

Manicassamy, Balaji, et al., "Analysis of in vivo dynamics of influenza virus infection in mice using a GFP reporter virus", Proc Natl Acad Sci. USA, 107(25), (2010), 11531-11536.

Manz, Benjamin, et al., "Disruption of the Viral Polymerase Complex Assembly as a Novel Approach to Attenuate Influenza A Virus", The Journal of Biological Chemistry, 286(10), (2011), 8414-8424.

Mark, A, et al., "Effect of Mutations and Deletions in a Bicistronic mRNA on the Synthesis of Influenza B Virus NB and NA Glycoproteins", Journal of Virology, vol. 77, No. 10, (May 2003), 6050-6054.

Matsuoka, et al., "Neuraminidase Stalk Length and Additional Glycosylation of the Hemagglutinin Influence the Virulence of Influenza H5N1 Viruses for Mice", Journal of Virology, vol. 83, No. 9,, (2009), 4704-4708.

(56) **References Cited**

OTHER PUBLICATIONS

Matsuzaki, Y., et al., "Epitope Mapping of the Hemagglutinin Molecule of A/(H1N1)pdm09 Influenza Virus by Using Monoclonal Antibody Escape Mutants", Journal of Virology, 88(21), (2014), 12364-12373.

McCown, M F, et al., "The influenza A virus M2 cytoplasmic tail is required for infectious virus production and efficient genome packaging. ", J Virol., 79(6), (Mar. 2005), 3595-3605.

McCown, M. F, et al., "Distinct domains of the influenza a virus M2 protein cytoplasmic tail mediate binding to the M1 protein and facilitate infectious virus production.", J Virol., 80(16), (Aug. 2006), 8178-8189.

McKimm, J. L., et al., "Mutations in a Conserved Residue in the Influenza Virus Neuraminidase Active Site Decreases Sensitivity to Neu5Ac2en-Derived Inhibitors", Journal of Virology, 72(3), (1998), 2456-2462.

Mebatsion, Teshome, et al., "Budding of Rabies Virus Particles in the Absence of the Spike Glycoprotein", Cell, 84(6), (1996), 941-951.

Mebatsion, Teshome, et al., "Matrix Protein of Rabies Virus Is Responsible for the Assembly and Budding of Bullet-Shaped Particles and Interacts with the Transmembrane Spike Glycoprotein G", Journal of Virology, 73 (1), (Jan. 1999), 242-250.

Mena, I., "Rescue of a Synthetic Choramphenicol Acetyltransferase RNA into influenza Virus-Like Particles obtained from recombinant plasmids", Journal of Virology, 70(8), (1996), 5016-5024.

Mena, I., et al., "Synthesis of Biologically Active Influenza Virus Core Proteins Using a Vaccinia Virus-T7 RNA Polymerase Expression System", Journal of General Virology, 75, (1994), 2109-2114.

Mitnaul, et al., "The Cytoplasmic Tail of Influenza a Virus Neuraminidase (NA) Affects NA Incorporation into Virons, Viron Morphology, and Virulence in Mice but is not essential for Virus Replication", Journal of Virology, 70 (2), (1996), 873-879.

Monto, Arnold S, et al., "Comparative efficacy of inactivated and live attenuated influenza vaccines.", N Engl J Med., 361(13), (Sep. 24, 2009), 1260-1267.

Moyer, S. A., et al., "Assembly and Transcription of Synthetic Vesicular Stomatitis Virus Nucleocapsids", Journal of Virology, 65(5), (1991), 2170-2178.

Murakami, "Enhanced Growth of Influenza Vaccine Seed Viruses in Vero Cells Mediated by Broadening the Optimal pH Range for Virus Membrane Fusion", J Virol 86(3), (2012), 1405-1410.

Murakami, Shin, et al., "Growth Determinants for H5N1 Influenza Vaccine Seed Viruses in MDCK Cells", Journal of Virology, vol. 82, No. 21, (Nov. 2008), 10502-10509.

Murphy, Brian R, et al., "Virulence of Avian Influenza A Viruses for Squirrel Monkeys", Infection and Immunity 37 (3), (Sep. 1982), 1119-1126.

Muster, T., et al., "An Influenza A Virus Containing Influenza B Virus 5' and 3' Noncoding Regions on the Neuraminidase Gene is Attenuated in Mice", Proc. Natl. Acad. Sci. USA, 88, (1991), 5177-5181.

Naito, S., et al., "Function and Structure of RNA Polymerase From Vesicular Stomatitis Virus", The Journal of Biological Chemistry, 251(14), (1976), 4307-4314.

Nara, P. L., et al., "Simple, Rapid, Quantitative, Syncytium-Forming Microassay for the Detection of Human Immunodeficiency Virus Neutralizing Antibody", Aids Research and Human Retroviruses, 3(3), (1987), 283-302.

Neirynck, S., "A universal influenza A vaccine based on the extracellular domain of the M2 protein", Nature Medicine, 5 (10), (Oct. 1999), 1157-1163.

Nemeroff, M. E., et al., "Influenza Virus NS1 Protein Interacts With the Cellular 30 kDa Subunit of CPSF and Inhibits 3' End Formation of Cellular Pre-mRNAs", Molecular Cell, 1(7), (1998), 991-1000.

Neumann, G., et al., "An improved reverse genetics system for influenza A virus generation and its implications for vaccine production", Proc. Natl. Acad. Sci. USA. 102(46), (2005), 16825-16829.

Neumann, G., et al., "Emergence and pandemic potential of swine-origin HIN1 influenza virus", Nature (London), 459(7249), (Jun. 2009), 931-939.

Neumann, G., et al., "Generation of influenza A virus from cloned cDNAs—historical perspective and outlook for the new millenium. ", Rev Med Virol., 12(1), XP002314285, (Jan.-Feb. 2002), 13-30.

Neumann, G., et al., "Generation of influenza A viruses entirely from cloned cDNAs", Proc. Natl. Acad. Sci. USA., 96(16), (1999), 9345-9350.

Neumann, G., et al., "Mutational analysis of influenza virus promoter elements in vivo", Journal of General Virology, 76, (1995), 1709-1717.

Neumann, G., et al., "Plasmid-driven formation of influenza virus-like particles", J Virol., 74(1), [Online]. Retrieved from the Internet: <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC111569/>, (Jan. 2000), 547-551.

Neumann, G., et al., "Reverse Genetics of Influenza Viruses—Applications in Research and Vaccine Design", Monographs in Virology, 27, (2008), 118-133.

Neumann, G., et al., "RNA Polymerase I-Mediated Expression of Influenza Viral RNA Molecules", Virology, 202(1), (1994), 477-479.

Neumann, Gabriele, et al., "Reverse Genetics Demonstrates that Proteolytic Processing of the Ebola Virus Glycoprotein Is Not Essential for Replication in Cell Culture", Journal of Virology, 76 (1), (Jan. 2002), 406-410.

Noda, Takeshi, et al., "Three-dimensional analysis of ribonucleoprotein complexes in influenza A virus", Nature Communications, 3, (2012), 1-6.

Odagiri, T., et al., "Nucleotide Sequence of the PA Gene of Influenza A/WSN/33 (H1N1)", Nucleic Acids Research, 18(3), Department of Virology, (Jan. 9, 1990), 1 page.

Orkin, S. H, et al., "Report and Recommendations of the Panel to Assess the NIH Investment in Research on Gene Therapy", http://www.nih.gov/news/panelrep.html, (Dec. 7, 1995), 37 pgs.

Ozaki, "Generation of High-Yielding Influenza A Viruses in African Green Monkey Kidney (Vero) Cells by Reverse Genetics", J Virol 78(4), (2004), 1851-1857.

Palese, P., et al., "47. Orthomyxoviridae: The Viruses and Their Replication", In: Fields Virology (5th Edition), (2007), 90 pgs.

Palese, P., "Negative-Strand RNA Viruses: Genetic Engineering and Applications", Proc. Natl. Acad. Sci. USA, 93(21), (1996), 11354-11358.

Park, Eun K., et al., "The M2 Ectodomain is important for its incorporation into influenza A virions", J. of Virology, vol. 72, No. 3, XP002196797, (Mar. 1998), 2449-2455.

Park, K. H., et al., "Rescue of a Foreign Gene by Sendai Virus", Proc. Natl. Acad. Sci. USA, 88, (1991), 5537-5541.

Pattnaik, A. K., et al., "Cells That Express All Five Proteins of Vesicular Stomatitis Virus From Cloned cDNAs Support Replication, Assembly, and Budding of Defective Interfering Particles", Proc. Natl. Acad. Sci. USA, 88(4), (1991), 1379-1383.

Peeters, B. P. H., et al., "Rescue of Newcastle Disease Virus From Cloned cDNA: Evidence That Cleavability of the Fusion Protein Is a Major Determinant for Virulence", Journal of Virology, 73(6), (1999), 5001-5009.

Pekosz, A., "Commentary—Reverse Genetics of Negative-Strand RNA Viruses: Closing the Circle", Proc. Natl. Acad. Sci. USA, 96, (1999), 8804-8806.

Pekosz, A., et al., "Influenza C virus CM2 integral membrane glycoprotein is produced from a polypeptide precursor by cleavage of an internal signal sequence", PNAS, vol. 95, XP002196653, (Oct. 1998), 13233-13238.

Percy, N., et al., "Expression of a Foreign Protein by Influenza A Virus", Journal of Virology, 68(7), (1994), 4486-4492.

Perez, Jasmine T., et al., "UNIT 15G.4—Insertion of a GFP Reporter Gene in Influenza Virus", Curr Protoc Microbiol., (2013), 20 pgs.

Piller, S C., et al., "Vpr protein of human immunodeficiency virus type 1 forms cation-selective channels in planar lipid bilayers", PNAS, 93, (1996), 111-1115.

Ping, J., et al., "Development of high-yield influenza B virus vaccine viruses", Proc. Natl. Acad. Sci. USA, 113(51), (2016), E8296-E8305, and 25 pgs of Supplemental Material.

(56) **References Cited**

OTHER PUBLICATIONS

Ping, Jihui, et al., "Development of high-yield influenza A virus vaccine viruses", Nature Communications, [online]. Retrieved from the Internet: <http://www.nature.eom/article-assets/npg/ncomms/2015/150902/ncomms9148/extref/ncomms9148-sl.pdf>, (Sep. 2, 2015), 50 pgs.

Pinto, L. H., et al., "Influenza Virus M2 Protein Has Ion Channel Activity", Cell, 69, (May 1992), 517-528.

Plant, E P, et al., "Mutations to A/PuertoRico/8/34 PB1 gene improves seasonal reassortant influenza A virus growth kinetics", Vaccine, 31(1), (Dec. 1, 2012), 207-212 pgs.

Pleschka, S., et al., "A Plasmid-Based Reverse Genetics System for Influenza A Virus", Journal of Virology, 70(6), (1996), 4188-4192.

Qiu, Y., et al., "The Influenza Virus NS1 Protein Binds to a Specific Region in Human U6 snRNA and Inhibits U6-U2 and U6-U4 snRNA Interactions During Splicing", RNA, 1, (1995), 304-316.

Qiu, Y., et al., "The Influenza Virus NS1 Protein Is a Poly(A)-Binding Protein That Inhibits Nuclear Export of mRNAs Containing Poly(A)", Journal of Virology, 68(4), (1994), 2425-2432.

Racaniello, V. R., et al., "Cloned Poliovirus Complimentary DNA Is Infectious in Mammalian Cells", Science, 214, (1981), 916-919.

Radecke, F., et al., "Rescue of Measles Viruses From Cloned DNA", The EMBO Journal, 14(23), (1995), 5773-5784.

Radecke, F., et al., "Reverse Genetics Meets the Nonsegmented Negative-Strand RNA Viruses", Reviews in Medical Virology, 7, (1997), 49-63.

Ramanunninair, Manojkumar, et al., "Molecular Signature of High Yield (Growth) Influenza A Virus Reassortants Prepared as Candidate Vaccine Seeds", PLoS ONE, 8(6): e65955, (2013), 1-16.

Reed, M. L, et al., "Amino Acid Residues in the Fusion peptide Pocket Regulate the pH of Activation of the H5N1 Influenza Virus Hemagglutinin Protein", . J. Virol., 83(8), (2009), 3568-3580.

Roberts, A., et al., "Minireview—Recovery of Negative-Strand RNA Viruses From Plasmid DNAs: A Positive Approach Revitalizes a Negative Field", Virology, 247(1), (1998), 1-6.

Romanova, J., et al., "Live cold-adapted influenza A vaccine produced in Vero cell line", Virus Research, 103, (2004), 187-193.

Rose, J. K., "Positive Strands to the Rescue Again: A Segmented Negative-Strand RNA Virus Derived From Cloned cDNAs", Proc. Natl. Acad. Sci. USA, 94, (1996), 14998-15000.

Ruigrok, R W, et al., "Characterization of three highly purified influenza virus strains by electron microscopy", J Gen Virol 65 (Pt 4), (Apr. 1984), 799-802.

Ruigrok, R W, et al., "Structural Characterization and Membrane Binding Properties of the Matrix Protein VP40 of Ebola Virus", Journal of Molecular Biology, 300(1), (2000), 103-112.

Sansom, M. S., et al., "Influenza virus M2 Protein: a molecular modelling study of the ion channel", Protein Engineering, 6 (1), (1993), 65-74.

Schickli, J. H, et al., "Plasmid-only Rescue of Influenza A Virus Vaccine Candidates", Philosophical Transactions of the Royal Society of London. Series B, Biological Sciences, 356(1416), (Dec. 29, 2001), 1965-1973.

Schlesinger, S., "RNA Viruses as Vectors for the Expression of Heterologous Proteins", Molecular Biotechnology, 3(2), (1995), 155-165.

Schnell, M. J., "Infectious Rabies Viruses From Cloned cDNA", The EMBO Journal, 13(18), (1994), 4195-4203.

Schnell, Matthias J, et al., "Requirement for a non-specific glycoprotein cytoplasmic domain sequence to drive efficient budding of vesicular stomatitis virus", EMBO Journal, 17 (5), (1998), 1289-1296.

Schotsaert, M, et al., "Universal M2 ectodomain-based influenza A vaccines: preclinical and clinical developments", Expert Rev V accines. Apr. 2009;8(4), 499-508.

Seong, B. L., et al., "A New Method for Reconstituting Influenza Polymerase and RNA in Vitro: A Study of the Promoter Elements for cRNA and vRNA Synthesis in Vitro and Viral Rescue in Vivo", Virology, 186(1), (1992), 247-260.

Shinya, Kyoko, et al., "Characterization of a Neuraminidase-Deficient Influenza A Virus as a Potential Gene Delivery Vector and a Live Vaccine", Journal of Virology, 78(6), (2004), 3083-3088.

Sidhu, M. S., et al., "Rescue of Synthetic Measles Virus Minireplicons: Measles Genomic Termini Direct Efficient Expression and Propagation of a Reporter Gene", Virology, 208, (1995), 800-807.

Skehel, J. J., et al., "On the Mechanism of Inhibition of Influenza Virus Replication by Amantadine Hydrochloride", The Journal of General Virology, 38 (1), (1977), 97-110.

Smeenk, et al., "Mutations in the Hemagglutinin and Matrix Genes of a Virulent Influenza Virus Variant, A/FM/1/47-MA, Control Different Stages in Pathogenesis", Virus Research 44, (1996), 79-95.

Subbarao, E. K., et al., "Sequential Addition of Temperature-Sensitive Missense Mutations into the PB2 Gene of Influenza A Transfectant Viruses Can Effect an Increase in Temperature Sensitivity and Attenuation and Permits the Rational Design of a Genetically Engineered Live Influen", Journal of Virology, 69(10), (1995), 5969-5977.

Subbarao, K., et al., "Evaluation of a Genetically Modified Reassortant H5N1 Influenza A Virus Vaccine Candidate Generated by Plasmid-based Reverse Genetics", Virology, vol. 305(1), (Jan. 5, 2003), 192-200.

Sugrue, R. J., et al., "Specific structural alteration of the influenza haemagglutinin by amantadine", The EMBO Journal, 9 (11), (1990), 3469-3476.

Sugrue, R. J., et al., "Structural Characteristics of the M2 Protein of Influenza A Viruses: Evidence That It Forms a Tetrameric Channel", Virology, 180, (1991), pp. 617-624.

Suguitan, A. L, et al., "Live, Attenuated Influenza A H5N1 Candidate Vaccines Provide Broad Cross-Protection in Mice and Ferrets", PLoS Med., 3(9), (2006), 1541-1555.

Sunstrom, N. A., et al., "Ion Channels formed by NB, an influenza B virus Protein", J. of Membrane Biology, vol. 150, XP002196654, (Dec. 1996), 127-132.

Sweet, T. M., et al., "Creation of amantadine resistant clones of influenza type A virus using a new transfection procedure.", J Virol Methods., 69(1-2), (Dec. 1997), 103-111.

Szewczyk, B., "Purification, Thioredoxin Renaturation, and Reconstituted Activity of the Three Subunits of the Influenza A Virus RNA Polymerase", Proc. Natl. Acad. Sci. USA, 85, (1988), 7907-7911.

Takeda, M., et al., "Influenza a virus M2 ion channel activity is essential for efficient replication in tissue culture.", J Virol., 76(3), (Feb. 2002), 1391-1399.

Takeuchi, K., et al., "Influenza Virus M2 Protein Ion Channel Activity Stabilizes the Native Form of Fowl Plague Virus Hemagglutinin during Intracellular Transport", Journal of Virology, 68 (2), (Feb. 1994), 911-919.

Tannock, G. A, et al., "Relative immunogenicity of the cold-adapted influenza virus A/Ann Arbor/6/60 (A/AA/6/60-ca), recombinants of A/AA/6/60-ca, and parental strains with similar surface antigens.", Infect Immun., 43(2), (Feb. 1984), 457-462.

Taylor, J., et al., "Newcastle Disease Virus Fusion Protein Expressed in a Fowlpox Virus Recombinant Confers Protection in Chickens", Journal of Virology, 64(4), (1990), 1441-1450.

Tobler, K, et al., "Effect of cytoplasmic tail truncations on the activity of the M(2) ion channel of influenza A virus", J Virol., 73(12), (Dec. 1999), 9695-9701.

Uraki, R., et al., "A Novel Bivalent Vaccine Based on a PB2-Knockout Influenza Virus Protects Mice from Pandemic H1N1 and Highly Pathogenic H5N1 Virus Challenges", Journal of Virology, 87(14), (2013), 7874-7881.

Verma, I. M, et al., "Gene Therapy—Promises, Problems and Prospects", Nature, 389, (1997), 239-242.

Voeten, J. T, et al., "Characterization of high-growth reassortant influenza A viruses generated in MDCK cells cultured in serum-free medium", Vaccine, vol. 17, (1999), 1942-1950.

Volchkov, Viktor E, et al., "Recovery of Infectious Ebola Virus from Complementary DNA: RNA Editing of the GP Gene and Viral Cytotoxicity", Science Magazine, 291, (Mar. 2001), 1965-1969.

(56) **References Cited**

OTHER PUBLICATIONS

Wagner, R., et al., "Interdependence of hemagglutinin glycosylation and neuraminidase as regulators of influenza virus growth: a study by reverse genetics", Journal of Virology, 74 (14), (Jul. 2000), 6316-6323.

Wang, C., et al., "Ion Channel Activity of Influenza A Virus M2 Protein: Characterization of the Amantadine Block", Journal of Virology, 67 (9), (Sep. 1993), 5585-5594.

Wang, Wenlig, et al., "Robust Immunity and Heterologous Protection against Influenza in Mice Elicited by a Novel Recombinant NP-M2e Fusion Protein Expressed in *E. coli*", PLoS ONE 7(12): e52488, (Dec. 2012), 1-13.

Ward, C. D., et al., "Direct Measurement of the Poliovirus RNA Polymerase Error Frequency In Vitro", Journal of Virology, 62(2), (1988), 558-562.

Wareing, M. D, et al., "Immunogenic and isotype-specific responses to Russian and US cold-adapted influenza a vaccine donor strains A/Leningrad/134/17/57, A/Leningrad/134/47/57, and A/Ann Arbor/6/60 (H2N2) in mice.", J Med Virol., 65(1), (Sep. 2001), 171-177.

Watanabe, S., et al., "Influenza A Virus Lacking M2 Protein as a Live Attenuated Vaccine", Journal of Virology, 83(11), (2009), 5947-5950.

Watanabe, T., et al., "Influenza A virus can undergo multiple cycles of replication without M2 ion channel activity", J Virol., 75(12), (Jun. 2001), 5656-5662.

Watanabe, T., et al., "Influenza A Virus with Defective M2 Ion Channel Activity as a Live Vaccine", Virology, 299(2), (Aug. 1, 2002), 266-270.

Watanabe, T., et al., "Novel Approach to the Development of Effective H5N1 Influenza A Virus Vaccines: Use of M2 Cytoplasmic Tail Mutants", Journal of Virology, 82(5), (2008), 2486-2492.

Watanabe, Tokiko, et al., "Exploitation of Nucleic Acid Packaging Signals To Generate a Novel Influenza Virus-Based Vector Stably Expressing Two Foreign Genes", Journal of Virology, 77(19), (Oct. 2003), 10575-10583.

Watanabe, Tokiko, et al., "Influenza A Virus Can Undergo Multiple Cycles of Replication without M2 Ion Channel Activity", Journal of Virology 75(12), (2001), 5656-5662.

Wei, Hung-Ju, et al., "Fabrication of influenza virus-like particles using M2 fusion proteins for imaging single viruses and designing vaccines", Vaccine, 29, (2011), 7163-7172.

Whelan, S. P. J., et al., "Efficient Recovery of Infectious Vesicular Stomatitis Virus Entirely from cDNA Clones", Proc. Natl. Acad. Sci. USA, 92, (1995), 8388-8392.

Williams, Mark A., et al., "Effect of Mutations and Deletions in a Bicistronic mRNA on the Synthesis of Influenza B Virus NB and NA Glycoproteins", Journal of Virology, 63(1), (1989), 28-35.

Wilson, Julie A, et al., "Epitopes Involved in Antibody-Mediated Protection from Ebola Virus", Science, 287(5458), (Mar. 2000), 1664-1666.

Winter, G., et al., "The use of synthetic oligodeoxynucleotide primers in cloning and sequencing segment 8 of influenza virus (A/PR/8/34)", Nucleic Acids Res., 9(2), (1981), 237-245.

Wu, Rui, et al., "A live bivalent influenza vaccine based on a H9N2 virus strain", Vaccine, 28, (2010), 673-680.

Xu, X., et al., "Reassortment and evolution of current human influenza A and B viruses", Virus Research, 103, (2004), 55-60.

Yamanaka, K., et al., "In vivo Analysis of the Promoter Structure of the Influenza Virus RNA Genome Using a Transfection System With an Engineered RNA", Proc. Natl. Acad. Sci. USA, 88, (1991), 5369-5373.

Yannarell, Dean A., et al., "Factors affecting the yield of cold-adapted influenza virus vaccine", Journal of Virological Methods, vol. 64, 161-169, (1997), 1 page.

Yi, Pu Lin, et al., "Adaptation of Egg-Grown and Transfectant Influenza Viruses for Growth in Mammalian Cells: Selection of Hemagglutinin Mutants with Elevated pH of Membrane Fusion", Virology, 233(2), (Jul. 7, 1997), 402-410.

Yu, Q., et al., "Functional cDNA Clones of the Human Respiratory Syncytial (RS) Virus N, P, and L Proteins Support Replication of RS Virus Genomic RNA Analogs and Define Minimal trans-Acting Requirements for RNA Replication", Journal of Virology, 69(4), (1995), 2412-2419.

Yusoff, K., et al., "Nucleotide Sequence Analysis of the L Gene of Newcastle Disease Virus: Homologies With Sendai and Vesicular Stomatitis Viruses", Nucleic Acids Research, 15(10), (1987), 3961-3976.

Zaghouani, H, et al., "Induction of Antibodies to the Envelope Protein of the Human Immunodeficiency Virus by Immunization With Monoclonal Anti-Idiotypes", Proc. Natl. Acad. Sci. USA, 88, (1991), 5645-5649.

Zaghouani, H., et al., "Cells Expressing an H Chain 1g Gene Carrying a Viral T Cell Epitope are Lysed by Specific Cytolytic T Cells", The Journal of Immunology, 148(11), (1992), 3604-3609.

Zebedee, S. L, et al., "Characterization of the Influenza Virus M2 Integral Membrane Protein and Expression at the Infected-Cell Surface from Cloned cDNA", Journal of Virology, 56(2), (Nov. 1985), 502-511.

Zhang, H., et al., "Expression of Functional Influenza Virus A Polymerase Proteins and Template From Cloned cDNAs in Recombinant Vaccinia Virus Infected Cells", Biochemical and Biophysical Research Communications, 200(1), (1994), 95-101.

Zobel, A., et al., "RNA Polymerase I Catalysed Transcription of Insert Viral cDNA", Nucleic Acids Research, 21(16), (1993), 3607-3614.

"U.S. Appl. No. 09/834,095, Advisory Action dated Jan. 8, 2004", 3 pgs.

"U.S. Appl. No. 09/834,095, Final Office Action dated Aug. 26, 2003", 12 pgs.

"U.S. Appl. No. 09/834,095, Non-Final Office Action dated Nov. 4, 2002", 12 pgs.

"U.S. Appl. No. 09/834,095, Notice of Allowance dated Sep. 27, 2004", 13 pgs.

"U.S. Appl. No. 09/834,095, Office Action dated Apr. 20, 2004", 11 pgs.

"U.S. Appl. No. 09/834,095, Response filed Feb. 4, 2003 to Office Action dated Nov. 4, 2002", 14 pgs.

"U.S. Appl. No. 09/834,095, Response filed Jun. 12, 2003 to Restriction Requirement dated Apr. 22, 2003", 2 pgs.

"U.S. Appl. No. 09/834,095, Response filed Jun. 18, 2004 to Office Action dated Apr. 20, 2004", 11 pgs.

"U.S. Appl. No. 09/834,095, Response filed Aug. 1, 2002 to Restriction Requirement dated Jul. 1, 2002", 3 pgs.

"U.S. Appl. No. 09/834,095, Response filed Nov. 26, 2003 to Final Office Action dated Aug. 26, 2003", 10 pgs.

"U.S. Appl. No. 09/834,095, Restriction Requirement dated Apr. 22, 2003", 5 pgs.

"U.S. Appl. No. 09/834,095, Restriction Requirement dated Jul. 1, 2002", 9 pgs.

"U.S. Appl. No. 09/834,095, Supplemental Amendment filed Aug. 4, 2004", 7 pgs.

"U.S. Appl. No. 10/827,995, Final Office Action dated Nov. 15, 2006", 10 pgs.

"U.S. Appl. No. 10/827,995, Non-Final Office Action dated Jun. 2, 2006", 15 pgs.

"U.S. Appl. No. 10/827,995, Non-Final Office Action dated Oct. 25, 2007", 7 pgs.

"U.S. Appl. No. 10/827,995, Notice of Allowance dated Feb. 17, 2009", 9 pgs.

"U.S. Appl. No. 10/827,995, Notice of Allowance dated Jul. 2, 2008", 9 pgs.

"U.S. Appl. No. 10/827,995, Notice of Allowance dated Oct. 17, 2008", 7 pgs.

"U.S. Appl. No. 10/827,995, Notice of Non-Compliant Amendment dated Jul. 25, 2007", 4 pgs.

"U.S. Appl. No. 10/827,995, Proposed Examiner's Amendment dated Jun. 5, 2008", 6 pgs.

"U.S. Appl. No. 10/827,995, Response filed Mar. 3, 2008 to Office Action dated Oct. 25, 2007", 10 pgs.

"U.S. Appl. No. 10/827,995, Response filed May 14, 2007 Final Office Action dated Nov. 15, 2006", 16 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"U.S. Appl. No. 10/827,995, Response filed Aug. 13, 2007 to Notice of Non-Compliant Amendment dated Jul. 25, 2007", 16 pgs.
"U.S. Appl. No. 10/827,995, Response filed Aug. 17, 2006 Non-Final Office Action dated Jun. 2, 2006", 15 pgs.
"U.S. Appl. No. 10/855,875 , Response filed May 17, 2012 to Non Final Office Action dated Mar. 15, 2012", 15 pgs.
"U.S. Appl. No. 10/855,875, Final Office Action dated Mar. 11, 2008", FOAR, 20 Pgs.
"U.S. Appl. No. 10/855,875, Final Office Action dated Dec. 10, 2010", 15 pgs.
"U.S. Appl. No. 10/855,875, Final Office Action dated Aug. 2, 2006", 34 pgs.
"U.S. Appl. No. 10/855,875, Non Final Office Action dated Mar. 15, 2012", 15 pgs.
"U.S. Appl. No. 10/855,875, Non-Final Office Action dated Feb. 19, 2010", 7 pgs.
"U.S. Appl. No. 10/855,875, Non-Final Office Action dated Aug. 7, 2009", 32 pgs.
"U.S. Appl. No. 10/855,875, Non-Final Office Action dated Nov. 6, 2008", 12 pgs.
"U.S. Appl. No. 10/855,875, Non-Final Office Action dated Nov. 30, 2005", 13 pgs.
"U.S. Appl. No. 10/855,875, Non-Final Office Action dated May 3, 2007", 13 pgs.
"U.S. Appl. No. 10/855,875, Notice of Allowance dated Mar. 4, 2013", 8 pgs.
"U.S. Appl. No. 10/855,875, Preliminary Amendment filed Feb. 2, 2007", 14 pgs.
"U.S. Appl. No. 10/855,875, Response filed Jan. 29, 2007 to Final Office Action dated Aug. 2, 2007", 14 pgs.
"U.S. Appl. No. 10/855,875, Response filed Mar. 18, 2011 to Final Office Action dated Dec. 10, 2010", 15 pgs.
"U.S. Appl. No. 10/855,875, Response filed Aug. 17, 2010 to Non Final Office Action dated Feb. 19, 2010", 20 pgs.
"U.S. Appl. No. 10/855,875, Response filed Dec. 7, 2009 to Non Final Office Action dated Aug. 7, 2009", 15 pgs.
"U.S. Appl. No. 10/855,875, Response filed Mar. 31, 2009 to Non Final Office Action dated Nov. 6, 2008", 14 pgs.
"U.S. Appl. No. 10/855,875, Response filed May 1, 2006 Non-Final Office Action dated Nov. 30, 2005", 13 pgs.
"U.S. Appl. No. 10/855,875, Response filed Aug. 18, 2008 to final Office Action dated Mar. 11, 2008", 15 pgs.
"U.S. Appl. No. 10/855,875, Response filed Sep. 20, 2005 to Restriction Requirement dated Jul. 26, 2005", 4 pgs.
"U.S. Appl. No. 10/855,875, Restriction Requirement dated Dec. 23, 2011", 9 pgs.
"U.S. Appl. No. 10/855,875, Restriction Requirement dated Jul. 26, 2005", 9 pgs.
"U.S. Appl. No. 10/855,875, Response filed Nov. 2, 2007 to Office Action dated May 3, 2007", 16 pgs.
"U.S. Appl. No. 11/043,768 Non-Final Office Action dated Sep. 27, 2010", 8 pgs.
"U.S. Appl. No. 11/043,768, Final Office Action dated Jun. 27, 2008", 8 pgs.
"U.S. Appl. No. 11/043,768, Non-Final Office Action dated Feb. 23, 2010", 6 pgs.
"U.S. Appl. No. 11/043,768, Non-Final Office Action dated Feb. 23, 2009", 7 pgs.
"U.S. Appl. No. 11/043,768, Non-Final Office Action dated Nov. 28, 2007", 9 pgs.
"U.S. Appl. No. 11/043,768, Notice of Allowance dated Jun. 29, 2011", 12 pgs.
"U.S. Appl. No. 11/043,768, Response filed May 2, 2011 to Final Office Action dated Feb. 3, 2011", 11 pgs.
"U.S. Appl. No. 11/043,768, Response filed Jun. 15, 2010 to Non Final Office Action dated Feb. 23, 2010", 9 pgs.
"U.S. Appl. No. 11/043,768, Response filed Jun. 23, 2009 to Non Final Office Action dated Feb. 23, 2009", 9 pgs.
"U.S. Appl. No. 11/043,768, Response filed Sep. 13, 2007 to Restriction Requirement dated Mar. 13, 2007", 10 pgs.
"U.S. Appl. No. 11/043,768, Response filed Oct. 26, 2010 to Non Final Office Action dated Sep. 27, 2010", 11 pgs.
"U.S. Appl. No. 11/043,768, Response filed Dec. 12, 2008 to Final Office Action dated Jun. 27, 2008", 9 pgs.
"U.S. Appl. No. 11/043,768, Response filed Mar. 10, 2008 to Office Action dated Nov. 28, 2007", 12 pgs.
"U.S. Appl. No. 11/043,768, Restriction Requirement dated Mar. 13, 2007", 9 pgs.
"U.S. Appl. No. 11/043,786, Final Office Action dated Feb. 3, 2011", 10 pgs.
"U.S. Appl. No. 11/729,557, Advisory Action dated May 9, 2011", 3 pgs.
"U.S. Appl. No. 11/729,557, Advisory Action dated Dec. 24, 2014", 3 pgs.
"U.S. Appl. No. 11/729,557, Final Office Action dated Feb. 2, 2011", 14 pgs.
"U.S. Appl. No. 11/729,557, Final Office Action dated Aug. 20, 2009", 13 Pgs.
"U.S. Appl. No. 11/729,557, Final Office Action dated Sep. 12, 2014", 14 pgs.
"U.S. Appl. No. 11/729,557, Non Final Office Action dated Feb. 18, 2015", 13 pgs.
"U.S. Appl. No. 11/729,557, Non Final Office Action dated Feb. 26, 2014", 16 pgs.
"U.S. Appl. No. 11/729,557, Non-Final Office Action dated Jan. 30, 2009", 20 pgs.
"U.S. Appl. No. 11/729,557, Non-Final Office Action dated Feb. 22, 2010", 16 pgs.
"U.S. Appl. No. 11/729,557, Non-Final Office Action dated Aug. 23, 2010", 15 pgs.
"U.S. Appl. No. 11/729,557, Notice of Allowance dated Sep. 30, 2015", 11 pgs.
"U.S. Appl. No. 11/729,557, Respons filed Jun. 22, 2010 to Non Final Office Action dated Feb. 22, 2010", 33 pgs.
"U.S. Appl. No. 11/729,557, Response filed Apr. 27, 2011 to Final Office Action dated Feb. 2, 2011", 14 pgs.
"U.S. Appl. No. 11/729,557, Response filed Apr. 30, 2009 to Non Final Office Action dated Jan. 30, 2009", 18 pgs.
"U.S. Appl. No. 11/729,557, Response filed May 22, 2014 to Non Final Office Action dated Feb. 26, 2014", 13 pgs.
"U.S. Appl. No. 11/729,557, Response filed May 28, 2008 to Restriction Requirement dated Nov. 28, 2007", 13 pgs.
"U.S. Appl. No. 11/729,557, Response filed Jun. 22, 2010 to Non Final Office Action dated Feb. 22, 2010", 16 pgs.
"U.S. Appl. No. 11/729,557, Response filed Jun. 22, 2015 to non Final Office Action dated Feb. 18, 2015", 13 pgs.
"U.S. Appl. No. 11/729,557, Response filed Oct. 28, 2010 to Non Final Office Action dated Aug. 23, 2010", 13 pgs.
"U.S. Appl. No. 11/729,557, Response filed Dec. 1, 2009 to Final Office Action dated Aug. 26, 2009", 16 pgs.
"U.S. Appl. No. 11/729,557, Response filed Dec. 11, 2014 to Final Office Action dated Sep. 12, 2014", 15 pgs.
"U.S. Appl. No. 11/729,557, Restriction Requirement dated Nov. 28, 2007", 9 pgs.
"U.S. Appl. No. 12/214,414, Advisory Action dated Feb. 2, 2016", 5 pgs.
"U.S. Appl. No. 12/214,414, Advisory Action dated Apr. 15, 2015", 6 pgs.
"U.S. Appl. No. 12/214,414, Advisory Action dated Oct. 21, 2011", 5 pgs.
"U.S. Appl. No. 12/214,414, Examiner Interview Summary dated Dec. 11, 2015", 3 pgs.
"U.S. Appl. No. 12/214,414, Final Office Action dated Jan. 20, 2015", 28 pgs.
"U.S. Appl. No. 12/214,414, Final Office Action dated Aug. 2, 2011", 7 pgs.
"U.S. Appl. No. 12/214,414, Non Final Office Action dated Jun. 12, 2014", 28 pgs.
"U.S. Appl. No. 12/214,414, Non Final Office Action dated Dec. 10, 2010", 6 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"U.S. Appl. No. 12/214,414, Non-Final Office Action dated Mar. 2, 2010", 9 pgs.
"U.S. Appl. No. 12/214,414, Notice of Allowance dated Jun. 7, 2016", 18 pgs.
"U.S. Appl. No. 12/214,414, Response filed Jan. 19, 2016 to Final Office Action dated Nov. 18, 2015", 14 pgs.
"U.S. Appl. No. 12/214,414, Response filed Feb. 18, 2016 to Final Office Action dated Nov. 18, 2015", 14 pgs.
"U.S. Appl. No. 12/214,414, Response filed Mar. 26, 2015 to Final Office Action dated Jan. 20, 2015", 13 pgs.
"U.S. Appl. No. 12/214,414, Response filed May 3, 2011 to Non Final Office Action dated Dec. 10, 2010", 12 pgs.
"U.S. Appl. No. 12/214,414, Response filed Jul. 20, 2015 to Advisory Action dated Apr. 15, 2015", 14 pgs.
"U.S. Appl. No. 12/214,414, Response filed Aug. 31, 2010 to Non Final Office Action dated Mar. 2, 2010", 11 pgs.
"U.S. Appl. No. 12/214,414, Response filed Oct. 3, 2011 to Non Final Office Action dated Aug. 2, 2011", 9 pgs.
"U.S. Appl. No. 12/214,414, Response filed Dec. 21, 2011 to Advisory Action dated Oct. 21, 2011", 10 pgs.
"U.S. Appl. No. 12/467,492, Restriction Requirement dated Nov. 22, 2010", 6 pgs.
"U.S. Appl. No. 12/912,411, Advisory Action dated Feb. 5, 2014", 3 pgs.
"U.S. Appl. No. 12/912,411, Examiner Interview Summary dated Feb. 11, 2014", 2 pgs.
"U.S. Appl. No. 12/912,411, Final Office Action dated Jan. 14, 2015", 10 pgs.
"U.S. Appl. No. 12/912,411, Final Office Action dated Oct. 25, 2013", 11 pgs.
"U.S. Appl. No. 12/912,411, Non Final Office Action dated Jun. 7, 2013", 8 pgs.
"U.S. Appl. No. 12/912,411, Non Final Office Action dated Sep. 24, 2014", 11 pgs.
"U.S. Appl. No. 12/912,411, Notice of Allowability dated May 20, 2015", 7 pgs.
"U.S. Appl. No. 12/912,411, Notice of Allowance dated Apr. 8, 2015", 11 pgs.
"U.S. Appl. No. 12/912,411, Response filed Jan. 27, 2014 to Final Office Action dated Oct. 25, 2013", 11 pgs.
"U.S. Appl. No. 12/912,411, Response filed Feb. 18, 2013 to Restriction Requirement dated Oct. 17, 2012", 9 pgs.
"U.S. Appl. No. 12/912,411, Response filed Feb. 25, 2014 to Final Office Action dated Oct. 25, 2013", 11 pgs.
"U.S. Appl. No. 12/912,411, Response filed Mar. 16, 2015 to Final Office Action dated Jan. 14, 2015", 9 pgs.
"U.S. Appl. No. 12/912,411, Response filed Oct. 7, 2013 to Non Final Office Action dated Jun. 7, 2013", 10 pgs.
"U.S. Appl. No. 12/912,411, Response filed Dec. 31, 2014 to Non Final Office Action dated Sep. 24, 2014", 12 pgs.
"U.S. Appl. No. 12/912,411, Restriction Requirement dated Oct. 17, 2012", 9 pgs.
"U.S. Appl. No. 13/070,110, Advisory Action dated Mar. 3, 2017", 5 pgs.
"U.S. Appl. No. 13/070,110, Examiner Interview Summary dated Jan. 16, 2018", 3 pgs.
"U.S. Appl. No. 13/070,110, Final Office Action dated Apr. 3, 2015", 18 pgs.
"U.S. Appl. No. 13/070,110, Final Office Action dated Jun. 12, 2013", 7 pgs.
"U.S. Appl. No. 13/070,110, Final Office Action dated Sep. 14, 2016", 12 pgs.
"U.S. Appl. No. 13/070,110, Non Final Office Action dated Jul. 21, 2017", 14 pgs.
"U.S. Appl. No. 13/070,110, Non Final Office Action dated Oct. 2, 2014", 24 pgs.
"U.S. Appl. No. 13/070,110, Non Final Office Action dated Dec. 11, 2015", 19 pgs.
"U.S. Appl. No. 13/070,110, Non Final Office Action dated Dec. 21, 2012", 7 pgs.
"U.S. Appl. No. 13/070,110, Notice of Allowance dated Mar. 26, 2018", 6 pgs.
"U.S. Appl. No. 13/070,110, Preliminary Amendment filed Jun. 6, 2011", 4 pgs.
"U.S. Appl. No. 13/070,110, Response filed Jan. 22, 2018 to Non Final Office Action dated Jul. 21, 2017", 10 pgs.
"U.S. Appl. No. 13/070,110, Response filed Feb. 14, 2017 to Final Office Action dated Sep. 14, 2016", 8 pgs.
"U.S. Appl. No. 13/070,110, Response filed Mar. 22, 2013 to Non Final Office Action dated Dec. 21, 2012", 8 pgs.
"U.S. Appl. No. 13/070,110, Response filed May 27, 2016 to Non Final Office Action dated Dec. 11, 2015", 13 pgs.
"U.S. Appl. No. 13/070,110, Response filed Jun. 20, 2017 to Advisory Action dated Mar. 3, 2017", 13 pgs.
"U.S. Appl. No. 13/070,110, Response filed Sep. 3, 2014 to Restriction Requirement dated Jul. 8, 2014", 7 pgs.
"U.S. Appl. No. 13/070,110, Response filed Oct. 2, 2015 to Final Office Action dated Apr. 3, 2015", 11 pgs.
"U.S. Appl. No. 13/070,110, Response filed Nov. 12, 2013 to Final Office Action dated Jun. 12, 2013", 9 pgs.
"U.S. Appl. No. 13/070,110, Response filed Dec. 30, 2014 to Non Final Office Action dated Oct. 2, 2014", 13 pgs.
"U.S. Appl. No. 13/070,110, Restriction Requirement dated Jul. 8, 2014", 7 pgs.
"U.S. Appl. No. 14/332,121, Non Final Office Action dated May 16, 2016", 9 pgs.
"U.S. Appl. No. 14/332,121, Notice of Allowance dated Feb. 15, 2017", 10 pgs.
"U.S. Appl. No. 14/332,121, Notice of Allowance dated Jun. 15, 2017", 8 pgs.
"U.S. Appl. No. 14/332,121, Notice of Allowance dated Oct. 11, 2017", 8 pgs.
"U.S. Appl. No. 14/332,121, Preliminary Amendment filed Sep. 30, 2014", 5 pgs.
"U.S. Appl. No. 14/332,121, Response filed Jan. 29, 2016 to Restriction Requirement dated Jul. 30, 2015", 9 pgs.
"U.S. Appl. No. 14/332,121, Response filed Sep. 7, 2017 to Notice of Allowability dated Jun. 15, 2017", 8 pgs.
"U.S. Appl. No. 14/332,121, Response filed Oct. 11, 2016 to Non Final Office Action dated May 16, 2016", 9 pgs.
"U.S. Appl. No. 14/332,121, Restriction Requirement dated Jul. 30, 2015", 9 pgs.
"U.S. Appl. No. 14/332,121, Supplemental Amendment filed Jan. 23, 2017", 10 pgs.
"U.S. Appl. No. 14/745,236, Advisory Action dated Nov. 15, 2017", 2 pgs.
"U.S. Appl. No. 14/745,236, Final Office Action dated Aug. 25, 2017", 16 pgs.
"U.S. Appl. No. 14/745,236, Non Final Office Action dated Feb. 2, 2017", 14 pgs.
"U.S. Appl. No. 14/745,236, Notice of Allowability dated Jul. 5, 2018", 4 pgs.
"U.S. Appl. No. 14/745,236, Notice of Allowance dated Feb. 5, 2018", 9 pgs.
"U.S. Appl. No. 14/745,236, PTO Response to Rule 312 Communication dated Jul. 10, 2018", 2 pgs.
"U.S. Appl. No. 14/745,236, Response filed May 2, 2017 to Non Final Office Action dated Feb. 2, 2017", 10 pgs.
"U.S. Appl. No. 14/745,236, Response filed Nov. 6, 2017 to Final Office Action dated Aug. 25, 2017", 12 pgs.
"U.S. Appl. No. 14/745,236, Response filed Dec. 14, 2017 to Final Office Action dated Aug. 25, 2017", 12 pgs.
"U.S. Appl. No. 14/745,236, Response filed Dec. 23, 2016 to Restriction Requirement dated Sep. 23, 2016", 8 pgs.
"U.S. Appl. No. 14/745,236, Restriction Requirement dated Sep. 23, 2016", 8 pgs.
"U.S. Appl. No. 14/816,807, Non Final Office Action dated Oct. 3, 2017", 7 pgs.
"U.S. Appl. No. 14/816,807, Notice of Allowance dated Apr. 20, 2018", 8 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"U.S. Appl. No. 14/816,807, Preliminary Amendment filed Aug. 11, 2015", 8 pgs.
"U.S. Appl. No. 14/816,807, PTO Response to Rule 312 Communication dated Jul. 6, 2018", 2 pgs.
"U.S. Appl. No. 14/816,807, Response filed Jan. 3, 2018 to Non Final Office Action dated Oct. 3, 2017", 8 pgs.
"U.S. Appl. No. 14/816,807, Response filed May 1, 2017 to Restriction Requirement dated Nov. 1, 2016", 9 pgs.
"U.S. Appl. No. 14/816,807, Restriction Requirement dated Nov. 1, 2016", 8 pgs.
"U.S. Appl. No. 15/000,851, Non Final Office Action dated Jan. 26, 2017", 15 pgs.
"U.S. Appl. No. 15/000,851, Notice of Allowance dated Nov. 8, 2017", 9 pgs.
"U.S. Appl. No. 15/000,851, Preliminary Amendment filed Feb. 3, 2016", 3 pgs.
"U.S. Appl. No. 15/000,851, Response filed Jul. 26, 2017 to Non Final Office Action dated Jan. 26, 2017", 16 pgs.
"U.S. Appl. No. 15/000,851, Response filed Oct. 12, 2016 to Restriction Requirement dated May 12, 2016", 11 pgs.
"U.S. Appl. No. 15/000,851, Restriction Requirement dated May 12, 2016", 6 pgs.
"U.S. Appl. No. 15/000,851, Supplemental Amendment filed Apr. 4, 2016", 10 pgs.
"U.S. Appl. No. 15/170,556, Non Final Office Action dated Feb. 8, 2019", 11 pgs.
"U.S. Appl. No. 15/170,556, Non Final Office Action dated Jul. 27, 2018", 10 pgs.
"U.S. Appl. No. 15/170,556, Preliminary Amendment filed Aug. 22, 2016", 9 pgs.
"U.S. Appl. No. 15/170,556, Response filed Apr. 5, 2018 to Restriction Requirement dated Feb. 16, 2018", 8 pgs.
"U.S. Appl. No. 15/170,556, Response filed Oct. 29, 2018 to Non Final Office Action dated Jul. 27, 2018", 9 pgs.
"U.S. Appl. No. 15/170,556, Restriction Requirement dated Feb. 16, 2018", 7 pgs.
"U.S. Appl. No. 15/203,581, Examiners Interview Summary dated Sep. 11, 2017", 1 pg.
"U.S. Appl. No. 15/203,581, Notice of Allowance dated Sep. 11, 2017", 12 pgs.
"U.S. Appl. No. 15/203,581, Preliminary Amendment filed Sep. 22, 2016", 4 pgs.
"U.S. Appl. No. 15/203,581, PTO Response to Rule 312 Communication dated Dec. 27, 2017", 2 pgs.
"U.S. Appl. No. 15/203,581, Response filed Aug. 15, 2017 to Restriction Requirement dated Jun. 16, 2017", 8 pgs.
"U.S. Appl. No. 15/203,581, Restriction Requirement dated Jun. 16, 2017", 8 pgs.
"U.S. Appl. No. 15/292,595, Non Final Office Action dated Sep. 25, 2017", 13 pgs.
"U.S. Appl. No. 15/292,595, Notice of Allowance dated Feb. 28, 2018", 9 pgs.
"U.S. Appl. No. 15/292,595, Preliminary Amendment filed Dec. 27, 2016", 5 pgs.
"U.S. Appl. No. 15/292,595, Response filed Dec. 22, 2017 to Non Final Office Action dated Sep. 25, 2017", 9 pgs.
"U.S. Appl. No. 15/436,245, Preliminary Amendment filed May 5, 2017", 3 pgs.
"U.S. Appl. No. 15/436,245, Restriction Requirement dated Oct. 11, 2018", 9 pgs.
"U.S. Appl. No. 15/593,039, Non Final Office Action dated Feb. 6, 2018", 8 pgs.
"U.S. Appl. No. 15/593,039, Notice of Allowance dated Jul. 11, 2018", 5 pgs.
"U.S. Appl. No. 15/593,039, Preliminary Amendment filed Jul. 25, 2017", 7 pgs.
"U.S. Appl. No. 15/593,039, PTO Response to Rule 312 Communication dated Oct. 9, 2018", 2 pgs.
"U.S. Appl. No. 15/593,039, Response filed Apr. 30, 2018 to Non Final Office Action dated Feb. 4, 2018", 8 pgs.
"U.S. Appl. No. 15/593,039, Response filed Dec. 18, 2017 to Restriction Requirement dated Oct. 18, 2017", 8 pgs.
"U.S. Appl. No. 15/593,039, Restriction Requirement dated Oct. 18, 2017", 6 pgs.
"U.S. Appl. No. 15/593,039, Supplemental Preliminary Amendment filed Jul. 26, 2017", 4 pgs.
"U.S. Appl. No. 15/865,364, Notice of Allowance dated Nov. 15, 2018", 7 pgs.
"U.S. Appl. No. 15/865,364, Preliminary Amendment filed Apr. 10, 2018", 10 pgs.
"U.S. Appl. No. 15/905,454, Preliminary Amendment filed Nov. 2, 2018", 5 pgs.
"U.S. Appl. No. 15/905,454, Restriction Requirement dated Jan. 3, 2019", 6 pgs.
"U.S. Appl. No. 15/966,092, Non Final Office Action dated Jun. 26, 2020", 22 pgs.
"U.S. Appl. No. 15/966,092, Notice of Allowability dated Mar. 2, 2021", 2 pgs.
"U.S. Appl. No. 15/966,092, Notice of Allowance dated Feb. 11, 2021", 5 pgs.
"U.S. Appl. No. 15/966,092, Response filed Oct. 26, 2020 to Non Final Office Action dated Jun. 26, 2020", 9 pgs.
"U.S. Appl. No. 12/214,414, Response filed Oct. 14, 2014 to Non Final Office Action dated Jun. 12, 2014", 16 pgs.
"Australian Application Serial No. 2001255336, Examiner's First Report dated Feb. 16, 2005", 2 pgs.
"Australian Application Serial No. 2001255336, Response filed Aug. 23, 2005 to Examiner's First Report dated Feb. 16, 2005", 10 pgs.
"Australian Application Serial No. 2004249133, First Examiner's Report dated May 5, 2008", 4 pgs.
"Australian Application Serial No. 2004249133, Response filed Mar. 30, 2009 to First Examiner's Report dated May 5, 2008", 30 pgs.
"Australian Application Serial No. 2007245192, Office Action dated Aug. 25, 2011", 2 pgs.
"Australian Application Serial No. 2007245192, Response filed Feb. 28, 2012 to Office Action dated Aug. 25, 2011", 22 pgs.
"Australian Application Serial No. 2012204138, First Examiner Report dated Jul. 16, 2013", 4 pgs.
"Australian Application Serial No. 2012204138, Response filed Dec. 24, 2013 to First Examiner Report dated Jul. 16, 2013", 21 pgs.
"Australian Application Serial No. 2014202470, First Examiner Report dated Jul. 20, 2015", 2 pgs.
"Australian Application Serial No. 2014202470, Respojnse filed Jul. 4, 2016 to Subsequent Examiners Report dated Feb. 1, 2016", 3 pgs.
"Australian Application Serial No. 2014202470, Response filed Jul. 20, 2016 to Subsequent Examiners Report dated Jul. 19, 2016", 15 pgs.
"Australian Application Serial No. 2014202470, Response filed Dec. 1, 2015 to First Examiner Report dated Jul. 20, 2015", 22 pgs.
"Australian Application Serial No. 2014202470, Subsequent Examiners Report dated Feb. 1, 2016", 2 pgs.
"Australian Application Serial No. 2014202470, Subsequent Examiners Report dated Jul. 19, 2016", 3 pgs.
"Brazilian Application Serial No. PI0410702-0, Office Action dated Feb. 23, 2012", (w/ English Translation), 4 pgs.
"Brazilian Application Serial No. PI0410702-0, Response filed May 7, 2012 to Office Action dated Feb. 23, 2012", (w/ English Translation of Claims), 11 pgs.
"Canadian Application Serial No. 2,406,180, Office Action dated Sep. 9, 2008", 5 pgs.
"Canadian Application Serial No. 2,406,180, Office Action dated Nov. 10, 2011", 3 pgs.
"Canadian Application Serial No. 2,406,180, Office action dated Nov. 23, 2009", 3 pgs.
"Canadian Application Serial No. 2,406,180, Office Action dated Dec. 10, 2010", 2 Pgs.
"Canadian Application Serial No. 2,406,180, Response filed Jan. 26, 2009 to Official Action dated Sep. 9, 2008", 22 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"Canadian Application Serial No. 2,406,180, Response filed May 21, 2010 to Office action dated Nov. 23, 2009", 13 pgs.
"Canadian Application Serial No. 2,406,180, Response filed Jun. 14, 2011 to Office Action dated Dec. 10, 2010", 10 pgs.
"Canadian Application Serial No. 2,522,081, Amendment After Allowance filed Aug. 10, 2012", 3 pgs.
"Canadian Application Serial No. 2,522,081, Office Action filed Nov. 18, 2011", 11 pgs.
"Canadian Application Serial No. 2,522,081, Office Action dated Jun. 6, 2011", 2 pgs.
"Canadian Application Serial No. 2,522,081, Office Action dated Aug. 30, 2010", 2 pgs.
"Canadian Application Serial No. 2,522,081, Office Action dated Oct. 8, 2009", 6 pgs.
"Canadian Application Serial No. 2,522,081, Response filed Feb. 28, 2011 to Office Action dated Aug. 30, 2010", 10 pgs.
"Canadian Application Serial No. 2,522,081, Response filed Apr. 8, 2010 to Office Action dated Oct. 8, 2009", 30 pgs.
"Canadian Application Serial No. 2,522,081, Response filed Nov. 18, 2011 to Office Action dated Jun. 6, 2011", 11 pgs.
"Canadian Application Serial No. 2,525,953, Amendment and Response filed Feb. 1, 2017 to Office Action dated Aug. 1, 2016", 28 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Jan. 21, 2016", 6 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Jul. 31, 2012", 4 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Aug. 1, 2016", 6 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Aug. 16, 2013", 3 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Oct. 3, 2017", 4 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Nov. 2, 2018", 6 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Nov. 6, 2014", 3 pgs.
"Canadian Application Serial No. 2,525,953, Office Action dated Jun. 22, 2011", 4 pgs.
"Canadian Application Serial No. 2,525,953, Response filed Jan. 31, 2013 to Office Action dated Jul. 31, 2012", 11 pgs.
"Canadian Application Serial No. 2,525,953, Response filed Feb. 1, 2017 to Office Action dated Aug. 1, 2016", 28 pgs.
"Canadian Application Serial No. 2,525,953, Response filed Feb. 14, 2014 to Office Action dated Aug. 16, 2013", 16 pgs.
"Canadian Application Serial No. 2,525,953, Response filed Apr. 3, 2018 to Office Action dated Oct. 3, 2017", 46 pgs.
"Canadian Application Serial No. 2,525,953, Response filed May 1, 2015 to Office Action dated Nov. 6, 2014", 23 pgs.
"Canadian Application Serial No. 2,525,953, Response filed Jul. 11, 2016 to Office Action dated Jan. 21, 2016", 21 pgs.
"Canadian Application Serial No. 2,525,953, Response filed Dec. 22, 2011 to Office Action dated Jun. 22, 2011", 17 pgs.
"Canadian Application Serial No. 2,647,985 , Office Action dated May 15, 2013", 3 pgs.
"Canadian Application Serial No. 2,647,985 , Response filed Sep. 30, 2013 to Office Action dated May 15, 2013", 20 pgs.
"Canadian Application Serial No. 2406180, Response filed May 7, 2012 to Office Action dated Nov. 10, 2011", 11 pgs.
"Chinese Application Serial No. 200480017037, First Office Action dated May 25, 2007", (w/ English Translation), 10 pgs.
"Chinese Application Serial No. 200480017037, Response filed Oct. 30, 2007 to First Office Action dated May 25, 2007", (w/ English Translation of Claims), 26 pgs.
"Chinese Application Serial No. 200480017037.X, Response filed May 14, 2010 to Third Office Action dated Mar. 1, 2010", (w/ English Translation of Claims), 16 pgs.
"Chinese Application Serial No. 200480017037.X, Response filed Aug. 4, 2009 to Second Office Action dated Mar. 20, 2009", (w/ English Translation of Amended Claims), 15 pgs.
"Chinese Application Serial No. 200480017037.X, Second Office Action dated Mar. 20, 2009", (English Translation), 7 pgs.
"Chinese Application Serial No. 200480017037.X, Third Office Action dated Mar. 1, 2010", (w/ English Translation), 9 pgs.
"Chinese Application Serial No. 200480021259.9 Office Action dated Sep. 11, 2009", (English Translation), 7 pgs.
"Chinese Application Serial No. 200480021259.9 Response filed Aug. 20, 2010 to Office Acton dated May 6, 2010", (w/ English Translation of Claims), 26 pgs.
"Chinese Application Serial No. 200480021259.9, First Offiice Action dated on Aug. 24, 2007", (w/ English Translation), 9 pgs.
"Chinese Application Serial No. 200480021259.9, Notice of Reexamination dated Jul. 3, 2012", (w/ English Translation), 10 pgs.
"Chinese Application Serial No. 200480021259.9, Office Action dated Jan. 11, 2011", (w/ English Translation), 15 pgs.
"Chinese Application Serial No. 200480021259.9, Office Action dated May 6, 2010", (w/ English Translation), 12 pgs.
"Chinese Application Serial No. 200480021259.9, Office Action dated Jul. 3, 2012", (w/ English Translation), 10 pgs.
"Chinese Application Serial No. 200480021259.9, Request for Reexamination dated Apr. 26, 2011", (w/ English Translation of Amended Claims), 23 pgs.
"Chinese Application Serial No. 200480021259.9, Response filed Mar. 7, 2008 to Offiice Action dated Aug. 24, 2007", (w/ English Translation of Claims), 13 pgs.
"Chinese Application Serial No. 200480021259.9, Response filed Oct. 16, 2012 to Office Action dated Jul. 3, 2012", (w/ English Translation of Claims), 13 pgs.
"Chinese Application Serial No. 200780020095.1, Decision on Rejection dated Jul. 22, 2013", (w/ English Translation), 11 pgs.
"Chinese Application Serial No. 200780020095.1, First Office Action dated Jun. 24, 2011", (w/ English Translation), 13 pgs.
"Chinese Application Serial No. 200780020095.1, Office Action dated Jan. 29, 2013", (w/ English Translation), 10 pgs.
"Chinese Application Serial No. 200780020095.1, Office Action dated Mar. 5, 2015", (w/ English Translation), 12 pgs.
"Chinese Application Serial No. 200780020095.1, Office Action dated Apr. 26, 2016", (w/ English Summary), 4 pgs.
"Chinese Application Serial No. 200780020095.1, Office Action dated May 3, 2012", (w/ English Translation), 10 pgs.
"Chinese Application Serial No. 200780020095.1, Office Action dated Nov. 2, 2016", (w/ English Translation), 11 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Jan. 6, 2017 to Office Action dated Nov. 2, 2016", (w/ English Translation of Claims), 15 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Jun. 9, 2013 to Office Action dated Jan. 29, 2013", (w/ English Translation of Claims), 10 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Jun. 23, 2015 to Office Action dated Mar. 5, 2015", (w/ English Translation of Claims), 16 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Jun. 30, 2016 to Office Action dated Apr. 26, 2016", (w/ English Translation of Claims), 22 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Sep. 17, 2012 to Office Action dated May 3, 2012", (w/ English Translation of Claims), 17 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Nov. 5, 2013 to to Decision on Rejection dated Jul. 22, 2013", (w/ English Translation of Claims), 12 pgs.
"Chinese Application Serial No. 200780020095.1, Response filed Nov. 8, 2011 to Office Action dated Jun. 24, 2011", (w/ English Translation of Amended Claims), 20 pgs.
"Chinese Application Serial No. 200480021259.9, Office Action dated May 8, 2009", (w/ English Translation), 6 pgs.
"Eurasian Application No. 200501890, Notice of Allowance dared Jun. 23, 2009", 1 pg.
"Eurasian Application Serial No. 200501890, Office Action dated Mar. 23, 2007", (w English Translation), 2 pgs.
"Eurasian Application Serial No. 200501890, Office Action dated Sep. 4, 2008", (English Translation), 1 pg.
"Eurasian Application Serial No. 200501890, Office Action dated Dec. 17, 2007", (w/ English Translation), 6 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"Eurasian Application Serial No. 200501890, Response filed Mar. 26, 08 to Office Action dated Dec. 17, 2007", (w/ English Translation of Claims), 15 pgs.
"Eurasian Application Serial No. 200501890, Response filed Jun. 14, 2007 to Office Action dated Mar. 23, 2007", (w/ English Translation of Claims), 11 pgs.
"Eurasian Application Serial No. 200501890, Response filed Dec. 17, 2008 to Office Action", (w/English Translation of Claims), 13 pgs.
"Eurasian Application Serial No. 200501890, Response filed Dec. 17, 2008 to Office Action dated Sep. 4, 2008", (w/ English Translation of Claims), 14 pgs.
"European Application 04750333.9, Communication dated Oct. 12, 2006", 6 pgs.
"European Application 04750333.9, Communication dated Dec. 8, 2006", 4 pgs.
"European Application 04750333.9, Communication dated Apr. 11, 2008", 6 pgs.
"European Application 04750333.9, Response filed Oct. 4, 2007 to Communication dated Dec. 8, 2006", 42 pgs.
"European Application 04750333.9, Response filed Nov. 2021, 06 to Communication dated Oct. 12, 2006", 4 pgs.
"European Application Serial No. 01928486.8 Office Action dated Oct. 1, 2009", 2 pgs.
"European Application Serial No. 01928486.8, Communication dated Aug. 10, 2007", 3 pgs.
"European Application Serial No. 01928486.8, Communication dated Sep. 20, 2005", 4 pgs.
"European Application Serial No. 01928486.8, Office Action dated Feb. 19, 2009", 3 pgs.
"European Application Serial No. 01928486.8, Response filed Jan. 30, 06 to Communication dated Sep. 20, 2005", 9 pgs.
"European Application Serial No. 01928486.8, Response filed Aug. 28, 2009 to Communication dated Feb. 19, 2009", 5 pgs.
"European Application Serial No. 01928486.8, Response filed Jan. 21, 2008 to Communication dated Aug. 10, 2007", 11 pgs.
"European Application Serial No. 01928486.8, Response filed Dec. 9, 2009 to Office Action dated Oct. 1, 2009", 11 pgs.
"European Application Serial No. 04750333.9, Office Action dated Jan. 22, 2009", 5 pgs.
"European Application Serial No. 04750333.9, Response filed Oct. 21, 2008 to Communication dated Apr. 11, 2008", 15 pgs.
"European Application Serial No. 04750333.9, Response filed Nov. 17, 2009 to Communication dated Jan. 22, 2009", 17 pgs.
"European Application Serial No. 04750333.9, Summons To Attend Oral Proceedings dated Aug. 3, 2011", 13 pgs.
"European Application Serial No. 04776133.3, Communication dated Mar. 30, 2006", 3 pgs.
"European Application Serial No. 04776133.3, Examination Notification Art. 94(3) dated Jul. 28, 2015", 4 pgs.
"European Application Serial No. 04776133.3, Examination Notification Art. 94(3) dated Nov. 25, 2013", 5 pgs.
"European Application Serial No. 04776133.3, Office Action dated Jan. 5, 2010", 4 pgs.
"European Application Serial No. 04776133.3, Response filed Jan. 25, 2007 to Communication dated Mar. 30, 2006", 20 pgs.
"European Application Serial No. 04776133.3, Response filed Apr. 30, 2014 to Examination Notification Art. 94(3) dated Nov. 25, 2013", 12 pgs.
"European Application Serial No. 04776133.3, Response filed Jul. 15, 2010 to Office Action dated Jan. 5, 2010", 9 pgs.
"European Application Serial No. 04776133.3, Response filed Sep. 18, 2015 to Examination Notification Art. 94(3) dated Jul. 28, 2015", 47 pgs.
"European Application Serial No. 07754132.4, Office Action dated Apr. 28, 2009", 4 pgs.
"European Application Serial No. 07754132.4, Office Action dated Sep. 5, 2011", 5 pgs.
"European Application Serial No. 07754132.4, Office Action dated Nov. 2, 2012", 4 pgs.
"European Application Serial No. 07754132.4, Response filed Feb. 5, 2010 to Office Action dated Apr. 28, 2009", 15 pgs.
"European Application Serial No. 07754132.4, Response filed Mar. 15, 2012 to Office Action dated Sep. 5, 2011", 21 pgs.
"European Application Serial No. 07754132.4, Response filed May 10, 2013 to Office Action dated Nov. 2, 2012", 14 pgs.
"European Application Serial No. 07754132.4, Response dated Jun. 26, 2013", 8 pgs.
"European Application Serial No. 10777154.5, Communication Pursuant to Article 94(3) EPC dated Apr. 4, 2018", 7 pgs.
"European Application Serial No. 10777154.5, Communication Pursuant to Article 94(3) EPC dated Oct. 12, 2017", 7 pgs.
"European Application Serial No. 10777154.5, Examination Notification Art. 94(3) dated Oct. 6, 2014", 7 pgs.
"European Application Serial No. 10777154.5, Office Action dated May 2, 2016", 6 pgs.
"European Application Serial No. 10777154.5, Office Action dated Jul. 4, 2012", 2 pgs.
"European Application Serial No. 10777154.5, Response filed Jan. 14, 2013 to Office Action dated Jul. 4, 2012", 12 pgs.
"European Application Serial No. 10777154.5, Response filed Feb. 21, 2018 to Communication Pursuant to Article 94(3) EPC dated Oct. 12, 2017", 12 pgs.
"European Application Serial No. 10777154.5, Response filed Sep. 7, 2018 to Communication Pursuant to Article 94(3) EPC dated Apr. 4, 2018", 18 pgs.
"European Application Serial No. 10777154.5, Response filed Sep. 8, 2016 to Office Action dated May 2, 2016", 69 pgs.
"European Application Serial No. 10777154.5, Summons to Attend Oral Proceedings dated Jan. 7, 2019", 5 pgs.
"European Application Serial No. 14745060.5, Communication Pursuant to Article 94(3) EPC dated Feb. 6, 2018", 5 pgs.
"European Application Serial No. 14745060.5, Communication Pursuant to Article 94(3) EPC dated Sep. 18, 2018", 4 pgs.
"European Application Serial No. 14745060.5, Office Action dated Feb. 23, 2016", 2 pgs.
"European Application Serial No. 14745060.5, Response filed Jun. 15, 2018 to Communication Pursuant to Article 94(3) EPC dated Feb. 6, 2018", 14 pgs.
"European Application Serial No. 14745060.5, Response filed Dec. 22, 2016 to Communication pursuant to Rules 161 (1) and 162 EPC dated Feb. 23, 2016", 6 pgs.
"Indian Application Serial No. 02082/KOLNP/2005, Examination Report dated Mar. 17, 2008", 1 pg.
"Indian Application Serial No. 02082/KOLNP/2005, Examination Report dated Dec. 28, 2007", 1 pg.
"Indian Application Serial No. 02082/KOLNP/2005, First Examination Report dated Jan. 25, 2007", 9 pgs.
"Indian Application Serial No. 02082/KOLNP/2005, Response filed Jan. 22, 2008 to Examination Report dated Dec. 28, 2007", 13 pgs.
"Indian Application Serial No. 02082/KOLNP/2005, Response filed Jun. 10, 2008 to Examination Report dated Mar. 17, 2008", 3 pgs.
"Indian Application Serial No. 02082/KOLNP/2005, Response filed Nov. 19, 2007 to First Examination Report dated Jan. 25, 2007", 26 pgs.
"Indian Application Serial No. 1026/KOLNP/2009, First Examiner Report dated Mar. 13, 2014", 2 pgs.
"Indian Application Serial No. 2272/KOLNP/2005, First Examination Report dated Mar. 17, 2008", 10 pgs.
"Indian Application Serial No. 2272/KOLNP/2005, Response filed Mar. 16, 2009 to Subsequent Examination Report dated Mar. 6, 2009", 12 pgs.
"Indian Application Serial No. 2272/KOLNP/2005, Response filed Oct. 11, 2008 to First Examination Report dated Mar. 17, 2008", 27 pgs.
"Indian Application Serial No. 2272/KOLNP/2005, Subsequent Examination Report dated Mar. 6, 2009", 1 pg.
"International Application No. PCT/US2004/016680, International Search Report", (dated Feb. 2, 2005), 7 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"International Application Serial No. PCT/US01/11963, Amendment filed Sep. 9, 2002 to Written Opinion dated Aug. 7, 2002", 12 pgs.
"International Application Serial No. PCT/US01/11963, International Preliminary Examination Report dated Oct. 15, 2002", 13 pgs.
"International Application Serial No. PCT/US01/11963, International Search Report dated May 7, 2002", 5 pgs.
"International Application Serial No. PCT/US01/11963, Response filed Sep. 9, 2002 to Written Opinion dated Aug. 7, 2002", 12 pgs.
"International Application Serial No. PCT/US01/11963, Written Opinion dated Jun. 14, 2002", 2 pgs.
"International Application Serial No. PCT/US01/11963, Written Opinion dated Aug. 7, 2002", 6 pgs.
"International Application Serial No. PCT/US2004/012050, International Search Report dated Feb. 2, 2005", 8 pgs.
"International Application Serial No. PCT/US2004/012050, International Search Report dated Feb. 2005", 8 pgs.
"International Application Serial No. PCT/US2004/012050, Written Opinion dated Feb. 2, 2005", 12 pgs.
"International Application Serial No. PCT/US2004/016680, International Preliminary Report on Patentability dated Dec. 15, 2005", 11 pgs.
"International Application Serial No. PCT/US2007/007562, International Preliminary Report on Patentability dated Oct. 9, 2008", 5 pgs.
"International Application Serial No. PCT/US2007/007562, International Search Report dated Jan. 14, 2008", 8 pgs.
"International Application Serial No. PCT/US2007/007562, Written Opinion dated Jan. 14, 2008", 9 pgs.
"International Application Serial No. PCT/US2008/007582, International Preliminary Report on Patentability dated Jan. 7, 2010", 9 pgs.
"International Application Serial No. PCT/US2008/007582, International Search Report and Written Opinion dated Feb. 18, 2009", 16 pgs.
"International Application Serial No. PCT/US2010/054128, Preliminary Report on Patentability dated May 10, 2012", 10 pgs.
"International Application Serial No. PCT/US2010/054128, Search Report dated Feb. 23, 2011", 6 pgs.
"International Application Serial No. PCT/US2010/054128, Written Opinion dated Feb. 23, 2011", 8 pgs.
"International Application Serial No. PCT/US2014/046731, International Preliminary Report on Patentability dated Jan. 28, 2016", 12 pgs.
"International Application Serial No. PCT/US2014/046731, International Search Report dated Nov. 25, 2014", 9 pgs.
"International Application Serial No. PCT/US2014/046731, Written Opinion dated Nov. 25, 2014", 10 pgs.
"International Application Serial No. PCT/US2015/036803, International Preliminary Report on Patentability dated Dec. 29, 2016", 10 pgs.
"International Application Serial No. PCT/US2015/036803, International Search Report dated Dec. 11, 2015", 8 pgs.
"International Application Serial No. PCT/US2015/036803, Invitation to Pay Additional Fees and Partial Search Report dated Oct. 2, 2015", 8 pgs.
"International Application Serial No. PCT/US2015/036803, Written Opinion dated Dec. 11, 2015", 8 pgs.
"International Application Serial No. PCT/US2016/041172, International Preliminary Report on Patentability dated Jan. 18, 2018", 10 pgs.
"International Application Serial No. PCT/US2016/041172, International Search Report dated Oct. 27, 2016", 6 pgs.
"International Application Serial No. PCT/US2016/041172, Written Opinion dated Oct. 27, 2016", 8 pgs.
"International Application Serial No. PCT/US2017/018443, International Preliminary Report on Patentability dated Aug. 30, 2018", 11 pgs.
"International Application Serial No. PCT/US2017/018443, International Search Report dated May 22, 2017", 9 pgs.
"International Application Serial No. PCT/US2017/018443, Written Opinion dated May 22, 2017", 9 pgs.
"International Application Serial No. PCT/US2020/014659, International Search Report dated Nov. 6, 2020", 7 pgs.
"International Application Serial No. PCT/US2020/014659, Invitation to Pay Additional Fees dated Sep. 16, 2020", 11 pgs.
"International Application Serial No. PCT/US2020/014659, Written Opinion dated Nov. 6, 2020", 10 pgs.
"Israeli Application Serial No. 238584, Office Action dated Jul. 24, 2017", 2 pgs.
"Israeli Application Serial No. 238584, Response filed Nov. 21, 2017 to Office Action dated Jul. 24, 2017", (w/ English Translation), 2 pgs.
"Israeli Application Serial No. 171831, Notification of Defects dated Nov. 10, 2008", (English Translation), 10 pgs.
"Israeli Application Serial No. 171372, Office Action dated Feb. 21, 2010", (Translation), 2 pgs.
"Israeli Application Serial No. 171372, Office Action dated Nov. 6, 2008", (Translation), 12 pgs.
"Israeli Application Serial No. 171372, Response filed Nov. 18, 10 to Office Action dated Feb. 21, 2010", (Translation), 19 pgs.
"Israeli Application Serial No. 171831, Office Action dated Feb. 21, 2010", (English Translation), 2 pgs.
"Israeli Application Serial No. 171831, Office Action dated Apr. 18, 2012", (English Translation), 2 pgs.
"Israeli Application Serial No. 171831, Response filed Jan. 20, 2011 to Office Action dated Feb. 21, 2010", (English Translation), 18 pgs.
"Israeli Application Serial No. 171831, Response filed Jun. 24, 2009 to Notification of Defects dated Nov. 10, 2008", (w/ English Translation of Claims), 10 pgs.
"Israeli Application Serial No. 171831, Response filed Nov. 6, 2012 to Office Action dated Apr. 18, 2012", (w/ English Translation of Amended Claims), 54 pgs.
"Israeli Application Serial No. 238584, Office Action dated Apr. 14, 2016", (English Translation), 3 pgs.
"Israeli Application Serial No. 238584, Office Action dated Jul. 24, 2017", (Translation), 2 pgs.
"Israeli Application Serial No. 238584, Office Action dated Aug. 23, 2018", (w/ English Translation), 6 pgs.
"Israeli Application Serial No. 238584, Response filed Aug. 3, 2016 to Office Action dated Apr. 14, 2016", (English Translation of Claims), 19 pgs.
"Israeli Application Serial No. 238584, Response filed Nov. 21, 2017 to Office Action dated Jul. 24, 2017", (Translation), 2 pgs.
"Israeli Application Serial No. 238584, Response filed Dec. 10, 2018 to Office Action dated Aug. 23, 2018", (w/ English Translation of Claims), 10 pgs.
"Israeli Application Serial No. 171372, Office Action dated Feb. 20, 2011", (Translation), 2 pgs.
"Japanese Application No. 2001-576868, Office Action dated May 31, 2011", (w/ English Translation), 5 pgs.
"Japanese Application No. 2001-576868, Response filed Apr. 26, 2011 to Office Action dated Nov. 2, 2010", (w/Translation of Amended Claims), 14 pgs.
"Japanese Application Serial No. 2001-576868, Office Action dated Nov. 2, 2010", (w/ English Translation), 10 pgs.
"Japanese Application Serial No. 2001-576868, Response filed Dec. 1, 2011 to Office Action dated May 3, 2011", (w/ English Translation of Amended Claims), 37 pgs.
"Japanese Application Serial No. 2006-513125, Office Action dated Mar. 9, 2010", (English Translation), 11 pgs.
"Japanese Application Serial No. 2006-513125, Response filed Aug. 30, 2010 to Office Action dated Mar. 9, 2010", (w/ English Translation of Amended Claims), 60 pgs.
"Japanese Application Serial No. 2006-533439, Decision of Final Rejection dated Aug. 14, 2012", (w/ English Translation), 5 pgs.
"Japanese Application Serial No. 2006-533439, Office Action dated Mar. 9, 2010", (w/ English Translation), 20 pgs.
"Japanese Application Serial No. 2006-533439, Office Action dated Mar. 27, 2012", (w/ English Translation), 8 pgs.

