

Reassortment of Influenza A Viruses in Wild Birds in Alaska before H5 Clade 2.3.4.4 Outbreaks

Nichola J. Hill, Islam T.M. Hussein, Kimberly R. Davis, Eric J. Ma, Timothy J. Spivey, Andrew M. Ramey, Wendy Blay Puryear, Suman R. Das, Rebecca A. Halpin, Xudong Lin, Nadia B. Fedorova, David L. Suarez, Walter M. Boyce, Jonathan A. Runstadler

Sampling of mallards in Alaska during September 2014–April 2015 identified low pathogenic avian influenza A virus (subtypes H5N2 and H1N1) that shared ancestry with highly pathogenic reassortant H5N2 and H5N1 viruses. Molecular dating indicated reassortment soon after interhemispheric movement of H5N8 clade 2.3.4.4, suggesting genetic exchange in Alaska or surrounds before outbreaks.

The emergence of highly pathogenic avian influenza (HPAI) A virus subtype H5 of clade 2.3.4.4 in East Asia followed by spread into North America in 2014 highlights the importance of ecologic interactions along the Pacific Rim to the incursion of novel viruses. Introduction of influenza A subtype H5N8 into North America is hypothesized to have occurred through wild bird movement across the Bering Strait (1,2); the virus then spread through Canada to the continental United States, concurrently infecting wild birds (ducks, geese, passerines, and raptors) and poultry (turkeys and chickens) (3). Reassortment of H5N8 with low pathogenic avian influenza (LPAI) A virus in North America generated 3 subtypes (H5N8, H5N2, and H5N1, collectively referred to as H5Nx) that followed different trajectories in local bird populations. HPAI H5N2 became the most widespread in US poultry, prompting the culling of ≈49 million chickens and turkeys in 15 states (4). During the outbreaks (November 2014–December 2015),

Author affiliations: Massachusetts Institute of Technology, Cambridge, Massachusetts, USA (N.J. Hill, I.T.M. Hussein, K.R. Davis, E.J. Ma, W.B. Puryear, J.A. Runstadler); University of Alaska Fairbanks, Alaska, USA (T.J. Spivey); US Geological Survey, Anchorage, Alaska, USA (T.J. Spivey, A.M. Ramey); Vanderbilt University Medical Center, Nashville, Tennessee, USA (S. Das); J. Craig Venter Institute, Rockville, Maryland, USA (R.A. Halpin, X. Lin, N.B. Fedorova); US Department of Agriculture, Athens, Georgia, USA (D.L. Suarez); University of California, Davis, California, USA (W.M. Boyce)

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surveillance efforts increased; consequently, later stages of the epidemic were better characterized (5,6) relative to the beginning. Analysis of wild bird viruses from Alaska preceding outbreaks remains one of the few avenues for elucidating how H5N8 entered and reassorted with North American lineage viruses.

Our sampling of mallards (*Anas platyrhynchos*) from urban ponds in Anchorage, Alaska, during September 2014–April 2015 identified LPAI H5N2 and H1N1 (online Technical Appendix Figure 1, Table 1, <https://wwwnc.cdc.gov/EID/article/23/4/16-1668-Techapp1.pdf>). These viruses were the closest relatives for 4 of the 8 North American segments that contributed to the H5Nx reassortants based on the time of most recent common ancestry (tMRCA) analysis (online Technical Appendix Figures 2–12). All North American segments of the H5N2 reassortant (basic polymerase protein 1, nucleoprotein, and neuraminidase) shared most recent common ancestry with LPAI H5N2 that circulated in Anchorage mallards and a concurrently sampled wild bird population at Izembek National Wildlife Refuge in western Alaska (1) (online Technical Appendix Figures 3, 5, 8, 9). Molecular dating indicated reassortment of H5N8 and LPAI H5N2 (or precursors) shortly after the interhemispheric movement of H5N8. We estimated that ancestors of the H5N2 reassortant emerged among wild birds in Alaska during August 2013–May 2014, based on tMRCAs of multiple segments (Figure 1, panel A), followed by emergence of the H5N2 reassortant during May–September 2014. Our analysis refines the hypothesis of Beringia introduction (1,2) by indicating that H5N8 reassorted with viruses shed by waterfowl in Alaska (or nearby high latitudes) shortly after introduction into North America (May 2014–October 2014, 95% highest posterior density January 2014–January 2015) (Figure 1, panel A). Accuracy of molecular dating hinges on the availability of virus sequences from relevant hosts, which were lacking from North American poultry and wild birds during the year preceding outbreaks (Figure 1, panel B). Our sampling was fortuitous, being one of the few in Alaska conducted before the outbreaks, underscoring the importance of routine sampling where interhemispheric mixing of viruses occurs with high frequency.

The rapid reassortment of H5N8 clade 2.3.4.4 within North America is premised on the movement of at least a single infected bird across the Bering Strait followed by

