Supporting Information

Smith et al. 10.1073/pnas.0904991106

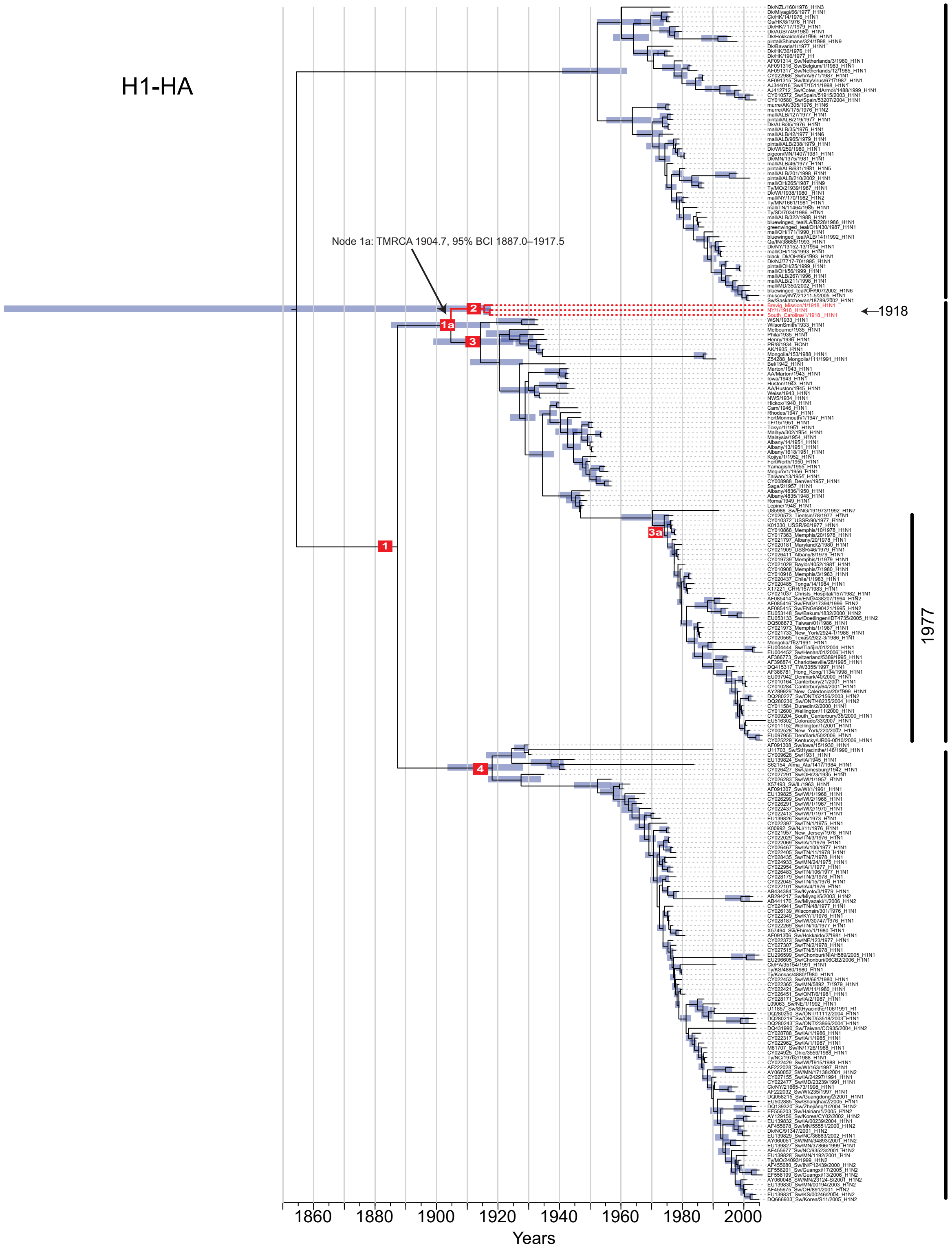

Fig. S1. Dated phylogeny of H1-HA genes of representative influenza A viruses isolated from birds, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

