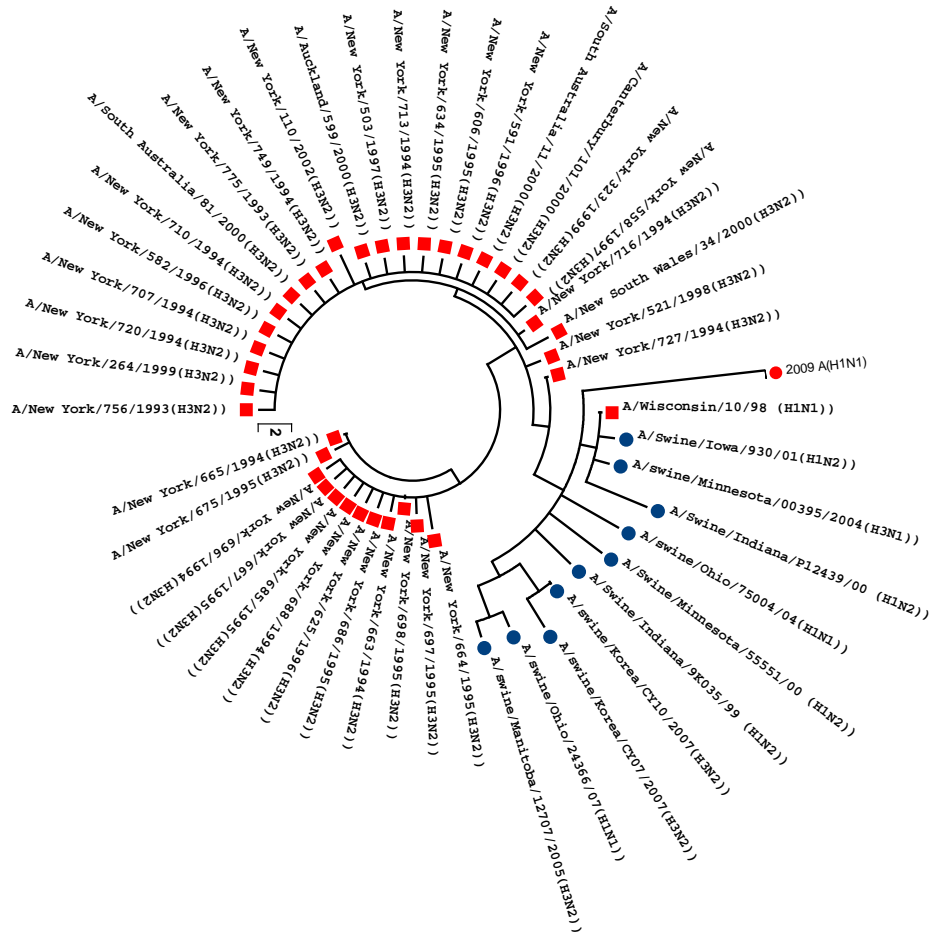


Supplementary Fig. 1. Possible origins of influenza 2009 A(H1N1) virus. **a**, PB2; **b**, PB1 and **c**, PA polymerases; **d**, hemagglutinin; **e**, nucleocapsid protein; **f**, neuraminidase; **g**, matrix protein 1; **h**, nonstructural protein 1. Protein sequences from the 2009 A(H1N1) virus were used for BLAST searches versus the all-species NCBI nr protein database. Top fifty best hits were retrieved from GenBank and used for phylogenetic tree reconstruction using the maximum parsimony method. Phylogenetic trees were constructed with the maximum parsimony method using the MEGA software version 4.0 and rooted using the earliest influenza virus isolates obtained with the analyses. The statistical significance of branch order was estimated by the generation of 100 replications of bootstrap resampling of the originally-aligned amino acid sequences. Scale bar indicates the number of changes over the whole sequence.

