



## Supporting Online Material for

### **Reassortment of Pandemic H1N1/2009 Influenza A Virus in Swine**

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## Supporting Online Material for

### **Transmission and reassortment of pandemic H1N1/2009 influenza A virus in swine**

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### **Materials and Methods**

Tracheal or nasal swabs were taken fortnightly from slaughtered swine at an abattoir in Hong Kong. Swab materials were inoculated into 9-to-10-day old chicken embryonated eggs and MDCK cells, and virus isolates identified and subtyped by hemagglutination inhibition (HI) assays as previously described (*SI*).

Post-H1N1/2009 vaccination (n=3), acute and convalescent post-H1N1/2009 infection human sera (n=2) and a ferret antiserum to A/California/4/09 were tested by HI assay for

reactivity to the viral antigens A/Brisbane 59/2007 (seasonal influenza H1N1), A/California/4/2009 (H1N1/2009) and reassortant virus A/swine/Hong Kong/201/2010 (*S1*).

Viral RNA extraction, cDNA synthesis, PCR, and sequencing were carried out as described (*S2,S3*). The genetic composition of A/swine/Hong Kong/201/2010 was confirmed by direct PCR detection and re-sequencing of the 8 gene segments from the original swab specimen. Furthermore, the original swab specimen and virus isolate were screened with H1N1/2009 specific primers which confirmed the absence of H1N1/2009 HA and internal genes.

We compared 32 newly sequenced Hong Kong swine influenza genomes with all genomes available in GenBank representing influenza A diversity from human, swine and avian hosts. Phylogenetic trees were constructed for each genomic segment independently. A best-fit nucleotide substitution model (*S4*) was calculated and maximum likelihood phylogenies reconstructed using the program Garli 0.96 (*S5*). Phylogenetic support was calculated with 1000 neighbor-joining bootstrap replicates in PAUP\* 4.0 (*S6*).

To assess the infectivity and transmission of A/swine/Hong Kong/201/2010, five 4 to 6-week-old seronegative piglets were infected intranasally with  $10^6$  plaque forming units (PFU) of the virus in 0.6ml of Eagle's minimal essential Medium (MEM) and co-housed in the same cage with two naïve piglets. Two other piglets were mock infected with an equivalent volume of MEM. All animals were moved to the BSL-3 lab 4 days prior to infection and baseline body weights were established 3 days prior to infection. Body weights were recorded daily at approximately the same time (9:30-10:30 am) for each individual. Nasal and rectal swabs were collected daily from each piglet and placed into 0.6 ml of cold sterile phosphate buffered saline and stored at  $-80^{\circ}\text{C}$ . Viral RNA was extracted from the clarified swab supernatant using MagMAX<sup>TM</sup> 96 Viral RNA Isolation Kit (Applied Biosystems) on the MagMAX<sup>TM</sup> Express

(Applied Biosystems). cDNA synthesis and determination of influenza M gene copy number were carried out as described previously (S2, S7). A virus preparation was titrated with standard plaque assay to construct a ten-fold dilution series ( $10^1$ - $10^6$  PFU/ml) that was used to determine the relative equivalent units (REU) for viral infectivity based on the cycle threshold (Ct) values obtained (S8, S9).

Blood was collected via venipuncture of the anterior vena cava from pigs. Specific antibodies against A/swine/Hong Kong/201/2010 were tested by HI.

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**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	A/California/4/2009	A/Sw/HK/201/2010	A/Sw/HK/NS29/2009	A/Sw/HK/4167/1999
	(Seasonal H1N1)	(Pandemic H1N1)	(Novel reassortant H1N1)	(EA lineage H1N1)	(CS lineage H1N1)
Human post H1N1/2009 vaccine (Patient A)	<10	160	<10	#	–
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. #– indicates titer not tested. Underline text indicates homologous titers. Abbreviations: CS, classical

swine; EA, European avian-like; HK, Hong Kong; Sw, swine.