(56) **References Cited**

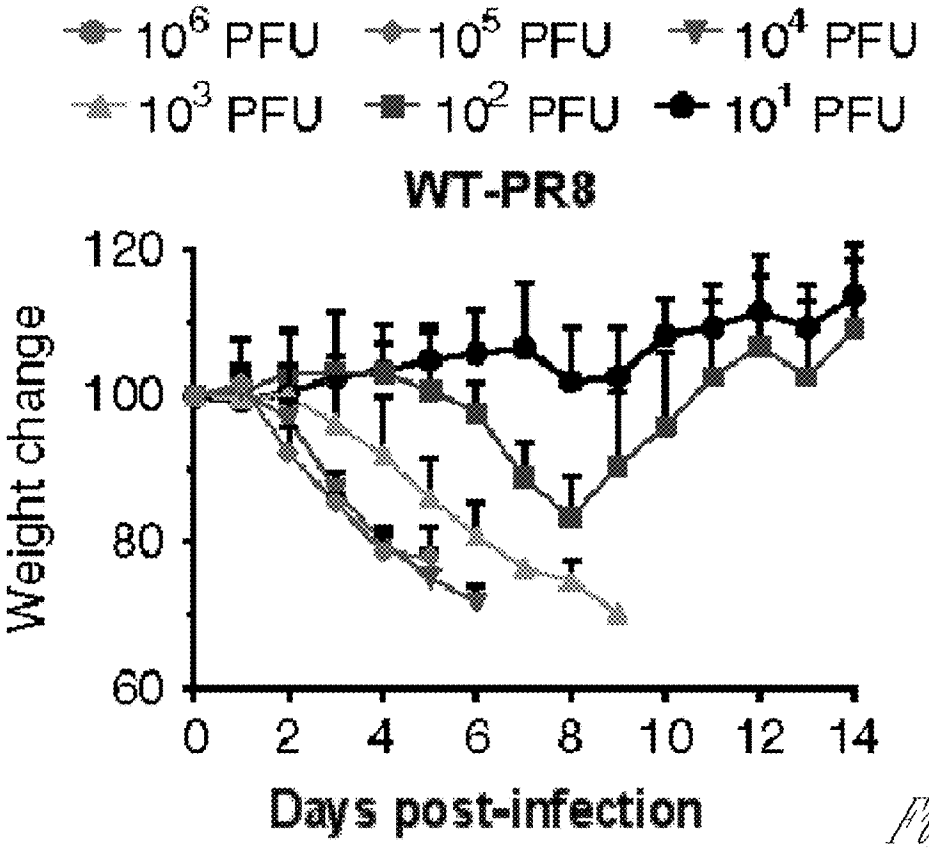
OTHER PUBLICATIONS

"Japanese Application Serial No. 2006-533439, Response filed May 21, 2012 to Office Action dated Mar. 27, 2012", (w/ English Translation of Amended Claims), 19 pgs.
"Japanese Application Serial No. 2006-533439, Response filed Aug. 3, 2011 to Office Action dated Feb. 15, 2011", (w/ English Translation of Amended Claims), 18 pgs.
"Japanese Application Serial No. 2006-533439,Office Action dated Feb. 15, 2011", (w/ English Translation), 13 pgs.
"Japanese Application Serial No. 2006-533439; Office Action Response dated Jul. 9, 2010", (w/English Translation of Claims), 25 pgs.
"Japanese Application Serial No. 2009-502945, Examiners Decision of Final Refusal dated Nov. 12, 2013", (w/ English Translation), 8 pgs.
"Japanese Application Serial No. 2009-502945, Office Action dated Oct. 23, 2012", (w/ English Translation), 16 pgs.
"Japanese Application Serial No. 2009-502945, Response filed Apr. 10, 2013 to Office Action dated Oct. 23, 2012", (w/ English Translation of Claims), 18 pgs.
"Japanese Application Serial No. 2011 -111048, Office Action dated Jun. 25, 2013", (w/ English Translation), 7 pgs.
"Japanese Application Serial No. 2011 -111048, Office Action dated Sep. 18, 2012", (w/ English Translation), 10 pga.
"Japanese Application Serial No. 2011-111048, Response filed Sep. 25, 2012 to Office Action dated Jun. 25, 2013", (w/ English Translation of Amended Claims), 18 pgs.
"Japanese Application Serial No. 2011-111048. Response dated Mar. 15, 2013", (w/ Translation of Amended Claims), 14 pgs.
"Japanese Application Serial No. 2012-273898, Office Action dated Jun. 10, 2014", (w/ English Translation), 7 pgs.
"Japanese Application Serial No. 2012-273898, Response filed Sep. 4, 2014 to Office Action dated Jun. 10, 2014", (w/ English Claims), 9 pgs.
"Japanese Application Serial No. 2012-536963, Amendment and Argument filed Jun. 26, 2015 to Office Action dated Jan. 6, 2015", (w/ English Translation of Amended Claims), 12 pgs.
"Japanese Application Serial No. 2012-536963, Examiners Decision of Final Refusal dated Nov. 17, 2015", (w/ English Translation), 8 pgs.
"Japanese Application Serial No. 2012-536963, Office Action dated Jan. 6, 2015", (w/ English Translation), 14 pgs.
"Japanese Application Serial No. 2012-536963, Voluntary Amendment dated Jun. 27, 2012", (w/ English Translation of Amended Claims), 17 pgs.
"Japanese Application Serial No. 2013-198377, Office Action dated Jan. 6, 2015", (w/ English Translation), 9 pgs.
"Japanese Application Serial No. 2014-049025 Response filed Sep. 4, 2015 to Office Action dated Jun. 16, 2015", (w/ English Translation of Amended Claims), 12 pgs.
"Japanese Application Serial No. 2014-049025, Examiners Decision of Final Refusal dated Feb. 2, 2016",(w/ English Translation), 5 pgs.
"Japanese Application Serial No. 2014-049025, Office Action dated Jun. 16, 2015", (w/ English Translation), 6 pgs.
"Japanese Application Serial No. 2016-053990, Office Action dated Jun. 6, 2017", (w/ English Translation), 4 pgs.
"Japanese Application Serial No. 2016-053990, Response filed Dec. 6, 2017 to Office Action dated Jun. 6, 2017", (w/ English Translation of Amended Claims), 14 pgs.
"Japanese Application Serial No. 2016-110879, Office Action dated May 30, 2017", (w/ English Translation), 7 pgs.
"Japanese Application Serial No. 2016-110879, Response filed Nov. 30, 2017 to Office Action dated May 30, 2017", (w/ English Translation of Claims), 25 pgs.
"Japanese Application Serial No. 2016-527046, Reasons For Rejection dated Aug. 14, 2018", (w/ English Translation), 14 pgs.
"Japanese Application Serial No. 2016-527046, Response filed Dec. 4, 2018 to Reasons For Rejection dated Aug. 14, 2018", (w/ English Translation of Amended Claims), 18 pgs.
"Japanese Application Serial No. 2006-513125,Final Office Action dated Jan. 18, 2011", (English Translation), 4 pgs.
"Korean Application Serial No. 10-2005-7020077, Response filed Apr. 28, 2008 to Examination Report dated Dec. 28, 2007", (w/ English Translation of Revised Claims), 41 pgs.
"Korean Application Serial No. 10-2005-7020077, Examination Report dated Dec. 28, 2007", (w/English Translation), 8 pgs.
"Korean Application Serial No. 10-2005-7020077, Notice of Preliminary Rejection dated Jun. 28, 2007", (w/ English Translation), 9 pgs.
"Korean Application Serial No. 10-2005-7020077, Response filed Aug. 28, 2007 to Notice of Preliminary Rejection dated Jun. 28, 2007", (w/ EnglishTranslation), 40 pgs.
"Korean Application Serial No. 10-2005-7022564, Notice of Preliminary Rejection dated Jul. 25, 2007", (w/ English Translation), 5 pgs.
"Korean Application Serial No. 10-2005-7022564, Office Action dated Aug. 6, 2008", (w/ English Translation), 4 pgs.
"Korean Application Serial No. 10-2005-7022564, Response and Amendment filed Dec. 29, 2008 to Office Action dated Aug. 6, 2008", (w/ English Translation), 16 pgs.
"Korean Application Serial No. 10-2005-7022564, Response filed Mar. 25, 2008 to Notice of Preliminary Rejection dated Jul. 25, 2007", (w/ English Translation of Claims), 35 pgs.
"Korean Application Serial No. 10-2005-7022564, Response filed Dec. 29, 2008 to Office Action dated Aug. 6, 2008", (w/ English Translation of Claims), 16 pgs.
"Mexican Application No. PA/a/2005/012712 Office Action dated Jul. 21, 209", (w/ English Translation), 9 pgs.
"Mexican Application Serial No. MX/a/2009/006341, Office Action dated Mar. 29, 2012", (English Translation), 1 pg.
"Mexican Application Serial No. MX/a/2009/006341, Response dated Jun. 4, 2012 to Mar. 29, 12", (w/ English Translation of Amended Claims), 16 pgs.
"Mexican Application Serial No. MX/a/20 12/009249 Response filed Sep. 10, 2015 to Office Action dated May 19, 2015", (w/ English Translation of Claims), 21 pgs.
"Mexican Application Serial No. MX/a/2012/009249, Office Action dated Feb. 5, 2016", (w/ English Claims), 2 pgs.
"Mexican Application Serial No. MX/a/2012/009249, Office Action dated May 19, 2015", (English Translation), 1 pg.
"Mexican Application Serial No. MX/a/2012/009249, Response filed Mar. 29, 2016 to Office Action dated Feb. 5, 2016", (English Translation of Claims), 18 pgs.
"Mexican Application Serial No. PA/a/2005/011250, Office Action dated Aug. 23, 2010", (w/ English Translation), 4 pgs.
"Mexican Application Serial No. PA/a/2005/011250, Response filed Dec. 20, 2010 to Office Action dated Aug. 23, 2010", (w/ English Translation of Claims), 14 pgs.
"Mexican Application Serial No. PA/a/2005/012712 , Office Action dated Aug. 11, 2009", (English Translation), 5 pgs.
"Mexican Application Serial No. PA/a/2005/012712 , Response filed Sep. 28, 2009 to Office Action dated Jul. 21, 2009", (w/ English Translation of Claims), 24 pgs.
"Mexican Application Serial No. PA/a/2005/012712, Office Action dated May 12, 2010", (w/English Translation), 19 pgs.
"Mexican Application Serial No. PA/a/2005/012712, Office Action dated Jun. 9, 2010", (w/English Translation), 11 pgs.
"Mexican Application Serial No. PA/a/2005/012712, Office Action dated Nov. 30, 2009", (w/English Translation), 14 pgs.
"Mexican Application Serial No. PA/a/2005/012712, Official Action dated Mar. 5, 2009", (English Translation), 2 pgs.
"Mexican Application Serial No. PA/a/2005/012712, Response filed Feb. 3, 2010 to Office Action dated Nov. 30, 2009", (w/ English Translation of Amended Claims), 22 pgs.
"Mexican Application Serial No. PA/a/2005/012712, Response filed Sep. 27, 2010 to Office Action dated May 12, 2010", (w/ English Translation of Claims), 19 pgs.
"Mexico Application Serial No. PA/a/2005/012712, Response filed Jun. 12, 2009 to Official Action dated Mar. 5, 2009", (w/ English Translation of Claims), 11 pgs.

(56) **References Cited**

OTHER PUBLICATIONS

"Neuraminidase, partial [Influenza A virus (A/swine/France/WVL13/1995(H1N1))]", GenBank Accession# AC025028, (May 22, 2009), 2 pgs.
"New Zealand Application Serial No. 542935, Examination Report dated Feb. 25, 2008", 2 pgs.
"New Zealand Application Serial No. 542935, Examination Report dated Jun. 14, 2006", 2 pgs.
"New Zealand Application Serial No. 542935, Response filed Jun. 30, 2008 to Examination Report dated Feb. 25, 2008", 32 pgs.
"New Zealand Application Serial No. 542935, Response filed Aug. 7, 2007 to Examination Report dated Jun. 14, 2006", 18 pgs.
"New Zealand Application Serial No. 542935, Voluntary Amendments dated Sep. 12, 2007", 10 pgs.
"New Zealand Application Serial No. 543446, Examination Report dated Feb. 29, 2008", 2 pgs.
"New Zealand Application Serial No. 543446, Examination Report dated May 12, 2008", 2 pgs.
"New Zealand Application Serial No. 543446, Response dated Mar. 20, 2008 to Examination Report dated Feb. 29, 2008", 2 pgs.
"Norweigan Application Serial No. 20056074, Office Action dated Jan. 17, 2017", (English Translation), 5 pgs.
"Norweigan Application Sertial No, 20056074, Office Action dated Apr. 25, 2017", (w/ English Translation), 3 pgs.
"Norweigan Application Serial No. 20056074, Office Action Response dated Apr. 18, 2017", (w/ English Claims 0, 27 pgs.
"Norweigan Application Serial No. 20056074, Response filed Jul. 25, 2017 to Office Action dated Apr. 25, 2017", (w/ English Translation of Amended Claims), 111 pgs.
"NorweiganApplication Serial No. 20056074, Office Action dated Apr. 25, 2017", (Translation), 3 pgs.
"Russian Federation Application No. 2005136233, Office Action dated Dec. 25, 2007", 2 pgs.
"Russian Federation Application No. 2005136233, Response filed May 29, 2008 to Office Action dated Dec. 25, 2007", (w/ Partial English Translation), 7 pgs.
"Russian Federation Application Serial No. 2005136233, First Office Action dated Feb. 27, 2007", (w/ English Translation), 5 pgs.
"Russian Federation Application Serial No. 2005136233, Response filed Jun. 14, 2007 to First Office Action dated Feb. 27, 2007", (English Translation of Claims), 6 pgs.
"Russian Federation Application Serial No. 2005136233, Response filed Nov. 20, 2007 to Office Action", (w/ English Translation of Amended Claims), 18 pgs.
"Singaporean Application Serial No. 200506858-0, Examination Report dated Feb. 9, 2007", 4 pgs.
"Singaporean Application Serial No. 200506858-0, Response filed Dec. 22, 2006 to Written Opinion dated Jul. 26, 2006", 18 pgs.
"Singaporean Application Serial No. 200506858-0, Written Opinion dated Jul. 26, 2006", 8 pgs.
"Singaporean Application Serial No. 200507468-7, Examination Report dated Mar. 19, 2008", 5 pgs.
"Singaporean Application Serial No. 200507468-7, Invitation to Respond to Written Opinion dated Jun. 12, 2007", 6 pgs.
"Singaporean Application Serial No. 200507468-7, Response filed Nov. 7, 2007 to Invitation to Respond to Written Opinion dated Jun. 12, 2007", 9 pgs.
"Ukrainian Application Serial No. 200512619, Response filed Jan. 21, 2010 to Office Action dated Jun. 17, 2009", (w/ English Claims), 14 pgs.
"Ukrainian Application Serial No. 200512619, Office Action dated Feb. 27, 2009", (w/ English Translation), 21 pgs.
"Ukrainian Application Serial No. 200512619, Office Action dated Jun. 17, 2009", (w/ English Translation), 4 pgs.
"Ukrainian Application Serial No. 200512619, Response filed Apr. 8, 2009 to Office Action dated Feb. 27, 2009", (w/ English Translation of Claims), 9 pgs.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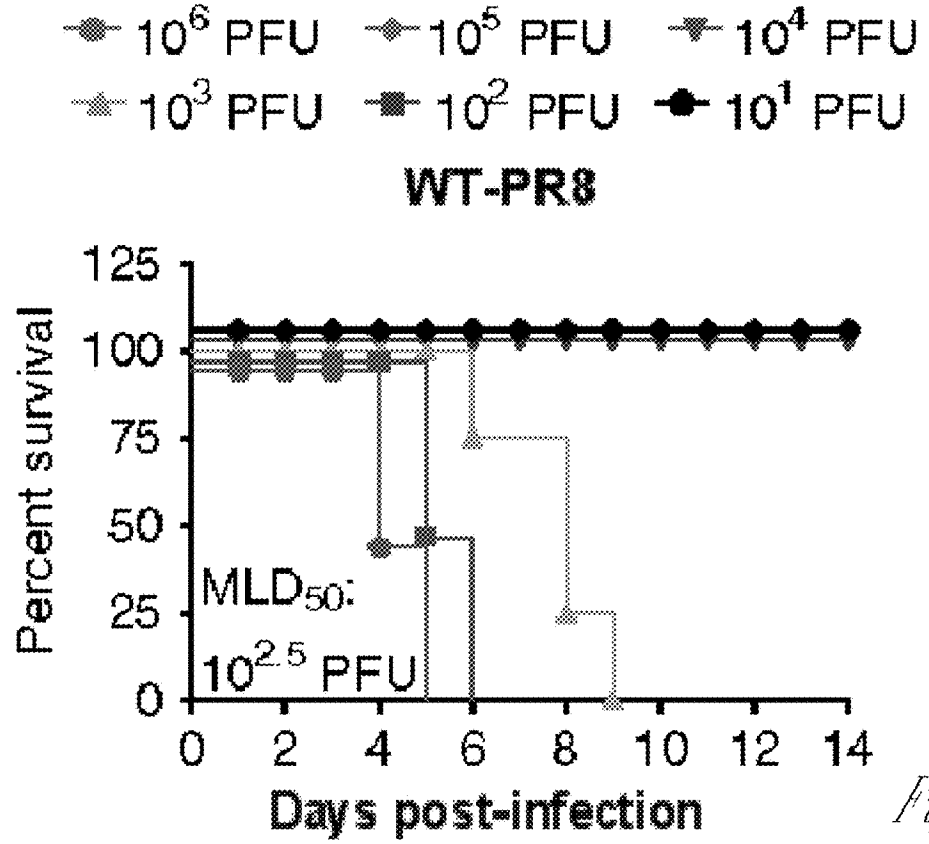
10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
WT-PR8
Weight change
120
100
80
60
0
2
4
6
8
10
12
14
Days post-infection

Fig. 1A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10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
WT-PR8
Percent survival
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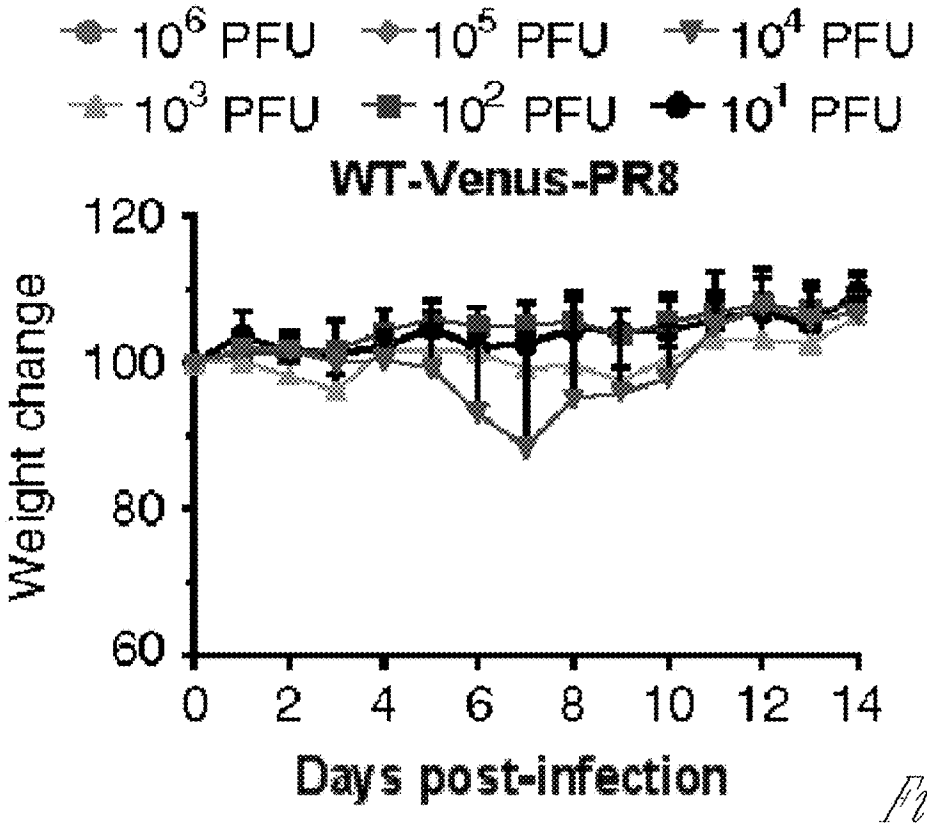
100
75
50
25
0
MLD_{50}:
$10^{2.5}$ PFU
0
2
4
6
8
10
12
14
Days post-infection

Fig. 1B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10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
WT-Venus-PR8
Weight change
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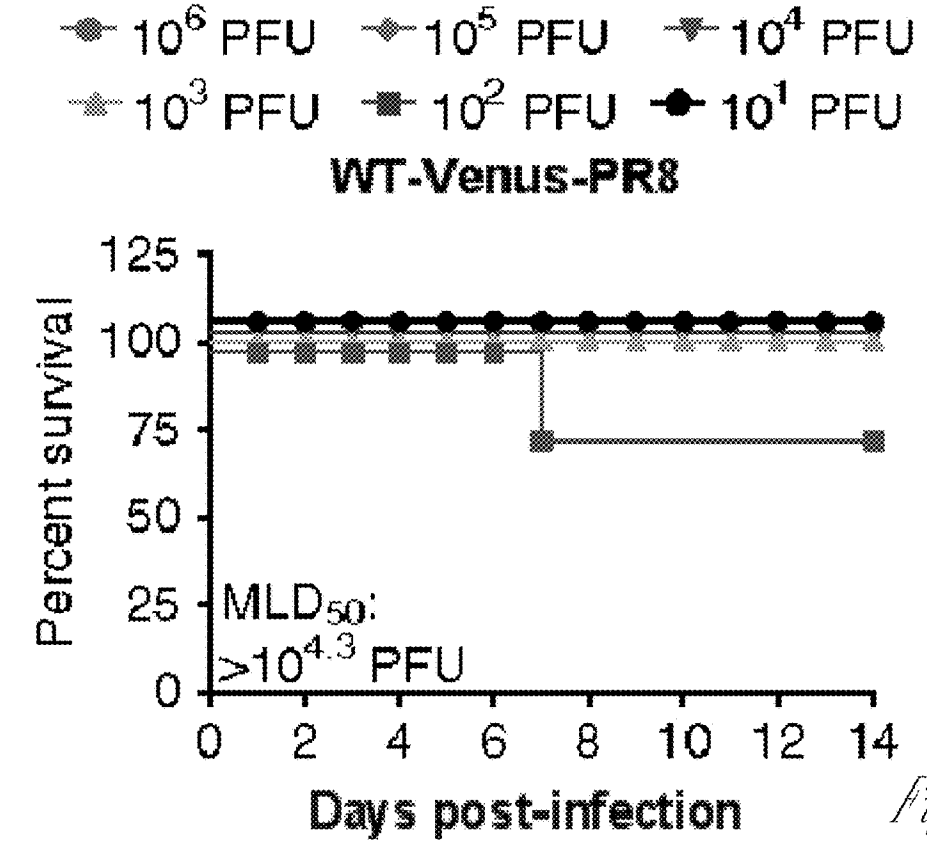
100
80
60
0
2
4
6
8
10
12
14
Days post-infection

Fig. 1C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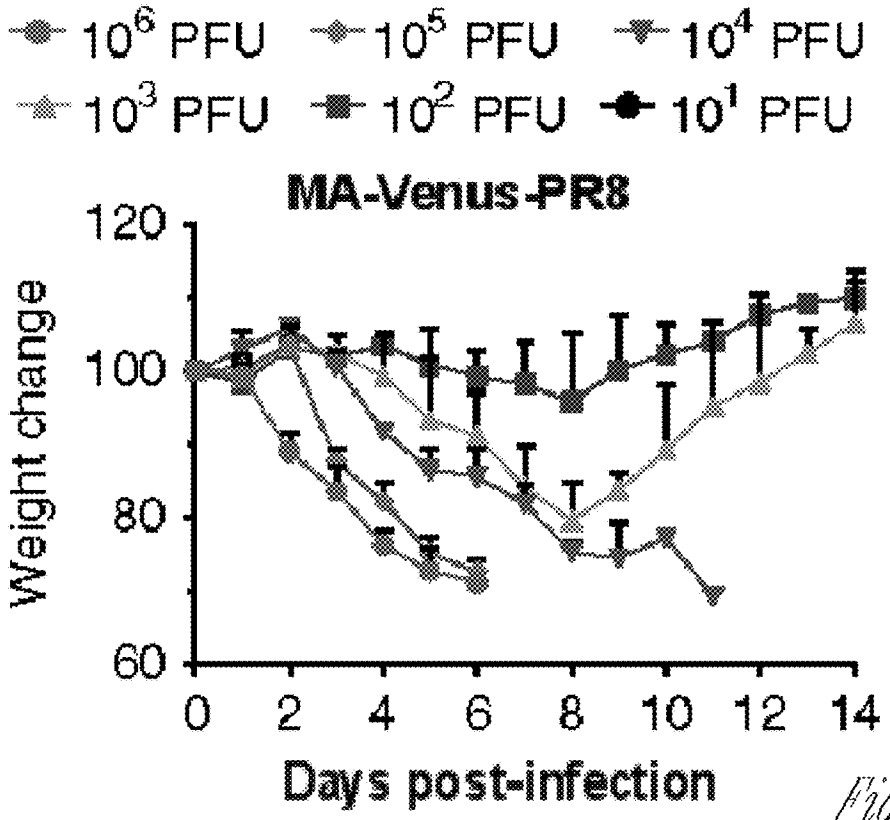
10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
WT-Venus-PR8
Percent survival
125
100
75
50
25
0
MLD_{50}:
$>10^{4.3}$ PFU
0
2
4
6
8
10
12
14
Days post-infection

Fig. 1D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10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
MA-Venus-PR8
Weight change
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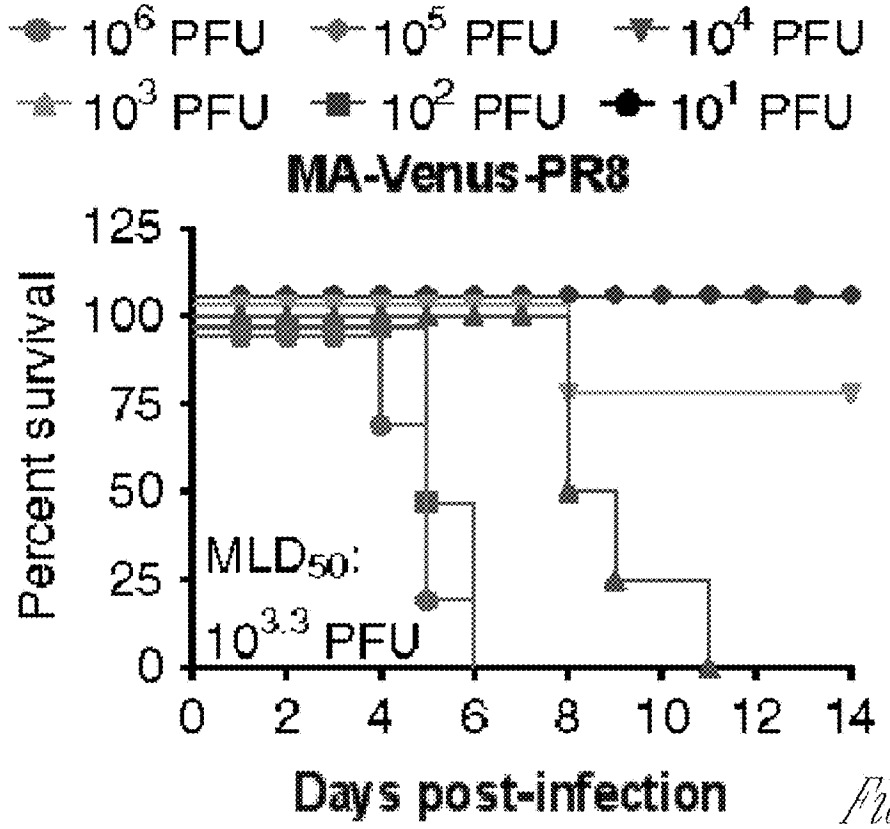
100
80
60
0
2
4
6
8
10
12
14
Days post-infection

Fig. 1E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10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
MA-Venus-PR8
Percent survival
125
100
75
50
25
0
MLD_{50}:
$10^{3.3}$ PFU
0
2
4
6
8
10
12
14
Days post-infection

Fig. 1F

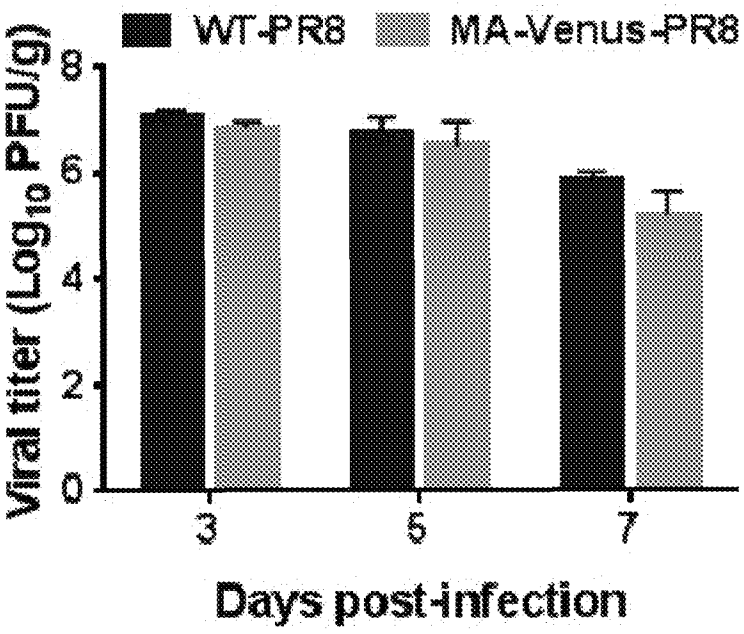

WT-PR8
MA-Venus-PR8
Viral titer (Log10 PFU/g)
0
2
4
6
8
3
5
7
Days post-infection

Fig. 1C

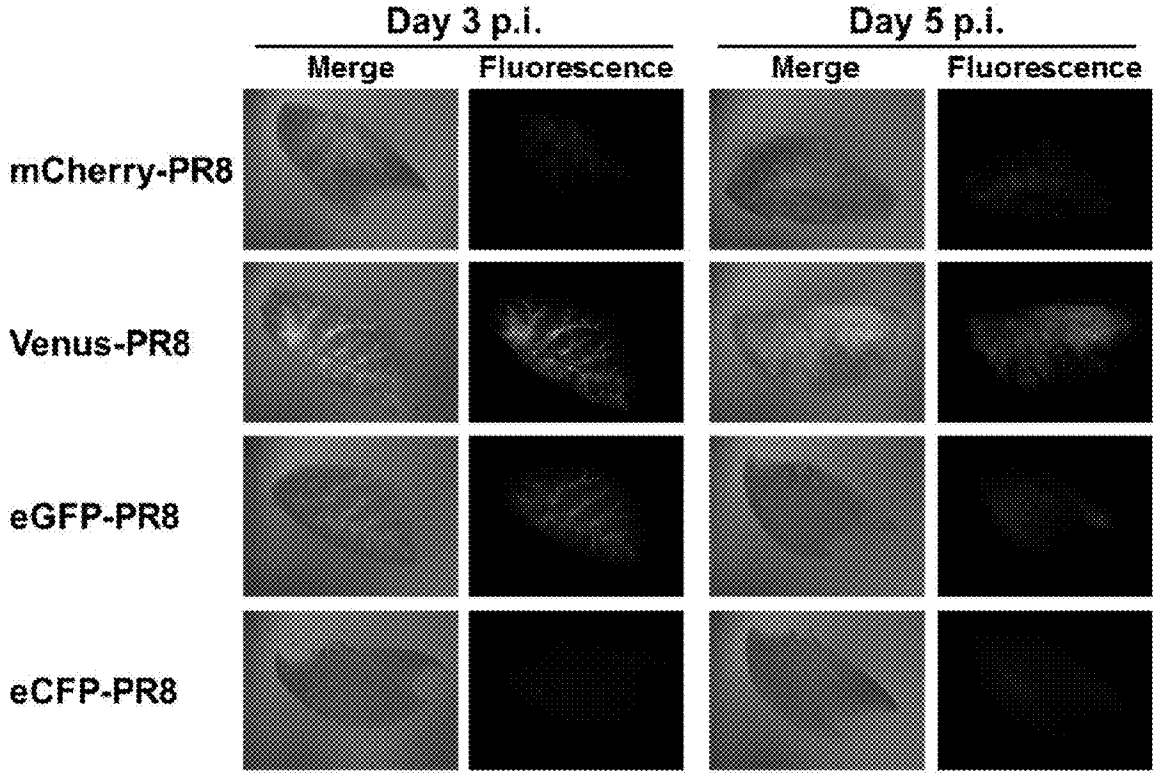


Fig.2A

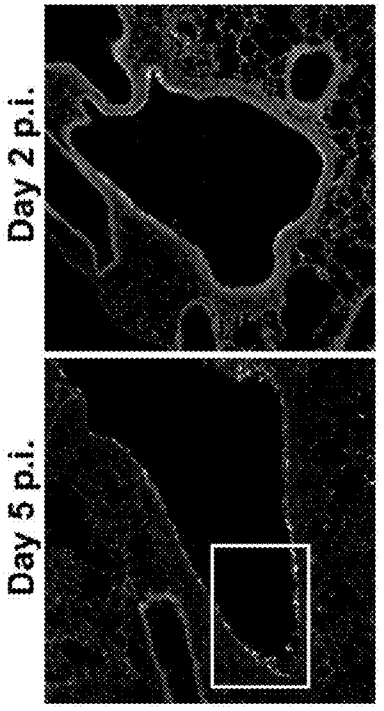


Fig.2B

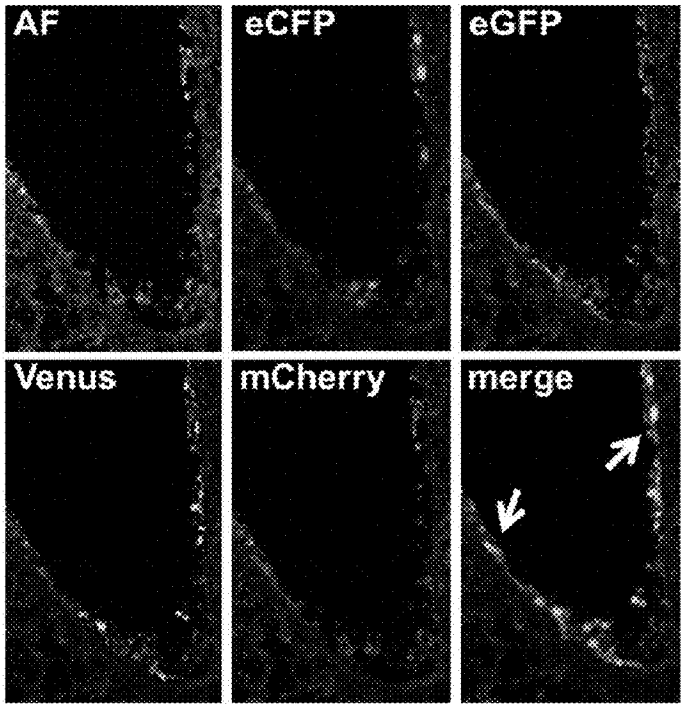


Fig.2C

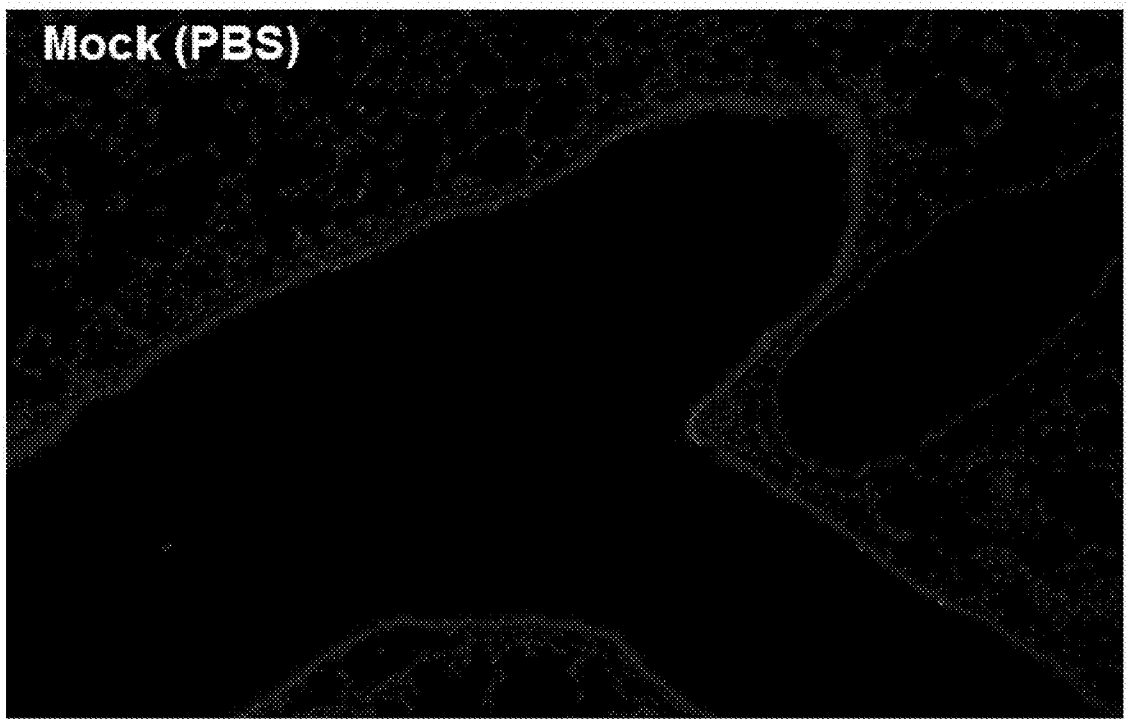


Fig. 3A

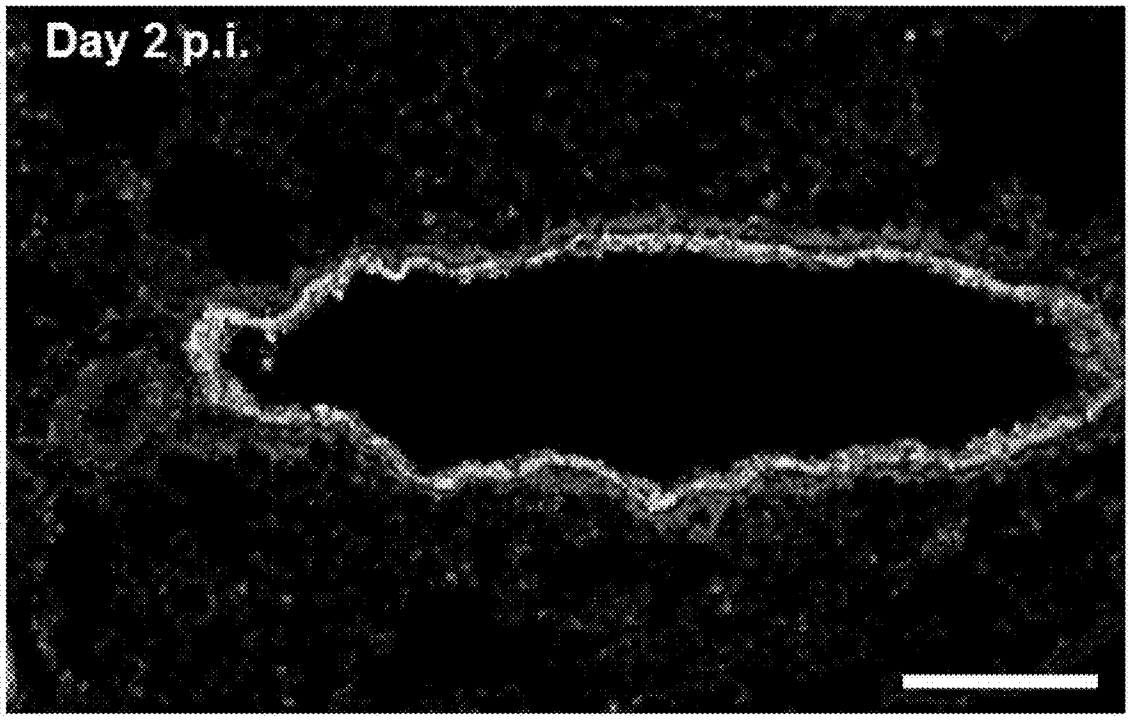


Fig. 3B

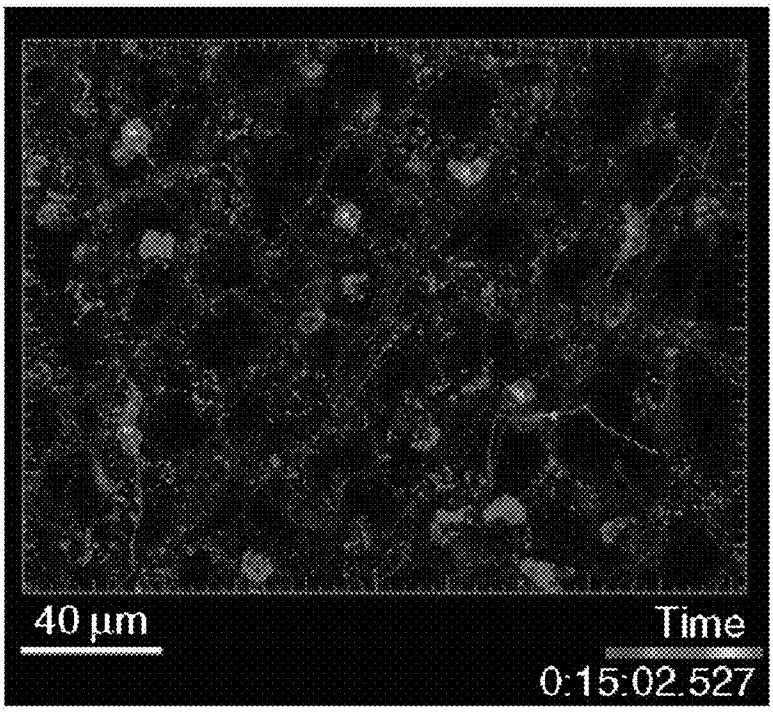


Fig. 3C

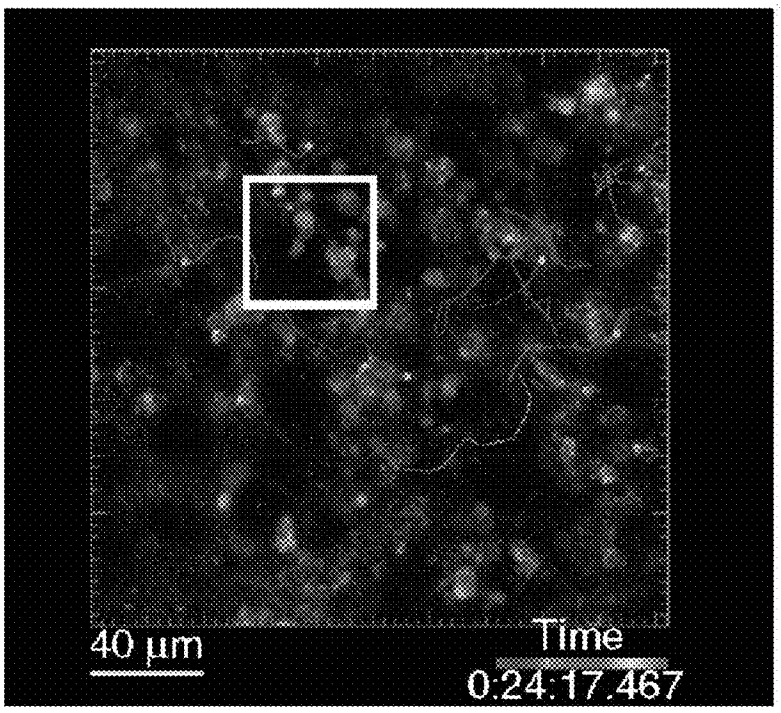


Fig. 3D

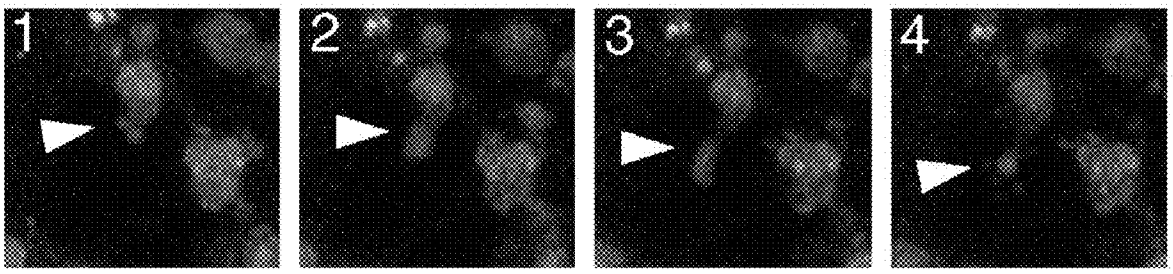


Fig. 3E Fig. 3F Fig. 3G Fig. 3H

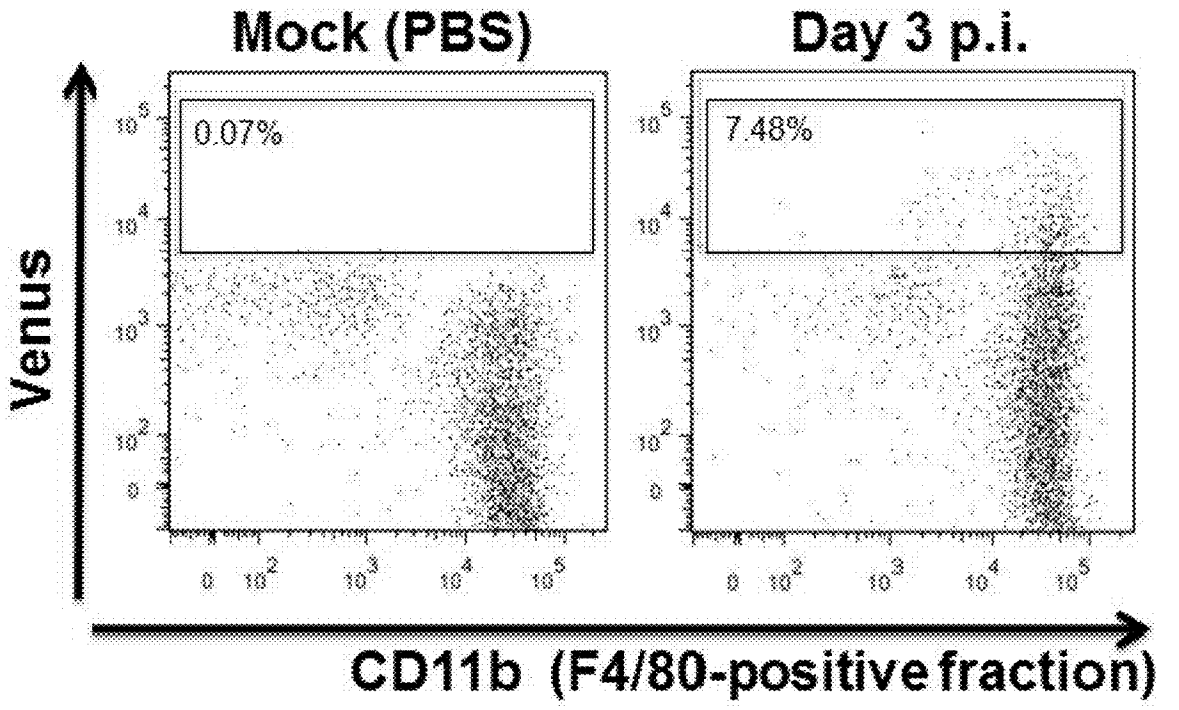


Fig. 3I

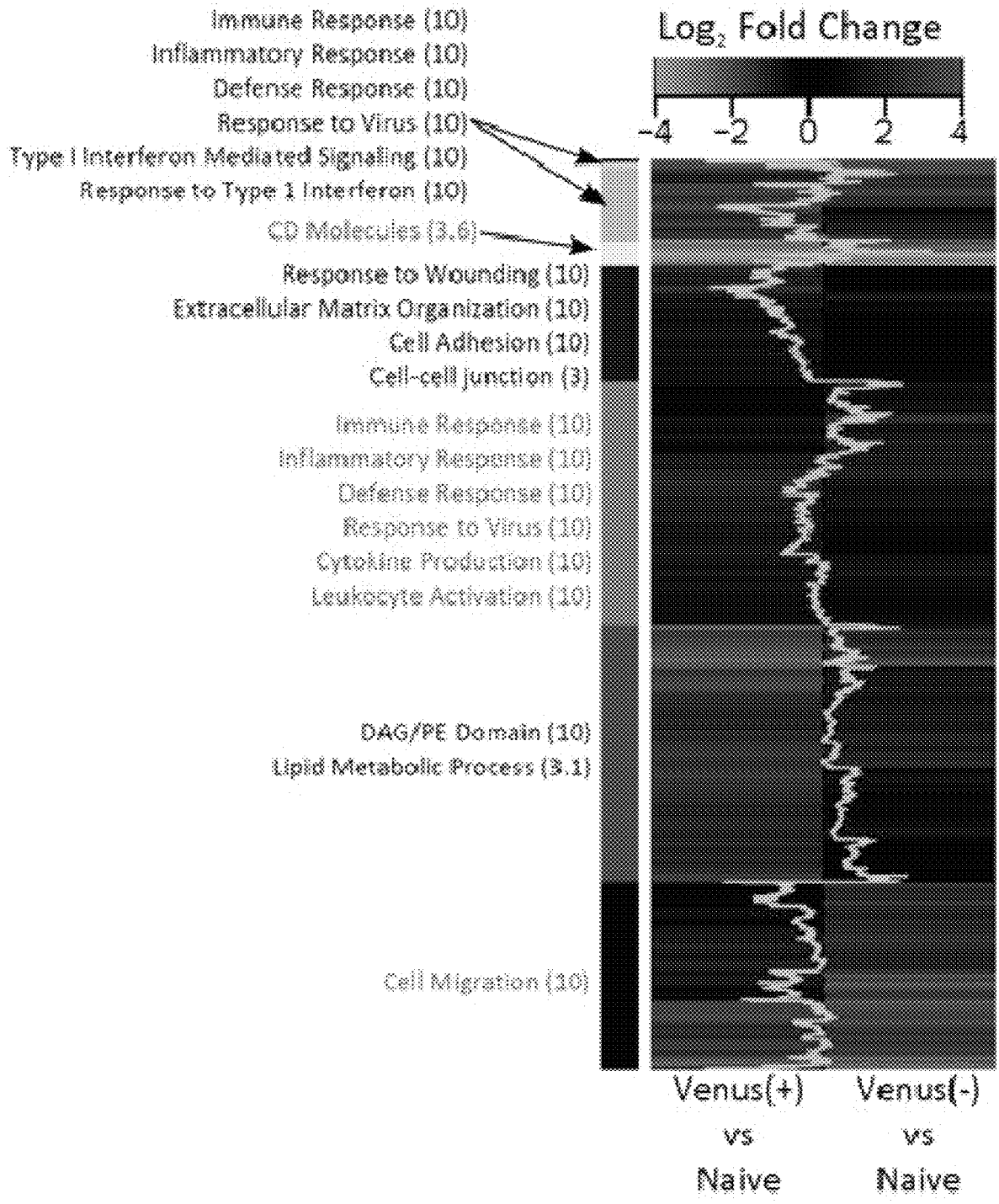

Log2 Fold Change
−4
−2
0
2
4
Immune Response (10)
Inflammatory Response (10)
Defense Response (10)
Response to Virus (10)
Type I Interferon Mediated Signaling (10)
Response to Type 1 Interferon (10)
CD Molecules (3.6)
Response to Wounding (10)
Extracellular Matrix Organization (10)
Cell Adhesion (10)
Cell-cell junction (3)
Immune Response (10)
Inflammatory Response (10)
Defense Response (10)
Response to Virus (10)
Cytokine Production (10)
Leukocyte Activation (10)
DAG/PE Domain (10)
Lipid Metabolic Process (3.1)
Cell Migration (10)
Venus(+) vs Naive
Venus(-) vs Naive

Fig. 3J

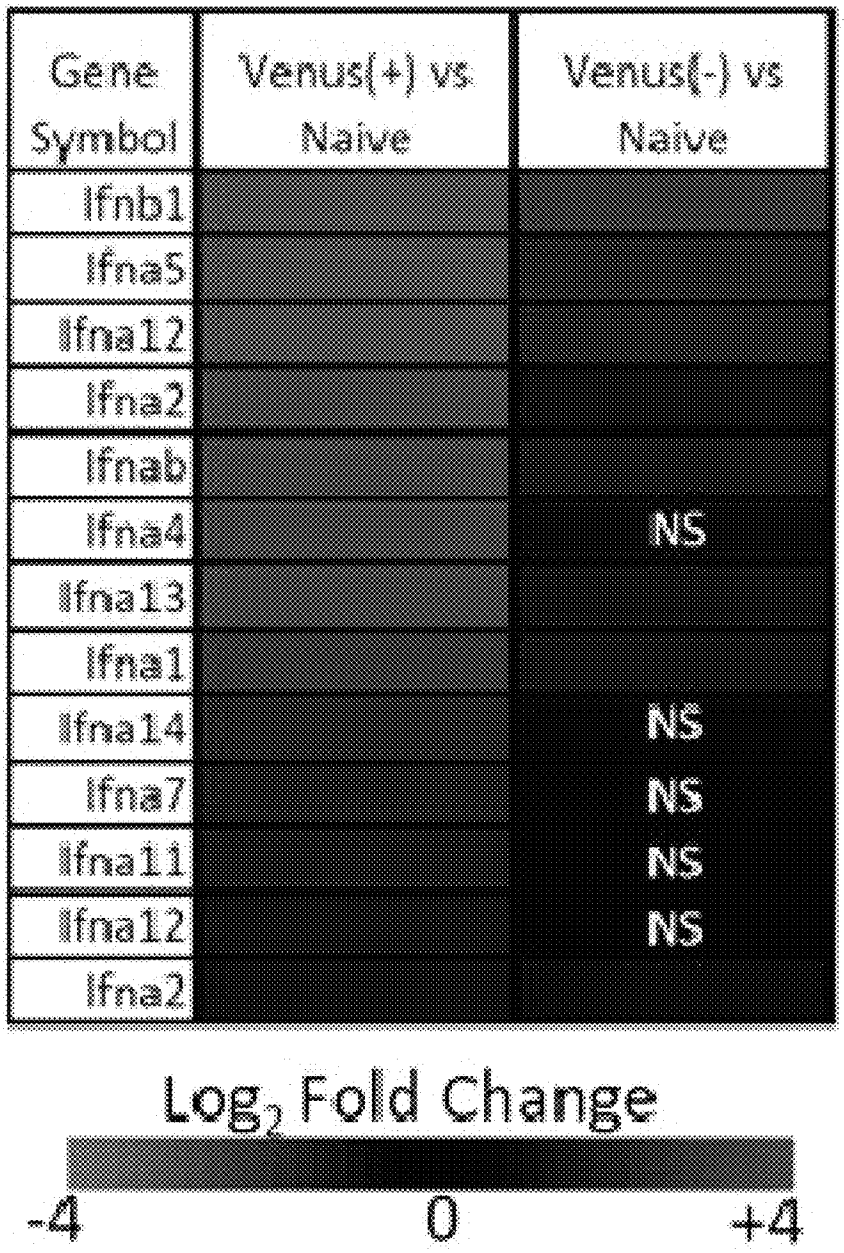

Gene Symbol
Venus(+) vs Naive
Venus(-) vs Naive
Ifnb1
Ifna5
Ifna12
Ifna2
Ifnab
Ifna4
NS
Ifna13
Ifna1
Ifna14
NS
Ifna7
NS
Ifna11
NS
Ifna12
NS
Ifna2
Log2 Fold Change
-4
0
+4