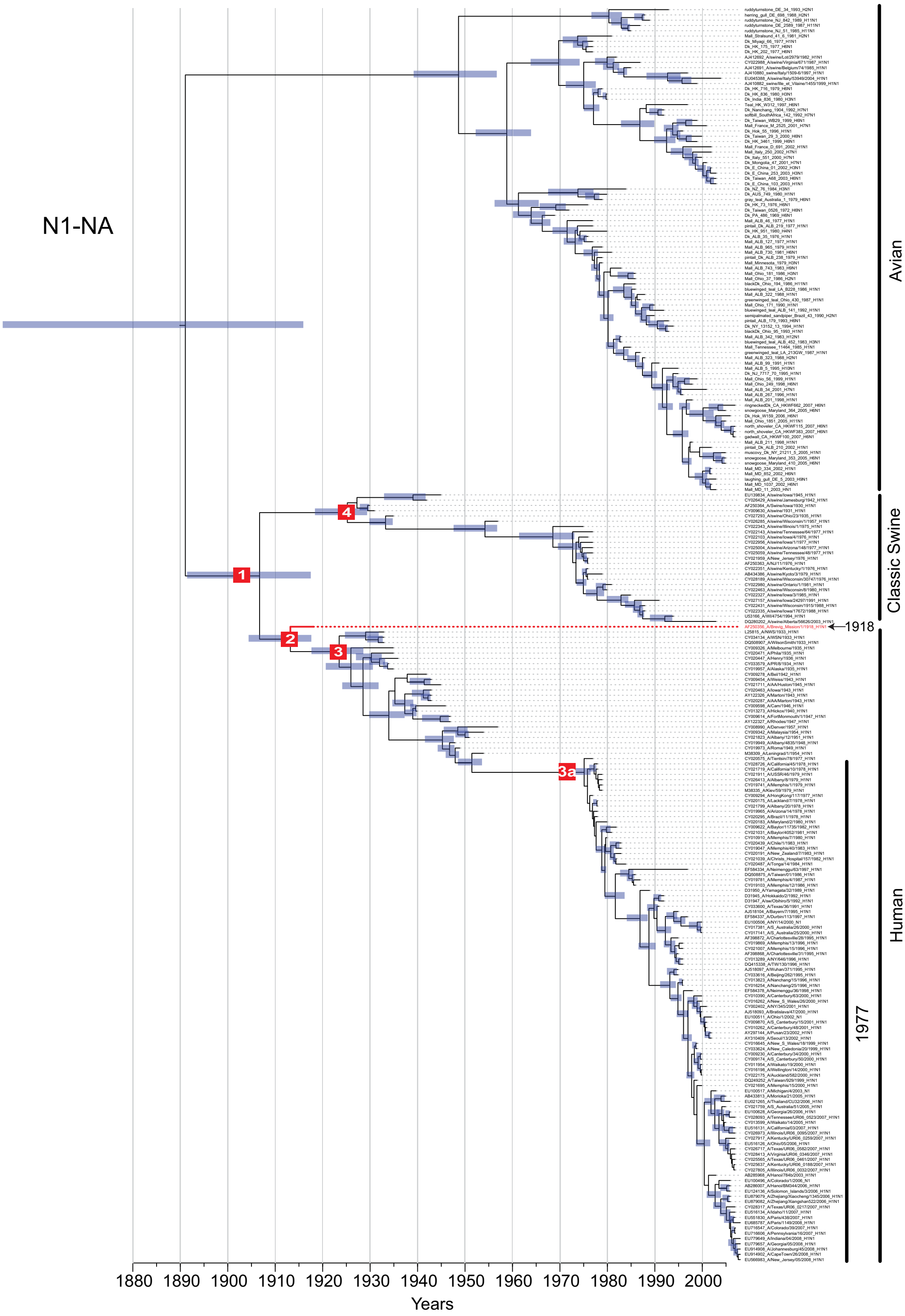

Fig. S2. Dated phylogeny of N1-NA genes of representative influenza A viruses isolated from birds, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

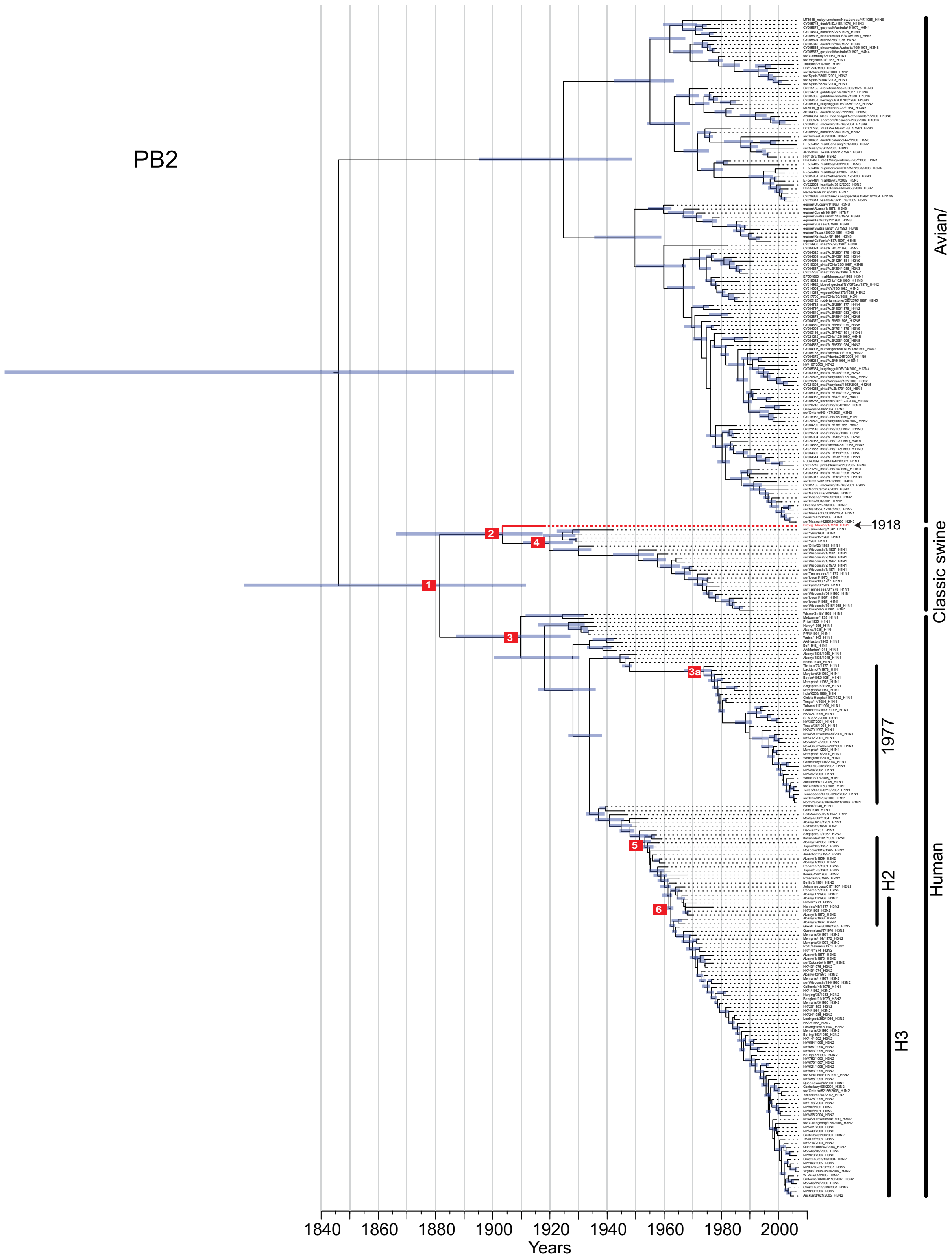

Fig. S3. Dated phylogeny of PB2 genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