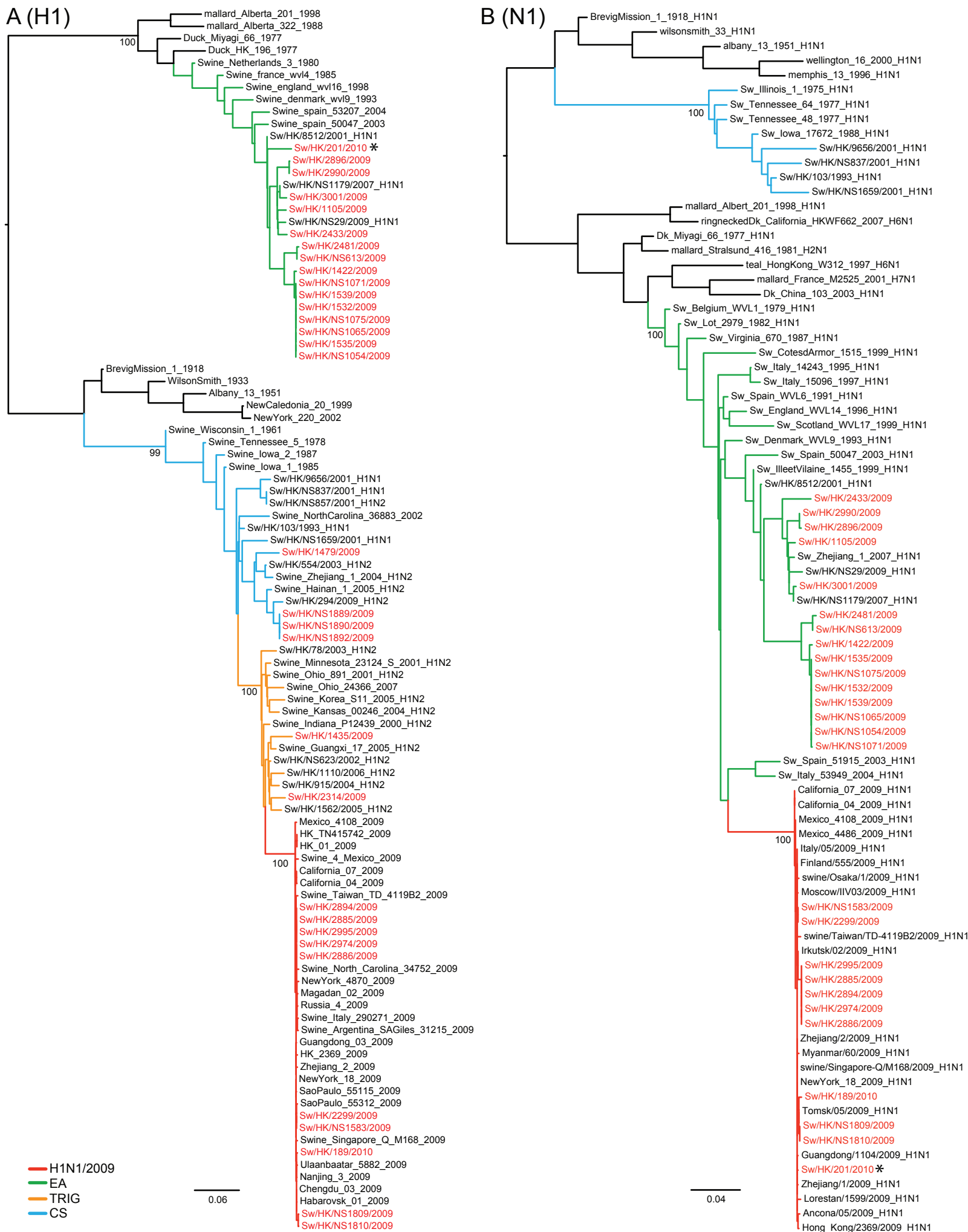
**Fig. S1.** Maximum likelihood phylogenies of the (A–H) H1-HA, N1-NA, PB2, PB1, PA, NP, M and NS genes, respectively, of representative influenza A viruses. \* denotes phylogenetic position of the novel reassortant virus A/swine/Hong Kong/201/2010. Only bootstrap supports for major swine H1N1/H1N2 and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