Fig. 3K

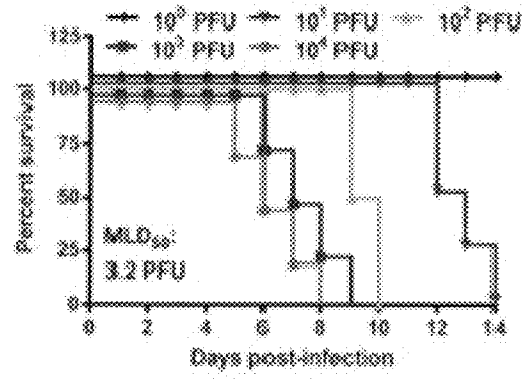


Fig. 4A

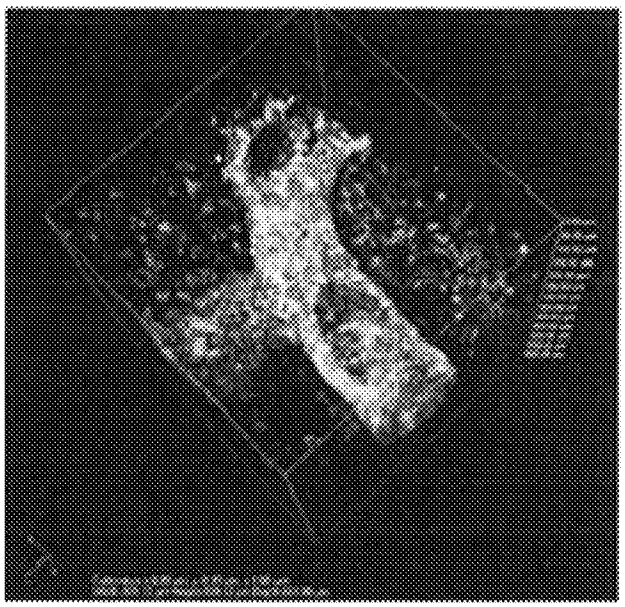


Fig. 4C

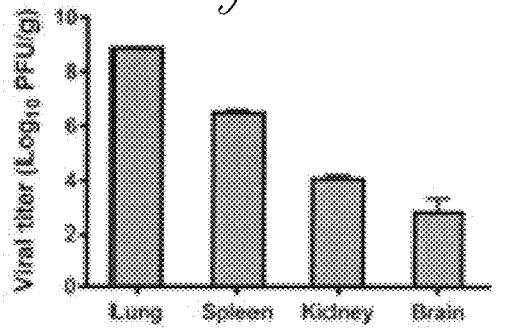


Fig. 4B

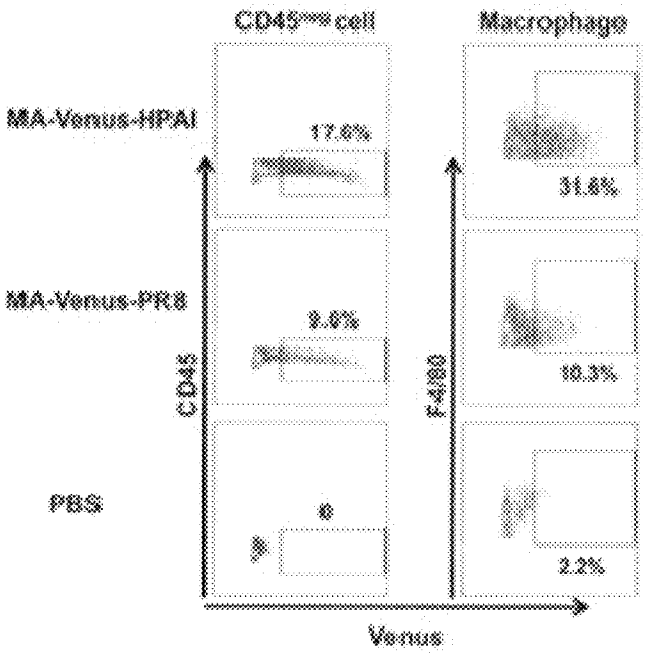


Fig. 4D

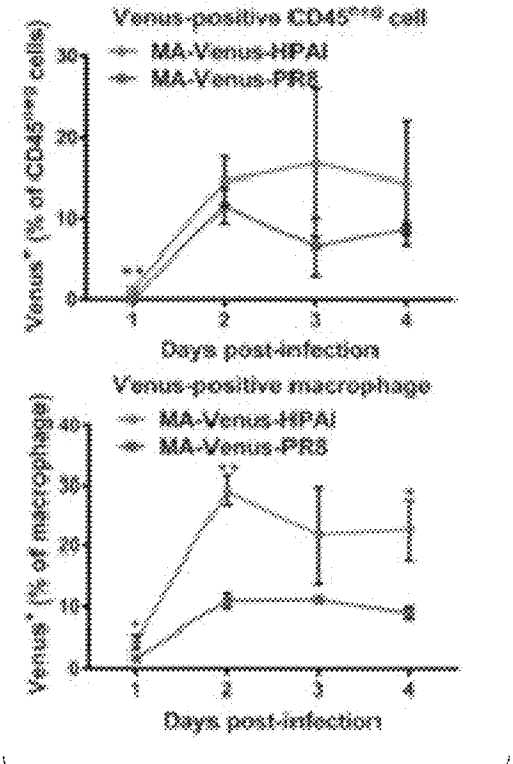


Fig. 4E

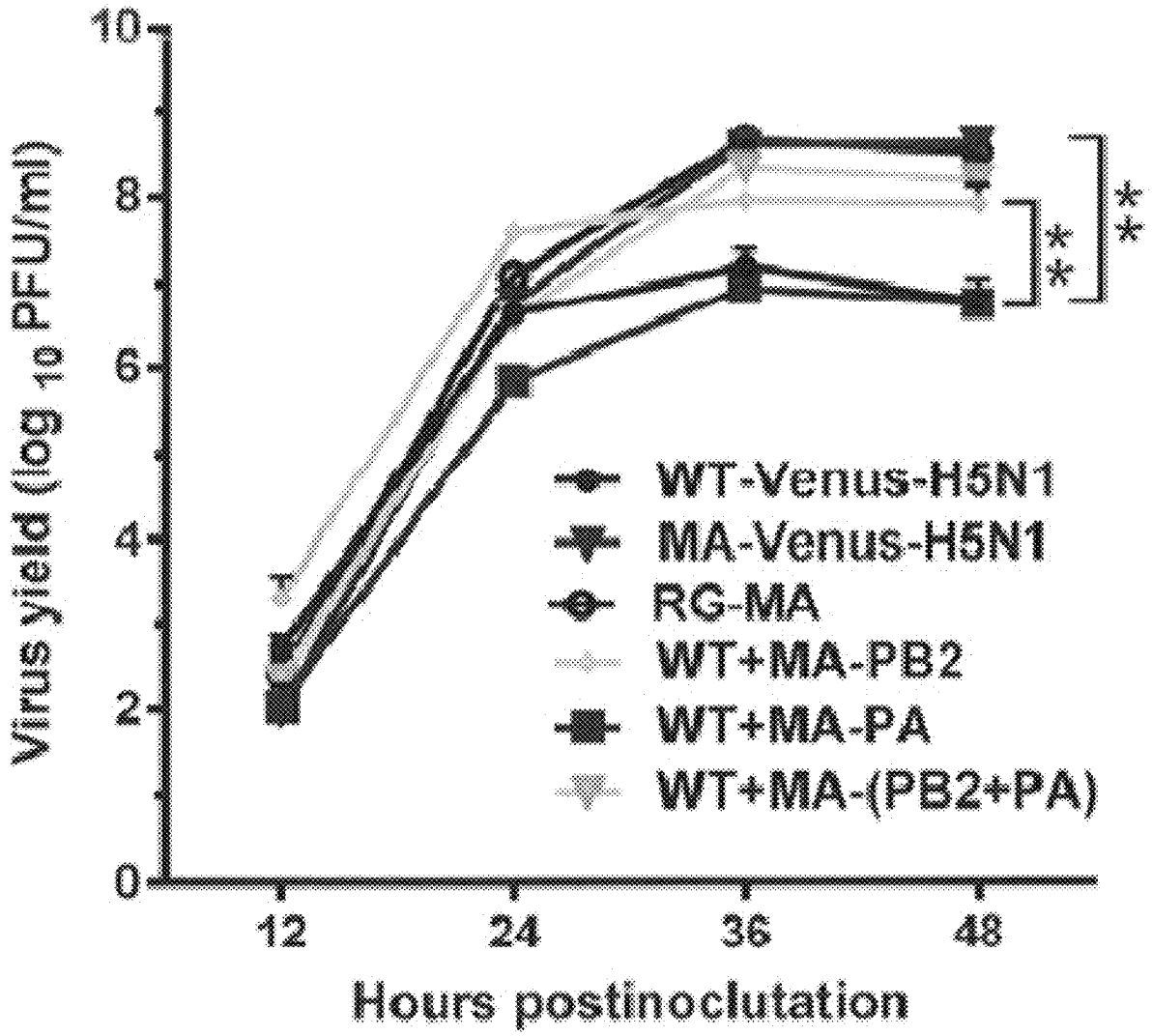

10
8
6
4
2
0
Virus yield (log 10 PFU/ml)
12
24
36
48
Hours postinoclutation
WT-Venus-H5N1
MA-Venus-H5N1
RG-MA
WT+MA-PB2
WT+MA-PA
WT+MA-(PB2+PA)
**
**

Fig. 5

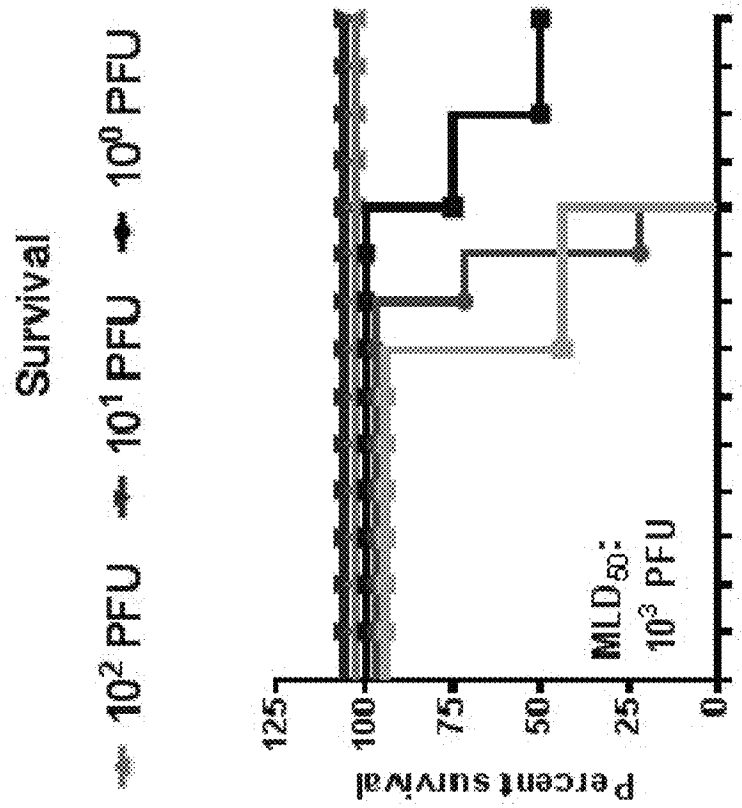

Survival
10^5 PFU
10^4 PFU
10^3 PFU
10^2 PFU
10^1 PFU
10^0 PFU
Percent survival
125
100
75
50
25
0
MLD_{50}:
10^3 PFU

Fig. 6B

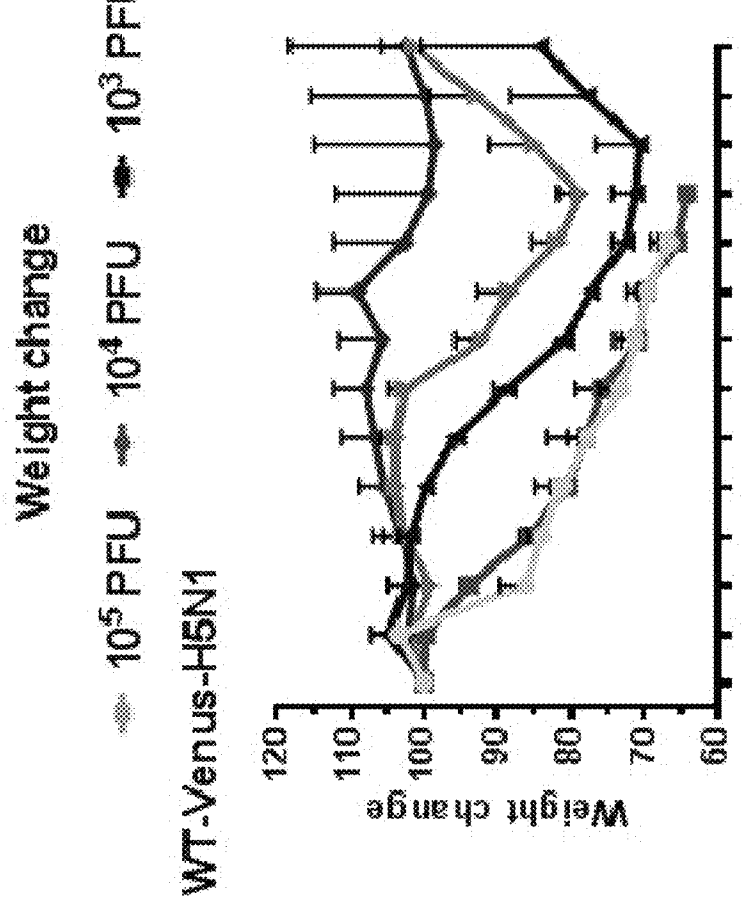

Weight change
WT-Venus-H5N1
10^5 PFU
10^4 PFU
10^3 PFU
Weight change
120
110
100
90
80
70
60

Fig. 6A

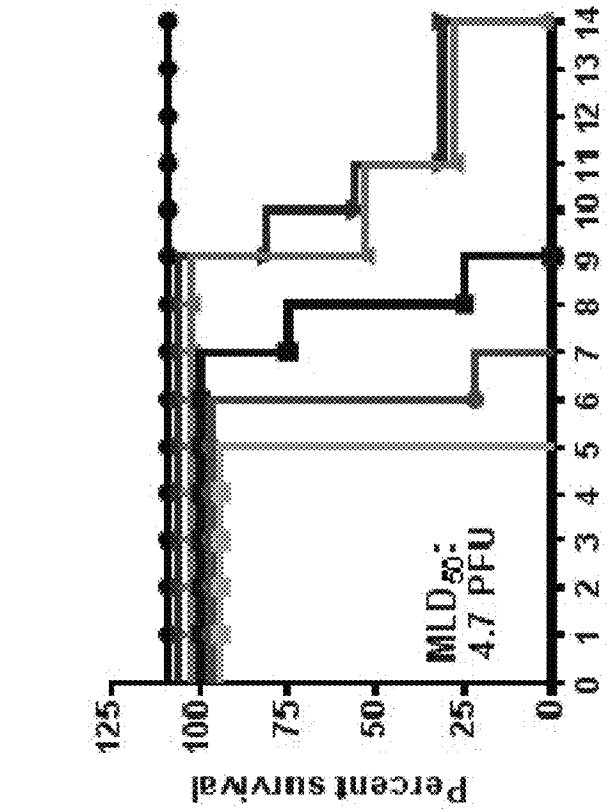
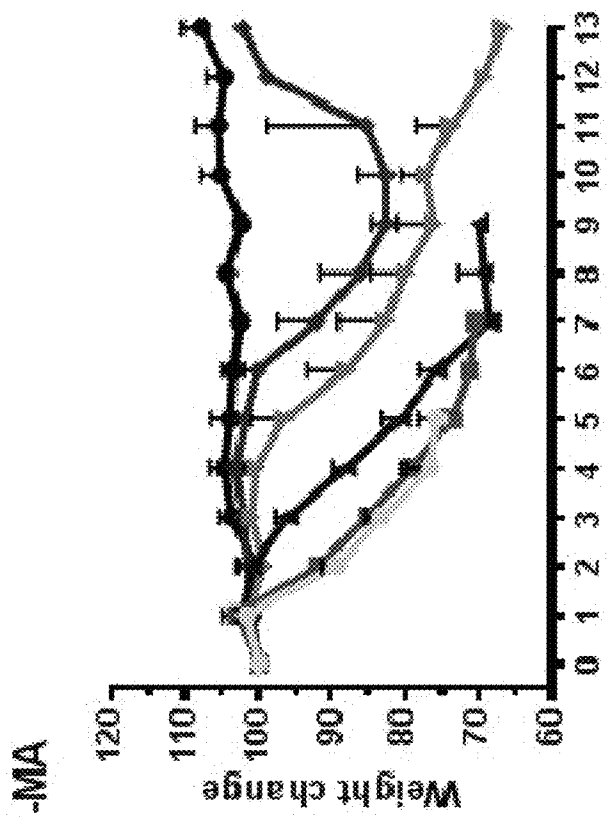


Fig. 6D



RG-MA

Fig. 6C

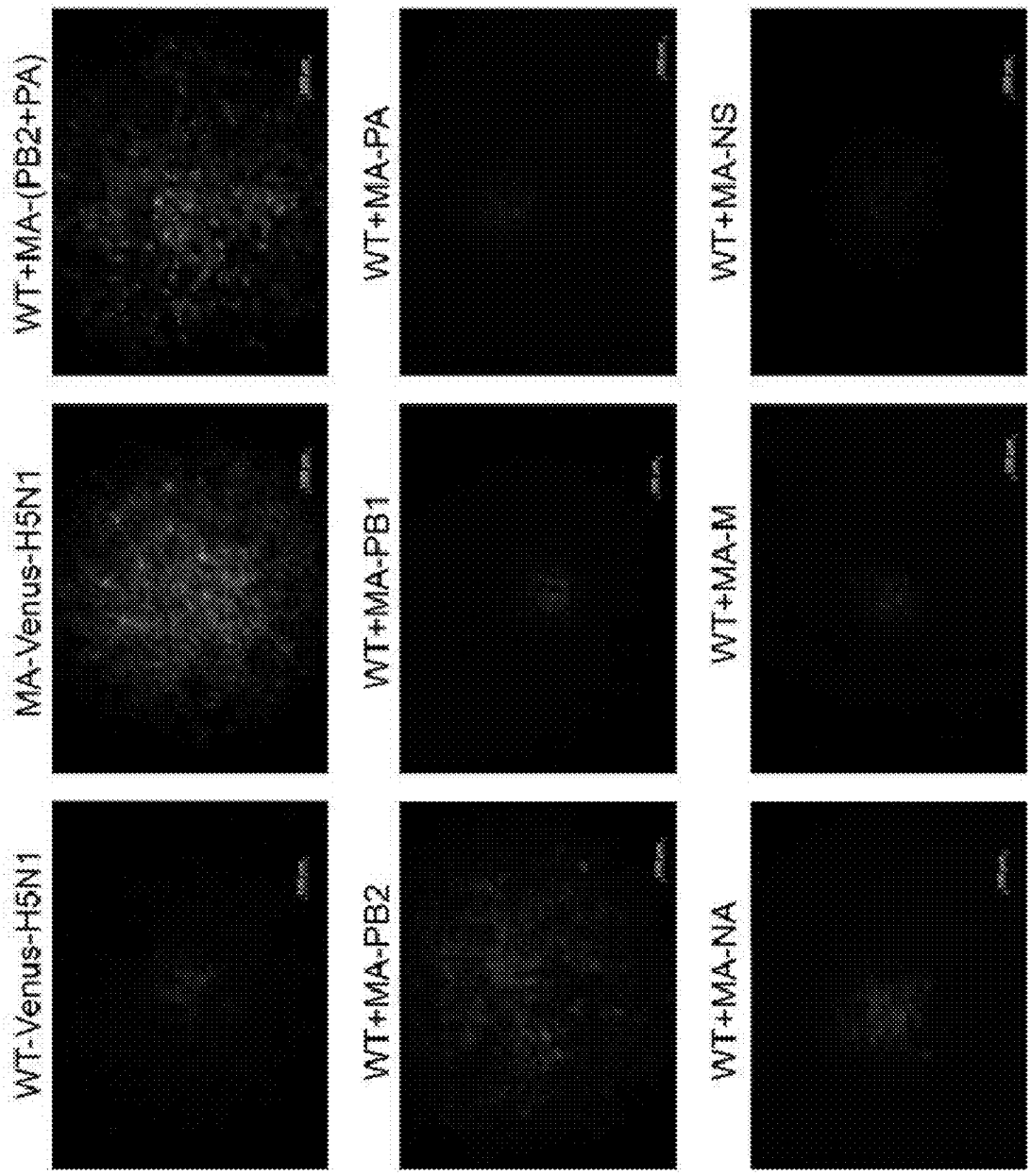

WT-Venus-H5N1
MA-Venus-H5N1
WT+MA-(PB2+PA)
WT+MA-PB2
WT+MA-PB1
WT+MA-PA
WT+MA-NA
WT+MA-M
WT+MA-NS

Fig. 7

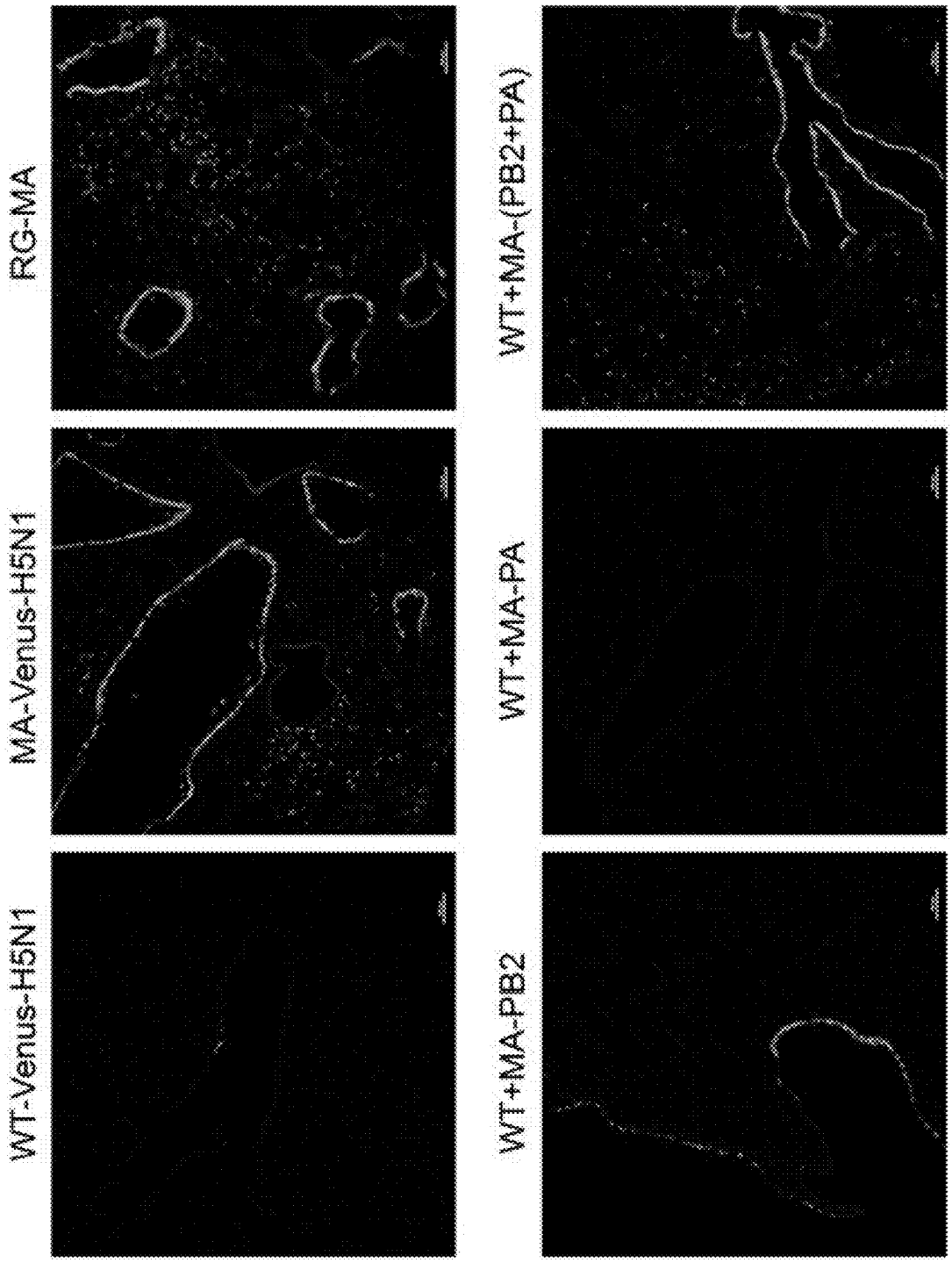


Fig. 8

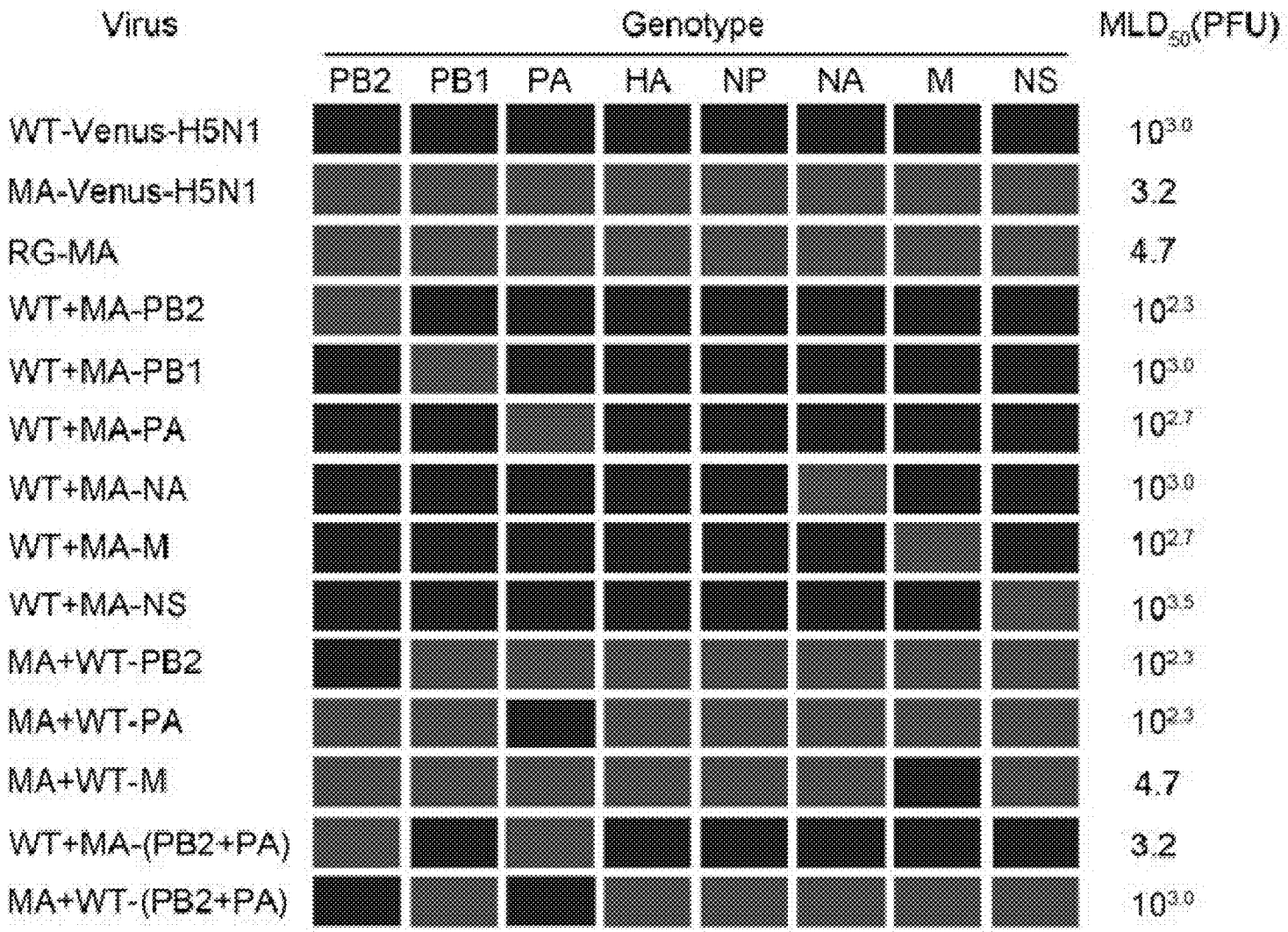

Virus
Genotype
MLD50(PFU)
PB2
PB1
PA
HA
NP
NA
M
NS
WT-Venus-H5N1
10^3.0
MA-Venus-H5N1
3.2
RG-MA
4.7
WT+MA-PB2
10^2.3
WT+MA-PB1
10^3.0
WT+MA-PA
10^2.7
WT+MA-NA
10^3.0
WT+MA-M
10^2.7
WT+MA-NS
10^3.5
MA+WT-PB2
10^2.3
MA+WT-PA
10^2.3
MA+WT-M
4.7
WT+MA-(PB2+PA)
3.2
MA+WT-(PB2+PA)
10^3.0

Fig. 9

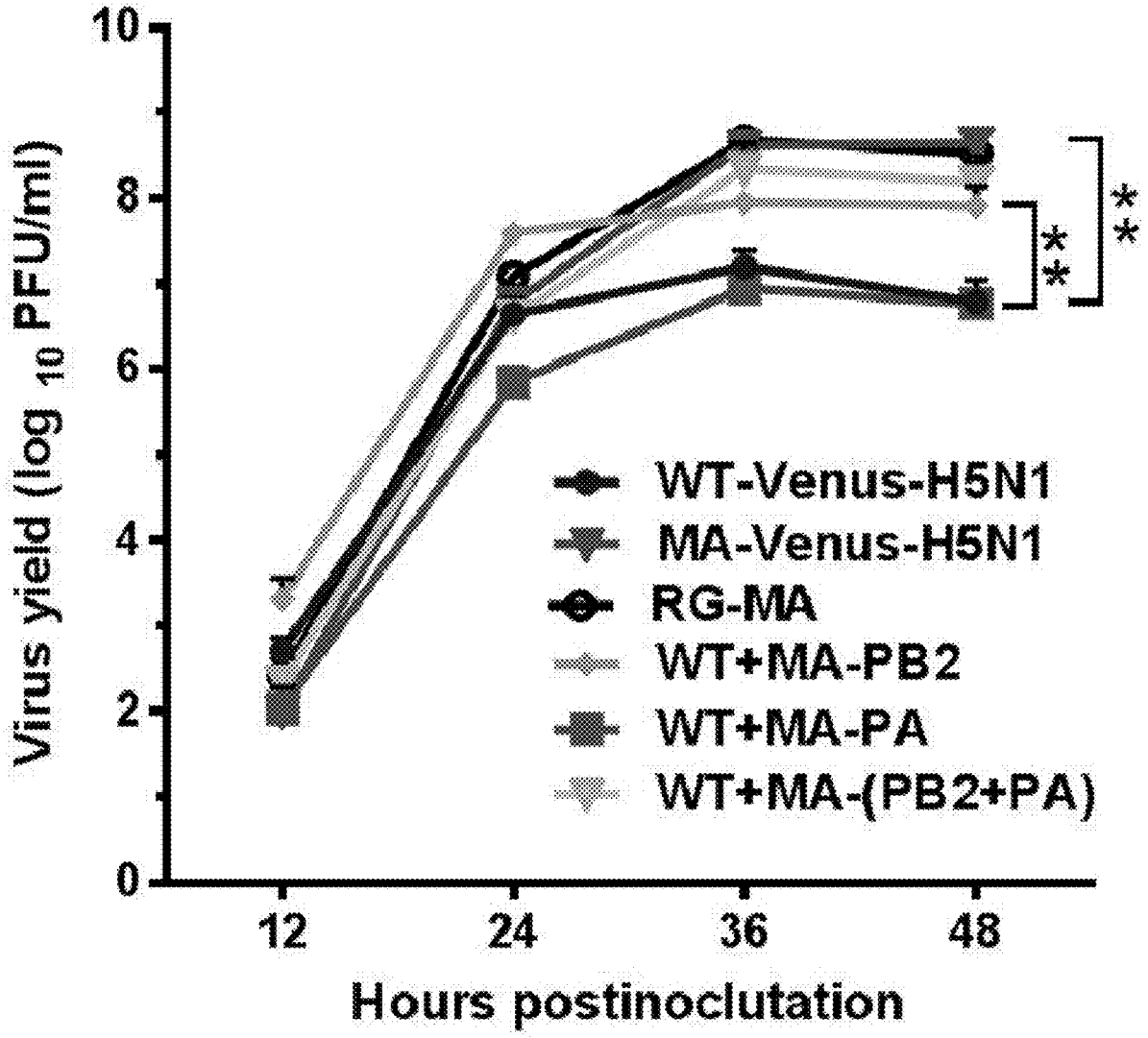

Virus yield (log 10 PFU/ml)
10
8
6
4
2
0
12
24
36
48
Hours postinoclutation
WT-Venus-H5N1
MA-Venus-H5N1
RG-MA
WT+MA-PB2
WT+MA-PA
WT+MA-(PB2+PA)
**
**

Fig. 10

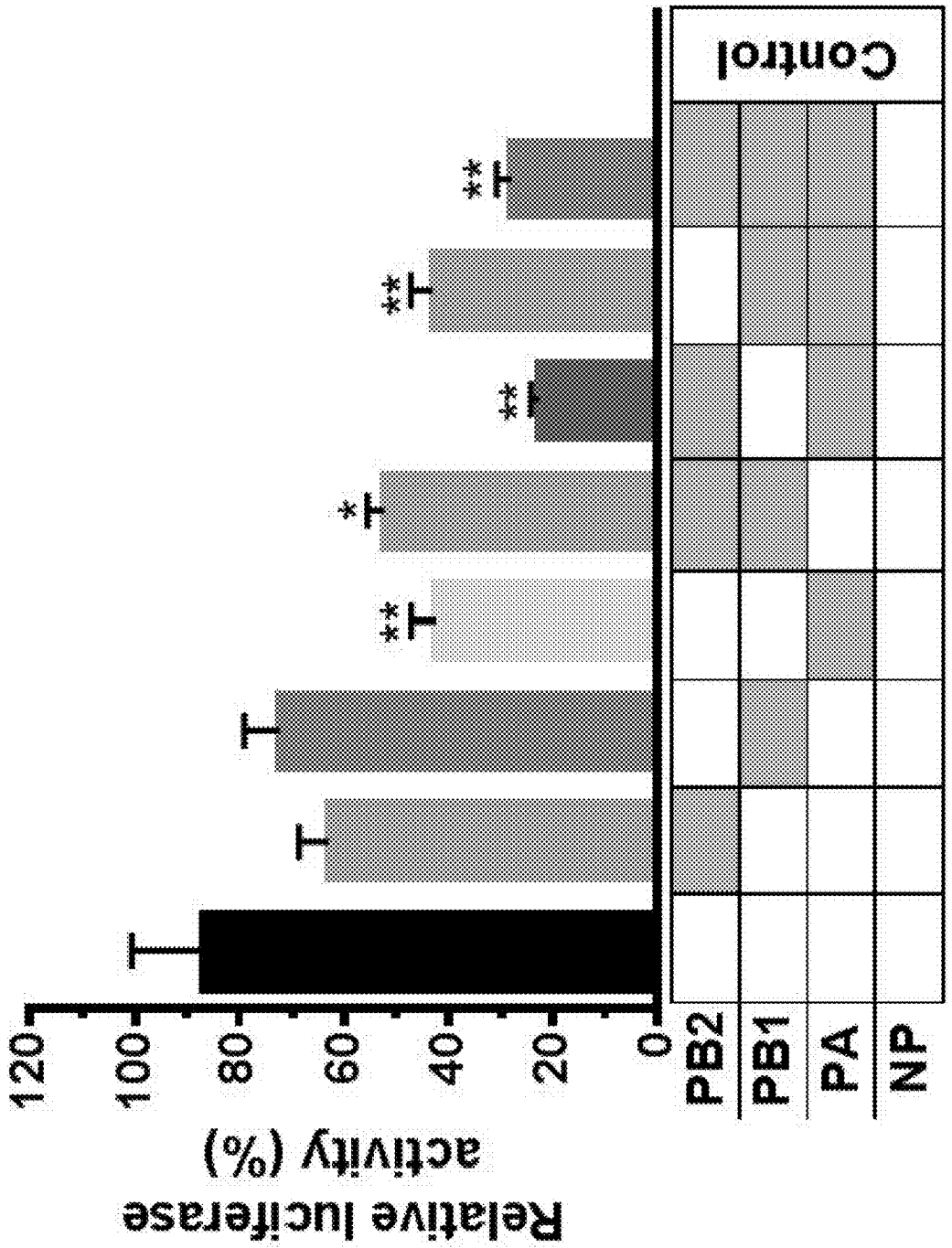

Relative luciferase activity (%)
120
100
80
60
40
20
0
PB2
PB1
PA
NP
Control
**
**
*
**
**
**

Fig. 11

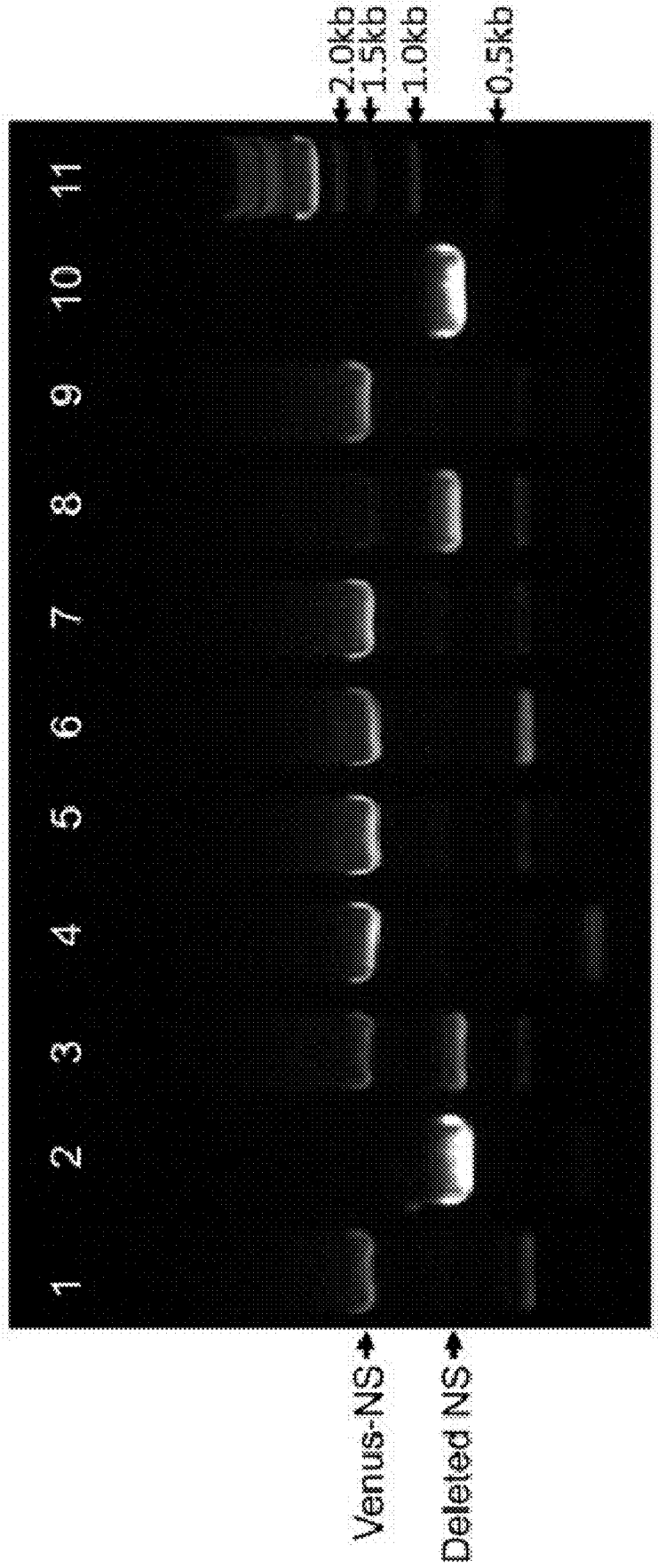


Fig. 12A

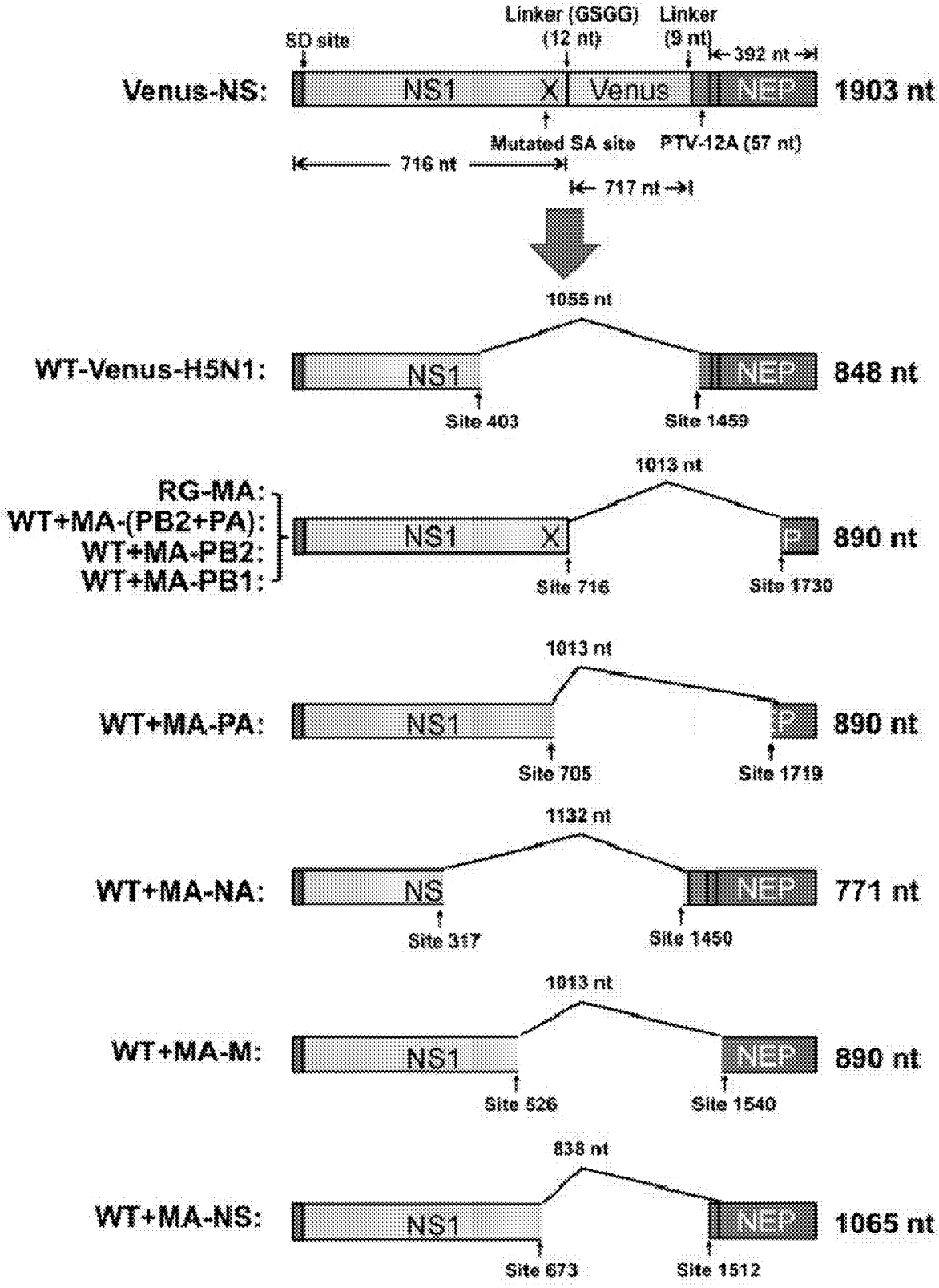

Linker (GSGG) (12 nt)
Linker (9 nt)
SD site
392 nt
Venus-NS:
NS1
X
Venus
NEP
1903 nt
Mutated SA site
PTV-12A (57 nt)
716 nt
717 nt
1055 nt
WT-Venus-H5N1:
NS1
NEP
848 nt
Site 403
Site 1459
1013 nt
RG-MA:
WT+MA-(PB2+PA):
WT+MA-PB2:
WT+MA-PB1:
NS1
X
P
890 nt
Site 716
Site 1730
1013 nt
WT+MA-PA:
NS1
P
890 nt
Site 705
Site 1719
1132 nt
WT+MA-NA:
NS
NEP
771 nt
Site 317
Site 1450
1013 nt
WT+MA-M:
NS1
NEP
890 nt
Site 526
Site 1540
838 nt
WT+MA-NS:
NS1
NEP
1065 nt
Site 673
Site 1512

Fig. 12B

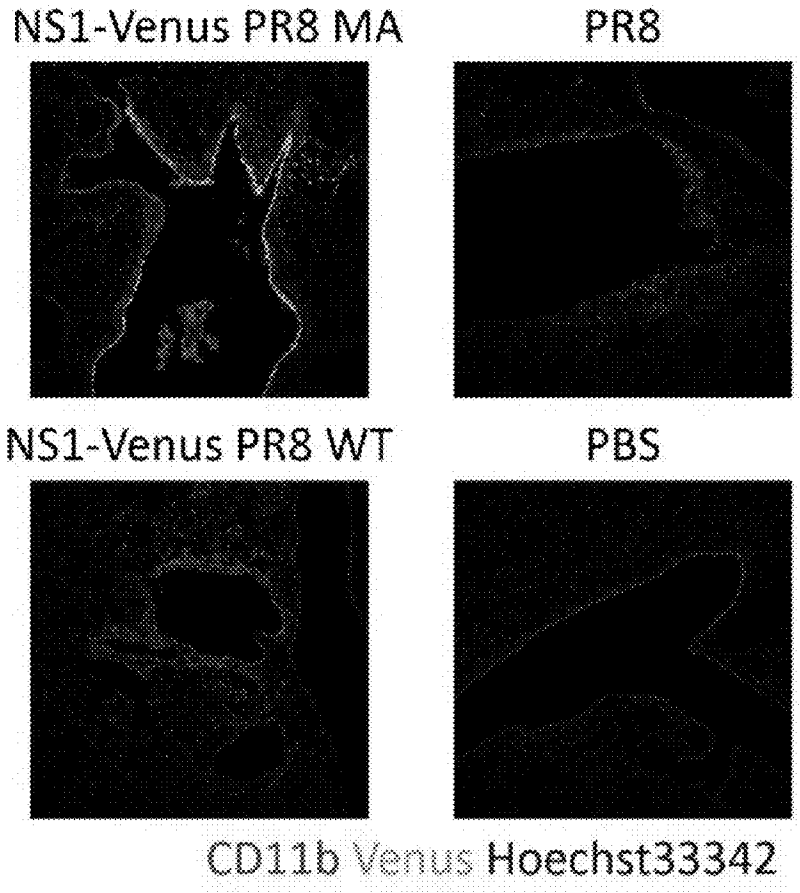

NS1-Venus PR8 MA
PR8
NS1-Venus PR8 WT
PBS
CD11b Venus Hoechst33342

Fig. 13

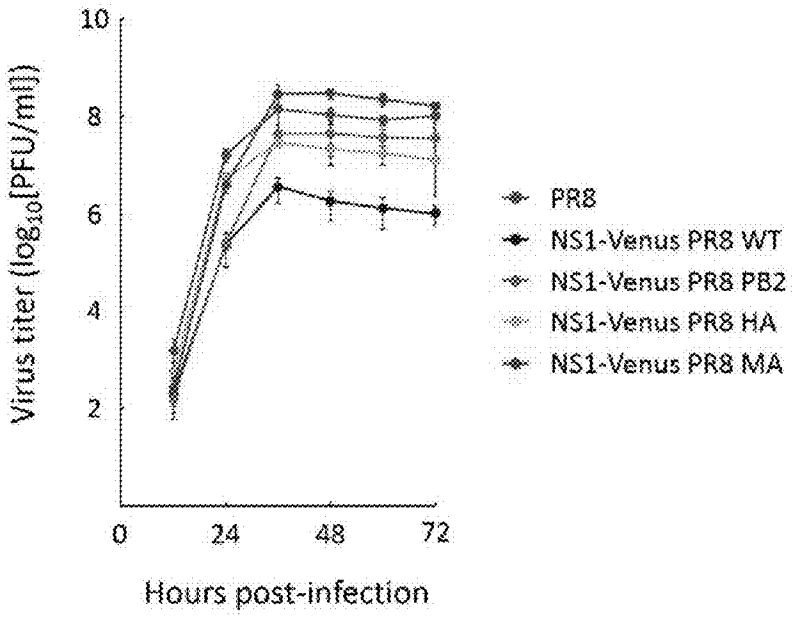

Virus titer (log_{10}[PFU/ml])
10
8
6
4
2
0
24
48
72
Hours post-infection
PR8
NS1-Venus PR8 WT
NS1-Venus PR8 PB2
NS1-Venus PR8 HA
NS1-Venus PR8 MA

Fig. 14

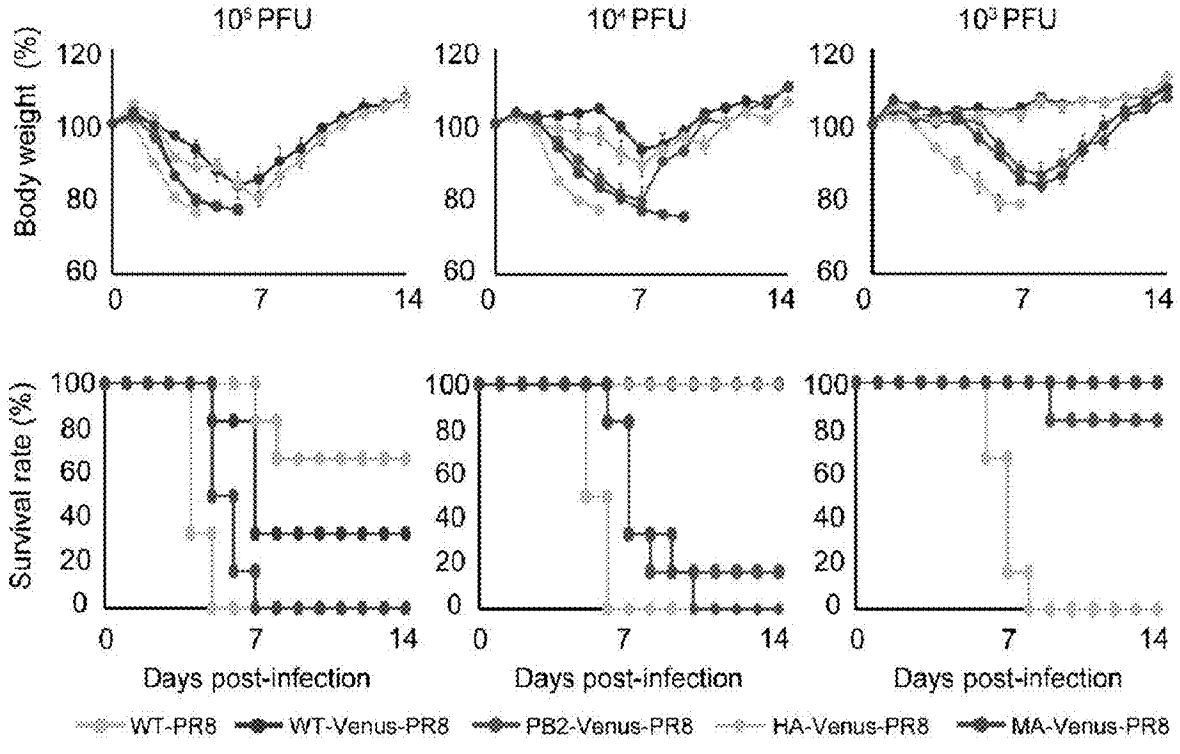

10^6 PFU
10^4 PFU
10^3 PFU
Body weight (%)
120
100
80
60
0
7
14
Survival rate (%)
100
80
60
40
20
0
Days post-infection
WT-PR8
WT-Venus-PR8
PB2-Venus-PR8
HA-Venus-PR8
MA-Venus-PR8

Fig. 15

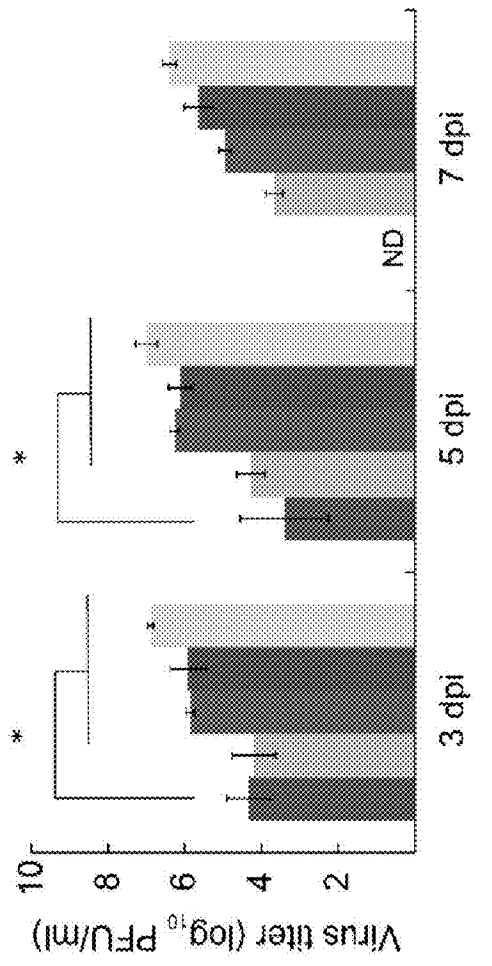


Fig. 16A

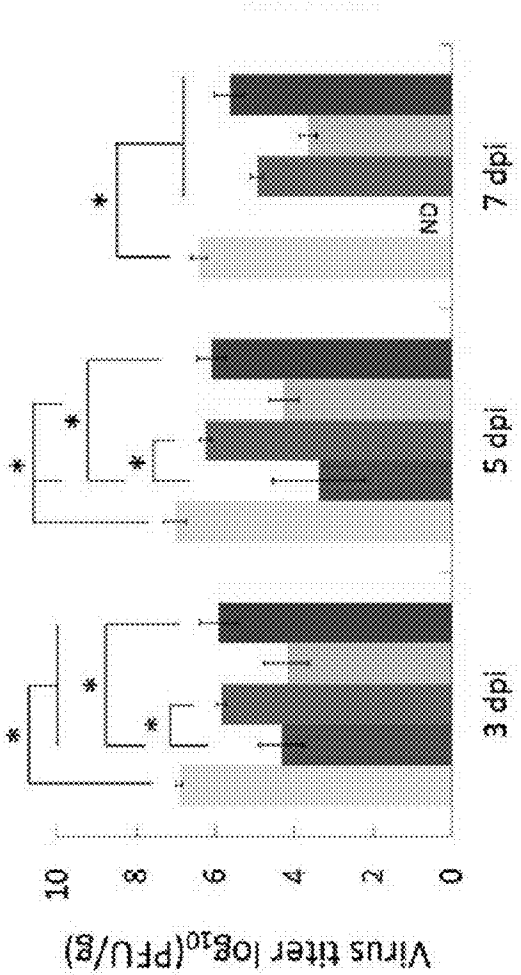


Fig. 16B

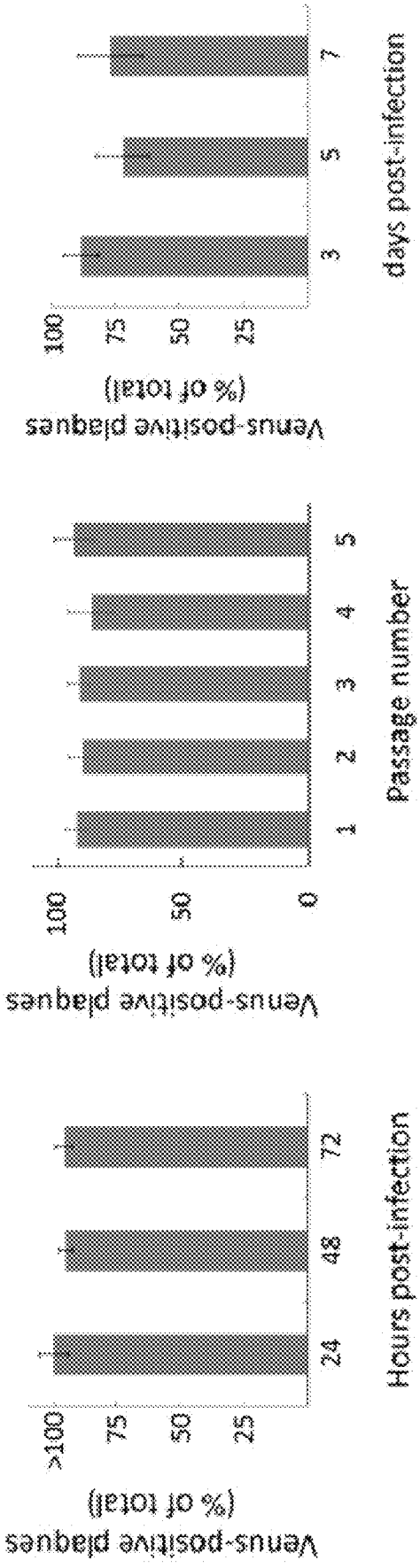

Venus-positive plaques
(% of total)
100
75
50
25
3
5
7
days post-infection
Venus-positive plaques
(% of total)
100
50
0
1
2
3
4
5
Passage number
Venus-positive plaques
(% of total)
>100
75
50
25
24
48
72
Hours post-infection

Fig. 17

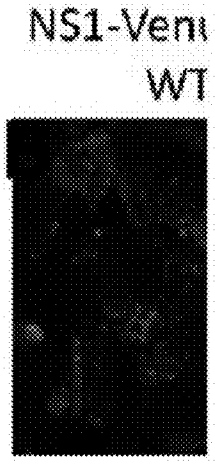


Fig. 18A

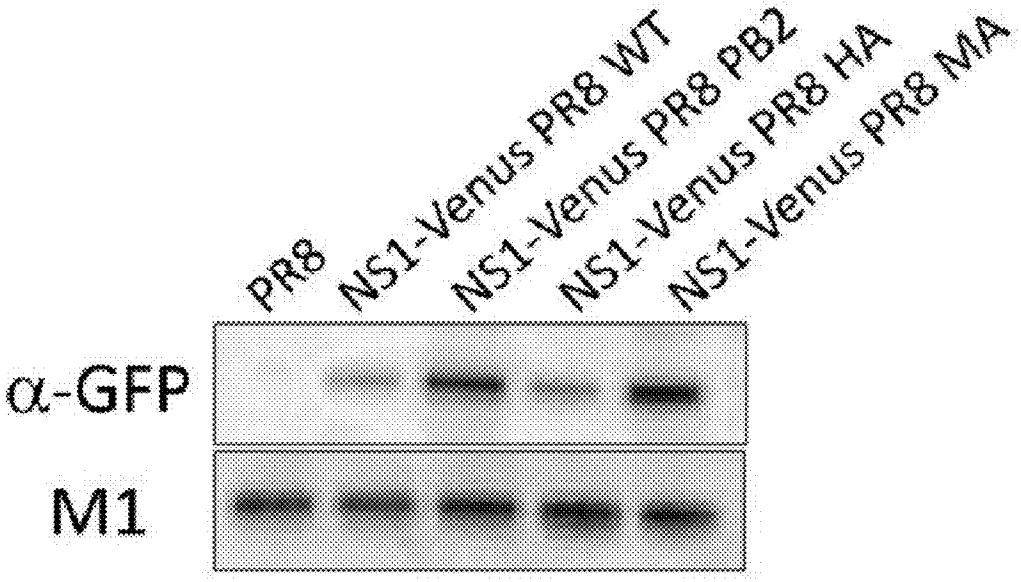


Fig. 18B

WT-Venus-PR8

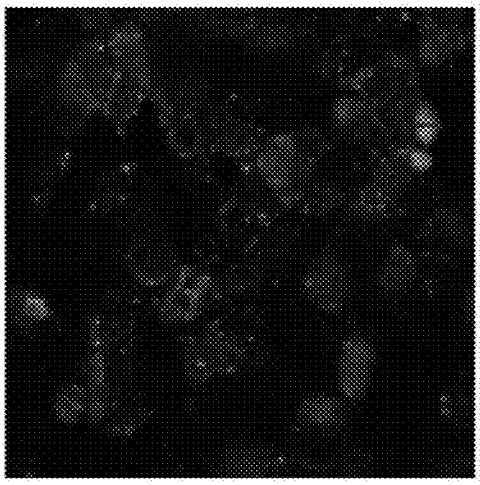


Fig. 18C

PB2-Venus-PR8

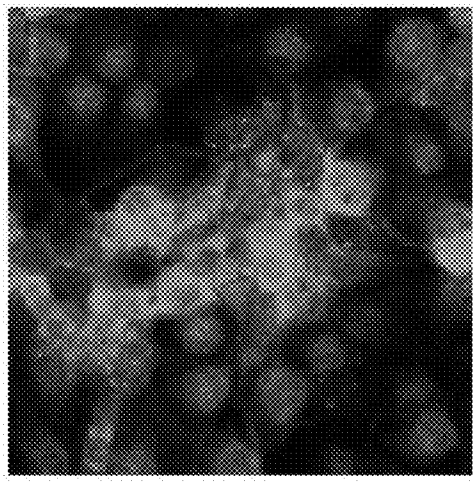


Fig. 18D

HA-Venus-PR8

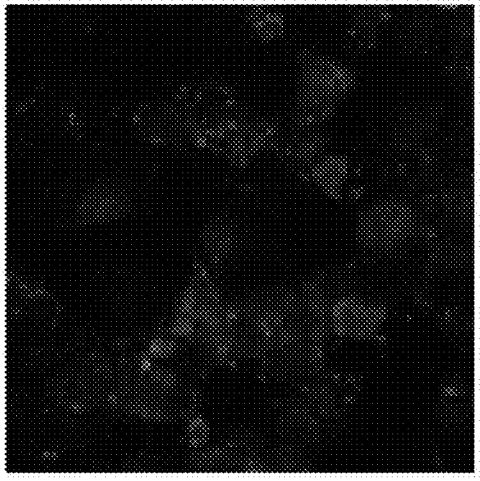


Fig. 18E

MA-Venus-PR8

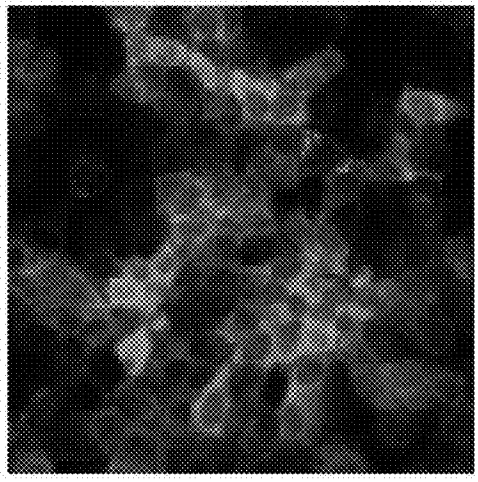


Fig. 18F

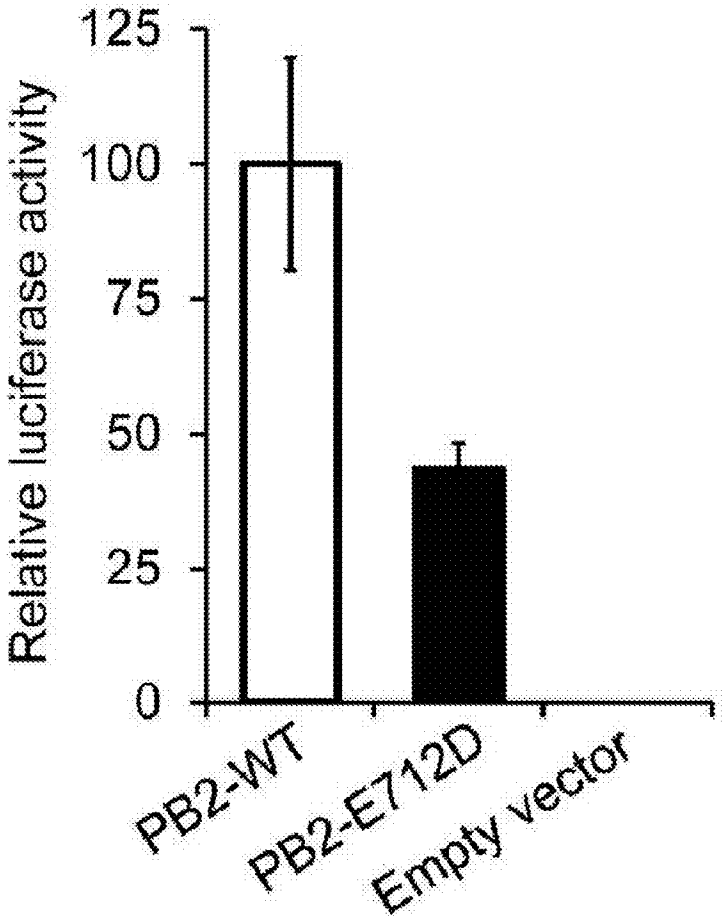

Relative luciferase activity
125
100
75
50
25
0
PB2-WT
PB2-E712D
Empty vector

Fig. 18C

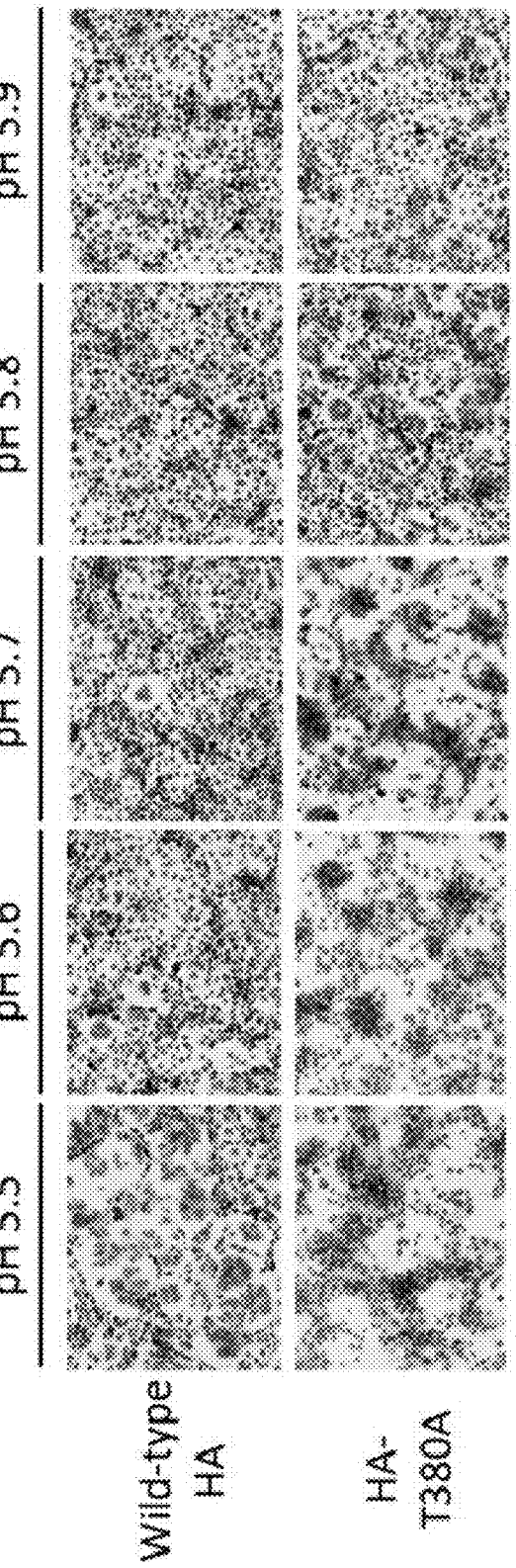


Fig. 19

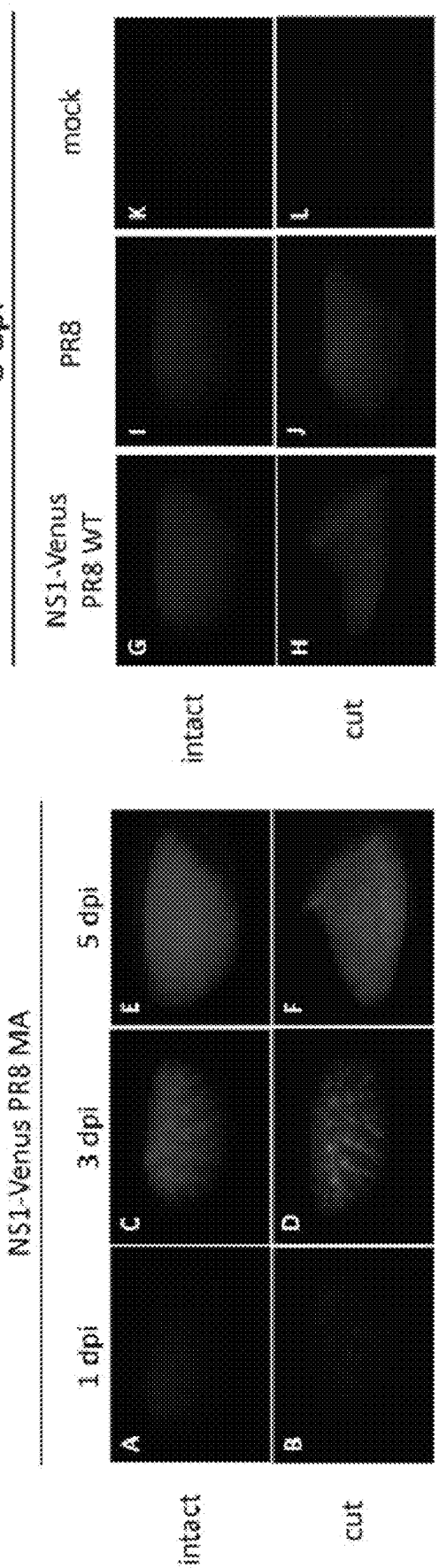

NS1-Venus PR8 MA
1 dpi
3 dpi
5 dpi
intact
cut
A
B
C
D
E
F
3 dpi
NS1-Venus PR8 WT
PR8
mock
intact
cut
G
H
I
J
K
L