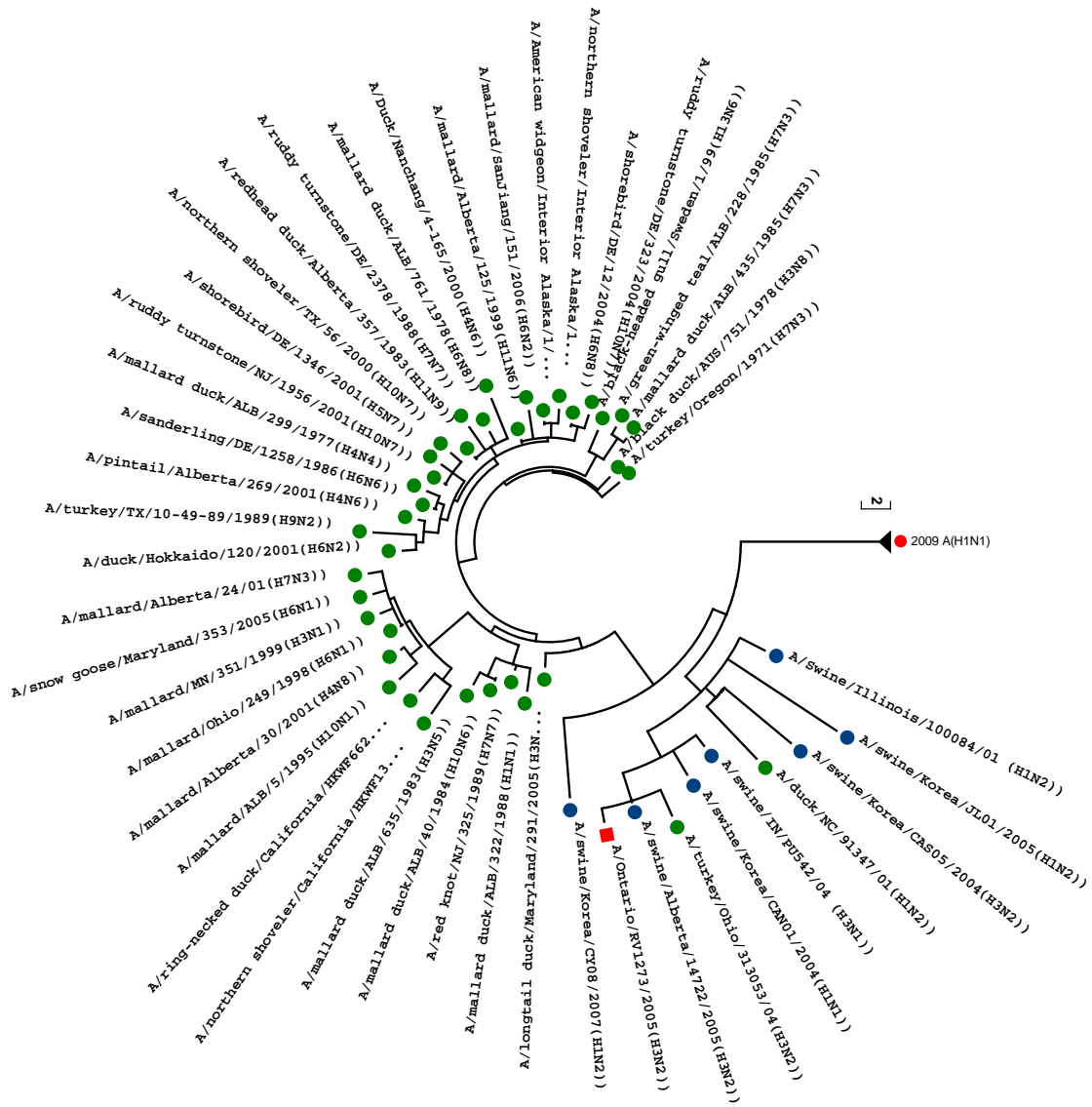
b

PB1



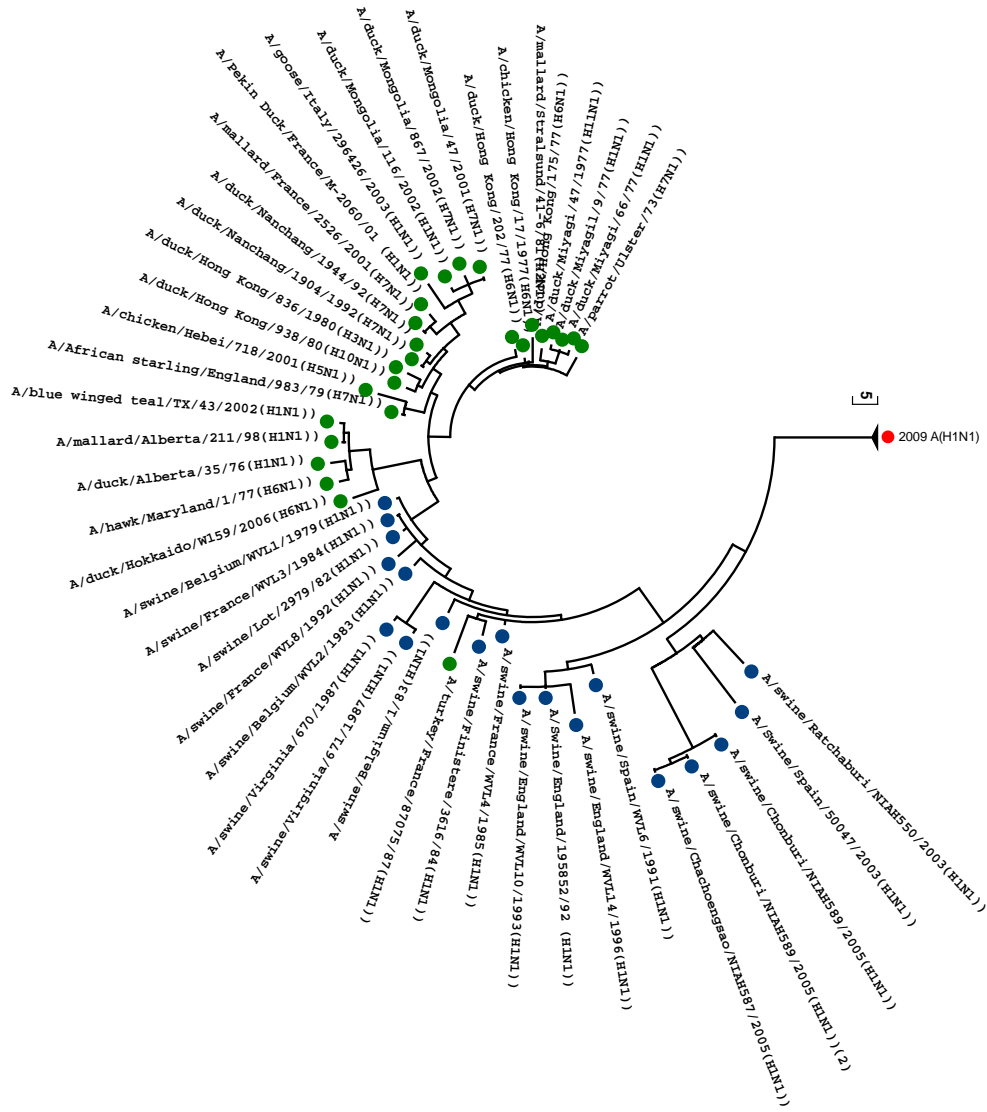
C

PA



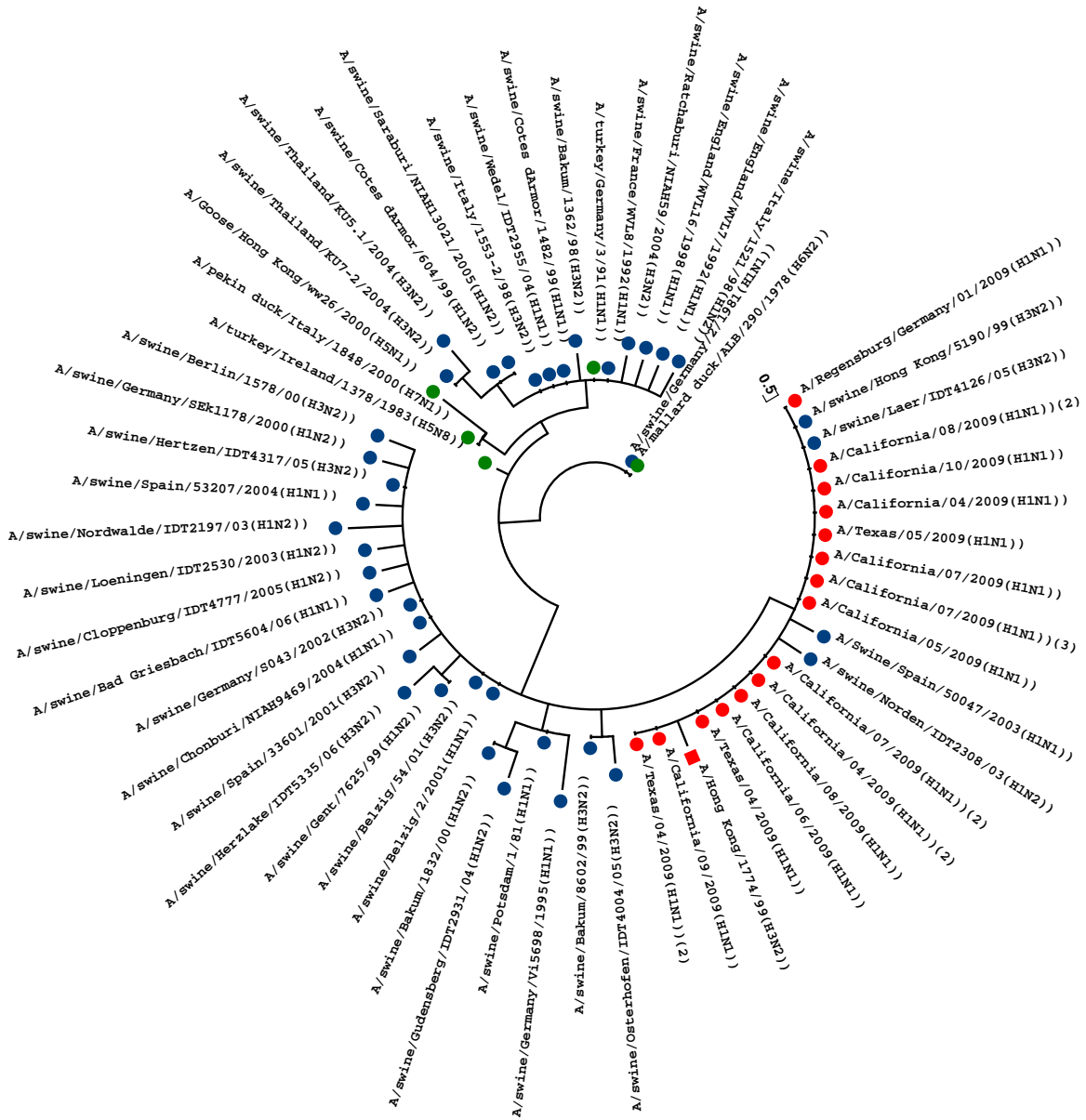
f

NA



g

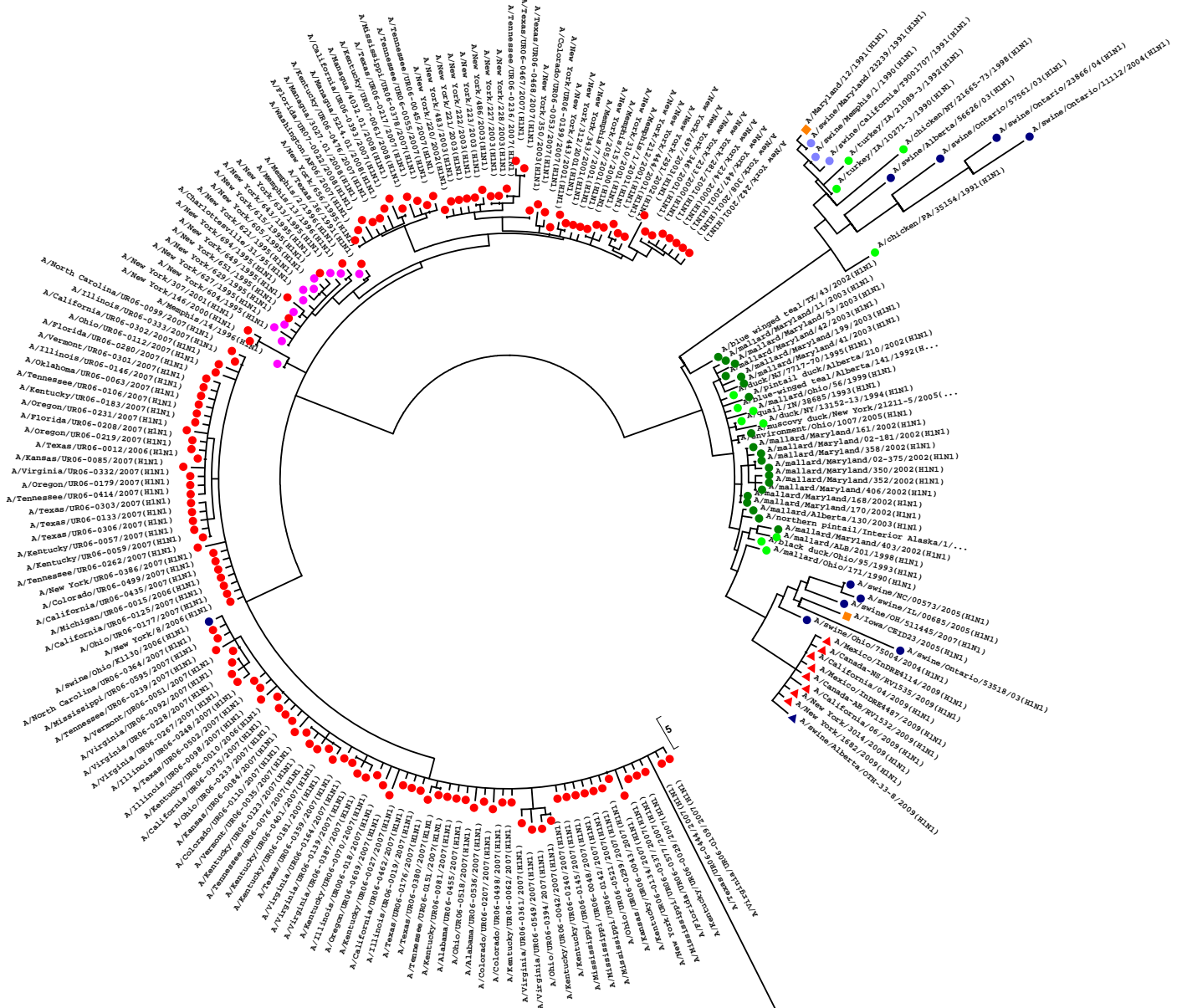
MP1



Supplementary Fig. 2. Genetic distinctness of the influenza 2009 A(H1N1) virus. **a**, PB2; **b**, PB1 and **c**, PA polymerases; **d**, hemagglutinin (HA); **e**, nucleocapsid protein (NP); **f**, neuraminidase (NA); **g**, matrix protein 1 (MP1); **h**, nonstructural protein 1 (NS1). Protein sequences from avian, swine and human influenza A (H1N1) viruses circulating in North-America from 1989 to 2009 were retrieved from the Influenza Virus Resource. Sequences were used for unrooted phylogenetic tree construction with the maximum parsimony method. Proteins from the influenza 2009 A(H1N1) virus (red triangles), earlier human (red and pink circles) swine (navy blue and purple circles) and avian (green circles) viruses are shown. Light colors (pink, purple and green) correspond to viruses found between 1989 and 1999 and dark colors (red, navy blue and green) to viruses found between 2000 and 2009. Orange squares represent pig-human interspecies transmission of influenza A cases occurred in Iowa, Maryland and Wisconsin, USA between 1991 and 2006. Scale bar indicates the number of changes over the whole sequence. Phylogenetic trees were constructed with the MEGA software version 4.0. The statistical significance of branch order was estimated by the generation of 100 replications of bootstrap resampling of the originally-aligned amino acid sequences. Scale bar indicates the number of changes over the whole sequence.

