

Supplemental figures:

The following 18 figures are the remaining phylogenetic trees that will be posted on a website once the paper is accepted for publication

Supplemental Fig. 1-5. The phylogenetic trees of the internal genes (PB2 nucleotide positions 65-603; PB1, 354-565; NP, 41-631; M, 40-668; and NS, 101-621) analyzed with PAUP using bootstrap and the neighbor-joining methods as distance measures. The trees are rooted as indicated in the title. The distance bar is shown under the tree, and bootstrap values (100 replicates) are given for selected nodes. The Canadian feral duck isolates sequenced in this study cluster in the North American avian clade and are in bold print; each of the distinct phylogenetic groupings is assigned a different pattern as indicated to the right; Black arrows identify swine and quail species that clustered with Canadian ducks. Abbreviations: Cal, California.

Supplemental Fig. 6. The phylogenetic tree of the matrix gene obtained by using the complete sequences of 221 M genes (nucleotides bases 26-1004) analyzed with PAUP using the bootstrap and the maximum parsimony methods as distance measures. The tree is rooted to *A/equine/Prague/56* (H7N7). The bar indicating the number of nucleotide changes is shown under the tree and bootstrap values (100 replicates) are given for selected nodes. Major phylogenetic divisions are indicated to the right of the tree and the two Canadian feral duck outliers (*A/pintail/Alberta/113/85* and *A/mallard/Alberta/98/85*) are identified at the base of the tree.

Supplemental Fig. 7,8. The phylogenetic trees of a fragment of the H1 hemagglutinin gene (fig.7) (nucleotides bases 494-659) and the complete HA1 of the H1 hemagglutinin

gene (fig.8) (nucleotides bases 33-1061) analyzed with PAUP using the bootstrap and the neighbor-joining methods as distance measures. The tree is rooted to A/Singapore/1/57 (H2N2). The distance bar is shown under the tree, and bootstrap values (100 replicates) are given for selected nodes. Major phylogenetic divisions are indicated to the right of the tree. The Canadian feral duck isolate is in bold at the base of the North American avian clade.

Supplemental Fig. 9-11. The phylogenetic trees of the hemagglutinin H2, H3, and H4 genes (H2 nucleotide positions 44-1060; H3, 78-1035; and H4, 30-1647) analyzed with PAUP using bootstrap and the neighbor-joining methods as distance measures. The trees are rooted as indicated in the title. The distance bar is shown under the tree, and bootstrap values (100 replicates) are given for selected nodes. The Canadian feral duck isolates sequenced in this study cluster in the North American avian clade and are in bold print. The Canadian feral duck isolates formed one phylogenetic grouping in the H2 tree and 2 separate phylogenetic groupings in the H3 and H4 trees. Each distinct phylogenetic grouping is assigned a different pattern as indicated to the right.

Supplemental Fig. 12. The phylogenetic tree of the HA1 of the H9 hemagglutinin gene (nucleotides bases, 43-1047) analyzed with PAUP using the bootstrap and the neighbor-joining methods as distance measures. The tree is rooted to A/duck/Alberta/60/76 (H12N5). The distance bar is shown under the tree, and bootstrap values (100 replicates) are given for selected nodes. Major phylogenetic divisions are indicated to the right of

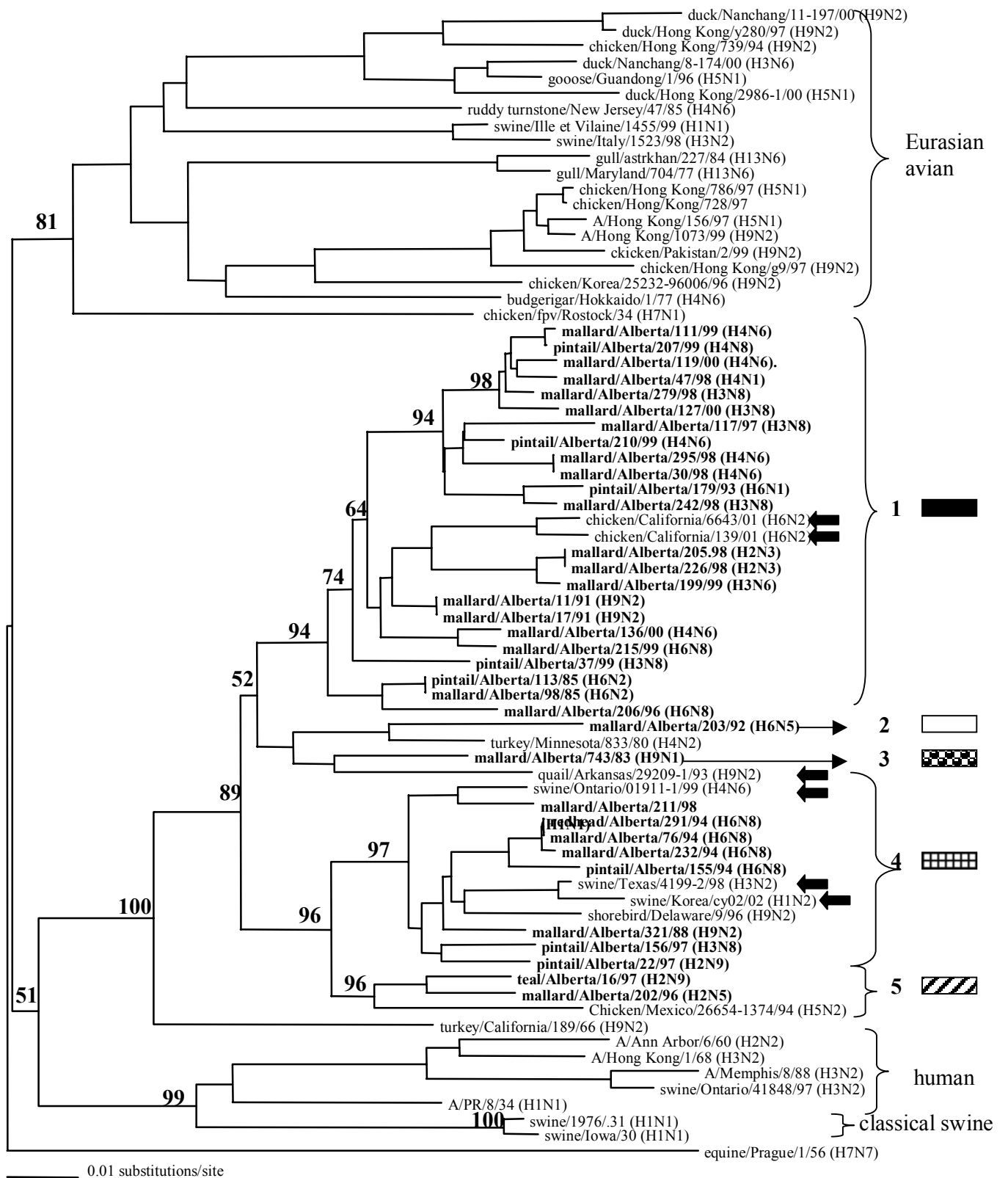
the tree. The Canadian feral duck isolates all cluster together in the Eurasian avian clade and are in bold.

Supplemental Fig. 13. The phylogenetic tree of the N1 gene (nucleotides bases, 21-1430) analyzed with PAUP using the bootstrap and the neighbor-joining methods as distance measures. The tree is rooted to *A/turkey/Minnesota/5001/78 (H6N8)*. The distance bar is shown under the tree, and bootstrap values (100 replicates) are given for selected nodes. Major phylogenetic divisions are indicated to the right of the tree. The Canadian feral duck isolates all cluster together in the North American avian clade and are in bold. Viruses in italics represent isolates that antigenically identified as N4 by the NA inhibition assay using reference sera to H4; however nucleotide sequence and phylogenetic analysis identified these NA genes as N1 subtypes. Included in this tree are sequences provided by Webby et al. (personal communication).