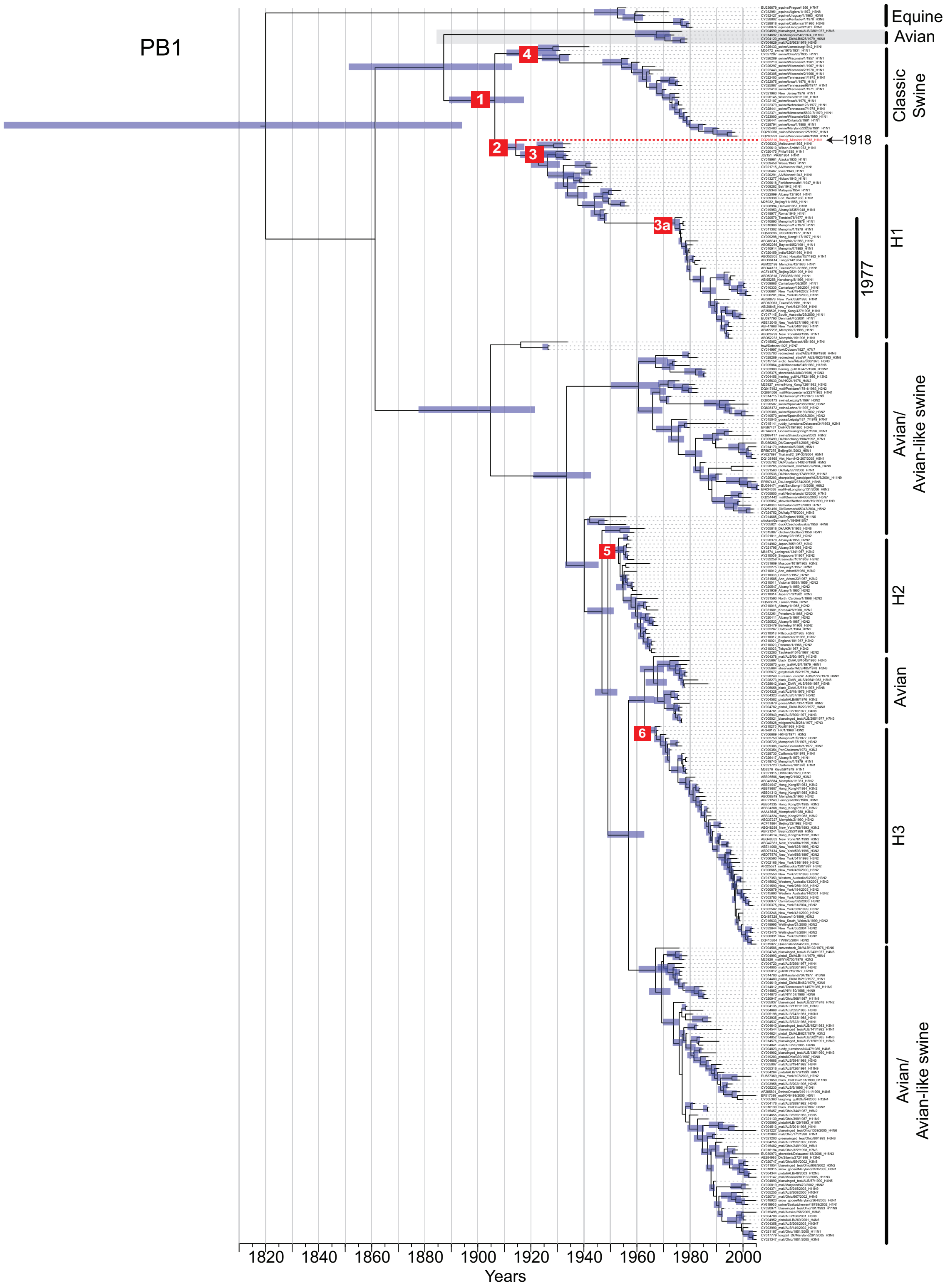

Fig. S4. Dated phylogeny of PB1 genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

