

H7 HA1 Site (H3 numbering)	H7N1	H7N2	H7N3	H7N7
-17		X		
-16		X	X	X
-15			X	X
22	X			
27			X	
28		X		
30			X	
31			X	
56		X		
64	X			
69	X			
71		X		X
77	X			
123	X	X		
135	X	X		
137		X		X
151	X	X		
184		X		
190		X		
193			X	
201	X			
203		X		
216		X		X
218	X	X	X	X
242		X		
255	X	X		
270		X	X	X
277		X		
284		X		X
290	X			
300	X	X		
304	X	X	X	
308		X		
322		X		

**Table S1: H7 HA1 sites with  $d_N/d_S > 1$  in stochastic mutational analysis on different NA subtype backgrounds.**

The  $d_N$  value for each site was divided by the average  $d_S$  across all sites for that subtype to obtain a  $d_N/d_S$  value for each site on each background NA subtype. Sites with  $d_N/d_S > 1$ , i.e. under putative positive selection, are reported in the table (denoted “X”). As is influenza convention, sites are numbered according to the H3 numbering for HA1 (positive sites numbers) and the peptide signal region (negative site numbers). Site numbers are coloured according to the domain: fusion (pink), vestigial esterase (green) or receptor binding (blue) following Yang *et al.* (2010) *PLoS Path.*

<b>Avian taxonomic order</b>	<b>Hosts in avian H7 HA dataset</b>
Anseriformes	Duck, goose, swan, teal, widgeon
Galliformes	Turkey, grouse, chicken, quail, pheasant, guinea-fowl, chukar
Struthioniformes	Ostrich, emu
Passeriformes	Starling, fairy bluebird, common iora
Pstittaciformes	Parrot, parakeet, conure, macaw
Charadriiformes	Gull, ruddy turnstone, shorebird/wader, red knot
Rheiformes	Rhea

**Table S2: Classification of avian hosts of H7 influenza virus by taxonomic order.**

The right-hand column lists the names of birds of a particular taxonomic order for which an isolate was present in the avian H7 HA sequence dataset.