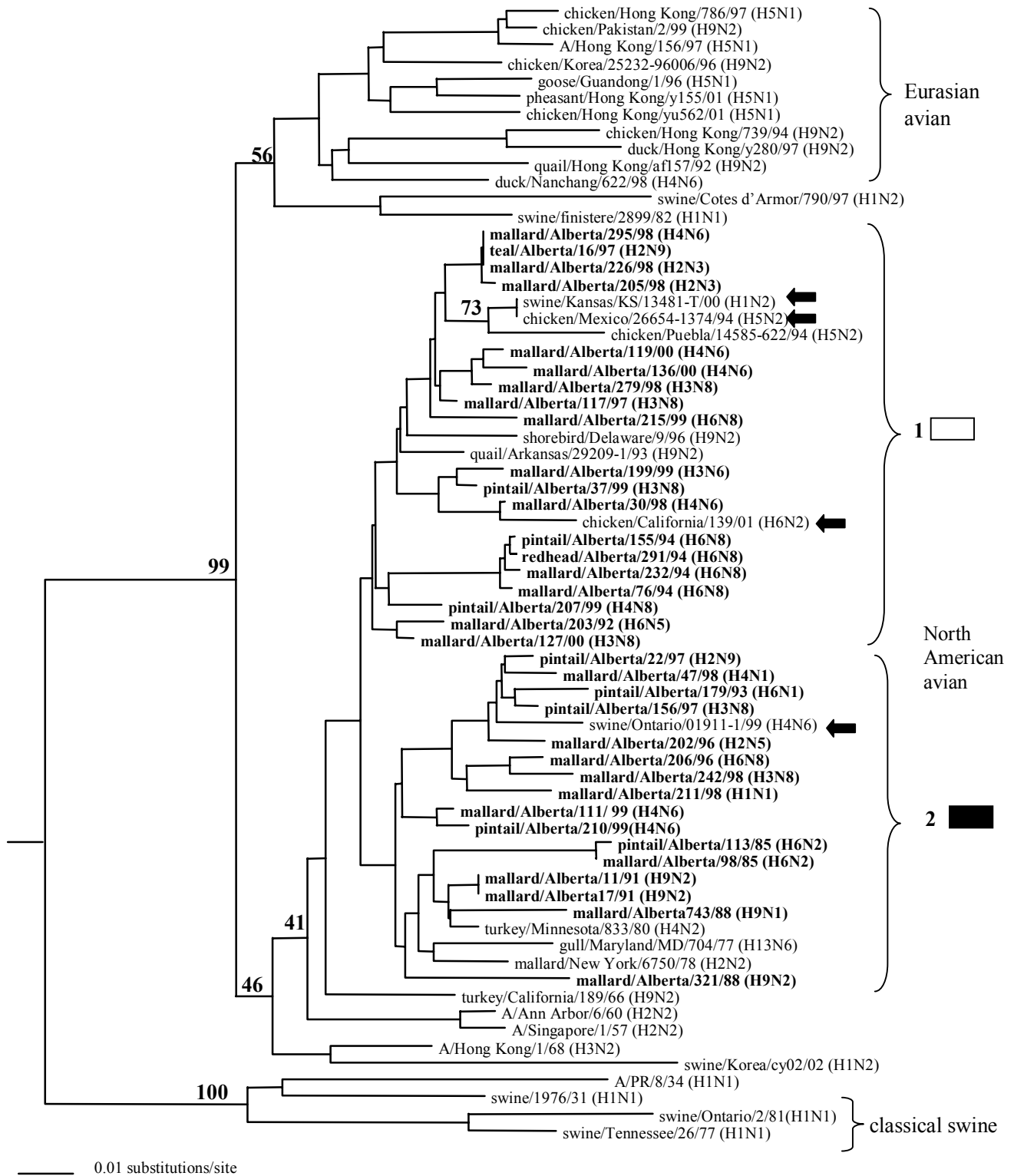
Supplemental Fig. 14-18. The phylogenetic trees of the N2, N3, N6, N8 and N9 genes (N2 nucleotide positions 27-1395; N3, 21-1430; and N6, 21-1433; N8, 21-1415; N9, 158-601) analyzed with PAUP using bootstrap and the neighbor-joining methods as distance measures. The trees are rooted as indicated in the title. The distance bar is shown under the tree, and bootstrap values (100 replicates) are given for selected nodes. The Canadian feral duck sequenced in this study cluster in the North American avian clade and are in bold print. The Canadian feral duck N2, N3, N6 and N9 genes all clustered into one phylogenetic grouping. The N8 genes formed two distinct phylogenetic groupings.

Each of the distinct phylogenetic groupings is assigned a different pattern as indicated to the right each of the viruses.

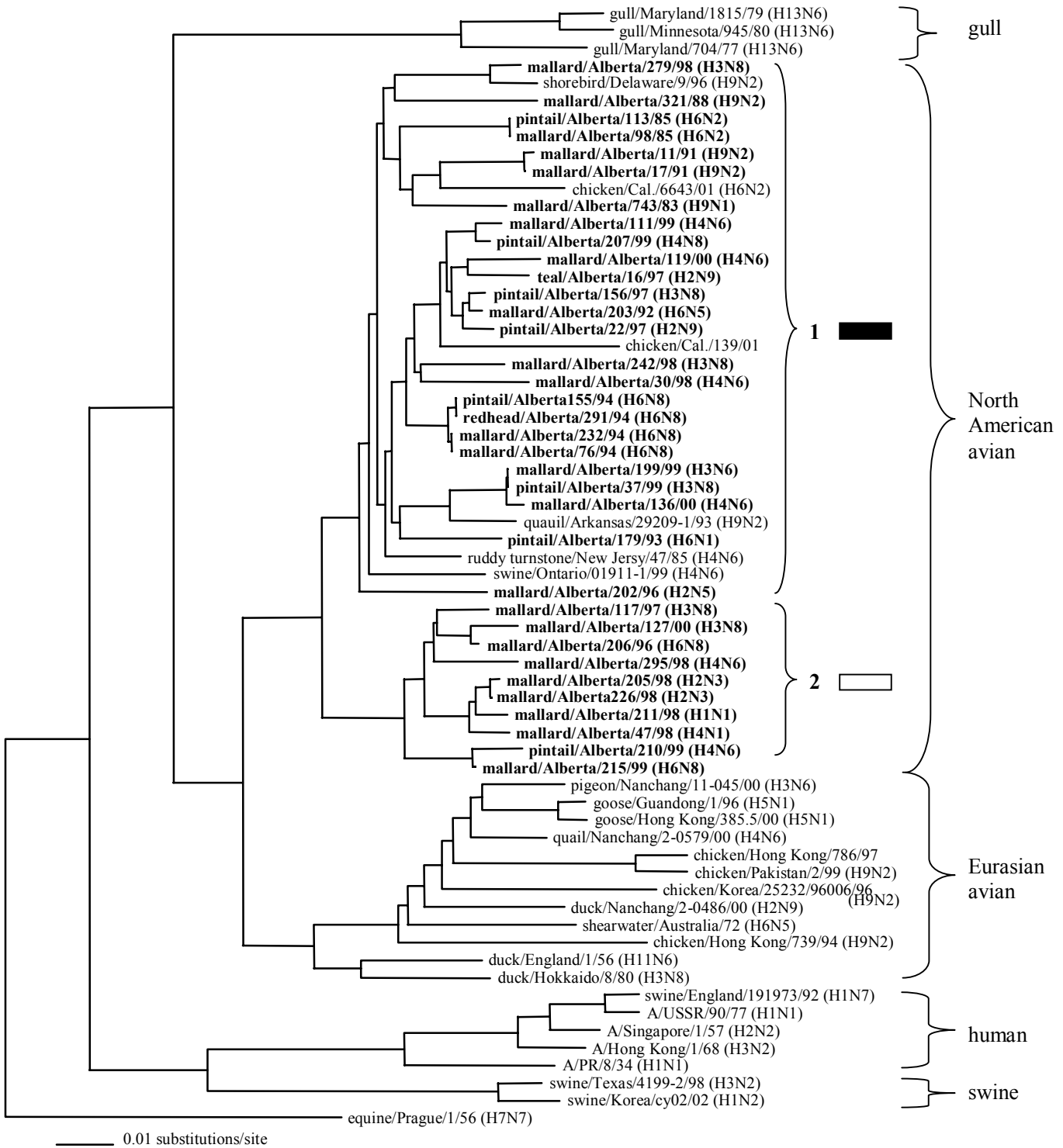
Supplemental Fig. 1. PB2 rooted to equine/prague/1/56