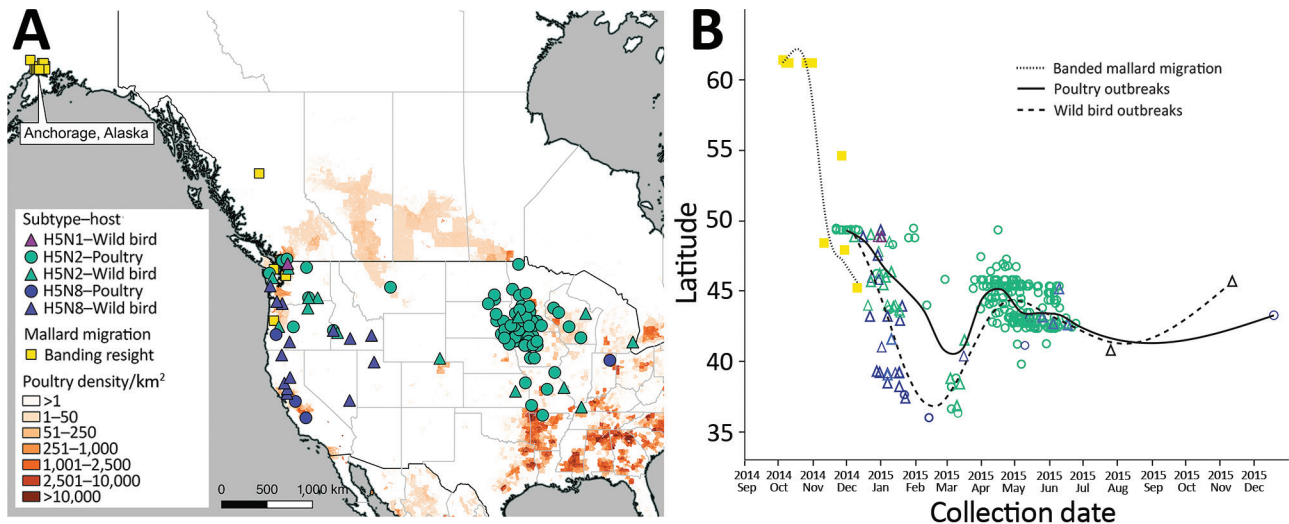


Figure 2. Spatial and temporal distribution of H5N1 and H5N8 influenza A virus outbreaks among wild birds and poultry across North America. A) Spatial distribution of H5N1 and H5N8 influenza A virus outbreaks in wild birds (triangles) and poultry (circles) across North America, color-coded by subtype, relative to poultry density. The location of mallards from Anchorage, Alaska, based on resighting of banded birds, is indicated. B) Temporal distribution of H5N1 and H5N8 influenza A virus detections during the course of the outbreaks relative to the migration of mallards banded in Anchorage.

on 2 segments suggest emergence after October 2014. The H5N1 and H5N8 reassortants possessed a highly similar polymerase acidic segment (online Technical Appendix Figure 6), suggesting a similar evolutionary trajectory of the two subtypes that later diverged. Our tMRCA estimates for H5N1 are consistent with reassortment during or after the breeding season for mallards in Alaska followed by southward dispersal along the Pacific Flyway during autumn (Figure 2). These results suggest that H5N1 is a multiple reassortant that acquired PB1 and NS segments in Alaska (or surrounds) followed by polymerase acidic and neuraminidase 2 from different host populations before detection in Washington (9) and Oregon (4) in early 2015.

Arrival of mallards banded in Anchorage at the high-density poultry region of the Fraser Valley, British Columbia, Canada, in November 2014 is compatible with the chronology of evolution and subsequent detection of the H5Nx subtypes (Figure 2). The migration chronology of banded mallards might be broadly representative of other dabbling duck species that breed in Alaska, such as the American green-winged teal (*Anas carolinensis*), American wigeon (*Anas americana*), and northern pintail (*Anas acuta*), in which H5Nx was detected at lower latitudes. Consequently, mallards and other waterfowl species probably were involved in the southward dispersal and reassortment of H5Nx followed by spillover to poultry. Observations of wild birds congregating at water bodies on poultry farms in the Fraser Valley support the scenario of indirect transmission from migratory birds to poultry, seeding outbreaks at lower latitudes (10). Later divergence of H5N2

into multiple lineages during May–November 2014 (online Technical Appendix Figure 8) implies that outbreaks were seeded by different H5N2 strains, although the mode of dispersal through wild bird migration, farm-to-farm poultry movement, or poultry workers remains unclear.

Since introduction of HPAI H5 of clade 2.3.4.4 into the Pacific Northwest in late 2014, little evidence exists for additional reassortment, despite continued spread of H5N2 and H5N8 until late 2015 (Figure 2, panel B). Lack of further reassortment implies a change from wild bird-mediated dispersal to intermittent spillover between wild birds and poultry or indirect transmission among poultry farms via fomites, wind, or other undetermined vectors. The spatiotemporal pattern of outbreaks in wild birds and poultry appeared correlated during this later phase (Figure 2, panel B). Correlation might be a function of outbreak investigation procedures that require concurrent sampling of poultry and wild birds inhabiting the control zone. However, our phylogenetic analysis lends support for frequent spillover given that lineages of H5Nx were mixed by host, rather than poultry and wild birds clustering separately (online Technical Appendix Figures 4–12). Our analysis and the August 2016 detection of HPAI H5N2 in mallards from Fairbanks, Alaska (11), an area lacking commercial poultry, implicates waterfowl as playing an important role in reassortment, spread, and possibly long-term circulation of H5Nx viruses.

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Dr. Hill is a postdoctoral associate at the Massachusetts Institute of Technology, Cambridge, Massachusetts, USA. Her primary research interests include the ecology and evolution of influenza viruses in natural and man-made systems.

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Address for correspondence: Jonathan A. Runstadler, Massachusetts Institute of Technology, Building 16-873, 77 Massachusetts Ave, Cambridge, MA 02139, USA; email: jrun@mit.edu

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Reassortment of Influenza A Viruses in Wild Birds in Alaska before H5 Clade 2.3.4.4 Outbreaks

Technical Appendix

Methods

Sampling of Wild Birds

The sampling locations were predominately at Cuddy Family Midtown Park, Anchorage, Alaska (61.184981°, -149.880597°) and Westchester Lagoon, Anchorage, Alaska (61.202333°, -149.90333°), two urban locations that attract overwintering mallards (online Technical Appendix Figure 1, panel A). Between September 2014 and April 2015 we sampled a total of 484 individual birds and recaptured 216. Baited swim and walk-in traps were used to capture mallards. We obtained a cloacal and tracheal swab from each bird and fitted each bird with an aluminum federal tarsus band. Polyester-tipped applicators were used to collect swabs, placed in viral transport media (VTM: Remel, KS) and kept on ice until transfer to -80 freezers in the laboratory.