1_h7n1_duck_mongolia_47_01	AB268557	51_h7n1_turkey_italy_3489_1999	CY025157
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3_h7n1_commoniora_singapore_f89_95	AF202228	53_h7n1_turkey_italy_2715_1999	CY025173
4_h7n1_fairybluebird_singapore_f92_94	AF202229	54_h7n1_turkey_italy_2732_1999	CY025181
5_h7n1_africanstarling_englandq_983_79	AF202232	55_h7n1_turkey_italy_1265_1999	CY025189
6_h7n1_ostrich_zimbabwe_222_96	AF202234	56_h7n1_duck_hongkong_301_72	DQ003216
7_h7n1_chicken_england_71_82	AF202236	57_h7n1_ostrich_italy_2332_00	DQ991312
8_h7n1_fpv_egypt_45	AF202237	58_h7n1_ostrich_italy_984_00	DQ991343
9_h7n1_conure_england_1234_94	AF202241	59_h7n1_rhea_northcarolina_39482_1993	EF470586
10_h7n1_parrot_england_1174_94	AF202243	60_h7n1_mallard_italy_250_02	EU158105
11_h7n1_ostrich_southafrica_1069_91	AF202244	61_h7n1_fpv_rostock_1934	M24457
12_h7n1_conure_england_766_94	AF202249	62_h7n1_ts1_1_a_fpv_rostock_1934	M24458
13_h7n1_parakeet_netherlands_267497_94	AF202251	1_h7n2_duck_hongkong_301_1978	AB302789
14_h7n1_parrot_northernireland_vf7367_73	AF202252	2_h7n2_chicken_newyork_131425_94	AF072384
15_h7n1_turkey_italy_12598_99	AJ489520	3_h7n2_turkey_newyork_44505_94	AF072386
16_h7n1_chicken_italy_13489_99	AJ493214	4_h7n2_chicken_newyork_138337_95	AF072388
17_h7n1_chicken_italy_267_00	AJ493215	5_h7n2_chicken_newyork_80302_96	AF072393
18_h7n1_turkey_italy_3889_99	AJ493466	6_h7n2_chicken_pennsylvania_117671_97	AF072395
19_h7n1_turkey_italy_4169_99	AJ493468	7_h7n2_chicken_newyork_67773_97	AF072396
20_h7n1_chicken_italy_4575_99	AJ493469	8_h7n2_turkey_pennsylvania_7975_97	AF072397
21_h7n1_turkey_italy_4602_99	AJ493470	9_h7n2_chicken_pennsylvania_135521_98	AF072398
22_h7n1_turkey_italy_4603_99	AJ493471	10_h7n2_quail_newyork_1398951_98	AF072399
23_h7n1_turkey_italy_3775_99	AJ493472	11_h7n2_turkey_israel_ramon_79	AF202235
24_h7n1_chicken_italy_445_99	AJ580353	12_h7n2_psittacine_italy_1_91	AF202242
25_h7n1_chicken_italy_1067_99	AJ584647	13_h7n2_gull_italy_6922_93	AF202248
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27_h7n1_turkey_italy_4169_1999	CY006037	15_h7n2_avian_ny_7041112_00	AY240878
28_h7n1_duck_nanchang_1904_1992	CY014612	16_h7n2_avian_ny_742112_00	AY240879
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31_h7n1_turkey_italy_1351_2001	CY021421	19_h7n2_avian_ny_77296_00	AY240882
32_h7n1_turkey_italy_2984_2000	CY021533	20_h7n2_chicken_fl_903484_01	AY240883
33_h7n1_turkey_italy_4426_2000	CY021541	21_h7n2_chicken_nj_1188785_01	AY240884
34_h7n1_chicken_italy_322_2001	CY021549	22_h7n2_chicken_nj_1503837_02	AY240885
35_h7n1_duck_italy_551_2000	CY021557	23_h7n2_chicken_nj_15124418_02	AY240886