**Fig. S2.** Mean body weight changes of swine challenged or exposed to A/swine/Hong Kong/201/2010.

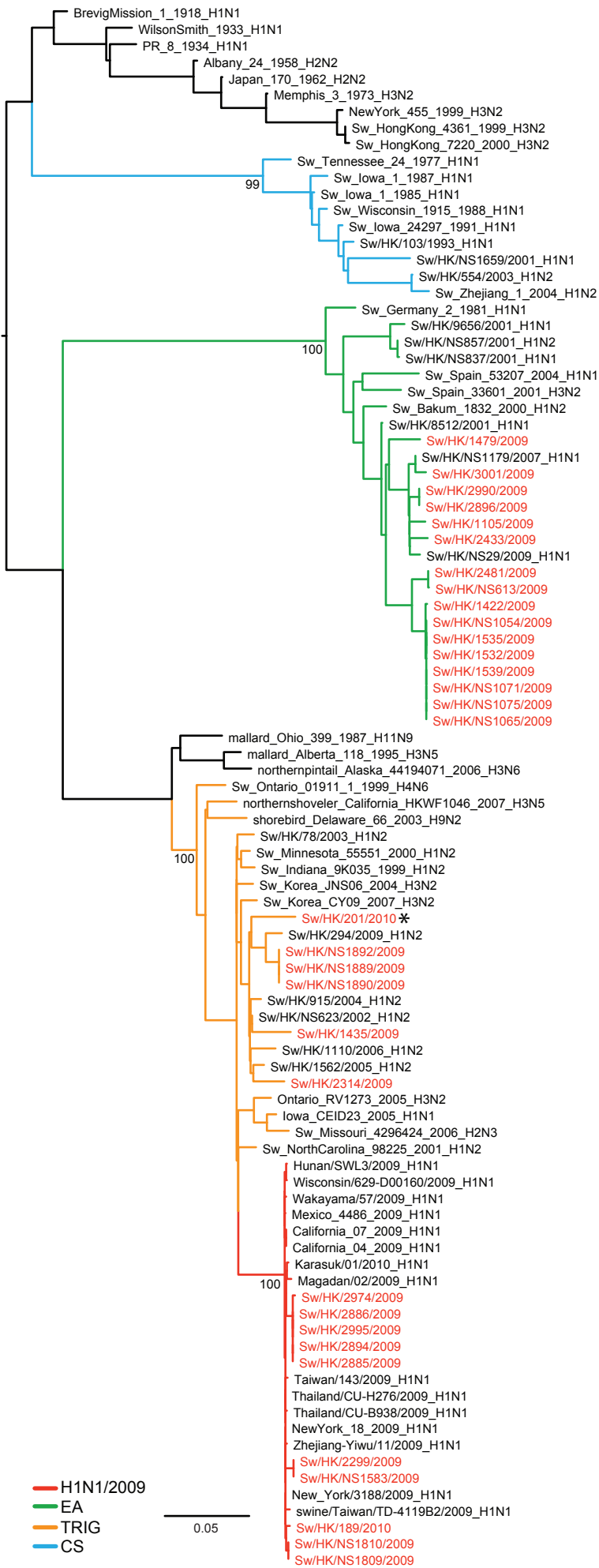
**Fig. S3.** Virus shedding of A/swine/Hong Kong/201/2010 in challenged or contact exposed swine. Virus shedding was not detected either in mock infected pigs or rectal swabs from any individual collected at any time point throughout the study. All infected and contact animals seroconverted to A/swine/Hong Kong/201/2010 (data not shown).