Banding Data and Outbreak Analysis

We obtained recovery/recapture data for mallards banded in Anchorage from the U.S. Geological Survey Bird Banding Laboratory. Of the 468 ducks banded, a total of 75 (16.03%) bands were reported between 2014 and 2016, mostly representing hunter-shot ducks. Band returns were mapped using QGIS 2.0 (Open Source Geospatial Foundation Project. <http://qgis.osgeo.org>) to describe connectivity of the Anchorage mallard population with other regions in North America. Poultry (chicken) density layers were obtained from the Gridded Livestock of the World (*1*) available online. Location and timing of all H5 clade 2.3.4.4 outbreaks were obtained from federal agency Web sites for the U.S. (U.S. Department of Agriculture [2]) and Canada (Canadian Food Inspection Agency [3]). A smoothing average for the spatiotemporal pattern of outbreaks was plotted separately for wild bird and poultry cases

separately (JMP Pro 12.2, SAS), as well as the chronology of mallard migration (Figure 2, panel B).

Virus Isolation and Sequencing

Viral RNA was extracted using the Omega Mag-Bind Viral DNA/RNA Kit (Omega Bio-Tek, Norcross, GA) and a Kingfisher magnetic particle processor (Thermo Scientific, Waltham, MA). RNA was screened for the presence of influenza A virus (IAV) using qScript XLT one-step RT-qPCR Tough Mix (Quanta Biosciences, Gathersburg, MD) targeting the matrix gene. PCR assays were run on an ABI 7500 real-time PCR System (Applied Biosystems, Foster City, CA). PCR-positive samples (Ct value <45) were subjected to a H5-specific rRT-PCR to identify potentially highly pathogenic samples (4). All H5-positive samples were sent to the U.S. National Poultry Research Center, USDA to culture potential HPAI viruses. To amplify virus, positive VTM (100ul) was inoculated into the allantoic cavity of 9–11 day old embryonating specific pathogen free chicken eggs (Charles River, CT) and incubated at 37°C for 72 hours or until embryo death, as detected by daily candling. RNA was extracted from the allantoic fluid and the matrix rRT-PCR repeated (5). Whole-genome sequencing was performed at the J. Craig Venter Institute in Rockville, MD as described by Nelson et al. (6) and all sequences deposited into GenBank (online Technical Appendix Table 1). Subtyping was confirmed by BLASTn of the sequence against isolates in GenBank and identifying the subtype match that showed highest percentage identity.

Multiple Sequence Alignment

Global IAV sequences were downloaded from the Influenza Research Database (IRD [7]) and Global Initiative on Sharing All Influenza Data (GISAID) during the period between 1/17/16 - 2/16/16. Only full genomic segments (PB2, PB1, PA, H5, NP, N2, N1, M and NS) of isolates collected during the period (1976 – 2016) were considered. Only sequences associated with a full date of collection (DD/MM/YYYY) were included. To facilitate filtering out duplicate sequences, taxa names were edited to remove apostrophes, brackets and all hyphens were replaced with underscores. Sequences containing misreads (NNNs) were deleted to improve the quality of alignments and subsequent trees. Sequences were then aligned using MUSCLE v3.8.31 (8), inspected visually in Geneious v7.1.5 to remove indels and taxa containing premature termination codons, then re-aligned once again using MUSCLE.

Down-Sampling before Tree Reconstruction

The aligned global sequence datasets were down-sampled to reduce the number of sequences to a size suitable for molecular clock Bayesian phylogenetic analysis (~300 taxa). The goal of down-sampling was 3-fold: 1) preserve all clade 2.3.4.4 isolates from North America; 2) preserve basal avian and mammalian lineages to accurately root the tree in deep evolutionary time; and 3) random down-sampling of non-clade 2.3.4.4 isolates stratified by time (3–5 isolates randomly preserved per year) to ensure confidence in tree topology from root to tips (online Technical Appendix Figure 13). Down-sampling was conducted using a series of Python scripts (available for download: [10.5281/zenodo.61923](https://doi.org/10.5281/zenodo.61923)). A preliminary phylogenetic tree using the global sequence alignment for each segment was constructed using the GTRGAMMA substitution model in RAxML v 8.1.16 (9). The resulting maximum likelihood trees were used to compute patristic distances between a designated ‘taxa-of-interest’ group and the rest of the global dataset. This taxa-of-interest group included recent isolates from Anchorage and Izembek (2014) and all clade 2.3.4.4 isolates from North America.

To determine the minimum number of closest relatives to the taxa-of-interest needed to construct a well-sampled Bayesian phylogenetic tree we evaluated 3 metrics in TreeStat v1.8.2: i) time of most recent common ancestry (tMRCA); ii) tree height/root age; and iii) treeness (tree shape). These values were generated for the closest 10 and 25 relatives of the in-group by constructing preliminary Bayesian trees in BEAST v 1.8.3 (10). At least 3 independent Bayesian Markov Chain Monte Carlo (MCMC) chains, of 40 – 80 million generations each, were run and sampled under the Bayesian skyride coalescent model and the uncorrelated lognormal distribution, to produce 10,000 trees. In all cases we used a GTR + gamma substitution model. MCMC chains were visually assessed in Tracer v1.6.0 (<http://tree.bio.ed.ac.uk/software/tracer>) to ensure convergence on the same optimal tree. After removing 10 – 30% burn-in from each chain we combined trees and constructed maximum clade credibility trees. High similarity between the closest 10 and 25 relatives for the 3 metrics tested (online Technical Appendix Table 2) validated our decision to use the closest 10 relatives to reduce computational burden without compromising the reproducibility of the Bayesian trees. This data-driven approach guided how to down-sample the internal segments. For the H5 and N2 segments, we included the closest 100 relatives, and for N1, we included the closest 25 relatives owing to the limited taxa available.