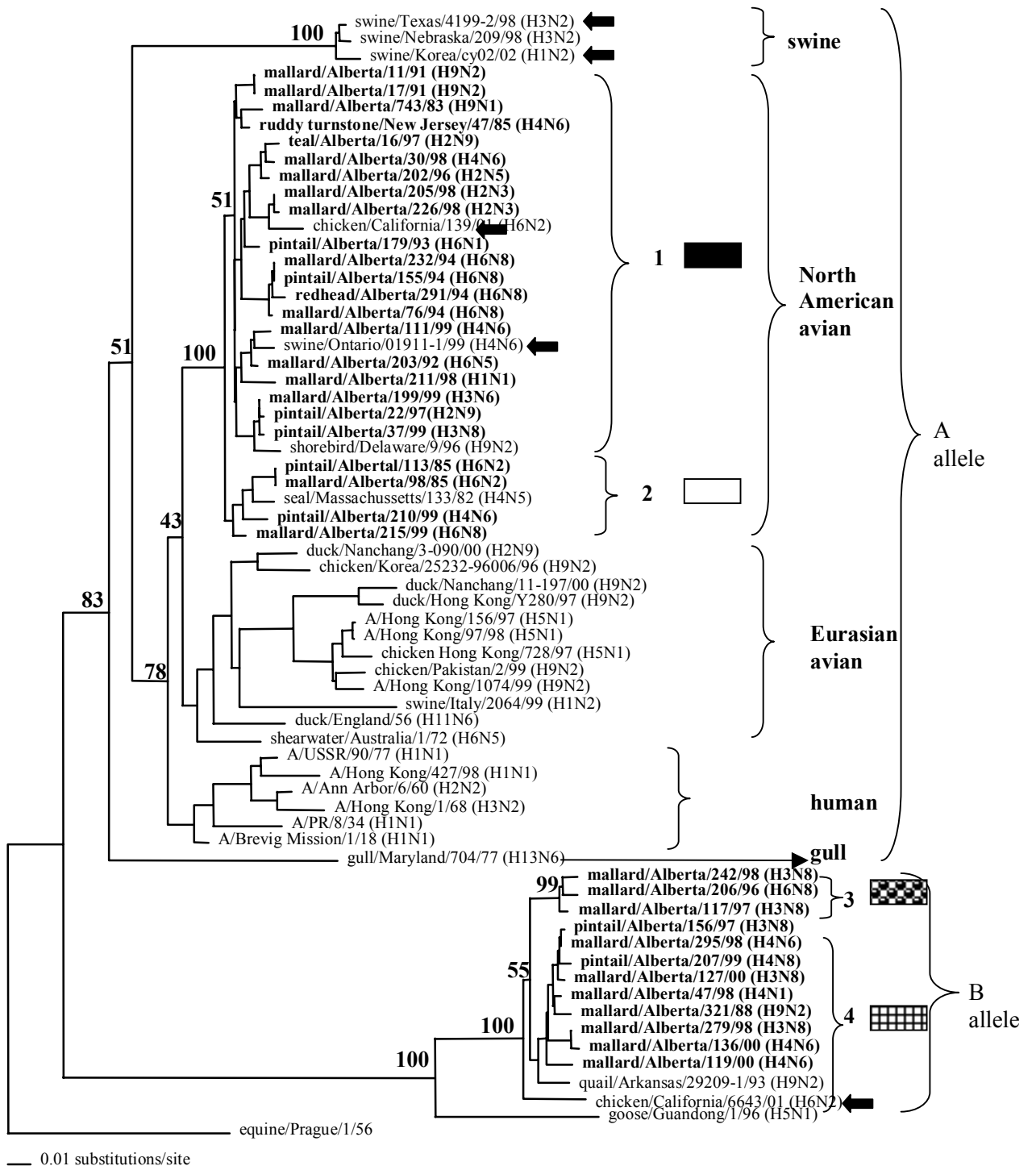
Supplemental Fig. 2. PB1 rooted to Equine/London/1416/73



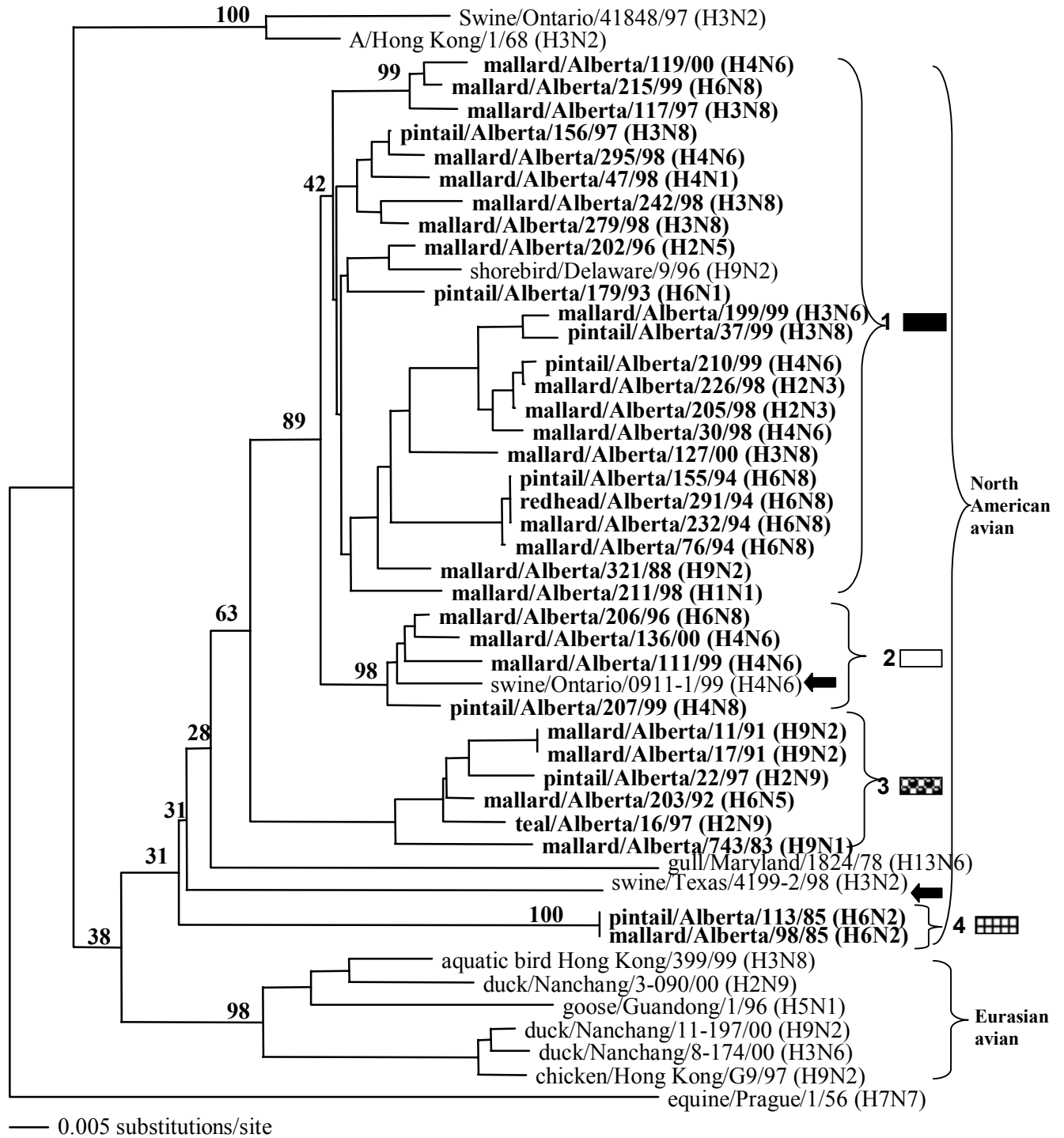
Supplemental Fig. 3. NP rooted to equine/prague/1/56



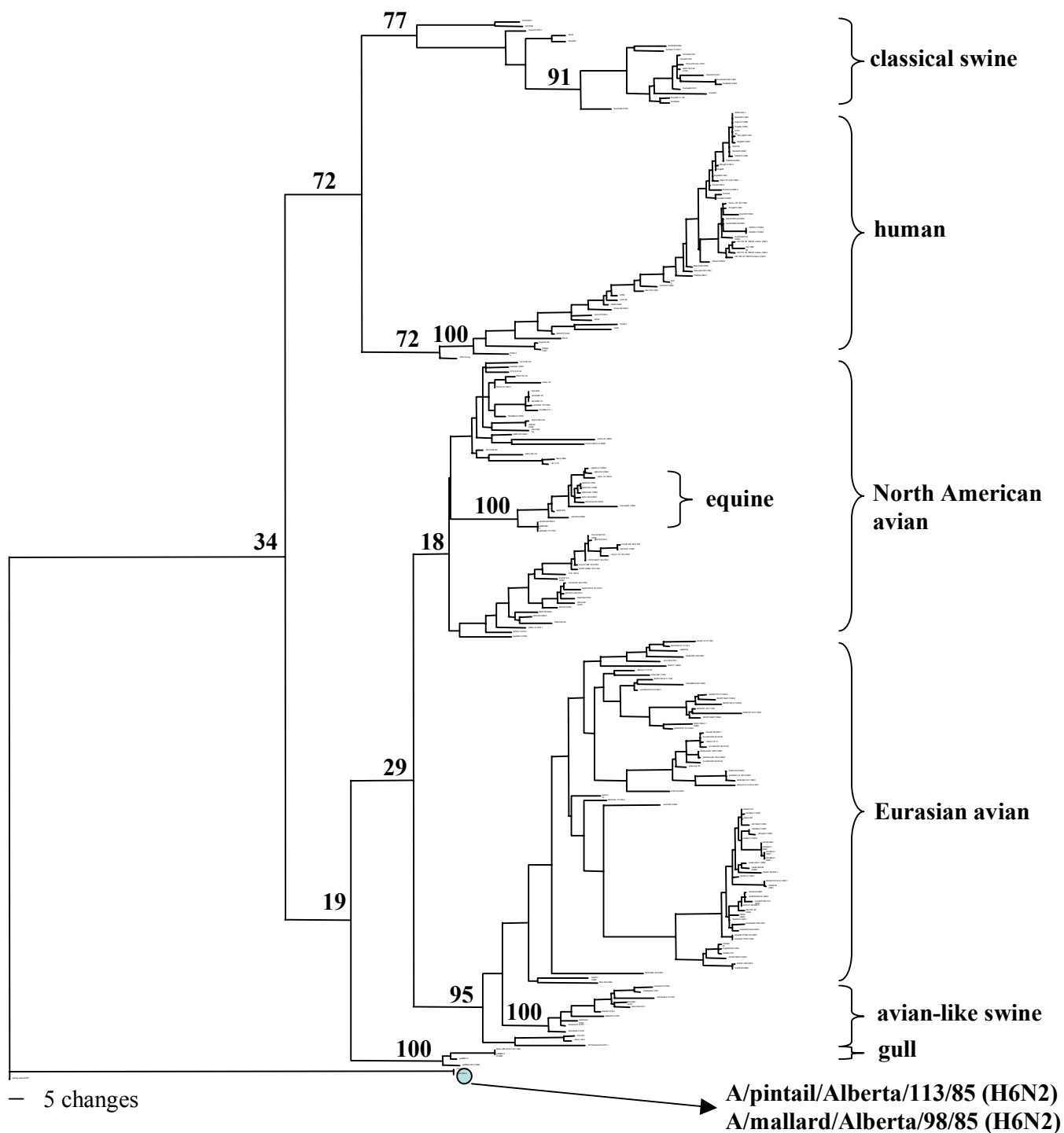
Supplemental Fig. 4. NS rooted to equine/prague/1/56