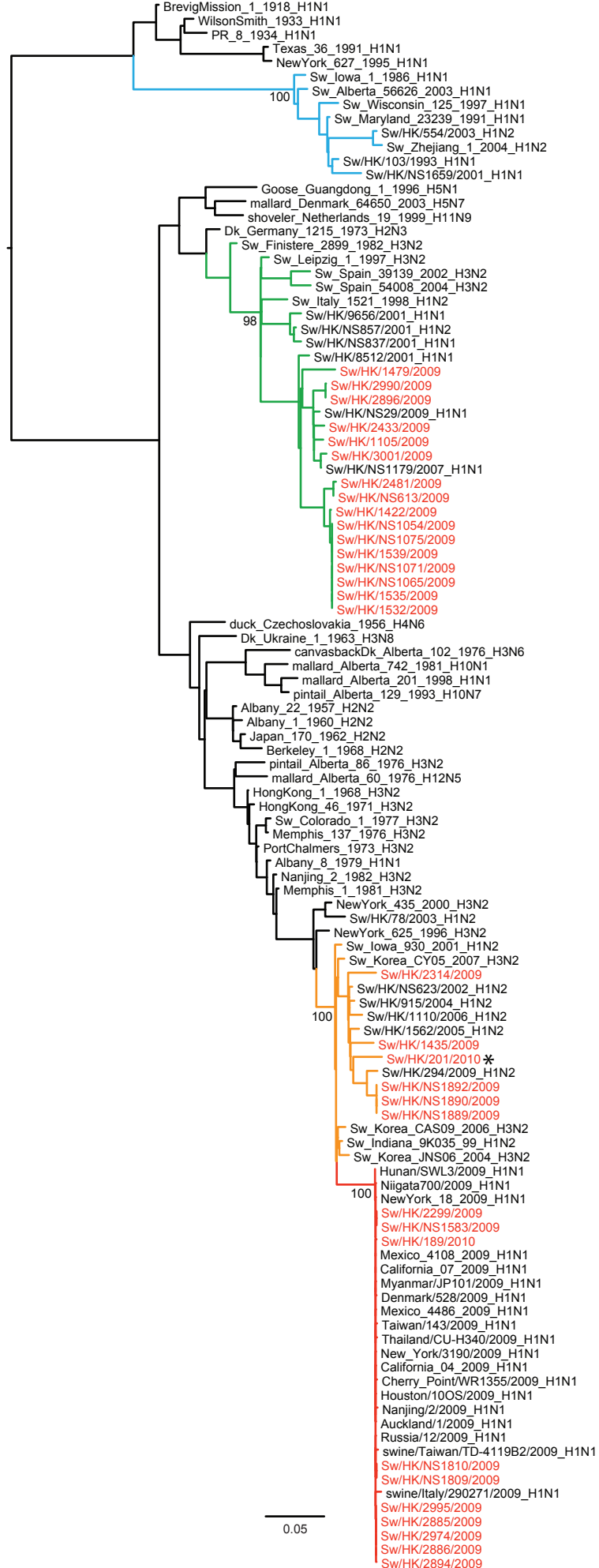
Figure S1



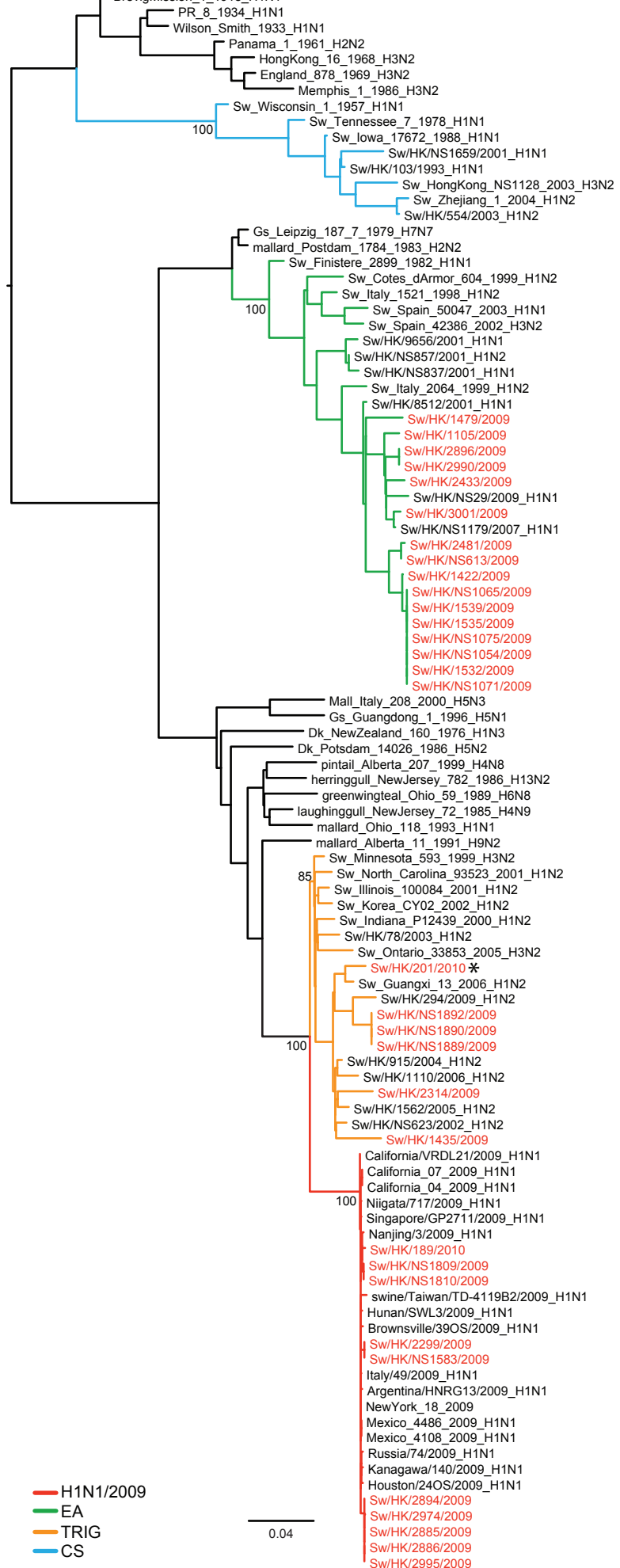
### C (PB2)