To achieve down-sampling stratified by time – a strategy we used to increase accuracy of molecular dating of divergence events, a maximum of 100 taxa were randomly selected from our global datasets, spanning 1996–2016, with an average of 3–5 isolates per year. The 1996 cutoff was chosen because it marks the emergence of the A/goose/Guangdong/1/1996 lineage. A compiled BEAST dataset was obtained by combining recent Alaskan isolates, the in-group of clade 2.3.4.4 isolates and randomly selected taxa. The down-sampled datasets contained the following numbers of taxa: PB2 = 321, PB1 = 334, PA = 309, H5 = 370, NP = 347, N2 = 311, N1 = 277, M = 362, and NS = 374.

Bayesian Phylogenetic Analysis

Dated phylogenetic trees for each segment were constructed using BEAST v1.8.3. At least 4 independent MCMC chains, of 40 – 80 million generations each, were run using the GMRF Bayesian skyride coalescent tree prior and uncorrelated lognormal distribution to produce 10,000 trees. To ensure MCMC chains converged on the same optimal tree, runs were visually inspected in Tracer v1.6.0. After removing 10 – 30% burn-in from each chain, the trees were combined to produce a single maximum clade credibility (MCC) tree.

Molecular Dating Analysis

The time of most recent common ancestry (tMRCA) for each taxon was inferred from the nodes of the MCC tree inspected in FigTree v1.4.3. The tMRCA dates and 95% highest posterior densities (95% HPD) for all segments were used to assess the order of gene introduction events (Figure 1, panel A). We also considered the posterior probabilities associated with each branch node when estimating gene segment introduction events. Only gene segment introductions associated with a posterior probability greater than 0.85 were considered such that bifurcating nodes with low support were ignored. We considered this an important step in view of the uneven sampling regime (targeting poultry farms) and low number of viruses sequenced during the outbreak period. As a result, not all influenza segments contributed equally to this analysis. For the matrix (M) and non-structural (NS) genes, low posterior probabilities for branch nodes (Technical Appendix Figure 12) combined with reverse branching (ambiguity in the exact timing of divergence events) precluded their use for estimating gene introduction events. These conserved segments were of limited value for estimating the rapid evolution of H5 clade 2.3.4.4, especially in view of the low number of sequences available before the outbreaks.

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Technical Appendix Table 1. List of 12 influenza A virus strains (H5N2 and H1N1) isolated from mallards in Anchorage, Alaska, that were precursors to the reassortment event with highly pathogenic H5N8 clade 2.3.4.4

