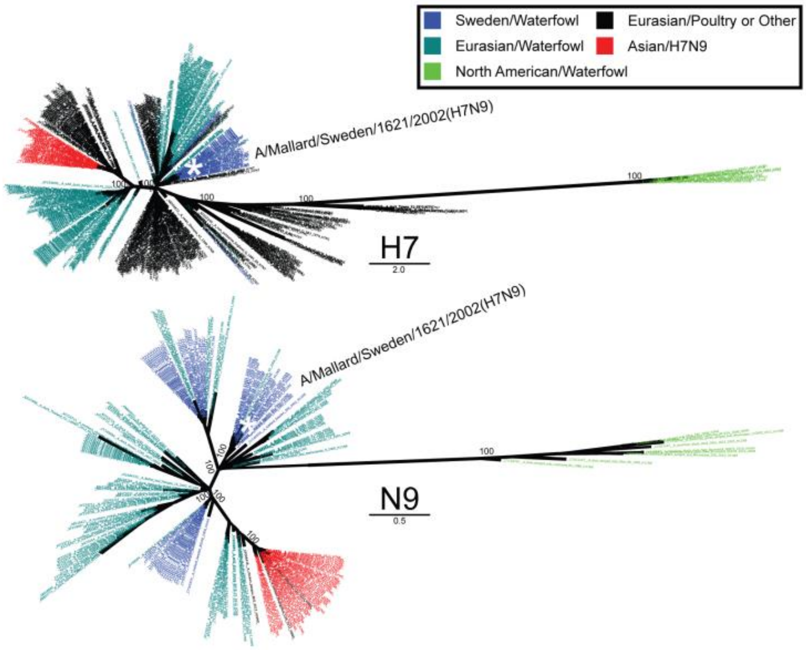

Figure S1: HA and NA phylogenetic trees of Eurasian H7 and N9 virus segments. Phylogenetic placement of the virus used in this study is denoted by an asterisk (*), and the different colors correspond to geographical or host species groupings. Scale bar represents number of substitutions per site. Posterior probabilities of major clades are included at corresponding nodes.

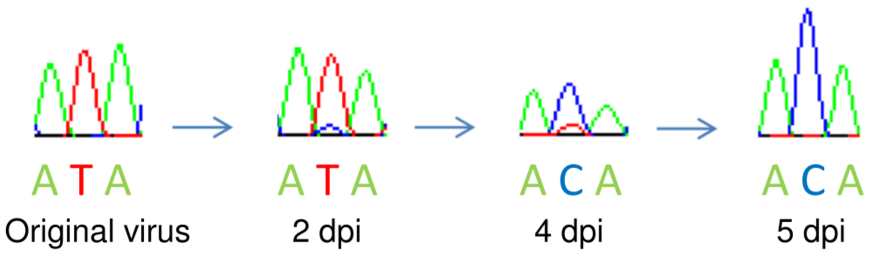

Figure S2. Electropherograms from Sanger sequencing over the N9 codon for amino acid residue 222. Presented sequences are from IAV isolates of fecal samples from a Mallard in generation one, i.e. one of the birds present from the start of the experiment. 2 dpi = 2 days post inoculation etc. ATA codes for isoleucine (I) and ACA for threonine (T).

Table S1. Primers for the amplification and sequencing of neuraminidase N9.

Primer	**Sequence (5’ to 3’)**	**Application**
N9_FWy	TCTATGCACTTCAGCCACTGCTA	NA-PCR, sequencing
N9_FWi2	TCACCGCCCACAGTATACAA	sequencing
N9_REVy (ic)	ATCAGGCCAGTTCCATTGTCCTA	NA-PCR, sequencing
N9_REVi (ic)	TACCTGGATAAGGGTCATTACACT	sequencing