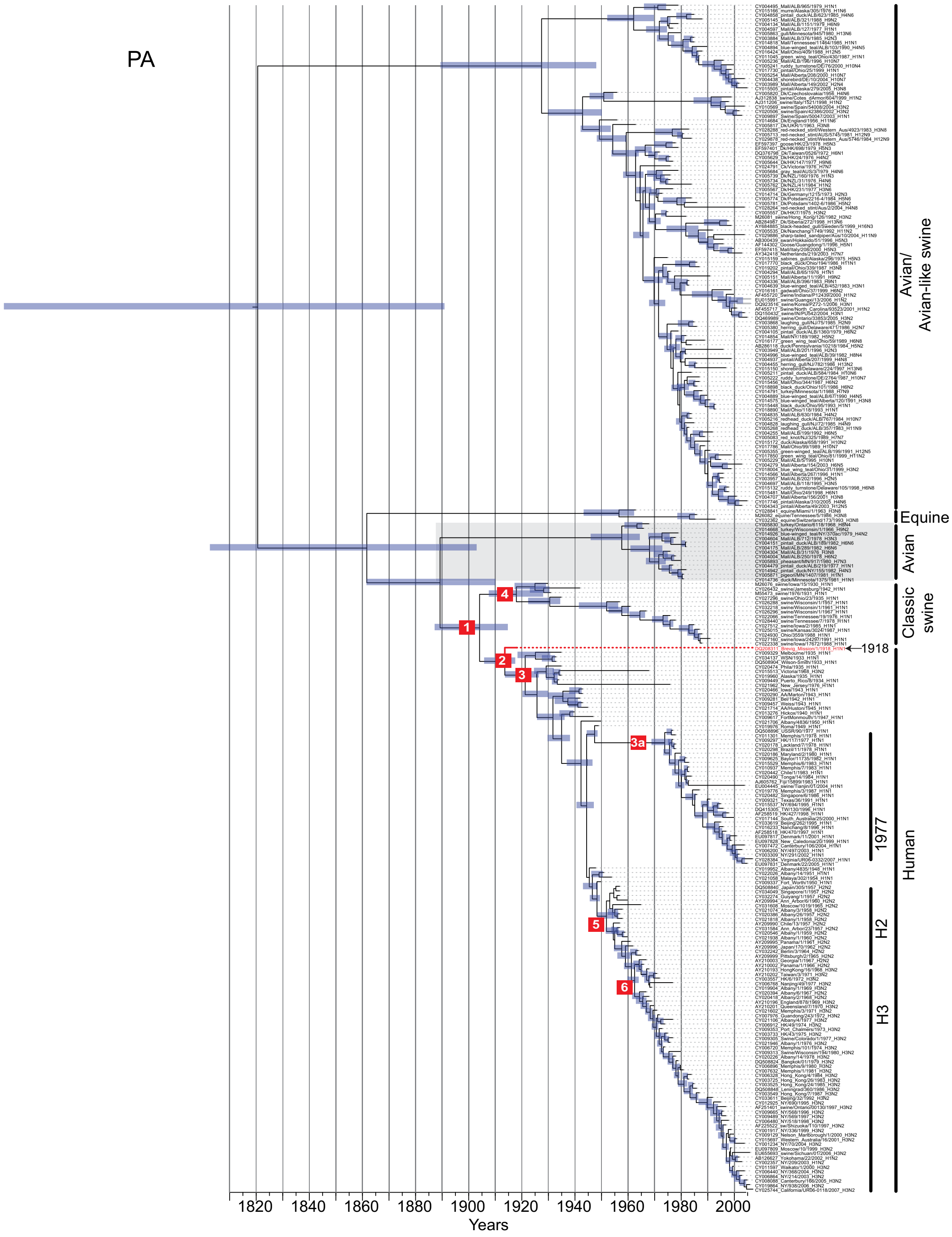

Fig. S5. Dated phylogeny of PA genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

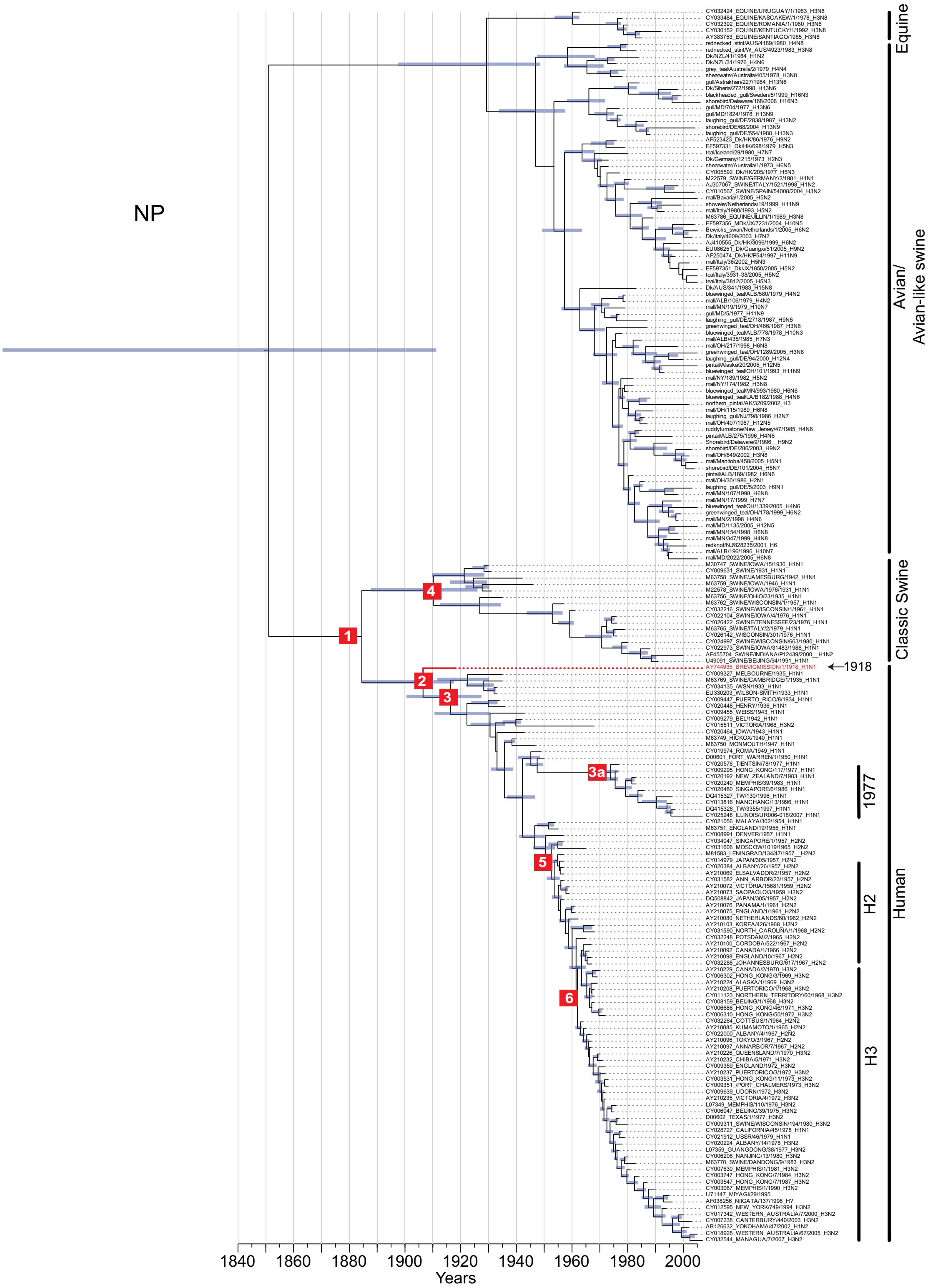

Fig. S6. Dated phylogeny of NP genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