36_h7n1_guineafowl_italy_155_2000	CY022661	24_h7n2_chicken_nj_158149_99	AY240887
37_h7n1_quail_italy_396_2000	CY022669	25_h7n2_chicken_nj_608_02	AY240888
38_h7n1_chicken_italy_1082_1999	CY022677	26_h7n2_chicken_ny_1190557_01	AY240890
39_h7n1_turkey_italy_977_1999	CY024754	27_h7n2_chicken_ny_1192567_01	AY240891
40_h7n1_chicken_italy_2335_2000	CY024762	28_h7n2_chicken_ny_13878_98	AY240893
41_h7n1_turkey_italy_1084_2000	CY024770	29_h7n2_chicken_ny_215868_99	AY240895
42_h7n1_turkey_italy_4708_1999	CY024858	30_h7n2_chicken_ny_224094_99	AY240896
43_h7n1_turkey_italy_4295_1999	CY024874	31_h7n2_chicken_ny_307493_00	AY240897
44_h7n1_turkey_italy_3488_1999	CY024890	32_h7n2_chicken_pa_1490921_02	AY240900
45_h7n1_pekinduck_italy_1848_2000	CY024898	33_h7n2_chicken_va_32_02	AY240906
46_h7n1_turkey_italy_4644_1999	CY025109	34_h7n2_chicken_ny_1485812_99	AY240907
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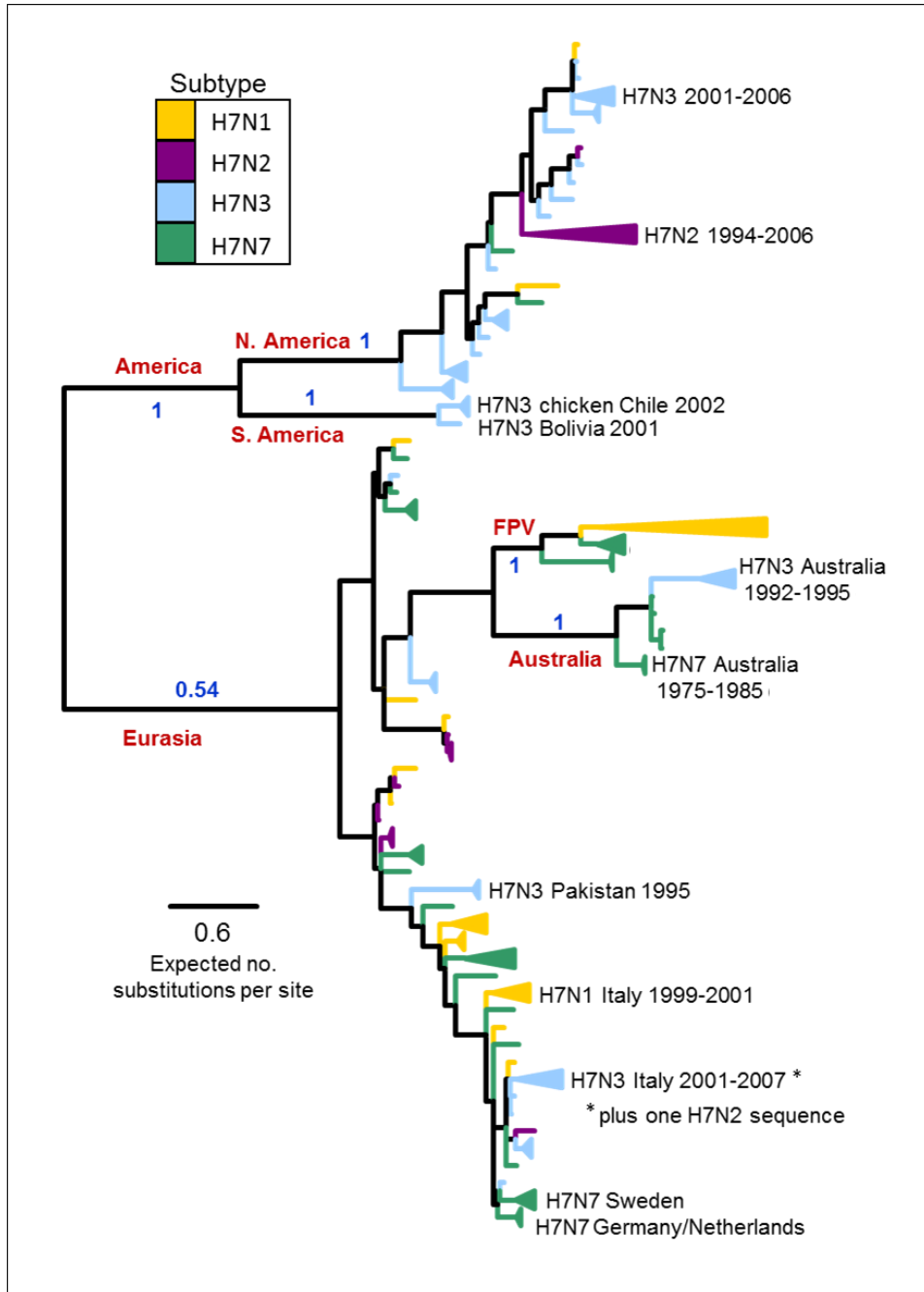
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48_h7n2_goose_newjersey_86003_98	AY240922	23_h7n3_turkey_italy_9742_2002	CY028660
49_h7n2_quail_ny_11430_99	AY240923	24_h7n3_turkey_italy_3829_2004	CY028676
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52_h7n2_chicken_hebei_1_2002	AY724257	27_h7n3_chicken_england_4054_2006	EF467826
53_h7n2_chicken_de_hobo_2004	AY831668	28_h7n3_turkey_italy_4479_2004	CY020581
54_h7n2_chicken_de_viva_2004	AY831669	29_h7n3_turkey_italy_4608_2003	CY021485
55_h7n2_chicken_md_minhma_2004	AY831670	30_h7n3_turkey_italy_2043_2003	CY022613
56_h7n2_dk_hongkong_293_1978	CY006029	31_h7n3_chicken_chile_176822_02	AY303630
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13_h7n3_bluewingedteal_ohio_658_2004	CY018901	63_h7n3_chicken_chile_4322_02	AY303631
64_h7n3_chicken_britishcolumbia_gsc_human_b_04	AY646078	22_h7n7_mallard_sweden_103_02	AY999987
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4_h7n7_nonpsittacine_englandq_1985_89	AF202240	31_h7n7_chicken_victoria_1976	CY024786
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6_h7n7_turkey_england_647_77	AF202247	33_h7n7_chicken_netherlands_03010132_03	EF015551
7_h7n7_macaw_england_626_80	AF202250	34_h7n7_mallard_italy_299_05	EU158104
8_h7n7_ostrich_southafrica_m320_96	AF202253	35_h7n7_duck_jiangxi_1742_03	EU158108
9_h7n7_chicken_germany_r28_03	AJ620350	36_h7n7_fpv_weybridge	L37794
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13_h7n7_mallard_sweden_56_02	AY999977	40_h7n7_chicken_victoria_1_1985	M17735
14_h7n7_mallard_sweden_82_02	AY999978	41_h7n7_starling_victoria_1_1985	M17736
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**Table S3: H7 avian influenza sequence dataset.**