Fig. 20

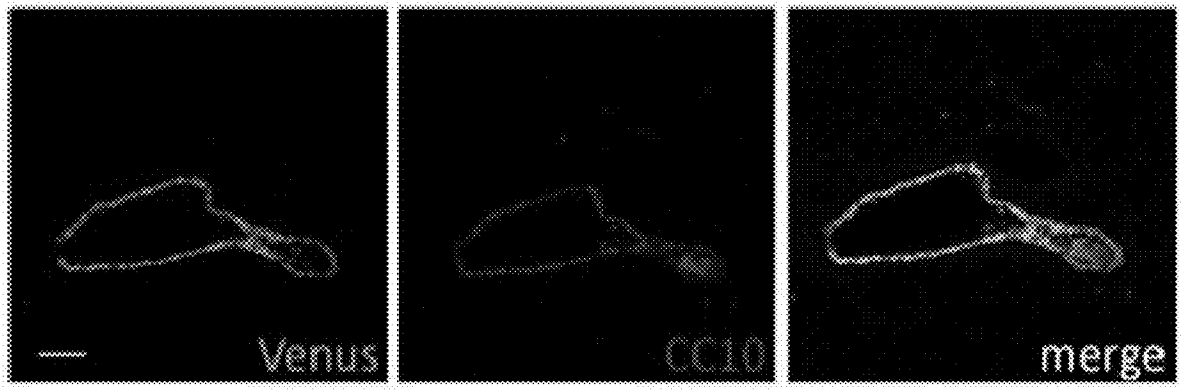


Fig.21A

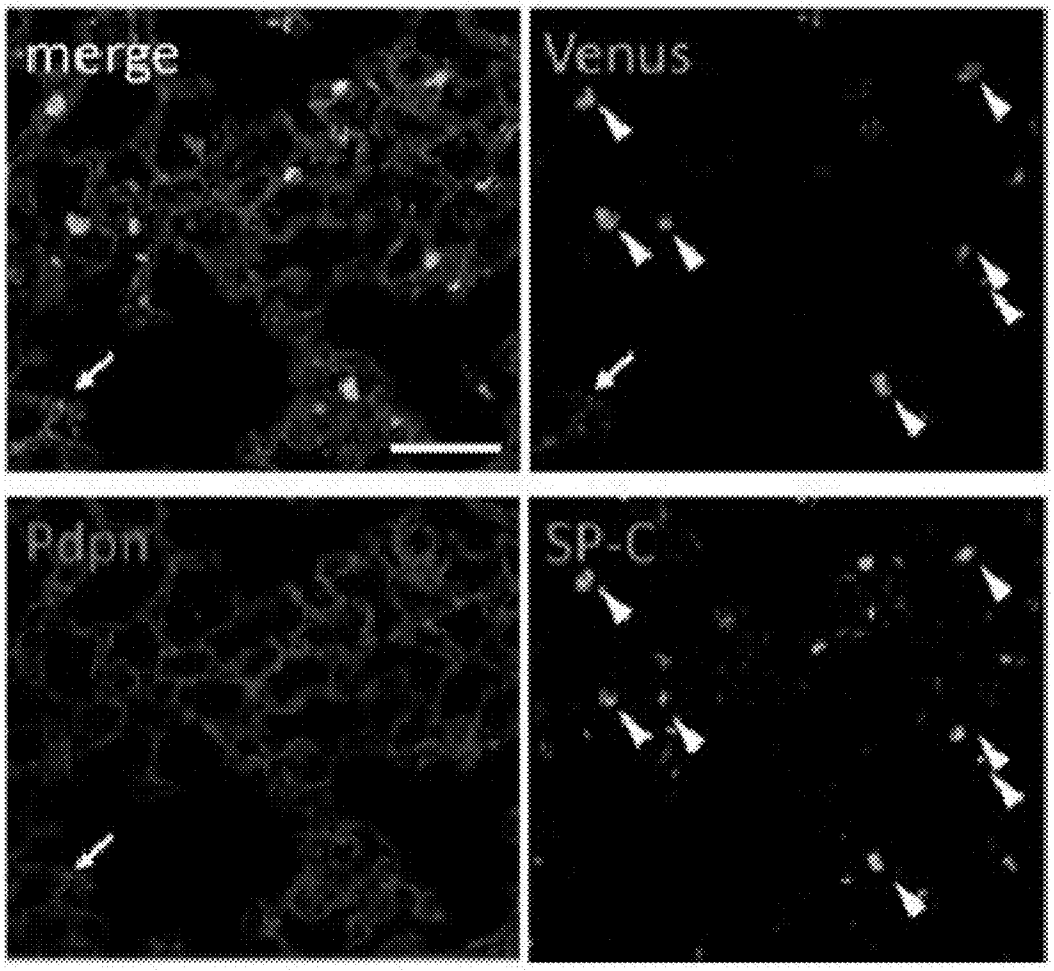


Fig.21B

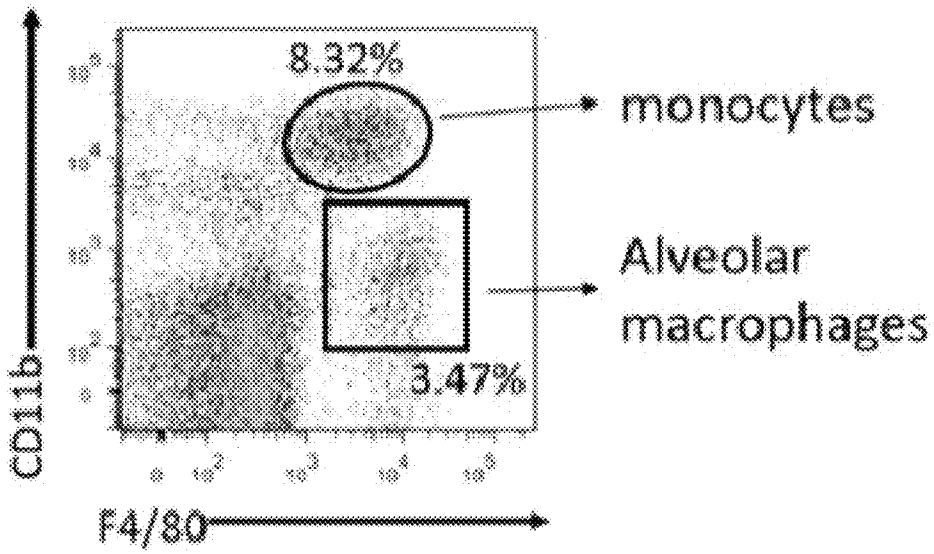


Fig. 22A

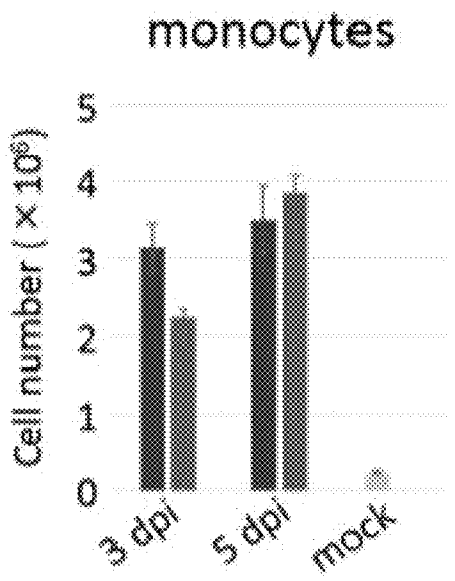


Fig. 22B

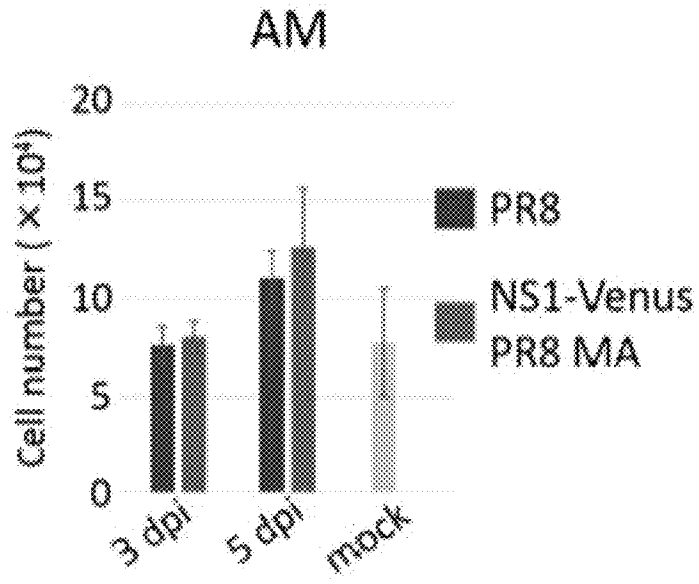


Fig. 22C

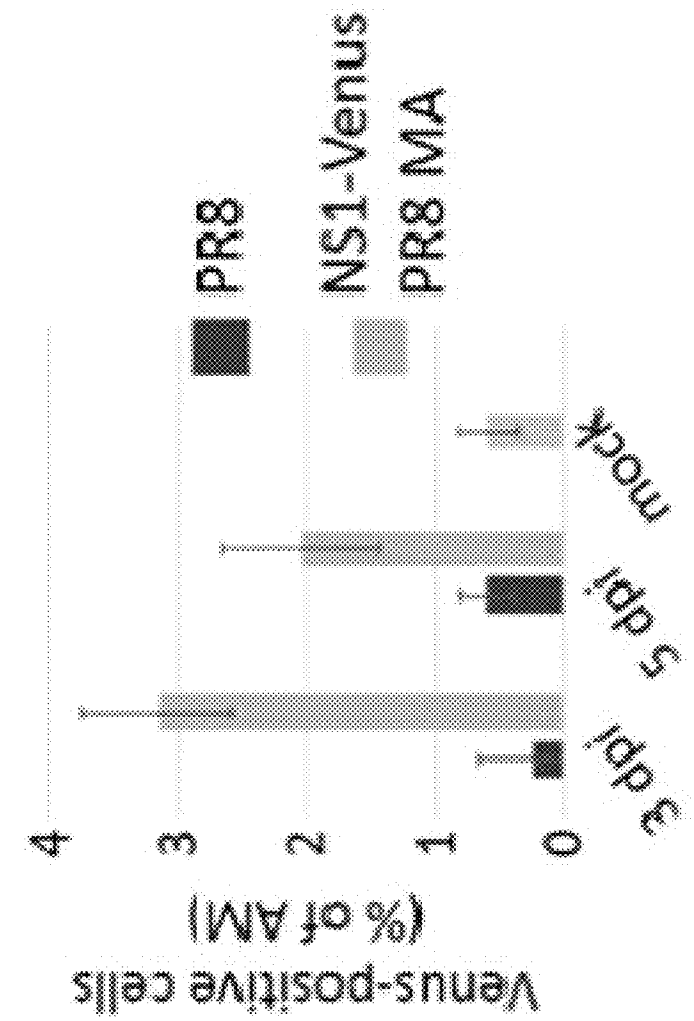


Fig. 22E

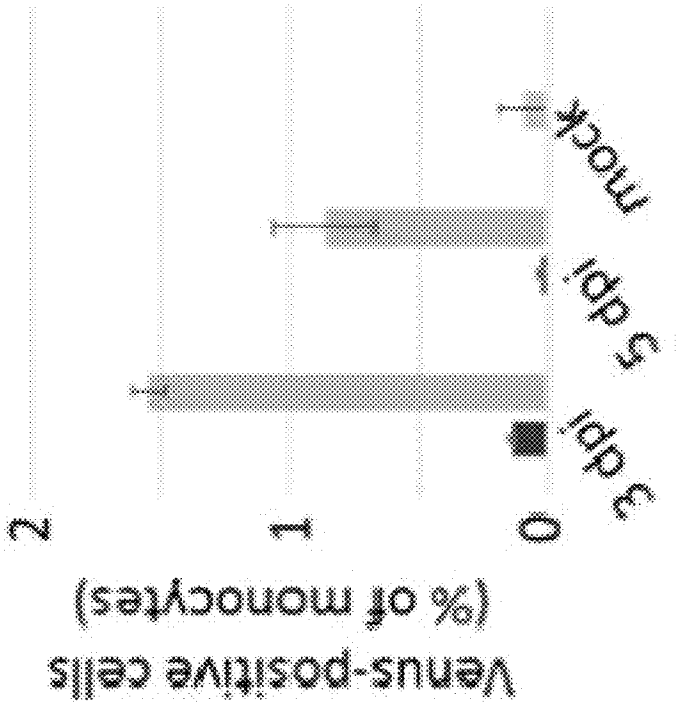


Fig. 22D

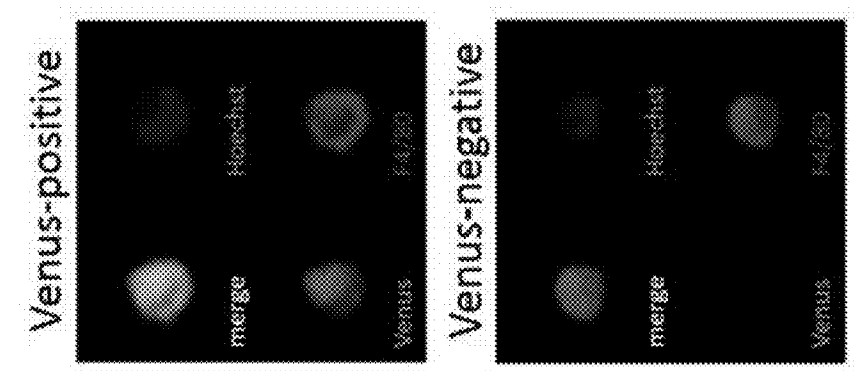


Fig.23B

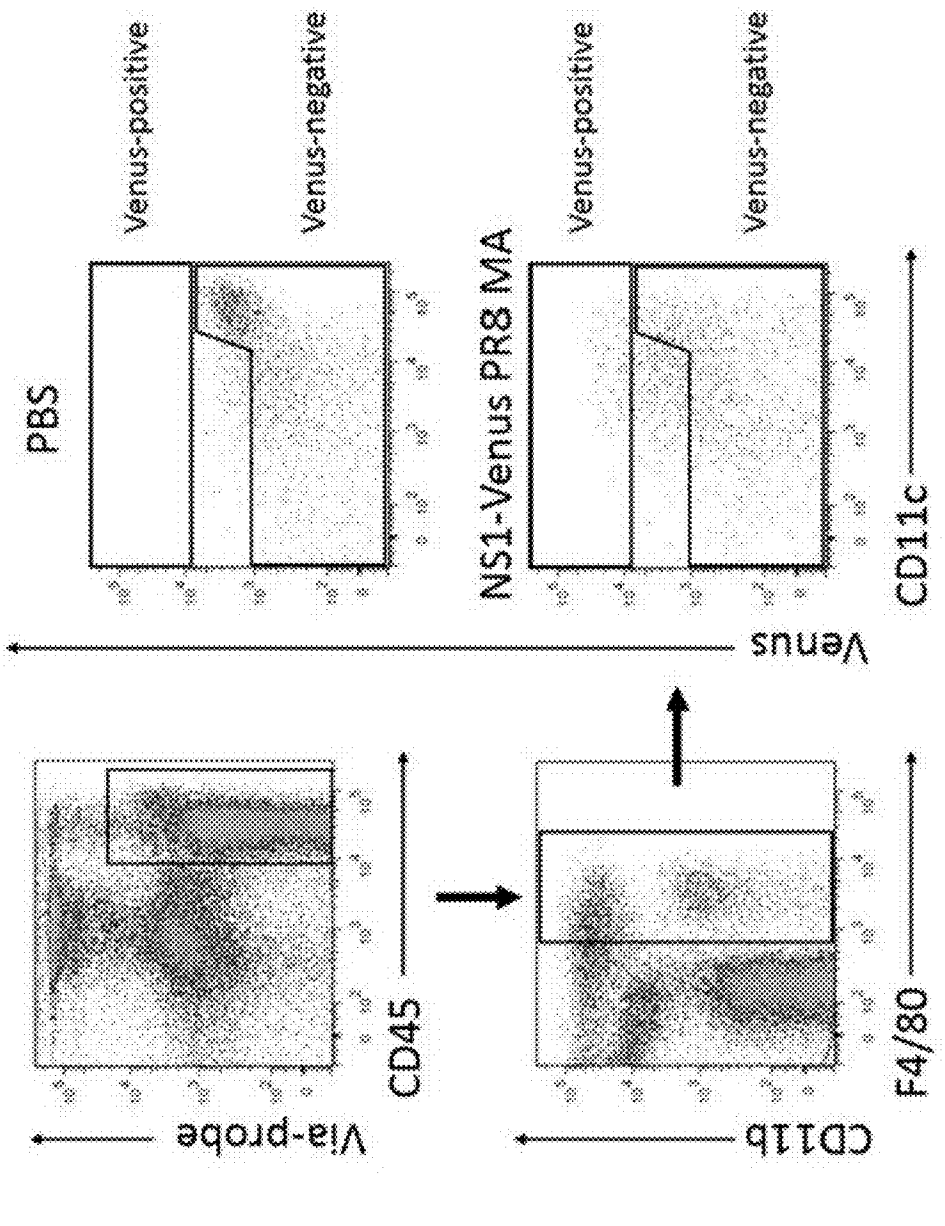


Fig.23A

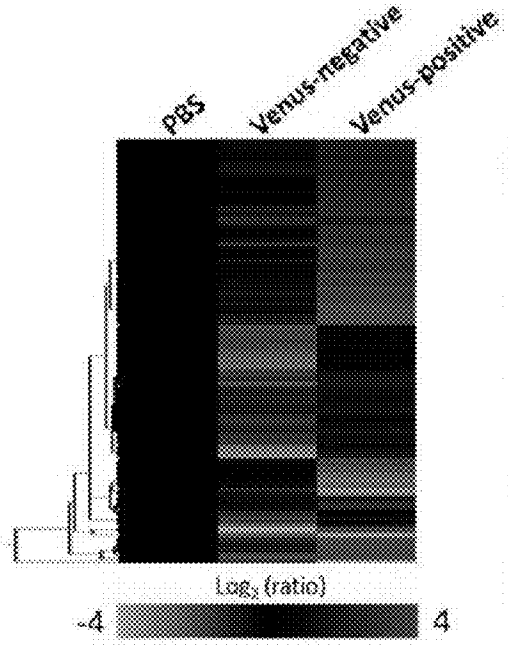


Fig. 24A

TOP 10 GO Term	p-value
extracellular region part	1.24E-32
extracellular region	5.10E-32
extracellular space	3.52E-30
extracellular matrix	6.85E-15
proteinaceous extracellular matrix	1.57E-13
extracellular matrix part	2.61E-12
receptor binding	2.60E-12
cytokine activity	6.08E-12
regulation of localization	6.60E-12
cardiovascular system development	5.56E-11

Fig. 24B

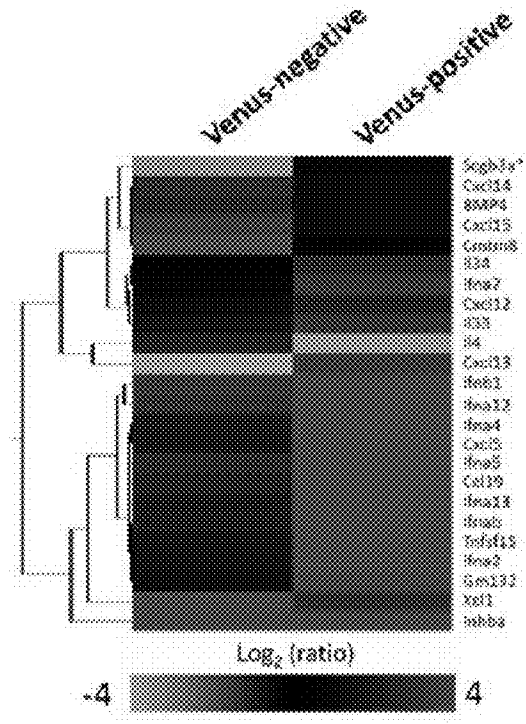


Fig. 24C

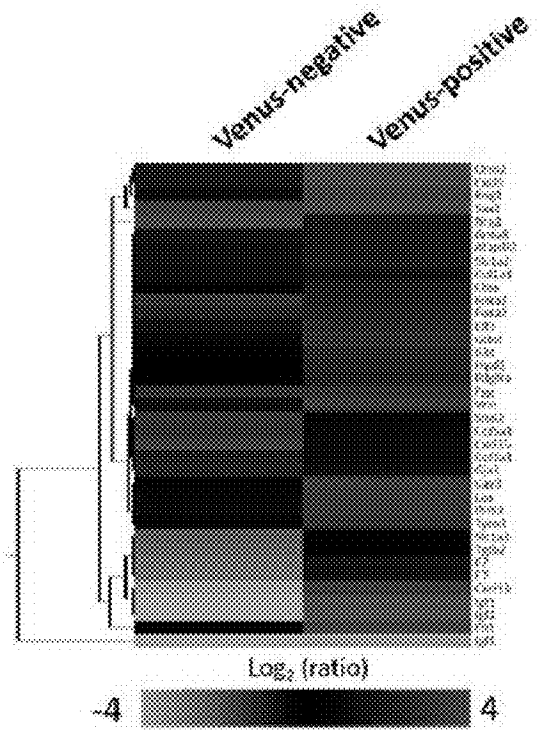


Fig. 24D

PR8(UW)

PA

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CAATCCGATG ATTGTCGAGC TTGCGGAAAA AACAATGAAA GAGTATGGGG
AGGACCTGAA AATCGAAACA AACAAATTTG CAGCAATATG CACTCACTTG
GAAGTATGCT TCATGTATTC AGATTTTCAC TTCATCAATG AGCAAGGCGA
GTCAATAATC GTAGAACTTG GTGATCCAAA TGCACTTTTG AAGCACAGAT
TTGAAATAAT CGAGGGAAGA GATCGCACAA TGGCCTGGAC AGTAGTAAAC
AGTATTTGCA ACACTACAGG GGCTGAGAAA CCAAAGTTTC TACCAGATTT
GTATGATTAC AAGGAGAATA GATTCATCGA AATTGGAGTA ACAAGGAGAG
AAGTTCACAT ATACTATCTG GAAAAGGCCA ATAAAATTAA ATCTGAGAAA
ACACACATCC ACATTTTCTC GTTCACTGGG GAAGAAATGG CCACAAAGGC
AGACTACACT CTCGATGAAG AAAGCAGGGC TAGGATCAAA ACCAGACTAT
TCACCATAAG ACAAGAAATG GCCAGCAGAG GCCTCTGGGA TTCCTTTCGT
CAGTCCGAGA GAGGAGAAGA GACAATTGAA GAAAGGTTTG AAATCACAGG
AACAATGCGC 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 TGTCATGGAA 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
CCACTTAAGG AATGACACCG ACGTGGTAAA CTTTGTGAGC ATGGAGTTTT
CTCTCACTGA CCCAAGACTT GAACCACATA AATGGGAGAA GTACTGTGTT
CTTGAGATAG GAGATATGCT TATAAGAAGT GCCATAGGCC AGGTTTCAAG
GCCCATGTTC TTGTATGTGA GAACAAATGG AACCTCAAAA ATTAAAATGA
AATGGGGAAT GGAGATGAGG CGTTGCCTCC TCCAGTCACT TCAACAAATT
GAGAGTATGA TTGAAGCTGA GTCCTCTGTC AAAGAGAAAG ACATGACCAA
AGAGTTCTTT GAGAACAAAT CAGAAACATG GCCCATTGGA GAGTCCCCCA
AAGGAGTGGA GGAAAGTTCC ATTGGGAAGG TCTGCAGGAC TTTATTAGCA

Fig. 25A

AAGTCGGTAT TCAACAGCTT GTATGCATCT CCACAACTAG AAGGATTTTC
AGCTGAATCA AGAAAACTGC TTCTTATCGT TCAGGCTCTT AGGGACAACC
TGGAACCTGG GACCTTTGAT CTTGGGGGGC TATATGAAGC AATTGAGGAG
TGCCTGATTA ATGATCCCTG GGTTTTGCTT AATGCTTCTT GGTTCAACTC
CTTCCTTACA CATGCATTGA GTTAGTTGTG GCAGTGCTAC TATTTGCTAT
CCATACTGTC CAAAAAAGTA CCTTGTTTCT ACT
(SEQ ID NO:1)

PB1

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CCTTACTTTT CTTAAAAGTG CCAGCACAAA ATGCTATAAG CACAACTTTC
CCTTATACTG GAGACCCTCC TTACAGCCAT GGGACAGGAA CAGGATACAC
CATGGATACT GTCAACAGGA CACATCAGTA CTCAGAAAAG GGAAGATGGA
CAACAAACAC CGAAACTGGA GCACCGCAAC TCAACCCGAT TGATGGGCCA
CTGCCAGAAG ACAATGAACC AAGTGGTTAT GCCCAAACAG ATTGTGTATT
GGAGGCGATG GCTTTCCTTG AGGAATCCCA TCCTGGTATT TTTGAAAACT
CGTGTATTGA AACGATGGAG GTTGTTCAGC AAACACGAGT AGACAAGCTG
ACACAAGGCC GACAGACCTA TGACTGGACT CTAAATAGAA ACCAACCTGC
TGCAACAGCA TTGGCCAACA CAATAGAAGT GTTCAGATCA AATGGCCTCA
CGGCCAATGA GTCTGGAAGG CTCATAGACT TCCTTAAGGA TGTAATGGAG
TCAATGAACA AAGAAGAAAT GGGGATCACA ACTCATTTTC AGAGAAAGAG
ACGGGTGAGA GACAATATGA CTAAGAAAAT GATAACACAG AGAACAATGG
GTAAAAAGAA GCAGAGATTG AACAAAAGGA GTTATCTAAT TAGAGCATTG
ACCCTGAACA CAATGACCAA AGATGCTGAG AGAGGGAAGC TAAAACGGAG
AGCAATTGCA ACCCCAGGGA TGCAAATAAG GGGGTTTGTA TACTTTGTTG
AGACACTGGC AAGGAGTATA TGTGAGAAAC TTGAACAATC AGGGTTGCCA
GTTGGAGGCA ATGAGAAGAA AGCAAAGTTG GCAAATGTTG TAAGGAAGAT
GATGACCAAT TCTCAGGACA CCGAACTTTC TTTCACCATC ACTGGAGATA
ACACCAAATG GAACGAAAAT CAGAATCCTC GGATGTTTTT GGCCATGATC
ACATATATGA CCAGAAATCA GCCCGAATGG TTCAGAAATG TTCTAAGTAT
TGCTCCAATA ATGTTCTCAA ACAAAATGGC GAGACTGGGA AAAGGGTATA
TGTTTGAGAG CAAGAGTATG AAACTTAGAA CTCAAATACC TGCAGAAATG
CTAGCAAGCA TCGATTTGAA ATATTTCAAT GATTCAACAA GAAAGAAGAT
TGAAAAAATC CGACCGCTCT TAATAGAGGG GACTGCATCA TTGAGCCCTG
GAATGATGAT GGGCATGTTC AATATGTTAA GCACTGTATT AGGCGTCTCC
ATCCTGAATC TTGGACAAAA GAGATACACC AAGACTACTT ACTGGTGGGA
TGGTCTTCAA TCCTCTGACG ATTTTGCTCT GATTGTGAAT GCACCCAATC
ATGAAGGGAT TCAAGCCGGA GTCGACAGGT TTTATCGAAC CTGTAAGCTA
CTTGGAATCA ATATGAGCAA GAAAAAGTCT TACATAAACA GAACAGGTAC
ATTTGAATTC ACAAGTTTTT TCTATCGTTA TGGGTTTGTT GCCAATTTCA
GCATGGAGCT TCCCAGTTTT GGGGTGTCTG GGATCAACGA GTCAGCGGAC
ATGAGTATTG GAGTTACTGT CATCAAAAAC AATATGATAA ACAATGATCT

Fig. 25B

TGGTCCAGCA ACAGCTCAAA TGGCCCTTCA GTTGTTCATC AAAGATTACA
GGTACACGTA CCGATGCCAT ATAGGTGACA CACAAATACA AACCCGAAGA
TCATTTGAAA TAAAGAAACT GTGGGAGCAA ACCCGTTCCA AAGCTGGACT
GCTGGTCTCC GACGGAGGCC CAAATTTATA CAACATTAGA AATCTCCACA
TTCCTGAAGT CTGCCTAAAA TGGGAATTGA TGGATGAGGA TTACCAGGGG
CGTTTATGCA ACCCACTGAA CCCATTTGTC AGCCATAAAG AAATTGAATC
AATGAACAAT GCAGTGATGA TGCCAGCACA TGGTCCAGCC AAAAACATGG
AGTATGATGC TGTTGCAACA ACACACTCCT GGATCCCCAA AAGAAATCGA
TCCATCTTGA ATACAAGTCA AAGAGGAGTA CTTGAGGATG AACAAATGTA
CCAAAGGTGC TGCAATTTAT TTGAAAAATT CTTCCCCAGC AGTTCATACA
GAAGACCAGT CGGGATATCC AGTATGGTGG AGGCTATGGT TTCCAGAGCC
CGAATTGATG CACGGATTGA TTTCGAATCT GGAAGGATAA AGAAAGAAGA
GTTCACTGAG ATCATGAAGA TCTGTTCCAC CATTGAAGAG CTCAGACGGC
AAAAATAGTG AATTTAGCTT GTCCTTCATG AAAAAATGCC TTGTTTCTAC
T
(SEQ ID NO:2)

PB2

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AAATCTAATG TCGCAGTCTC GCACCCGCGA GATACTCACA AAAACCACCG
TGGACCATAT GGCCATAATC AAGAAGTACA CATCAGGAAG ACAGGAGAAG
AACCCAGCAC TTAGGATGAA ATGGATGATG GCAATGAAAT ATCCAATTAC
AGCAGACAAG AGGATAACGG AAATGATTCC TGAGAGAAAT GAGCAAGGAC
AAACTTTATG GAGTAAAATG AATGATGCCG GATCAGACCG AGTGATGGTA
TCACCTCTGG CTGTGACATG GTGGAATAGG AATGGACCAA TAACAAATAC
AGTTCATTAT CCAAAAATCT ACAAAACTTA TTTTGAAAGA GTCGAAAGGC
TAAAGCATGG AACCTTTGGC CCTGTCCATT TTAGAAACCA AGTCAAAATA
CGTCGGAGAG TTGACATAAA TCCTGGTCAT GCAGATCTCA GTGCCAAGGA
GGCACAGGAT GTAATCATGG AAGTTGTTTT CCCTAACGAA GTGGGAGCCA
GGATACTAAC ATCGGAATCG CAACTAACGA TAACCAAAGA GAAGAAAGAA
GAACTCCAGG ATTGCAAAAT TTCTCCTTTG ATGGTTGCAT ACATGTTGGA
GAGAGAACTG GTCCGCAAAA CGAGATTCCT CCCAGTGGCT GGTGGAACAA
GCAGTGTGTA CATTGAAGTG TTGCATTTGA 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 CAGGAGATTG ATTCAGCTGA TAGTGAGTGG GAGAGACGAA
CAGTCGATTG CCGAAGCAAT AATTGTGGCC ATGGTATTTT CACAAGAGGA

Fig.25C

TTGTATGATA AAAGCAGTCA GAGGTGATCT GAATTTCGTC AATAGGGCGA
ATCAACGATT GAATCCTATG CATCAACTTT TAAGACATTT TCAGAAGGAT
GCGAAAGTGC TTTTTCAAAA TTGGGGAGTT GAACCTATCG ACAATGTGAT
GGGAATGATT GGGATATTGC CCGACATGAC TCCAAGCATC GAGATGTCAA
TGAGAGGAGT GAGAATCAGC AAAATGGGTG TAGATGAGTA CTCCAGCACG
GAGAGGGTAG TGGTGAGCAT TGACCGTTTT TTGAGAATCC GGGACCAACG
AGGAAATGTA CTACTGTCTC CCGAGGAGGT CAGTGAAACA CAGGGAACAG
AGAAACTGAC AATAACTTAC TCATCGTCAA TGATGTGGGA GATTAATGGT
CCTGAATCAG TGTTGGTCAA TACCTATCAA TGGATCATCA GAAACTGGGA
AACTGTTAAA ATTCAGTGGT CCCAGAACCC TACAATGCTA TACAATAAAA
TGGAATTTGA ACCATTTCAG TCTTTAGTAC CTAAGGCCAT TAGAGGCCAA
TACAGTGGGT TTGTAAGAAC TCTGTTCCAA CAAATGAGGG ATGTGCTTGG
GACATTTGAT ACCGCACAGA TAATAAAACT TCTTCCCTTC GCAGCCGCTC
CACCAAAGCA AAGTAGAATG CAGTTCTCCT CATTTACTGT GAATGTGAGG
GGATCAGGAA TGAGAATACT TGTAAGGGGC AATTCTCCTG TATTCAACTA
TAACAAGGCC ACGAAGAGAC TCACAGTTCT CGGAAAGGAT GCTGGCACTT
TAACTGAAGA CCCAGATGAA GGCACAGCTG GAGTGGAGTC CGCTGTTCTG
AGGGGATTCC TCATTCTGGG CAAAGAAGAC AAGAGATATG GGCCAGCACT
AAGCATCAAT GAACTGAGCA ACCTTGCGAA AGGAGAGAAG GCTAATGTGC
TAATTGGGCA AGGAGACGTG GTGTTGGTAA TGAAACGGAA ACGGGACTCT
AGCATACTTA CTGACAGCCA GACAGCGACC AAAAGAATTC GGATGGCCAT
CAATTAGTGT CGAATAGTTT AAAAACGACC TTGTTTCTAC T (SEQ ID NO:3)

NP

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GATGGAGAAC GCCAGAATGC CACTGAAATC AGAGCATCCG TCGGAAAAAT
GATTGGTGGA ATTGGACGAT TCTACATCCA AATGTGCACC GAACTCAAAC
TCAGTGATTA TGAGGGACGG TTGATCCAAA ACAGCTTAAC AATAGAGAGA
ATGGTGCTCT CTGCTTTTGA CGAAAGGAGA AATAAATACC TTGAAGAACA
TCCCAGTGCG GGGAAAGATC CTAAGAAAAC TGGAGGACCT ATATACAGGA
GAGTAAACGG AAAGTGGATG AGAGAACTCA TCCTTTATGA CAAAGAAGAA
ATAAGGCGAA TCTGGCGCCA AGCTAATAAT GGTGACGATG CAACGGCTGG
TCTGACTCAC ATGATGATCT GGCATTCCAA TTTGAATGAT GCAACTTATC
AGAGGACAAG AGCTCTTGTT CGCACCGGAA TGGATCCCAG GATGTGCTCT
CTGATGCAAG GTTCAACTCT CCCTAGGAGG TCTGGAGCCG CAGGTGCTGC
AGTCAAAGGA GTTGGAACAA TGGTGATGGA ATTGGTCAGA ATGATCAAAC
GTGGGATCAA TGATCGGAAC TTCTGGAGGG GTGAGAATGG ACGAAAAACA
AGAATTGCTT ATGAAAGAAT GTGCAACATT CTCAAAGGGA AATTTCAAAC
TGCTGCACAA AAAGCAATGA TGGATCAAGT GAGAGAGAGC CGGAACCCAG
GGAATGCTGA GTTCGAAGAT CTCACTTTTC TAGCACGGTC TGCACTCATA
TTGAGAGGGT CGGTTGCTCA CAAGTCCTGC CTGCCTGCCT GTGTGTATGG
ACCTGCCGTA GCCAGTGGGT ACGACTTTGA AAGGGAGGGA TACTCTCTAG
TCGGAATAGA CCCTTTCAGA CTGCTTCAAA ACAGCCAAGT GTACAGCCTA

Fig. 25D

ATCAGACCAA ATGAGAATCC AGCACACAAG AGTCAACTGG TGTGGATGGC
ATGCCATTCT GCCGCATTTG AAGATCTAAG AGTATTAAGC TTCATCAAAG
GGACGAAGGT GCTCCCAAGA GGGAAGCTTT CCACTAGAGG AGTTCAAATT
GCTTCCAATG AAAATATGGA GACTATGGAA TCAAGTACAC TTGAACTGAG
AAGCAGGTAC TGGGCCATAA GGACCAGAAG TGGAGGAAAC ACCAATCAAC
AGAGGGCATC TGCGGGCCAA ATCAGCATAC AACCTACGTT CTCAGTACAG
AGAAATCTCC CTTTTGACAG AACAACCATT ATGGCAGCAT TCAATGGGAA
TACAGAGGGG AGAACATCTG ACATGAGGAC CGAAATCATA AGGATGATGG
AAAGTGCAAG ACCAGAAGAT GTGTCTTTCC AGGGGCGGGG AGTCTTCGAG
CTCTCGGACG AAAAGGCAGC GAGCCCGATC GTGCCTTCCT TTGACATGAG
TAATGAAGGA TCTTATTTCT TCGGAGACAA TGCAGAGGAG TACGACAATT
AAAGAAAAAT ACCCTTGTTT CTACT
(SEQ ID NO:4)

M

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CGTACGTACT CTCTATCATC CCGTCAGGCC CCCTCAAAGC CGAGATCGCA
CAGAGACTTG AAGATGTCTT TGCAGGGAAG AACACCGATC TTGAGGTTCT
CATGGAATGG CTAAAGACAA GACCAATCCT GTCACCTCTG ACTAAGGGGA
TTTTAGGATT TGTGTTCACG CTCACCGTGC CCAGTGAGCG AGGACTGCAG
CGTAGACGCT TTGTCCAAAA TGCCCTTAAT GGGAACGGGG ATCCAAATAA
CATGGACAAA GCAGTTAAAC TGTATAGGAA GCTCAAGAGG GAGATAACAT
TCCATGGGGC CAAAGAAATC TCACTCAGTT ATTCTGCTGG TGCACTTGCC
AGTTGTATGG GCCTCATATA CAACAGGATG GGGGCTGTGA CCACTGAAGT
GGCATTTGGC CTGGTATGTG CAACCTGTGA ACAGATTGCT GACTCCCAGC
ATCGGTCTCA TAGGCAAATG GTGACAACAA CCAATCCACT AATCAGACAT
GAGAACAGAA TGGTTTTAGC CAGCACTACA GCTAAGGCTA TGGAGCAAAT
GGCTGGATCG AGTGAGCAAG CAGCAGAGGC CATGGAGGTT GCTAGTCAGG
CTAGACAAAT GGTGCAAGCG ATGAGAACCA TTGGGACTCA TCCTAGCTCC
AGTGCTGGTC TGAAAAATGA TCTTCTTGAA AATTTGCAGG CCTATCAGAA
ACGAATGGGG GTGCAGATGC AACGGTTCAA GTGATCCTCT CACTATTGCC
GCAAATATCA TTGGGATCTT GCACTTGACA TTGTGGATTC TTGATCGTCT
TTTTTTCAAA TGCATTTACC GTCGCTTTAA ATACGGACTG AAAGGAGGGC
CTTCTACGGA AGGAGTGCCA AAGTCTATGA GGGAAGAATA TCGAAAGGAA
CAGCAGAGTG CTGTGGATGC TGACGATGGT CATTTTGTCA GCATAGAGCT
GGAGTAAAAA ACTACCTTGT TTCTACT (SEQ ID NO:5)

NS

AGCAAAAGCA GGGTGACAAA AACATAATGG ATCCAAACAC TGTGTCAAGC
TTTCAGGTAG ATTGCTTTCT TTGGCATGTC CGCAAACGAG TTGCAGACCA
AGAACTAGGC GATGCCCCAT TCCTTGATCG GCTTCGCCGA GATCAGAAAT
CCCTAAGAGG AAGGGGCAGT ACTCTCGGTC TGGACATCAA GACAGCCACA

Fig. 25E

CGTGCTGGAA AGCAGATAGT GGAGCGGATT CTGAAAGAAG AATCCGATGA
GGCACTTAAA ATGACCATGG CCTCTGTACC TGCGTCGCGT TACCTAACTG
ACATGACTCT TGAGGAAATG TCAAGGGACT GGTCCATGCT CATACCCAAG
CAGAAAGTGG CAGGCCCTCT TTGTATCAGA ATGGACCAGG CGATCATGGA
TAAGAACATC ATACTGAAAG CGAACTTCAG TGTGATTTTT GACCGGCTGG
AGACTCTAAT ATTGCTAAGG GCTTTCACCG AAGAGGGAGC AATTGTTGGC
GAAATTTCAC CATTGCCTTC TCTTCCAGGA CATACTGCTG AGGATGTCAA
AAATGCAGTT GGAGTCCTCA TCGGAGGACT TGAATGGAAT GATAACACAG
TTCGAGTCTC TGAAACTCTA CAGAGATTCG CTTGGAGAAG CAGTAATGAG
AATGGGAGAC CTCCACTCAC TCCAAAACAG AAACGAGAAA TGGCGGGAAC
AATTAGGTCA GAAGTTTGAA GAAATAAGAT GGTTGATTGA AGAAGTGAGA
CACAAACTGA AGATAACAGA GAATAGTTTT GAGCAAATAA CATTTATGCA
AGCCTTACAT CTATTGCTTG AAGTGGAGCA AGAGATAAGA ACTTTCTCGT
TTCAGCTTAT TTAGTACTAA AAAACACCCT TGTTTCTACT
(SEQ ID NO:6)

HA

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GCAGACACAATATGTATAGGCTACCATGCGAACAATTCAACCGACACTGTTGACAC
AGTACTCGAGAAGAATGTGACAGT
GACACACTCTGTTAACCTGCTCGAAGACAGCCACAACGGAAAACTATGTAGATTAA
AAGGAATAGCCCCACTACAATTGG
GGAAATGTAACATCGCCGGATGGCTCTTGGGAAACCCAGAATGCGACCCACTGCTT
CCAGTGAGATCATGGTCCTACATT
GTAGAAACACCAAACTCTGAGAATGGAATATGTTATCCAGGAGATTTCATCGACTAT
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ACAACAGAATCTCTATCAGAATGAAAATGCTTATGTCTCTGTAGTGACTTCAAATTA
TAACAGGAGATTTACCCCGGAAA
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GGCTTTGGGTCCGGCATCATCAC
CTCAAACGCATCAATGCATGAGTGTAACACGAAGTGTCAAACACCCCTGGGAGCTA
TAAACAGCAGTCTCCCTTACCAGA
ATATACACCCAGTCACAATAGGAGAGTGCCCAAAATACGTCAGGAGTGCCAAATTG
AGGATGGTTACAGGACTAAGGAAC

Fig. 25F

ATTCCGTCCATTCAATCCAGAGGTCTATTTGGAGCCATTGCCGGTTTTATTGAAGGG
GGATGGACTGGAATGATAGATGG
ATGGTATGGTTATCATCATCAGAATGAACAGGGATCAGGCTATGCAGCGGATCAAA
AAAGCACACAAAATGCCATTAACG
GGATTACAAACAAGGTGAACACTGTTATCGAGAAAATGAACATTCAATTCACAGCT
GTGGGTAAAGAATTCAACAAATTA
GAAAAAAGGATGGAAAATTTAAATAAAAAAGTTGATGATGGATTTCTGGACATTTG
GACATATAATGCAGAATTGTTAGT
TCTACTGGAAAATGAAAGGACTCTGGATTTCCATGACTCAAATGTGAAGAATCTGTA
TGAGAAAGTAAAAAGCCAATTAA
AGAATAATGCCAAAGAAATCGGAAATGGATGTTTTGAGTTCTACCACAAGTGTGAC
AATGAATGCATGGAAAGTGTAAGA
AATGGGACTTATGATTATCCCAAATATTCAGAAGAGTCAAAGTTGAACAGGGAAAA
GGTAGATGGAGTGAAATTGGAATC
AATGGGGATCTATCAGATTCTGGCGATCTACTCAACTGTCGCCAGTTCACTGGTGCT
TTTGGTCTCCCTGGGGGCAATCA
GTTTCTGGATGTGTTCTAATGGATCTTTGCAGTGCAGAATATGCATCTGAGATTAGA
ATTTCAGAGATATGAGGAAAAAC
ACCCTTGTTTCTACT (SEQ ID NO:7)

NA
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ATCTGTCTGGTAGTCGGACTAATT
AGCCTAATATTGCAAATAGGGAATATAATCTCAATATGGATTAGCCATTCAATTCAA
ACTGGAAGTCAAAACCATACTGG
AATATGCAACCAAAACATCATTACCTATAAAAATAGCACCTGGGTAAAGGACACAA
CTTCAGTGATATTAACCGGCAATT
CATCTCTTTGTCCCATCCGTGGGTGGGCTATATACAGCAAAGACAATAGCATAAGAA
TTGGTTCCAAAGGAGACGTTTTT
GTCATAAGAGAGCCCTTTATTTCATGTTCTCACTTGGAATGCAGGACCTTTTTTCTGA
CCCAAGGTGCCTTACTGAATGA
CAAGCATTCAAGTGGGACTGTTAAGGACAGAAGCCCTTATAGGGCCTTAATGAGCT
GCCCTGTCGGTGAAGCTCCGTCCC
CGTACAATTCAAGATTTGAATCGGTTGCTTGGTCAGCAAGTGCATGTCATGATGGCA
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TCAGGTCCAGATAATGGAGCAGTGGCTGTATTAAAATACAACGGCATAATAACTGA
AACCATAAAAAGTTGGAGGAAGAA
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TTTCGGTGACAACCCGCGTCCCG

Fig. 25G

AAGATGGAACAGGCAGCTGTGGTCCAGTGTATGTTGATGGAGCAAACGGAGTAAAG
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GACTGATAGTAAGTTCTCTGTGAGGCAAGATGTTGTGGCAATGACTGATTGGTCAGG
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ID NO:8)