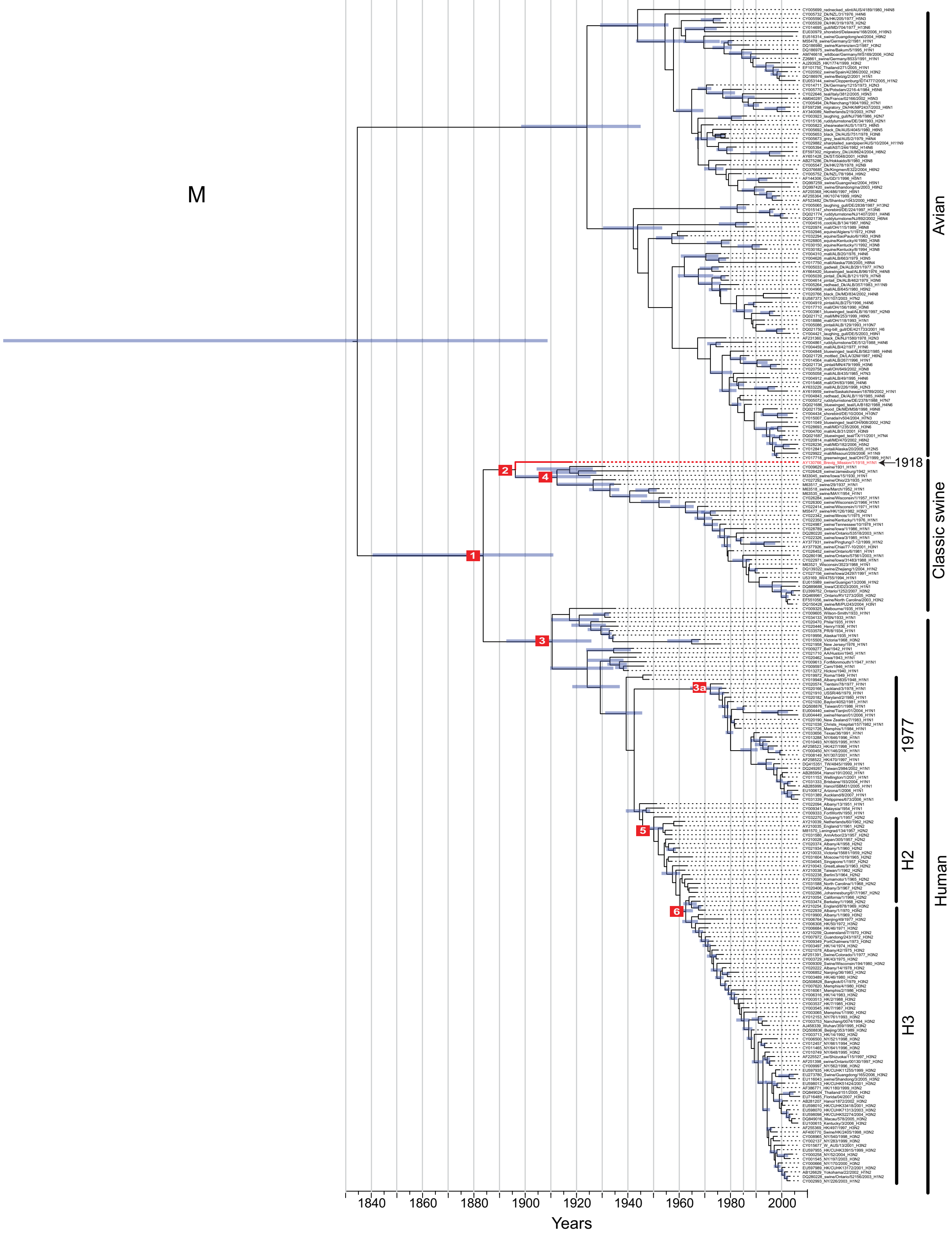

Fig. S7. Dated phylogeny of M genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