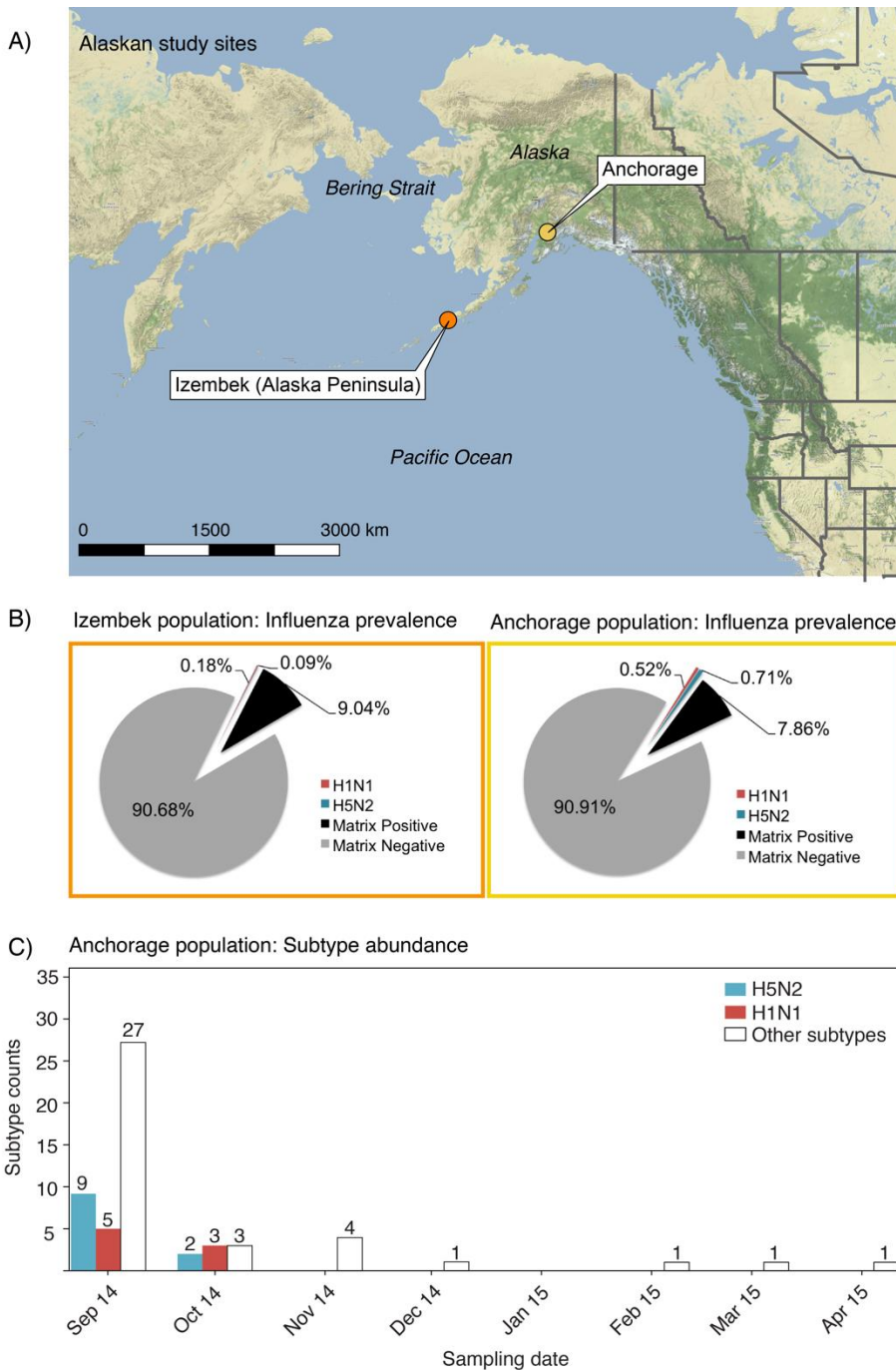
Strain name	Accession numbers	Subtype	Sampling date	Swab type	Mallard age	Band number
A/mallard/Southcentral Alaska/12ML00957/2014	CY206693-CY206700	H1N1	19-Sep-14	Cloacal	Hatch-year	2047–55491
A/mallard/Southcentral Alaska/12ML00991/2014	CY194156-CY194163	H5N2	22-Sep-14	Cloacal	Hatch-year	2047–55121
A/mallard/Southcentral Alaska/12ML00985/2014	CY194147-CY194155	H5/3N2	22-Sep-14	Cloacal	Hatch-year	2047–55110
A/mallard/Southcentral Alaska/12ML00988_AAF1/2014	CY194181-CY194188	H5N2	22-Sep-14	Oral	Hatch-year	2047–55104
A/mallard/Southcentral Alaska/12ML00977/2014	CY194139-CY194146	H5N2	22-Sep-14	Cloacal	Hatch-year	2047–55107
A/mallard/Southcentral Alaska/12ML00995/2014	CY206733-CY206740	H1N1	22-Sep-14	Cloacal	Hatch-year	2047–55113
A/mallard/Southcentral Alaska/12ML01009/2014	CY206741-CY206748	H1N1	22-Sep-14	Cloacal	Hatch-year	2047–55117
A/mallard/Southcentral Alaska/12ML01048_AAF1/2014	CY194213-CY194220	H5N2	23-Sep-14	Cloacal	Hatch-year	2047–55138
A/mallard/Southcentral Alaska/12ML01045/2014	CY206781-CY206788	H1N1	23-Sep-14	Cloacal	Hatch-year	2047–55136
A/mallard/Southcentral Alaska/12ML01175/2014	CY206797-CY206805	H1N1	20-Oct-14	Cloacal	After hatch-year	2047–55005
A/mallard/Southcentral Alaska/12ML01443/2014	CY206806-CY206813	H1N1	24-Oct-14	Cloacal	Hatch-year	2047–55025
A/mallard/Southcentral Alaska/12ML01469/2014	CY194164-CY194172	H5/9N2	24-Oct-14	Cloacal	Hatch-year	2047–55065

Technical Appendix Table 2. Time of most recent common ancestry (tMRCA) for each of the 8 influenza segments