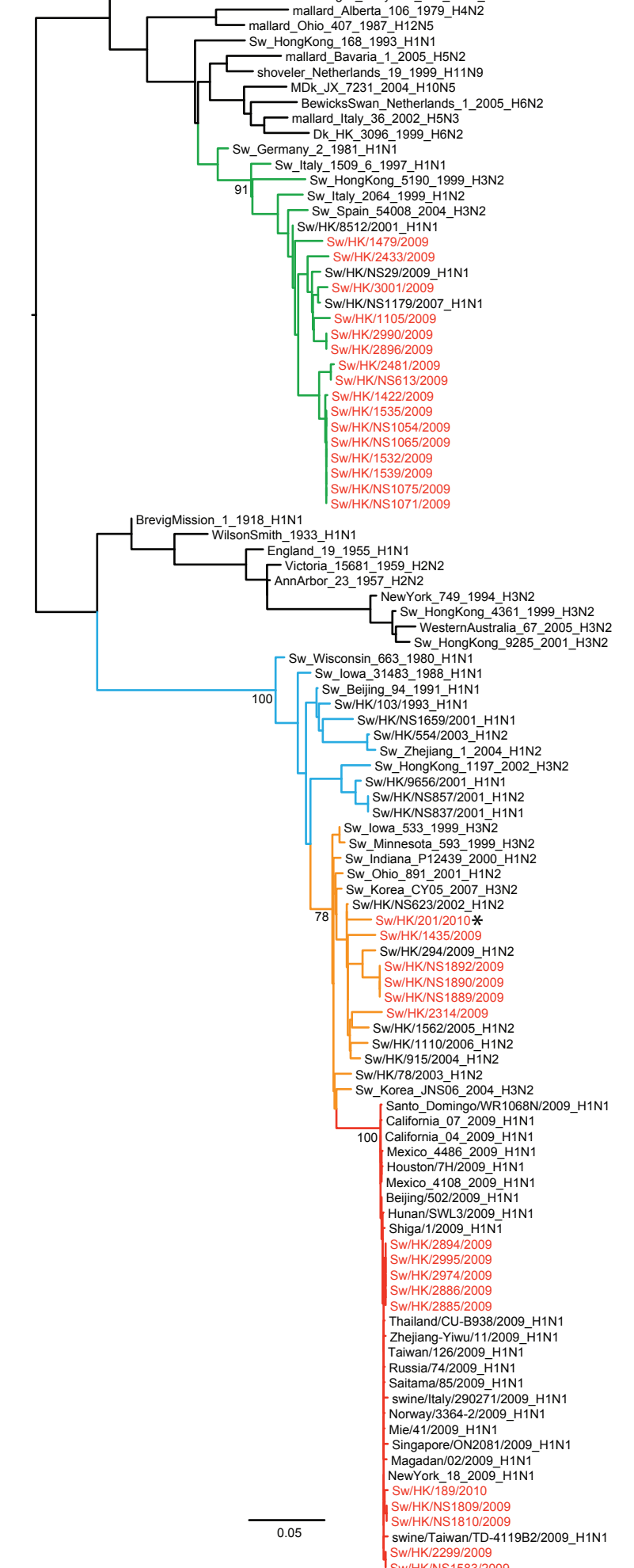
### D (PB1)