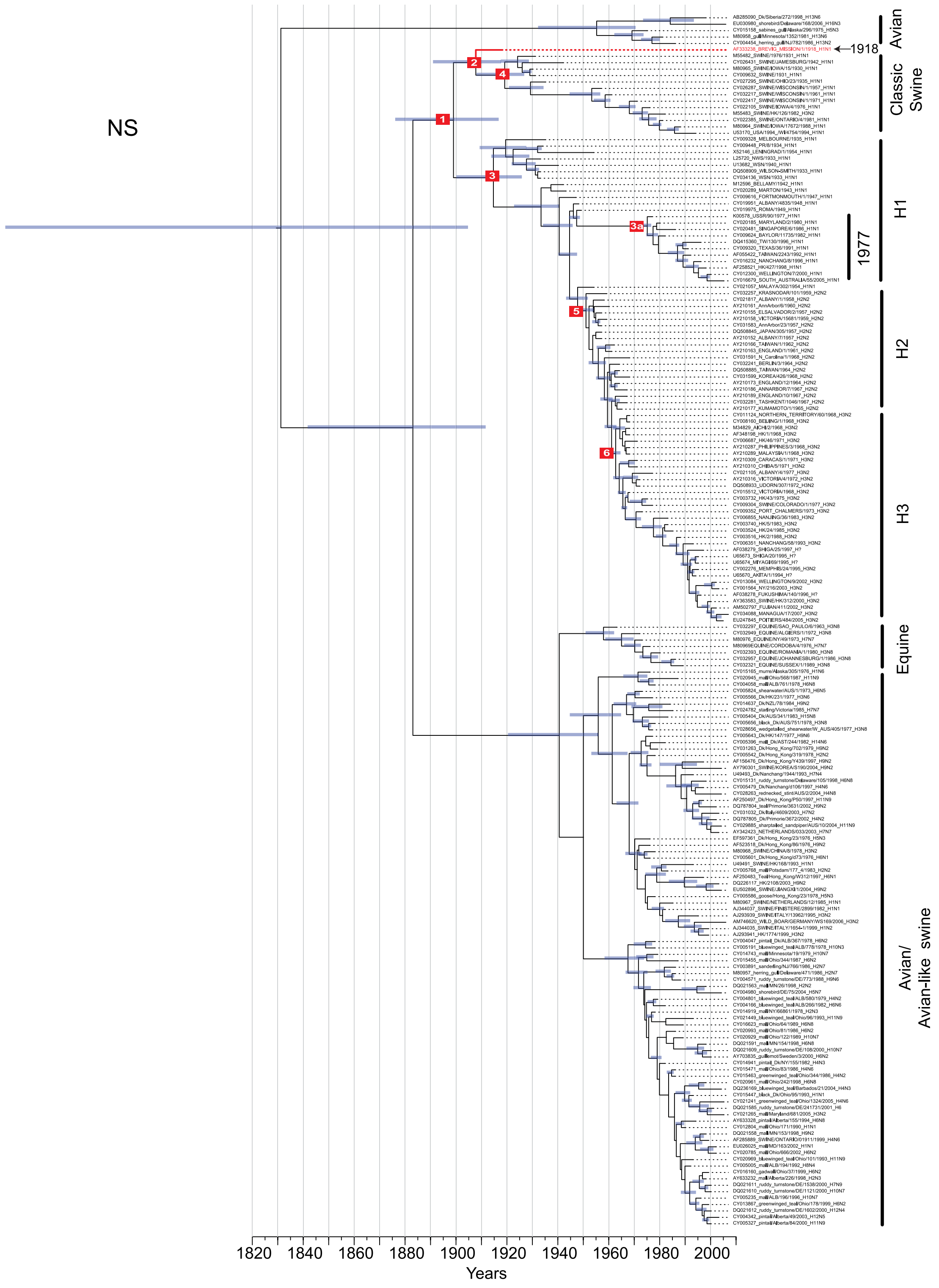

Fig. S8. Dated phylogeny of NS genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

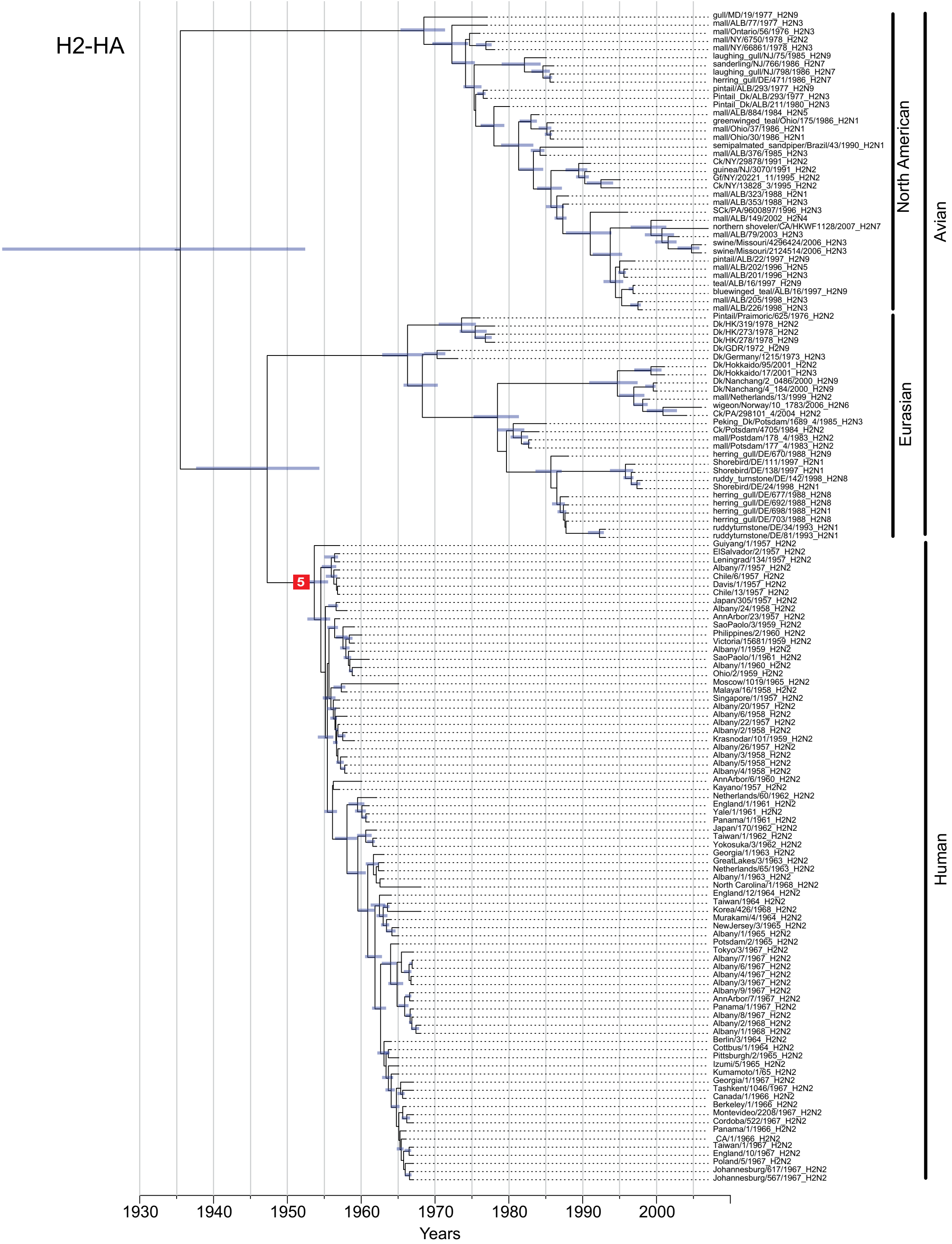

Fig. S9. Dated phylogeny of H2-HA genes of representative influenza A viruses isolated from birds and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