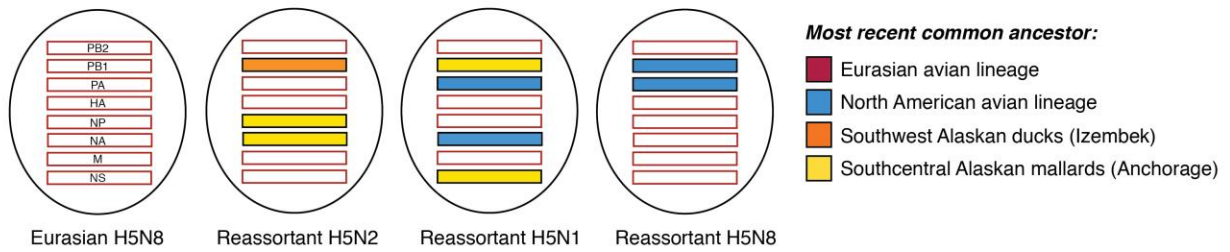
Segment	Emergence event	Posterior probability	tMRCA	Maximum tMRCA	Minimum tMRCA
PB2	Eurasian ancestor of North American clade 2.3.4.4	0.999	23-Feb-14	27-Jul-14	6-Sep-13
PB2	H5N8 clade 2.3.4.4 emerges in North America	1.000	5-Jul-14	27-Sep-14	4-Apr-14
PB2	H5N1 reassortant emerges	0.881	2-Nov-14	17-Dec-14	12-Sep-14
PB2	H5N2 reassortant emerges	0.960	9-Sep-14	19-Oct-14	15-Jun-14
PB2	Alaskan ancestor of H5N2 reassortant	1.000	4-May-14	14-Aug-14	27-Dec-13
PB2	Alaskan ancestor of H5N1 reassortant	1.000	2-Nov-13	15-Apr-14	2-May-13
PB1	Eurasian ancestor of North American clade 2.3.4.4	1.000	12-May-14	2-Nov-14	21-Oct-13
PB1	H5N8 clade 2.3.4.4 emerges in North America	1.000	22-Oct-14	8-Jan-15	9-Jul-14
PB1	Alaskan ancestor of H5N2 reassortant	0.999	22-Aug-13	16-Apr-14	1-Dec-12
PB1	H5N2 reassortant emerges	1.000	15-Sep-14	19-Dec-14	13-May-14
PB1	Alaskan ancestor of reassortant H5N1	1.000	31-May-14	30-Oct-14	16-Nov-13
PB1	H5N1 reassortant emerges	1.000	25-Dec-14	1-Feb-15	23-Oct-14
PB1	H5N8 reassortant emerges	1.000	28-Dec-14	9-Feb-15	6-Nov-14
PA	Eurasian ancestor of North American clade 2.3.4.4	1.000	24-Jan-14	22-Jun-14	6-Aug-13
PA	H5N8 clade 2.3.4.4 emerges in North America	1.000	16-May-14	25-Aug-14	21-Jan-14
PA	North American ancestor of H5N8 & H5N1 reassortant	1.000	10-Mar-14	7-Nov-14	7-May-13
PA	H5N2 reassortant emerges	1.000	19-Aug-14	10-Oct-14	13-Jun-14
PA	H5N8 reassortant emerges	1.000	18-Oct-14	4-Jan-15	29-Jun-14
PA	H5N1 reassortant emerges	0.995	21-Oct-14	31-Dec-14	27-Jul-14
H5	Eurasian ancestor of North American clade 2.3.4.4	1.000	25-Apr-14	30-Jun-14	10-Feb-14
H5	H5N8 clade 2.3.4.4 emerges in North America	0.999	10-Jun-14	5-Aug-14	9-Apr-14
H5	North American ancestor of H5N8 & H5N1 reassortant	0.992	1-Nov-14	20-Nov-14	27-Sep-14
H5	H5N1 reassortant emerges	1.000	8-Dec-14	26-Dec-14	14-Nov-14
H5	H5N2 reassortant emerges	0.998	27-Jul-14	18-Sep-14	2-Jun-14
H5	Alaskan ancestor of H5N2 reassortant	1.000	3-Mar-14	29-Jun-14	7-Oct-13
H5	H5N8 reassortant emerges	0.225	9-Dec-14	11-Jan-15	15-Oct-14
NP	Eurasian ancestor of North American clade 2.3.4.4	0.990	24-Dec-13	15-Aug-14	15-Jun-13
NP	H5N2 reassortant emerges	0.993	9-Jul-14	24-Sep-14	26-Oct-13
NP	Alaskan ancestor of H5N2 reassortant	0.992	9-Jan-14	23-May-14	11-Dec-12

Segment	Emergence event	Posterior probability	tMRCA	Maximum tMRCA	Minimum tMRCA
NP	Alaskan ancestor of H5N1 reassortant	0.806	3-May-14	28-Jul-14	7-Sep-13
N1	H5N1 reassortant emerges	1.000	9-Jul-14	9-Nov-14	16-Jun-14
N2	H5N2 reassortant emerges	0.992	6-May-14	18-Aug-14	7-Jan-14
N2	Alaskan ancestor of H5N2 reassortant	0.918	15-Dec-13	12-Mar-14	1-Jan-13
M	Eurasian ancestor of North American clade 2.3.4.4	0.005	1-Jan-14	19-Jan-14	18-Oct-13
NS	Eurasian ancestor of North American clade 2.3.4.4	0.001	24-Sep-13	12-Dec-13	25-Aug-13
NS	Alaskan ancestor of reassortant H5N1	0.996	21-Mar-14	29-Aug-14	3-Jan-14
NS	H5N1 reassortant emerges	0.999	24-Sep-14	26-Dec-14	16-Sep-14
NS	H5N2 reassortant emerges	0.001	7-Sep-13	19-Jan-14	22-Aug-13