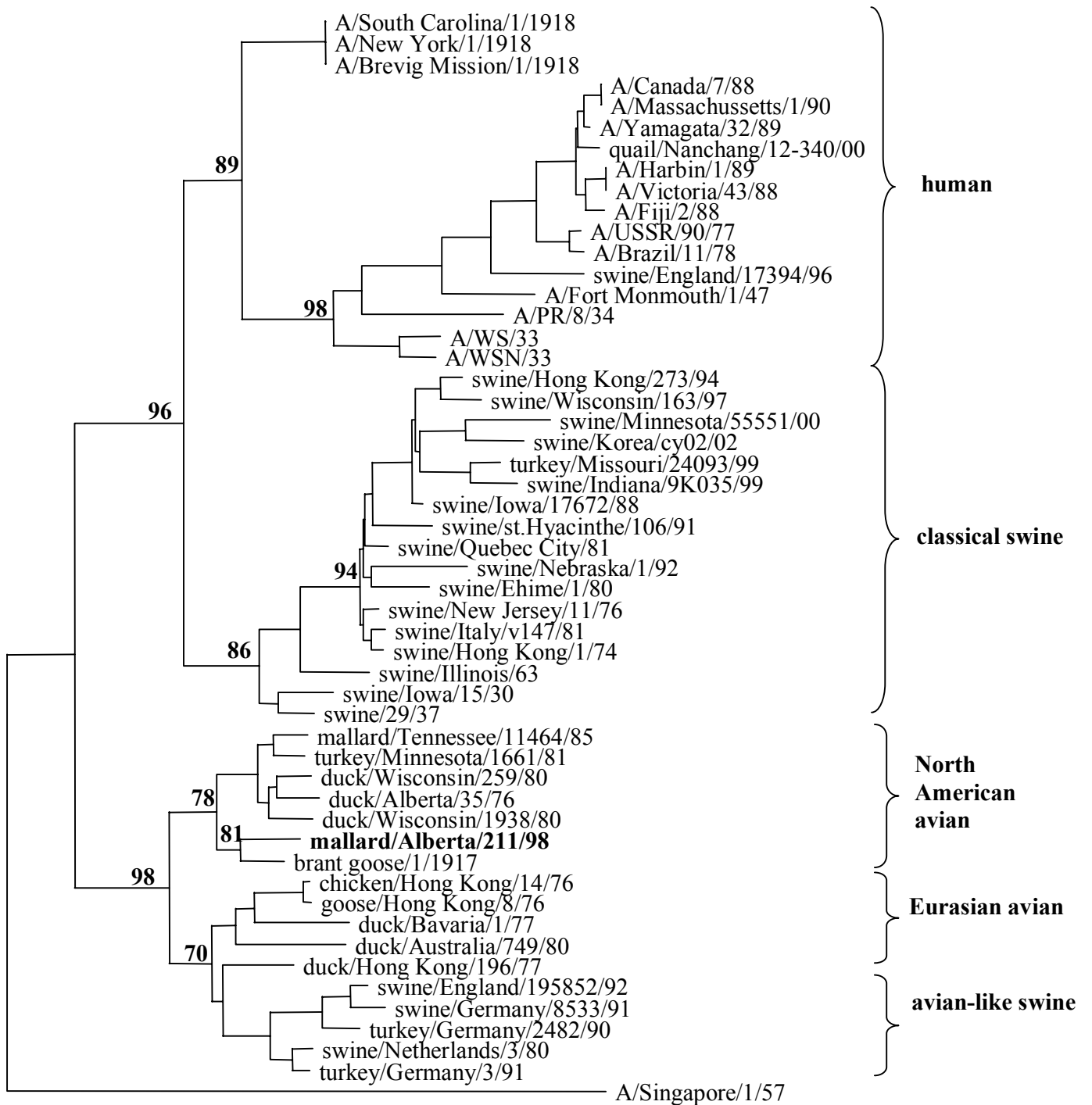
Supplemental Fig.5. M rooted to equine/prague/1/56



Supplemental Fig. 6. Matrix gene maximum parsimony tree rooted to A/equine/Prague/1/56 (H7N7) (221 taxa)