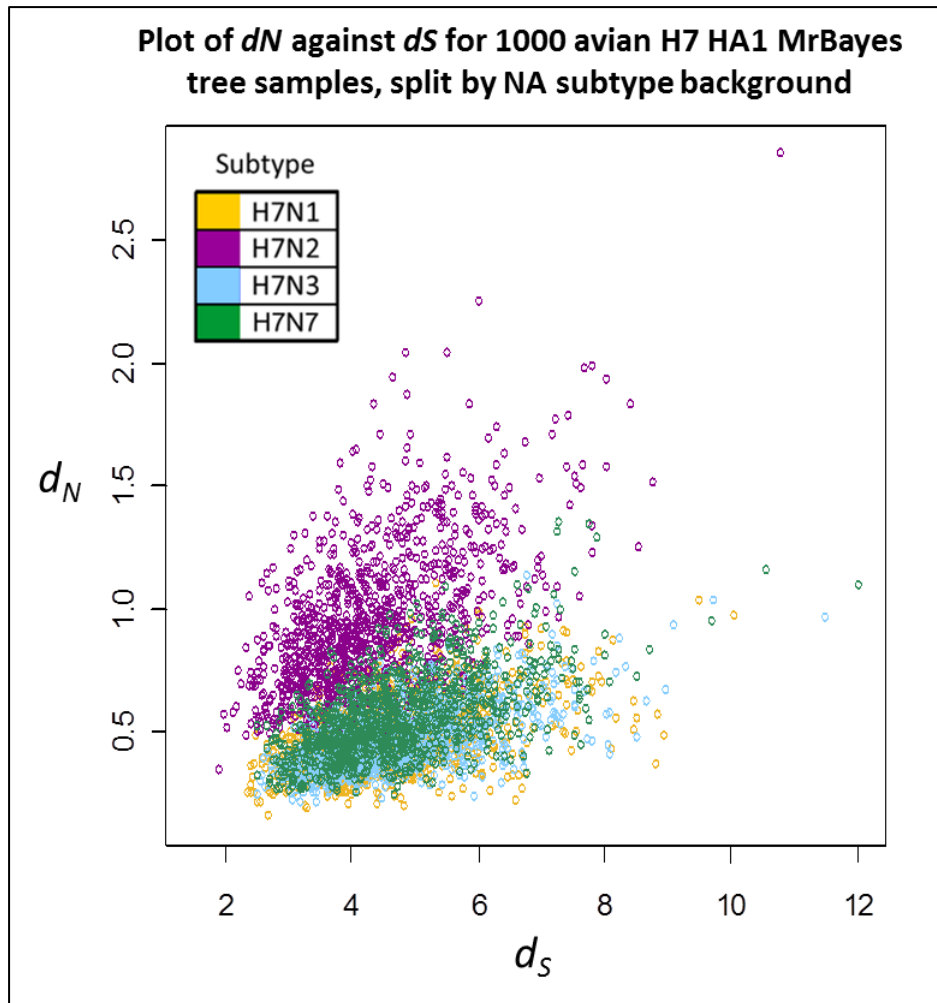
GenBank accession numbers are provided (Note: only the HA1 sub-segment of the influenza HA was used for the phylogenetic and mutational mapping analyses. Identical sequences and early European sequences sampled between 1927 and 1945 were excluded from the mutational mapping analyses). Sequence names were re-formatted for compatibility with sequence analysis software. Sequences were downloaded from the NCBI influenza virus resource:

(<http://www.ncbi.nlm.nih.gov/genomes/FLU/Database/>)



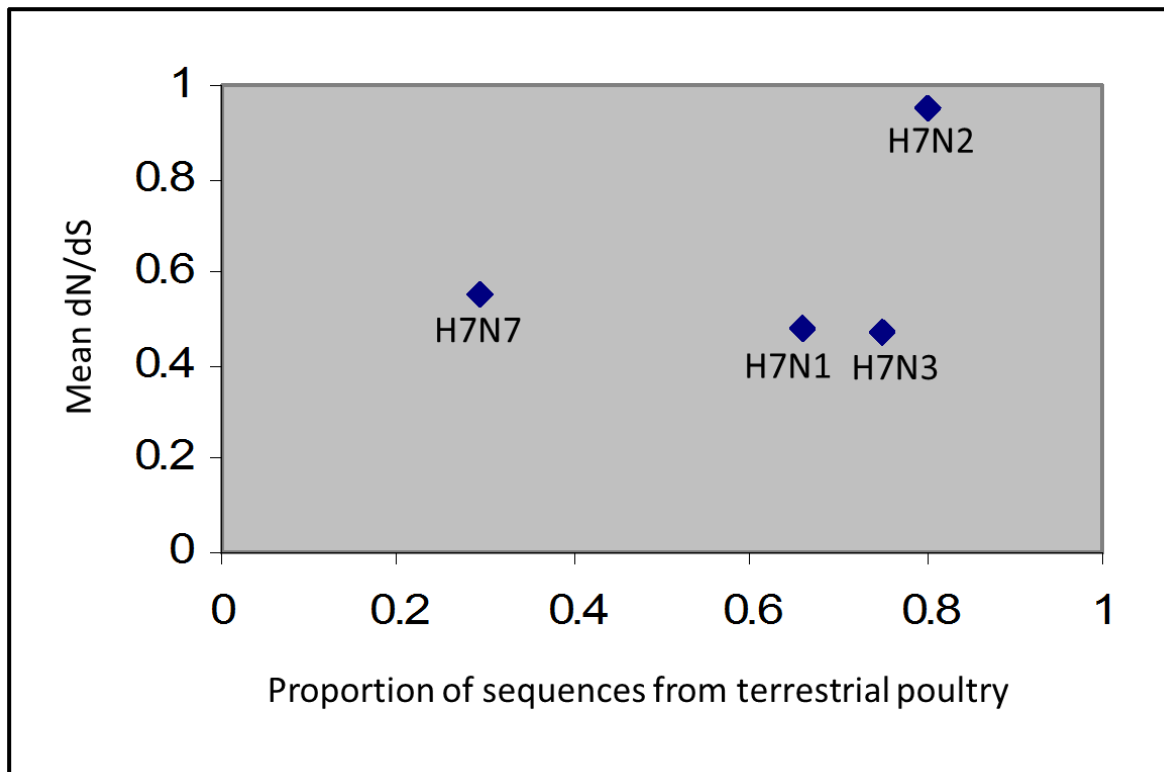
**Figure S1**

**H7 HA1 MrBayes consensus phylogeny.** The tree was inferred under the GTR +  $\Gamma$  model of DNA substitution, with 6 rate categories, and constructed from 1000 post-burnin MCMC phylogeny samples from MrBayes. Major geographical lineages are labelled in red and posterior probabilities of clades are labelled in blue. An H15 sequence was used as an outgroup, but was removed in this figure for the purpose of presentation. Lineages are coloured by the background NA subtype of the virus at the tips of the tree, and clades of sequences of the same subtype have been collapsed for the purpose of presentation. Note: FPV = 'fowl plague virus', a term used to describe H7 avian influenza viruses isolated in the 1920s-1940s.



**Figure S2**

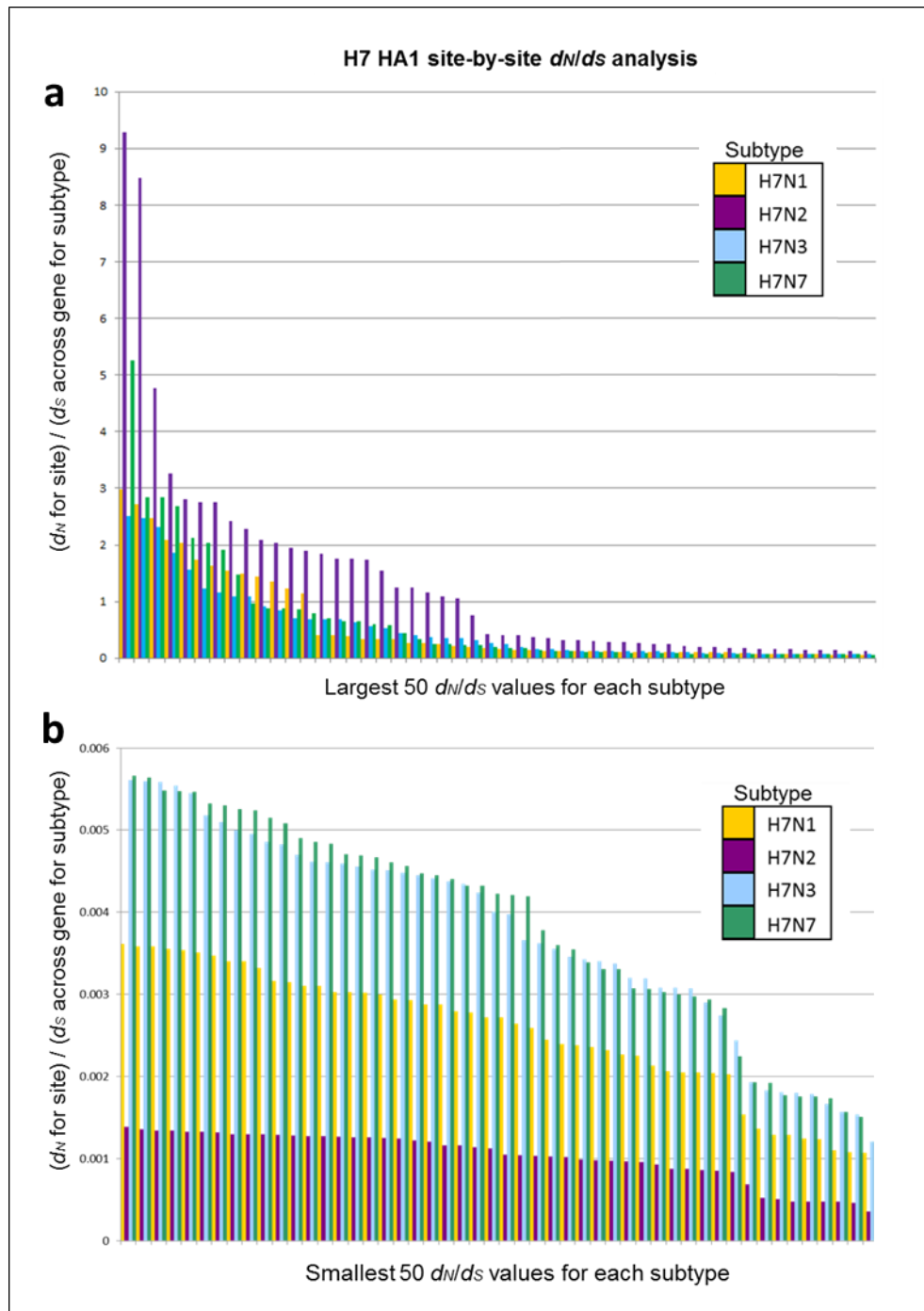
**The rate of non-synonymous substitution ( $d_N$ ) plotted against the rate of synonymous substitution ( $d_S$ ) for avian influenza H7 HA1 from viruses with different background NA subtypes.** For each of the 1000 MCMC tree samples from MrBayes, the value of  $d_N$  was plotted against the value of  $d_S$  for H7N1, H7N2, H7N3 and H7N7, so that the rates for different subtypes could be directly compared. It may be observed that, whilst the  $d_S$  values were similar for all four subtypes, there was little overlap between the H7N2  $d_N$  values and those for the other subtypes. For each subtype, the linear regression line for the  $d_N$  value for a tree sample against the  $d_S$  value for the tree sample is shown.