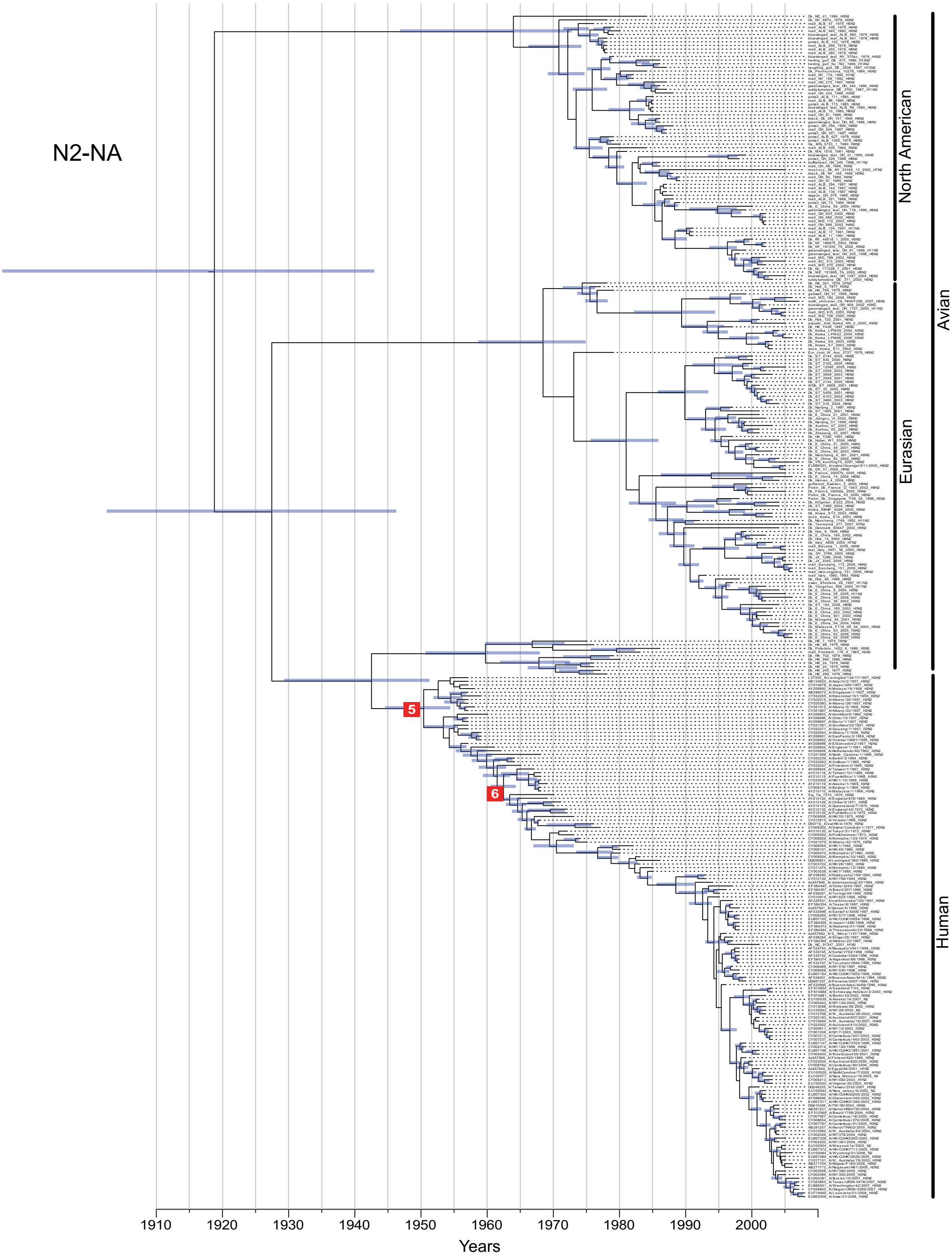

Fig. S10. Dated phylogeny of N2-NA genes of representative influenza A viruses isolated from birds, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