Cambridge

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Fig. 25H

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Fig. 25I

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Fig. 25J

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Fig. 25K

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Fig. 25L

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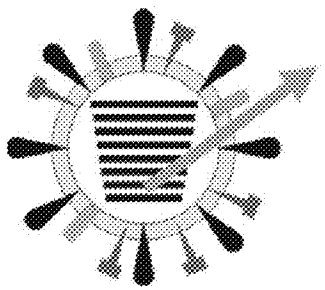
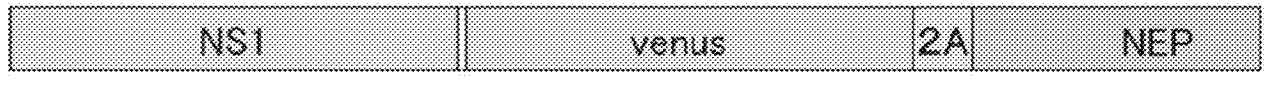
gaaataagat ggttgattga agaagtgaga cacaaactga aggtaacaga gaatagtttt     780
gagcaaataa catttatgca agccttacat ctattgcttg aagtggagca agagataaga     840
actttctcat ttcagcttat
ttaataataa aaaacaccct
tgtttctact
890 (SEQ ID NO 15)
```

Fig. 25M





NS1: ORF of NS1 gene
2A: autoproteolytic cleavage site
NEP: ORF of nuclear export protein

Fig.26

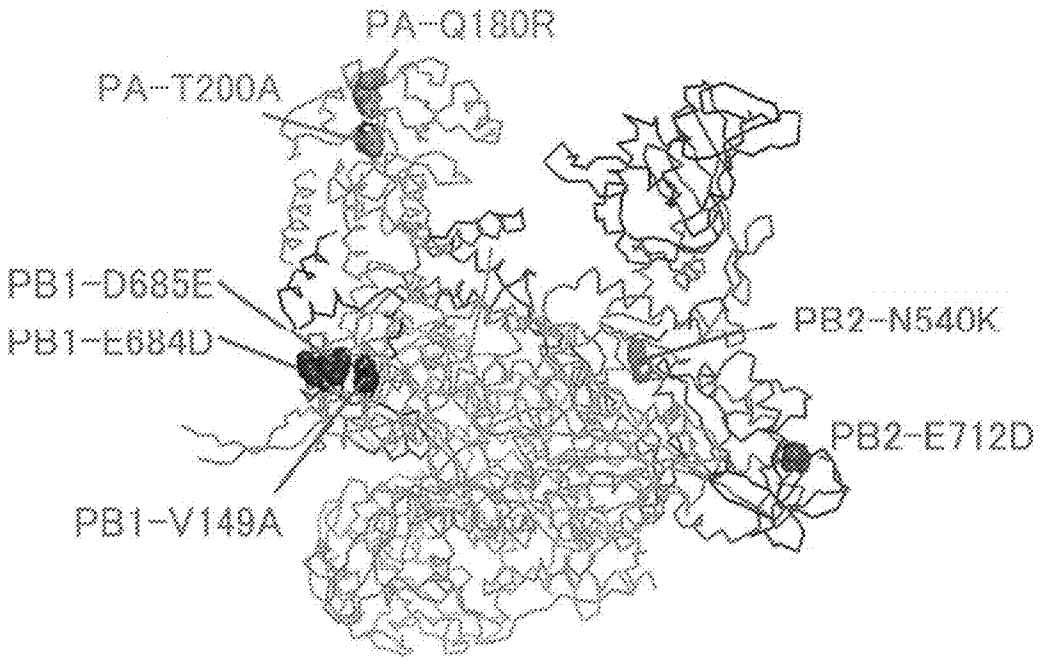


Fig.27

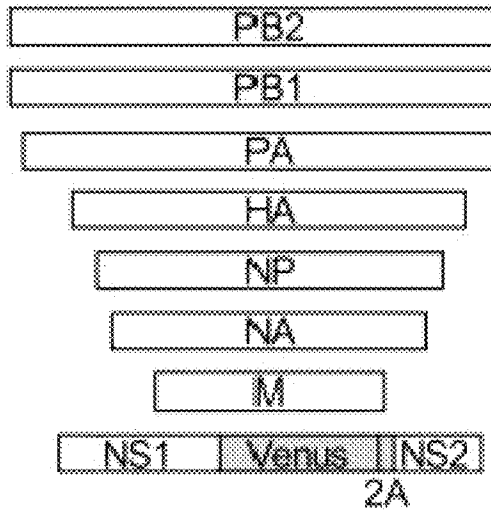


Fig. 28A

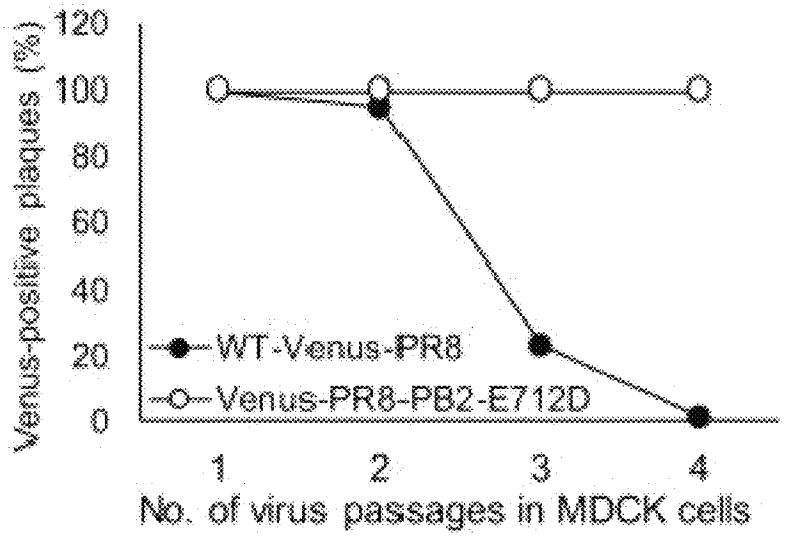


Fig. 28B

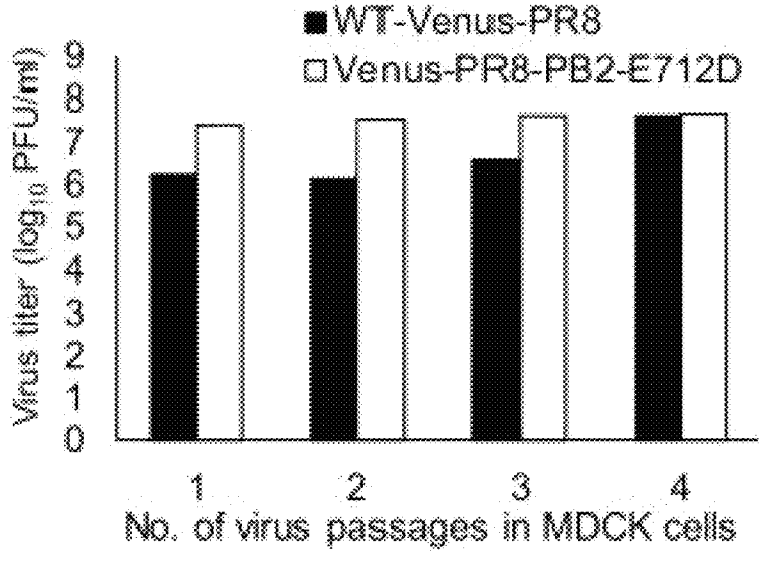


Fig. 28C

	Number of mutations							
	PB2	PB1	PA	HA	NP	NA	M	NS
WT-PR8	3	3	7	9	2	10	1	6
PR8-PB2-E712D	3	4	6	8	3	8	5	7
PR8-PB1-V43I	2	13	3	4	9	4	0	4
PR8-PB1-T123A	2	2	12	10	16	12	1	11

Fig. 29A

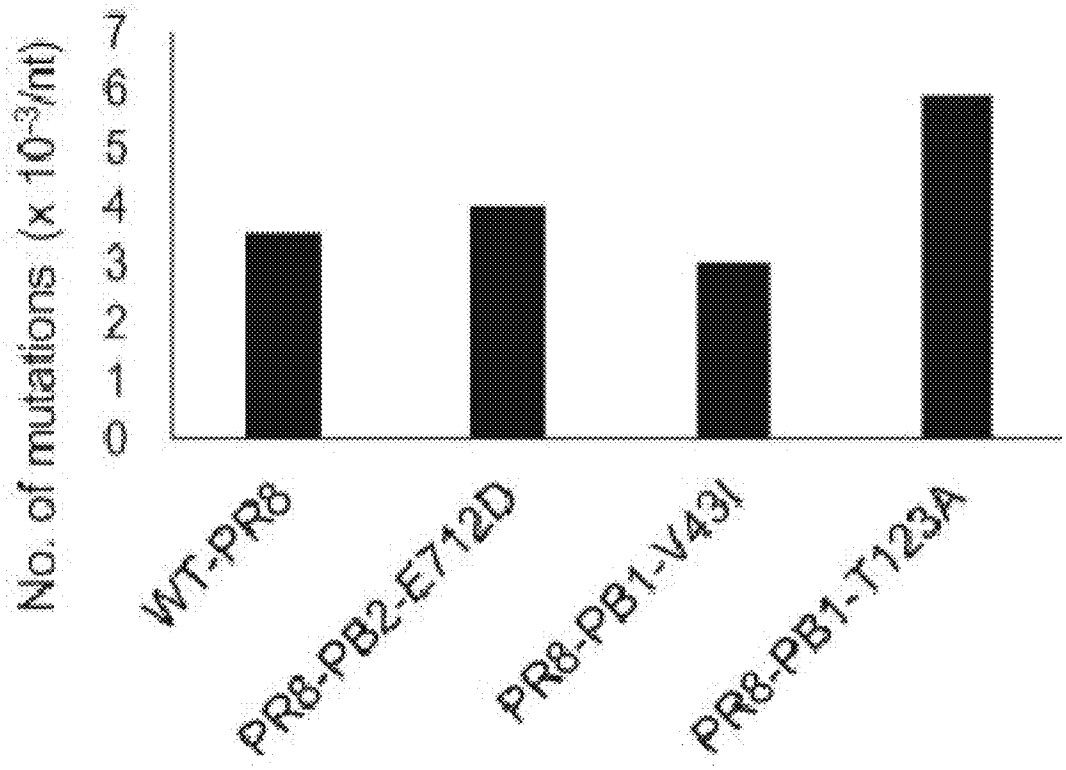


Fig. 29B

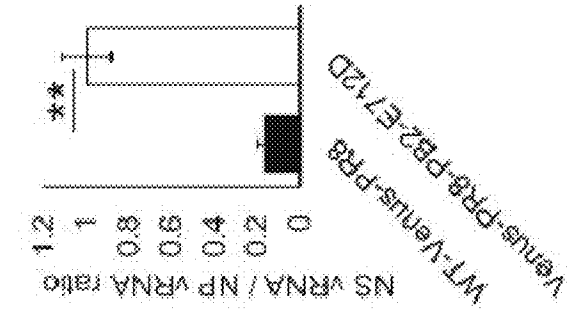


Fig. 30A

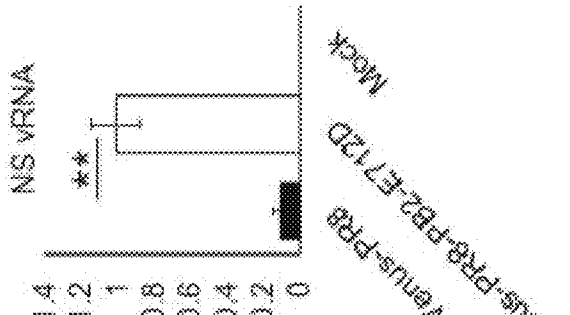


Fig. 30B

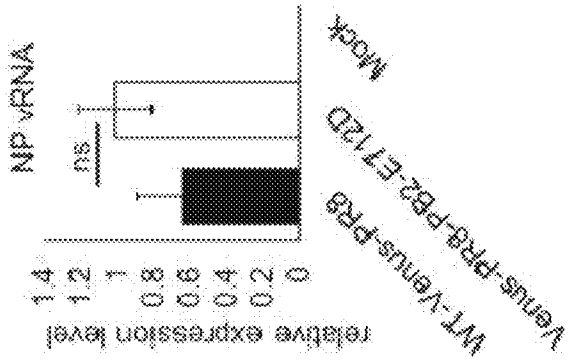


Fig. 30C

Fig. 30D

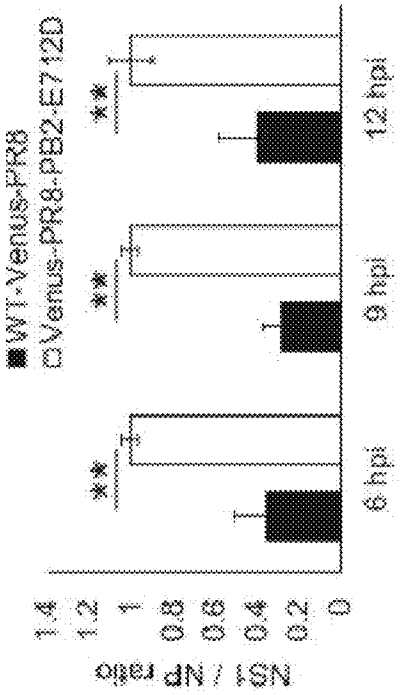


Fig. 30E

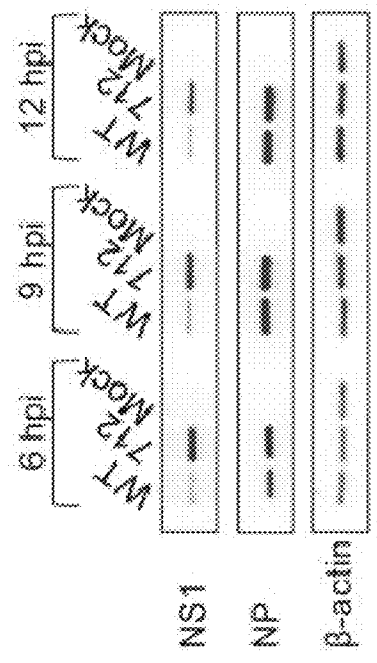


Fig. 30F

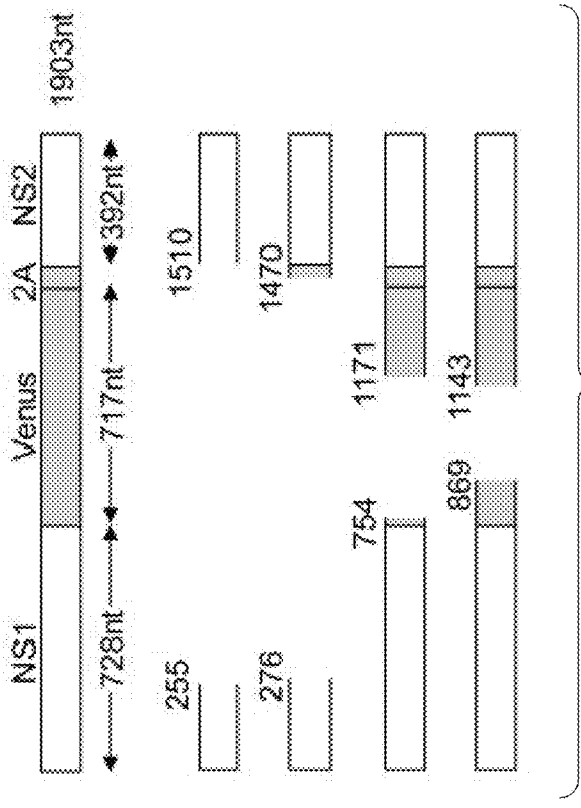


Fig. 31A

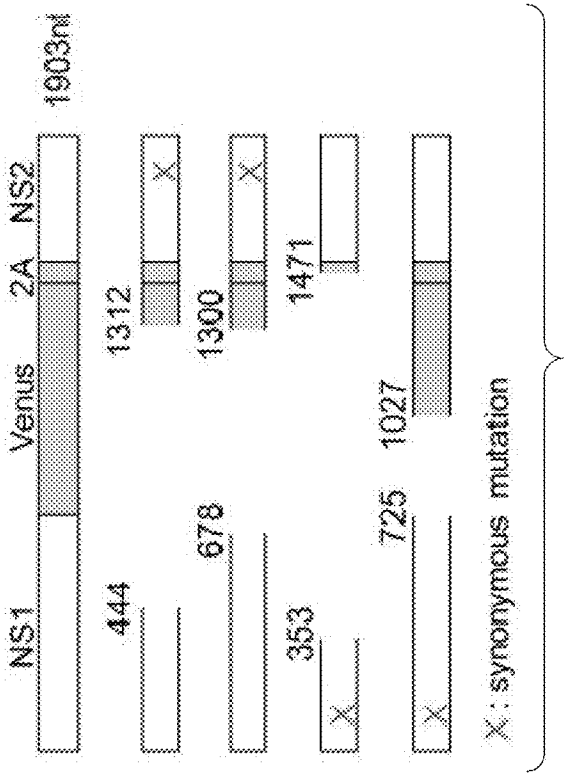


Fig. 31C

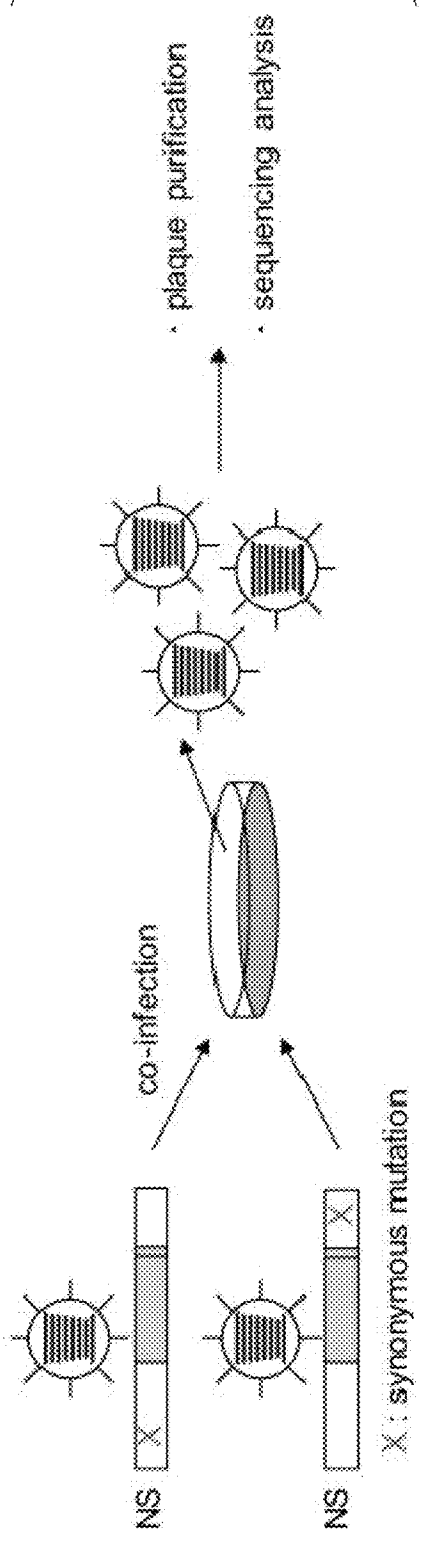


Fig. 31B

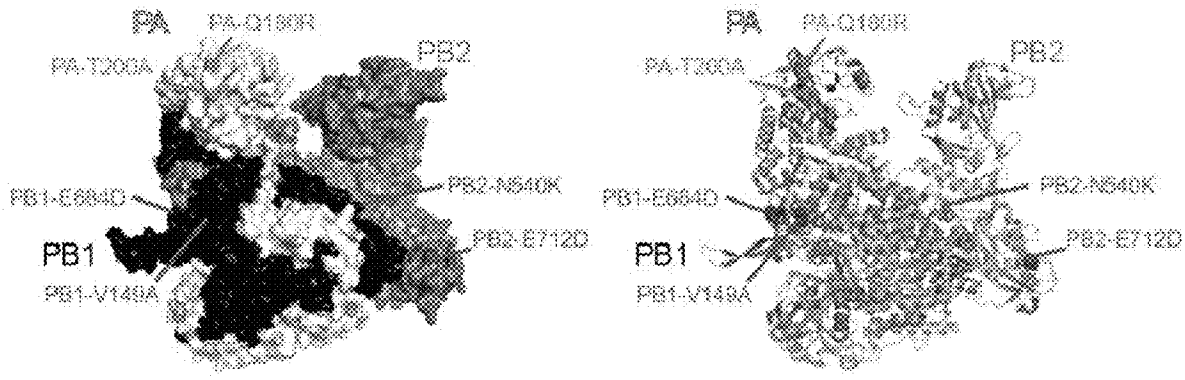


Fig. 32A

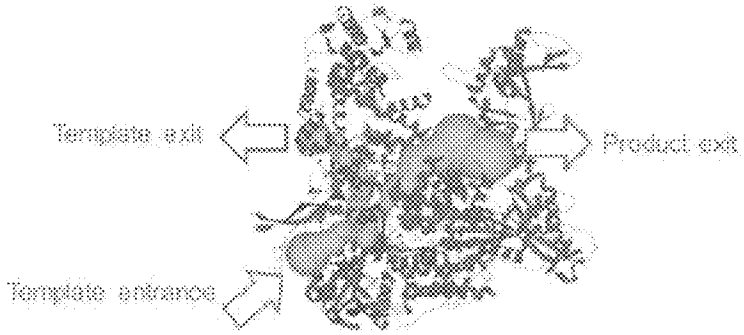


Fig. 32B

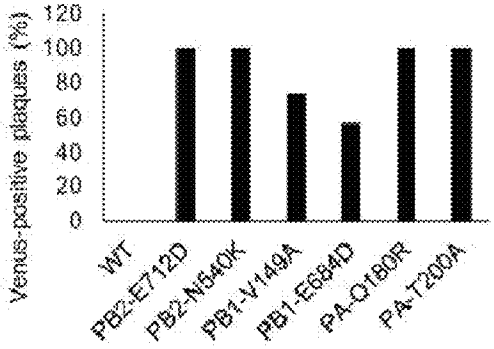


Fig. 32C

	Percentage of strains containing indicated amino acid
PB2-D712	0.002% (1/55658)
PB2-K540	0.002% (1/55658)
PB1-A149	0.004% (2/46649)
PB1-D684	0.002% (1/46649)
PA-R190	0.005% (3/55556)
PA-A200	0.007% (4/55556)

Fig. 32D

MUTATIONS THAT CONFER GENETIC STABILITY TO GENES IN INFLUENZA VIRUSES

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of the filing date of U.S. application Ser. No. 62/795,821, filed on Jan. 23, 2019, the disclosure of which is incorporated by reference herein.

STATEMENT OF GOVERNMENT RIGHTS

This invention was made with government support under HHSN272201400008C awarded by the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND

Influenza A virus is a respiratory pathogen that causes annual epidemics and sporadic pandemics (Wright et al., 2013). Moreover, highly pathogenic avian H5N1 and the recently emerged H7N9 influenza viruses have caused an appreciable number of human infections with high mortality rates (Watanabe et al., 2013; Zhang et al., 2013). Influenza viruses infect respiratory epithelial cells and alveolar macrophages in mammalian hosts (Yu et al., 2010). The host immune system recognizes the RNA genome of influenza viruses via cytosolic sensors (Diebold et al., 2004; Pichlmair et al., 2006), which trigger innate immune responses that lead to the production of type I interferons (IFNs) and proinflammatory cytokines and chemokines (Honda and Taniguchi, 2006). Type I IFNs upregulate the production of antiviral proteins including myxovirus resistance (Mx), oligoadenylate synthetase (OAS), and interferon-stimulated gene 15 (ISG15) (Garcia-Sastre et al., 2011). Dysregulation of the innate immune responses to influenza virus infection causes lung pathology mediated by infiltrating immune cells, including macrophages and neutrophils (Heron et al., 2008; Perrone et al., 2008). Although several studies have addressed host responses to influenza virus infections (Fakuyama and Kawaoka, 2011), the mechanisms of influenza virus-induced pathology are still not fully understood.

To analyze the immune responses to influenza virus infection in vivo, viruses have been generated that expressed a fluorescent reporter protein (Kittel et al., 2004; Shinya et al., 2004). However, these viruses were significantly attenuated (Kittel et al., 2004; Shinya et al., 2004) and may not accurately reflect natural infections. For example, Manicassamy et al. (2010) generated a GFP-expressing influenza virus, which they used to assess the route of antigen presentation upon influenza virus infection (Helft et al., 2012). However, the GFP gene was not stably maintained during replication in mouse lung or cultured cells (Manicassamy et al., 2010).

Highly pathogenic avian influenza viruses (HPAI) of the H5N1 subtype continue to evolve in nature, threatening animal and public health. These viruses were first identified in Guangdong province in China in 1996 (Li et al., 2006), and have since been found in over 63 countries in multiple avian species, repeatedly infecting mammals such as pigs and humans (Li et al., 2010; Neumann et al., 2010). By December 2013, 648 human cases of H5N1 virus infection had been confirmed by the World health organization (WHO), of which 384 were fatal, yielding a mortality rate of almost 60% (http://www.who.int). In addition, novel subtypes of influenza viruses, such as H7N9 and H10N8 virus, have spontaneously appeared and sporadically infected humans causing fatal outcomes (Chen et al., 2014; Li et al., 2013) (http://www.who.int). Thus, the current threat from influenza viruses reminds us of the urgent need to gain a thorough understanding of their pathogenic mechanism in order to develop more effective strategies for control, including dynamic processes of influenza virus infection and virus-target cells in vivo remain unclear.

SUMMARY

The present disclosure relates to mutations in influenza virus viral segment(s) that increase genetic stability, for instance, of an additional, non-influenza viral gene, such as a "heterologous" gene sequence that is inserted into one of the viral segments, e.g., fused to an intact or modified (for example, truncated or internally deleted) viral protein coding region, or that is present on an additional viral segment. In one embodiment, one or more of the mutations may be employed to enhance the stability of influenza viruses that are not augmented with heterologous gene sequences. In one embodiment, the heterologous gene sequence is a marker gene, e.g., a fluorescent protein gene such as one for GFP, BFP, RFP, or YFP, a luciferase gene, a beta-glucuronidase gene, or beta-lactamase gene. In one embodiment, the heterologous sequence is for a prophylactic gene product. In one embodiment, the heterologous sequence encodes a therapeutic gene product.

As disclosed herein, influenza viruses expressing fluorescent proteins of different colors (Color-flu viruses) were generated. Viruses containing the foreign matter gene were passaged. Upon adaptation to mice, stable expression of the fluorescent proteins in infected animals allowed their detection by different types of microscopy and by flow cytometry. The use of fluorescent influenza viruses, each of which stably expresses one of four different fluorescent proteins, allows for simultaneous monitoring and live imaging. Using these viruses, several studies were performed to demonstrate the versatility of these viruses. For example, this system was used to analyze the progression of viral spread in mouse lungs, for live imaging of virus-infected cells, and for differential gene expression studies in virus antigen-positive and -negative live cells in the lungs of Color-flu-infected mice. Thus, Color-flu viruses are powerful tools to analyze virus infections at the cellular level in vivo to better understand influenza pathogenesis. Moreover, different stabilizing mutations in the resulting viruses were identified. These mutations include the T380A in HA protein (numbering is that for H1) and E712D in PB2 protein of A/PR/8/34 (H1N1) virus, and V25A, R443K, K737R and P167S amino acid replacements in the PB2, PA, PB1 and NS1 proteins of A/Vietnam/1203/2004 (H5N1) virus, respectively. The individual mutations in the H5 virus alone resulted in the virus containing a foreign gene more stable in vitro, and the combination of all of them provided even greater stability in vivo. These mutations are useful for any HA/NA combination.

In one embodiment, a recombinant virus has one or more stabilizing mutations, e.g., one or more substitutions in one or more influenza virus proteins that enhance the stability or replication (for instance, enhance the titer) of the recombinant virus with the one or more substitutions relative to a corresponding virus without the one or more substitutions (a parental virus) and/or one or more substitutions in one or more influenza virus proteins that enhance the stability or replication of a heterologous gene sequence present on one

of the viral segments in the recombinant virus relative to a corresponding virus without the one or more substitutions that has the heterologous gene sequence in the respective viral segment and/or one or more substitutions in one or more influenza virus proteins that enhance the stability or replication of a heterologous gene sequence that is present on an additional viral segment in the recombinant virus relative to a corresponding virus without the one or more substitution and that has the additional viral segment with the heterologous gene sequence. The one or more substitutions include but are not limited to substitutions in any of influenza PA, PA-X, PB1, PB1-F2, PB2, NP, NS1, NS2, M1, M2, NA, and/or HA (e.g., a HA of influenza A virus), substitutions encoded in the corresponding viral segments therefor (PA, PB1, PB2, NP, NS, M, NA, and/or HA), or a combination of substitutions in any one of those influenza virus proteins or genes, or a combination of one or more substitutions in two or more of those proteins or genes. In one embodiment, the one or more substitutions that enhance the stability or replication of an influenza virus are in the PA protein, e.g., a substitution for glutamine at position 180, for threonine at position 200, or for arginine at position 443 in PA (which is located on the protein surface) that enhances, for example, RNA replication, PA proteolytic activity and/or interaction with one or more viral or cellular proteins. In one embodiment, the substitution for arginine at position 443 in PA is a conservative substitution. In one embodiment, the substitution for arginine at position 443 in PA is a non-conservative substitution. In one embodiment, the substitution for glutamine at position 180 in PA is a conservative substitution. In one embodiment, the substitution for glutamine at position 180 in PA is a non-conservative substitution. In one embodiment, the substitution for threonine at position 200 in PA is a conservative substitution. In one embodiment, the substitution for threonine at position 200 in PA is a non-conservative substitution. In one embodiment, the one or more substitutions that enhance the stability or replication of an influenza virus are in the PB2 protein, e.g., a substitution for valine at position 25, a substitution for asparagine at position 540, and/or for glutamic acid at position 712 in PB2 that, for example, enhances polymerase activity, interaction with MAVS (for position 25) and/or protein folding or stability (for position 712). In one embodiment, the substitution for valine at position 25 in PB2 is a conservative substitution. In one embodiment, the substitution for valine at position 25 in PB2 is a non-conservative substitution. In one embodiment, the substitution for asparagine at position 540 in PB2 is a conservative substitution. In one embodiment, the substitution for asparagine at position 540 in PB2 is a non-conservative substitution. In one embodiment, the substitution for glutamic acid at position 712 in PB2 is a conservative substitution. In one embodiment, the substitution for glutamic acid at position 712 in PB2 is a non-conservative substitution. In one embodiment, the one or more substitutions that enhance the stability or replication of an influenza virus are in the PB1 protein, e.g., a substitution for valine at position 149, for lysine at position 737, for glutamic acid at position 684, and/or for aspartic acid at position 685, in PB1 (which may be located on the protein surface) that, for instance, alter polymerase or endonuclease activity. In one embodiment, the substitution for lysine at position 737 in PB1 is a conservative substitution. In one embodiment, the substitution for lysine at position 737 in PB1 is a non-conservative substitution. In one embodiment, the substitution for valine at position 149 in PB1 is a conservative substitution. In one embodiment, the substitution for valine at position 149 in PB1 is a non-conservative substitution. In one embodiment, the substitution for glutamic acid at position 684 in PB1 is a conservative substitution. In one embodiment, the substitution for glutamic acid at position 684 in PB1 is a non-conservative substitution. In one embodiment, the substitution for aspartic acid at position 685 in PB1 is a conservative substitution. In one embodiment, the substitution for aspartic acid at position 685 in PB1 is a non-conservative substitution. In one embodiment, the one or more substitutions that enhance the stability or replication, e.g., by altering the interferon interfering activity or transcription regulatory activity of NS1 of an influenza virus, are in the NS1 protein, e.g., a substitution for proline at position 167 in NS1 which may alter interaction with cellular proteins. In one embodiment, the substitution for proline at position 167 in NS1 is a conservative substitution. In one embodiment, the substitution for proline at position 167 in NS1 is a non-conservative substitution. In one embodiment, the one or more substitutions that enhance the stability or replication of an influenza virus are in the HA protein, e.g., a substitution for threonine at position 380 in HA (which is in an alpha helix of HA-2). In one embodiment, the substitution for threonine at position 380 in HA is a conservative substitution. In one embodiment, the substitution for threonine at position 380 in HA is a non-conservative substitution. In one embodiment, the residue at position 443 in PA is K or H. In one embodiment, the residue at position 737 in PB1 is H or R. In one embodiment, the residue at position 25 in PB2 is A, L, T, I, or G. In one embodiment, the residue at position 712 in PB2 is D. In one embodiment, the residue at position 167 in NS1 is C, M, A, L, I, G or T.

The viruses may be employed as vaccines or as gene delivery vectors.

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 or C DNA (see Fields *Virology* (Fields et al. (eds.), Lippincott, Williams and Wickens (2006), which is specifically incorporated by reference herein).

In one embodiment, PB1, PB2, PA, NP, M, and NS encode proteins 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, although the disclosed positions and substitutions in viral proteins may be made in a viral segment from any influenza virus isolate or may be used to select viral segments with specified residues at the one or more disclosed positions. In one embodiment, PB1, PB2, PA, NP, M, and NS encode proteins that are 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 ID NOs:1-6 or 10-15, and has a characteristic residue as described herein that provides for stability.

A recombinant influenza virus of the disclosure may be prepared by selecting viral segments for inclusion in a recombinant virus, such as a reassortant virus, having one or more stabilizing mutations in one or more influenza virus proteins. For example, a HA viral segment encoding a HA

with a residue at position 380 that is not threonine may be selected; a PA viral segment encoding a PA with a residue at position 443 that is not arginine may be selected; a PA viral segment encoding a PA with a residue at position 180 that is not glutamine may be selected; a PA viral segment encoding a PA with a residue at position 200 that is not threonine may be selected; a PB1 viral segment encoding a PB1 with a residue at position 737 that is not lysine may be selected; a PB1 viral segment encoding a PB1 with a residue at position 149 that is not valine may be selected; a PB1 viral segment encoding a PB1 with a residue at position 684 that is not glutamic acid may be selected; a PB1 viral segment encoding a PB1 with a residue at position 685 that is not aspartic acid may be selected; a PB2 viral segment encoding a PB2 with a residue at position 25 that is not valine, a residue that is not asparagine at position 540, or a residue at position 712 that is not glutamic acid may be selected; a NS viral segment encoding a NS1 with a residue at position 167 that is not proline may be selected; or any combination thereof. In one embodiment, the residue at position 443 in PA is K or H. In one embodiment, the residue at position 180 in PA is R, K or H. In one embodiment, the residue at position 200 in PA is A, G, I, L or V. In one embodiment, the residue at position 737 in PB1 is H or R. In one embodiment, the residue at position 149 in PB1 is A, T, G, I or L. In one embodiment, the residue at position 684 in PB1 is D or N. In one embodiment, the residue at position 685 in PB1 is E or Q. In one embodiment, the residue at position 25 in PB2 is A, L, T, I, or G. In one embodiment, the residue at position 712 in PB2 is D. In one embodiment, the residue at position 540 in PB2 is K, R or H. In one embodiment, the residue at position 167 in NS1 is S, C, M, A, L, I, G or T. In one embodiment, the residue at position 380 in HA is A, I, V, L or G.

In one embodiment, the influenza virus of the disclosure is a recombinant influenza virus having two or more of selected amino acid residues at specified positions in one or more of PA, PB1, PB2, HA, and/or NS1. In one embodiment, the recombinant reassortant influenza virus has a lysine or histidine at position 443 in PA, a histidine or arginine at position 737 in PB1, a leucine, isoleucine, threonine, alanine or glycine at position 25 in PB2 and/or an aspartic acid, histidine, arginine, lysine or asparagine at position 712 in PB2; a leucine, alanine, valine, isoleucine, or glycine at position 380 in HA, or serine, cysteine, methionine, alanine, valine, glycine, isoleucine or leucine at position 167 in NS1.

A recombinant influenza virus of the disclosure having an extra viral segment with a heterologous gene sequence (a "9 segment" virus) which virus has enhanced stability and/or replication may be prepared by selecting viral segments for inclusion in the recombinant virus having one or more of the stabilizing mutations in an influenza virus protein. For example, a HA viral segment encoding a HA with a residue at position 380 that is not threonine may be selected; a PA viral segment encoding a PA with a residue at position 443 that is not arginine may be selected; a PB1 viral segment encoding a PB1 with a residue at position 737 that is not lysine may be selected; a PB2 viral segment encoding a PB2 with a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid may be selected; a NS viral segment enclosing a NS1 with a residue at position 167 that is not proline may be selected; or any combination thereof. The extra viral segment may be derived from any of the naturally occurring viral segments. In one embodiment, the residue at position 443 in PA is K or H. In one embodiment, the residue at position 737 in PB1 is H or R. In one embodiment, the residue at position 25 in PB2 is A, L, T, I, or G. In one embodiment, the residue at position 180 in PA is R, K or H. In one embodiment, the residue at position 200 in PA is A, G, I, L or V. In one embodiment, the residue at position 149 in PB1 is A, T, G, I or L. In one embodiment, the residue at position 684 in PB1 is D or N. In one embodiment, the residue at position 685 in PB1 is E or Q. In one embodiment, the residue at position 540 in PB2 is K, R or H. In one embodiment, the residue at position 712 in PB2 is D. In one embodiment, the residue at position 167 in NS1 is C, M, A, L, I, G or T. The heterologous gene sequence may be of length that results in the viral segment with that heterologous gene sequence having a length that is up to 4 kb, 4.2 kb, 4.5 kb, 4.7 kb, 5 kb, 5.2 kb, 5.5 kb, 5.7 kb or 6 kb in length. In one embodiment, the heterologous gene in the extra viral segment replaces influenza virus protein coding sequences (e.g., there is a deletion of influenza virus coding sequences without deleting encapsidation (incorporation) sequences in coding sequences that are linked to encapsidation sequences in non-coding sequences at one or both ends of the viral segment). In one embodiment, the heterologous gene sequence in the extra viral segment is in genomic orientation. In one embodiment, the heterologous gene sequence in the extra viral segment is fused in frame to N-terminal influenza virus protein coding sequences. In one embodiment, the heterologous gene sequence in the extra viral segment is fused in frame to C-terminal influenza virus protein coding sequences. The heterologous gene may encode a RNA, e.g., a microRNA, or a protein, e.g., a gene product that is prophylactic or therapeutic. In one embodiment, the gene product is an antigen from a different influenza virus isolate, or an antigen from a bacteria, a virus other than influenza virus, a parasite, or a fungus.

A recombinant influenza virus of the disclosure having a heterologous gene sequence in one of the eight viral segments (an "8 segment" virus) with enhanced stability and/or replication may be prepared by selecting viral segments for inclusion in the recombinant virus having one or more of the stabilizing mutations in an influenza virus protein. For example, a HA viral segment encoding a HA with a residue at position 380 that is not threonine may be selected; a PA viral segment encoding a PA with a residue at position 443 that is not arginine may be selected; a PB1 viral segment encoding a PB1 with a residue at position 737 that is not lysine may be selected; a PB2 viral segment encoding a PB2 with a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid may be selected; a NS viral segment enclosing a NS1 with a residue at position 167 that is not proline may be selected; or any combination thereof. In one embodiment, the residue at position 443 in PA is K or H. In one embodiment, the residue at position 737 in PB1 is H or R. In one embodiment, the residue at position 25 in PB2 is A, L, T, I, or G. In one embodiment, the residue at position 712 in PB2 is D. In one embodiment, the residue at position 180 in PA is R, K or H. In one embodiment, the residue at position 200 in PA is A, G, I, L or V. In one embodiment, the residue at position 149 in PB1 is A, T, G, I or L. In one embodiment, the residue at position 684 in PB1 is D or N. In one embodiment, the residue at position 685 in PB1 is E or Q. In one embodiment, the residue at position 540 in PB2 is K, R or H. In one embodiment, the residue at position 167 in NS1 is C, M, A, L, I, G or T.

A recombinant influenza virus of the disclosure having a heterologous gene sequence in one of the influenza virus viral segments that also lacks a viral segment (a "7 segment" virus), which virus has enhanced stability and/or replication,

may be prepared by selecting viral segments for inclusion in the recombinant virus having one or more of the stabilizing mutations in an influenza virus protein. For example, a HA viral segment encoding a HA with a residue at position 380 that is not threonine may be selected; a PA viral segment encoding a PA with a residue at position 443 that is not arginine may be selected; a PB1 viral segment encoding a PB1 with a residue at position 737 that is not lysine may be selected; a PB2 viral segment encoding a PB2 with a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid may be selected; a NS viral segment enclosing a NS1 with a residue at position 167 that is not proline may be selected; or any combination thereof. The viral segment that is omitted may be any one of the naturally occurring viral segments and optionally the encoded protein is provided in trans. In one embodiment, the 7 segment virus includes a PA viral segment, or the PA protein is provided in trans, and the residue at position 443 in PA is K or H. In one embodiment, the 7 segment virus includes a PB1 viral segment, or the PB1 protein is provided in trans, and the residue at position 737 in PB1 is H or R. In one embodiment, the 7 segment virus includes a PB2 viral segment, or the PB2 protein is provided in trans, and the residue at position 25 in PB2 is A, L, T, I, or G. In one embodiment, the 7 segment virus includes a PB2 viral segment, or the PB2 protein is provided in trans, and the residue at position 712 in PB2 is D. In one embodiment, the 7 segment virus includes a PA viral segment, or the PA protein is provided in trans, and the residue at position 180 in PA is R, K or H. In one embodiment, the 7 segment virus includes a PA viral segment, or the PA protein is provided in trans, and the residue at position 200 in PA is A, G, I, L or V. In one embodiment, the 7 segment virus includes a PB1 viral segment, or the PB1 protein is provided in trans, and the residue at position 149 in PB1 is A, T, G, I or L. In one embodiment, the 7 segment virus includes a PB1 viral segment, or the PB1 protein is provided in trans, and the residue at position 684 in PB1 is D or N. In one embodiment, the 7 segment virus includes a PB1 viral segment, or the P protein is provided in trans, and the residue at position 685 in P61 is E or Q. In one embodiment, the 7 segment virus includes a PB2 viral segment, or the PB2 protein is provided in trans, and the residue at position 540 in PB2 is K, R or H. In one embodiment, the 7 segment virus includes a NS viral segment, or the NS1 protein is provided in trans, and the residue at position 167 in NS1 is C, M, A, L, I, G or T. The heterologous gene sequence may be of length that results in the viral segment with that heterologous gene sequence having a length that is up to 4 kb, 4.2 kb, 4.5 kb, 4.7 kb, 5 kb, 5.2 kb, 5.5 kb, 5.7 kb or 6 kb in length. In one embodiment, the heterologous gene replaces influenza virus protein coding sequences (e.g., there is a deletion of influenza virus coding sequences without deleting encapsidation (incorporation) sequences in coding sequences that are linked to encapsidation sequences in non-coding sequences at one or both ends of the viral segment). In one embodiment, the heterologous gene sequence in the extra viral segment is in genomic orientation. In one embodiment, the heterologous gene sequence is fused in frame to N-terminal influenza virus protein coding sequences. In one embodiment, the heterologous gene sequence in the extra viral segment is fused in frame to C-terminal influenza virus protein coding sequences. The heterologous gene may encode a RNA, e.g., a microRNA, or a protein, e.g., a gene product that is prophylactic or therapeutic. In one embodiment, the gene product is an antigen from a different influenza virus isolate, or an antigen from a bacteria, a virus other than influenza virus, a parasite, or a fungus.

The heterologous gene sequence may be inserted into any viral segment. The heterologous gene sequence may be of length that results in the viral segment with that heterologous gene sequence having a length that is up to 4 kb, 4.2 kb, 4.5 kb, 4.7 kb, 5 kb, 5.2 kb, 5.5 kb, 5.7 kb or 6 kb in length. In one embodiment, the heterologous gene replaces internal influenza virus sequences in the viral segment. In one embodiment, the insertion of a heterologous gene sequence may result in a "knock-out" of the respective influenza virus gene product and to prepare such a virus, influenza virus protein(s) may be provided in trans to complement that type of mutation. In one embodiment, the heterologous gene sequences are in addition to influenza virus coding sequences in the viral segment. In one embodiment, the heterologous gene sequence is fused in frame to N-terminal influenza virus protein coding sequences. In one embodiment, the heterologous gene in is fused in frame to C-terminal influenza virus protein coding sequences. The heterologous gene may encode a RNA or a protein, e.g., a gene product that is prophylactic or therapeutic. In one embodiment, the gene product is an antigen from a different influenza virus isolate, an antigen from a bacteria, a virus other than influenza virus, a parasite, or a fungus. In one embodiment, the heterologous gene sequence is in the NA viral segment. In one embodiment, the heterologous gene sequence is in the HA viral segment. In one embodiment, the heterologous gene sequence is in the M viral segment. In one embodiment, the heterologous gene sequence is in the NS viral segment. In one embodiment, the heterologous gene sequence is in the NP viral segment, e.g., see Liu et al., 2012; Wang et al. 2010; Arilor et al., 2010; Dos Santos Afonso et al., 2005). In one embodiment, the heterologous gene sequence is in the PA viral segment. In one embodiment, the heterologous gene sequence is in the PB1 viral segment. In one embodiment, the heterologous gene sequence is in the PB2 viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the PA coding sequence in the PA viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the PB1 coding sequence in the PB1 viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the PB2 coding sequence in the PB2 viral segment (see, e.g., Avilov et al. 2012). In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the NS coding sequence in the NS viral segment (Manicassamy et al. 2010). In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the NS1 coding sequence in the NS viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the NS2 coding sequence in the NS viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the HA coding sequence in the HA viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the NA coding sequence in the NA viral segment (see, e.g., Perez et al. 2004). In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the M1 coding sequence in the M viral segment. In one embodiment, the heterologous gene sequence is 5' or 3' to, replaces at least some of or is inserted into, the M2 coding sequence in the M viral segment (see, e.g., Wei et al. 2011).

Further provided is a vaccine comprising the recombinant virus of the disclosure, e.g., a live attenuated vaccine or where the recombinant virus is cold adapted, one or more vectors comprising one or more viral segments with one or more of the disclosed substitutions, as well as methods of making and using the recombinant virus. In one embodiment, the vector for vRNA production comprises a promoter such as a RNA polymerase I promoter, a RNA polymerase II promoter, a RNA polymerase III promoter, a T3 promoter or a T7 promoter.

Also provided is a method to generate influenza viruses with an altered property, e.g., enhanced replication or stability, in a selected avian or mammalian host. The method includes serially passaging an isolate of an influenza virus in an individual host organism, and identifying individual viruses with the altered property and optionally molecularly characterizing the individual viruses.

Further provided is a set of recombinant influenza viruses, each member of the set encoding a distinct optically detectable marker, e.g., the open reading frame of which is fused to the open reading frame of an influenza virus protein, the open reading frame of which is on a ninth viral segment for influenza A or B viruses, or the open reading frame of which replaces at least a portion of one of the viral protein coding regions. For example, one of the members includes a luminescent protein gene, e.g., a luciferase gene, a fluorescent protein gene, for instance, green fluorescent protein gene, yellow fluorescent protein gene, or red fluorescent protein gene, photoprotein genes such as *Aequorin* photoprotein gene or obelin photoprotein gene, chloramphenical acetyltransferase gene, a phosphatase gene such as alkaline phosphatase gene, a peroxidase gene such as horseradish peroxidase gene, beta-galactosidase gene, beta-lactamase gene or beta-glucuronidase gene.

BRIEF DESCRIPTION OF THE FIGURES

FIGS. **1A-1G**. Characteristics of mouse-adapted Venus-PR8 in mice. (A-F) Four B6 mice per group were intranasally inoculated with WT-PR8, WT-Venus-PR8, or MA-Venus-PR8. Body weight and survival of mice were monitored for 14 days. (G) Lungs of animals infected with 10^4 PFU of PR8 or MA-Venus PR8 (three mice per group) were harvested at days 3, 5, and 7 p.i. Virus titers were analyzed by use of a plaque assay in MDCK cells.

FIGS. **2A-2C**. Distribution of Color-flu viruses in lungs. (A) Lung tissues were harvested from B6 mice at days 3 and 5 p.i. with Color-flu viruses (10^5 PFU of MA-eCFP, eGFP, Venus, and mCherry-PR8). The open reading frame (ORF) of the NS1 gene without a stop codon was fused with the N-terminus of fluorescent reporter genes (Venus, eCFP, eGFP, and mCherry) via a sequence encoding the protein linker GSGG. The fluorescent genes are followed by a sequence encoding the GSG linker, a foot-and-mouth virus protease 2A autoproteolytic site with 57 nucleotides from porcine teschovirus-1, and by the ORF of NEP. In addition, silent mutations were introduced into the endogenous splice acceptor site of the NS1 ORF to prevent splicing. Whole-mount images of transparent lung tissues were obtained by using a fluorescent stereomicroscope. (B, C) B6 mice were intranasally inoculated with a mixture of MA-eCFP, eGFP, Venus, and mCherry-PR8 (2.5×10^4 PFU per strain). Scale bar, 5 mm. (B) The sections of lungs at days 2 and 5 p.i. were analyzed by using an inverted fluorescence microscope with a Nuance FX multispectral imaging system with InForm software. Scale bar, 100 μm. (C) Enlarged images of the indicated area in (B) were unmixed and separated into autofluorescence (AF), eCFP, eGFP, Venus, and mCherry fluorescence. Arrows in the merged image indicate cells infected with different color variants of Color-flu viruses.

FIGS. **3A-3K**. Analysis of macrophage infiltration. (A-D) Lung tissues were harvested from PBS-inoculated mice (mock) or mice infected with 10^5 PFU of MA-Venus-PR8 at day 2 p.i., and tissues were fixed and processed for histological analysis. Sections were incubated with PE-anti-Mac3 antibody to detect macrophages (red) and counterstained with Hoechst dye (blue) to visualize nuclei. The fluorescent signal of the Venus protein is shown in green. The scale bar represents 200 μm. (E-H) Kinetics of the interaction between virus infected cells and lung macrophages. Images of eGFP positive cells (green) and CD11b+ macrophage (red) in lung tissue from naïve B6 mice (upper left panel) and B6 mice on day 3 p.i. with 10^5 PFU MA-eGFP-PR8 (upper right panel) were obtained by using two-photon microscope. Sequential images in lower panel (1-4) show an enlarged view of the box in the upper right panel. Arrowheads indicate the blebbing of eGFP positive cells. Scale bar, 40 μm. (I) Infection of macrophages by influenza viruses. Single cell suspensions were obtained from lungs of PBS-inoculated (mock) mice or mice infected with 10^5 PFU of MA-Venus-PR8 at day 3 p.i., stained with antibodies against CD45, CD11b, and F4/80, and analyzed by flow cytometry. The panel shows Venus expression versus the CD11b staining profile from cells gated on F4/80 and CD45 expression levels. (J) Gene expression analysis. Total RNA was isolated from sorted macrophages of PBS-inoculated (naive) mice, and from sorted Venus-positive (Venus(+)) and Venus-negative (Venus(−)) macrophages of mice inoculated with 10^5 PFU of MA-Venus-PR8 at day 3 p.i. (9 mice per treatment), and microarray analysis was performed. (J) Differentially expressed (DE) transcripts were identified by comparing gene expression levels in naive macrophages with those in Venus(+) macrophages from infected mice. Likewise, gene expression levels were compared for naive macrophages and Venus(−) macrophages obtained from infected mice. DE transcripts were organized by hierarchical clustering and each cluster was analyzed for enriched biological functions. A heat map of the clustered transcripts for each condition is displayed (a color key is shown at the top of the panel), and the different clusters are illustrated by the color bar on the left of the heat map. Enriched annotations for each cluster are listed to the left of each cluster, with the enrichment score for each annotation in parentheses. The blue line in the heat map illustrates fold changes of DE transcripts when comparing Venus(+) with Venus(−) macrophages. A shift of the blue line to the left indicates that the DE transcript is more highly expressed in Venus(+) macrophages, whereas a shift to the right indicates that the DE transcript is more highly expressed in Venus(−) macrophages. (K) This panel shows a heat map comparing expression levels of type I interferons (IFNs) between Venus(+) and Venus(−) macrophages. A color key is shown at the bottom of the panel. NS denotes comparisons that were not statistically significant between Venus(−) cells from infected animals and naive macrophages from uninfected animals.

FIGS. **4A-4E**. Characterization of MA-Venus-HPAI virus. (A) Four B6 mice per group were intranasally inoculated with MA-Venus-HPAI virus. Mouse body weight and survival were monitored for 14 days. (B) Lungs, spleens, kidneys, and brains were harvested from B6 mice at day 3 p.i. with 10^5 PFU of MA-Venus-HPAI virus. Virus titers of tissue homogenates were determined by use of plaque assays in MDCK cells. Each data point represents mean±s.d. (n=3) (C, D) Lung tissues were harvested from B6 mice at day 1

and day 2 p.i. with 10^5 PFU of MA-Venus-HPAI virus and PR8. Images of transparent lung tissues (bronchus, red; alveolar, green) were obtained by a two-photon microscope. Each data point represents mean±s.d. (n=3). Statistical significance was calculated using the Student's t-test. (D) The distribution of Venus-positive cells was evaluated via volume analysis of the Venus-positive bronchus and alveolar area using 3D images of the transparent lung tissues. (E) Cells were collected from lungs of B6 mice at days 1, 2, 3, and 4 p.i. with 10^5 PFU of MA-Venus-PR8 or MA-Venus-HPAI virus, and stained for CD45, CD11b, and F4/80. Venus expression in CD45-negative cells, and the Venus versus F4/80 staining profile gated on CD45-positive cells were analyzed by flow cytometry. A representative data plot form day 2 p.i. is shown with the percentage of Venus-positive cells.

FIG. **5**. Virus yield of various viruses.

FIGS. **6**A-**6**D. Virulence of WT-Venus-H5N1 virus and RG-MA virus in mice. Groups of four mice were intranasally infected with WT-Venus-H5N1 virus at doses of 10^1 to 10^5 PFU or with RG-MA virus at doses of 10^0 to 10^5 PFU, and their body weight changes (A-C) and survival (B-D) were monitored for two weeks.

FIG. **7**. Venus expression of various H5N1 viruses in MDCK cells. MDCK cells were infected with Venus-H5N1-related viruses, and at 24 hpi the Venus expression of each virus plaque was observed by using fluorescent microscopy (Axio Observer.Z1, Zeiss). A representative image of each virus is shown.

FIG. **8**. Venus expression of various H5N1 viruses in mouse lung. Groups of three mice were intranasally infected with 10^5 PFU (50 μl) of virus. The mice were euthanized on day 2 p.i., and their lungs were collected and fixed in 4% PFA and then embedded in O.C.T Compound. The frozen tissues were cut into 5-μm slices and then stained with Hoechst 33342. Venus signal was detected by using the Nikon confocal microscope system A1$^+$. Blue represents nuclei stained by Hoechst 33342; green represents Venus expression.

FIG. **9**. Genotypes of Venus-H5N1-related reassortants and their virulence in mice. The colors indicate the origins of the viral segments: blue, WT-Venus-H5N1 virus; red, MA-Venus-H5N1 virus. MLD_{50} values were determined by inoculating groups of four mice with 10-fold serial dilutions contain 10^0 to 10^5 PFU of virus in a 50-μL volume and were calculated by using the method of Reed and Muench (30).

FIG. **10**. Growth kinetics of reassortants in MDCK cells. MDCK cells were infected with virus at an MOI of 0.0001, and culture supernatants were collected at the indicated times and then titrated in MDCK cells. The reported values are means±standard deviations (SD) from two independent experiments. **, P<0.01 compared with that of WT-Venus-H5N1 virus-infected cells.

FIG. **11**. Polymerase activity of different RNP combinations derived from the WT-Venus-H5N1 and MA-Venus-H5N1 viruses. 293 cells were transfected in triplicate with a luciferase reporter plasmid and an internal control plasmid, together with plasmids expressing PB1, PB2, PA, and NP from either WT-Venus-H5N1 or MA-Venus-H5N1 virus. Segments derived from WT-Venus-H5N1 virus are shown in white, whereas those derived from MA-Venus-H5N1 virus are in green. Cells were incubated at 37° C. for 24 hours, and cell lysates were analyzed to measure firefly and Renilla luciferase activities. The values shown are means±SD of the three independent experiments and are standardized to the activity of WT-Venus-H5N1 (100%). *, P<0.05 compared with that of WT-Venus-H5N1 virus. **, P<0.01 compared with that of WT-Venus-H5N1 virus.

FIG. **12**A. Venus-NS and deleted NS segments of Venus-H5N1-related reassortants. Viruses were passaged five times in MDCK cells and the vRNAs from the fifth passages were extracted by using a QIAamp® Viral RNA Mini Kit (QIAGEN). The respective NS segments were then amplified by using PCR with NS-specific primers and run on an agarose gel. Lane 1, WT+MA—NS; lane 2, WT+MA—M; lane 3, WT+MA—NA; lane 4, WT+MA—PA; lane 5, WT+MA—PB1; lane 6, WT+MA—PB2; lane 7, WT+MA–(PB2+PA); lane 8, WT-Venus-H5N1; lane 9, RG-MA; lane 10, PR8; and lane 11, 1-kb DNA marker.

FIG. **12**B. Schematic of deleted viruses.

FIG. **13**. High expression of Venus reassortants in mouse lung.

FIG. **14**. Comparison of the growth capabilities of mutant viruses in MDCK cells. MDCK cells were infected at a MOI of 0.001 with PR8, NS1-Venus PR8 WT, NS1-Venus PR8 MA, and mutant NS1-Venus PR8 viruses that possess amino acid substitutions found in NS1-Venus PR8 MA virus. Virus titers were determined every 12 hours by means of plaque assays. Results are expressed as the mean titer ($\log_{10}$ [PFU/ml])±standard deviation.

FIG. **15**. Body weight changes and survival rates for mice infected with viruses carrying Venus. Four mice per group were intranasally infected with 10^3, 10^4 and 10^5 PFU of each NS1-Venus PR8 virus. Body weights were measured and survival rates were monitored for 14 days after infection.

FIGS. **16**A-**16**B. Virus titers in mouse lung. Nine mice per group were intranasally infected with 10^3 PFU of PR8 (A) or the respective NS1-Venus PR8 virus (B). Three mice per group were euthanized on days 3, 5, and 7 after infection and their lungs collected to determine virus titers. Virus titers were determined by means of plaque assays. Results are expressed as the mean of the titer ($\log_{10}$ PFU/g)±standard deviation. Statistical significance was calculated by using the Turkey-Kramer method. Asterisks indicate significant differences from titers from mice infected with PR8 or NS1-Venus WT virus (P<0.05). ND: Not detected (detection limit, 5 PFU/lung).

FIG. **17**. The stability of Venus expression by NS1-Venus PR8 MA virus in vitro and in vivo. The positive rate of Venus expression was examined in MDCK cells and in mouse lung. Left panel: MDCK cells were infected with NS1-Venus PR8 MA virus at an MOI of 0.001, and supernatants were collected every 24 hours. The positive rate of Venus expression was estimated by dividing the number of plaques that expressed Venus by the total number of plaques. Middle panel: NS1-Venus PR8 MA virus was serially passaged in MDCK cells five times and the positive rates of Venus expression were estimated. Right panel: Nine mice were infected with 10^3 PFU of NS1-Venus PR8 MA virus. Three mice were euthanized at each time point and plaque assays were performed using lung homogenates. The positive rates of Venus expression were estimated as described above.

FIGS. **18**A-**18**G. Comparison of Venus expression in cells infected with each NS1-Venus PR8 virus. (A-B) Venus protein expression in cells infected with each NS1-Venus PR8 virus was detected by means of western blotting. MDCK cells were infected with each virus at an MOI of 1. Twelve hours after infection, virus-infected cells were lysed and western blotting was performed. An anti-GFP antibody was used to detect Venus protein, and M1 protein was detected as a control. The bands appeared at approximately 27 kDa were shown in M1 panel. Representative results of

two independent experiments are shown. (C-F) Observation of Venus expression by use of confocal microscopy. MDCK cells were infected with each virus at an MOI of 1. Twelve hours after infection, cells were fixed, and Venus expression was observed. Representative results of two independent experiments are shown. Indicated viruses were used to infect MDCK cells (MOI of 1) and confocal microscopy was performed 12 hours later. (G) HEK293 cells were infected with viral protein expression plasmids for NP, PA, PB1 and PB2 or PB-2-E712D, together with a plasmid expressing a vRNA encoding firefly luciferase.

FIG. **19**. Polykaryon formation by HEK293 cells infected with wild-type PR8 or PR8 that possesses the HA-T380A mutation after exposure to low pH buffer. The threshold for membrane fusion was examined at a pH range of 5.5-5.9. HEK293 cells were infected with PR8 or PR8 that possesses the HA-T380A substitution. Eighteen hours after infection, HA on the cell surface was digested with TPCK-trypsin, and exposure to the indicated pH buffer. After fixation with methanol, the cells were stained with Giemsa's solution. Representative pictures are shown.

FIG. **20**. Time-course observation of Venus-expressing cells in transparent lungs. Venus-expressing cells in whole lung lobe were observed. Three mice per group were intranasally infected with NS1-Venus PR8 MA, NS1-Venus PR8 WT or PR8 virus and lungs were collected on the indicated days. Mock-treated lungs served as a negative control. To image Venus-expressing cells deeper, lung samples were treated with SCALEVIEW A2, which make samples transparent, and were separated into each lobe and observed by using a stereo fluorescence microscope. After imaging the whole lung lobe (intact), samples were dissected to exposure the bronchi (cut). Samples from mice infected with PR8 or NS1-Venus PR8 WT virus were prepared on day 3 post-infection to compare with NS1-Venus PR8 MA virus-infected lungs in which the Venus signal was the brightest during infection. Representative images are shown.

FIGS. **21**A-**21**B. Analysis of Venus expression in $CC10^+$ cells and $SP—C^+$ cells in lungs. Lung sections from mice infected with NS1-Venus PR8 MA virus were stained with several antibodies specific for the epithelial cells in the lung. Mice were infected with 10^4 PFU of NS1-Venus PR8 MA virus and lungs were collected at 3 and 5 days post-infection. (A) Lung section of mice infected with NS1-Venus PR8 MA virus were prepared at 3 days post-infection and stained with an anti-CC10 polyclonal antibody (red). Scale bar: 100 μm. (B) Lung section of mice infected with NS1-Venus PR8 MA virus were prepared at 5 days post-infection and stained with an anti-SP-C polyclonal antibody (cyan) and an anti-podoplanin (Pdpn) polyclonal antibody (red). Venus-positive cells in the alveolar region comprised SP-C-positive cells (white arrowhead) and podoplanin-positive cells (white arrow). Scale bar: 50 μm.

FIGS. **22**A-**22**E. Flow cytometric analysis of Venus-positive cells in specific cell types of the lung. Venus-positive cells in the indicated cell types were analyzed by using flow cytometry. Mice were infected with 10^5 PFU of PR8 or NS1-Venus PR8 MA virus and lungs were collected at 3 and 5 days post-infection. Single cell suspensions were stained with antibodies. (A) Representative dot plot for $CD45^+$ live cells from the lung of mice inoculated with PBS are shown. (B, C) Total numbers of each specific cell species at the indicated time points are shown. Results are expressed as the mean cell numbers per lung±standard deviation. $CD45^+$ and via-$probe^-$ cells were analyzed for monocytes and alveolar macrophages. (D, E) The numbers of Venus-positive cells in cells defined in A and B at the indicated time points are shown. Results are expressed as the mean cell numbers±standard deviation. AM: alveolar macrophage.

FIGS. **23**A-**23**B. Sorting strategy to collect Venus-positive and Venus-negative cells in the $F4/80^+$ population. Mice were infected with 10^5 PFU of NS1-Venus PR8 MA virus and lungs were collected at 3 days post-infection. Single cell suspensions were stained with a set of antibodies. Lungs from mice inoculated with PBS were similarly stained to confirm the autofluorescence of alveolar macrophages. (A) Representative dot plots showing the gating strategy to collect Venus-positive and -negative cells in a population of $CD45^+$, via-$probe^-$ $F4/80^+$ cells. The Venus-positive gate was shown not to include alveolar macrophages. (B) Venus-positive and -negative cells collected from the lungs of mice infected with NS1-Venus PR8 MA virus were observed by using an immunofluorescence assay.

FIGS. **24**A-**24**D. Genes differentially expressed between Venus-positive and -negative $F4/80^+$ cells. Mice were infected with 10^5 PFU of NS1-Venus PR8 MA virus and lungs were collected at 3 days post-infection. Single cell suspensions were stained in the same manner as described in FIG. **10**. Venus-positive and -negative cells were separately harvested by using FACSAria II and subjected to microarray analysis. $F4/80^+$ cells isolated from the lungs of mice inoculated with PBS were used as a control. (A) A total of 633 genes were selected by student's T test ($P<0.05$) and by filtering the genes whose expression changed at least 4.0-fold between the Venus-positive and -negative groups from the genes whose expression changed at least 2.0-fold from the level of the PBS group. (B) These selected genes were functionally annotated by using Gene Ontology (GO) grouping. Statistical significance were determined by using Fisher's exact test ($P<0.01$). (C) Hierarchical analysis of genes annotated in "cytokine activity" enriched by genes that were significantly differentially expressed between Venus-positive and -negative $F4/80^+$ cells. (D) Hierarchical analysis of genes annotated in "response to wounding" enriched by genes that were significantly differentially expressed between Venus-positive and -negative $F4/80^+$ cells.

FIGS. **25**A-**25**M. Exemplary parental sequences for PR8HG and the Cambridge strain of PR8 (SEQ ID Nos: 1-19).

FIG. **26**. Schematic of fusion protein comprising a heterologous protein.

FIG. **27**. Schematic of mutations in polymerase complex proteins that stabilize heterologous gene products mapped on the structure of the complex (PDB ID:4WSB).

FIGS. **28**A-**28**C. A) Schematic structure of the eight viral RNA segments contained in WT-Venus-PR8. 2A, protease 2A autoproteolytic site. (B) Each virus was passaged in MDCK cells. The proportion of Venus-expressing plaques in virus stocks from different passages was determined in MDCK cells by using fluorescence microscopy. (C) The virus stocks from different passages were titrated by use of plaque assays in MDCK cells.

FIGS. **29**A-**29**B. Effect of PB2-E712D on the mutation rate. (A) Each virus was passaged five times in MDCK cells, and the mutations introduced into each segment during the passages were counted. (B) The mutation number per nucleotide in each segment was calculated, and the mean values for all eight segments are shown.

FIGS. **30**A-**30**F. RNA and protein expression in infected cells. (A to C) MDCK cells were infected with each virus at an MOI of 1. The relative expression levels of IFN-β mRNA (A), NS vRNA (B), and NP vRNA (C) were determined by quantitative real-time PCR at 9 h postinfection. (D) The NS vRNA/NP vRNA ratio was calculated. (E) MDCK cells

were infected with WT-Venus-PR8 (WT) or Venus-PR8—PB2-E712D (712) at an MOI of 1. Cells were lysed at the indicated time points, and the expression of NS1, NP, and β-actin was detected by Western blotting. (F) NS1/NP ratios were determined based on the band intensity of the Western blotting. Means±the standard deviations of triplicate experiments, taking each value in Venus-PR8—PB2-E712D-infected cells as 1, are shown in panels A, B, C, D, and F. **, $P<0.01$; ns, not significant (Student t test); hpi, hours postinfection.

FIGS. **31**A-**31**C. Internal deletions occurred in the NS segment of WT-Venus-PR8. (A) Schematic sequence of the NS segment in WT-Venus-PR8 viruses that lost Venus expression after serial passages in MDCK cells. Selected examples are shown. (B) The procedure for the coinfection experiment is illustrated. The synonymous mutation was introduced into the 3' or 5' region of the NS segment of WT-Venus-PR8. The viruses were then used to coinfect MDCK cells. Viruses not expressing Venus were plaque purified, and the sequences of their NS segments were analyzed. (C) Examples of the sequences of the NS segment of Venus-negative viruses obtained after coinfection experiments. The red "X" indicates an introduced synonymous mutation.

FIGS. **32**A-**32**D. Additional mutations that stabilizes the Venus gene inserted into the NS segment. (A) Identified amino acid mutations were mapped onto the influenza polymerase complex (PDB ID 4WSB). (B) Polymerase internal tunnels (shown as yellow tubes). The vRNA promoter binds to the polymerase, and the template vRNA enters the polymerase complex. The template vRNA passes through the active site, where RNA synthesis occurs, and then leaves via the template exit. The RNA products synthesized at the active site, leave via the product exit. (C) Each mutant Venus-PR8 virus was passaged four times in MDCK cells, and the proportion of Venus-expressing plaques after passaging was determined in MDCK cells by using fluorescence microscopy. (D) Percentages of influenza A virus strains containing mutations that stabilize the Venus gene in Venus-PR8 (i.e., the number of strains containing the indicated amino acid/total number of strains available in the Influenza Research Database).

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 disclosure, 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, e.g., 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, less than about 0.01, or 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.n1m.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.

"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.

Encapsidation Sequences

The viral segment for incorporation of heterologous gene sequences into a recombinant influenza virus includes at each end non-coding sequences that provide for encapsidation (incorporation or packaging) into virions. The viral segments also include adjacent coding sequences, from one or both ends, that contribute to encapsidation, e.g., enhance encapsidation relative to viral segments that lack the adjacent coding sequences but have with the heterologous gene sequence. The vectors with the viral segment having the heterologous gene sequence thus include encapsidation sequences that at the 3' end of vRNA that may include adjacent 5' coding sequences, at the 5' end of vRNA that may include 3' coding sequences, or at the 3' end of vRNA that may include adjacent 5' coding sequences and at the 5' end of vRNA that may include 3' coding sequences. For example, HA encapsidation sequences include sequences at the 3' end of HA vRNA including 33-nt of non-coding sequences and at least 3, 6, 9, or 15 or up to about 216 nt of HA coding sequence and/or at the 5' end of HA vRNA including about 45 nt of non-coding sequence and up to about 75, 80, 268 or 291 of HA coding sequence (Watanabe et al. 2003). HS encapsidation sequences include sequences at the 3' end of NS vRNA including at least 30, 60, 90 or 150 nt of coding sequence and at the 5' end of NS vRNA including at least 30, 60, 90 or 100 nt of coding sequence (Fujii et al. 2005).

In one embodiment, the 3' NA incorporation sequences correspond to nucleotides 1 to 183, nucleotides 1 to 90, nucleotides 1 to 45, nucleotides 1 to 21, nucleotides 1 to 19 or any integer between 19 and 183, of the N-terminal NA coding region, and may include a mutation at the NA initiation codon. In another embodiment, the 5' NA incorporation sequences correspond to sequences in the C-terminal coding region of NA, sequences corresponding to the 3' most 39, 78, or 157, or any integer between 1 and 157, nucleotides for C-terminal NA coding region.

In one embodiment, the 5' HA incorporation sequences correspond to sequences in the C-terminal coding region of HA, sequences corresponding to the 3' most 75, 80, 268, 291, or 518, or any integer between 1 and 518, nucleotides of the C-terminal HA coding region. The 3' HA incorporation sequences correspond to nucleotides 1 to 3, 1 to 6, 1 to 9, 1 to 15, 1 to 216, 1 to 468, or any integer between 1 and 468, of the N-terminal HA coding region.

In one embodiment, the 3' PB1 or PB2 incorporation sequences correspond to nucleotides 1 to 250, nucleotides 1 to 200, nucleotides 1 to 150, nucleotides 1 to 160 or 1 to 130 or any integer between 1 and 250, of the N-terminal PB1 or PB2 coding region. In one embodiment, the 5' PB1 or PB2 incorporation sequences correspond to the 3' most nucleotides, e.g., the 3' 1 to 250 nucleotides, 1 to 200 nucleotides, nucleotides 1 to 150, nucleotides 1 to 160, 1 to 170 or 1 to 190, or any integer between 1 and 250, of the C-terminal PB1 or PB2 coding region.

In one embodiment, the 3' PA incorporation sequences correspond to nucleotides 1 to 250, nucleotides 1 to 200, nucleotides 1 to 150, or any integer between 1 and 250, of the N-terminal PA coding region. In one embodiment, the 5' PA incorporation sequences correspond to the 3' most nucleotides, e.g., the 3' 1 to 250 nucleotides, 1 to 200 nucleotides, nucleotides 1 to 150, nucleotides 1 to 160, 1 to 170 or 1 to 190, or any integer between 1 and 250, of the C-terminal PA coding region.

In one embodiment, the 3' M incorporation sequences correspond to nucleotides 1 to 250, nucleotides 1 to 242, nucleotides 1 to 240 or any integer between 1 and 250, of the N-terminal M coding region, and may include a mutation at the M initiation codon. In another embodiment, the 5' M incorporation sequences correspond to sequences in the C-terminal coding region of M, sequences corresponding to the 3' most 50, 100, or 220, or any integer between 1 and 250, nucleotides for C-terminal M coding region.

In one embodiment, the 3' NS or NP incorporation sequences correspond to nucleotides 1 to 250, nucleotides 1 to 200, nucleotides 1 to 150, nucleotides 1 to 30, or any integer between 1 and 250, e.g., 1 to 60, 1 to 70, 1 to 80 or 1 to 90 of the N-terminal NS or NP coding region, and may include a mutation at the NS or NP initiation codon. In another embodiment, the 5' NS or NP incorporation sequences correspond to sequences in the C-terminal coding region of NS or NP, sequences corresponding to the 3' most 10, 30, 150, 200 or 250, or any integer between 1 and 250, nucleotides for the C-terminal NS or NP coding region, e.g., nucleotides 1 to 250, nucleotides 1 to 200, nucleotides 1 to 150, nucleotides 1 to 30, or any integer between 1 and 250, e.g., 1 to 60, 1 to 70, 1 to 80 or 1 to 90 of the C-terminal NS or NP codon region.

Accordingly, the disclosure provides influenza virus vectors which include sequences corresponding to the 3' and 5' noncoding regions of a particular vRNA, incorporation sequences of the corresponding vRNA, and a heterologous nucleic acid segment. Thus, in one embodiment, the vector includes the 3' noncoding region of NA vRNA, 3' or 5' NA vRNA incorporation sequences, and optionally both 3' and 5' NA incorporation sequences, a heterologous nucleic acid segment, and the 5' noncoding region of NA vRNA. In another embodiment, the vector includes the 3' noncoding region of HA vRNA, 5' or 3' HA vRNA incorporation sequences or both 5' and 3' HA incorporation sequences, a heterologous nucleic acid segment, and the 5' noncoding region of HA vRNA. In another embodiment, the vector includes the 3' noncoding region of NS vRNA, NS incorporation sequences, a heterologous nucleic acid segment, and the 5' noncoding region of NS vRNA. In another embodiment, the vector includes the 3' noncoding region of M vRNA, 5' or 3' M incorporation sequences or both 5' and 3' M incorporation sequences, a heterologous nucleic acid segment, and the 5' noncoding region of M vRNA. In yet another embodiment, the vector includes the 3' noncoding region of PB2 vRNA, a heterologous nucleic acid segment, PB2 incorporation sequences, and the 5' noncoding region of PB2 vRNA. When two incorporation sequences are employed in a vector, they may be separated by the heterologous nucleic acid segment. Each vector may be employed so as to prepare vRNA for introduction to a cell, or to express vRNA in a cell, in which other influenza virus vRNAs and proteins necessary for virus production, are present.

In another embodiment, the heterologous gene sequence comprises sequences corresponding to an open reading frame for a therapeutic gene. In yet a further embodiment, the heterologous gene sequence comprises sequences corresponding to an open reading frame for an immunogenic peptide or protein of a pathogen or a tumor cell, e.g., one useful to induce a protective immune response. For example, the heterologous nucleic acid segment may encode an immunogenic epitope useful in cancer therapy or a vaccine. The vector comprising the heterologous nucleic acid segment may be prepared such that transcription of vector vRNA results in mRNA encoding a fusion protein with an influenza protein such as NA. Thus, it is envisioned that the heterologous nucleic acid segment may be fused with viral incorporation sequences so as to encode a fusion protein, e.g., a fusion with the N-terminal 21 residues of NA. The fusion protein may comprise sequences from two different influenza virus proteins including sequences from two different NA or HA proteins. In another embodiment, the heterologous nucleic acid segment may comprise sequences corresponding to an IRES linked 5N to an open reading frame.

In one embodiment of the disclosure, the heterologous gene sequence may encode a heterologous protein (a non-influenza viral protein such as a glycoprotein or a cytosolic, nuclear or mitochondrial specific protein), which may confer a detectable phenotype. In one embodiment, the heterologous gene sequence may be fused to truncated portions of PB2 coding sequences, e.g., those corresponding to 5' or 3' PB2 coding incorporation sequences, optionally forming a chimeric protein. In one embodiment, the heterologous nucleotide sequence replaces or is introduced to sequences in the viral segment corresponding to the coding region for that segment, so as not to disrupt the incorporation sequences in the coding region of the viral segment. For instance, the heterologous nucleotide sequence 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, after infection of a host cell with the biologically contained PB2-KO virus, a heterologous protein is produced which is a fusion with the N-terminus and/or C-terminus of the remaining residues of the deleted PB2 protein.

The vRNA for the additional viral segment or a viral segment having the heterologous gene sequence may be incorporated into virions at an efficiency that is at least 1%, 5%, 10%, or 30%, or at least 50%, that of a corresponding wild-type vRNA.

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 has only seven viral segments.

Cell Lines that can be Used

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, 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 disclosure includes an isolated recombinant influenza virus of the disclosure, 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 disclosure. In one embodiment, the influenza viruses of the disclosure 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 bromelin, and then purified. The subunit vaccine may be combined with an attenuated virus of the disclosure 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 an attenuated virus of the disclosure 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, such as those including a recombinant virus of the disclosure can be used for preventing or treating influenza virus infection. 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 are 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. See, for example, Isakova-Sivall et al., 2014. 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 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 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 rimantadine); 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 the attenuated viruses.

EXEMPLARY EMBODIMENTS

A reporter influenza virus, e.g., allowing visualization of virus-infected cells to understand influenza virus-induced pathology, was prepared by inserting the gene for the Venus fluorescent protein into the NS segment of influenza A/Puerto Rico/8/34 (PR8, H1N1) virus to yield WT-Venus-PR8. Although the inserted Venus gene was deleted during serial passages of WT-Venus-PR8, and WT-Venus-PR8 was significantly attenuated, the PB2-E712D mutation was found to stabilize the Venus gene. As disclosed herein, the mechanisms by which Venus gene deletion occurs and how the polymerase mutation stabilizes the Venus gene were investigated. Deep sequencing analysis revealed that PB2-E712D does not cause an appreciable change in the mutation rate, suggesting that the stability of the Venus gene is not affected by polymerase fidelity. Using quantitative real-time PCR it was found that WT-Venus-PR8 induces high-level interferon beta (IFN-β) expression. The induction of IFN-β expression seemed to result from the reduced transcription/replication efficiency of the modified NS segment in WT-Venus-PR8. In contrast, the transcription/replication efficiency of the modified NS segment was enhanced by the PB2-E712D mutation. Loss of the Venus gene in WT-Venus-PR8 appeared to be caused by internal deletions in the NS segment. Moreover, to further the understanding of the Venus stabilization mechanisms, additional amino acid mutations in the virus polymerase complex were identified that stabilize the Venus gene. It was found that some of these amino acids are located near the template exit or the product exit of the viral polymerase, suggesting that these amino acids contribute to the stability of the Venus gene by affecting the binding affinity between the polymerase complex and the RNA template and product.

The disclosure provides an isolated recombinant influenza virus having PA, PB1, PB2, NP, NS, M, NA, and HA viral segments, wherein at least one of the viral segments is a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, wherein the recombinant influenza virus has enhanced genetic stability or enhanced replication relative to a corresponding recombinant influenza virus with a residue at position 540 in PB2 that is asparagine, a residue at position 180 in PA that is glutamine, a residue at position 200 in PA that is threonine, a residue at position 149 in PB1 that is valine, a residue at position 684 in PB1 that is glutamic acid or a residue at position 685 in PB1 that is aspartic acid. In one embodiment, the residue at position 540 of PB2 is K, R, D, E, Q, or H, the residue at position 712 of PB2 is D, N, S, H, T, Y, or C, the residue at position 180 in PA is R, K, D, E, N, or H, the residue at position 200 in PA is A, I, L, C, S, M, F, P, G, or V, the residue at position 149 in PB1 is A, T, I, L, C, S, M, F, P, or G, the residue at position 684 is D, Q, S, H, T, Y, C, K, R, or N, or the residue at position 685 in PB1 is E, N, R, H, K, S, T, Y, C, or Q. In one embodiment, the residue at position 540 of PB2 is K, R, H, D, S, H, T, Y, or C, the residue at position 712 of PB2 is D, K, H, R, Q, or N, the residue at position 180 in PA is R, K, D, N, S, H, T, Y, or H, the residue at position 200 in PA is A, I, L, G, S, M, or V, the residue at position 149 in PB1 is A, T, I, L, S, M, or G, the residue at position 684 is D, Q, H, L, R or N, or the residue at position 685 in PB1 is E, N, R, H, K or Q. In one embodiment, the residue at position 540 of PB2 is K, R or H, the residue at position 712 of PB2 is D or N, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in P61 is E or Q. In one embodiment, the PA further comprises a residue at position 443 that is not arginine, the PB1 further comprises a residue at position 737 that is not lysine, the PB2 further comprises a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid, the NS viral segment encodes a NS1 with a residue at position 167 that is not proline, the HA viral segment encodes a HA with a residue at position 380 that is not threonine, or any combination thereof. In one embodiment, the residue at position 443 of PA is K or H, the residue at position 737 of PB1 is H or R, the residue at position 25 of PB2 is A, L, T, I, or G, the residue at position 712 of PB2 is D, the residue at position 167 of NS1 is S, C, M, A, L, I, G or T, or any combination thereof. In one embodiment, at least one of the viral segments includes a heterologous gene sequence encoding a gene product. In one embodiment, the heterologous sequence is in the NS viral segment, M viral segment, NP viral segment, PA viral segment, PB1 viral segment, or the PB2 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the PA coding sequence in the PA viral segment, 5' or 3' to the PB1 coding sequence in the PB1 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the PB2 coding sequence in the PB2 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the NS1 coding sequence in the NS viral segment. In one embodiment, the recombinant virus comprises a further viral segment comprising a heterologous gene sequence encoding a gene product. In one embodiment, the further viral segment is a NS viral segment, a M viral segment, a NP viral segment, a PA viral segment, a PB1 viral segment or a PB2 viral segment. In one embodiment, the

virus has a HA that is H1, H2, H3, H5, H7, H9, or H10. In one embodiment, the virus is an influenza B virus.

Also provided is an isolated recombinant influenza virus having PA, PB1, PB2, NP, NS, M, NA, and HA viral segments, wherein at least one of the viral segments is a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, and wherein at least one of the other viral segments is a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, wherein the recombinant influenza virus has enhanced genetic stability or replication relative to a corresponding recombinant influenza virus with a residue at position 540 in PB2 that is asparagine, a residue in PB2 at position 712 that is glutamic acid, a residue at position 180 in PA that is glutamine, a residue at position 200 in PA that is threonine, a residue at position 149 in PB1 that is valine, a residue at position 684 in PB1 that is glutamic acid or a residue at position 685 in PB1 that is aspartic acid. In one embodiment, the residue at position 540 of PB2 is K, R, D, E, Q, or H, the residue at position 712 of PB2 is D, N, S, H, T, Y, or C, the residue at position 180 in PA is R, K, D, E, N, or H, the residue at position 200 in PA is A, I, L, C, S, M, F, P, G, or V, the residue at position 149 in PB1 is A, T, I, L, C, S, M, F, P, or G, the residue at position 684 is D, Q, S, H, T, Y, C, K, R, or N, or the residue at position 685 in PB1 is E, N, R, H, K, S, T, Y, C, or Q. In one embodiment, the residue at position 540 of PB2 is K, R, H, D, S, H, T, Y, or C, the residue at position 712 of PB2 is D, K, H, R, Q, or N, the residue at position 180 in PA is R, K, D, N, S, H, T, Y, or H, the residue at position 200 in PA is A, I, L, G, S, M, or V, the residue at position 149 in PB1 is A, T, I, L, S, M, or G, the residue at position 684 is D, Q, H, L, R or N, or the residue at position 685 in PB1 is E, N, R, H, K or Q. In one embodiment, the residue at position 540 of PB2 is K, R or H, the residue at position 712 of PB2 is D or N, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q. In one embodiment, the PA further comprises a residue at position 443 that is not arginine, the PB1 further comprises a residue at position 737 that is not lysine, the PB2 further comprises a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid, the NS viral segment encodes a NS1 with a residue at position 167 that is not proline, the HA viral segment encodes a HA with a residue at position 380 that is not threonine, or any combination thereof. In one embodiment, the residue at position 443 of PA is K or H, the residue at position 737 of PB1 is H or R, the residue at position 25 of PB2 is A, L, T, I, or G, the residue at position 712 of PB2 is D, the residue at position 167 of NS1 is S, C, M, A, L, I, G or T, or any combination thereof. In one embodiment, at least one of the viral segments includes a heterologous gene sequence encoding a gene product. In one embodiment, the heterologous sequence is in the NS viral segment, M viral segment, NP viral segment, PA viral segment, PB1 viral segment, or the PB2 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the PA coding sequence in the PA viral segment, 5' or 3' to the PB1 coding sequence in the PB1 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the PB2 coding sequence in the PB2 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the NS1 coding sequence in the NS viral segment. In one embodiment, the recombinant virus comprises a further viral segment comprising a heterologous gene sequence encoding a gene product. In one embodiment, the further viral segment is a NS viral segment, a M viral segment, a NP viral segment, a PA viral segment, a PB1 viral segment or a PB2 viral segment. In one embodiment, the virus has a HA that is H1, H2, H3, H5, H7, H9, or H10. In one embodiment, the virus is an influenza B virus.

Further provided is an isolated recombinant influenza virus having PA, PB1, PB2, NP, NS, M, NA, and HA viral segments, wherein the recombinant virus has two or more viral segments comprising a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, wherein the recombinant influenza virus has enhanced genetic stability or replication relative to a corresponding recombinant influenza virus with a residue at position 540 in PB2 that is asparagine, a residue in PB2 at position 712 that is glutamic acid, a residue at position 180 in PA that is glutamine, a residue at position 200 in PA that is threonine, a residue at position 149 in PB1 that is valine, a residue at position 684 in PB1 that is glutamic acid or a residue at position 685 in PB1 that is aspartic acid. In one embodiment, the residue at position 540 of PB2 is K, R, D, E, Q, or H, the residue at position 712 of PB2 is D, N, S, H, T, Y, or C, the residue at position 180 in PA is R, K, D, E, N, or H, the residue at position 200 in PA is A, I, L, C, S, M, F, P, G, or V, the residue at position 149 in PB1 is A, T, I, L, C, S, M, F, P, or G, the residue at position 684 is D, Q, S, H, T, Y, C, K, R, or N, or the residue at position 685 in PB1 is E, N, R, H, K, S, T, Y, C, or Q. In one embodiment, the residue at position 540 of PB2 is K, R, H, D, S, H, T, Y, or C, the residue at position 712 of PB2 is D, K, H, R, Q, or N, the residue at position 180 in PA is R, K, D, N, S, H, T, Y, or H, the residue at position 200 in PA is A, I, L, G, 5, M, or V, the residue at position 149 in PB1 is A, T, I, L, S, M, or G, the residue at position 684 is D, Q, H, L, R or N, or the residue at position 685 in PB1 is E, N, R, H, K or Q. In one embodiment, the residue at position 540 of PB2 is K, R or H, the residue at position 712 of PB2 is D or N, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q. In one embodiment, the PA further comprises a residue at position 443 that is not arginine, the PB1 further comprises a residue at position 737 that is not lysine, the PB2 further comprises a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid, the NS viral segment encodes a NS1 with a residue at position 167 that is not proline, the HA viral segment encodes a HA with a residue at position 380 that is not threonine, or any combination thereof. In one embodiment, the residue at position 443 of PA is K or H, the residue at position 737 of PB1 is H or R, the residue at position 25 of PB2 is A, L, T, I, or G, the residue at position 712 of PB2 is D, the residue at position 167 of NS1 is S, C, M, A, L, I, G or T, or any combination thereof. In one embodiment, at least one of the viral segments includes a heterologous gene sequence encoding a gene product. In one embodiment, the

heterologous sequence is in the NS viral segment, M viral segment, NP viral segment, PA viral segment, PB1 viral segment, or the PB2 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the PA coding sequence in the PA viral segment, 5' or 3' to the PB1 coding sequence in the PB1 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the PB2 coding sequence in the PB2 viral segment. In one embodiment, the heterologous sequence is 5' or 3' to the NS1 coding sequence in the NS viral segment. In one embodiment, the recombinant virus comprises a further viral segment comprising a heterologous gene sequence encoding a gene product. In one embodiment, the further viral segment is a NS viral segment, a M viral segment, a NP viral segment, a PA viral segment, a PB1 viral segment or a PB2 viral segment. In one embodiment, the virus has a HA that is H1, H2, H3, H5, H7, H9, or H10. In one embodiment, the virus is an influenza B virus.

The disclosure also provides a vaccine having the isolated recombinant virus.

The disclosure provides a plurality of influenza virus vectors for preparing a reassortant, comprising a vector for vRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA production comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the PB1, PB2, or PA DNAs in the vectors for vRNA production encode at least one of: a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or a combination thereof; and optionally 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 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 residue at position 540 of PB2 is K, R or H, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q. In one embodiment, at least one of the viral segments includes a heterologous gene sequence encoding a gene product. In one embodiment, the vectors comprise a further vector having a viral segment comprising a heterologous gene sequence encoding a gene product.

A method to prepare influenza virus is provided, comprising: contacting a cell with a vector for vRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA production comprising a promoter operably linked to an influenza virus NS DNA linked to a transcription termination sequence, wherein the PB1, PB2, or PA DNAs in the vectors for vRNA production encode i) a PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, and at least one: a PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, ii) a PB2 with residue at position 540 that is not asparagine, a PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, or iii) two or more of: a PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, a PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof; and optionally 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. In one embodiment, the cell is a Vero cell, a human cell or a MDCK cell. In one embodiment, the wherein 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 residue at position 540 of PB2 is K, R or H, the residue at position 712 of PB2 is D or N, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q.

The heterologous sequence, e.g., for a therapeutic or prophylactic gene of interest, which may be in an additional influenza segment, e.g., in one of the segments of a 9 segment influenza A or B virus, in one of 8 viral segments, or in one of the segments in a 7 segment virus, may be an immunogen for a cancer associated antigen or for a pathogen such as a bacteria, a noninfluenza virus, fungus In one embodiment, the influenza viruses of the disclosure may be vaccine vectors for influenza virus and for at least one other pathogen, such as a viral or bacterial pathogen, or for a pathogen other than influenza virus, pathogens including but not limited to, lentiviruses such as HIV, hepatitis B virus, hepatitis C virus, herpes viruses such as CMV or HSV, Foot and Mouth Disease Virus, Measles virus, Rubella virus, Mumps virus, human Rhinovirus, Parainfluenza viruses, such as respiratory syncytial virus and human parainfluenza virus type 1, Coronavirus, Nipah virus, Hantavirus, Japanese encephalitis virus, Rotavirus, Dengue virus, West Nile virus, *Streptococcus pneumoniae, Mycobacterium tuberculosis, Bordetella pertussis*, or *Haemophilus* influenza. For example, the biologically contained influenza virus of the disclosure may include sequences for H protein of Measles virus, viral envelope protein E1 of Rubella virus, HN protein of Mumps virus, RV capsid protein VP1 of human Rhinovirus, G protein of Respiratory syncytial virus, S protein of Coronavirus, G or F protein of Nipah virus, G protein of Hantavirus, E protein of Japanese encephalitis virus, VP6 of Rotavirus, E protein of Dengue virus, E protein of West Nile virus, PspA of *Streptococcus pneumonia*, HSP65 from *Mycobacterium tuberculosis*, IRP1-3 of *Bordetella pertussis*, or the heme utilization protein, protective surface antigen D15, heme binding protein A, or outer membrane protein P1, P2, P5 or P6 of *Haemophilus* influenza. The gene therapy vector may include a heterologous sequence useful to inhibit or treat, e.g., cancer, AIDS, adenosine deaminase, muscular dystrophy, ornithine transcarbamylase deficiency and central nervous system tumors, or pathogens, or may encode an antibody or fragment thereof, e.g., scFv or a single chain antibody.

Pharmaceutical Compositions

Pharmaceutical compositions of the present disclosure, suitable for inoculation, e.g., nasal, parenteral or oral administration, comprise one or more influenza virus isolates, e.g., one or more attenuated 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 disclosure 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, 0.1 to 2 μg, 0.5 to 5 μg, 1 to 10 μg, 10 μg to 20 μg, 15 μg to 30 μg, or 10 to 30 μg, of HA from each of the strains entering into their composition. The vaccine forming the main constituent of the vaccine composition of the disclosure 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 disclosure 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 disclosure 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-alpha, thiosemicarbarzones, 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 disclosure 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 disclosure, 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 disclosure 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 disclosure 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, 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 disclosure 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 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 disclosure 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 disclosure 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 disclosure, including one which is attenuated 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 disclosure, 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^{20}, e.g., 10^3-10^{12}, 10^2-10^{10}, 10^5-10^{11}, 10^6-10^{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 μg, 1 to 20 μg, 30 to 100 μg, 10 to 50 μg, 50 to 200 μg, or 150 to 300 μg, 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., 0.1 μg to 1 μg, 0.5 μg to 5 μg, 1 μg to 10 μg, 10 μg to 20 μg, 15 μg to 30 μg, or 30 μg to 100 μg 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 μg or any range or value therein, or the amount recommended by the U.S. Public Health

Service (PHS), which is usually 15 μg, per component for older children >3 years of age, and 7.5 μg 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.

The invention will be further described by the following non-limiting examples.

Example I

Methods

Generation of Color-Flu

The NS segments of PR8 fused with different fluorescent reporter genes including eCFP, eGFP, Venus, and mCherry were constructed by overlapping fusion PCR as described in Manicassamy et al. (2010). In brief, the open reading frame (ORF) of the NS1 gene without the stop codon was fused with the N-terminus of fluorescent reporter genes via a sequence encoding the amino acid linker GSGG. The fluorescent reporter ORFs were followed by a sequence encoding the GSG linker, a foot-and-mouth virus protease 2A autoproteolytic site with 57 nucleotides from porcine teschovirus-1 in Manicassamy et al. (2010), and by the ORF of nuclear export protein (NEP) (FIG. **5**). In addition, silent mutations were introduced into the endogenous splice acceptor site of the NS1 gene to abrogate splicing (Basler et al., 2001). The constructed NS segments (designated eCFP-NS, eGFP-NS, Venus-NS, and mCherry-NS) were subsequently cloned into a pPoII vector for reverse genetics as described in Newmann et al. (1999). The plasmid encoding the Venus reporter protein was a kind gift from Dr. A. Miyawaki (Laboratory for Cell Function Dynamics, RIKEN Brain Science Institute, Wako, Japan) (Nagai et al., 2002). WT-Venus-PR8 was generated by using the reverse genetics system as described in Newmann et al. (1999). Since WT-Venus-PR8 pathogenicity and Venus expression levels were appreciably attenuated in mice, WT-Venus-PR8 was serially passaged in mice. After six passages, a variant (MA-Venus-PR8) was obtained with increased pathogenicity and strong Venus expression. A stock of MA-Venus-PR8 was generated in MDCK cells. Since serial passage in animals typically results in virus populations composed of genetic variants, MA-Venus-PR8 was recreated by using reverse genetics. Likewise, MA-eCFP-PR8, -eGFP-PR8, and -mCherry-PR8 were generated with the same genetic backbone as MA-Venus-PR8.

To generate a Venus-HPAI virus by reverse genetics, the NS segment of A/Vietnam/1203/2004 (H5N1; VN1203) was replaced with Venus-NS of PR8, and the virus was adapted to mice as described for MA-Venus-PR8. A stock of MA-Venus-HPAI virus was made in MDCK cells. The set of these influenza viruses carrying various fluorescent proteins was collectively termed "Color-flu".

Mouse Experiments

Female, 6-week-old C57BL/6 ('B6') mice were purchased from Japan SLC, Inc. (Shizuoka, Japan). Mice were intranasally inoculated with Color-flu viruses, at the dosages indicated in the figure panels, in 50 μL of PBS under sevoflurane anesthesia, and body weights and survival were monitored for 14 days. Lungs were harvested from PBS-inoculated or Color-flu-infected mice for virus titration, flow cytometric analysis, and histological experiments at the times indicated in the figure panels. All animal experiments were performed in accordance with the regulations of the University of Tokyo Committee for Animal Care and Use and were approved by the Animal Experiment Committee of the Institute of Medical Science of the University of Tokyo.

Histology and Cytology

Lungs were fixed in 4% paraformaldehyde (PFA) phosphate buffer solution. Fixed tissues were embedded in OCT compound (Sakura Finetek, Tokyo, Japan), frozen by liquid N2 and stored at −80° C. Cryostat 6-μm sections were treated for 30 minutes with PBS containing 1% BSA (PBS-BSA) to block nonspecific binding, and then incubated with phycoerythrin (PE)-Mac3 (M3/84, BD Biosciences, San Jose, Calif.). To examine the cytology of the MDCK cells, cells were infected with Color-flu virus and then fixed in 4% PFA phosphate buffer solution. Nuclei were stained with Hoechst33342 (Invitrogen, Carlsbad, Calif.). Sections and cells were visualized by using a confocal microscope (Nikon A1, Nikon, Tokyo, Japan), controlled by NIS-Elements software. For quantitative multi-color imaging analysis, the slides were visualized by use of an inverted fluorescence microscope (Nikon Eclipse TS100) with a Nuance FX multispectral imaging system with InForm software (PerkinElmer, Waltham, Mass.).

Whole-Mount Imaging of Lung Tissue

Mice were euthanized and intracardially perfused with PBS to remove blood cells from the lung. The lungs were isolated after intratracheal perfusion with 4% PFA phosphate buffer solution. The lung tissues were cleared with SCALEVIEW-A2 solution (Olympus, Tokyo, Japan) according to the manufacturer's instructions. Images were acquired by using a stereo fluorescence microscope (M205FA, Leica Microsystems, Wetzlar, Germany) equipped with a digital camera (DFC365FX, Leica Microsystems).

Two-Photon Laser Microscopy

A total of 10^5 PFU of MA-eGFP-PR8 was intranasally inoculated into B6 mice. To label lung macrophages, 50 μL of PE-CD11b (M1/70, BioLegend, San Diego, Calif.) was injected intravenously to the mice at day 3 p.i. Thirty minutes after the antibody injection, the lungs of the mice were harvested. The kinetics of eGFP- and PE-positive cells in the lungs were imaged with a multi-photon microscope (LSM 710 NLO, Carl Zeiss, Oberkochen, Germany). During the analysis, the lungs were maintained in complete medium (RPMI 1640 with 10% fetal calf serum) in a humid chamber (37° C., 5% CO_2). The data were processed with LSM software Zen 2009 (Carl Zeiss). For three-dimensional imaging of HPAI virus-infected lung tissues, B6 mice were intranasally inoculated with 10^5 PFU of MA-Venus-HPAI virus. The lung tissues were collected from the mice at day 2 p.i., and treated with SCALEVIEW-A2 solution (Olympus) to make tissues transparent as described above. Three-dimensional images of lung tissues were obtained from a multi-photon microscope (Nikon A1R MP).

Flow Cytometric Analysis and Cell Sorting

To obtain single-cell suspensions, lungs were dissociated with Collagenase D (Roche Diagnostics, Mannheim, Germany; final concentration: 2 μg/mL) and DNase I (Worthington Biochemical, Lakewood, N.J.; final concentration: 40 U/mL) for 30 minutes at 37° C. by grinding the tissue through nylon filters (BD Biosciences). Red blood cells (RBCs) were lysed by treatment with RBC lysing buffer (Sigma Aldrich, St. Louis, Mo.). To block nonspecific binding of antibodies, cells were incubated with purified anti-mouse CD16/32 (Fc Block, BD Biosciences, San Diego, Calif.). Cells were stained with appropriate combinations of fluorescent antibodies to analyze the population of each

immune cell subset. The following antibodies were used: anti-CD45 (30-F11: eBioscience, San Diego, Calif.), anti-CD11b (M1/70: BioLegend), anti-F4/80 (BM8: eBioscience), and anti-CD11c (HL3: BD Biosciences). All samples were also incubated with 7-aminoactinomycin D (ViaProbe, BD Biosciences) for dead cell exclusion. Data from labeled cells were acquired on a FACSAria II (BD Biosciences) and analyzed with FlowJo software version 9.3.1 (Tree Star, San Carlos, Calif.). To isolate Venus-positive and -negative macrophages from lungs, stained cells were sorted using a FACSAria II (BD Biosciences).

Microarray Analysis

Total RNA of sorted macrophages was extracted using TRIzol reagent (Life Technologies, Carlsbad, Calif.) and precipitated with isopropanol. RNA amplification was performed using the Arcturus Riboamp Plus RNA Amplification Kit (Life technologies) in accordance with the manufacturer's instructions. RNA was labeled by using the Agilent Low Input Quick Amp Labeling kit, one color (Agilent Technologies, Santa Clara, Calif.) and hybridized to the SurePrint G3 Mouse GE 8×60 K microarray (Agilent Technologies). Arrays were scanned with a DNA Microarray Scanner with SureScan High-Resolution Technology, (G2565CA; Agilent Technologies), and data were acquired using Agilent Feature Extraction software ver. 10.7.3.1. (Agilent Technologies). Probe annotations were provided by Agilent Technologies (AMADID 028005). Probe intensities were background corrected and normalized using the normal-exponential and quantile methods, respectively. The $\log_2$ of the intensities were then fit to a linear model that compared the groups of interest[34]. All reported p values were adjusted for multiple hypothesis comparisons using the Benjamini-Hochberg method. Transcripts were considered differentially expressed if there was at least a 2-fold change in the mean probe intensity between contrasts with an adjusted $p<0.01$. Hierarchical clustering was performed in R. The resultant gene clusters were then analyzed with ToppCluster (Kaimal et al., 2010) to identify gene annotations that were enriched in each cluster. The reported scores are the $-\log_{10}$ of the Benjamini-Hochberg adjusted p-value.

Western Blot Analysis

Whole lysates of MDCK cells were electrophoresed through SDS-polyacrylamide gels (Bio-Rad Laboratories, Hercules, Calif.) and transferred to a PVDF membrane (Millipore, Billerica, Mass.). The membrane was blocked with Blocking One (Nacalai Tesque, Kyoto, Japan) and incubated with a rabbit anti-GFP polyclonal antibody (MBL, Nagoya, Japan), mouse anti-NS1 antibody (188/5), rabbit antiserum to A/WSN/33(H1N1)(R309) or mouse anti-actin antibody (A2228; Sigma-Aldrich), followed by HR-conjugated anti-mouse or anti-rabbit IgG antibody (GE Healthcare, Waukesha, Wis.). After the membrane was washed with PBS-Tween, specific proteins were detected using ECL Plus Western Blotting Detection System (GE Healthcare. The specific protein bands were visualized by the use of the VersaDoc Imaging System (Bio-Rad).

Results

To generate a fluorescent influenza virus expressing a reporter protein fused to the NS1 open reading frame, Venus was chosen, a GFP variant with eight mutations including F46L, which improves chromophore formation and increases brightness compared with GFP (Wagai et al., 2002). As expected based on previous findings of attenuation for influenza viruses expressing reporter proteins (Kittel et al., 2004; Shinhya et al., 2004), the mouse pathogenicity of A/Puerto Rico/8/34 (PR8; H1N1) virus expressing Venus (WT-Venus-PR8) was substantially lower than that of wild-type PR8 (WT-PR8); the dose required to kill 50% of infected mice (MLD_{50}) was more than $10^{4.5}$ plaque-forming units (PFU) for WT-Venus-PR8 compared with $10^{2.5}$ PFU for WT-PR8. WT-Venus-PR8 was serially passaged in C57BL/6 (B6) mice. After six consecutive passages, a variant (designated MA-Venus-PR8; possessing a T-to-A mutation at position 380 of the hemagglutinin protein, and an E-to-D mutation at position 712 of the polymerase subunit PB2) was identified with appreciably higher pathogenicity ($MLD_{50}=10^{3.5}$ PFU) compared with WT-Venus-PR8, although it was still less pathogenic than the original PR8 virus (FIG. **1**A). To assess the replicative ability of MA-Venus-PR8 in mouse lungs, B6 mice were intranasally infected with 10^4 PFU of MA-Venus-PR8 or PR8 virus. At all time points tested, the lung virus titers were similar for MA-Venus-PR8- and PR8-infected mice (FIG. **1**B). To test the stability of Venus expression, plaque assays were performed using lung homogenate from infected mice and found that only one of 150 plaques on each of days 3, 5, and 7 post-infection (p.i.) was Venus-negative, attesting to the high genetic stability of Venus expression in this recombinant virus. In contrast, only 70% of NS1-GFP virus expressed the reporter protein (Manicassamy et al., 2010). The robust virulence and genetic stability of MA-Venus-PR8 indicate that this virus represents a highly attractive reporter system to visualize influenza virus-infected cells in vivo.

TABLE 1

Replication and virulence of Color-flu in mice*.

Virus	Mean virus titer (log10 PFU/g ± s.d.) in the mouse lung on the indicated day p.i.			
	Day 3 p.i.	Day 5 p.i.	Day 7 p.i.	MLD_{50} (PFU)
MA-eCFP-PR8	8.1 ± 0.2**	8.0 ± 0.1	6.3 ± 0.1	$10^{3.0}$
MA-eGFP-PR8	8.6 ± 0.1	8.3 ± 0.1	6.3 ± 0.1	$10^{3.5}$
MA-Venus-PR8	8.6 ± 0.2	8.4 ± 0.1	6.5 ± 0.3	$10^{3.3}$
MA-mCherry-PR8	7.7 ± 0.3**	7.5 ± 0.7	6.1 ± 0.4	$10^{2.7}$
WT-Venus-PR8	5.6 ± 0.3**	5.3 ± 0.3**	5.2 ± 0.2**	$>10^{4.3}$
WT-PR8	8.8 ± 0.1	8.2 ± 0.5	6.9 ± 0.2	$10^{2.5}$
MA-PR8	8.9 ± 0.1	9.0 ± 0.0	7.9 ± 0.2**	$10^{2.3}$

*B6 mice were inoculated intranasally with 10^4 PFU of each virus in a 50 mL volume. Three mice from each group were killed on days 3, 5 and 7 p.i., and virus titres in the lungs were determined in MDCK cells.

**Statistical significance was calculated by using the Student's t-test; the P value was <0.01 compared with the titres in the lungs of mice infected with WT-PR8 virus.

To increase the versatility of fluorescent influenza viruses as imaging tools, additional MA-PR8 variants were generated that expressed different spectral GFP mutants, namely, eCFP (ex. 434 nm, em. 477 nm) and eGFP (ex. 489 nm, em. 508 nm) (Patterson, 2001). A mCherry variant (ex. 587 nm, em. 610 nm), which emits fluorescence at a longer wavelength than Venus (ex. 515 nm, em. 528 nm) (Nagai et al., 2002; Shaner et al., 2004), was also generated. These influenza viruses encoding the multi-spectral fluorescent reporter proteins were collectively named "Color-flu". To determine the pathogenicity of Color-flu viruses, the virus titres in mouse lung tissues and the MLD_{50} values of MA-eCFP, eGFP and mCherry-PR8 were compared with those of MA-Venus-PR8 and MA-PR8. All of virus strains showed comparatively high replication in the lungs and the MLD_{50} values were similar among the Color-flu viruses (Table 1). The stability of the fluorescent expression of the Color-flu viruses was tested in vivo and in vitro by plaque assay. When virus was collected from the lungs of mice on day 7 p.i., the percentages of fluorescent-positive plaques were 98.0% (MA-eCFP-PR8), 100.0% (MA-eGFP-PR8) and 96.4% (MA-mCherry-PR8). The percentages of fluorescent-positive plaques in the sample from the culture medium of MDCK cells after 72 hours p.i. was found to be 100.0% (MA-eCFP-PR8), 99.2% (MA-eGFP-PR8) and 98.2% (MA-mCherry-PR8). In addition, the stability of an NS1-fluorescent protein chimera in virus-infected cells was examined by infecting MDCK cells with MA-Venus-PR8 virus and detecting NS1-Venus chimeric protein by using anti-GFP and anti-NS1 antibodies. The NS1-Venus chimeric protein was not degraded until the time point examined (that is, 12 hours p.i.), indicating that the fluorescent signal is mainly emitted from the NS1-fluorescent protein chimera and not from degradation products in cells infected with Color-flu viruses. These findings indicate that the pathogenicity and stability of the Color-flu viruses were not affected by the different fluorescent reporter genes.

To assess the expression of Color-flu viruses in mouse lungs, we collected lungs from B6 mice infected with each of the Color-flu viruses and processed them for visualization as described in the Methods section. All four colors were clearly visible in whole transparent lung tissue when analyzed with a fluorescent stereomicroscope (FIG. **2**A). Fluorescent signals were mainly seen in the bronchial epithelial layer at day 3 p.i. At day 5 p.i., fluorescent signals extended to the peripheral alveolar regions. These data indicated that all four Color-flu viruses are useful for analyzing the distribution of influenza virus-infected cells in mouse lungs. To assess the expression of Color-flu viruses in mouse lungs, lungs were collected from B6 mice infected with each of the Color-flu viruses and processed them for visualization as described in the Methods section. All four colors were clearly visible in whole transparent lung tissue when analyzed with a fluorescent stereomicroscope (FIG. **2**A). Fluorescent signals were mainly seen in the bronchial epithelial layer at day 3 p.i. At day 5 p.i., fluorescent signals extended to the peripheral alveolar regions. These data indicate that all four Color-flu viruses are useful for analyzing the distribution of influenza virus-infected cells in mouse lungs.

Next, the Nuance™ spectral imaging system was employed to test whether the fluorescent signals of all four Color-flu viruses could be detected simultaneously. Lung tissues were collected from B6 mice intranasally inoculated with a mixture of the four strains (2.5×10^4 PFU each in a total volume of 50 μL). Analysis of lung sections obtained at days 2 and 5 p.i. showed that the fluorescent signals of all four Color-flu viruses were distinguishable from each other (FIG. **2**B). At day 2 p.i., clusters of the same fluorescent color were found in bronchial epithelial cells, suggesting local spread of the individual viruses. At this time point, a limited number of alveolar cells were infected. At day 5 p.i., we detected a cluster of alveolar cells expressing a single fluorescent protein, indicative of the initiation of infection with a single virus and its local spread (FIG. **2**B). Interestingly, epithelial cells simultaneously expressing two or three fluorescent proteins were detected, albeit at a low frequency, suggesting co-infection of these cells (FIG. **2**C). The ability to visualize cells co-infected with different influenza viruses in vivo is a major advance in technology and will allow insights into influenza co-infection and reassortment processes.

Next, the utility of Color-flu viruses was tested for the analysis of host responses to infection. Since macrophages are involved in innate immunity and acute inflammation in influenza virus-infected lungs, lung sections that were stained with an antibody to macrophages (PE-Mac3) were examined by using confocal microscopy. Macrophages infiltrated regions containing Venus-positive bronchial epithelial cells at day 2 p.i. of mice with MA-Venus-PR8 (FIG. **3**A); by contrast, only a few Mac3-positive cells were detected in the alveoli of lungs from mock-infected animals. On the basis of this finding, live imaging was employed to further study the interaction between influenza virus-infected epithelial cells and macrophages in mouse lungs. In the lung tissue of naive B6 mice, CD11b+ alveolar macrophages were detected by use of a two-photon laser microscope. Most of these macrophages did not migrate (i.e., showed little movement) during the observation period (49 minutes; data not shown). In mice infected with MA-eGFP-PR8 virus, many CD11b+ macrophages appeared to be 'attached' to eGFP-positive epithelial cells (data not shown); moreover, some of these eGFP-positive epithelial cells exhibited blebbing similar to apoptotic cells. Interestingly, a number of CD11b+ macrophages quickly moved around the eGFP-positive epithelial cells, suggesting possible macrophage responses to inflammatory signals such as IFNs or chemokines. The present system can thus be used to monitor the in vivo interactions between virus-infected and immune cells.

A number of studies have assessed the transcriptomics and proteomics profiles of influenza virus-infected mice (Go et al., 2012; Zhao et al., 2012). Since these studies used whole lung samples, the results are the sum of virus-infected and uninfected cells, leading to the dilution of host responses and not allowing one to distinguish the profiles of infected cells from those of uninfected, bystander cells. As a first step to overcome this shortcoming, macrophages (known to be infected by influenza viruses (FIG. **3**B)) from the lungs of mice infected with MA-Venus-PR8 were sorted on the basis of their fluorescent protein expression and performed microarray analysis. Macrophages isolated from the lungs of mice inoculated with PBS (naive macrophages) served as controls. In fluorescent-positive macrophages, 6,199 tran-

scripts were differently expressed relative to naive macrophages. By contrast, in fluorescent-negative macrophages obtained from infected mice, only 4,252 transcripts were differentially expressed relative to the naive macrophages. This difference likely reflects differences in gene transcription induced by active influenza virus infection. However, it should be noted that the fluorescent-negative cell populations obtained from infected animals may have included infected cells in which the fluorescent signal had not yet been detected as would be expected at an early stage of virus infection. In fact, confocal microscopy revealed that it took 9 hours to detect fluorescent protein expression in the majority of MDCK cells. Hierarchical clustering of differentially expressed transcripts, followed by functional enrichment analysis of each cluster, indicated that both fluorescent-positive and fluorescent-negative macrophages obtained from infected animals exhibit activation of pathways associated with the immune response, cytokine production, and inflammation (FIG. **3**D, green cluster). The upregulation of these pathways in the fluorescent-negative cells may have resulted from cell activation by IFN and cytokines released from infected cells, and/or from cells that were at an early stage of virus infection (as discussed earlier). Yet, a subset of enriched annotations, for example, type I IFN-mediated signaling (FIG. **3**D, light blue cluster), included transcripts that were more highly expressed in fluorescent-positive macrophages. In addition, it was observed that type I IFN genes were among the most upregulated transcripts in the fluorescent-positive macrophages (FIG. **3**E). Taken together, this enhanced type I IFN activity is consistent with the suggestion that the fluorescent-positive cells had been infected whereas the fluorescent-negative cells included both uninfected (but potentially 'stimulated') cells and cells at early stages of influenza virus infection. Indeed, it took at least 5 hours to detect fluorescent protein expression after infection with Color-flu viruses, although all of the fluorescent proteins (that is, eCFP, eGFP, Venus, and mCherry) were detectable in the majority of cells by 9 hours p.i. These findings open new avenues in infectious disease research to compare gene expression (or other types of expression) patterns of reporter protein-positive cells with those of reporter protein-negative cells (but potentially stimulated by released cytokines and/or are at an early stage of infection).

Finally, as discussed in more detail in Example II, it was tested whether the concept of mouse-adapted fluorescent influenza viruses could be applied to other influenza virus strains, such as highly pathogenic avian influenza A (H5N1) (HPAI) viruses, which are a research priority due to the threat they pose to humans. An MA-Venus-HPAI virus based on A/Vietnam/1203/2004 (VN1203; H5N1) was generated, employing the same strategy used to create MA-Venus-PR8; however, the PR8 NS gene was used to express NS1-Venus chimeric protein because Venus virus with the VN1203 NS gene did not contribute to pathogenicity in mice. The pathogenicity of MA-Venus-HPAI virus for B6 mice was comparable to that of VN1203, with MLD_{50} values for both viruses being less than 5 PFU (FIG. **4**A and Hatta et al., 2007). MA-Venus-HPAI virus also shared with other HPAI viruses the ability to spread systemically and replicate in various organs including spleen, kidney, and brain (FIG. **4**B and Hatta et al., 2007). Moreover, taking advantage of the strong fluorescent signal emitted by MA-Venus-HPAI virus-infected cells, a three-dimensional image of an HPAI virus-infected bronchus deep inside the lung tissues was successfully constructed (FIG. **4**C and data not shown). This type of three-dimensional imaging analysis will improve the understanding of the spatial distribution of influenza virus-infected bronchi. When the distribution of virus-infected cells was compared between HPAI virus and PR8-infected lungs, it was found that HPAI virus spreads from the bronchial epithelium to alveolar sites more quickly than did PR8 (FIGS. **4**C and D). By using flow cytometric analysis, it was found that CD45-negative, non-hematopoietic cells and F4/80-positive macrophages more frequently expressed Venus in the lungs of mice infected with MA-Venus-HPAI virus than in the lungs of animals inoculated with MA-Venus-PR8 (FIGS. **4**E and F), supporting findings that H5N1 HPAI viruses induce more severe inflammatory responses in the lung than does PR8, demonstrating the utility of Color-flu viruses for comparative studies of influenza pathogenesis.

Discussion

In this study, Color-flu viruses were generated to study influenza virus infections at the cellular level. Color-flu viruses combine several improvements over existing systems, including robust viral replication, virulence, stable fluorescent protein expression, and a set of four different colors that can be visualized simultaneously. Color-flu viruses are applicable to all influenza virus strains. These improvements allowed global transcriptomics analyses of infected and bystander cells and, for the first time, live-imaging of influenza virus-infected cells in the mouse lung.

Previous versions of fluorescent influenza viruses (Kittel et al., 2004; Shinya et al., 2004) including our original construct (i.e., WT-Venus-PR8) were appreciably attenuated in mice. These attenuated fluorescent viruses may still be useful for identifying initial target cells. However, the immune responses elicited by these highly attenuated, non-lethal viruses most likely differ considerably from those of the mouse-lethal parent virus, making their use for pathogenesis studies problematic. This problem was solved by passaging viruses in mice. This strategy proved to be successful for two different influenza virus strains, suggesting its broad applicability. A second drawback of previously tested fluorescent influenza viruses is the genetic instability of the added reporter protein (Manicassamy et al., 2010). However, almost 100% of virus plaques examined from mouse lung samples on day 7 post-infection expressed the reporter protein.

At present, Color-flu viruses cannot be monitored in live animals non-invasively because fluorescent reporter proteins must be within a "biological optical window (650-900 nm)" to be detected for imaging of tissues in live animals using fluorescent probes (Weisslander, 2001; Jobsis, 1977), and none of the fluorescent reporter proteins including mCherry, which has the longest emission among the reporter proteins of Color-flu, is inside this biological optical window. Heaton et al. (2013) generated a luciferase reporter-expressing influenza virus that can be used to monitor virus replication in live animals; however, this system needs systemic inoculation of substrate into the animals at every observation point. In addition, the resolution of their imaging system (based on the IVIS® system) is not adequate for the analysis of cellular immune mechanisms in vivo, which we are able to achieve with the present system.

Newer technologies for imaging analysis (Ghoznari et al., 2013) have enabled the development of a set of four different influenza color variants that can be distinguished from one

another by using Nuance™, hence allowing their simultaneous detection. In fact, our pilot study identified lung epithelial cells expressing two or three different fluorescent proteins (FIG. 2C). This may be the first visualization of mouse lung cells infected with more than one influenza virus strain. In future studies, these color variants could be used to address long-standing questions in influenza virus research, such as the frequency of viral co-infections in vivo, which may be critical to better understand influenza virus reassortment and, hence, the generation of novel influenza viruses such as the pandemic viruses of 1957 (Schaltissek et al., 1978; Kanaoka et al., 1989), 1968 (Schaltissek et al., 1978; Kanaoka et al., 1989), and 2009 (Smith et al., 2009; Itoh et al., 2009).

