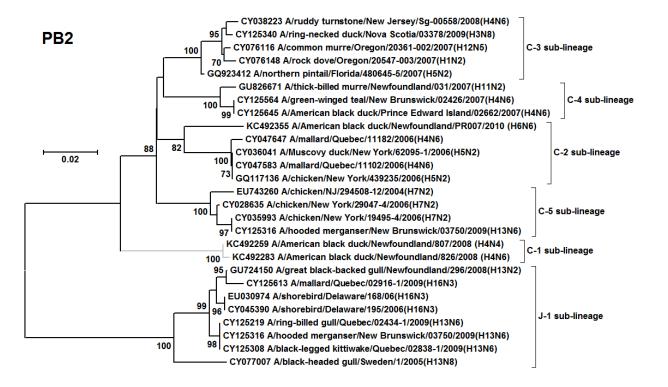
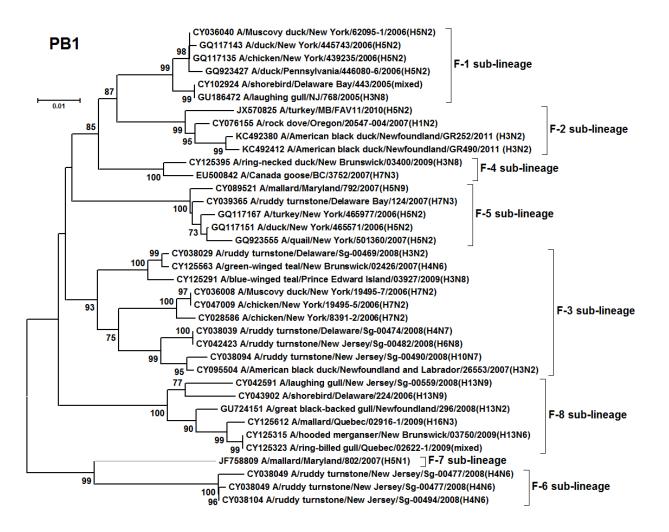
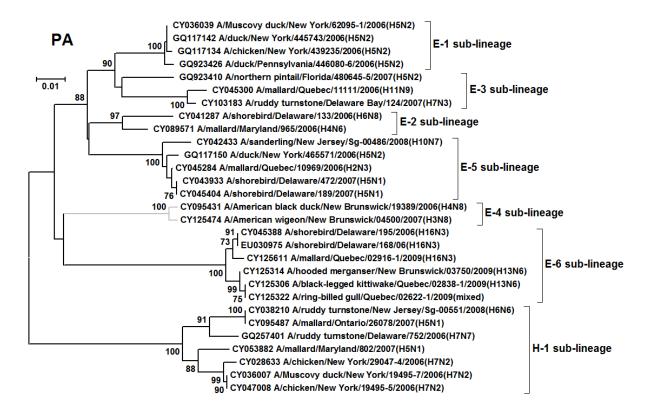
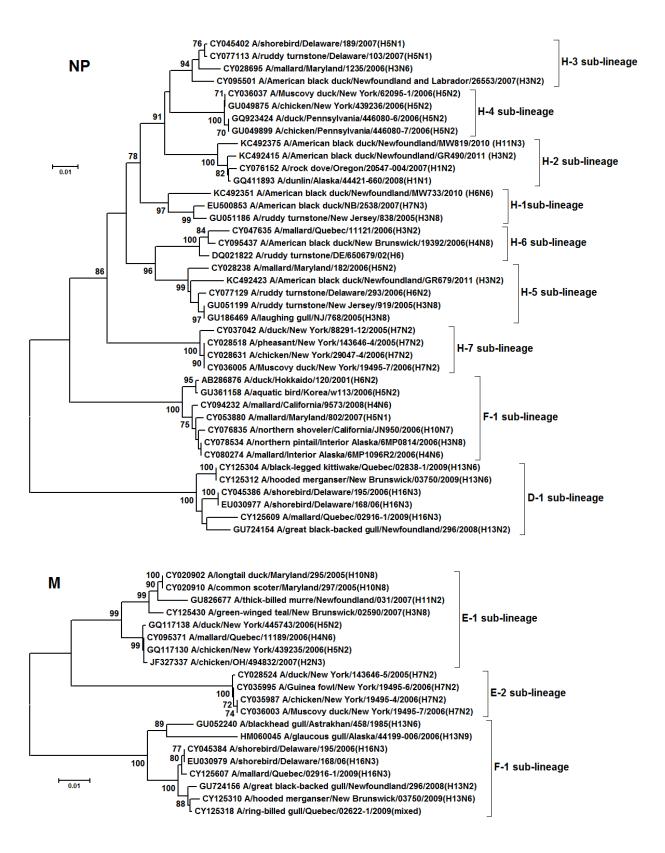
Figure S2. Identification of Atlantic flyway duck AIV genes in other bird hosts.

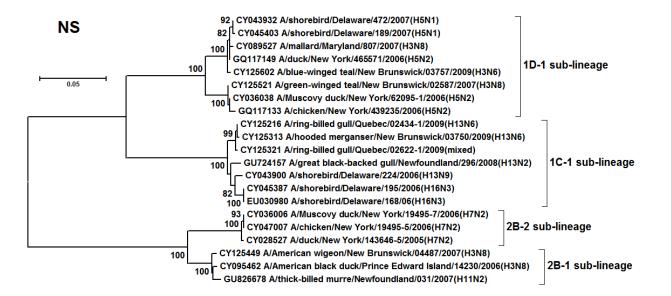
Phylogenetic trees were constructed to highlight the distribution of the genes found in the 109 Atlantic flyway duck AIVs in non-duck host species. The neighbour-joining trees were constructed with MEGA5 and support values based on 1000 bootstrap replicates are shown as percentages where ≥70%. The sub-lineages are labelled on the right of the phylogenetic trees. Black branch lines indicate detection of the sub-lineage in non-duck species, whereas grey branch lines indicate the detection of the sub-lineage only in ducks. For the H16 tree, the 3 gullrelated lineages (H16A to C) established in the Flugenome database were labelled in red.











H1 GQ411892 A/dunlin/Alaska/44421-660/2008(H1N1) CY076141 A/rock dove/Oregon/20547-003/2007(H1N2) CY076149 A/rock dove/Oregon/20547-004/2007(H1N2) - KC464566 A/American black duck/ Newfoundland/1146/2009 (H1N1) KC464574 A/American black duck/ Newfoundland/1148/2009 (H1N1) KC464582 A/American black duck/ Newfoundland/1150/2009 (H1N1) CY077310 A/northern pintail/Interior Alaska/7MP0278/2007(H1N1) CY097781 A/swine/Alberta/25/2009(H1N1)