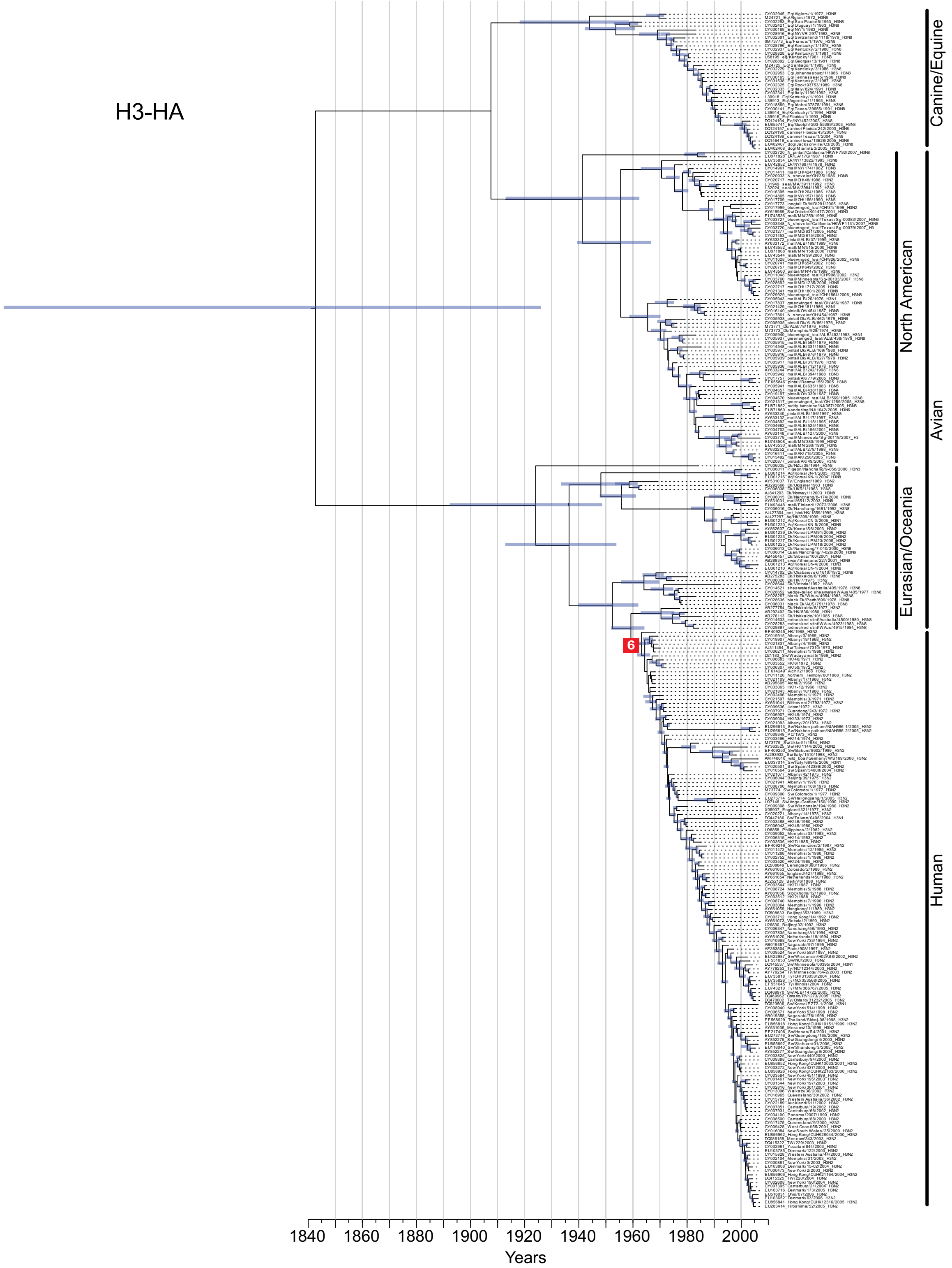

Fig. S11. Dated phylogeny of H3-HA genes of representative influenza A viruses isolated from birds, horses, swine, and humans. Node numbers (*red boxes*) represent major influenza lineages. Node bars indicate 95% BCI of mean divergence times. Timeline is in years.

Table S1. Dataset size, outgroup, and best-fit clock model for each gene segment

Dataset	No. of Viruses	Length	Outgroup*	Best-Fit Clock Model
H1-HA	245	1698	H2 subtype	uced[†]
H2-HA	144	1686	H1 subtype	uced
H3-HA	302	1698	H4 subtype	uced
N1-NA	238	1410	N4 subtype	uced
N2-NA	323	1404	N3 subtype	uced
PB2	294	2277	Influenza B	uced
PB1	318	2271	Influenza B	uced
PA	259	2148	Influenza B	uced
NP	192	1476	Influenza B	uced
M	265	756	Influenza B	uced
NS allele B	189	690	NS allele A	uced

*Outgroup used to determine basal tree topology.

[†] Uncorrelated exponential clock (uced) model

Table S2. Bayes factors were estimate by comparing the marginal likelihoods for each of the 3 clock models—strict clock, uncorrelated exponential relaxed clock (uecd), and uncorrelated lognormal relaxed clock (ucld)—for the H1-HA, N1-NA, PB2, PB1, PA, NP, M, NS, H2-HA, N2-NA, and H3-HA genes

Gene_clock	ln P (model | data)	SE	H1_strict	H1_uced	H1_ucld
H1_strict	−35748.572	0.476	–	−1032.911	−990.337
H1_uced	−34715.661	0.645	1032.911	–	42.574
H1_ucld	−34758.235	0.685	990.337	−42.574	–
Gene_clock	ln P(model | data)	± SE	N1_strict	N1_uced	N1_ucld
N1_strict	−23873.2	0.492	–	−336.032	−297.846
N1_uced	−23537.2	0.565	336.032	–	38.186
N1_ucld	−23575.4	0.835	297.846	−38.186	–
Gene_clock	ln P(model | data)	± SE	PB2_strict	PB2_uced	PB2_ucld
PB2_strict	−50702.563	0.596	–	−548.82	−533.421
PB2_uced	−50153.744	0.539	548.82	–	15.399
PB2_ucld	−50169.142	0.721	533.421	−15.399	–
Gene_clock	ln P(model | data)	± SE	PB1_strict	PB1_uced	PB1_ucld
PB1_strict	50587.2	0.489	–	−463.464	−437.377
PB1_uced	50123.7	0.825	463.464	–	26.087
PB1_ucld	50149.8	1.021	437.377	−26.087	–
Gene_clock	ln P(model | data)	± SE	PA_strict	PA_uced	PA_ucld
PA_strict	−41906.1	0.499	–	−574.653	−535.262
PA_uced	−41331.5	0.71	574.653	–	39.391
PA_ucld	−41370.8	0.649	535.262	−39.391	–
Gene_clock	ln P(model | data)	± SE	NP_strict	NP_uced	NP_ucld
NP_strict	−26763.351	0.437	–	−311.363	−290.631
NP_uced	−26451.988	0.563	311.363	–	20.732
NP_ucld	−26472.72	0.475	290.631	−20.732	–
Gene_clock	ln P(model | data)	± SE	M_strict	M_uced	M_ucld
M_strict	−13475.974	0.575	–	−245.448	−220.641
M_uced	−13230.525	0.778	245.448	–	24.807
M_ucld	−13255.333	0.647	220.641	−24.807	–
Gene_clock	ln P(model | data)	± SE	NSB_strict	NSB_uced	NSB_ucld
NS_strict	−10916.772	0.513	–	−213.301	−198.515
NS_uced	−10703.471	0.675	213.301	–	14.785
NS_ucld	−10718.256	0.52	198.515	−14.785	–
Gene_clock	ln P(model | data)	± SE	H2_strict	H2_uced	H2_ucld
H2_strict	−15657.0	0.451	–	−138.822	−126.274
H2_uced	−15518.2	0.578	138.822	–	12.548
H2_ucld	−15530.8	0.48	126.274	−12.548	–
Gene_clock	ln P(model | data)	± SE	N2_strict	N2_uced	N2_ucld
N2_strict	−31805.185	0.655	–	−537.032	−502.949
N2_uced	−31268.153	0.663	537.032	–	34.082
N2_ucld	−31302.236	0.792	502.949	−34.082	–
Gene_clock	ln P(model | data)	± SE	H3_strict	H3_uced	H3_ucld
H3_strict	−32456.128	0.528	–	−617.834	−593.74
H3_uced	−31838.294	0.676	617.834	–	24.094
H3_ucld	−31862.388	0.696	593.74	−24.094	–