By employing the described tool sets, influenza virus-infected cells were detected in whole lung tissues of mice, allowing the observation of the location and distribution of influenza viruses in the lung. Moreover, interactions of virus-infected epithelial cells with immune cells were observed. Such studies will allow direct monitoring influenza disease progression from acute bronchitis to severe viral pneumonia, which causes considerable morbidity and mortality in highly pathogenic influenza virus infections (Gambotto et al., 2008; Shieh et al., 2009).

In conclusion, Color-flu viruses in combination with advanced imaging technologies allow for detection at the cellular level in animals.

Example II

As disclosed in Example I, an H5N1 virus with the Venus (Nagai et al., 2002) (a variant of eGFP) reporter gene (designated wild-type Venus-H5N1 virus, and abbreviated as WT-Venus-H5N1 virus) was prepared using reverse genetics; this virus showed moderate virulence and low Venus expression in mice. After six passages in mice a mouse-adapted Venus-H5N1 virus was acquired (abbreviated as MA-Venus-H5N1 virus) that stably expressed high levels of Venus in vivo and was lethal to mice; a dose required to kill 50% of infected mice (MLD_{50}) was 3.2 plaque-forming units (PFU), while that of its parent WT-Venus-H5N1 virus was 10^3 PFU. However, the mechanism for this difference in virulence and Venus stability was unclear.

In this study, the molecular mechanism that determines the virulence and Venus stability of Venus-H5N1 virus in mice was explored. By using reverse genetics, various reassortants between WT-Venus-H5N1 and MA-Venus-H5N1 virus were rescued and their virulence in mice examined to identify determinants for pathogenicity. Further, the determinants for Venus expression and Venus stability in vitro and in vivo were investigated. The findings further the understanding of the pathogenicity of influenza virus in mammals and will benefit the development of influenza virus-related vaccines and therapy.

Materials and Methods

Cells.

Human embryonic kidney 293 and 293T cells were maintained in Dulbecco's modified Eagle's medium (DMEM) with 10% fetal calf serum, and Madin-Darby canine kidney (MDCK) cells were maintained in minimal essential medium (MEM) supplemented with 5% newborn calf serum. All the cells were incubated at 37° C. in 5% CO_2.

Construction of Plasmids.

Plasmids for virus rescue was constructed as described in Neumann et al. (1999). To measure viral polymerase activity, the open reading frames of the PB1, PB2, PA, and NP of influenza virus were amplified by PCR with gene-specific primers and cloned into the pCAGGS/MCS protein expression plasmid (Dias et al., 2009). The primer sequences are listed below:

TABLE 2

Gene	Primer	sequence (5'-3')
VN1203-PB2	Upper	CCCATCGATACCATGGAGAGGATAAAAGAATTACGAGATC (SEQ ID NO: 20)
	Low	CTAGCTAGCCTACTAATTGATGGCCATCCGAATTCTTTTG (SEQ ID NO: 21)
VN1203-PB1	Upper	TACGAGCTCACCATGGATGTCAATCCGACTTTACTTTT (SEQ ID NO: 22)
	Low	CTAGCTAGCCTACTATTTTTGCCGTCTGAGTTCTTCAATG (SEQ ID NO: 23)
VN1203-PA	Upper	CCCATCGATACCATGGAAGACTTTGTGCGACAATGC (SEQ ID NO: 24)
	Low	CTAGCTAGCCTACTATTTCAGTGCATGTGCGAGGAAGGA (SEQ ID NO: 25)
VN1203-NP	Upper	TTCATCGATACCATGGCGTCTCAAGGCACCAAAC (SEQ ID NO: 26)
	Low	CGCGCTAGCCTATTAATTGTCATACTCCTCTGCATTGTCT (SEQ ID NO: 27)

All of the constructs were completely sequenced to ensure the absence of unwanted mutations.

Plasmid-Based Reverse Genetics.

Influenza A viruses were generated by using plasmid-based reverse genetics, as described previously (Murakami, 2008; Ozawa et al.; 2007). Viral titers of the rescued viruses were determined by use of plaque assays in MDCK cells. All rescued viruses were sequenced to confirm the absence of unwanted mutations.

Mouse Experiments.

Six-week-old female C57/BL6 (B6) mice (Japan SLC, Inc., Shizuoka, Japan) were used in this study. To measure viral replication in mice, six mice in each group were anesthetized with isoflurane and then intranasally inoculated with 10^5 PFU (50 μL) of virus. On days 1 and 3 post-infection (p.i.) three mice were euthanized, and their organs including the lungs, kidneys, spleens, and brains were collected and titrated in MDCK cells. To determine the 50% mouse lethal dose (MLD_{50}) of the viruses, four mice from each group were inoculated intranasally with 10-fold serial

dilutions containing 10^0 to 10^5 PFU (50 μL) of virus, respectively. Body weight and survival were monitored daily for 14 days. The MLD_{50} was calculated by using the method of Reed and Muench (1938). All mouse experiments were performed in accordance with the University of Tokyo's Regulations for Animal Care and Use and were approved by the Animal Experiment Committee of the Institute of Medical Science, the University of Tokyo.

Virus Passage in Mice and MDCK Cells.

Mouse adaptation of virus was performed as described in Example I. For virus passages in MDCK cells, confluent MDCK cells were infected with virus at a multiplicity of infection (MOI) of 0.0001. At 48 hours post-infection (hpi) the supernatants were collected and titered in MDCK cells. The new, harvested viruses were used to infect MDCK cells for the next passage. This procedure was repeated five times.

Growth Kinetics Assays.

Each virus was inoculated into triplicate wells of subconfluent MDCK cells at an MOI of 0.0001. The cells were supplemented with MEM containing 0.3% bovine serum albumin (BSA) and 1 μg/mL tolylsulfonyl phenylalanyl chloromethyl ketone (TPCK) trypsin and incubated at 37° C. in 5% CO_2. Culture supernatants were harvested at the indicated hours post-infection. The viral titers of the supernatants at the different time-points were determined by use of plaque assays in MDCK cells.

Mini-Genome Luciferase Assay.

Polymerase activity was tested with a mini-genome assay by using the dual-luciferase system as previously described in Murakami (2008) and Ozawa et al. (2007). Briefly, 293 cells were transfected with viral protein expression plasmids for NP, PB1, PB2, and PA from the WT-Venus-H5N1 or MA-Venus-H5N1 virus (0.2 μg each), with a plasmid expressing a reporter vRNA encoding the firefly luciferase gene under the control of the human RNA polymerase I promoter (pPolI/NP(0)Fluc(0), 0.2 μg), and with pRL-null (Promega, 0.2 μg), which encodes the Renilla luciferase, as an internal transfection control. At 24 hours post-transfection, cell lysate was prepared with the Dual-Luciferase Reporter Assay System (Promega) and luciferase activity was measured by using the GloMax 96 microplate luminometer (Promega). The assay was standardized against Renilla luciferase activity. All experiments were performed in triplicate.

Laboratory Facility.

All studies with H5N1 viruses were performed in enhanced biosafety level 3 containment laboratories at the University of Tokyo (Tokyo, Japan), which are approved for such use by the Ministry of Agriculture, Forestry, and Fisheries, Japan.

Statistical Analysis.

The data were analyzed by using the R software (www.r-project.org), version 3.1. For comparisons of measurements from multiple groups collected at a single time point, we used one-way ANOVA followed by Tukey's Post hoc test. For comparisons of multiple groups with measurements collected independently at different time-points (i.e., viral growth curves from mice, collected in MDCK cells), we used two-way ANOVA followed by Tukey's Post hoc test. For comparisons of multiple groups with dependent measurements (i.e., viral growth 7 curves in cell culture for which aliquots were collected from the same culture at different time points), a linear mixed-effects model was fitted to the data using the R package NLME, and the time, the virus strain, and the interaction between these two factors were considered. Next, a contrast matrix was built to compare the strains in a pairwise fashion at the same time points (e.g., group_1 vs group_2 at 24 hours post-infection, group_1 vs group_3 at 24 hours post-infection, group_2 vs group_3 at 24 hours post-infection), using the R package PHIA. Because the comparisons were performed individually, the final p-values were adjusted by using Holm's method to account for multiple comparisons. In all cases, the results were considered statistically significant if we obtained In all cases, the results were considered statistically significant if we obtained p-values (or adjusted p-values) <0.05.

Sequence Analysis.

The PB2 and PA sequences from the NCBI Influenza Virus Database were aligned by using the MUSCLE program (Edgar, 2004), with the default parameters and a maximum of 100 iterations. The alignment was visualized by using Clustal X (Larkin et al., 2007), and the frequency of amino acid occurrences at specific positions was determined by using custom written Perl scripts.

Results

Comparison Between WT-Venus-H5N1 and MA-Venus-H5N1 Viruses.

As in Example I, the NS segment of A/Viet Nam/1203/2004 (H5N1) (abbreviated as VN1203) was substituted with a Venus-fused NS segment of Venus-PR8 virus by using reverse genetics, and acquired an H5N1 virus that expressed the Venus fluorescent reporter gene (WT-Venus-H5N1 virus). A pathogenicity analysis in mice revealed that this virus exhibited attenuated virulence in mice compared with that of the parental VN1203 with an MLD_{50} value of 10^3 PFU (compared with 0.7 PFU for VN1203) (FIGS. **6**A and **6**B and Haifa et al. (2007)). Moreover, WT-Venus-H5N1 virus mainly replicated in respiratory organs (Table 3), and its Venus expression was very weak in both MDCK cells (FIG. **7**) and in mice after virus infection (FIG. **8**).

TABLE 3

Replication and virulence of H5N1 reassortants and mutants in mice[a]

	Mean virus titer (log_{10} PFU/g ± SD) on the indicated day p.i.							
	Lung		Spleen		Kidney		Brain	
Virus	Day 1 p.i.	Day 3 p.i.	Day 1 p.i.	Day 3 p.i.	Day 1 p.i.	Day 3 p.i.	Day 1 p.i.	Day 3 p.i.
WT-Venus-H5N1	6.5 ± 0.2	6.3 ± 0.2	—[b]	—	—	—	—	—
MA-Venus-H5N1	9.1 ± 0.1[c]	8.9 ± 0.0[c]	3.4 ± 0.2	6.5 ± 0.1	2.4 ± 0.1	4.1 ± 0.1	—	2.8 ± 0.6
RG-MA	9.1 ± 0.1[c]	9.2 ± 0.1[c]	2.8 ± 0.4	7.1 ± 0.0	2.3, —, —	4.0 ± 0.1	—	2.3 ± 0.2
WT + MA-PB2	7.7 ± 0.0[c]	8.0 ± 0.1[c]	—	4.1, 4.4, —	—	—	—	—
WT + MA-PA	7.1 ± 0.1[c]	6.8 ± 0.1[d]	—	—	—	—	—	—

TABLE 3-continued

Replication and virulence of H5N1 reassortants and mutants in mice[a]

Virus	Mean virus titer (log_{10} PFU/g ± SD) on the indicated day p.i.							
	Lung		Spleen		Kidney		Brain	
	Day 1 p.i.	Day 3 p.i.	Day 1 p.i.	Day 3 p.i.	Day 1 p.i.	Day 3 p.i.	Day 1 p.i.	Day 3 p.i.
WT + MA-(PB2 + PA)	8.6 ± 0.3[c]	8.7 ± 0.1[c]	2.9 ± 0.4	6.8 ± 0.0	2.0, 1.7, —	4.3 ± 0.7	—	2.7 ± 0.8

[a]Six-week-old SPF C57/BL6 mice were inoculated intranasally with 10^5 PFU of each virus in a 50-μl volume. Three mice from each group were euthanized on days 1 and 3 p.i., and virus titers were determined in samples of lung, spleen, kidney, and brain in MDCK cells.
[b]—, no virus was isolated from the sample.
[c]P value was <0.01 compared with the titers in the lungs of mice infected with WT-Venus-H5N1 virus.
[d]P value was <0.05 compared with the titers in the lungs of mice infected with WT-Venus-H5N1 virus.

After six passages of WT-Venus-H5N1 virus in mice, MA-Venus-H5N1 virus was obtained. MA-Venus-H5N1 virus was lethal to mice with an MLD_{50} of 3.2 PFU (Example I). This virus replicated systemically in mice; on day 1 p.i., high viral titers were detected in lungs, spleens, and kidneys, and on day 3 p.i. virus could be detected in brains (Table 3). Moreover we detected high Venus expression of MA-Venus-H5N1 virus in MDCK cells (FIG. **7**) and in mice (FIG. **8**). Therefore, compared with WT-Venus-H5N1, MA-Venus-H5N1 virus showed much higher pathogenicity in mice and a higher replicative ability. Moreover, this virus exhibited high Venus expression during its replication in vitro and in vivo.

To identify the genetic mutations that had occurred during mouse adaptation, the genome of MA-Venus-H5N1 virus was sequenced and compared to that of WT-Venus-H5N1 virus. At the amino acid level, a total of seven differences were found between the two viruses in their PB1, PB2, PA, NA, M2, and NS1 genes (Table 4). Thus single or multiple amino-acid changes among these seven different amino acids may contribute to the difference in virulence in mice and in Venus expression between these two viruses.

TABLE 4

Amino acid differences between WT-Venus-H5N1 and MA-Venus-H5N1 viruses.

Viral segment	Amino acid position	Amino acid in: WT-Venus-H5N1	Amino acid in: MA-Venus-H5N1
PB2	25	Val (V)	Ala (A)
PB1	737	Lys (K)	Arg (R)
PA	443	Arg (R)	Lys (K)
	35	Ser (S)	Arg (R)
NA	284	Val (V)	Leu (L)
M2	64	Ala (A)	Asp (D)
NS1	167	Pro (P)	Ser (S)

V25A of PB2 and R443K of PA Determine the Pathogenicity and Venus Expression of Venus-H5N1 Virus in Mice.

To investigate the genetic basis for the difference in the virulence and Venus expression of Venus-H5N1 virus after mouse adaptation, a reverse genetics system was established for MA-Venus-H5N1 virus, which was named RG-MA virus. RG-MA virus exhibited similar viral titers in organs, MLD_{50} value (FIGS. **6**C and **6**D and FIG. **9**), and Venus expression in mice (FIG. **9**) to those of its original virus (MA-Venus-H5N1 virus).

To identify the amino acids responsible for the difference in virulence and Venus expression between WT-Venus-H5N1 and MA-Venus-H5N1 virus, six single-gene recombinant viruses were generated, each bearing the PB2, PB1, PA, NA, M, or NS gene from MA-Venus-H5N1 virus and the other seven genes from WT-Venus-H5N1 virus. The recombinant viruses that contained the PB1, NA, or NS gene of MA-Venus-H5N1 virus (designated WT+MA—PB1, WT+MA—NA, or WT+MA—NS) displayed similar pathogenicity in mice to that of WT-Venus-H5N1 (MLD_{50}, 10^3 PFU) (FIG. **9**), whereas the reassortants with the PB2, PA, or M gene of MA-Venus-H5N1 (designated WT+MA—PB2, WT+MA—PA, or WT+MA—M) exhibited higher pathogenicity in mice than WT-Venus-H5N1 (FIG. **9**). WT+MA—PB2 and WT+MA—PA replicated more efficiently in mouse lungs than did WT-Venus-H5N1; moreover virus was detected in the spleens of two of three mice infected with WT+MA—PB2.

The effect of the PB2, PA, or M genes derived from WT-Venus-H5N1 on the virulence of MA-Venus-H5N1 was also examined by generating three single-gene recombinant viruses, each containing the PB2, PA, or M gene from WT-Venus-H5N1 virus and the remaining segments from MA-Venus-H5N1 virus (designated MA+WT−PB2, MA+WT−PA, or MA+WT−M). The MLD_{50} values of MA+WT−PB2 and MA+WT−PA were $10^{2.3}$ PFU, significantly higher than that of MA-Venus-H5N1 (MLD_{50}, 3.2 PFU), whereas the virulence of MA+WT−M in mice was similar with that of MA-Venus-H5N1 (FIG. **9**). These data suggest that the PB2 and PA genes played a role in the pathogenicity of MA-Venus-H5N1 virus in mice.

To assess the potential synergetic effects of the PB2 and PA genes on viral pathogenicity in mice, a reassortant carrying both the PB2 and PA genes of MA-Venus-H5N1 [MA−(PB2+PA)] on the WT-Venus-H5N1 virus backbone and a reciprocal reassortant on the MA-Venus-H5N1 virus backbone [designated WT+MA−(PB2+PA) and MA+WT−(PB2+PA)] were rescued, and assessed for virulence in mice. The substitution of the PB2 and PA genes from MA-Venus-H5N1 virus into WT-Venus-H5N1 virus significantly enhanced its virulence in mice, with an MLD_{50} value of 3.2 PFU (FIG. **9**), and also enhanced virus spread and replication in mice, similar to that of MA-Venus-H5N1 virus, and vice versa. Given that a single mutation is present in PB2 and in PA after mouse adaptation, these data indicate that V25A of PB2 and R443K of PA synergistically contribute to the virulence of MA-Venus-H5N1 virus in mice.

When checking the Venus expression of the above reassortants in MDCK cells, it was found that the MA—PB2 gene markedly increased Venus expression (FIG. **7**). In addition, Venus expression of WT+MA—PB2 virus in the lungs was also appreciably enhanced (FIG. **8**). The other single-gene substitutions including MA—PA did not affect Venus expression; however, the double substitution of MA—PB2 and MA—PA on the WT-Venus-H5N1 virus backbone increased Venus expression in MDCK cells and in mouse lung compared with those achieved by WT-Venus-H5N1 and WT+MA—PB2 virus (FIGS. **7** and **8**). These data indicate that V25A of the PB2 protein plays a vital role in the Venus expression of MA-Venus-H5N1 virus in vitro and in vivo, and that R443K of the PA protein enhances the PB2 effect on Venus expression.

The Amino Acid at Position 25 in the PB2 Protein Significantly Enhances Viral Replication in Mammalian Cells.

The replicative ability of these viruses was further examined in MDCK cells and it was found that the MA-Venus-H5N1 virus had similar replicative capability with RG-MA virus and grew more efficiently than WT-Venus-H5N1 virus, and that the titers of MA-Venus-H5N1 virus were significantly higher than those of WT-Venus-H5N1 virus at 36 and 48 hpi (FIG. **10**). The contribution of the PB2 and PA viral segments to the replication of the two viruses was then investigated. Significantly higher titers of WT+MA—PB2 and WT+MA−(PB2+PA) were observed compared with those of WT-Venus-H5N1 virus at several time points post-infection, yet the replication efficiency of WT+MA—PA was comparable to that of WT-Venus-H5N1 virus (FIG. **10**). The titers of WT+MA−(PB2+PA) were higher than those of WT+MA—PB2 at 36 and 48 hpi although the difference was not statistically significant (FIG. **10**). These results indicate that the MA—PB2 gene enhances the replication of Venus-H5N1 virus in MDCK cells, and that this increase can be further enhanced by the presence of MA—PA, although MA—PA alone does not alter virus replication in MDCK cells.

The Mutations in the Polymerase Genes after Mouse Adaptation Decrease Viral Polymerase Activity in Mammalian Cells.

The polymerase activity of the viral ribonucleoprotein (RNP) complex has been correlated with viral replication and virulence (Gabriel et al., 2005; Leung et al., 2010; Li et al., 2008; Salomen et al., 2006). The activity of the eight RNP combinations of PB1, PB2, and PA from either WT-Venus-H5N1 or MA-Venus-H5N1 virus was determined by measuring luciferase activity. The polymerase activity of the mouse-adapted virus was near 4-fold less than that of WT-Venus-H5N1 virus (FIG. **11**). The substitution of any MA gene decreased the activity of the polymerase complex of WT-Venus-H5N1 virus, but the polymerase activity of complexes containing the double substitution of MA—PB2 and MA—PA was significantly decreased compared with that of WT-Venus-H5N1 virus and was similar with that of MA-Venus-H5N1 virus. These results indicate that the polymerase activity of RNP complexes was notably decreased after mouse adaptation, which is not in agreement with the enhanced replication and virulence.

Molecular Determinants of Venus Stability in Venus-H5N1 Virus In Vitro and In Vivo.

To assess Venus stability in the WT-Venus-H5N1 and RG-MA viruses in vitro, the two viruses were passaged five times in MDCK cells. During these passages Venus-negative plaques were picked up from WT-Venus-H5N1 virus, but not from RG-MA virus, suggesting that the Venus gene is more stable after mouse adaptation (Table 5). To identify the molecular determinants of this Venus stability, various reassortants were passaged five times in MDCK cells. Venus-negative plaques were acquired from reassortants with the MA—PB1, MA—NA, or MA—M gene, but we did not obtain any Venus-negative plaques from the fifth passages of Venus-H5N1 virus with the MA—PB2, MA—PA, MA−(PB2+PA), or MA—NS gene (Table 5). These data suggest that the MA—PB2, —PA, and —NS genes may play roles in Venus stability.

TABLE 5

Venus stability in Venus-H5N1 reassortants in MDCK cells[a].

Virus	No. of passages in MDCK cells	No. of plaques checked	No. of Venus-negative plaques picked	No. of Venus-negative plaques after recheck
WT-Venus-H5N1	2	73	5	4
	3	111	5	1
	4	79	5	0
	5	61	12	2
RG-MA	2	66	1	0
	3	144	8	0
	4	73	1	0
	5	75	2	0
WT + MA-PB2	5	84	2	0
WT + MA-PB1	5	126	4	1
WT + MA-PA	5	104	16	0
WT + MA-(PB2+PA)	5	123	6	0
WT + MA-NS	5	199	11	0
WT + MA-NA	5	73	16	1
WT + MA-M[b]	5	69	10	10

[a]Each virus was passaged five times in MDCK cells as describe in the Materials and Methods. Venus expression of different passage stocks was detected in MDCK cells by using fluorescence microscopy. Venus-negative plaques were picked up and amplified in MDCK cells. Amplified Venus-negative plaques were rechecked for Venus expression to exclude false-negative plaques.

[b]69 plaques of the fifth passage stock of WT+30MA-M were checked by using fluorescence microscopy, all of which were "Venus-negative". Ten of these plaques were picked up to further confirm the lack of Venus expression, all of which were confirmed to be Venus-negative.

To further evaluate the roles of these different genes on Venus stability, the NS segments of the fifth-passage stocks from different reassortants were amplified by using PCR and NS-specific primers. Except for the Venus-NS segment (1.9 kb), the deleted NS segments were detectable, at a level similar to that for the NS segment of PR8, at less than 1 kb. The deleted NS segments of WT-Venus-H5N1 and of the reassortants with the MA—NA and MA—M genes were much brighter than those of the other reassortants (FIG. **12**), further implying that the MA—NA and MA—M genes do not contribute to Venus stability in vitro. Although RG-MA virus and the reassortants with MA—NS, MA—PA, or MA—PB2 were more stable, the deleted Venus-NS segments were still amplified by using PCR albeit to a lesser degree (FIG. **12**). The deleted NS segments from the various reassortants were extracted and sequenced, and the different deletion forms were identified from the different reassortants (FIG. **13**).

In addition, to examine Venus stability in vivo, B6 mice were inoculated with 10^5 PFU of WT-Venus-H5N1 virus, RG-MA virus, or WT+MA−(PB2+PA) virus. Lungs were collected on day 4 p.i., before the mice died, and were homogenized in PBS. The supernatants were inoculated into MDCK cells, and at 48 hpi Venus-negative plaques were picked up and amplified in MDCK cells. It should be noted that sometimes the Venus signal of the plaque correlates with the condition of the cultured cells and the detection time. Therefore the Venus expression of amplified Venus-negative plaques was rechecked in MDCK cells to exclude false

negatives. More than 95 plaques were detected from each lung, and only one plaque without Venus expression was acquired from one of three mice infected with RG-MA virus, twelve Venus-negative plaques from three mice infected with WT+MA−(PB2+PA), and more than 15 Venus-negative plaques from each mouse infected with WT-Venus-H5N1 virus (Table 6). These results indicate that WT-Venus-H5N1 virus is the most unstable of these viruses in vivo, and that the PB2 and PA genes from MA-Venus-H5N1 virus enhance Venus stability, albeit to a lesser extent than occurs in MA-Venus-H5N1 virus. The mutations on PB1, PB2, PA, and NS may therefore synergistically contribute to Venus stability in MA-Venus-H5N1 virus in vivo.

TABLE 6

Venus stability in Venus-H5N1 viruses in mice[a].

Virus	Mouse No.	No. of plaques checked	No. of Venus-negative plaques picked	No. of Venus-negative plaques after recheck
RG-MA	1#	105	4	1
	2#	109	6	0
	3#	127	5	0
WT + MA-(PB2 + PA)	4#	116	12	6
	5#	111	8	3
	6#	115	14	3
WT-Venus-H5N1	7#	145	31	22
	8#	120	27	18
	9#	95	19	15

[a]Six-week-old SPF C57/BL6 mice were infected intranasally with 10^5 PFU of each virus in a 50-μl volume. Three mice from each group were euthanized on day 4 p.i. and their lung tissues were collected and homogenized in PBS. The supernatants of the lung samples were inoculated into MDCK cells to check for Venus expression, and Venus-negative plaques were picked up and amplified in MDCK cells. Amplified Venus-negative plaques were rechecked for Venus expression to exclude false-negative plaques.

Discussion

Previously, a visualizable H5N1 virus expressing a Venus reporter gene that became more lethal to mice and more stable after mouse adaptation was constructed (Example I). In this study, the whole genome of this virus (MA-Venus-H5N1) was sequenced, and seven amino acids that differed from the WT-Venus-H5N1 virus sequence were identified. To explore the molecular determinants for the differences in virulence and Venus expression in mice between these two viruses, a series of reassortants of both viruses was generated using reverse genetics. The double mutation of PB2 (V25A) and PA (R443K) was found to dramatically enhance the pathogenicity of WT-Venus-H5N1 in mice. V25A of PB2 also significantly increased Venus expression and viral replication in MDCK cells and in mice, and that R443K of PA further enhanced these effects. The stability of different reassortants was examined in vitro, the reassortants with MA—PB2, MA—PA, or MA—NS were found to be more stable. These results suggest that the PB2 and PA proteins play roles in the pathogenicity and Venus stability of Venus-expressing H5N1 viruses in mammalian hosts.

The pathogenicity of highly pathogenic H5N1 avian influenza viruses in mammals is determined by multiple viral genes. For example, the HA protein plays crucial roles in the systemic replication and lethal infection of H5 subtype viruses in chickens (Kawaoka and Webster, 1986) and mammals (Hatta et al., 2001; Suguitan et al., 2012). The HA and NS genes of H5N1 virus also contribute to high virulence in ferrets (Imai et al., 2010). The NS1 protein helps to subvert the antiviral immune response of the host and is essential for the pathogenicity of H5N1 viruses in mice (Jiao et al., 2005). Mutations in the M1 protein also affect the virulence of H5N1 viruses in mice (Fan et al., 2009). The amino acids at position 627 and 701 of PB2 are key determinants of the high virulence of H5N1 influenza viruses in mammals (Hatta et al., 2001; Li et al., 2005). Lastly, the PA protein is reported to contribute to the virulence of H5N1 avian influenza viruses in domestic ducks (Song et al., 2011) and in mice (Hu et al., 2013). Here, it was found that V25A of PB2 and R443K of PA synergistically contribute the pathogenicity of H5N1 virus in mice.

Based on all of the influenza virus sequences (23514 PB2 proteins and 24240 PA proteins) available in the public database (www.fludb.org), it was found that 25V in PB2 and 443 R in PA are extremely conserved, whereas 25A in PB2 is present in only two viruses [A/Mallard/ON/499/2005 (H5N1), accession number EF392844; and A/Zhejiang/92/2009(H1N1), accession number CY095997] and 443 K in PA is present in only one strain, isolated from a quail [A/Quail/Shantou/1425/2001(H9N2), accession number EF154846]. Although the virulence of these viruses in mice is unknown, the present study is the first to suggest that the combination of 25 A in PB2 and 443 K in PA contributes to the increased virulence of a virus in mice and is a unique feature of MA-Venus-H5N1 virus.

The RNA polymerase of influenza A virus consists of the PB1, PB2, and PA subunits, and is implicated in numerous essential processes in the viral life cycle (Naffakh et al., 2005). PB1 performs polymerase and endonuclease activities, PB2 is responsible for capped-RNA recognition, and PA is involved in RNA replication and proteolytic activity (Obayasjo et al., 2005). The interfaces of these polymerase subunits are essential for transcription initiation (He et al., 2008; Sugiyama et al., 2009). Residues 1-37 at the N-terminus of the PB2 protein play a vital role in binding to the PB1 protein and affect the RNA polymerase activity, and these residues are highly conserved among all subtypes of influenza virus (Sugiyama et al., 2009). The amino acid at position 25 of PB2 is located within the third α-helix (amino acids 25 to 32) of its PB1-binding domain (Sugiyama et al., 2009). In this study, the amino acid at position 25 in PB2 was found to be changeable, and V25A in PB2 was found to increase viral replication in mammalian cells and in mice, resulting in higher pathogenicity of the H5N1 virus in mice. The R443 residue of the PA protein also plays a role in replication activity (Obayashi et al., 2008; Regan et al., 2006), and the mutation R443A in PA prevents the production of infectious virus (Regan et al., 2006). In this study, reassortants with R443K in their PA protein were rescued, and demonstrated that R443K in PA enhances viral replication in mouse lungs, reinforcing it was the virulence of H5N1 virus in mice. The present data thus further emphasize the role of the amino acid at position 443 of the PA protein for influenza virus.

Earlier reports have shown that the polymerase activity of the viral RNP complex closely correlates with viral replication and virulence (Gabriel et al., 2005; Leung et al., 2010; Li et al., 2008; Salomon et al., 2006). Viruses with higher polymerase activity in mammalian cells generally show higher virulence in mice (Zhang et al., 2014) and ferrets (Salomen et al., 2006). However, viruses with high polymerase activity are not always lethal to mice, which suggests that high pathogenicity of a virus in its host may require a certain level of polymerase activity (Gabriel et al., 2005), In this study, it was found that MA-Venus-H5N1 virus was more lethal to mice than was its wild-type counterpart, yet it had much lower polymerase activity, and any RNP combination with a polymerase gene from MA-Venus-H5N1 also had lower activity. These results may imply that the

polymerase activity of the vRNP complex closely correlates with the viral genome, and that the lower level of polymerase activity is more compatible with the reconstructed genome of Venus-H5N1, which benefits its high pathogenicity in mice.

With the development of living imaging in vivo, the ability to visualize influenza viruses carrying fluorescent reporter genes will be of great benefit influenza virus-related research (Heaton et al, 2013; Helft et al., 2012; Manicassamy et al., 2010; Pan et al., 2013; Example I). An effective virus for this purpose should have good replicative ability and show considerable pathogenicity in its host. Moreover, it should both highly and stably express its fluorescent reporter protein. Many attempts to construct influenza A viruses carrying the GFP reporter gene have been reported (Kittel et al., 2004; Manicassamy et al., 2010); however, some of these viruses showed low replication or poor pathogenicity in mice (Kittle et al., 2004), while some produced relatively low fluorescent signals or did not stably express GFP during virus replication in vitro and in vivo (Manicassamy et al., 2010). The present data demonstrate that not only is MA-Venus-H5N1 virus highly pathogenic to mice, but it also highly and stably expresses Venus fluorescent protein in vitro and in vivo. In the present analysis of the molecular determinants of Venus expression and Venus stability, it was found that V25A in PB2 played a role in determining Venus expression, which was further enhanced by the presence of R443K in PA. The analysis of Venus stability revealed that the single gene of MA—PB1, —PB2, —PA, or —NS determines Venus stability in vitro, but in vivo the situation is more complex and mutations in PB1, PB2, PA, and NS may synergistically codetermine Venus stability in MA-Venus-H5N1 virus.

In summary, molecular determinants in a mouse-adapted Venus-H5N1 virus were identified that play a crucial role in the pathogenicity of the virus in mice, and in its Venus expression and Venus stability in vitro and in vivo. These molecular markers will benefit future research on anti-influenza virus drug and vaccine development.

Example III

Materials and Methods

Cells and Viruses.

Madin-Darby canine kidney (MDCK) cells were maintained in minimum essential medium (MEM) containing 5% of newborn calf serum (NCS). Human embryonic kidney 293T (HEK293T) and HEK293 cells were maintained in Dulbecco's modified Eagle medium supplemented with 10% fetal calf serum (FCS). A/Puerto Rico/8/34 (H1N1; PR8) (Horimoto et al., 2007) and each NS1-Venus PR8 virus were generated by using reverse genetics and were propagated in MDCK cells at 37° C. for 48 hours in MEM containing L-(tosylamido-2-phenyl) ethyl chloromethyl ketone (TPCK)-treated trypsin (0.8 μg/mL) and 0.3% bovine serum albumin (BSA) (Sigma Aldrich).

Adaptation of NS1-Venus PR8 Virus in Mice.

Six- to eight-week-old female C57BL/6 mice (Japan SLC) were intranasally infected with 50 μL of 2.3×10^6 plaque-forming units (PFU) of NS1-Venus PR8 virus. Lungs were harvested 3-6 days post-infection (dpi) and homogenized in 1 mL of phosphate-buffered saline (PBS). To obtain a clone with high proliferative ability and Venus expression, plaque purification of the lung homogenate using MDCK cells was performed. A large, highly Venus-expressing plaque was picked and the cloned virus was propagated in MDCK cells at 37° C. for 48 hours, then 50 μL of the supernatant was used as an inoculum for the next passage. These procedures were repeated six times.

Sequence Analysis.

Sequence analysis of viral RNA was performed as described previously (Sakabe et al., 2011). Briefly, viral RNAs were extracted by using a QIAamp Viral RNA mini kit (QIAGEN) and Superscript III™ reverse transcriptase (Invitrogen) and an oligonucleotide complementary to the 12-nucleotide sequence at the 3' end of the viral RNA (Katz et al., 1990) were used for reverse transcription of viral RNAs. Each segment was amplified by using PCR with Phusion High Fidelity DNA polymerase (Finnzymes) and primers specific for each segment of the PR8 virus. The PCR products were purified and their sequences determined by using ABI 3130 xl (Applied Biosystems).

Plasmid Construction and Reverse Genetics.

Plasmids containing the cloned cDNAs of PR8 genes between the human RNA polymerase 1 promoter and the mouse RNA polymerase I terminator (referred to as PoII plasmid) were used for reverse genetics and as templates for mutagenesis. The mutations found in NS1-Venus PR8 virus after passage were introduced into the plasmid constructs of PR8 by using site-directed mutagenesis (referred to as pPoIIR-PR8—PB2-E712D and pPoIIR-PR8-HA-T380A, respectively). Reverse genetics was performed as described previously (Neumann et al., 1999). The eight PoII plasmids were cotransfected into HEK293T cells together with eukaryotic protein expressing plasmids for PB2, PB1, PA, and NP derived from PR8 by using the TransIT-293 transfection reagent (Mirus). Forty-eight hours after transfection, the supernatant was harvested and propagated once in MDCK cells at 37° C. for 48 hours in MEM containing TPCK-treated trypsin (0.8 □g/mL) and 0.3% BSA. Cell debris was removed by centrifugation at 2,100×g for 20 minutes at 4° C., and the supernatants were stored at −80° C. until use. The virus titers were determined by means of a plaque assay using MDCK cells.

Polykaryon Formation Assay.

Polykaryon formation assay was performed as described previously (Imai et al., 2012) with modifications. HEK293 cells propagated in 24-well plates were infected with wild-type PR8 or PR8 possessing the hemagglutinin (HA) mutation found in NS1-Venus PR8 MA virus in DMEM containing 10% FCS at a multiplicity of infection (MOI) of 10. At 18 hours post-infection, cells were washed with MEM containing 0.3% BSA and treated with TPCK-treated trypsin (1 μg/mL) in MEM containing 0.3% BSA for 15 minutes at 37° C. to cleave the HA on the cell surface into HA1 and HA2. Trypsin was inactivated by washing the cells with DMEM containing 10% FCS. To initiate polykaryon formation, cells were exposed to low-pH buffer (145 mM NaCl, 20 mM sodium citrate (pH 6.0-5.4)) for 2 minutes at 37° C. Then the low-pH buffer was replaced with DMEM containing 10% FCS and the cells were incubated for 2 hours at 37° C. The cells were then fixed with methanol and stained with Giemsa's solution. A microscope mounted with a digital camera (Nikon) was used to obtain photographic images.

Western Blotting.

MDCK cells were infected with each virus at an MOI of 1 without trypsin. The cells were lysed with Novex® Tris-Glycine SDS sample buffer (Invitrogen) 12 hours after infection and subjected to SDS-polyacrylamide gel electrophoresis. Then, the proteins were transferred to a PVDF membrane in transfer buffer (100 mM Tris, 190 mM glycine). After membrane blocking, the membranes were incubated with a rabbit anti-GFP polyclonal antibody (MBL) or rabbit antiserum to A/WSN/33(H1N1)(R309), which was

available in our laboratory. This antiserum reacts with influenza viral proteins including HA, NP, and matrix protein (M1). After incubation with the primary antibodies followed by washing with PBS containing 0.05% Tween-20 (PBS-T), the membranes were incubated with ECL™ anti-rabbit IgG HRP-linked whole antibody (GE Healthcare). Finally, specific proteins were detected by using the ECL Plus Western Blotting Detection System (GE Healthcare). The VersaDoc Imaging System (Bio-Rad) was used to obtain photographic images.

Pathogenicity and Replication of Viruses in Mice.

Six-week-old female C57BL/6 mice were intranasally infected with 50 μL of 10^3, 10^4 or 10^5 PFU of each virus. Four mice per group were monitored for survival and body weight changes for 14 days after infection. Three mice per group were infected with 10^3 PFU of each virus and euthanized on the indicated days. Their lungs were collected to determine viral titers by means of plaque assay on MDCK cells.

Immunofluorescence Assay.

Six-week-old female C57BL/6 mice were intranasally infected with 50 μL of 10^4 PFU of each virus. Three mice per group were euthanized on the indicated days. To fix the lungs, they were intratracheally injected with 800 μL of 4% paraformaldehyde (PFA) phosphate buffer solution and then removed. After incubation with 10 mL of 4% PFA at 4° C. for 4 hours, the buffer was replaced with 10%, 20%, and 30% sucrose in PBS in a stepwise fashion. Then lungs were embedded in Optimum Cutting Temperature (OCT) Compound (Tissue-Tek) and frozen in liquid nitrogen. Frozen sections (6 μm in thickness) were permeabilized in 0.2% Triton X-100 in PBS and incubated with primary antibodies at 4° C. for 12 hours. Primary antibodies were goat anti-Clara cell 10 kDa protein (CC10) (Santa Cruz, sc-9772), rabbit anti-surfactant protein C (SP—C) (Santa Cruz, sc-13979), golden Syrian hamster anti-podoplanin (eBioscience, eBio8.1.1), and rabbit anti-calcitonin gene-related peptide (CGRP) (Sigma-Aldrich, C8198). After being washed with PBS, the sections were incubated with species-specific fluorescence dye-conjugated secondary antibodies at room temperature for 30 minutes. Nuclei were stained with Hoechst33342 (Invitrogen). A Nikon A1 confocal microscope (Nikon) was used to observe the sections.

Preparation of Transparent Samples.

Transparent samples were prepared by using SCALEVIEW A2 (Olympus) in accordance with a previous report (Hama et al., 2012). Six-week-old female C57BL/6 mice were intranasally infected with 50 μL of 10^5 PFU of each virus. Intracardial perfusion was performed on the indicated days and lungs were fixed with 4% PFA in PBS for 4 hours at 4° C. Lungs were incubated with 10%, 20%, and 30% sucrose in PBS as described above, embedded in OCT compound, and frozen in liquid nitrogen. After the samples were thawed and rinsed in PBS, they were fixed again with 4% PFA in PBS for 30 minutes at room temperature. Then the lungs were transferred to SCALEVIEW A2 and incubated at 4° C. for at least 2 weeks. SCALEVIEW A2 was exchanged every 2-3 days. Transparent samples were observed by using a stereo fluorescence microscope (Leica M205FA) mounted with a digital camera (DFC365FX) and filter GFP 3 (480/40 LP510).

Flow Cytometry.

To prepare single-cell suspensions, lungs were minced with scissors and digested with 20 mg of collagenase D (Roche) and 200 units of DNase (Worthington) for 30 minutes at 37° C. Samples were then passed through 100-μm cell strainers and red blood cells were lysed by red blood cell lysis buffer (Sigma Aldrich). Single-cell suspensions were stained with a combination of the following antibodies: allophycocyanin-conjugated anti-F4/80 (eBioscience, BM8), allophycocyanin-cyanine 7-conjugated anti-CD11b (BioLegend, M1/70), phycoerythrin-cyanine 7-conjugated anti-CD11c (BD PharMingen, HL3), and eFluor 450-conjugated CD45 (eBioscince, 30-F11). Dead cells were stained with via-probe (Becton Dickinson). Stained samples were analyzed with FACSAria II (Becton Dickinson and Company) and FlowJo software (TreeStar).

RNA Isolation and Integrity.

Venus-positive and -negative cells from three pooled lungs were collected in TRIzol Reagent (Invitrogen). Total RNA was extracted by isopropanol precipitation with glycogen as a carrier. Isolated total RNA integrity was assessed by determining UV 260/280 absorbance ratios and by examining 28S/18S ribosomal RNA bands with an Agilent 2100 bioanalyzer (Agilent Technologies) according to the manufacturer's instructions.

Microarray Analysis.

Forty nanograms of total RNAs was amplified by using the Arcturus® Riboamp® Plus RNA Amplification Kit (Life technologies). Cy3-labeled complementary RNA probe synthesis was initiated with 100 ng of total RNA by using the Agilent Low Input Quick Amp Labeling kit, one color (Agilent Technologies) according to the manufacturer's instructions. The Agilent SurePrint G3 Gene Mouse GE 8×60 K microarray was also used. Slides were scanned with an Agilent's High-Resolution Microarray Scanner, and image data were processed by using Agilent Feature Extraction software ver. 10.7.3.1. All data were subsequently uploaded into GeneSpring GX ver 12.5 for data analysis. For the data analysis, each gene expression array data set was normalized to the in silico pool for samples from mice inoculated with PBS. Statistically significant differences in gene expression between the Venus-positive cells and -negative cells were determined by using one-way analysis of variance (ANOVA) followed by the Turkey HSD post-hoc test ($P<0.05$) and the Benjamin-Hochberg false discovery rate correction. Differentially expressed genes were further filtered to include genes whose expression changed 2.0-fold relatively to the level in the PBS group. Genes that passed the statistical analysis were further assigned to a gene ontology (GO) grouping.

Results

Establishment of a Mouse-Adapted NS1-Venus PR8 Virus.

Although NS1-Venus PR8 WT virus was successfully rescued by reverse genetics, this virus was a virulent in mice (MLD_{50}:>10^5 PFU), and the expression of Venus was very weak in MDCK cells and in the lung sections of mice infected with this virus. To increase the virulence and Venus expression of NS1-Venus PR8 WT virus, the virus was serially passed in mice via intranasal infection with plaque-purified high Venus-expressing clones (see Examples I and II). After six serial passages, the virulence of the virus appeared to have increased; therefore, this mouse-adapted NS1-Venus PR8 WT virus was sequenced to look for mutations.

The sequence analysis revealed that two amino acid substitutions had occurred after passaging (Table 7).

TABLE 7

Amino acid substitutions in NS1-Venus PR8 MA virus.

Protein	amino acid position	amino acid encoded PR8	amino acid encoded NS1-Venus PR8 MA
PB2	712	E	D
HA	380	T	A

One of the mutations was in PB2 (a glutamine acid-to-asparagine acid substitution at position of 712), and the other was in HA (a threonine-to-alanine substitution at position of 380). To confirm their contribution to pathogenicity in mice, these mutations were introduced into a correspondent polI plasmid, and reverse genetics used to generate NS1-Venus PR8, which possessed the two mutations (referred to as NS1-Venus PR8 MA virus). The pathogenicity of NS1-Venus PR8 MA virus was higher than that of NS1-Venus PR8 WT virus (MLD_{50}: 2.1×10^4 PFU). Furthermore, the Venus signal in the lungs from mice infected with NS1-Venus PR8 MA virus was strong, whereas in the lung infected with NS1-Venus PR8 WT and that infected with PR8, no Venus signal was detected (data not shown). NS1-Venus PR8 MA, therefore, showed promise as a useful reporter virus.

Comparison of Mutant Virus Replication in MDCK Cells.

To compare the growth of these viruses in a cell line, two single-gene reassortants were generated that possessed the PB2 or HA gene of NS1-Venus PR8 MA virus and the remaining genes from NS-Venus PR8 WT virus for use in experiments with the NS1-Venus PR8 WT and NS1-Venus PR8 MA viruses. MDCK cells were infected with these viruses at an MOI of 0.001 and viral titers in supernatants were determined every 12 hours by means of a plaque assay (FIG. **14**). Although NS1-Venus PR8 WT virus grew to $10^{6.5}$ PFU/mL, NS1-Venus PR8 MA virus grew to more than 10^8 PFU/mL, comparable to wild-type PR8 virus. While the viral titers of NS1-Venus PR8 PB2 virus and NS1-Venus PR8 HA virus reached approximately $10^{7.5}$ PFU/mL, these were lower than that of NS1-Venus PR8 MA virus. Therefore, the growth capability of NS1-Venus PR8 MA virus was remarkably improved in MDCK cells, and the mutations in the PB2 and HA genes acted in an additive manner.

Comparison of the Pathogenicity and Replication in Mice of the Mutant Viruses.

Next, to assess their pathogenicities, C57BL/6 mice were infected with 10^5, 10^4 or 10^3 PFU of these viruses and monitored their body weights and survival (FIG. **15**). The body weights of the mice infected with 10^5 PFU of these viruses dramatically decreased and 1 out of 4 mice infected with NS1-Venus PR8 WT virus and all of the mice infected with NS1-Venus PR8 PB2 and NS1-Venus PR8 MA virus had to be euthanized during the observation period. In addition, mice infected with 10^4 PFU of NS1-Venus PR8 PB2 and NS1-Venus PR8 MA virus showed pronounced body weight loss, and 1 out of 4 mice infected with NS1-Venus MA virus and 2 out of 4 mice infected with NS1-Venus PR8 PB2 virus succumbed to their infection. On the other hand, although the body weights of the mice infected with 10^4 PFU of NS1-Venus PR8 HA and NS1-Venus PR8 WT virus decreased slightly, all of the mice survived. In the case of infection with 10^3 PFU, while the body weights of the mice infected with NS1-Venus PR8 PB2 and NS1-Venus PR8 MA decreased slightly, all of these mice also survived. Mice infected with 10^3 PFU of NS1-Venus PR8 WT and NS1-Venus PR8 HA showed little body weight loss, and all of the mice survived. The viral titers of these viruses were determined in mouse lung (FIG. **16**). Mice were infected with 10^3 PFU of the viruses and lungs were collected on days 3, 5, and 7 after infection. The maximum virus lung titer from mice infected with NS1-Venus PR8 PB2 virus was $>10^6$ PFU/g, which was similar to that from mice infected with NS1-Venus PR8 MA virus. In contrast, virus titers in lungs from mice infected with NS1-Venus PR8 WT and NS1-Venus PR8 HA virus were significantly lower than those in lungs from mice infected with NS1-Venus PR8 PB2 and NS1-Venus PR8 MA virus at all time points. Finally, viruses were not detected in lungs from mice infected with NS1-Venus PR8 WT at 7 days after infection. Taken together, these results demonstrate that only the PB2 mutation affected the pathogenicity and replication of NS1-Venus PR8 MA virus in mice.

The Stability of Venus Expression by NS1-Venus PR8 MA Virus During Replication In Vitro and In Vivo.

In the Manicassamy study (Manicassamy et al., 2010), the proportion of GFP-negative virus increased over time. This is one of the obstacles to utilizing this virus for live imaging studies. The stability of Venus expression by NS1-Venus PR8 MA virus was assessed during replication in MDCK cells (FIG. **17**A). More than 90% of plaques were Venus-positive even 72 hours after infection. The positive rate of Venus expression was monitored during repeated passages of the virus in cell culture (FIG. **17**B). Approximately 90% of plaques expressed Venus even after 5 passages, suggesting that Venus expression by NS1-Venus PR8 MA virus was stable in cell culture. Finally, Venus expression was confirmed to be stable during virus replication in vivo (FIG. **17**C). A plaque assay was performed using lung homogenates and estimated the positive rate of Venus expression essentially as described above. Although the percentage of Venus-positive plaques was more than 85% at 3 days after infection, that of Venus-positive plaques was approximately 75% at 7 days after infection. Taken together, these results indicate that Venus expression by NS1-Venus PR8 MA virus is stable during replication in vitro, and the percentage of Venus-positive plaques in mouse lung was similar to that reported previously (Manicassamy et al., 2010).

The PB2-E712D Substitution is Responsible for High Venus Expression.

The Venus expression level of NS1-Venus PR8 MA virus was substantially higher than that of NS1-Venus PR8 WT virus. Since PB2 is one of the subunit of the influenza virus polymerase, it was hypothesized that the PB2-E712D substitution was important for the augmentation of Venus expression. To compare the Venus protein expression, western blots of the viral protein and Venus in infected cells were performed (FIG. **18**A). Twelve hours post-infection, although the amount of M1 protein was similar for all of the viruses, the amount of Venus protein was higher in cells infected with NS1-Venus PR8 PB2 and NS1-Venus PR8 MA virus compared with the other two viruses that possessed the parental PB2 gene. Venus expression in infected cells was also observed by using a confocal laser microscope (FIG. **18**B). As expected, the Venus signals in the cells infected with NS1-Venus PR8 PB2 and NS1-Venus PR8 MA virus were stronger than in the cells infected with the two viruses that possessed parental PB2 gene. Taken together, these results demonstrate that the PB2-E712D substitution was responsible for the high Venus expression.

To demonstrate that the PB2-E712D mutation increased the Venus expression levels, MDCK cells were infected with the indicated viruses at an MOI of 1 and performed confocal microscopy 12 hours later (FIG. **18**C). As expected, the

levels of the NS1-Venus fusion protein were higher in cells infected with MA-Venus-PR8 or PB2-Venus-PR8 than in those infected with WT-Venus-PR8 or HA-Venus-PR8 (FIG. **18**C).

Collectively, the data indicate that the PB2-E712D substitution is primarily responsible for the increased replicative ability, Venus expression, and virulence in mice of MA-Venus-PR8 virus. To assess whether the PB2-E712D mutation directly affects the viral polymerase activity in a mini-replicon assay, HEK293 cells were transfected with viral protein expression plasmids for NP, PA, PB1, and PB2 or PB2-E712D, together with a plasmid expressing a vRNA encoding the firefly luciferase gene; the pRL-null luciferase protein expression plasmid (Promega) served as a transfection control. Luciferase activities were measured by using a Dual-Glo luciferase assay system (Promega) at 48 hours post-transfection (Ozawa et al., 2007). Unexpectedly, the polymerase activity of PB2-E712D was lower than that of the parental PB2 (FIG. **18**D). Similar results were obtained with canine MDCK cells (data not shown). In the context of a minireplicon that measures viral replication and transcription, the PB2-E712D mutation is thus attenuating; in contrast, this mutation enhances viral growth in the context of replicating virus. These findings indicate that the PB2 protein functions not only in viral replication/transcription, but performs additional roles in the viral life cycle.

The HA-T380A Substitution Raises the Threshold for Membrane Fusion.

The HA vRNA of MA-Venus-PR8 did not significantly increase the virulence of WT-Venus-PR8 in mice; however, HA-Venus-PR8 virus grew more efficiently in MDCK cells than WT-Venus-PR8 (FIG. **14**), suggesting a contribution of the HA-T380A mutation to, at least, virus replication in cultured cells. Because the HA-T380A substitution is located on an a-helix in the HA2 subunit (Gamblin et al., 2004), its effect on HA membrane-fusion activity was evaluated by using a polykaryon formation assay (Imai et al., 2012). Briefly, HEK293 cells were infected with WT-PR8 or a mutant PR8 virus encoding HA-T380A at an MOI of 10. Eighteen hours later, cells were treated with TPCK-treated trypsin (1 μg/mL) for 15 minutes at 37° C., exposed to low-pH buffer (145 mM NaCl, 20 mM sodium citrate (pH 6.0-5.4)) for 2 minutes, incubated for 2 hours in maintenance medium at 37° C., fixed with methanol, and stained with Giemsa's solution. The wild-type HA had a threshold for membrane fusion of pH 5.5, whereas the threshold for HA-T380A was pH 5.8 (FIG. **19**), leading to the conformational change in HA at an earlier stage of endosome maturation during influenza virus entry (Lozach et al., 2011). Changes in the pH threshold for membrane fusion may affect HA thermostability (Ruigrok et al., 1986), an effect that we did not observe at 50° C. (data not shown).

Time-Course Observation of Virus Propagation in Whole Mouse Lung.

NS1-Venus PR8 MA virus allows the observation of virus-infected cells without immunostaining because the Venus expression by this virus is sufficiently high to permit the visualization of infected cells with a microscope. To observe how influenza virus propagates in the lung, transparent lungs are treated with SCALEVIEW A2, a reagent that make samples optically transparent without decreasing fluorescence intensity were used (FIG. **20**). Mice were intranasally infected with 10^5 PFU of PR8, NS1-Venus PR8 WT, and NS1-Venus PR8 MA virus, and lungs were collected on days 1, 3, and 5 after infection. After treatment with SCALEVIEW A2, the samples were observed using a stereo fluorescence microscope. Venus signals that were directly observed were ambiguous because of insufficient transparency. Therefore, the transparent samples were dissected in the direction of the long axis to expose the bronchi (FIG. **20**, lower panel, "cut"). Venus expression was not observed in the transparent samples from mice infected with NS1-Venus PR8 WT virus at any time point (FIGS. **20**G and H). Samples collected at 3 days post-infection are shown. In the case of NS1-Venus PR8 MA virus-infected lungs, although Venus signals were not observed at 1 day post-infection (FIGS. **20**A and B), Venus expression was clearly observed in a large portion of the epithelial cells of the bronchi at 3 days post-infection (FIGS. **20**C and D). Venus expression was also occasionally observed in alveolar epithelial cells around the bronchus. At 5 days post-infection, most of the Venus-positive cells found in the bronchial epithelium had disappeared and the number of Venus-positive cells in the bronchiole and alveoli had increased (FIGS. **20**E and F). On the basis of these observations, it may be that the Venus-positive cells found in the bronchi at 3 days post-infection died and the influenza virus spread from the bronchi to the bronchioles and alveoli over time. No obvious Venus signals were observed in the transparent lungs from the mice inoculated with PR8 or PBS (FIGS. **20**I-L). These results demonstrate that NS1-Venus PR8 MA virus and transparent reagent SCALEVIEW A2 permit the visualization of the dynamics of influenza virus infection in whole lung lobes.

Identification of the Target Cells of NS1-Venus PR8 MA Virus in Mouse Lung.

Transparent lungs infected with NS1-Venus PR8 MA virus revealed that influenza virus first infected the bronchial epithelium and subsequently invaded the alveoli over time. Next, to identify the target cells of NS1-Venus PR8 MA virus, an immunofluorescence assay of frozen sections was performed using several antibodies specific for lung cells (FIG. **21**). The epithelial cells of the bronchi and bronchioles include Clara cells, ciliated cells, goblet cells, and a small number of neuroendocrine cells, whereas alveoli comprise type I and type II alveolar epithelial cells. Of these cell types, I focused on Clara cells and type II alveolar epithelial cells because Clara cells constitute the bulk of the lumen of bronchi and bronchioles (Rawlins et al., 2006), and type II alveolar epithelial cells have previously been reported to be a target of influenza virus (Baskin et al., 2009). At 3 days post-infection, a large proportion of the bronchiole cells were Venus-positive and almost all of these cells were CC10-positive (FIG. **21**A). In addition, cuboidal Venus signals in the alveolar regions were merged with SP—C positive cells (FIG. **21**B, white arrowheads). Although rare, Venus-positive type I alveolar epithelial cells were observed at 5 days post-infection (FIG. **21**B, white arrow). However, Venus expression in neuroendocrine cells was never detected (data not shown).

Flow cytometry was performed to determine whether alveolar macrophages and monocytes were infected with NS1-Venus PR8 MA virus, because these immune cells are present in lung and function as the first line of defense against inhaled microbes and particulates. Alveolar macrophages were distinguished monocytes on the basis of the CD11b expression level in the $F4/80^+$ population (FIG. **22**A). Mice were infected with 10^5 PFU of PR8 or NS1-Venus PR8 MA virus and the total number of these cells were compared. After influenza virus infection, although the number of alveolar macrophages was rarely different from that of the control group, the number of monocyte dramatically increased because monocytes infiltrated sites of infection from blood vessels (FIGS. **22**B and C). As to the

proportion of Venus-positive cells, 3.16%±0.59% of the alveolar macrophages were Venus-positive cells and 1.55%±0.07% of the monocytes were Venus-positive at 3 days post-infection (FIGS. **22**D and E). Further, the number of Venus-positive cells decreased slightly between 3 days and 5 days after NS1-Venus PR8 MA virus infection. For the PR8 infection, the number of Venus-positive cells was comparable to that in mock-treated mice. Taken together, these results demonstrate that the Clara cells in the bronchus and bronchiolus, type II alveolar epithelial cells, monocytes, and alveolar macrophages in the alveolar regions of the lung are target cells of influenza virus.

Differential Gene Expressions Between Venus-Positive and -Negative Cells in the F4/80$^+$ Cell Population.

Because alveolar macrophages and monocytes act as the first line of defense against inhaled microbes, it is possible that infection of these cells with influenza virus might influence their ability to prevent the spread of infection. To assess this, the gene expression profiles between the Venus-positive and -negative cells among the alveolar macrophage and monocyte populations were compared by means of microarray analysis. Because the number of Venus-positive alveolar macrophages and monocytes that could be collected from one mouse by using flow cytometry was too small to perform a microarray analysis, these cells were analyzed together as F4/80$^+$ cells and pooled from three mice. Live mononuclear cells were gated as CD45$^+$ and via-probe$^-$ cells. As shown in FIG. **22**A, the cells were confirmed as alveolar macrophages and monocytes on the basis of CD11b expression levels in the F4/80$^+$ population. Venus-positive and -negative F4/80 cells were sorted from a fraction of the live mononuclear cells by FACSAria II. Since CD11c^{high} alveolar macrophages possess high autofluorescence, the possibility existed for overlap with the Venus signal. Therefore, CD11c^{high} alveolar macrophages with intermediate expression of Venus were excluded from the Venus-positive fraction (FIG. **23**A). From confocal microscopic observation of the sorted cells, these cells could be collected properly based on Venus expression (FIG. **23**B). In addition, given that Venus expression was observable throughout the cell, these cells would have been infected with virus, but did not engulf the infected cells. The microarray analysis revealed thousands of genes whose expression statistically changed at least 2.0-fold relative to the level of F4/80$^+$ cells from mice inoculated with PBS (data not shown). Among these genes, 633 genes whose expression statistically differed by at least 4.0-fold between Venus-positive and -negative F4/80$^+$ cells were identified (FIG. **24**A). Gene Ontology analysis revealed that these genes were involved in extracellular activity (FIG. **24**B). For genes annotated in "cytokine activity," a total of 24 genes had changed expression levels, including several cytokines, such as type I interferon (IFN), and chemokines (FIG. **24**C). All of these genes except for the genes for interleukin (IL)-4 and Cxcl13 [chemokine (C—X—C motif) ligand 13] were up-regulated in Venus-positive cells relative to Venus-negative cells. Moreover, when I focused on the genes annotated in "response to wounding", most genes including those for collagen type 1α1 (Col1a1), collagen type 3α1 (Col3a1), collagen type 5α1 (Col5a1), hyaluronoglucosamidase 1 (Hyal1), and fibrinogen γ chain (Fgg) were up-regulated in Venus-positive F4/80$^+$ cells (FIG. **24**D). Taken together, these results demonstrate that a small number of cells relative to the total number of F4/80$^+$ cells was infected with influenza virus and that the gene expression levels of several cytokines and chemokines were enhanced in the virus-infected cells at the site of infection. Furthermore, F4/80$^+$ cells infected with NS1-Venus PR8 MA virus enhanced the expression of genes involved in the response to wounding which would be caused by infection and inflammation.

Example IV

A vector is described above that can express a heterologous gene product from a fusion construct with the viral NS1 protein (FIG. **26**). In particular, a PB2-E712D mutation stabilized expression of a heterologous gene product. The test virus, WT-Venus-PR8, was serially passaged to identify other mutations in the polymerase complex which contribute to stabilization (FIG. **27**).

Example V

An E-to-D mutation at position 712 of the polymerase subunit PB2 (PB2-E712D) stabilized the inserted Venus gene (Fukuyama et al., 2015; Katsura et al., 2016). Also, a H5N1 virus carrying the Venus gene, which was inserted into the NS segment from PR8 (Venus-H5N1), was prepared (Fukuyama et al., 2015). Although, like WT-Venus-PR8, WT-Venus-H5N1 showed moderate virulence and low Venus expression, we acquired a variant that became more lethal to mice and stably expressed Venus after mouse adaptation. A V-to-A mutation at position 25 of the polymerase subunit PB2 and a R-to-K mutation at position 443 of the polymerase subunit PA contributed to the stable maintenance of the Venus gene (Zhao et al., 2015). These results indicated that the composition of the viral polymerase plays a role in the stabilization of the inserted foreign gene. However, the mechanisms by which the Venus gene can be deleted and how polymerase mutations stabilize the Venus gene have remained unknown.

As disclosed below, the mechanisms of Venus gene stabilization were investigated by comparing events upon infection with WT-Venus-PR8 and Venus-PR8 possessing the PB2-E712D mutation (Venus-PR8—PB2-E712D). Polymerase fidelity and RNA and protein expression in infected cells were examined, and sequencing analysis coupled with coinfection experiments were performed to determine how the Venus gene is deleted. Moreover, additional mutations that contribute to the stabilization of the Venus gene were identified to further the understanding of the stabilization mechanisms.

Materials and Methods

Cells and Viruses.

Madin-Darby canine kidney (MDCK) cells were cultured in minimal essential medium (Gibco) with 5% newborn calf serum at 37° C. in 5% CO_2. Human embryonic kidney 293T (HEK293T) cells were cultured in Dulbecco's modified Eagle medium supplemented with 10% fetal calf serum. WT-Venus-PR8 and Venus-PR8 mutants with NS segments encoding the Venus fluorescent protein (Fukuyama et al., 2015) were generated by using reverse genetics (Neumann et al., 1999) and propagated in MDCK cells at 37° C.

Venus Stability.

MDCK cells were infected with WT-Venus-PR8 or each Venus-PR8 mutant at an MOI of 0.001. The supernatants were collected at 48 h postinfection and titrated by using plaque assays in MDCK cells. Obtained viruses were similarly passaged four times. The proportion of Venus-expressing plaques in virus stocks from different passages was determined in MDCK cells by observing more than 65 plaques in each virus stock using fluorescence microscopy.

To exclude false-positive plaques, Venus-negative plaques were picked up, amplified in MDCK cells, and reassessed for Venus expression.

Deep Sequencing Analysis

WT-PR8, PR8—PB2-E712D, PR8—PB1-V43I (Cheung et al., 2014; Naito et al., 2015), and PR8—PB1-T123A (Pauly et al., 2017) were generated by reverse genetics (Neumann et al., 1999), and MDCK cells were infected at an MOI of 0.001. The supernatants were collected at 48 h postinfection and titrated by using plaque assays in MDCK cells. The obtained viruses were passaged five times in the same way. Virus RNA was extracted from viruses before passaging and from viruses passaged five times by using a QIAamp viral RNA minikit (Qiagen). Reverse transcription-PCR (RT-PCR) was performed by using a Superscript III high-fidelity RT-PCR kit (Invitrogen). DNA amplicons were purified by 0.45× of Agencourt AMpure XP magnetic beads (Beckman Coulter), and 1 ng was used for barcoded library preparation with a Nextera XT DNA kit (Illumina). After bead-based normalization (Illumina), libraries were sequenced on the MiSeq platform in a paired-end run using the MiSeq v2, 300 cycle reagent kit (Illumina). The raw sequence reads were analyzed by using the ViVan pipeline (Isakov et al., 2015). Here, a cutoff of 1% as the minimum frequency was used. Moreover, we defined an empirical cutoff for the minimum read coverage: for a variant with 1% frequency, at least 1,000 reads should cover that region. Likewise, for a variant with 0.1% frequency, 10,000 reads should cover that region. Namely, if the coverage was <1,000/(frequency), the variant was removed. The sequencing data of the five-times passaged viruses were compared to those of the viruses before passaging. The number of nucleotide mutations that were not observed before passaging but observed only after passaging was counted. The number of mutations per nucleotide was calculated for each segment and the mean values for all eight segments in each virus were compared.

Quantitative Real-Time PCR.

MDCK cells were infected with WT-Venus-PR8 or Venus-PR8—PB2-E712D at an MOI of 1 or mock infected with medium. The total RNA was extracted from cells at 9 h postinfection by using an RNeasy minikit (Qiagen). Quantification of RNA was performed as described previously (Kawakami et al., 2011). The primers for IFN-β, NS vRNA, NP vRNA, and β-actin were described previously (Kawakami et al., 2011; Kupke et al., 2018; Park et al., 2015). Data were analyzed with the $2^{-\Delta\Delta CT}$ method (Livak et al., 2001) and normalized to the expression of β-actin mRNA.

Western Blotting.

MDCK cells were infected with each virus at an MOI of 1 or mock infected with medium. Cells were lysed at the indicated time points with Tris-glycine SDS sample buffer (Invitrogen). The cell lysates were sonicated, heated for 10 min at 95° C., and then subjected to SDS-PAGE. SDS-PAGE was performed on Any kD Mini-PROTEAN TGX precast protein gels (Bio-Rad). Proteins on SDS-PAGE gels were transferred to a polyvinylidene fluoride membrane (Millipore) and detected by using the indicated primary antibodies (rabbit anti-NS1 [GeneTex], mouse anti-Aichi NP [2S 347/4], mouse anti-β-actin [Sigma-Aldrich]), followed by secondary antibodies (sheep horseradish peroxidase [HRP]-conjugated anti-mouse IgG [GE Healthcare] or donkey HRP-conjugated anti-rabbit IgG [GE Healthcare]). Signals of specific proteins were detected by using ECL Prime Western blotting detection reagent (GE Healthcare). Images were captured with a ChemiDoc Touch imaging system (Bio-Rad) and quantified by using Image Lab software (Bio-Rad).

Coinfection Analysis.

Three nucleotides in the 3' or 5' region, which does not overlap the packaging signal sequence (Fujii et al., 2005) of the NS segment of WT-Venus-PR8, were substituted synonymously. These modified viruses were used to coinfect MDCK cells at an MOI of 0.001 each or an MOI of 5 each. The supernatant was collected at 2 days or 8 h postinfection, respectively, and infected to MDCK cells. Venus-negative plaques were picked up and amplified in MDCK cells, and then the sequences of the NS segments in the obtained viruses were analyzed.

Identification of Additional Mutations that Stabilize the Venus Gene.

WT-Venus-PR8 was infected to MDCK cells at an MOI of 0.001. The supernatant was collected at 2 days postinfection and infected to MDCK cells. Next, Venus-positive plaques were picked up and amplified in MDCK cells repeatedly until mutants stably expressing Venus fluorescence were obtained. The sequences of the mutants were analyzed to identify amino acid mutations in PB2, PB1, and PA. To determine whether these mutations contributed to the stability of the Venus gene, mutants containing each of the identified amino acid mutations were generated by reverse genetics (Neumann et al., 1999), and the Venus stability of each mutant was examined as described above. Confirmed amino acid positions were plotted on the crystal structure of the influenza virus polymerase complex (PDB ID 4WSB) by using the PyMOL molecular graphics system. In FIG. **32**B, the polymerase internal tunnels were visualized by using the MOLEonline web interface (Pravda et al., 2018), and the information was deposited in ChannelsDB (Pravda et al., 2018). The percentage of strains that contained the identified amino acid was determined by using the "Sequencing Feature Variant Type" tool in the Influenza Research Database (Zhang et al., 2017; Noronha et al., 2012).

Statistical Analysis.

Statistically significant differences between WT-Venus-PR8 and Venus-PR8—PB2-E712D were assessed by using a two-tailed unpaired Student t test. A P value of <0.05 was considered significantly different.

Results

Loss of Venus Expression in WT-Venus-PR8 Restores Replication Efficiency.

WT-Venus-PR8 and Venus-PR8-PB2-E712D were prepared by using reverse genetics as previously described (Neumann et al., 1999). The gene of the Venus fluorescent protein was inserted into the NS segment as illustrated in FIG. **28**A (Fukuyama et al., 2015). First, it was confirmed how quickly Venus expression was lost in WT-Venus-PR8 and the relationship between Venus deletion and virus titer. The viruses were passaged in MDCK cells at a multiplicity of infection (MOI) of 0.001 and the proportion of Venus-positive plaques measured (FIG. **28**B). It was confirmed that the expression of Venus was lost immediately in WT-Venus-PR8, whereas all plaques of Venus-PR8—PB2-E712D showed Venus expression after four passages. Although WT-Venus-PR8 showed a lower titer than Venus-PR8—PB2-E712D in MDCK cells, as described previously (Katsura et al., 2016), the virus titer increased during virus passages as the proportion of Venus-positive plaques decreased (FIG. **28**C). This result suggests that the loss of the Venus gene in the mutated WT-Venus-PR8 restored the replicative efficiency of the virus.

The PB2-E712D Mutation does not Cause an Appreciable Change in Polymerase Fidelity.

It was hypothesized that the PB2-E712D mutation increases viral polymerase fidelity in order to retain the inserted Venus gene during passages. To test this hypothesis, WT-PR8, as well as PR8—PB2-E712D, which possesses aspartic acid at position 712 of PB2 and therefore differs from WT-PR8 by only this amino acid, were generated by reverse genetics and their mutation rates compared. Here, viruses were used that did not contain the Venus gene to make it easier to measure the mutation rates. PR8—PB1-V43I, which has been reported to be a high-fidelity mutant virus (Cheung et al., 2014; Naito et al., 2015), and PR8—PB1-T123A, which has been reported to be a low-fidelity mutant virus (Pauly et al., 2017), were also generated by reverse genetics and used as controls. To estimate the mutation rates, these viruses were passaged in MDCK cells at an MOI of 0.001 and deep sequencing of the entire genome performed; the sequencing data for the five-times passaged viruses were compared to those of viruses before passaging. The number of nucleotide changes in the five-times passaged viruses that were not present before passaging were counted. The number of mutations introduced during the five passages are shown in FIG. **29**A by segment. Also, the number of mutations per nucleotide was calculated for normalization, and the mean values for all eight segments were compared (FIG. **29**B). It was confirmed that PR8—PB1-V43I, the high-fidelity control, had fewer mutations, and that PR8—PB1-T123A, the low-fidelity control, had more mutations than WT-PR8. Although PR8—PB1-V43I had fewer mutations than WT-PR8, the difference between PR8—PB1-V43I and WT-PR8 was small. Since a previous report suggested that PB1-V43I does not alter the mutation rate (Pauly et al., 2017), the influence of PB1-V43I on the mutation rate might be dependent on the virus strain or experimental conditions. Moreover, there was no clear difference in mutation number between WT-PR8 and PR8—PB2-E712D. Although the possibility that the PB2-E712D mutation affects virus polymerase fidelity cannot be excluded, the effect does not seem to be large enough to cause an appreciable difference in Venus stability. Therefore, this result suggests that the stability of the Venus gene is not influenced by the fidelity of the virus polymerase.

Transcription/Replication of the Modified RNA Segment is Impaired in WT-Venus-PR8.

Some reports suggest that recombinant viruses containing a foreign gene insertion in their NS segment can propagate more efficiently in interferon (IFN)-deficient Vero cells than in IFN-competent cells such as MDCK cells (Kittel et al., 2004; Ferko et al., 2001; Kuznetsova et al., 2014). Therefore, the expression levels of IFN-3 in virus-infected cells was quantified by using quantitative real-time PCR. MDCK cells were infected with WT-Venus-PR8 or Venus-PR8—PB2-E712D at an MOI of 1 or mock infected with medium only, and the relative expression levels of IFN-β in infected cells were quantified at 9 h postinfection. WT-Venus-PR8 induced a higher level of IFN-β expression than did Venus-PR8—PB2-E712D (FIG. **30**A). This result suggests that WT-Venus-PR8 does not efficiently inhibit IFN-β expression. Given that NS1 plays a key role in suppressing IFN expression and IFN-mediated antiviral responses in the host (Garcia-Sastre et al., 1998; Opitz et al., 2007), the NS vRNA in infected cells was quantified by using influenza virus strand-specific real-time PCR (Kawakami et al., 2011; Kupke et al., 2018). The amount of NS vRNA in WT-Venus-PR8-infected cells was 90% lower than that in Venus-PR8—PB2-E712D-infected cells (FIG. **30**B), whereas there was no significant difference in their NP vRNA expression levels (FIG. **30**C). The NS vRNA/NP vRNA ratio in WT-Venus-PR8-infected cells was 80% lower than that in Venus-PR8—PB2-E712D-infected cells (FIG. **30**D). This result suggests that the transcription/replication of the NS segment is specifically impaired in WT-Venus-PR8. The sequences of all of the plasmids used to generate viruses by reverse genetics were confirmed before use, and the NS segments of WT-Venus-PR8 and Venus-PR8—PB2-E712D were derived from the same NS-Venus plasmid. Therefore, it is unlikely that either WT-Venus-PR8 or Venus-PR8—PB2-E712D has a mutated promoter sequence in its NS segment. Accordingly, the difference in the transcription/replication efficiency of the NS segment was likely caused by the PB2-E712D. Moreover, it was confirmed the expression level of the NS1 protein by Western blotting (FIG. **30**E). Due to the reduced transcription/replication efficiency of the NS segment, the expression level of the NS1 protein in WT-Venus-PR8-infected cells was much lower than that in Venus-PR8—PB2-E712D-infected cells. In contrast, the expression level of NP was almost the same. The NS1/NP ratio, quantified based on the band intensity, was significantly reduced in WT-Venus-PR8-infected cells (FIG. **30**F). It therefore appears that the low level of NS1 expression leads to the high expression of IFN-β in WT-Venus-PR8-infected cells. Furthermore, the high expression of IFN-β causes attenuation of WT-Venus-PR8, although it is possible that other factors are involved.

The Inserted Venus Gene is Deleted Via Internal Deletion.

To explore how deletion of the Venus gene occurs, the sequence of the NS segment in WT-Venus-PR8 that lost Venus expression after serial passages was determined. Plaque assays were performed using three independently passaged WT-Venus-PR8 virus stocks and it was found that the majority of the plaques were Venus negative. More than five plaques from each stock were sequenced and it was found that one or two deletion patterns were in each virus stock. Large deletions occurred in the NS segment and most of the Venus sequence was lost (FIG. **31**A). However, no specific patterns with regard to the deletion, such as the number of nucleotide deletions, the site of the deletion(s), or specific sequences at which deletions occurred, were identified. It was hypothesized that the large deletion resulted from internal deletion caused by polymerase jumping, which is a known mechanism of defective interfering viral RNA production (Davis et al., 1980; Jennings et al., 1983), or by gene recombination, which plays a role in RNA virus adaptation through rearrangement of the virus genome (Xiao et al., 2016; Simon et al., 2011; Mitanul et al., 2000; Khatchikian et al., 1989). Synonymous mutations were introduced into the 3' or 5' region of the NS segment of WT-Venus-PR8 (FIG. **31**B) and then MDCK cells were infected at an MOI of 0.001 or 5 with each of these mutant viruses, after which supernatants were collected at 2 days or 8 h postinfection, respectively. The supernatant was then incubated with MDCK cells. Venus-negative plaques were picked up and amplified in MDCK cells, and then we determined the NS segment sequence in the viruses that lost Venus expression. We found that the truncated NS segments had a synonymous mutation on only one side (FIG. **31**C). No viruses were found that had NS segments with synonymous mutations on both sides or without a synonymous mutation in both low- and high-MOI coinfections. This result indicates that the large deletion in the NS segment resulted from internal deletion in each NS segment and not gene recombination between NS segments.

Additional Mutations Stabilize the Venus Gene.

To further understand the mechanisms of the Venus deletion and stabilization, additional mutations were attempted in the polymerase complex that stabilizes the Venus gene. MDCK cells were infected with WT-Venus-PR8 at an MOI of 0.001, and then Venus-positive plaques were picked and amplified in MDCK cells. After consecutive passaging and plaque purification of Venus-positive viruses, mutants were obtained that stably expressed enhanced Venus fluorescence. Sequence analysis revealed that mutations were introduced into the polymerase genes PB2, PB1, and PA of each mutant (FIG. **32**A). PA-180 and PA-200 are located on the surface of the polymerase complex, as is PB2-712, whereas PB2-540, PB1-149, and PB1-684 are located inside the complex. PA-180 and PA-200 are located in the endonuclease domain, PB1-149 and PB1-684 are located near the exit of the RNA template, and PB2-540 is located near the exit of newly synthesized RNA products (FIG. **32**B), while the function of the region around PB2-712 has remained unclear (Reich et al., 2014; Pflug et al., 2017; Gerlach et al., 2015). To determine whether these mutations contribute to the stabilization of the Venus gene, mutant viruses were generated containing each of the mutations by using reverse genetics and measured the Venus retention ratio after four passages in MDCK cells (FIG. **32**C). The mutant viruses showed enhanced Venus stability compared to WT-Venus-PR8, indicating that these amino acids play roles in the stabilization of the Venus gene. Although further analysis is needed to clarify how these amino acids contribute to the stability of the Venus gene, considering that PB2-540, PB1-149, and PB1-684 are located near the polymerase internal tunnels (Reich et al., 2014; Pflug et al., 2017; Gerlach et al., 2015) that the template and product go through during the transcription/replication reaction, these amino acids may affect the binding stability of the RNA template, product, and polymerase complex. Moreover, when we examined whether these mutations were found in previously isolated influenza A viruses in the Influenza Research Database (FIG. **32**D), we found that these amino acids are extremely rare, suggesting that they are not evolutionarily beneficial.

Discussion

Recombinant influenza viruses expressing foreign genes would be useful tools; however, long insertions in virus genomes are often unstable and cause attenuation of the recombinant viruses. We previously found that amino acids in the influenza virus polymerase complex play crucial roles in the stabilization of foreign gene insertions; the Venus gene inserted into the NS segment was stabilized by PB2-E712D in an H1N1 virus (Fukuyama et al., 2015; Katsura et al., 2016) and by PB2-V25A and PA-R443K in an H5N1 virus (Zhao et al., 2016). However, the mechanisms by which these amino acids contribute to the stabilization remained unclear. In the present study, we explored the mechanism of PB2-E712D-induced stabilization of the Venus gene inserted into the NS segment of an H1N1 virus. It was found that the transcription/replication efficiency of the modified segment was significantly reduced in WT-Venus-PR8 compared to Venus-PR8—PB2-E712D. This finding suggests that the PB2-E712D mutation stabilizes the inserted foreign gene due to the enhanced transcription/replication efficiency of the modified RNA segment. In contrast, the transcription/replication efficiency of segments that do not contain additional sequences is not changed in the presence or absence of the PB2-E712D mutation. Moreover, polymerase activity is reduced, not enhanced, by the PB2-E712D mutation in a minireplicon assay (Katsura et al., 2016). These results indicate that the alteration of the transcription/replication efficiency caused by PB2-E712D is specific to modified RNA segments. The insertion of foreign genes appears to impair the transcription/replication of the modified segments, and the polymerase overcomes this impairment in the presence of the PB2-E712D mutation.

In WT-Venus-PR8, in which the Venus gene is inserted into the NS segment, the transcription/replication efficiency of this segment is significantly reduced. As a result, the expression of the NS1 protein is also reduced. Since NS1 plays a role in inhibiting IFN-mediated antiviral responses (Garcia-Sastre et al., 2008; Optiz et al., 2007) WT-Venus-PR8 cannot inhibit IFN-β expression efficiently, which may lead to virus attenuation. The viral titer of WT-Venus-PR8 increases during serial passages in MDCK cells as the virus loses Venus expression (FIGS. **28**B and **28**C), suggesting that mutated WT-Venus-PR8 that does not contain the Venus gene propagates more efficiently than the original WT-Venus-PR8. Therefore, it is likely that the immediate loss of Venus expression in WT-Venus-PR8 results from the selection of variants without the Venus gene during serial passaging. Venus-PR8—PB2-E712D restores the transcription/replication efficiency of the NS segment, leading to efficient virus replication. Therefore, viruses expressing Venus are not purged by selective pressure in the presence of the PB2-E712D mutation, which enables Venus-PR8-PB2-E712D to stably maintain the inserted Venus gene.

How is the transcription/replication efficiency reduced on modified RNA segments specifically, and how is it enhanced by the PB2-E712D mutation? The RNA secondary structure and the binding affinity between the polymerase complex and the RNA templates likely hold the answer to these questions. Insertion of a foreign gene must change the RNA secondary structure, and transcription/replication by the viral polymerase complex may be negatively influenced by this unusual RNA secondary structure. Although we do not conclusively know how the PB2-E712D mutation overcomes the impairment of transcription/replication, one possible explanation is that the binding affinity between the polymerase complex and the RNA templates is increased.

The sequence analysis of WT-Venus-PR8 that lost Venus expression, coupled with the coinfection experiments (FIGS. **29**B and **29**C), suggested that the inserted sequence is deleted due to an internal deletion. Internal deletions often occur during influenza virus replication cycles regardless of the presence of a foreign gene insertion and have been reported to play roles in virus adaptation (Lui et al., 1993; Lui et al., 1985; Yang et al., 1987) and the generation of defective interfering viral RNA (Davis et al., 1980; Jennings et al., 1983). Internal deletion is believed to be caused by polymerase complex dissociation from RNA templates during transcription/replication (Jennings et al., 1983; Lazarini et al., 2001; Dimmock et al., 2014; Lopez et al., 2014). Amino acid mutations in the polymerase complex affect the frequency of occurrence of internal deletions (Fodor et al., 2003; Vasilijevic et al., 2017; Slaine et al., 2018; Te Velthuis et al., 2018). PB2-E712D may also be involved in the occurrence of internal deletions. Therefore, the stabilization of the Venus gene in Venus-PR8—PB2-E712D may be caused not only by the enhancement of the transcription/replication on the modified segment but also by the reduced frequency of internal deletions.

Additional mutations in the influenza virus polymerase complex were identified that stabilize the inserted Venus gene, which may help us to further understand the stabilization mechanisms based on the positions of these mutations in the viral polymerase complex. Some of the identified amino acids are located near the polymerase internal tunnels,

which are near the RNA template or newly synthesized RNA product during the transcription/replication reactions (Reich et al., 2014; Pflug et al., 2017; Gerlach et al., 2015). These amino acids might directly affect the binding affinity between the polymerase complex, template, and product. A previous report, which showed that PB2 amino acids located at the template exit channel are involved in the formation of short aberrant RNAs (Te Velthuis et al., 2018), supports the possibility that amino acids near the polymerase internal tunnels affect the binding affinity between the polymerase complex, template, and product. However, PA-180 and PA-200, which are located at the endonuclease domain, are not near the polymerase internal tunnels, which is also true for PB2-712. Therefore, these amino acids may affect the binding affinity indirectly, or there may be other mechanisms involved in the stabilization of the Venus gene. These mutations could be used to establish recombinant influenza viruses expressing a foreign gene. However, these amino acids may not necessarily cause the stabilization of a foreign gene in all influenza virus strains, since PB2-V25A, which stabilizes the Venus gene in Venus-H5N1, had a negative effect on virus replication in Venus-PR8 and did not cause Venus stabilization (our unpublished data).

Although the identified amino acids seem to enhance the genetic stability of virus genomes, they have been rarely found in virus isolates (FIG. **32**D). It seems likely that mutations that support the maintenance of inserted sequences are not evolutionarily beneficial to the virus. Insertions of additional sequences into virus genomes are often deleterious for virus replication. These mutations are probably rare in virus populations to avoid the accumulation of deleterious insertions. Viruses may purge deleterious insertions by reducing the transcription/replication efficiency of RNA segments that contain insertions that form abnormal secondary structures. In conclusion, although the amino acid mutations we identified in this study are useful for generating recombinant viruses, they do not seem to be beneficial to the virus in nature in the long run.

REFERENCES

Arilor et al., *J. Virol.,* 86:1433 (2010).
Avilov et al., *Vaccine,* 34:741 (2012).
Basler et al., *Proc. Natl. Acad. Sci. USA,* 98:2746 (2001).
Chen et al., *The Lancet,* 383:714 (2014).
Dias et al., *Nature,* 458:914 (2009).
Diebold et al., *Science,* 303:1529 (2004).
Dos Santos Afonso et al., *Virology,* 341:34 (2015).
Edgar, *Nucl Acids Res.,* 32:1792 (2004).
Fan et al., *Virology,* 384:28 (2009).
Fujii et al., *J. Virol.,* 79:3766 (2005).
Fukuyama et al., *Nat. Comm.,* 6:6600 (2015).
Fukuyama & Kawaoka, *Curr. Opin. Immunol.,* 23:481 (2011).
Gabriel et al., *Proc. Natl. Acad. Sci. USA,* 102:18590 (2005).
Gambotto et al., *Lancet,* 371:1464 (2008).
Garcia-Sastre, *Virus Res.,* 162:12 (2011).
Ghaznavi et al., *Annu. Rev. Pathol.,* 8:331 (2013).
Go et al., *BMC genomics,* 13:627 (2012).
Hatta et al., *PLoS Pathog.,* 3:1374 (2007).
Hatta et al., *Science,* 293:1840 (2001).
He et al., *Nature,* 454:1123 (2008).
Heaton et al., *J. Virol.,* 87:8272 (2013).
Helft et al., *J. Clin. Invest.,* 122:4037 (2012).
Herold et al., *J. Exp. Med.,* 205:3065 (2008).
Honda & Taniguchi, *Nat. Rev. Immunol.,* 6:644 (2006).
Hu et al., *J. Virol.,* 87:2660 (2013).
Imai et al., *PLoS Pathog.,* 6:e1001106 (2010).
Isakova-Sivak et al., *Clin. Vaccine Immunol.,* PMID: 24648485, epub Mar. 19 (2014).
Itoh et al., *Nature,* 460:1021 (2009).
Jiao et al., *J. Viral.,* 82:1146 (2008).
Jobsis, *Science,* 198:1264 (1977).
Kaimal et al., *Nucleic Acids Res.,* 38:W96 (2010).
Kawaoka and Webster, *Proc. Natl. Acad. Sci. USA,* 85:324 (1988).
Kawaoka et al., *J. Virol.,* 63:4603 (1989).
Kittel et al., *Virology,* 324:67 (2004).
Larkin et al., *Bioinform.,* 23:2947 (2007).
Leung et al., *Virology,* 401:96 (2010).
Li et al., *J. Virol.,* 79:12058 (2005).
Li et al., *J. Virol.,* 80:11115 (2006).
Li et al., *J. Virol.,* 82:11880 (2008).
Li et al., *J. Virol.,* 84:8389 (2010).
Li et al., *N. Eng. J. Med.,* 370:520 (2013).
Liu et al., *Zhonghna si Yan,* 26:70 (2012).
Manicassamy et al., *Proc. Natl. Acad. Sci. USA,* 107:11531 (2010).
Murakami et al., *J. Virol.,* 82:1605 (2008).
Naffakh et al., *Annu. Rev. Microbiol.,* 62:403 (2008)
Nagai et al., *Nat. Biotechnol.,* 20:87 (2002).
Neumann et al., *Cell Res.,* 20:51 (2010).
Neumann et al., *Proc. Natl. Acad. Sci. USA,* 96:9345 (1999).
Obayashi et al., *Nature,* 454:1127 (2008).
Ozawa et al., *J. Virol.,* 81:30 (2007).
Pan et al., *Nature Commun.,* 4:2369 (2013).
Patterson et al., *J. Cell Sci.,* 114:837 (2001).
Perez et al., *J. Virol.,* 78:3083 (2004).
Perrone et al., *PLoS Pathog.,* 4:e1000115 (2008).
Pichlmair et al., *Science,* 314:997 (2006).
Reed and Muench, *Am. J. Hyg.,* 27:493 (1938).
Regan et al., *J. Virol.,* 80:252 (2006).
Salomon et al., *J. Exp. Med.,* 203:689 (2006).
Scholtissek et al., *Virology,* 87:13 (1978).
Shaner et al., *Nat. Biotechnol.,* 22:1567 (2004).
Shieh et al., *Am. J. Pathol.,* 177:166 (2010).
Shinya et al., *J. Virol.,* 78:3083 (2004).
Smith et al., *Nature,* 459:1122 (2009).
Smyth, *Stat. Appl. Genet. Mol. Biol.,* 3:3 (2004).
Song et al., *J. Virol.,* 85:2180 (2011).
Sugiyama et al., *EMBO J.,* 28:1803 (2009).
Suguitan et al., *J. Viral.,* 86:2706 (2012).
Wang et al., *PLoS One,* 7:e52488 (2010).
Watanabe et al., *J. Virol.,* 77:10575 (2003).
Watanabe et al., *Nature,* 501:551 (2013).
Wei et al., *Vaccine,* 29:7163 (2011).
Weissleder, *Nature Biotech.,* 19:316 (2001).
Wright and Kawaoka, Fields Virology 6th edition, (Philadelphia, Pa., 2013).
Yamayoshi et al., *J. Virol.,* 88:3127 (2013).
Yu et al., *J. Virol.,* 85:6844 (2011).
Zhang et al., *J. Gen. Virol.,* 95:779 (2014)
Zhang et al., *Science,* 341:410 (2013).
Zhao et al., *Proteomics,* 12:1970 (2012).

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 apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details herein may be varied considerably without departing from the basic principles of the invention.

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aagcacagat ttgaaataat cgagggaaga gatcgcacaa tggcctggac agtagtaaac 300

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gagggaaggc gaaagaccaa cttgtatggt ttcatcataa 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 cgttgcctcc tccagtcact tcaacaaatt 1800

gagagtatga ttgaagctga gtcctctgtc aaagagaaag acatgaccaa agagttcttt 1860

gagaacaaat cagaaacatg gcccattgga gagtccccca aaggagtgga ggaaagttcc 1920

attgggaagg tctgcaggac tttattagca aagtcggtat tcaacagctt gtatgcatct 1980

ccacaactag aaggattttc agctgaatca agaaaactgc ttcttatcgt tcaggctctt 2040

agggacaacc tggaacctgg gacctttgat cttgggggggc tatatgaagc aattgaggag 2100

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tgcctgatta atgatccctg ggttttgctt aatgcttctt ggttcaactc cttccttaca 2160

catgcattga gttagttgtg gcagtgctac tatttgctat ccatactgtc caaaaaagta 2220

ccttgtttct act 2233

<210> SEQ ID NO 2
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 2

agcgaaagca ggcaaaccat ttgaatggat gtcaatccga ccttactttt cttaaaagtg 60

ccagcacaaa atgctataag cacaactttc 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 tcctggtatt tttgaaaact 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 actcattttc agagaaagag acgggtgaga 600

gacaatatga ctaagaaaat gataacacag agaacaatgg gtaaaaagaa gcagagattg 660

aacaaaagga gttatctaat tagagcattg accctgaaca caatgaccaa agatgctgag 720

agagggaagc taaaacggag agcaattgca accccaggga tgcaaataag ggggtttgta 780

tactttgttg agacactggc aaggagtata tgtgagaaac ttgaacaatc agggttgcca 840

gttggaggca atgagaagaa agcaaagttg gcaaatgttg taaggaagat gatgaccaat 900

tctcaggaca ccgaactttc tttcaccatc actggagata acaccaaatg gaacgaaaat 960

cagaatcctc ggatgttttt ggccatgatc acatatatga ccagaaatca gcccgaatgg 1020

ttcagaaatg ttctaagtat tgctccaata atgttctcaa acaaaatggc gagactggga 1080

aaagggtata tgtttgagag 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 tggtcttcaa tcctctgacg attttgctct gattgtgaat 1380

gcacccaatc atgaagggat tcaagccgga gtcgacaggt tttatcgaac ctgtaagcta 1440

cttggaatca atatgagcaa gaaaaagtct tacataaaca gaacaggtac atttgaattc 1500

acaagttttt tctatcgtta tgggtttgtt gccaatttca gcatggagct tcccagtttt 1560

ggggtgtctg ggatcaacga gtcagcggac atgagtattg gagttactgt catcaaaaac 1620

aatatgataa acaatgatct tggtccagca acagctcaaa tggcccttca gttgttcatc 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 tggtccagcc 1980

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aaaaacatgg agtatgatgc tgttgcaaca acacactcct ggatccccaa aagaaatcga 2040

tccatcttga atacaagtca aagaggagta cttgaggatg aacaaatgta ccaaaggtgc 2100

tgcaatttat ttgaaaaatt cttccccagc agttcataca gaagaccagt cgggatatcc 2160

agtatggtgg aggctatggt ttccagagcc cgaattgatg cacggattga tttcgaatct 2220

ggaaggataa agaaagaaga gttcactgag atcatgaaga tctgttccac cattgaagag 2280

ctcagacggc aaaaatagtg aatttagctt gtccttcatg aaaaaatgcc ttgtttctac 2340

t 2341

<210> SEQ ID NO 3
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 3

agcgaaagca ggtcaattat attcaatatg gaaagaataa aagaactacg aaatctaatg 60

tcgcagtctc gcacccgcga gatactcaca aaaaccaccg tggaccatat ggccataatc 120

aagaagtaca catcaggaag acaggagaag aacccagcac ttaggatgaa atggatgatg 180

gcaatgaaat atccaattac agcagacaag aggataacgg aaatgattcc tgagagaaat 240

gagcaaggac aaactttatg gagtaaaatg aatgatgccg gatcagaccg agtgatggta 300

tcacctctgg ctgtgacatg gtggaatagg aatggaccaa taacaaatac agttcattat 360

ccaaaaatct acaaaactta ttttgaaaga gtcgaaaggc taaagcatgg aacctttggc 420

cctgtccatt ttagaaacca agtcaaaata cgtcggagag ttgacataaa tcctggtcat 480

gcagatctca gtgccaagga ggcacaggat gtaatcatgg aagttgtttt ccctaacgaa 540

gtgggagcca ggatactaac atcggaatcg caactaacga taaccaaaga gaagaaagaa 600

gaactccagg attgcaaaat ttctcctttg atggttgcat acatgttgga gagagaactg 660

gtccgcaaaa cgagattcct cccagtggct ggtggaacaa gcagtgtgta cattgaagtg 720

ttgcatttga ctcaaggaac atgctgggaa cagatgtata ctccaggagg ggaagtgagg 780

aatgatgatg ttgatcaaag cttgattatt gctgctagga acatagtgag 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 gagtgcatga gggatatgaa gagttcacaa tggttgggag aagagcaaca 1140

gccatactca gaaaagcaac caggagattg attcagctga tagtgagtgg gagagacgaa 1200

cagtcgattg ccgaagcaat aattgtggcc atggtatttt cacaagagga ttgtatgata 1260

aaagcagtca 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 ctccagcacg 1500

gagagggtag tggtgagcat tgaccgtttt ttgagaatcc gggaccaacg aggaaatgta 1560

ctactgtctc ccgaggaggt cagtgaaaca cagggaacag agaaactgac aataacttac 1620

tcatcgtcaa tgatgtggga gattaatggt cctgaatcag tgttggtcaa tacctatcaa 1680

tggatcatca gaaactggga aactgttaaa attcagtggt cccagaaccc tacaatgcta 1740

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tacaataaaa tggaatttga accatttcag tctttagtac ctaaggccat tagaggccaa 1800

tacagtgggt ttgtaagaac tctgttccaa caaatgaggg atgtgcttgg gacatttgat 1860

accgcacaga taataaaact tcttcccttc gcagccgctc caccaaagca aagtagaatg 1920

cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatact tgtaaggggc 1980

aattctcctg tattcaacta taacaaggcc acgaagagac tcacagttct cggaaaggat 2040

gctggcactt taactgaaga cccagatgaa ggcacagctg gagtggagtc cgctgttctg 2100

aggggattcc tcattctggg caaagaagac aagagatatg ggccagcact aagcatcaat 2160

gaactgagca accttgcgaa aggagagaag gctaatgtgc taattgggca aggagacgtg 2220

gtgttggtaa tgaaacggaa acgggactct agcatactta ctgacagcca gacagcgacc 2280

aaaagaattc ggatggccat caattagtgt cgaatagttt aaaaacgacc ttgtttctac 2340

t 2341

<210> SEQ ID NO 4
<211> LENGTH: 1565
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 4

agcaaaagca gggtagataa tcactcactg agtgacatca aaatcatggc gtctcaaggc 60

accaaacgat cttacgaaca gatggagact gatggagaac gccagaatgc cactgaaatc 120

agagcatccg tcggaaaaat gattggtgga attggacgat tctacatcca aatgtgcacc 180

gaactcaaac tcagtgatta tgagggacgg ttgatccaaa acagcttaac aatagagaga 240

atggtgctct ctgcttttga cgaaaggaga aataaatacc ttgaagaaca tcccagtgcg 300

gggaaagatc ctaagaaaac tggaggacct atatacagga gagtaaacgg aaagtggatg 360

agagaactca tcctttatga caaagaagaa ataaggcgaa tctggcgcca agctaataat 420

ggtgacgatg caacggctgg tctgactcac atgatgatct ggcattccaa tttgaatgat 480

gcaacttatc agaggacaag agctcttgtt cgcaccggaa tggatcccag gatgtgctct 540

ctgatgcaag gttcaactct ccctaggagg tctggagccg caggtgctgc agtcaaagga 600

gttggaacaa tggtgatgga attggtcaga atgatcaaac gtgggatcaa tgatcggaac 660

ttctggaggg gtgagaatgg acgaaaaaca agaattgctt atgaaagaat gtgcaacatt 720

ctcaaaggga aatttcaaac tgctgcacaa aaagcaatga tggatcaagt gagagagagc 780

cggaacccag ggaatgctga gttcgaagat ctcacttttc tagcacggtc tgcactcata 840

ttgagagggt cggttgctca caagtcctgc ctgcctgcct gtgtgtatgg acctgccgta 900

gccagtgggt acgactttga aagggaggga tactctctag tcggaataga ccctttcaga 960

ctgcttcaaa acagccaagt gtacagccta atcagaccaa atgagaatcc agcacacaag 1020

agtcaactgg tgtggatggc atgccattct gccgcatttg aagatctaag agtattaagc 1080

ttcatcaaag ggacgaaggt gctcccaaga gggaagcttt ccactagagg agttcaaatt 1140

gcttccaatg aaaatatgga gactatggaa tcaagtacac ttgaactgag aagcaggtac 1200

tgggccataa ggaccagaag tggaggaaac accaatcaac agagggcatc tgcgggccaa 1260

atcagcatac aacctacgtt ctcagtacag agaaatctcc cttttgacag aacaaccatt 1320

atggcagcat tcaatgggaa tacagagggg agaacatctg acatgaggac cgaaatcata 1380

aggatgatgg aaagtgcaag accagaagat gtgtctttcc aggggcgggg agtcttcgag 1440

ctctcggacg aaaaggcagc gagcccgatc gtgccttcct ttgacatgag taatgaagga 1500

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tcttatttct tcggagacaa tgcagaggag tacgacaatt aaagaaaaat acccttgttt 1560

ctact 1565

<210> SEQ ID NO 5
<211> LENGTH: 1027
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 5

agcaaaagca ggtagatatt gaaagatgag tcttctaacc gaggtcgaaa cgtacgtact 60

ctctatcatc ccgtcaggcc ccctcaaagc cgagatcgca cagagacttg aagatgtctt 120

tgcagggaag aacaccgatc ttgaggttct catggaatgg ctaaagacaa gaccaatcct 180

gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg 240

aggactgcag cgtagacgct ttgtccaaaa tgcccttaat gggaacgggg atccaaataa 300

catggacaaa gcagttaaac tgtataggaa gctcaagagg gagataacat tccatggggc 360

caaagaaatc tcactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata 420

caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga 480

acagattgct gactcccagc atcggtctca taggcaaatg gtgacaacaa ccaatccact 540

aatcagacat gagaacagaa tggttttagc cagcactaca gctaaggcta tggagcaaat 600

ggctggatcg agtgagcaag cagcagaggc catggaggtt gctagtcagg ctagacaaat 660

ggtgcaagcg atgagaacca ttgggactca tcctagctcc agtgctggtc tgaaaaatga 720

tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa 780

gtgatcctct cactattgcc gcaaatatca ttgggatctt gcacttgaca ttgtggattc 840

ttgatcgtct ttttttcaaa tgcatttacc gtcgctttaa atacggactg aaaggagggc 900

cttctacgga aggagtgcca aagtctatga gggaagaata tcgaaaggaa cagcagagtg 960

ctgtggatgc tgacgatggt cattttgtca gcatagagct ggagtaaaaa actaccttgt 1020

ttctact 1027

<210> SEQ ID NO 6
<211> LENGTH: 890
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 6

agcaaaagca gggtgacaaa aacataatgg atccaaacac tgtgtcaagc tttcaggtag 60

attgctttct ttggcatgtc cgcaaacgag ttgcagacca agaactaggc gatgccccat 120

tccttgatcg gcttcgccga gatcagaaat ccctaagagg aaggggcagt actctcggtc 180

tggacatcaa gacagccaca cgtgctggaa agcagatagt ggagcggatt ctgaaagaag 240

aatccgatga ggcacttaaa atgaccatgg cctctgtacc tgcgtcgcgt tacctaactg 300

acatgactct tgaggaaatg tcaagggact ggtccatgct catacccaag cagaaagtgg 360

caggccctct ttgtatcaga atggaccagg cgatcatgga taagaacatc atactgaaag 420

cgaacttcag tgtgattttt gaccggctgg agactctaat attgctaagg gctttcaccg 480

aagagggagc aattgttggc gaaatttcac cattgccttc tcttccagga catactgctg 540

aggatgtcaa aaatgcagtt ggagtcctca tcggaggact tgaatggaat gataacacag 600

ttcgagtctc tgaaactcta cagagattcg cttggagaag cagtaatgag aatgggagac 660

ctccactcac tccaaaacag aaacgagaaa tggcgggaac aattaggtca gaagtttgaa 720

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gaaataagat ggttgattga agaagtgaga cacaaactga agataacaga gaatagtttt 780

gagcaaataa catttatgca agccttacat ctattgcttg aagtggagca agagataaga 840

actttctcgt ttcagcttat ttagtactaa aaaacaccct tgtttctact 890

<210> SEQ ID NO 7
<211> LENGTH: 1775
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 7

agcaaaagca ggggaaaata aaaacaacca aaatgaaggc aaacctactg gtcctgttat 60

gtgcacttgc agctgcagat gcagacacaa tatgtatagg ctaccatgcg aacaattcaa 120

ccgacactgt tgacacagta ctcgagaaga atgtgacagt gacacactct gttaacctgc 180

tcgaagacag ccacaacgga aaactatgta gattaaaagg aatagcccca ctacaattgg 240

ggaaatgtaa catcgccgga tggctcttgg gaaacccaga atgcgaccca ctgcttccag 300

tgagatcatg gtcctacatt gtagaaacac caaactctga gaatggaata tgttatccag 360

gagatttcat cgactatgag gagctgaggg agcaattgag ctcagtgtca tcattcgaaa 420

gattcgaaat atttcccaaa gaaagctcat ggcccaacca caacacaaac ggagtaacgg 480

cagcatgctc ccatgagggg aaaagcagtt tttacagaaa tttgctatgg ctgacggaga 540

aggagggctc atacccaaag ctgaaaaatt cttatgtgaa caaaaaaggg aaagaagtcc 600

ttgtactgtg gggtattcat cacccgccta acagtaagga acaacagaat ctctatcaga 660

atgaaaatgc ttatgtctct gtagtgactt caaattataa caggagattt accccggaaa 720

tagcagaaag acccaaagta agagatcaag ctgggaggat gaactattac tggaccttgc 780

taaaacccgg agacacaata atatttgagg caaatggaaa tctaatagca ccaatgtatg 840

ctttcgcact gagtagaggc tttgggtccg gcatcatcac ctcaaacgca tcaatgcatg 900

agtgtaacac gaagtgtcaa acacccctgg gagctataaa cagcagtctc ccttaccaga 960

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ccggttttat tgaaggggga tggactggaa tgatagatgg atggtatggt tatcatcatc 1140

agaatgaaca gggatcaggc tatgcagcgg atcaaaaaag cacacaaaat gccattaacg 1200

ggattacaaa caaggtgaac actgttatcg agaaaatgaa cattcaattc acagctgtgg 1260

gtaaagaatt caacaaatta gaaaaaagga tggaaaattt aaataaaaaa gttgatgatg 1320

gatttctgga catttggaca tataatgcag aattgttagt tctactggaa aatgaaagga 1380

ctctggattt ccatgactca aatgtgaaga atctgtatga gaaagtaaaa agccaattaa 1440

agaataatgc caaagaaatc ggaaatggat gttttgagtt ctaccacaag tgtgacaatg 1500

aatgcatgga aagtgtaaga aatgggactt atgattatcc caaatattca gaagagtcaa 1560

agttgaacag ggaaaaggta gatggagtga aattggaatc aatggggatc tatcagattc 1620

tggcgatcta ctcaactgtc gccagttcac tggtgctttt ggtctccctg ggggcaatca 1680

gtttctggat gtgttctaat ggatctttgc agtgcagaat atgcatctga gattagaatt 1740

tcagagatat gaggaaaaac acccttgttt ctact 1775

<210> SEQ ID NO 8
<211> LENGTH: 1413
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

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<400> SEQUENCE: 8

agcaaaagca ggggtttaaa atgaatccaa atcagaaaat aataaccatt ggatcaatct 60

gtctggtagt cggactaatt agcctaatat tgcaaatagg gaatataatc tcaatatgga 120

ttagccattc aattcaaact ggaagtcaaa accatactgg aatatgcaac caaaacatca 180

ttacctataa aaatagcacc tgggtaaagg acacaacttc agtgatatta accggcaatt 240

catctctttg tcccatccgt gggtgggcta tatacagcaa agacaatagc ataagaattg 300

gttccaaagg agacgttttt gtcataagag agccctttat ttcatgttct cacttggaat 360

gcaggacctt ttttctgacc caaggtgcct tactgaatga caagcattca agtgggactg 420

ttaaggacag aagcccttat agggccttaa tgagctgccc tgtcggtgaa gctccgtccc 480

cgtacaattc aagatttgaa tcggttgctt ggtcagcaag tgcatgtcat gatggcatgg 540

gctggctaac aatcggaatt tcaggtccag ataatggagc agtggctgta ttaaaataca 600

acggcataat aactgaaacc ataaaaagtt ggaggaagaa aatattgagg acacaagagt 660

ctgaatgtgc ctgtgtaaat ggttcatgtt ttactataat gactgatggc ccgagtgatg 720

ggctggcctc gtacaaaatt ttcaagatcg aaaaggggaa ggttactaaa tcaatagagt 780

tgaatgcacc taattctcac tatgaggaat gttcctgtta ccctgatacc ggcaaagtga 840

tgtgtgtgtg cagagacaat tggcatggtt cgaaccggcc atgggtgtct ttcgatcaaa 900

acctggatta tcaaatagga tacatctgca gtggggtttt cggtgacaac ccgcgtcccg 960

aagatggaac aggcagctgt ggtccagtgt atgttgatgg agcaaacgga gtaaagggat 1020

tttcatatag gtatggtaat ggtgtttgga taggaaggac caaaagtcac agttccagac 1080

atgggtttga gatgatttgg gatcctaatg gatggacaga gactgatagt aagttctctg 1140

tgaggcaaga tgttgtggca atgactgatt ggtcagggta tagcggaagt ttcgttcaac 1200

atcctgagct gacagggcta gactgtatga ggccgtgctt ctgggttgaa ttaatcaggg 1260

gacgacctaa agaaaaaaca atctggacta gtgcgagcag catttctttt tgtggcgtga 1320

atagtgatac tgtagattgg tcttggccag acggtgctga gttgccattc agcattgaca 1380

agtagtctgt tcaaaaaact ccttgtttct act 1413

<210> SEQ ID NO 9
<211> LENGTH: 759
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 9

Met Glu Arg Ile Lys Glu Leu Arg Asn Leu Met Ser Gln Ser Arg Thr
1 5 10 15

Arg Glu Ile Leu Thr Lys Thr Thr Val Asp His Met Ala Ile Ile Lys
20 25 30

Lys Tyr Thr Ser Gly Arg Gln Glu Lys Asn Pro Ala Leu Arg Met Lys
35 40 45

Trp Met Met Ala Met Lys Tyr Pro Ile Thr Ala Asp Lys Arg Ile Thr
50 55 60

Glu Met Ile Pro Glu Arg Asn Glu Gln Gly Gln Thr Leu Trp Ser Lys
65 70 75 80

Met Asn Asp Ala Gly Ser Asp Arg Val Met Val Ser Pro Leu Ala Val
85 90 95

Thr Trp Trp Asn Arg Asn Gly Pro Met Thr Asn Thr Val His Tyr Pro
100 105 110

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Lys Ile Tyr Lys Thr Tyr Phe Glu Arg Val Glu Arg Leu Lys His Gly
        115                 120                 125

Thr Phe Gly Pro Val His Phe Arg Asn Gln Val Lys Ile Arg Arg Arg
    130                 135                 140

Val Asp Ile Asn Pro Gly His Ala Asp Leu Ser Ala Lys Glu Ala Gln
145                 150                 155                 160

Asp Val Ile Met Glu Val Val Phe Pro Asn Glu Val Gly Ala Arg Ile
                165                 170                 175

Leu Thr Ser Glu Ser Gln Leu Thr Ile Thr Lys Glu Lys Lys Glu Glu
            180                 185                 190

Leu Gln Asp Cys Lys Ile Ser Pro Leu Met Val Ala Tyr Met Leu Glu
        195                 200                 205

Arg Glu Leu Val Arg Lys Thr Arg Phe Leu Pro Val Ala Gly Gly Thr
    210                 215                 220

Ser Ser Val Tyr Ile Glu Val Leu His Leu Thr Gln Gly Thr Cys Trp
225                 230                 235                 240

Glu Gln Met Tyr Thr Pro Gly Gly Glu Val Lys Asn Asp Asp Val Asp
                245                 250                 255

Gln Ser Leu Ile Ile Ala Ala Arg Asn Ile Val Arg Arg Ala Ala Val
            260                 265                 270

Ser Ala Asp Pro Leu Ala Ser Leu Leu Glu Met Cys His Ser Thr Gln
        275                 280                 285

Ile Gly Gly Ile Arg Met Val Asp Ile Leu Lys Gln Asn Pro Thr Glu
    290                 295                 300

Glu Gln Ala Val Asp Ile Cys Lys Ala Ala Met Gly Leu Arg Ile Ser
305                 310                 315                 320

Ser Ser Phe Ser Phe Gly Gly Phe Thr Phe Lys Arg Thr Ser Gly Ser
                325                 330                 335

Ser Val Lys Arg Glu Glu Glu Val Leu Thr Gly Asn Leu Gln Thr Leu
            340                 345                 350

Lys Ile Arg Val His Glu Gly Ser Glu Glu Phe Thr Met Val Gly Arg
        355                 360                 365

Arg Ala Thr Ala Ile Leu Arg Lys Ala Thr Arg Arg Leu Ile Gln Leu
    370                 375                 380

Ile Val Ser Gly Arg Asp Glu Gln Ser Ile Ala Glu Ala Ile Ile Val
385                 390                 395                 400

Ala Met Val Phe Ser Gln Glu Asp Cys Met Ile Lys Ala Val Arg Gly
                405                 410                 415

Asp Leu Asn Phe Val Asn Arg Ala Asn Gln Arg Leu Asn Pro Met His
            420                 425                 430

Gln Leu Leu Arg His Phe Gln Lys Asp Ala Lys Val Leu Phe Gln Asn
        435                 440                 445

Trp Gly Val Glu Pro Ile Asp Asn Val Met Gly Met Ile Gly Ile Leu
    450                 455                 460

Pro Asp Met Thr Pro Ser Ile Glu Met Ser Met Arg Gly Val Arg Ile
465                 470                 475                 480

Ser Lys Met Gly Val Asp Glu Tyr Ser Ser Thr Glu Arg Val Val Val
                485                 490                 495

Ser Ile Asp Arg Phe Leu Arg Val Arg Asp Gln Arg Gly Asn Val Leu
            500                 505                 510

Leu Ser Pro Glu Glu Val Ser Glu Thr Gln Gly Thr Glu Lys Leu Thr
        515                 520                 525
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Ile Thr Tyr Ser Ser Ser Met Met Trp Glu Ile Asn Gly Pro Glu Ser
    530                 535                 540

Val Leu Val Asn Thr Tyr Gln Trp Ile Ile Arg Asn Trp Glu Thr Val
545                 550                 555                 560

Lys Ile Gln Trp Ser Gln Asn Pro Thr Met Leu Tyr Asn Lys Met Glu
                565                 570                 575

Phe Glu Pro Phe Gln Ser Leu Val Pro Lys Ala Ile Arg Gly Gln Tyr
            580                 585                 590

Ser Gly Phe Val Arg Thr Leu Phe Gln Gln Met Arg Asp Val Leu Gly
        595                 600                 605

Thr Phe Asp Thr Ala Gln Ile Ile Lys Leu Leu Pro Phe Ala Ala Ala
    610                 615                 620

Pro Pro Lys Gln Ser Arg Met Gln Phe Ser Ser Phe Thr Val Asn Val
625                 630                 635                 640

Arg Gly Ser Gly Met Arg Ile Leu Val Arg Gly Asn Ser Pro Val Phe
                645                 650                 655

Asn Tyr Asn Lys Ala Thr Lys Arg Leu Thr Val Leu Gly Lys Asp Ala
            660                 665                 670

Gly Thr Leu Thr Glu Asp Pro Asp Glu Gly Thr Ala Gly Val Glu Ser
        675                 680                 685

Ala Val Leu Arg Gly Phe Leu Ile Leu Gly Lys Glu Asp Arg Arg Tyr
    690                 695                 700

Gly Pro Ala Leu Ser Ile Asn Glu Leu Ser Asn Leu Ala Lys Gly Glu
705                 710                 715                 720

Lys Ala Asn Val Leu Ile Gly Gln Gly Asp Val Val Leu Val Met Lys
                725                 730                 735

Arg Lys Arg Asp Ser Ser Ile Leu Thr Asp Ser Gln Thr Ala Thr Lys
            740                 745                 750

Arg Ile Arg Met Ala Ile Asn
        755
```