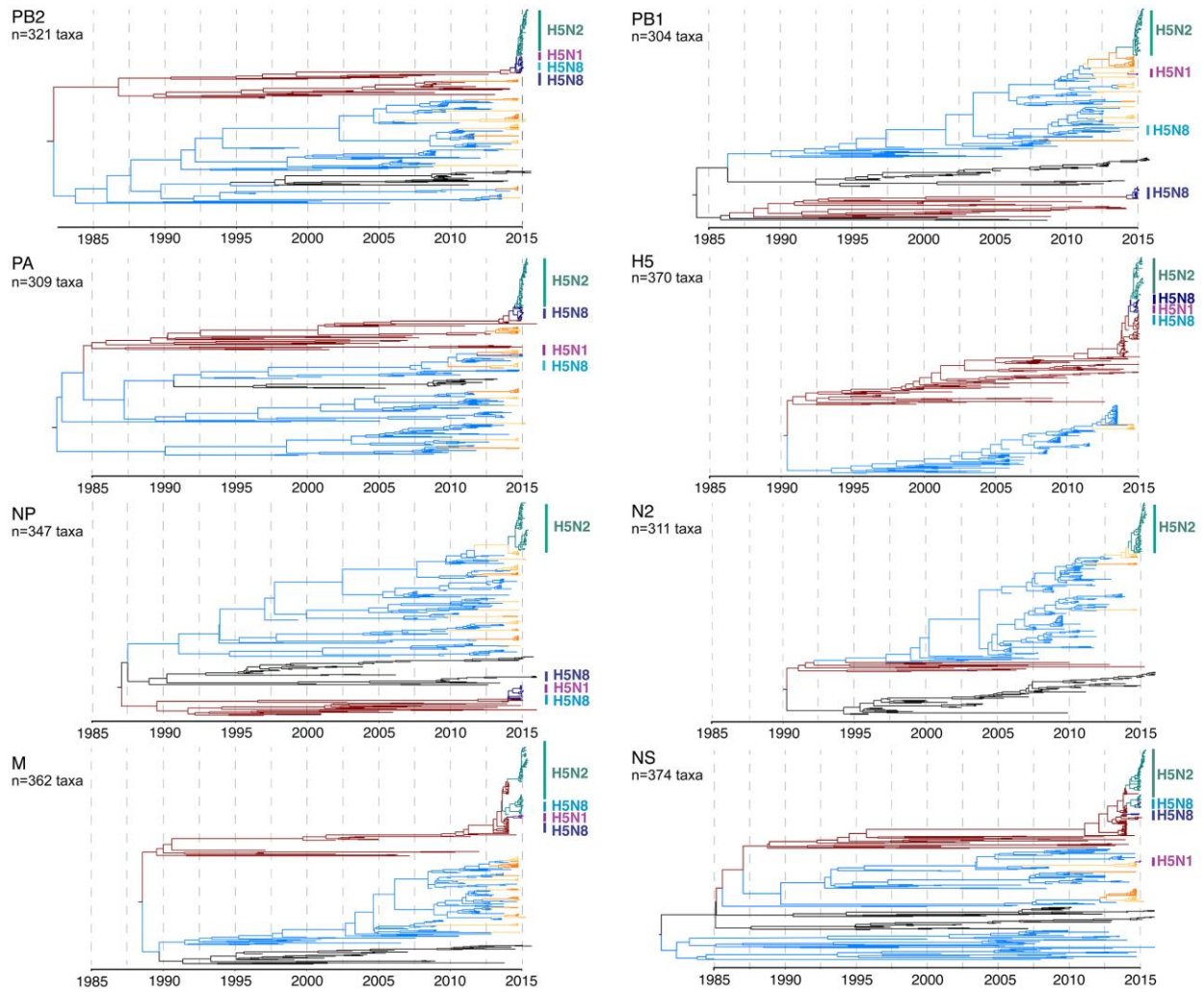
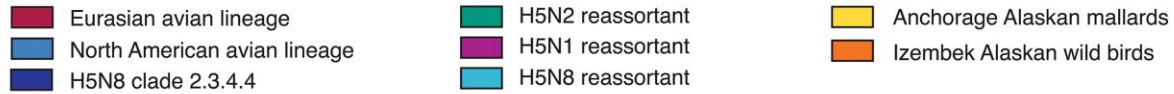
*tMRCA estimates with posterior probabilities >0.85 are highlighted in bold. Segments with Alaskan ancestry based on phylogenetic trees (online Technical Appendix Figures 4–12) are shaded in gray.



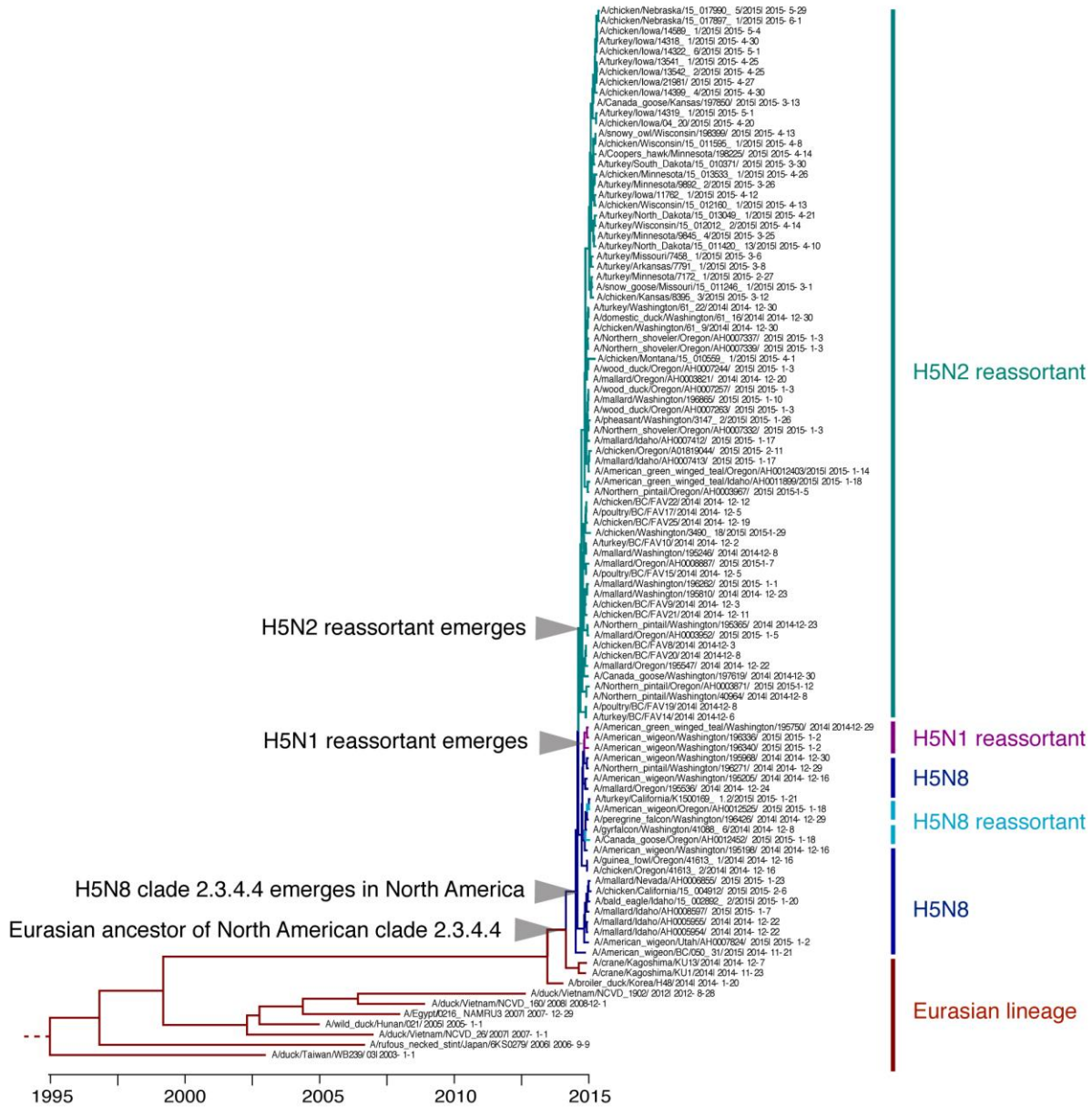
Technical Appendix Figure 1. Location of the Anchorage study site relative to the concurrently sampled Izembek site and prevalence of influenza A virus and the low pathogenic H5N2 subtype at each of the 2 sites. A) Location of the Anchorage study site relative to the concurrently sampled Izembek site, Alaska Peninsula. These were the only sites sampled in Alaska before the 2014 outbreaks. B) Prevalence of influenza A virus and the low pathogenic H5N2 subtype at each of the 2 sites, 2014–2015. C) Abundance of the low pathogenic H5N2 and H1N1 subtypes over the course of the winter among the Anchorage mallard population.