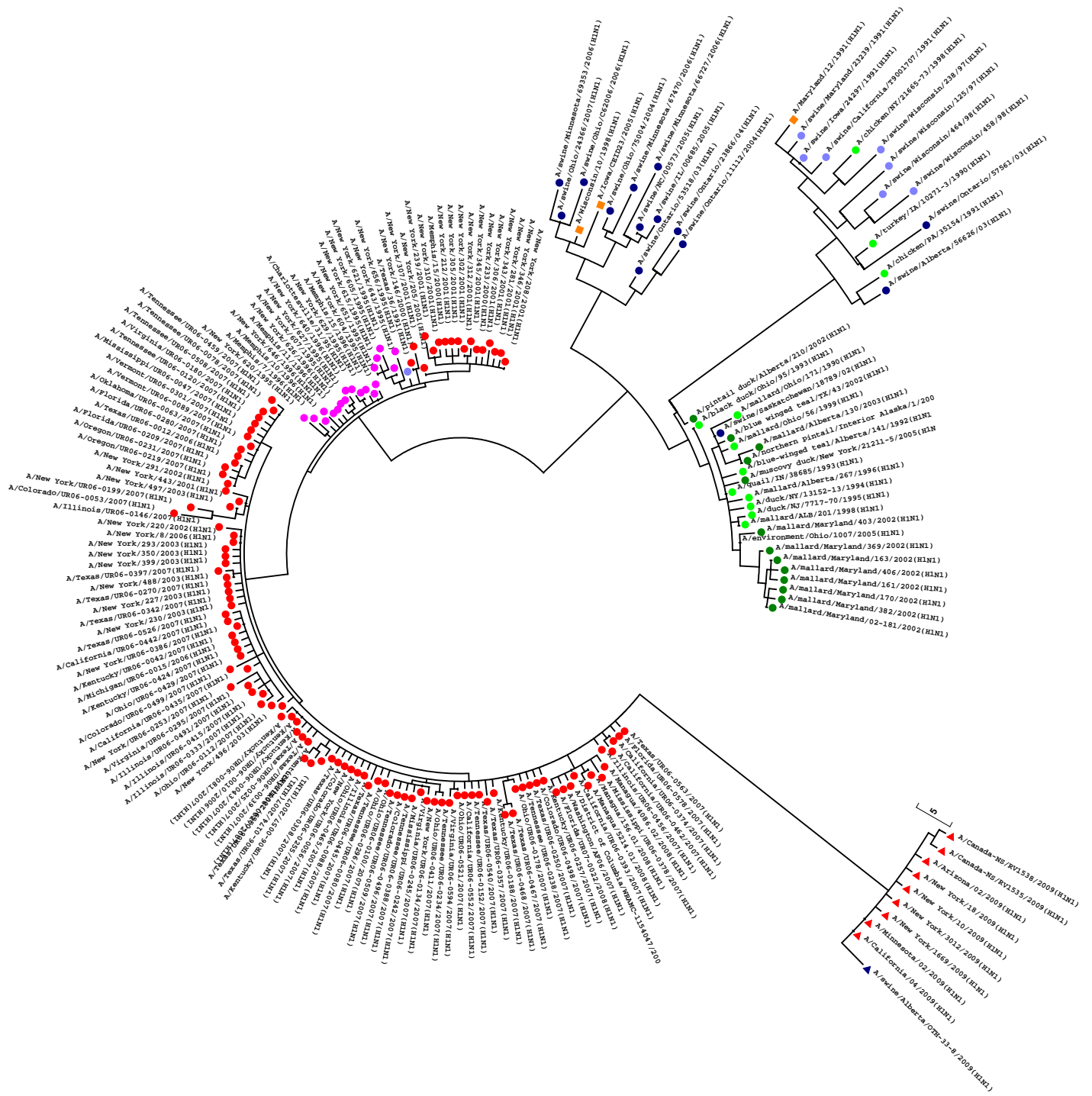
a

PB2



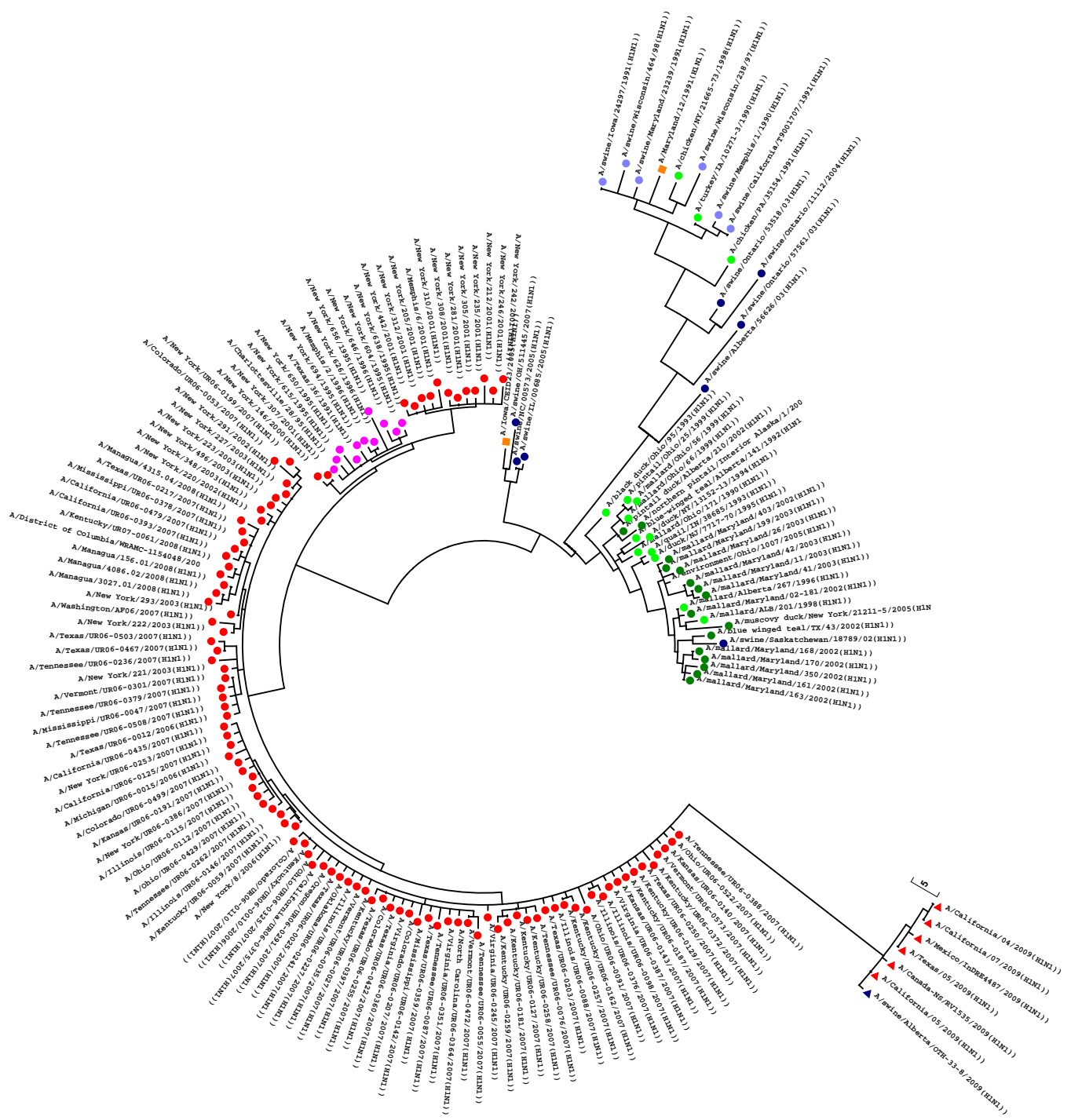
b

PB1



C

PA



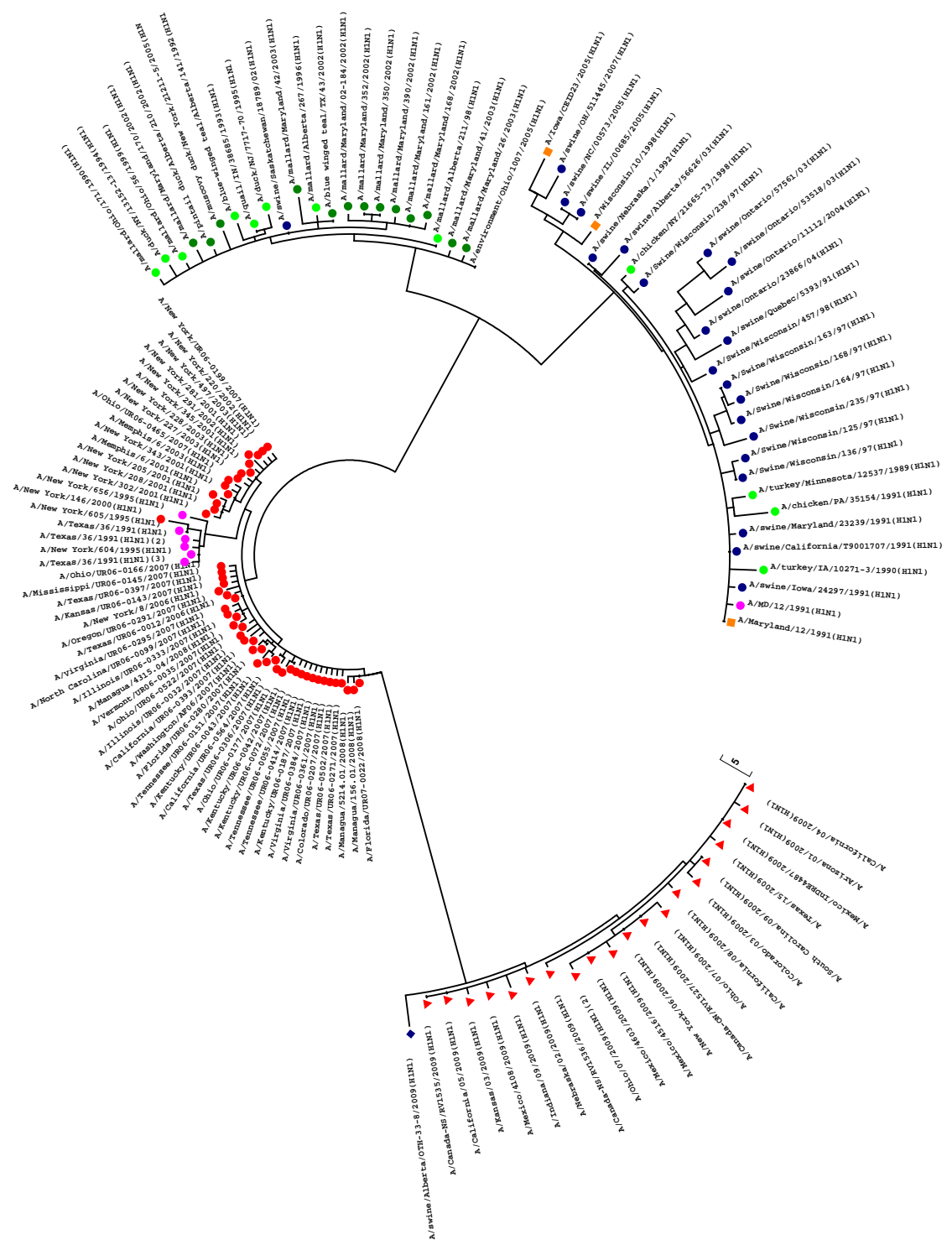
d

HA



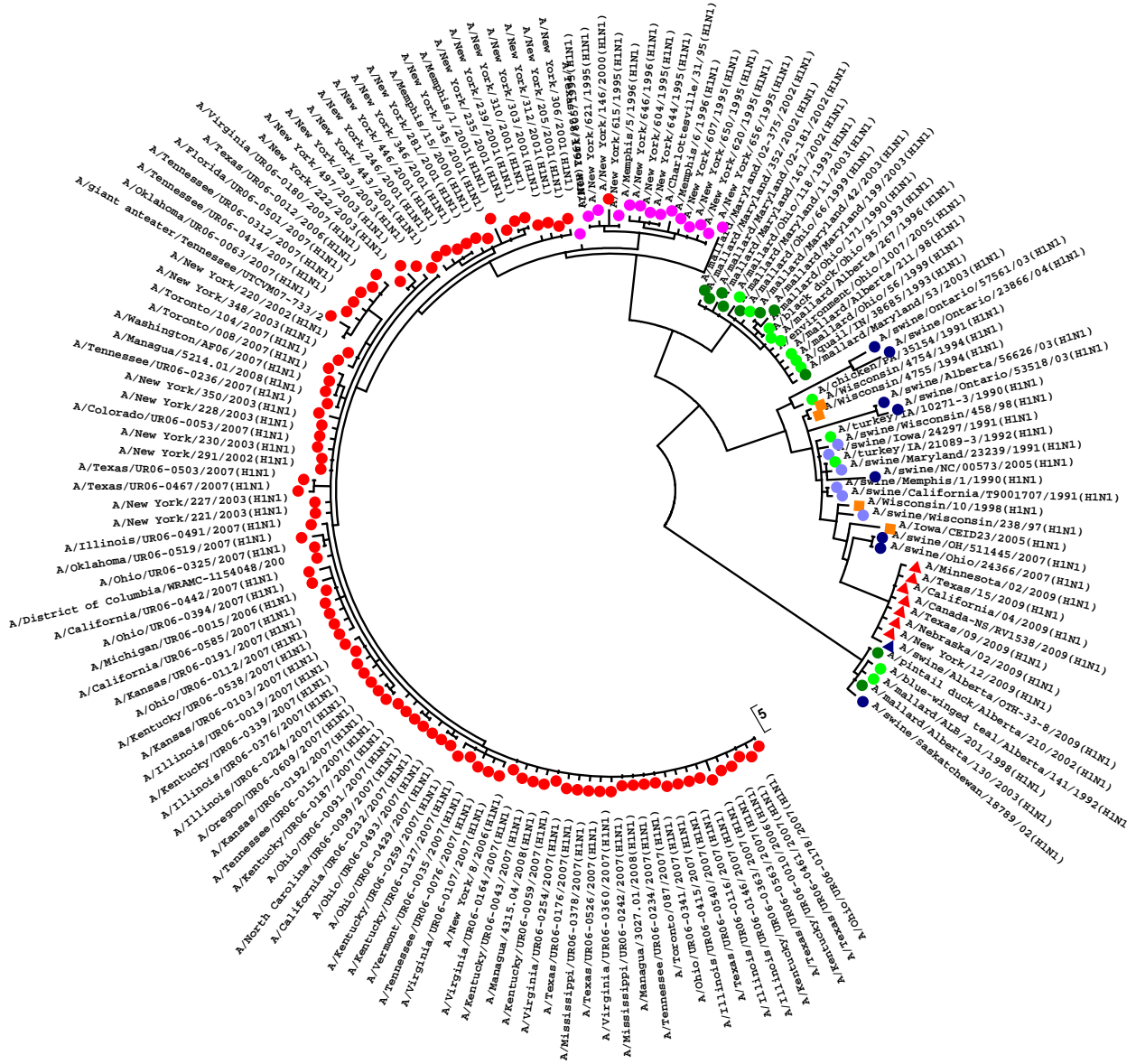
e

NP



h

NS1



Supplementary table 1. Closest protein homology of influenza 2009 A(H1N1) viruses

Gene	Best Hit	Identity	Lineage
PB2	A/Swine/Illinois/100085A/01 (H1N2)	98%	Swine
PB1	A/Wisconsin/10/98 (H1N1)	98%	Human
PA	A/Swine/Illinois/100084/01 (H1N2)	98%	Swine
HA	A/Swine/Indiana/P12439/00 (H1N2)	95%	Swine
