

Supplementary material:

Table 1: GenBank number of some influenza virus

Influenza virus	GenBank Number							
	PB2	PB1	PA	HA	NP	NA	M	NS
A/California/04/2009(H1N1) [1,2]	FJ966079.1	FJ966080.1	FJ966081.1	FJ966082.1	FJ966083.1	FJ966084.1	FJ966085.1	FJ966086.1
A/Swine/Indiana/P12439/00(H1N2)[13]	AF455736.1	AF455728.1	AF455720.1	AF455680.1	AF455704.1	AF455696.1	AF455688.1	AF455712.1
A/Swine/Iowa/533/99(H3N2)[14]	AF251418.1	AF251413.1	AF251417.1	AF251411.1	AF251415.2	AF251412.3	AF251414.1	AF251416.1
A/Siena/3/1995(H3N2)	CY038510.1	CY038509.1	CY038508.1	CY038503.1	CY038506.1	CY038505.1	CY038504.1	CY038507.1
A/Turkey/Utah/24721-10/95(H7N3)	EU980473.1	EU980472.1	EU980471.1	EF470585.1	EU980470.1	EU980469.1	AF073201.1	AF074284.1
A/swine/England/WVL7/1992(H1N1)[15]	CY038004.1	CY038005.1	CY038006.1	CY038007.1	CY038008.1	CY038009.1	CY038010.1	CY038011.1
A/swine/California/T9001707/1991(H1N1)	CY028787.1	CY028786.1	CY028785.1	CY028780.1	CY028783.1	CY028782.1	CY028781.1	CY028784.1
A/New Jersey/1976(H1N1)[11]	CY021964.1	CY021963.1	CY021962.1	CY021957.1	CY021960.1	CY021959.1	CY021958.1	CY021961.1
A/duck/Germany/1215/1973(H2N3)[16]	CY014716.1	CY014715.1	CY014714.1	CY014710.1	CY014712.1	AY207522.1	CY014711.1	CY014713.1
A/swine/Jamesburg/1942(H1N1)	CY026434.1	CY026433.1	CY026432.1	CY026427.1	CY026430.1	CY026429.1	CY026428.1	CY026431.1
A/Brevig Mission/1/1918(H1N1) [8]	DQ208309.1	DQ208310.1	DQ208311.1	AF116575.1	AY744935.1	AF250356.2	AY130766.1	AF333238.1
A/Japan/305/1957(H2N2) [10]	CY045811.1	CY045810.1	CY045809.1	CY045804.1	CY045807.1	CY045806.1	CY045805.1	CY045808.1
A/Hong Kong/1/1968(H3N2) [10]	CY044268.1	CY044267.1	CY044266.1	CY044261.1	CY044264.1	CY044263.1	CY044262.1	CY044265.1

Table 2: Homology calculation of all the segment sequences of some influenza virus

Influence virus(strain)	homology of all the segment sequences								Influence virus(strain)
	PB2	PB1	PA	HA	NP	NA	M	NS	
A/California/07/2009(H1N1)	96.49%	96.17%	95.82%	95.30%	96.66%	51.98%	87.98%	95.11%	A/Swine/Indiana/P12439/00 (H1N2)
	83.99%	86.24%	86.75%	74.38%	84.00%	94.16%	919%	81.83%	A/swine/England/WVL7/1992(H1N1)
A/Swine/Indiana/P12439/00 (H1N2)	98.77%	98.77%	98.33%	52.44%	99.20%	98.79%	97.76%	97.85%	A/Swine/Iowa/533/99 (H3N2)
	86.75%	81.05%	84.33%	91.30%	86.84%	51.11%	90.91%	85.20%	A/New Jersey/1976(H1N1)
A/swine/England/WVL7/1992(H1N1)	84.82%	83.11%	84.15%	77.50%	86.55%	85.04%	90.94%	87.48%	A/swine/Jamesburg/1942(H1N1)
	94.56%	93.54%	89.03%	65.80%	94.44%	52.78%	94.62%	93.74%	A/duck/Germany/1215/1973(H2N3)
A/Swine/Iowa/533/99 (H3N2)	84.36%	98.81%	83.08%	97.65%	83.80%	98.01%	89.58%	82.94%	A/Siena/3/1995(H3N2)
	95.81%	88.35%	95.91%	54.58%	83.57%	54.94%	91.58%	86.52%	A/Turkey/Utah/24721-10/95 (H7N3)
	83.90%	80.18%	81.45%	53.40%	97.78%	52.34%	98.88%	97.28%	A/swine/California/T9001707/1991(H1N1)

Table 3: Whole genome sequence compare

Strain	1	2	3	4	5	6	7	8	9	10	11	12	13
1 A/California/04/2009(H1N1)	100%												
2 A/Swine/Indiana/P12439/00 (H1N2)	90.82%	100%											
3 A/Swine/Iowa/533/99 (H3N2)	85.29%	92.58%	100%										
4 A/Siena/3/1995 (H3N2)	78.32%	83.86%	90.02%	100%									
5 A/Turkey/Utah/24721-10/95 (H7N3)	80.94%	81.57%	82.59%	78.64%	100%								
6 A/swine/England/WVL7/1992 (H1N1)	85.42%	80.69%	78.05%	76.86%	79.95%	100%							
7 A/swine/California/T9001707/1991(H1N1)	85.86%	84.21%	79.15%	76.29%	76.37%	81.79%	100%						
8 A/New Jersey/1976 (H1N1)	84.57%	82.27%	77.41%	79.53%	78.36%	83.56%	90.19%	100%					
9 A/duck/Germany/1215/1973 (H2N3)	80.84%	81.23%	80.29%	78.23%	85.38%	85.36%	77.95%	79.77%	100%				
10 A/Hong Kong/1/1968 (H3N2)	77.93%	82.65%	87.68%	93.63%	79.78%	78.12%	77.00%	81.37%	79.09%	100%			
11 A/Japan/305/1957(H2N2)	79.38%	83.90%	82.64%	87.61%	79.90%	80.05%	79.02%	83.99%	84.78%	91.00%	100%		
12 A/swine/Jamesburg/1942(H1N1)	85.09%	82.43%	78.50%	78.50%	79.04%	84.31%	89.04%	91.31%	80.38%	79.72%	82.14%	100%	
13 A/Brevig Mission/1/1918 (H1N1)	85.14%	82.16%	79.65%	80.98%	80.98%	85.59%	87.66%	92.59%	81.52%	82.20%	84.35%	95.19%	100%