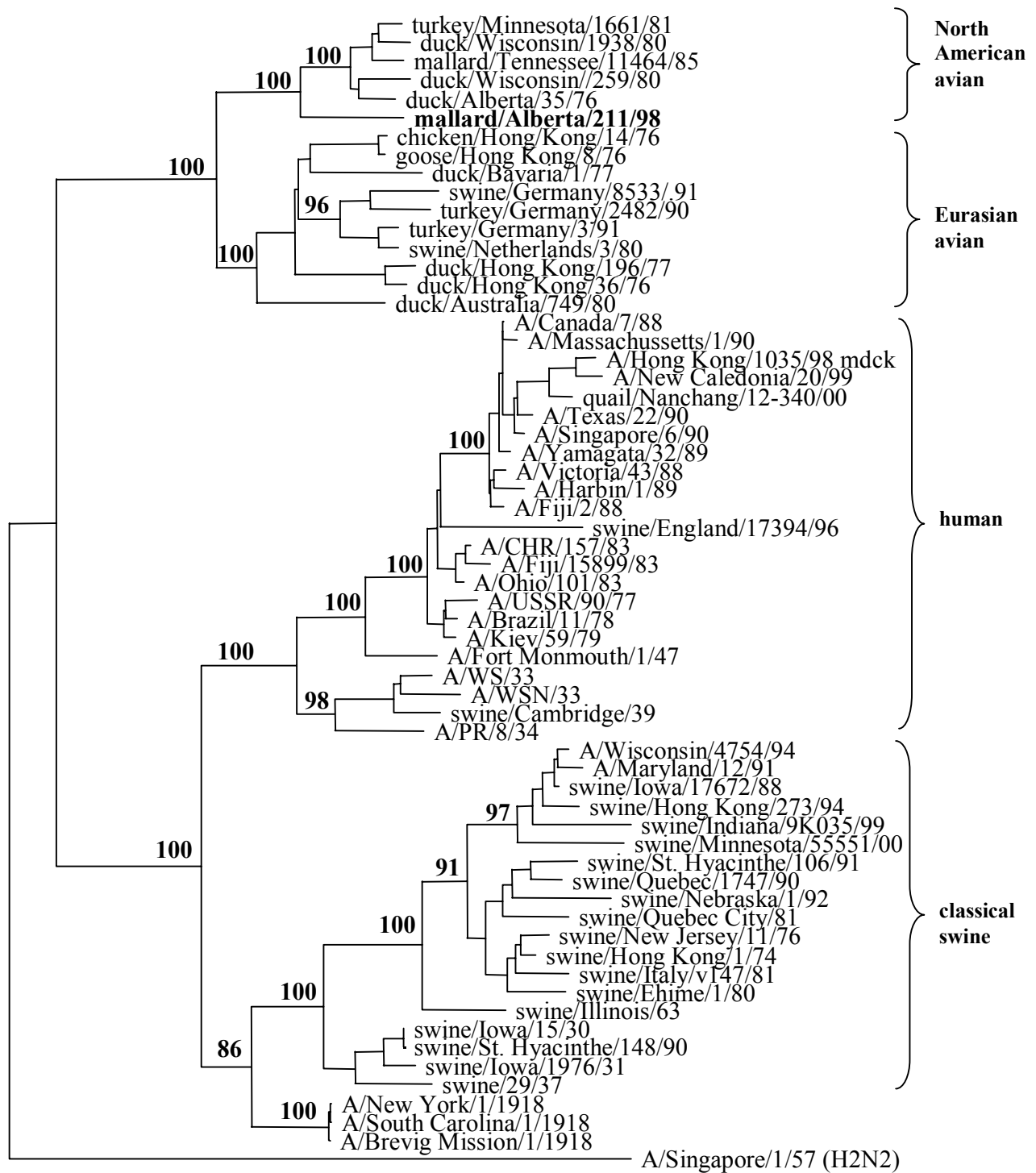


Supplemental Fig. 7. H1 nt 494-659 rooted to A/Singapore/1/57



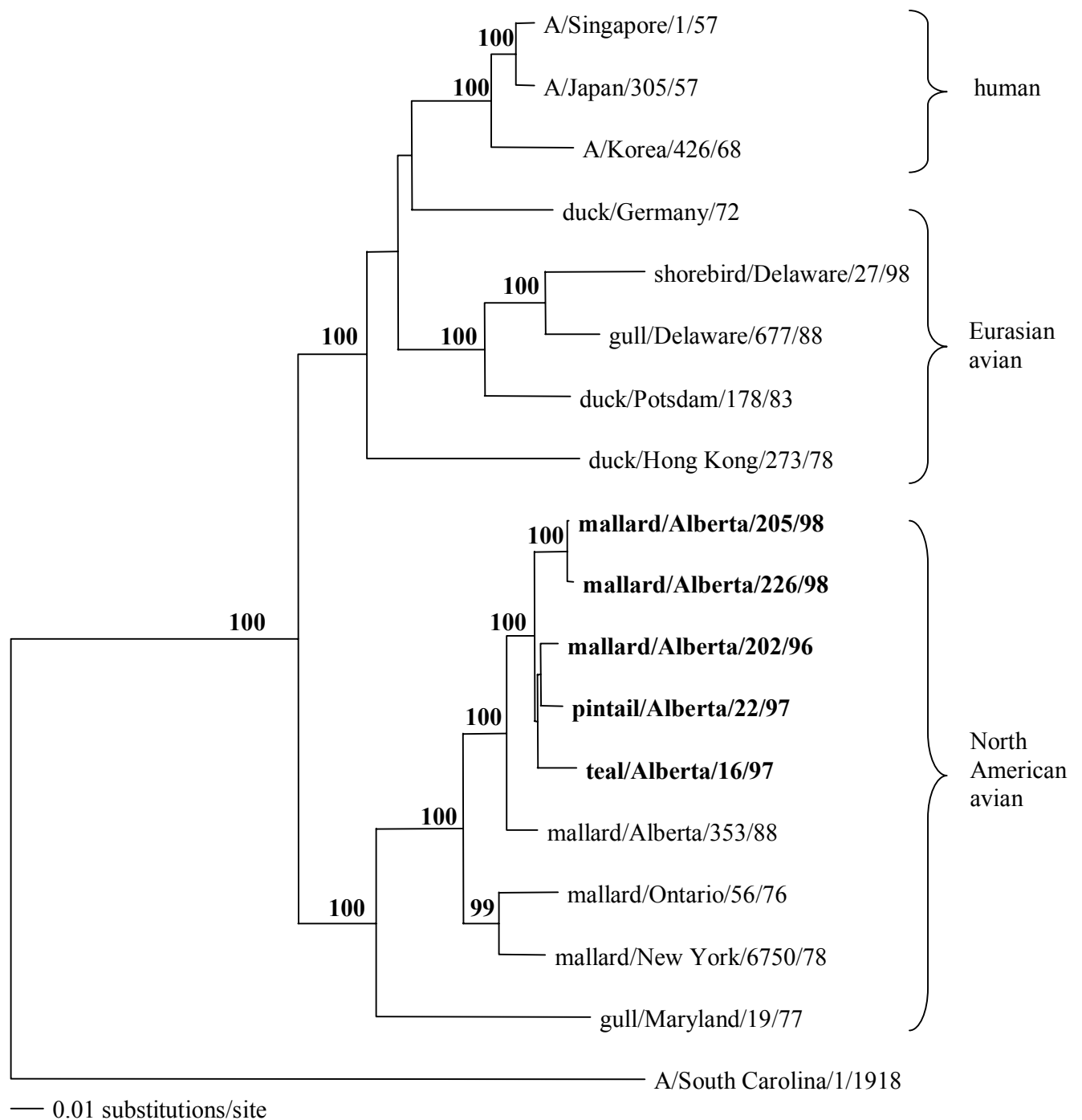
— 0.01 substitutions/site

Supplemental Fig. 8. H1 HA1 rooted to A/Singapore/1/57

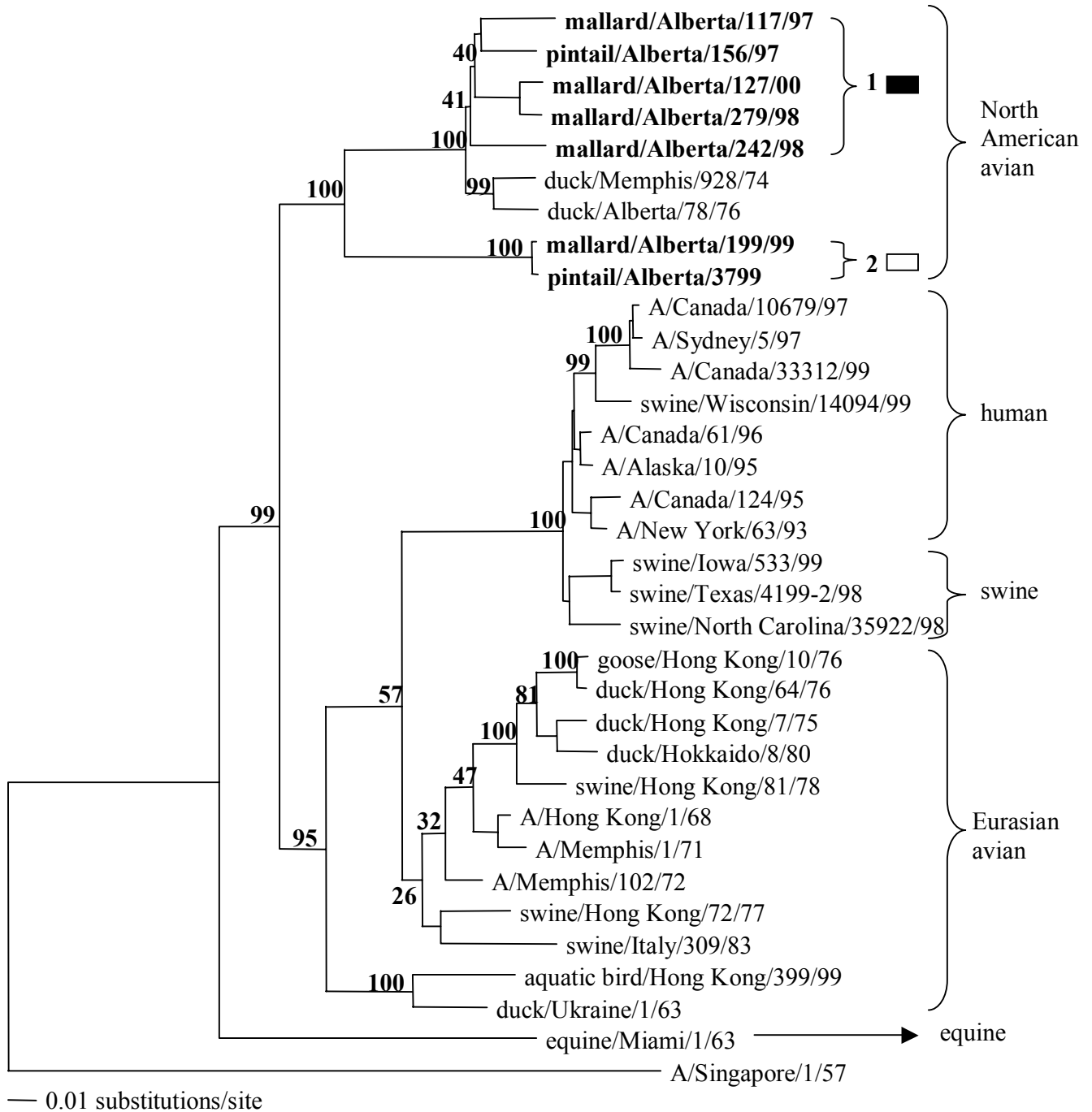