<210> SEQ ID NO 10
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 10

```
agcgaaagca ggtcaattat attcaatatg gaaagaataa aagaactaag aaatctaatg     60

tcgcagtctc gcacccgcga gatactcaca aaaaccaccg tggaccatat ggccataatc    120

aagaagtaca catcaggaag acaggagaag aacccagcac ttaggatgaa atggatgatg    180

gcaatgaaat atccaattac agcagacaag aggataacgg aaatgattcc tgagagaaat    240

gagcaaggac aaactttatg gagtaaaatg aatgatgccg gatcagaccg agtgatggta    300

tcacctctgg ctgtgacatg gtggaatagg aatggaccaa tgacaaatac agttcattat    360

ccaaaaatct acaaaactta ttttgaaaga gtcgaaaggc taaagcatgg aacctttggc    420

cctgtccatt ttagaaacca agtcaaaata cgtcggagag ttgacataaa tcctggtcat    480

gcagatctca gtgccaagga ggcacaggat gtaatcatgg aagttgtttt ccctaacgaa    540

gtgggagcca ggatactaac atcggaatcg caactaacga taaccaaaga gaagaaagaa    600

gaactccagg attgcaaaat ttctcctttg atggttgcat acatgttgga gagagaactg    660

gtccgcaaaa cgagattcct cccagtggct ggtggaacaa gcagtgtgta cattgaagtg    720

ttgcatttga ctcaaggaac atgctgggaa cagatgtata ctccaggagg ggaagtgaag    780
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aatgatgatg ttgatcaaag cttgattatt gctgctagga acatagtgag aagagctgca 840

gtatcagcag acccactagc atctttattg gagatgtgcc acagcacaca gattggtgga 900

attaggatgg tagacatcct taagcagaac ccaacagaag agcaagccgt ggatatatgc 960

aaggctgcaa tgggactgag aattagctca tccttcagtt ttggtggatt cacatttaag 1020

agaacaagcg gatcatcagt caagagagag gaagaggtgc ttacgggcaa tcttcaaaca 1080

ttgaagataa gagtgcatga gggatctgaa gagttcacaa tggttgggag aagagcaaca 1140

gccatactca gaaaagcaac caggagattg attcagctga tagtgagtgg gagagacgaa 1200

cagtcgattg ccgaagcaat aattgtggcc atggtatttt cacaagagga ttgtatgata 1260

aaagcagtta gaggtgatct gaatttcgtc aatagggcga atcagcgact gaatcctatg 1320

catcaacttt taagacattt tcagaaggat gcgaaagtgc tttttcaaaa ttggggagtt 1380

gaacctatcg acaatgtgat gggaatgatt gggatattgc ccgacatgac tccaagcatc 1440

gagatgtcaa tgagaggagt gagaatcagc aaaatgggtg tagatgagta ctccagcacg 1500

gagagggtag tggtgagcat tgaccggttc ttgagagtca gggaccaacg aggaaatgta 1560

ctactgtctc ccgaggaggt cagtgaaaca cagggaacag agaaactgac aataacttac 1620

tcatcgtcaa tgatgtggga gattaatggt cctgaatcag tgttggtcaa tacctatcaa 1680

tggatcatca gaaactggga aactgttaaa attcagtggt cccagaaccc tacaatgcta 1740

tacaataaaa tggaatttga accatttcag tctttagtac ctaaggccat tagaggccaa 1800

tacagtgggt ttgtaagaac tctgttccaa caaatgaggg atgtgcttgg gacatttgat 1860

accgcacaga taataaaact tcttcccttc gcagccgctc caccaaagca aagtagaatg 1920

cagttctcct catttactgt gaatgtgagg ggatcaggaa tgagaatact tgtaaggggc 1980

aattctcctg tattcaacta caacaaggcc acgaagagac tcacagttct cggaaaggat 2040

gctggcactt taaccgaaga cccagatgaa ggcacagctg gagtggagtc cgctgttctg 2100

aggggattcc tcattctggg caaagaagac aggagatatg ggccagcatt aagcatcaat 2160

gaactgagca accttgcgaa aggagagaag gctaatgtgc taattgggca aggagacgtg 2220

gtgttggtaa tgaaacgaaa acgggactct agcatactta ctgacagcca gacagcgacc 2280

aaaagaattc ggatggccat caattagtgt cgaatagttt aaaaacgacc ttgtttctac 2340

t 2341

<210> SEQ ID NO 11
<211> LENGTH: 2341
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 11

agcgaaagca ggcaaaccat ttgaatggat gtcaatccga ccttactttt cttaaaagtg 60

ccagcacaaa atgctataag cacaactttc ccttataccg gagaccctcc ttacagccat 120

gggacaggaa caggatacac catggatact gtcaacagga cacatcagta ctcagaaaag 180

ggaagatgga caacaaacac cgaaactgga gcaccgcaac tcaacccgat tgatgggcca 240

ctgccagaag acaatgaacc aagtggttat gcccaaacag attgtgtatt ggaagcaatg 300

gctttccttg aggaatccca tcctggtatt tttgaaaact cgtgtattga aacgatggag 360

gttgttcagc aaacacgagt agacaagctg acacaaggcc gacagaccta tgactggact 420

ttaaatagaa accagcctgc tgcaacagca ttggccaaca caatagaagt gttcagatca 480

aatggcctca cggccaatga gtcaggaagg ctcatagact tccttaagga tgtaatggag 540

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tcaatgaaaa aagaagaaat ggggatcaca actcattttc agagaaagag acgggtgaga 600

gacaatatga ctaagaaaat gataacacag agaacaatag gtaaaaggaa acagagattg 660

aacaaaaggg gttatctaat tagagcattg accctgaaca caatgaccaa agatgctgag 720

agagggaagc taaaacggag agcaattgca accccaggga tgcaaataag ggggtttgta 780

tactttgttg agacactggc aaggagtata tgtgagaaac ttgaacaatc agggttgcca 840

gttggaggca atgagaagaa agcaaagttg gcaaatgttg taaggaagat gatgaccaat 900

tctcaggaca ccgaactttc tttcaccatc actggagata acaccaaatg gaacgaaaat 960

cagaatcctc ggatgttttt ggccatgatc acatatatga ccagaaatca gcccgaatgg 1020

ttcagaaatg ttctaagtat tgctccaata atgttctcaa acaaaatggc gagactggga 1080

aaagggtata tgtttgagag caagagtatg aaacttagaa ctcaaatacc tgcagaaatg 1140

ctagcaagca ttgatttgaa atatttcaat gattcaacaa gaaagaagat tgaaaaaatc 1200

cgaccgctct taatagaggg gactgcatca ttgagccctg gaatgatgat gggcatgttc 1260

aatatgttaa gcactgtatt aggcgtctcc atcctgaatc ttggacaaaa gagatacacc 1320

aagactactt actggtggga tggtcttcaa tcctctgacg attttgctct gattgtgaat 1380

gcacccaatc atgaagggat tcaagccgga gtcgacaggt tttatcgaac ctgtaagcta 1440

cttggaatca atatgagcaa gaaaaagtct tacataaaca gaacaggtac atttgaattc 1500

acaagttttt tctatcgtta tgggtttgtt gccaatttca gcatggagct tcccagtttt 1560

ggggtgtctg ggatcaacga gtcagcggac atgagtattg gagttactgt catcaaaaac 1620

aatatgataa acaatgatct tggtccagca acagctcaaa tggcccttca gttgttcatc 1680

aaagattaca ggtacacgta ccgatgccat agaggtgaca 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 tggtccagcc 1980

aaaaacatgg agtatgatgc tgttgcaaca acacactcct ggatccccaa aagaaatcga 2040

tccatcttga atacaagtca aagaggagta cttgaagatg aacaaatgta ccaaaggtgc 2100

tgcaatttat ttgaaaaatt cttccccagc agttcataca gaagaccagt cgggatatcc 2160

agtatggtgg aggctatggt ttccagagcc cgaattgatg cacggattga tttcgaatct 2220

ggaaggataa agaaagaaga gttcactgag atcatgaaga tctgttccac cattgaagag 2280

ctcagacggc aaaaatagtg aatttagctt gtccttcatg aaaaaatgcc ttgtttctac 2340

t 2341

<210> SEQ ID NO 12
<211> LENGTH: 2233
<212> TYPE: DNA
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 12

agcgaaagca ggtactgatt caaaatggaa gattttgtgc gacaatgctt caatccgatg 60

attgtcgagc ttgcggaaaa aacaatgaaa gagtatgggg aggacctgaa aatcgaaaca 120

aacaaatttg cagcaatatg cactcacttg gaagtatgct tcatgtattc agatttccac 180

ttcatcaatg agcaaggcga gtcaataatc gtagaacttg gtgatcctaa tgcacttttg 240

aagcacagat ttgaaataat cgagggaaga gatcgcacaa tggcctggac agtagtaaac 300

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agtatttgca acactacagg ggctgagaaa ccaaagtttc taccagattt gtatgattac 360

aaggaaaata gattcatcga aattggagta acaaggagag aagttcacat atactatctg 420

gaaaaggcca ataaaattaa atctgagaaa acacacatcc acattttctc gttcactggg 480

gaagaaatgg ccacaagggc cgactacact ctcgatgaag aaagcagggc taggatcaaa 540

accaggctat tcaccataag acaagaaatg gccagcagag gcctctggga ttcctttcgt 600

cagtccgaga gaggagaaga gacaattgaa gaaaggtttg aaatcacagg aacaatgcgc 660

aagcttgccg accaaagtct cccgccgaac ttctccagcc ttgaaaattt tagagcctat 720

gtggatggat tcgaaccgaa cggctacatt gagggcaagc tgtctcaaat gtccaaagaa 780

gtaaatgcta gaattgaacc ttttttgaaa acaacaccac gaccacttag acttccgaat 840

gggcctccct gttctcagcg gtccaaattc ctgctgatgg atgccttaaa attaagcatt 900

gaggacccaa gtcatgaagg agagggaata ccgctatatg atgcaatcaa atgcatgaga 960

acattctttg gatggaagga acccaatgtt gttaaaccac acgaaaaggg aataaatcca 1020

aattatcttc tgtcatggaa gcaagtactg gcagaactgc aggacattga gaatgaggag 1080

aaaattccaa agactaaaaa tatgaaaaaa acaagtcagc taaagtgggc acttggtgag 1140

aacatggcac cagaaaaggt agactttgac gactgtaaag atgtaggtga tttgaagcaa 1200

tatgatagtg atgaaccaga attgaggtcg cttgcaagtt ggattcagaa tgagttcaac 1260

aaggcatgcg aactgacaga ttcaagctgg atagagcttg atgagattgg agaagatgtg 1320

gctccaattg aacacattgc aagcatgaga aggaattatt tcacatcaga ggtgtctcac 1380

tgcagagcca cagaatacat aatgaagggg gtgtacatca atactgcctt acttaatgca 1440

tcttgtgcag caatggatga tttccaatta attccaatga taagcaagtg tagaactaag 1500

gagggaaggc gaaagaccaa cttgtatggt ttcatcataa aaggaagatc ccacttaagg 1560

aatgacaccg acgtggtaaa ctttgtgagc atggagtttt ctctcactga cccaagactt 1620

gaaccacaca aatgggagaa gtactgtgtt cttgagatag gagatatgct tctaagaagt 1680

gccataggcc aggtttcaag gcccatgttc ttgtatgtga ggacaaatgg aacctcaaaa 1740

attaaaatga aatggggaat ggagatgagg cgttgtctcc tccagtcact tcaacaaatt 1800

gagagtatga ttgaagctga gtcctctgtc aaagagaaag acatgaccaa agagttcttt 1860

gagaacaaat cagaaacatg gcccattgga gagtctccca aaggagtgga ggaaagttcc 1920

attgggaagg tctgcaggac tttattagca aagtcggtat ttaacagctt gtatgcatct 1980

ccacaactag aaggattttc agctgaatca agaaaactgc ttcttatcgt tcaggctctt 2040

agggacaatc tggaacctgg gacctttgat cttgggggc tatatgaagc aattgaggag 2100

tgcctaatta atgatccctg ggttttgctt aatgcttctt ggttcaactc cttccttaca 2160

catgcattga gttagttgtg gcagtgctac tatttgctat ccatactgtc caaaaaagta 2220

ccttgtttct act 2233

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

<400> SEQUENCE: 13

agcaaaagca gggtagataa tcactcactg agtgacatca aaatcatggc gtcccaaggc 60

accaaacggt cttacgaaca gatggagact gatggagaac gccagaatgc cactgaaatc 120

agagcatccg tcggaaaaat gattggtgga attggacgat tctacatcca aatgtgcaca 180

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gaacttaaac tcagtgatta tgagggacgg ttgatccaaa acagcttaac aatagagaga 240

atggtgctct ctgcttttga cgaaaggaga 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

gcaacttatc agaggacaag ggctcttgtt cgcaccggaa tggatcccag gatgtgctct 540

ctgatgcaag gttcaactct ccctaggagg tctggagccg caggtgctgc agtcaaagga 600

gttggaacaa tggtgatgga attggtcagg atgatcaaac gtgggatcaa tgatcggaac 660

ttctggaggg gtgagaatgg acgaaaaaca agaattgctt atgaaagaat gtgcaacatt 720

ctcaaaggga aatttcaaac tgctgcacaa aaagcaatga tggatcaagt gagagagagc 780

cggaacccag ggaatgctga gttcgaagat ctcacttttc 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

ttcatcaaag ggacgaaggt ggtcccaaga gggaagcttt ccactagagg agttcaaatt 1140

gcttccaatg aaaatatgga gactatggaa tcaagtacac ttgaactgag aagcaggtac 1200

tgggccataa ggaccagaag tggaggaaac accaatcaac agagggcatc tgcgggccaa 1260

atcagcatac aacctacgtt ctcagtacag agaaatctcc cttttgacag aacaaccgtt 1320

atggcagcat tcactgggaa tacagagggg agaacatctg acatgaggac cgaaatcata 1380

aggatgatgg aaagtgcaag accagaagat gtgtctttcc aggggcgggg agtcttcgag 1440

ctctcggacg aaaaggcagc gagcccgatc gtgccttcct ttgacatgag taatgaagga 1500

tcttatttct tcggagacaa tgcagaggag tacgacaatt aaagaaaaat acccttgttt 1560

ctact 1565

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

<400> SEQUENCE: 14

agcaaaagca ggtagatatt gaaagatgag tcttctaacc gaggtcgaaa cgtacgttct 60

ctctatcatc ccgtcaggcc ccctcaaagc cgagatcgca cagagacttg aagatgtctt 120

tgcagggaag aacaccgatc ttgaggttct catggaatgg ctaaagacaa gaccaatcct 180

gtcacctctg actaagggga ttttaggatt tgtgttcacg ctcaccgtgc ccagtgagcg 240

aggactgcag cgtagacgct ttgtccaaaa tgcccttaat gggaacgggg atccaaataa 300

catggacaaa gcagttaaac tgtataggaa gctcaagagg gagataacat tccatggggc 360

caaagaaatc tcactcagtt attctgctgg tgcacttgcc agttgtatgg gcctcatata 420

caacaggatg ggggctgtga ccactgaagt ggcatttggc ctggtatgtg caacctgtga 480

acagattgct gactcccagc atcggtctca taggcaaatg gtgacaacaa ccaacccact 540

aatcagacat gagaacagaa tggttttagc cagcactaca gctaaggcta tggagcaaat 600

ggctggatcg agtgagcaag cagcagaggc catggaggtt gctagtcagg ctaggcaaat 660

ggtgcaagcg atgagaacca ttgggactca tcctagctcc agtgctggtc tgaaaaatga 720

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tcttcttgaa aatttgcagg cctatcagaa acgaatgggg gtgcagatgc aacggttcaa    780

gtgatcctct cgctattgcc gcaaatatca ttgggatctt gcacttgata ttgtggattc    840

ttgatcgtct ttttttcaaa tgcatttacc gtcgctttaa atacggactg aaaggagggc    900

cttctacgga aggagtgcca aagtctatga gggaagaata tcgaaaggaa cagcagagtg    960

ctgtggatgc tgacgatggt cattttgtca gcatagagct ggagtaaaaa actaccttgt   1020

ttctact                                                             1027


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

<400> SEQUENCE: 15

agcaaaagca gggtgacaaa gacataatgg atccaaacac tgtgtcaagc tttcaggtag     60

attgctttct ttggcatgtc cgcaaacgag ttgcagacca agaactaggt 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 taaaaacatc atactgaaag    420

cgaacttcag tgtgattttt gaccggctgg agactctaat attgctaagg gctttcaccg    480

aagagggagc aattgttggc gaaatttcac cattgccttc tcttccagga catactgctg    540

aggatgtcaa aaatgcagtt ggagtcctca tcggaggact tgaatggaat gataacacag    600

ttcgagtctc tgaaactcta cagagattcg cttggagaag cagtaatgag aatgggagac    660

ctccactcac tccaaaacag aaacgagaaa tggcgggaac aattaggtca gaagtttgaa    720

gaaataagat ggttgattga agaagtgaga cacaaactga aggtaacaga gaatagtttt    780

gagcaaataa catttatgca agccttacat ctattgcttg aagtggagca agagataaga    840

actttctcat ttcagcttat ttaataataa aaaacaccct tgtttctact               890


<210> SEQ ID NO 16
<211> LENGTH: 757
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 16

Met Asp Val Asn Pro Thr Leu Leu Phe Leu Lys Val Pro Ala Gln Asn
1               5                   10                  15

Ala Ile Ser Thr Thr Phe Pro Tyr Thr Gly Asp Pro Pro Tyr Ser His
            20                  25                  30

Gly Thr Gly Thr Gly Tyr Thr Met Asp Thr Val Asn Arg Thr His Gln
        35                  40                  45

Tyr Ser Glu Lys Gly Arg Trp Thr Thr Asn Thr Glu Thr Gly Ala Pro
    50                  55                  60

Gln Leu Asn Pro Ile Asp Gly Pro Leu Pro Glu Asp Asn Glu Pro Ser
65                  70                  75                  80

Gly Tyr Ala Gln Thr Asp Cys Val Leu Glu Ala Met Ala Phe Leu Glu
                85                  90                  95

Glu Ser His Pro Gly Ile Phe Glu Asn Ser Cys Ile Glu Thr Met Glu
            100                 105                 110
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Val Val Gln Gln Thr Arg Val Asp Lys Leu Thr Gln Gly Arg Gln Thr
        115                 120                 125

Tyr Asp Trp Thr Leu Asn Arg Asn Gln Pro Ala Ala Thr Ala Leu Ala
    130                 135                 140

Asn Thr Ile Glu Val Phe Arg Ser Asn Gly Leu Thr Ala Asn Glu Ser
145                 150                 155                 160

Gly Arg Leu Ile Asp Phe Leu Lys Asp Val Met Glu Ser Met Lys Lys
                165                 170                 175

Glu Glu Met Gly Ile Thr Thr His Phe Gln Arg Lys Arg Arg Val Arg
            180                 185                 190

Asp Asn Met Thr Lys Lys Met Ile Thr Gln Arg Thr Ile Gly Lys Arg
        195                 200                 205

Lys Gln Arg Leu Asn Lys Arg Gly Tyr Leu Ile Arg Ala Leu Thr Leu
    210                 215                 220

Asn Thr Met Thr Lys Asp Ala Glu Arg Gly Lys Leu Lys Arg Arg Ala
225                 230                 235                 240

Ile Ala Thr Pro Gly Met Gln Ile Arg Gly Phe Val Tyr Phe Val Glu
                245                 250                 255

Thr Leu Ala Arg Ser Ile Cys Glu Lys Leu Glu Gln Ser Gly Leu Pro
            260                 265                 270

Val Gly Gly Asn Glu Lys Lys Ala Lys Leu Ala Asn Val Val Arg Lys
        275                 280                 285

Met Met Thr Asn Ser Gln Asp Thr Glu Leu Ser Phe Thr Ile Thr Gly
    290                 295                 300

Asp Asn Thr Lys Trp Asn Glu Asn Gln Asn Pro Arg Met Phe Leu Ala
305                 310                 315                 320

Met Ile Thr Tyr Met Thr Arg Asn Gln Pro Glu Trp Phe Arg Asn Val
                325                 330                 335

Leu Ser Ile Ala Pro Ile Met Phe Ser Asn Lys Met Ala Arg Leu Gly
            340                 345                 350

Lys Gly Tyr Met Phe Glu Ser Lys Ser Met Lys Leu Arg Thr Gln Ile
        355                 360                 365

Pro Ala Glu Met Leu Ala Ser Ile Asp Leu Lys Tyr Phe Asn Asp Ser
    370                 375                 380

Thr Arg Lys Lys Ile Glu Lys Ile Arg Pro Leu Leu Ile Glu Gly Thr
385                 390                 395                 400

Ala Ser Leu Ser Pro Gly Met Met Met Gly Met Phe Asn Met Leu Ser
                405                 410                 415

Thr Val Leu Gly Val Ser Ile Leu Asn Leu Gly Gln Lys Arg Tyr Thr
            420                 425                 430

Lys Thr Thr Tyr Trp Trp Asp Gly Leu Gln Ser Ser Asp Asp Phe Ala
        435                 440                 445

Leu Ile Val Asn Ala Pro Asn His Glu Gly Ile Gln Ala Gly Val Asp
    450                 455                 460

Arg Phe Tyr Arg Thr Cys Lys Leu Leu Gly Ile Asn Met Ser Lys Lys
465                 470                 475                 480

Lys Ser Tyr Ile Asn Arg Thr Gly Thr Phe Glu Phe Thr Ser Phe Phe
                485                 490                 495

Tyr Arg Tyr Gly Phe Val Ala Asn Phe Ser Met Glu Leu Pro Ser Phe
            500                 505                 510
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Gly Val Ser Gly Ile Asn Glu Ser Ala Asp Met Ser Ile Gly Val Thr
        515                 520                 525

Val Ile Lys Asn Asn Met Ile Asn Asn Asp Leu Gly Pro Ala Thr Ala
    530                 535                 540

Gln Met Ala Leu Gln Leu Phe Ile Lys Asp Tyr Arg Tyr Thr Tyr Arg
545                 550                 555                 560

Cys His Arg Gly Asp Thr Gln Ile Gln Thr Arg Arg Ser Phe Glu Ile
                565                 570                 575

Lys Lys Leu Trp Glu Gln Thr Arg Ser Lys Ala Gly Leu Leu Val Ser
            580                 585                 590

Asp Gly Gly Pro Asn Leu Tyr Asn Ile Arg Asn Leu His Ile Pro Glu
        595                 600                 605

Val Cys Leu Lys Trp Glu Leu Met Asp Glu Asp Tyr Gln Gly Arg Leu
    610                 615                 620

Cys Asn Pro Leu Asn Pro Phe Val Ser His Lys Glu Ile Glu Ser Met
625                 630                 635                 640

Asn Asn Ala Val Met Met Pro Ala His Gly Pro Ala Lys Asn Met Glu
                645                 650                 655

Tyr Asp Ala Val Ala Thr Thr His Ser Trp Ile Pro Lys Arg Asn Arg
            660                 665                 670

Ser Ile Leu Asn Thr Ser Gln Arg Gly Val Leu Glu Asp Glu Gln Met
        675                 680                 685

Tyr Gln Arg Cys Cys Asn Leu Phe Glu Lys Phe Phe Pro Ser Ser Ser
    690                 695                 700

Tyr Arg Arg Pro Val Gly Ile Ser Ser Met Val Glu Ala Met Val Ser
705                 710                 715                 720

Arg Ala Arg Ile Asp Ala Arg Ile Asp Phe Glu Ser Gly Arg Ile Lys
                725                 730                 735

Lys Glu Glu Phe Thr Glu Ile Met Lys Ile Cys Ser Thr Ile Glu Glu
            740                 745                 750

Leu Arg Arg Gln Lys
        755


<210> SEQ ID NO 17
<211> LENGTH: 716
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 17

Met Glu Asp Phe Val Arg Gln Cys Phe Asn Pro Met Ile Val Glu Leu
1               5                   10                  15

Ala Glu Lys Thr Met Lys Glu Tyr Gly Glu Asp Leu Lys Ile Glu Thr
            20                  25                  30

Asn Lys Phe Ala Ala Ile Cys Thr His Leu Glu Val Cys Phe Met Tyr
        35                  40                  45

Ser Asp Phe His Phe Ile Asn Glu Gln Gly Glu Ser Ile Ile Val Glu
    50                  55                  60

Leu Gly Asp Pro Asn Ala Leu Leu Lys His Arg Phe Glu Ile Ile Glu
65                  70                  75                  80

Gly Arg Asp Arg Thr Met Ala Trp Thr Val Val Asn Ser Ile Cys Asn
                85                  90                  95
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Thr Thr Gly Ala Glu Lys Pro Lys Phe Leu Pro Asp Leu Tyr Asp Tyr
            100                 105                 110

Lys Glu Asn Arg Phe Ile Glu Ile Gly Val Thr Arg Arg Glu Val His
        115                 120                 125

Ile Tyr Tyr Leu Glu Lys Ala Asn Lys Ile Lys Ser Glu Lys Thr His
    130                 135                 140

Ile His Ile Phe Ser Phe Thr Gly Glu Glu Met Ala Thr Arg Ala Asp
145                 150                 155                 160

Tyr Thr Leu Asp Glu Glu Ser Arg Ala Arg Ile Lys Thr Arg Leu Phe
                165                 170                 175

Thr Ile Arg Gln Glu Met Ala Ser Arg Gly Leu Trp Asp Ser Phe Arg
            180                 185                 190

Gln Ser Glu Arg Gly Glu Glu Thr Ile Glu Glu Arg Phe Glu Ile Thr
        195                 200                 205

Gly Thr Met Arg Lys Leu Ala Asp Gln Ser Leu Pro Pro Asn Phe Ser
    210                 215                 220

Ser Leu Glu Asn Phe Arg Ala Tyr Val Asp Gly Phe Glu Pro Asn Gly
225                 230                 235                 240

Tyr Ile Glu Gly Lys Leu Ser Gln Met Ser Lys Glu Val Asn Ala Arg
                245                 250                 255

Ile Glu Pro Phe Leu Lys Thr Thr Pro Arg Pro Leu Arg Leu Pro Asn
            260                 265                 270

Gly Pro Pro Cys Ser Gln Arg Ser Lys Phe Leu Leu Met Asp Ala Leu
        275                 280                 285

Lys Leu Ser Ile Glu Asp Pro Ser His Glu Gly Glu Gly Ile Pro Leu
    290                 295                 300

Tyr Asp Ala Ile Lys Cys Met Arg Thr Phe Phe Gly Trp Lys Glu Pro
305                 310                 315                 320

Asn Val Val Lys Pro His Glu Lys Gly Ile Asn Pro Asn Tyr Leu Leu
                325                 330                 335

Ser Trp Lys Gln Val Leu Ala Glu Leu Gln Asp Ile Glu Asn Glu Glu
            340                 345                 350

Lys Ile Pro Lys Thr Lys Asn Met Lys Lys Thr Ser Gln Leu Lys Trp
        355                 360                 365

Ala Leu Gly Glu Asn Met Ala Pro Glu Lys Val Asp Phe Asp Asp Cys
    370                 375                 380

Lys Asp Val Gly Asp Leu Lys Gln Tyr Asp Ser Asp Glu Pro Glu Leu
385                 390                 395                 400

Arg Ser Leu Ala Ser Trp Ile Gln Asn Glu Phe Asn Lys Ala Cys Glu
                405                 410                 415

Leu Thr Asp Ser Ser Trp Ile Glu Leu Asp Glu Ile Gly Glu Asp Val
            420                 425                 430

Ala Pro Ile Glu His Ile Ala Ser Met Arg Arg Asn Tyr Phe Thr Ser
        435                 440                 445

Glu Val Ser His Cys Arg Ala Thr Glu Tyr Ile Met Lys Gly Val Tyr
    450                 455                 460

Ile Asn Thr Ala Leu Leu Asn Ala Ser Cys Ala Ala Met Asp Asp Phe
465                 470                 475                 480

Gln Leu Ile Pro Met Ile Ser Lys Cys Arg Thr Lys Glu Gly Arg Arg
                485                 490                 495

Lys Thr Asn Leu Tyr Gly Phe Ile Ile Lys Gly Arg Ser His Leu Arg
            500                 505                 510
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Asn Asp Thr Asp Val Val Asn Phe Val Ser Met Glu Phe Ser Leu Thr
        515                 520                 525

Asp Pro Arg Leu Glu Pro His Lys Trp Glu Lys Tyr Cys Val Leu Glu
    530                 535                 540

Ile Gly Asp Met Leu Leu Arg Ser Ala Ile Gly Gln Val Ser Arg Pro
545                 550                 555                 560

Met Phe Leu Tyr Val Arg Thr Asn Gly Thr Ser Lys Ile Lys Met Lys
                565                 570                 575

Trp Gly Met Glu Met Arg Arg Cys Leu Leu Gln Ser Leu Gln Gln Ile
            580                 585                 590

Glu Ser Met Ile Glu Ala Glu Ser Ser Val Lys Glu Lys Asp Met Thr
        595                 600                 605

Lys Glu Phe Phe Glu Asn Lys Ser Glu Thr Trp Pro Ile Gly Glu Ser
    610                 615                 620

Pro Lys Gly Val Glu Glu Ser Ser Ile Gly Lys Val Cys Arg Thr Leu
625                 630                 635                 640

Leu Ala Lys Ser Val Phe Asn Ser Leu Tyr Ala Ser Pro Gln Leu Glu
                645                 650                 655

Gly Phe Ser Ala Glu Ser Arg Lys Leu Leu Leu Ile Val Gln Ala Leu
            660                 665                 670

Arg Asp Asn Leu Glu Pro Gly Thr Phe Asp Leu Gly Gly Leu Tyr Glu
        675                 680                 685

Ala Ile Glu Glu Cys Leu Ile Asn Asp Pro Trp Val Leu Leu Asn Ala
    690                 695                 700

Ser Trp Phe Asn Ser Phe Leu Thr His Ala Leu Ser
705                 710                 715


<210> SEQ ID NO 18
<211> LENGTH: 498
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 18

Met Ala Ser Gln Gly Thr Lys Arg Ser Tyr Glu Gln Met Glu Thr Asp
1               5                   10                  15

Gly Glu Arg Gln Asn Ala Thr Glu Ile Arg Ala Ser Val Gly Lys Met
            20                  25                  30

Ile Gly Gly Ile Gly Arg Phe Tyr Ile Gln Met Cys Thr Glu Leu Lys
        35                  40                  45

Leu Ser Asp Tyr Glu Gly Arg Leu Ile Gln Asn Ser Leu Thr Ile Glu
    50                  55                  60

Arg Met Val Leu Ser Ala Phe Asp Glu Arg Arg Asn Lys Tyr Leu Glu
65                  70                  75                  80

Glu His Pro Ser Ala Gly Lys Asp Pro Lys Lys Thr Gly Gly Pro Ile
                85                  90                  95

Tyr Arg Arg Val Asn Gly Lys Trp Met Arg Glu Leu Ile Leu Tyr Asp
            100                 105                 110

Lys Glu Glu Ile Arg Arg Ile Trp Arg Gln Ala Asn Asn Gly Asp Asp
        115                 120                 125

Ala Thr Ala Gly Leu Thr His Met Met Ile Trp His Ser Asn Leu Asn
    130                 135                 140

Asp Ala Thr Tyr Gln Arg Thr Arg Ala Leu Val Arg Thr Gly Met Asp
145                 150                 155                 160

Pro Arg Met Cys Ser Leu Met Gln Gly Ser Thr Leu Pro Arg Arg Ser
                165                 170                 175
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Gly Ala Ala Gly Ala Ala Val Lys Gly Val Gly Thr Met Val Met Glu
            180                 185                 190

Leu Val Arg Met Ile Lys Arg Gly Ile Asn Asp Arg Asn Phe Trp Arg
        195                 200                 205

Gly Glu Asn Gly Arg Lys Thr Arg Ile Ala Tyr Glu Arg Met Cys Asn
    210                 215                 220

Ile Leu Lys Gly Lys Phe Gln Thr Ala Ala Gln Lys Ala Met Met Asp
225                 230                 235                 240

Gln Val Arg Glu Ser Arg Asn Pro Gly Asn Ala Glu Phe Glu Asp Leu
                245                 250                 255

Thr Phe Leu Ala Arg Ser Ala Leu Ile Leu Arg Gly Ser Val Ala His
            260                 265                 270

Lys Ser Cys Leu Pro Ala Cys Val Tyr Gly Pro Ala Val Ala Ser Gly
        275                 280                 285

Tyr Asp Phe Glu Arg Glu Gly Tyr Ser Leu Val Gly Ile Asp Pro Phe
    290                 295                 300

Arg Leu Leu Gln Asn Ser Gln Val Tyr Ser Leu Ile Arg Pro Asn Glu
305                 310                 315                 320

Asn Pro Ala His Lys Ser Gln Leu Val Trp Met Ala Cys His Ser Ala
                325                 330                 335

Ala Phe Glu Asp Leu Arg Val Leu Ser Phe Ile Lys Gly Thr Lys Val
            340                 345                 350

Val Pro Arg Gly Lys Leu Ser Thr Arg Gly Val Gln Ile Ala Ser Asn
        355                 360                 365

Glu Asn Met Glu Thr Met Glu Ser Ser Thr Leu Glu Leu Arg Ser Arg
    370                 375                 380

Tyr Trp Ala Ile Arg Thr Arg Ser Gly Gly Asn Thr Asn Gln Gln Arg
385                 390                 395                 400

Ala Ser Ala Gly Gln Ile Ser Ile Gln Pro Thr Phe Ser Val Gln Arg
                405                 410                 415

Asn Leu Pro Phe Asp Arg Thr Thr Val Met Ala Ala Phe Thr Gly Asn
            420                 425                 430

Thr Glu Gly Arg Thr Ser Asp Met Arg Thr Glu Ile Ile Arg Met Met
        435                 440                 445

Glu Ser Ala Arg Pro Glu Asp Val Ser Phe Gln Gly Arg Gly Val Phe
    450                 455                 460

Glu Leu Ser Asp Glu Lys Ala Ala Ser Pro Ile Val Pro Ser Phe Asp
465                 470                 475                 480

Met Ser Asn Glu Gly Ser Tyr Phe Phe Gly Asp Asn Ala Glu Glu Tyr
                485                 490                 495

Asp Asn


<210> SEQ ID NO 19
<211> LENGTH: 252
<212> TYPE: PRT
<213> ORGANISM: Influenza virus

<400> SEQUENCE: 19

Met Ser Leu Leu Thr Glu Val Glu Thr Tyr Val Leu Ser Ile Ile Pro
1               5                   10                  15

Ser Gly Pro Leu Lys Ala Glu Ile Ala Gln Arg Leu Glu Asp Val Phe
            20                  25                  30

Ala Gly Lys Asn Thr Asp Leu Glu Val Leu Met Glu Trp Leu Lys Thr
        35                  40                  45
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Arg Pro Ile Leu Ser Pro Leu Thr Lys Gly Ile Leu Gly Phe Val Phe
    50                  55                  60

Thr Leu Thr Val Pro Ser Glu Arg Gly Leu Gln Arg Arg Arg Phe Val
65                  70                  75                  80

Gln Asn Ala Leu Asn Gly Asn Gly Asp Pro Asn Asn Met Asp Lys Ala
                85                  90                  95

Val Lys Leu Tyr Arg Lys Leu Lys Arg Glu Ile Thr Phe His Gly Ala
            100                 105                 110

Lys Glu Ile Ser Leu Ser Tyr Ser Ala Gly Ala Leu Ala Ser Cys Met
        115                 120                 125

Gly Leu Ile Tyr Asn Arg Met Gly Ala Val Thr Thr Glu Val Ala Phe
    130                 135                 140

Gly Leu Val Cys Ala Thr Cys Glu Gln Ile Ala Asp Ser Gln His Arg
145                 150                 155                 160

Ser His Arg Gln Met Val Thr Thr Thr Asn Pro Leu Ile Arg His Glu
                165                 170                 175

Asn Arg Met Val Leu Ala Ser Thr Thr Ala Lys Ala Met Glu Gln Met
            180                 185                 190

Ala Gly Ser Ser Glu Gln Ala Ala Glu Ala Met Glu Val Ala Ser Gln
        195                 200                 205

Ala Arg Gln Met Val Gln Ala Met Arg Thr Ile Gly Thr His Pro Ser
    210                 215                 220

Ser Ser Ala Gly Leu Lys Asn Asp Leu Leu Glu Asn Leu Gln Ala Tyr
225                 230                 235                 240

Gln Lys Arg Met Gly Val Gln Met Gln Arg Phe Lys
                245                 250
```