**Figure S3**

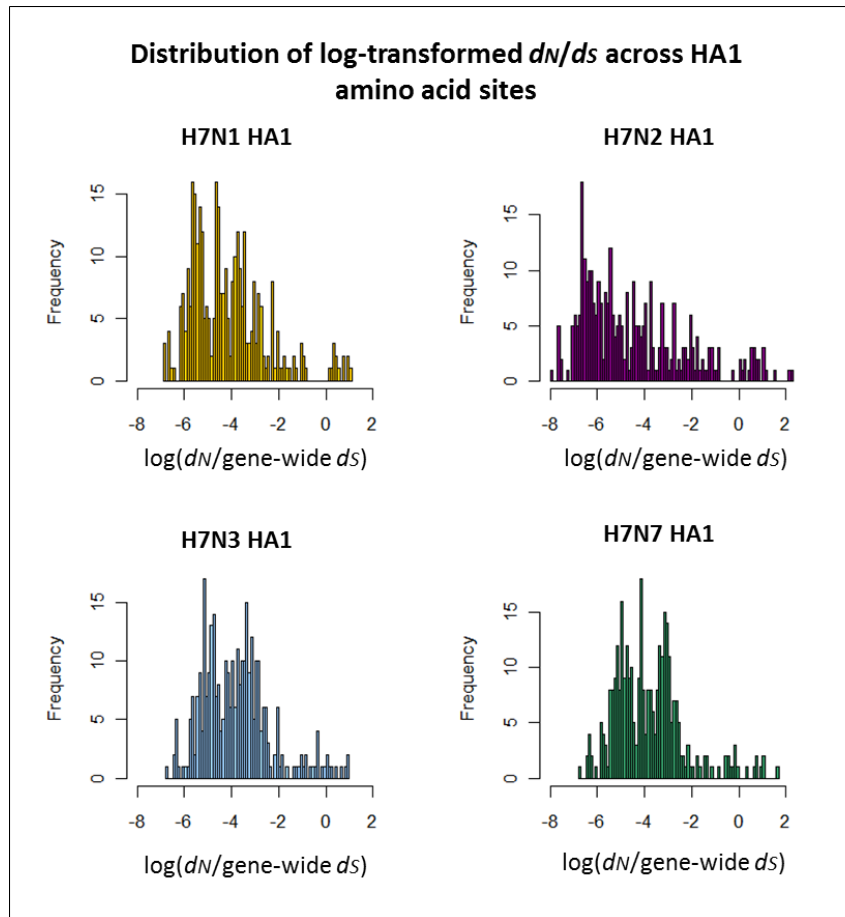
**Relationship between proportion of sequences from terrestrial poultry (Galliformes) and mean  $d_N/d_S$  for each background NA subtype.** For each background NA subtype, the proportion of sequences in the dataset which were from terrestrial poultry was plotted against the mean  $d_N/d_S$  for H7 avian influenza HA1, inferred by stochastic mutational mapping. A Spearman's rank correlation test did not indicate a significant correlation between  $d_N/d_S$  and proportion of sequences from terrestrial poultry ( $p = 0.9167$ ).