# E (PA)



# F (NP)

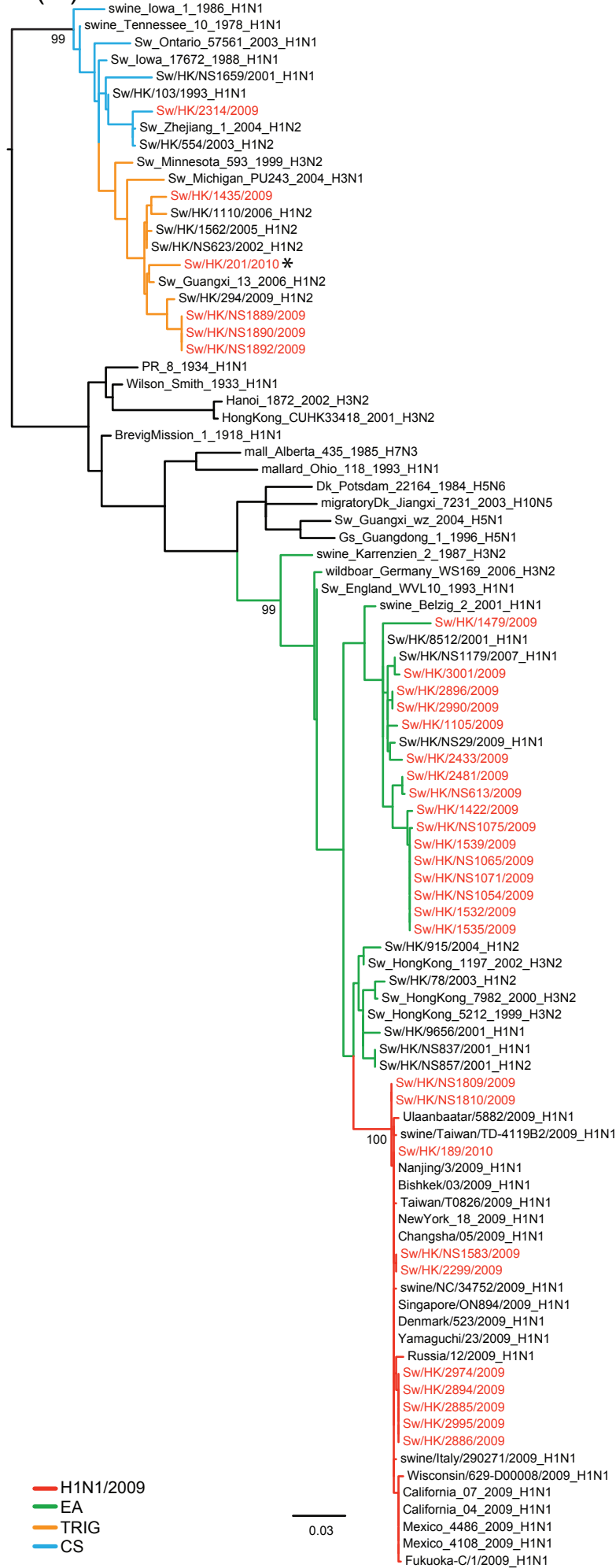


— H1N1/2009  
— EA  
— TRIG  
— CS

0.04

0.05