<210> SEQ ID NO 20
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 20

cccatcgata ccatggagag gataaaagaa ttacgagatc 40

<210> SEQ ID NO 21
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 21

ctagctagcc tactaattga tggccatccg aattcttttg 40

<210> SEQ ID NO 22
<211> LENGTH: 38
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 22

tacgagctca ccatggatgt caatccgact ttacttttt 38

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<210> SEQ ID NO 23
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 23

ctagctagcc tactattttt gccgtctgag ttcttcaatg 40

<210> SEQ ID NO 24
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 24

cccatcgata ccatggaaga ctttgtgcga caatgc 36

<210> SEQ ID NO 25
<211> LENGTH: 39
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 25

ctagctagcc tactatttca gtgcatgtgc gaggaagga 39

<210> SEQ ID NO 26
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 26

ttcatcgata ccatggcgtc tcaaggcacc aaac 34

<210> SEQ ID NO 27
<211> LENGTH: 40
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: A synthetic oligonucleotide

<400> SEQUENCE: 27

cgcgctagcc tattaattgt catactcctc tgcattgtct 40

What is claimed is:

1. An isolated recombinant influenza virus having PA, PB1, PB2, NP, NS, M, NA, and HA viral segments, wherein i) at least one of the viral segments is a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, wherein the recombinant influenza virus has enhanced stability and/or enhanced replication relative to a corresponding recombinant influenza virus with a residue at position 540 in PB2 that is asparagine, a residue at position 180 in PA that is glutamine, a residue at position 200 in PA that is threonine, a residue at position 149 in PB1 that is valine, a residue at position 684 in PB1 that is glutamic acid or a residue at position 685 in PB1 that is aspartic acid; ii) at least one of the viral segments is a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, and wherein at least one of the other viral segments is a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, wherein the recombinant influenza virus has enhanced stability and/or enhanced replication relative to a corresponding recombinant influenza virus with a residue at position 540 in PB2

that is asparagine, a residue in PB2 at position 712 that is glutamic acid, a residue at position 180 in PA that is glutamine, a residue at position 200 in PA that is threonine, a residue at position 149 in PB1 that is valine, a residue at position 684 in PB1 that is glutamic acid or a residue at position 685 in PB1 that is aspartic acid; or iii) the recombinant virus has two or more viral segments comprising a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, wherein the recombinant influenza virus has enhanced stability and/or enhanced replication relative to a corresponding recombinant influenza virus with a residue at position 540 in PB2 that is asparagine, a residue in PB2 at position 712 that is glutamic acid, a residue at position 180 in PA that is glutamine, a residue at position 200 in PA that is threonine, a residue at position 149 in PB1 that is valine, a residue at position 684 in PB1 that is glutamic acid or a residue at position 685 in PB1 that is aspartic acid.

2. The virus of claim **1** wherein the residue at position 540 of PB2 is K, R, D, E, Q, or H, the residue at position 712 of PB2 is D, N, Q, S, H, T, Y, or C, the residue at position 180 in PA is R, K, D, E, N, or H, the residue at position 200 in PA is A, I, L, C, S, M, F, P, G, or V, the residue at position 149 in PB1 is A, T, I, L, C, S, M, F, P, or G, the residue at position 684 is D, Q, S, H, T, Y, C, K, R, or N, or the residue at position 685 in PB1 is E, N, R, H, K, S, T, Y, C, or Q; the residue at position 540 of PB2 is K, R, H, D, S, H, T, Y, or C, the residue at position 712 of PB2 is D, K, H, R, Q, or N, the residue at position 180 in PA is R, K, D, N, S, H, T, Y, or H, the residue at position 200 in PA is A, I, L, G, S, M, or V, the residue at position 149 in PB1 is A, T, I, L, S, M, or G, the residue at position 684 is D, Q, H, L, R or N, or the residue at position 685 in PB1 is E, N, R, H, K or Q; or the residue at position 540 of PB2 is K, R or H, the residue at position 712 of PB2 is D or N, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q.

3. The virus of claim **1** wherein the PB2 has a residue at position 540 that is not asparagine, the PA has a residue at position 180 that is not glutamine and a residue at position 200 that is not threonine, and the PB1 has a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid; the PB2 has a residue at position 540 that is not asparagine, the PA has a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, and the PB1 has a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid; the PB2 has a residue at position 540 that is not asparagine or a residue at 712 that is not aspartic acid, the PA has a residue at position 180 that is not glutamine and a residue at position 200 that is not threonine, and the PB1 has a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid; or the PB2 has a residue at position 540 that is not asparagine and a residue at 712 that is not aspartic acid, the PA has a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, and the PB1 has a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid.

4. The virus of claim **1** wherein the PA further comprises a residue at position 443 that is not arginine, the PB1 further comprises a residue at position 737 that is not lysine, the PB2 further comprises a residue at position 25 that is not valine or a residue at position 712 that is not glutamic acid, the NS viral segment encodes a NS1 with a residue at position 167 that is not proline, the HA viral segment encodes a HA with a residue at position 380 that is not threonine, or any combination thereof.

5. The virus of claim **4** wherein the residue at position 443 of PA is K or H, the residue at position 737 of PB1 is H or R, the residue at position 25 of PB2 is A, L, T, I, or G, the residue at position 712 of PB2 is D, the residue at position 167 of NS1 is S, C, M, A, L, I, G or T, or any combination thereof.

6. The virus of claim **1** wherein at least one of the viral segments includes a heterologous gene sequence encoding a gene product.

7. The recombinant virus of claim **6** wherein the heterologous sequence is in the NS viral segment, M viral segment, NP viral segment, PA viral segment, PB1 viral segment, or the PB2 viral segment.

8. A vaccine having the isolated recombinant virus of claim **1**.

9. The vaccine of claim **8** wherein the virus encodes a non-influenza microbial protein, a heterologous influenza protein or a cancer associated antigen.

10. A plurality of influenza virus vectors for preparing a reassortant, comprising

a) a vector for vRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA production comprising a promoter operably linked to an influenza virus NS cDNA linked to a transcription termination sequence, wherein the PB1, PB2, or PA DNAs in the vectors for vRNA production encode at least one of: a PB2 viral segment encoding PB2 with residue at position 540 that is not asparagine, a PA viral segment encoding PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 viral segment encoding PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or a combination thereof; and optionally

b) 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.

11. The vectors of claim **10** wherein the PB1, PB2, PA, NP, NS, and M DNAs in the vectors for vRNA 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.

12. The vectors of claim **10** wherein the residue at position 540 of PB2 is K, R or H, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q.

13. The vectors of claim **10** wherein at least one of the viral segments includes a heterologous gene sequence encoding a gene product.

14. A method to prepare influenza virus, comprising: contacting a cell with:

a vector for vRNA production comprising a promoter operably linked to an influenza virus PA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB1 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus PB2 DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus HA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NP DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus NA DNA linked to a transcription termination sequence, a vector for vRNA production comprising a promoter operably linked to an influenza virus M DNA linked to a transcription termination sequence, and a vector for vRNA production comprising a promoter operably linked to an influenza virus NS DNA linked to a transcription termination sequence, wherein the PB1, PB2, or PA DNAs in the vectors for vRNA production encode

i) a PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, and at least one: a PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, ii) a PB2 with residue at position 540 that is not asparagine, a PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof, or iii) two or more of: a PB2 with residue at position 540 that is not asparagine or a residue at position 712 that is not glutamic acid, a PA with a residue at position 180 that is not glutamine or a residue at position 200 that is not threonine, or a PB1 with a residue at position 149 that is not valine, a residue at position 684 that is not glutamic acid or a residue at position 685 that is not aspartic acid, or any combination thereof; and optionally

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.

15. The method of claim **14** wherein the cell is an avian cell or a mammalian cell.

16. The method of claim **15** wherein the cell is a Vero cell, a human cell or a MDCK cell.

17. The method of claim **14** wherein the wherein 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.

18. The method of claim **14** wherein the residue at position 540 of PB2 is K, R or H, the residue at position 712 of PB2 is D or N, the residue at position 180 in PA is R, K or H, the residue at position 200 in PA is A, I, L, G or V, the residue at position 149 in PB1 is A, T, I, L or G, the residue at position 684 is D or N, or the residue at position 685 in PB1 is E or Q.

19. The method of claim **14** wherein the influenza virus includes a heterologous gene sequence encoding a gene product.

20. The method of claim **19** wherein the heterologous sequence is 5' or 3' to the PA coding sequence in the PA viral segment, 5' or 3' to the PB1 coding sequence in the PB1 viral segment, 5' or 3' to the PB2 coding sequence in the PB2 viral segment or 5' or 3' to the NS1 coding sequence in the NS viral segment.

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