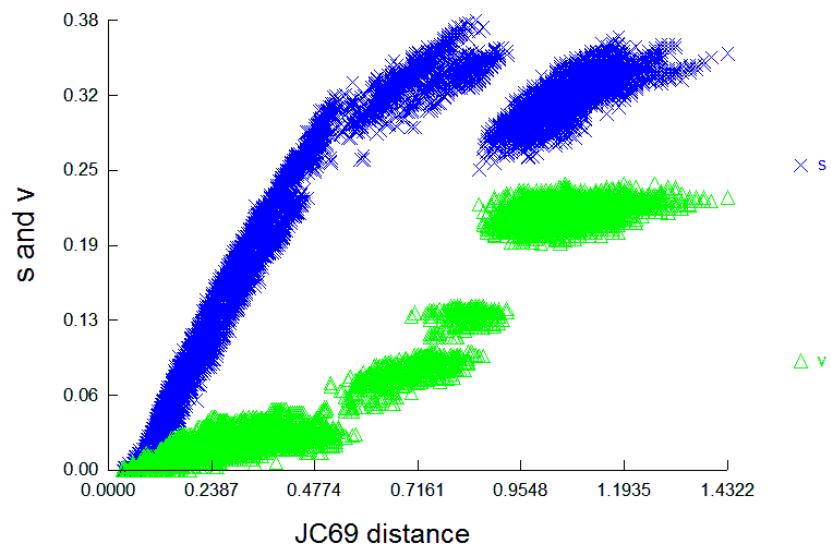
**Figure S4**

**Site-by-site  $d_N/d_S$  values across the avian influenza H7 HA1, ranked by size.** For each NA background subtype, the  $d_N$  value for each site was divided by the average  $d_S$  across all sites for that subtype. The site-by-site  $d_N/d_S$  values were ranked by size: (a) the largest 50 values were plotted for each subtype and (b) the smallest 50 values were plotted for each subtype. For all of the largest 50  $d_N/d_S$  values,  $d_N/d_S$  on the N2 NA background was larger than the values of the same rank on the N1, N3 or N7 NA backgrounds. For all of the smallest 50  $d_N/d_S$  values for the H7 HA1 sites, the value of  $d_N/d_S$  on the N2 NA background was smaller than the values of the same rank on the N1, N3 or N7 NA backgrounds.



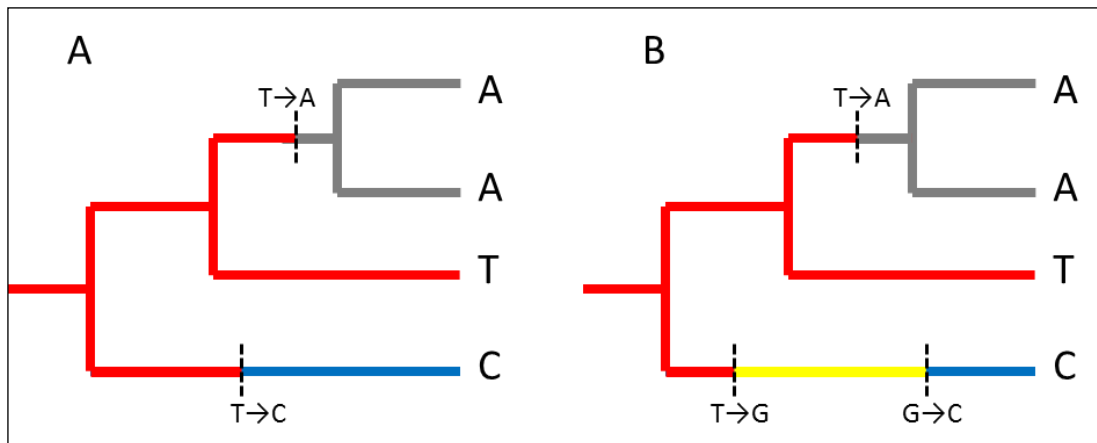
**Figure S5**

**Histograms showing frequency of different  $\log(d_N/\text{gene-wide } d_S)$  values across the H7 HA1 alignment for H7N1, H7N2, H7N3 and H7N7 lineages.** Sites with  $\log(d_N/d_S) > 0$  correspond to  $d_N/d_S > 1$ , and sites with  $\log(d_N/d_S) < 0$  correspond to  $d_N/d_S < 1$ . H7N2 was the only subtype for which  $\log(d_N/d_S)$  values less than -7, or greater than 2, was observed.



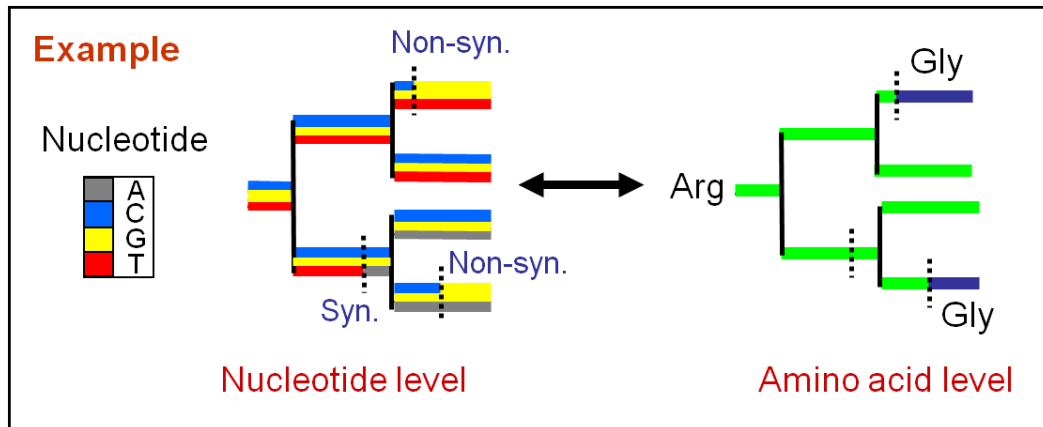
**Figure S6**

**Plot of transitions (s) and transversions (v) against genetic distance for H7 HA dataset.** Although some saturation was observed at higher genetic distances, the number of transitions remains higher than the number of transversions at all genetic distances.