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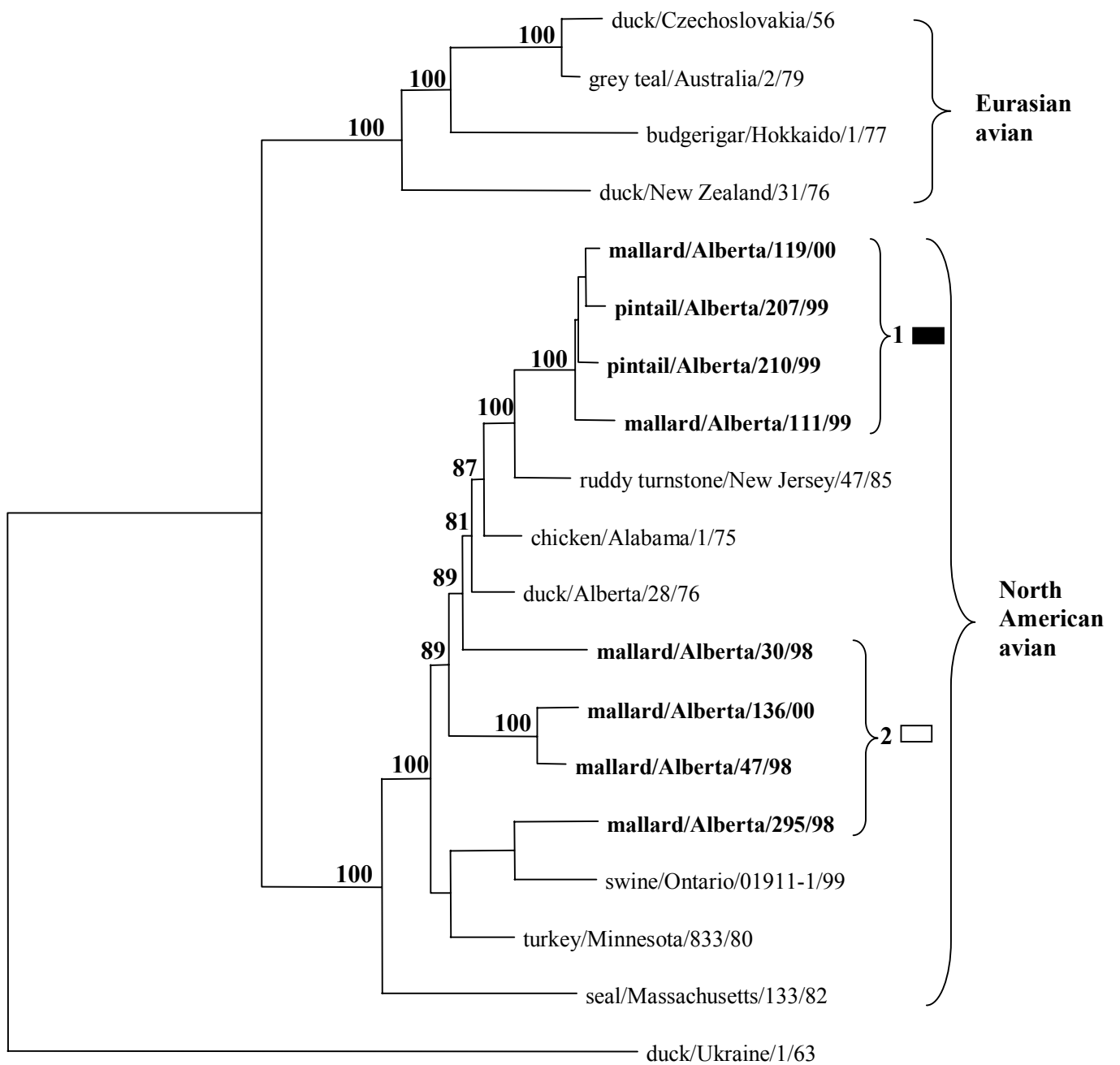
Supplemental Fig. 9. H2 rooted to A/South Carolina/1/1918



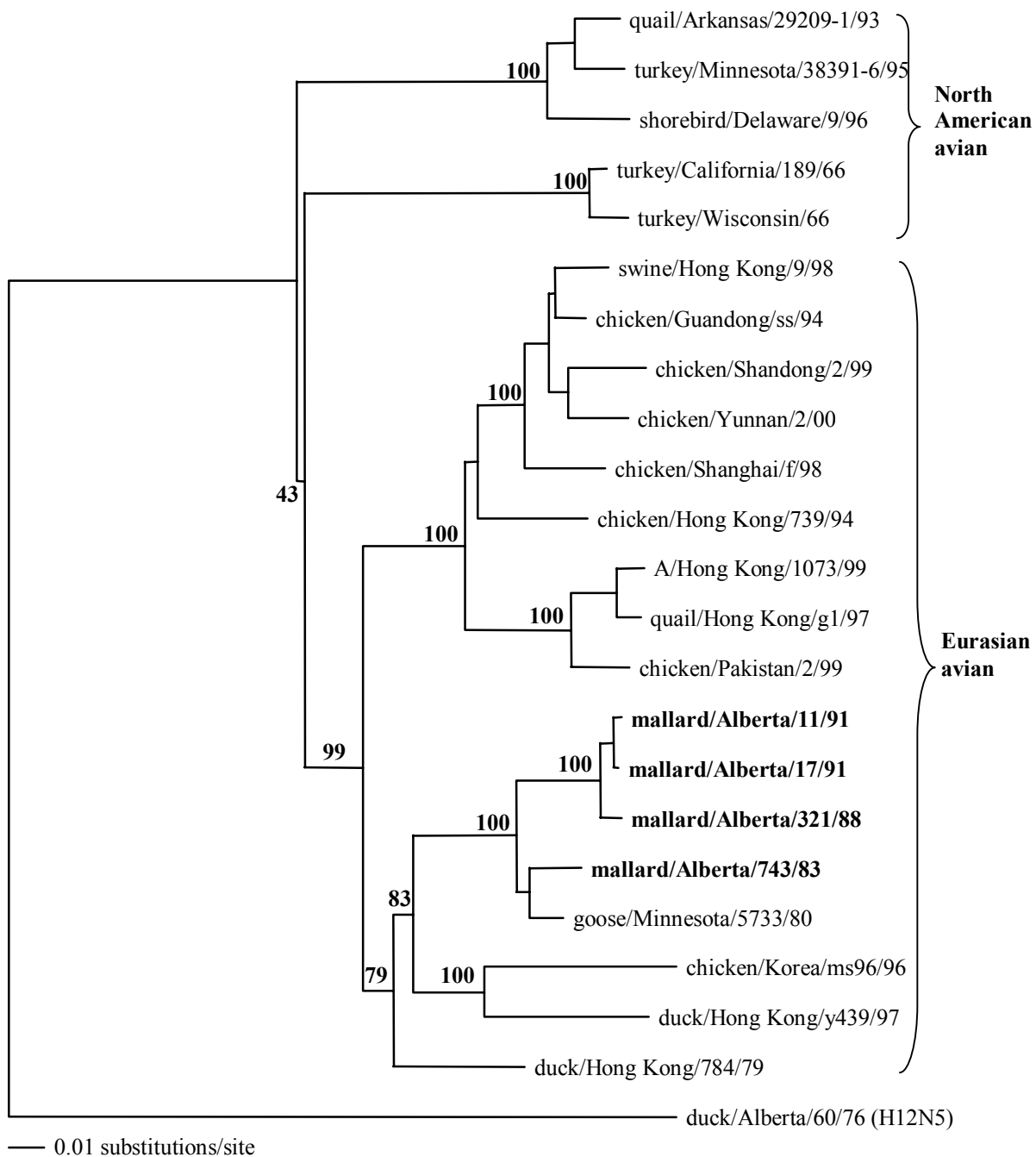
Supplemental Fig. 10. H3 rooted to A/Singapore/1/57



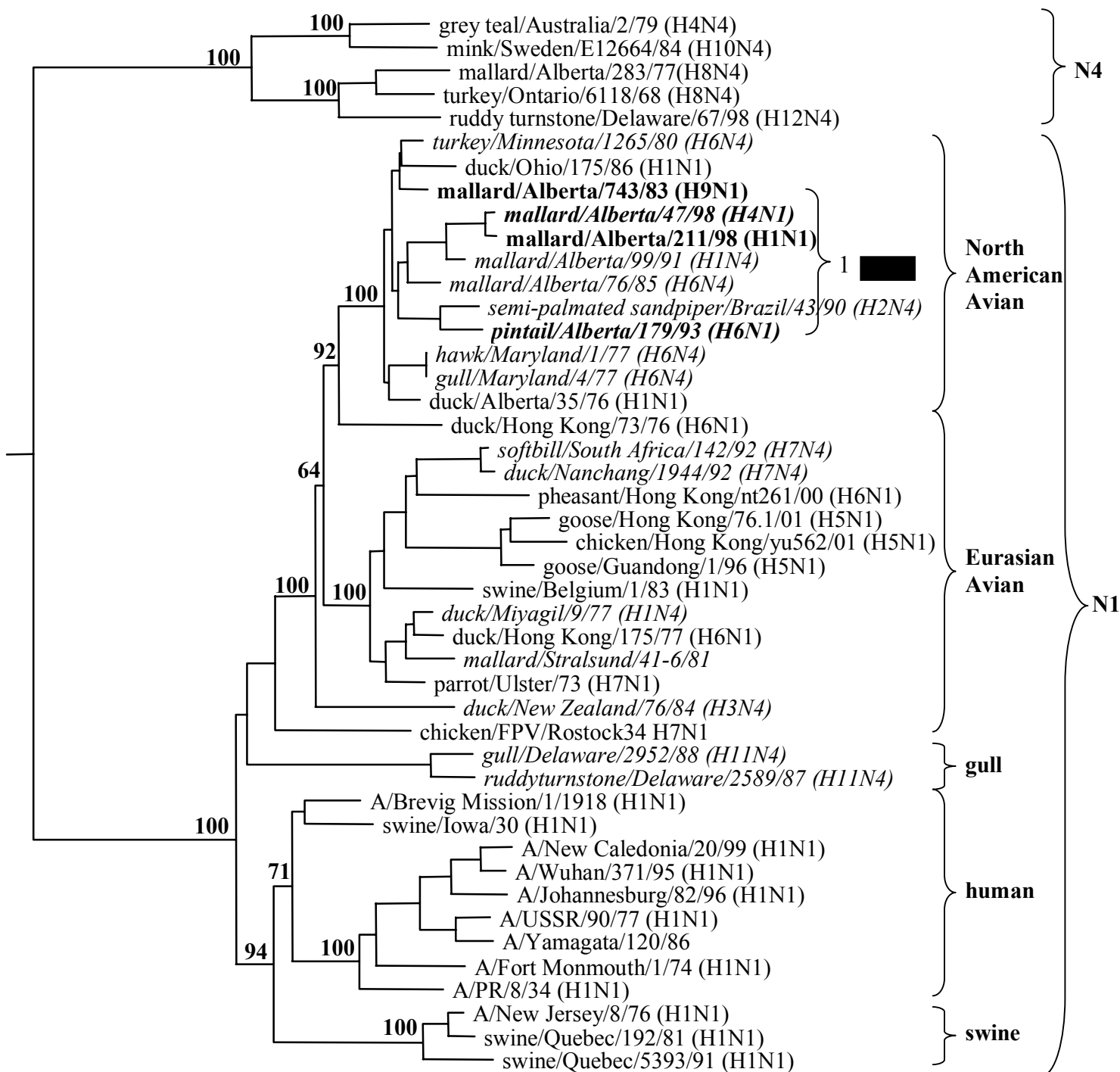
Supplemental Fig. 11. H4 rooted to duck/Ukraine/1/63