NP	A/swine/Guangxi/13/2006 (H1N2)	98%	Swine
NA	A/swine/Spain/WVL6/1991 (H1N1)	94%	Swine
MP1	A/swine/Laer/IDT4126/05 (H3N2)	99%	Swine
NS1	A/SW/IN/14810-T/01 (H1N2)	94%	Swine

Supplementary table 2. Closest protein homology of influenza 2009 A(H1N1) viruses with swine influenza viruses that have infected humans

Protein	Cases	Identity	Lineage	Reference
PB2	A/Iowa/CEID23/2005(H1N1)	98%	Human	[1]
PB1	A/New York/727/1994(H3N2)	98%	Human	ABG48024
PA	A/Ontario/RV1273/2005(H3N2)	97%	Human	[2]
HA	A/Wisconsin/10/98 (H1N1)	93%	Human	AAO88265
NP	A/Iowa/CEID23/2005(H1N1)	97%	Human	[1]
	A/MD/12/1991(H1N1)	98%	Human	AAA51491
	A/Ohio/3559/1988(H1N1)	98%	Human	ABU80404
	A/Ohio/3523/1988(H1N1)	97%	Human	AAA73104
NA	Novel protein	Nf	Nf	Nf
MP1	A/Hong Kong/1774/99(H3N2)	99%	Human	[3]
NS1	/Wisconsin/10/1998(H1N1)	93%	Human	AAO88260
	A/Ontario/RV1273/2005(H3N2)	94%	Human	[2]

Nf = Not found

Supplementary table 3. Reported cases of pig-human interspecies transmission of influenza A (H1N1) occurred in Iowa, Maryland and Wisconsin, USA between 1991 and 2006. These influenza virus subtypes possess genetic distinctness compared to main cluster of human influenza A (H1N1) viruses

Influenza A virus subtype	Evidence linking pig-human infection	Reference
A/Iowa/CEID23/2005 (H1N1)	Yes	[1]
A/Wisconsin/10/1998	Insufficient data	[4]
A/Wisconsin/4754/1994	Yes	[5]
A/Maryland/12/1991	Yes	[5]
A/MD/12/1991	Yes	[5]
A/Wisconsin/4755/1994	Yes	[5]
A/Wisconsin/87/2005	Yes	[6]
A/Iowa/01/2006	Yes	[6]

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