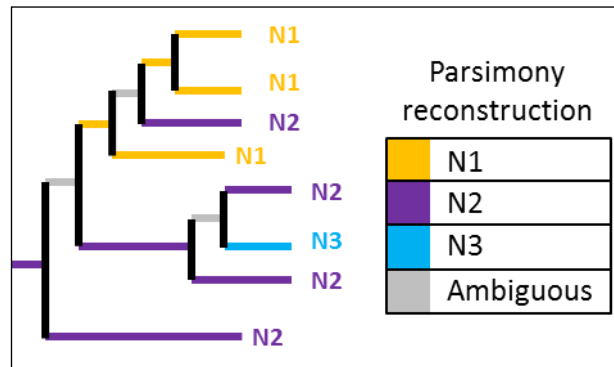
**Figure S7**

**Example nucleotide mutational maps.** Stochastic mutational mapping is used to infer mutational histories for nucleotide sites. Mutational histories report the nature and location of molecular changes along a phylogeny. Multiple mutational mappings may be sampled for each site. For example, maps (A) and (B) are both valid reconstructions for the observed pattern of variation.



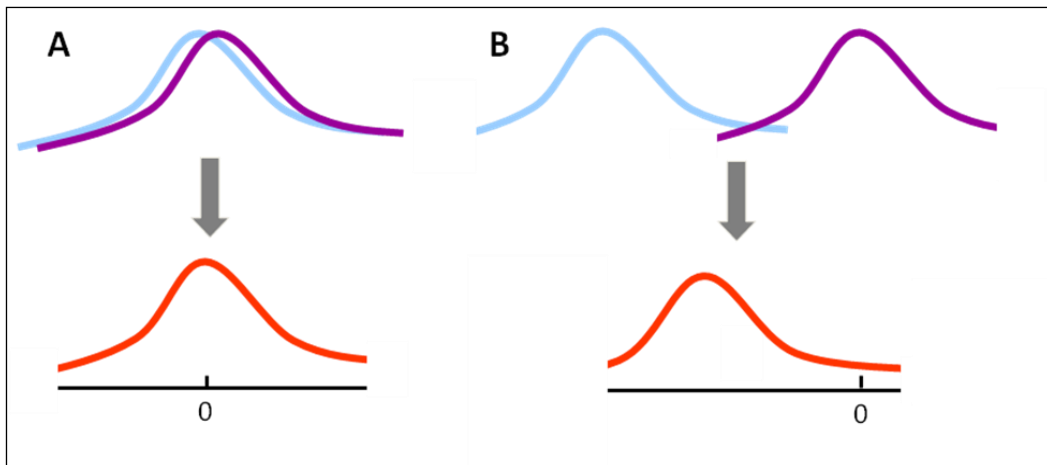
**Figure S8**

**Example codon map obtained using stochastic mutational mapping.** For each codon site, the first and second codon position nucleotide maps for a site were rescaled to the branch lengths of the third position map and combined to produce a map at the amino-acid level. Nucleotide changes could then be labelled as synonymous or non-synonymous for calculating  $d_N$ ,  $d_S$  and  $d_N/d_S$ . In this example there are three nucleotide changes, one of which is synonymous (CGT → CGA) and two of which are non-synonymous (CGT → GGT and CGA → GGA).



**Figure S9**

**Example parsimony reconstruction of background NA subtypes on a phylogeny of H7 HA sequences.** Branches are coloured according to the inferred ancestral subtype of the node immediately preceding them towards the tips of the tree. A single-pass algorithm was implemented, which labels some branches as 'ambiguous'. This avoids the problem associated with erroneous assignment of subtypes in the subsequent calculation of evolutionary rates along branches associated with a particular NA subtype.



**Figure S10**

**Testing for differences between posterior distributions of evolutionary rates for different NA background subtypes. (A)** When the location of the distributions (examples shown here in blue and purple) is very similar, the distribution of differences of randomised pairings between them (shown in red) will be roughly centred on zero. **(B)** When the distributions differ in their location, the distribution of differences between randomised pairings will be skewed, with zero at one of the tail ends. The proportion of pairings lying to each side of zero thus provides a measure of the difference in location of the distributions.