Supplemental Fig. 12. H9 rooted to duck/Alberta/60/76 (H12N5)

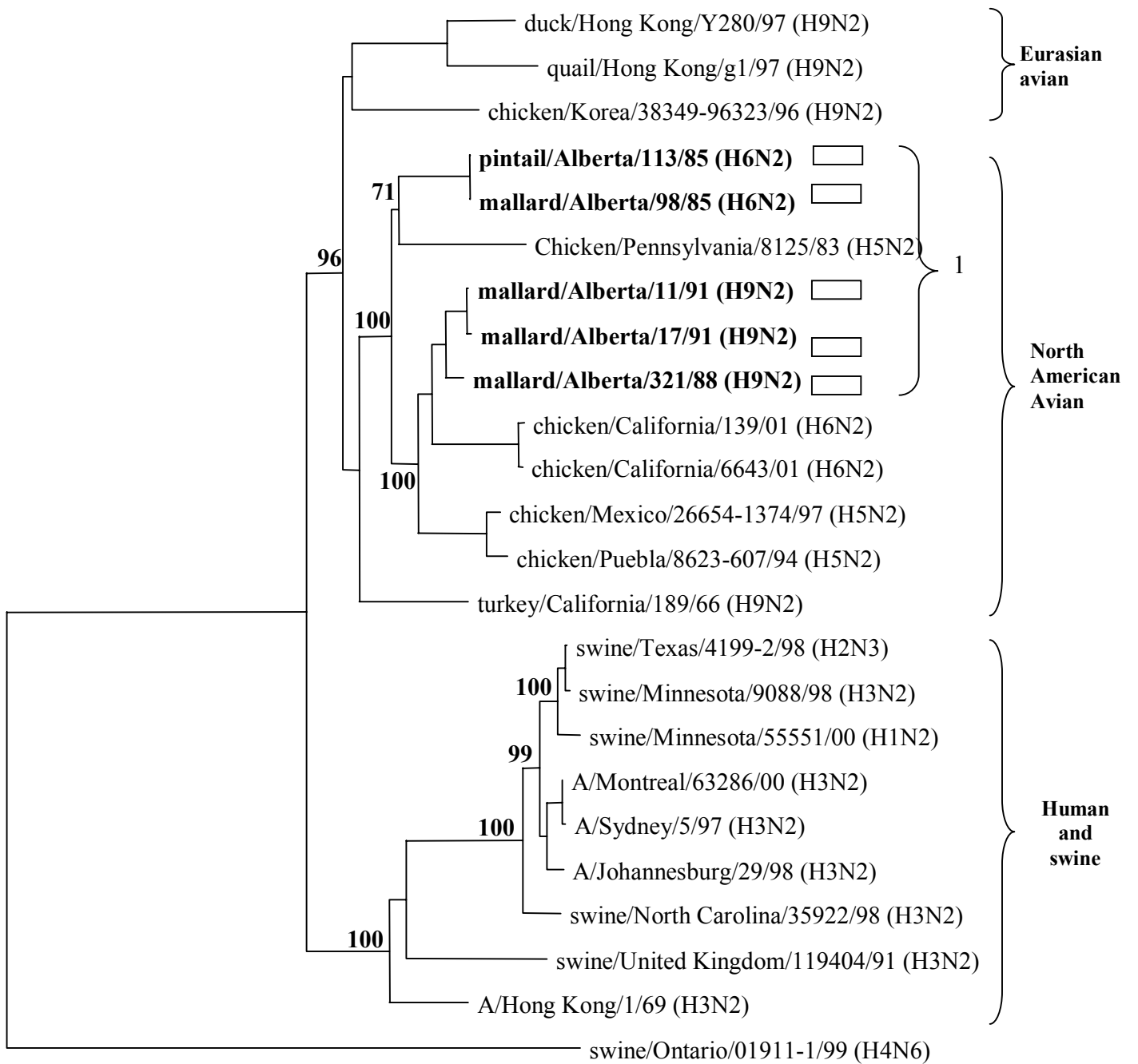


Supplemental Fig. 13. N1 and N4 trees rooted to A/turkey/Minnesota/5001/78 (H6N8)