# G (M)



# H (NS)

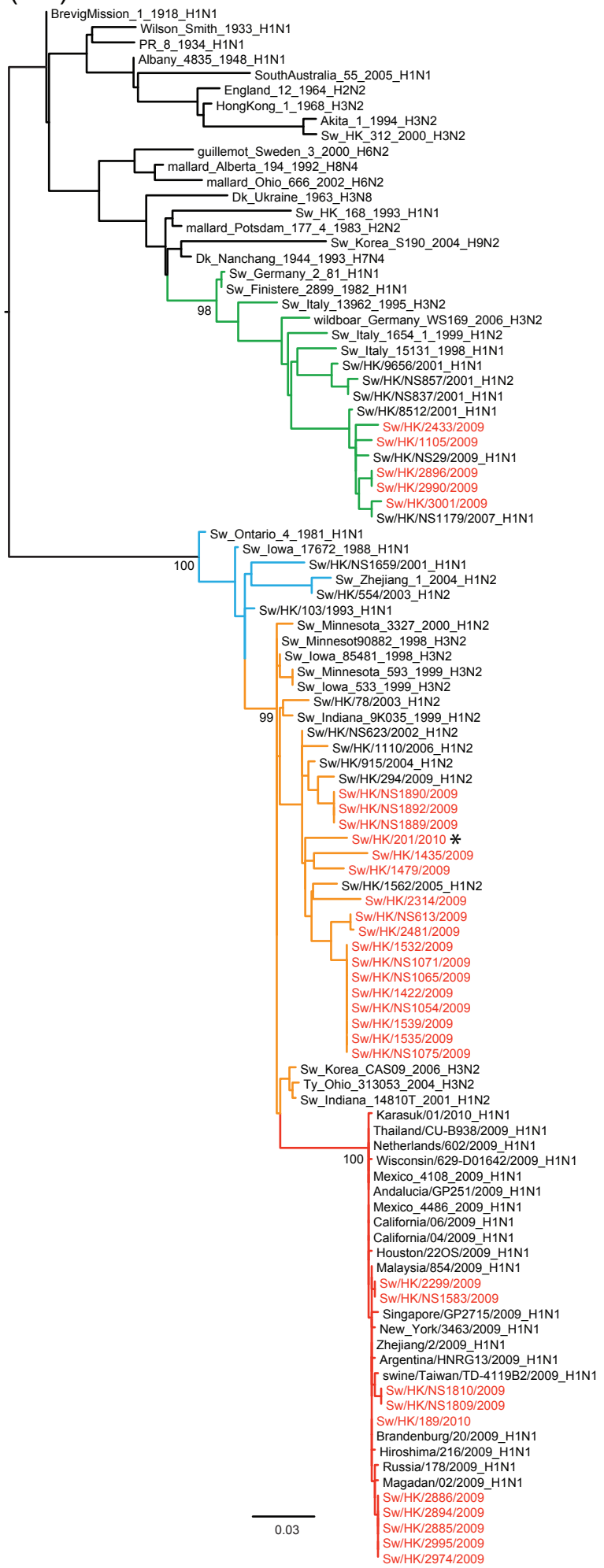


Figure S2

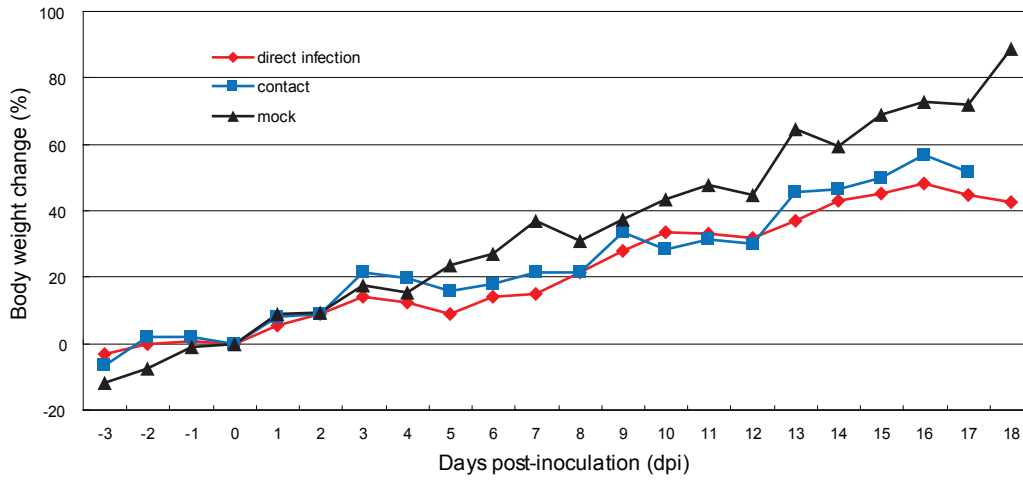


Figure S3

