

**Table S1.** Summary of isolation of influenza A viruses (H1N1 and H1N2) from swine, June 2009 to February 2010, Hong Kong

Sampling occasion	Sample number	Influenza A positive	
		H1N1/2009	H1N1 / H1N2
11 Jun 2009	252	0	1
25 Jun 2009	252	0	1
9 Jul 2009	252	0	0
23 Jul 2009	252	0	3
13 Aug 2009	252	0	7
27 Aug 2009	252	0	0
10 Sep 2009	252	0	0
24 Sep 2009	252	0	0
8 Oct 2009	252	0	0
22 Oct 2009	252	2	1
5 Nov 2009	252	0	2
19 Nov 2009	252	0	0
3 Dec 2009	247	2	3
17 Dec 2009	244	5	3
7 Jan 2010	206	1	1
21 Jan 2010	180	0	0
4 Feb 2010	200	0	0
<b>TOTAL</b>	<b>4101</b>	<b>10</b>	<b>22</b>

**Table S2.** Antigenic analysis of influenza A viruses (H1N1/H1N2) by hemagglutination inhibition test

Serum	Antibody titers* to viral antigen				
	A/Brisbane/59/2007 (Seasonal H1N1)	A/California/4/2009 (Pandemic H1N1)	A/Sw/HK/201/2010 (Novel reassortant H1N1)	A/Sw/HK/NS29/2009 (EA lineage H1N1)	A/Sw/HK/4167/1999 (CS lineage H1N1)
Human post H1N1/2009 vaccine (Patient A)	<10	160	<10	– <sup>#</sup>	–
Human post H1N1/2009 vaccine (Patient B)	10	320	320	–	–
Human post H1N1/2009 vaccine (Patient C)	320	80	<10	–	–
Human post H1N1/2009 infection (Patient D) acute	<10	<10	<10	–	–
Human post H1N1/2009 infection (Patient D) convalescent	<10	160	40	–	–
Human post H1N1/2009 infection (Patient E) acute	<10	<10	<10	–	–
Human post H1N1/2009 infection (Patient E) convalescent	20	160	10	–	–
Ferret anti-A/California/4/2009 serum	<10	<u>1280</u>	<10	80	2560
Ferret anti-A/swine/Hong Kong/NS29/2009 serum	<10	160	10240	<u>5120</u>	1280
Ferret anti-A/swine/Hong Kong/4167/1999 serum	<20	5120	160	640	<u>20480</u>

\*Reciprocal antibody titers are presented. <sup>#</sup>– indicates test not done. Underline text indicates homologous titers. Abbreviations: CS, classical swine; EA, European avian-like; HK, Hong Kong; Sw, swine.

**Fig. S1.** Maximum likelihood phylogenies of the **(A–H)** H1-HA, N1-NA, PB2, PB1, PA, NP, M and NS genes, respectively, of representative influenza A viruses. \* denotes phylogenetic position of the novel reassortant virus A/swine/Hong Kong/201/2010. Only bootstrap supports for major swine H1N1/H1N2 and H1N1/2009 lineages (>70%) are shown. Bar represents nucleotide substitutions per site.

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