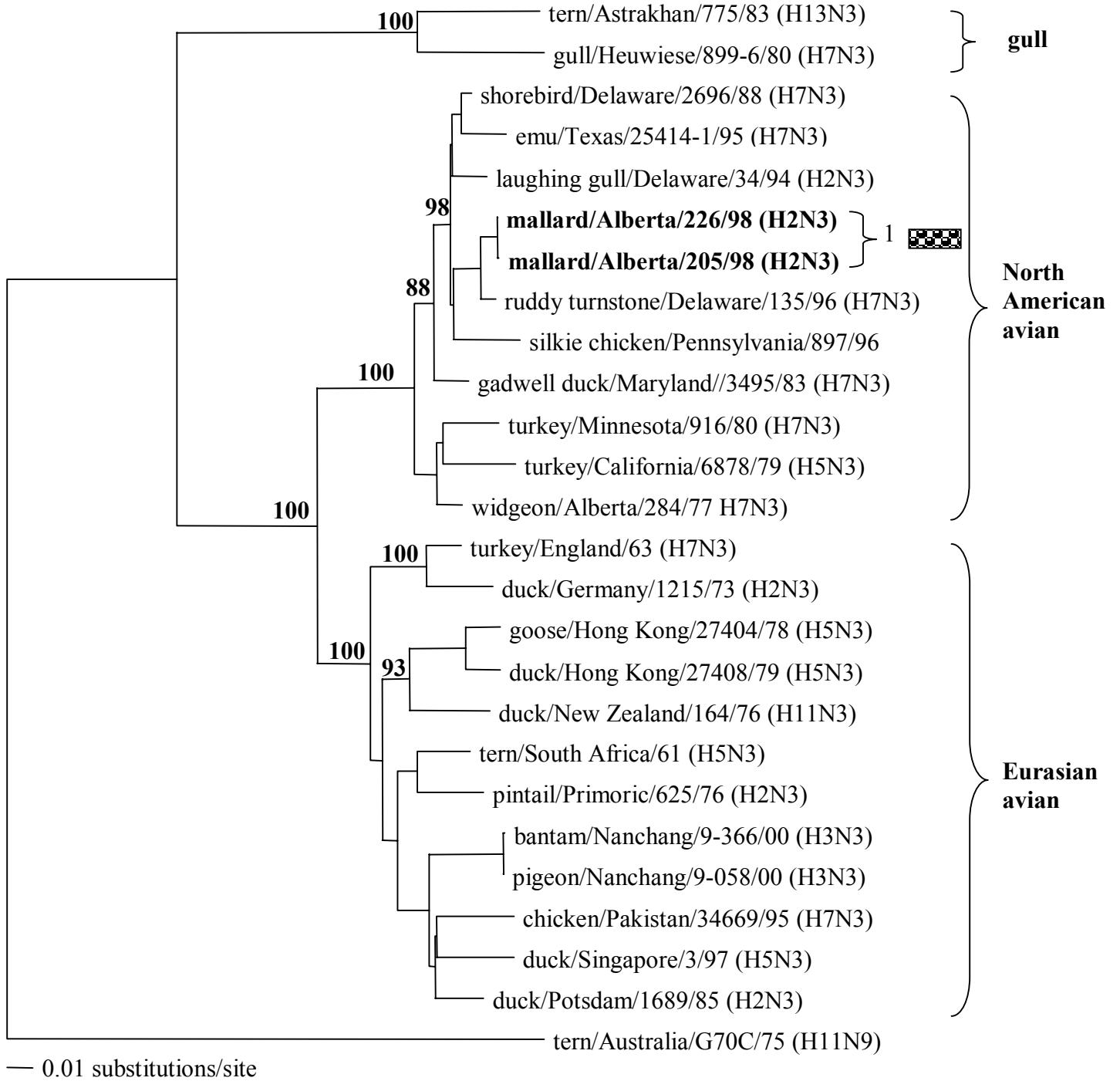


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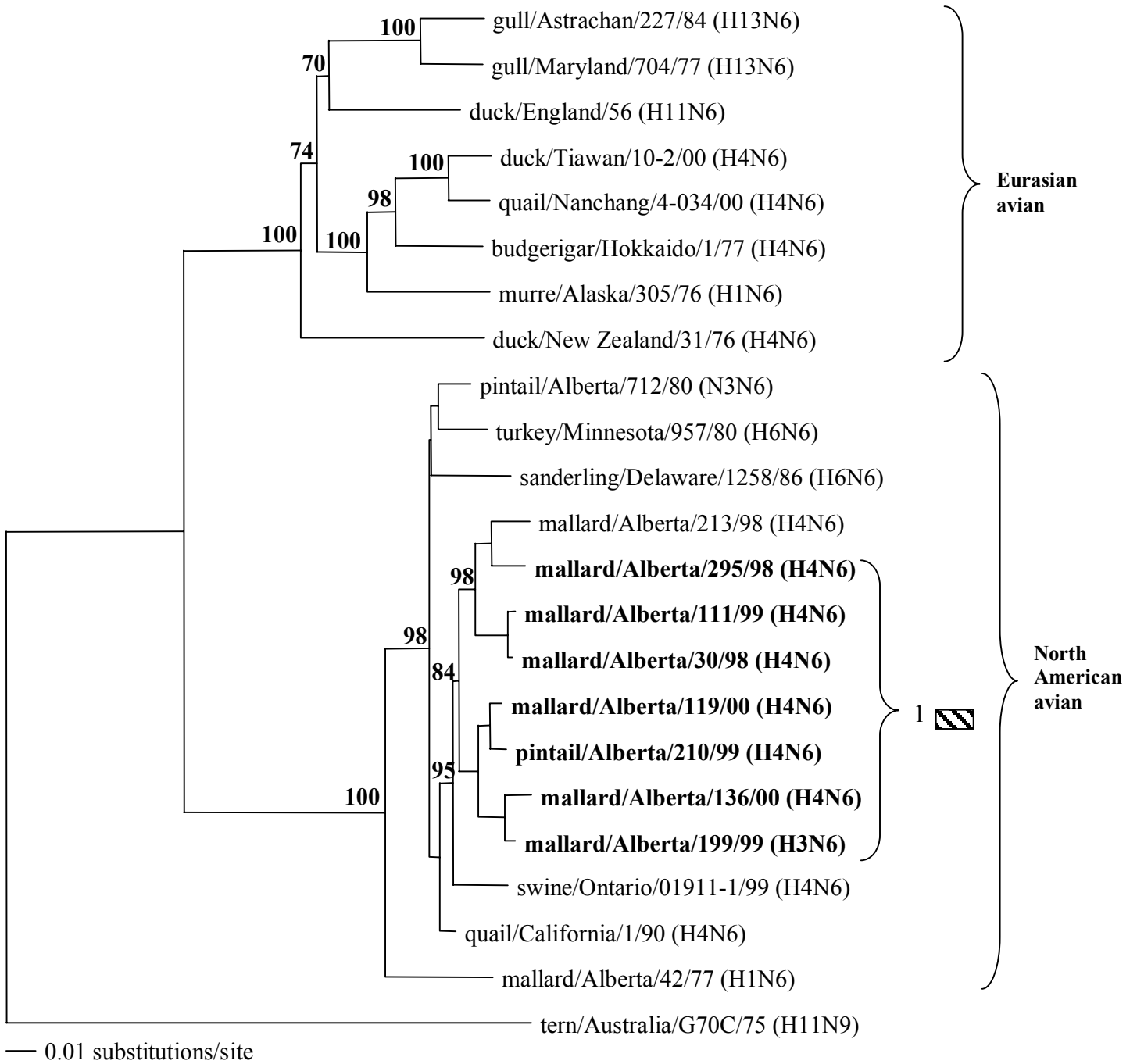
Supplemental Fig. 14. N2 rooted to swine/Ontario/01911-1/99 (H4N6)



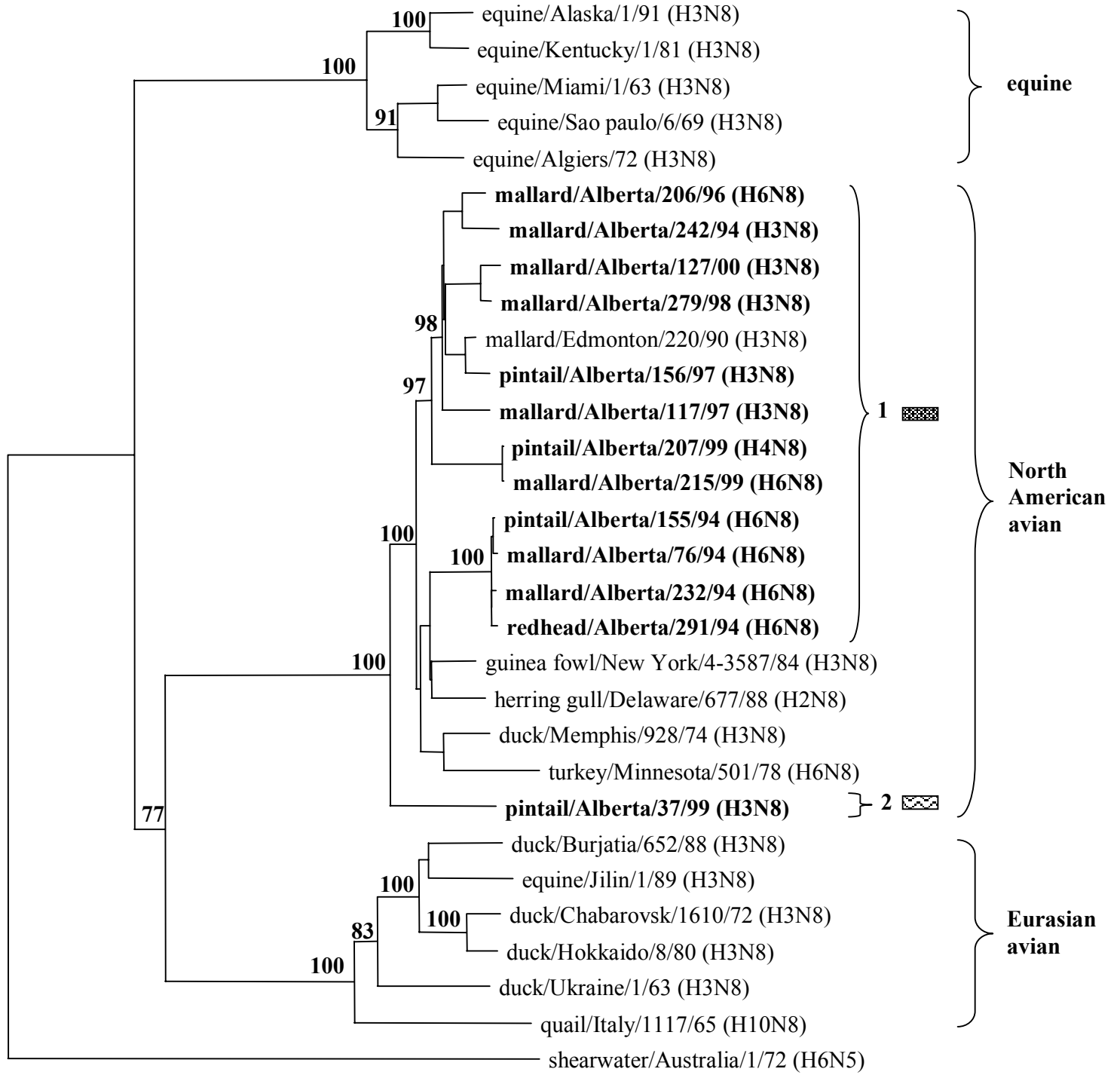
Supplemental Fig. 15. N3 rooted to tern/Australia/G70C/75 (H11N9)



Supplemental Fig. 16. N6 rooted to tern/Australia/G70C/75 (H11N9)



Supplemental Fig. 17. N8 rooted to Shearwater/Australia/1/72 (H6N5)



Supplemental Fig. 18. N9 rooted to swine/Ontario/01911-1/99 (H4N6)