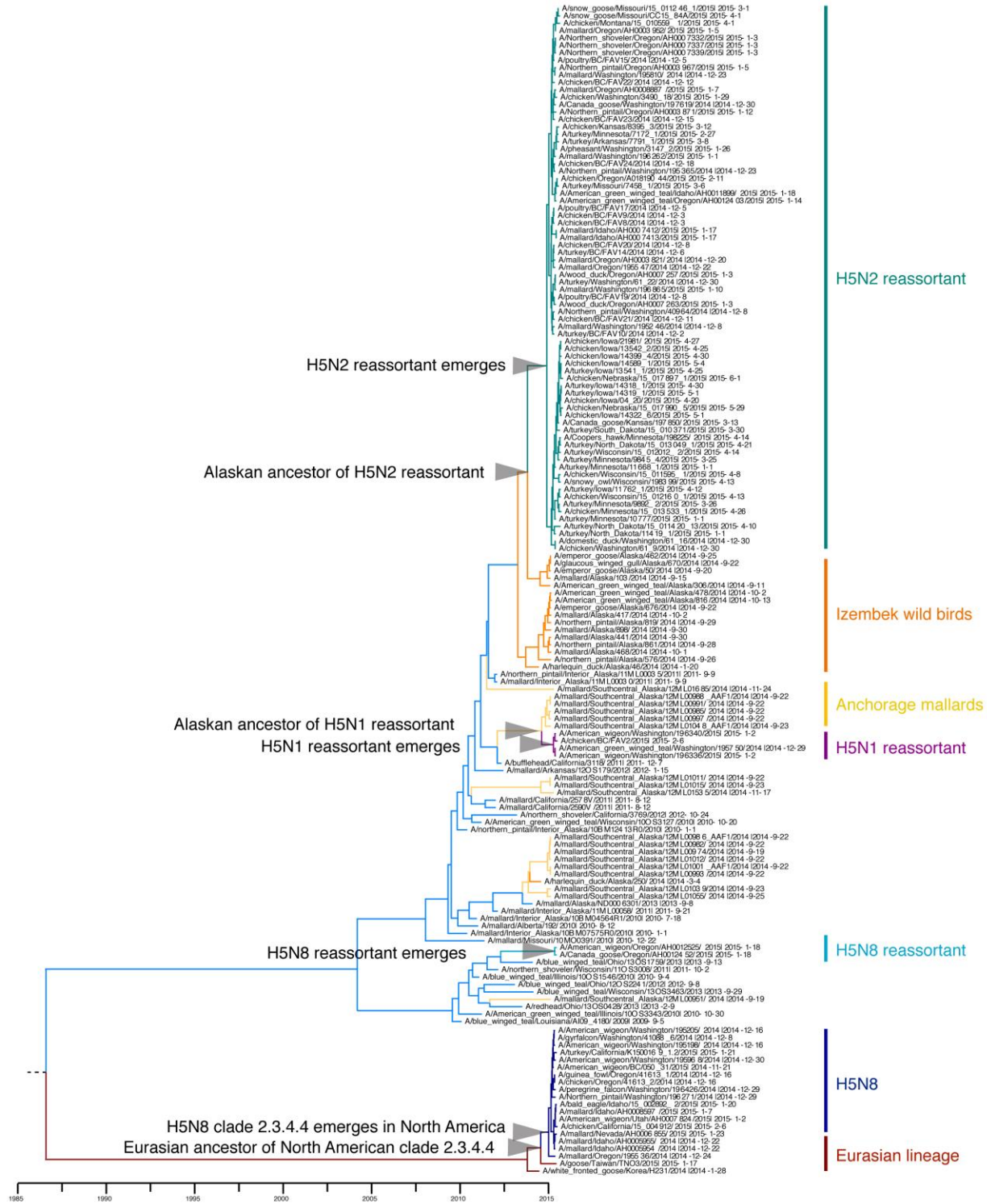
Technical Appendix Figure 2. Proposed genotypes of highly pathogenic influenza A virus H5Nx (reassortant H5N2, H5N1 and H5N8). Segments are color coded according to the most recent common ancestor for each genotype, based on phylogenetic tree reconstructions (Technical Appendix Figures 4–13).



Technical Appendix Figure 3. Phylogenetic tree reconstruction using Bayesian inference was used to date the ancestry of clade 2.3.4.4 viruses for each of the 8 influenza segments. The ancestry of the 3 subtypes: H5N8 (blue), H5N2 (green), H5N1 (purple) is shown relative to viruses shed by the Alaskan wild populations from Anchorage (yellow) and Izembek (orange).



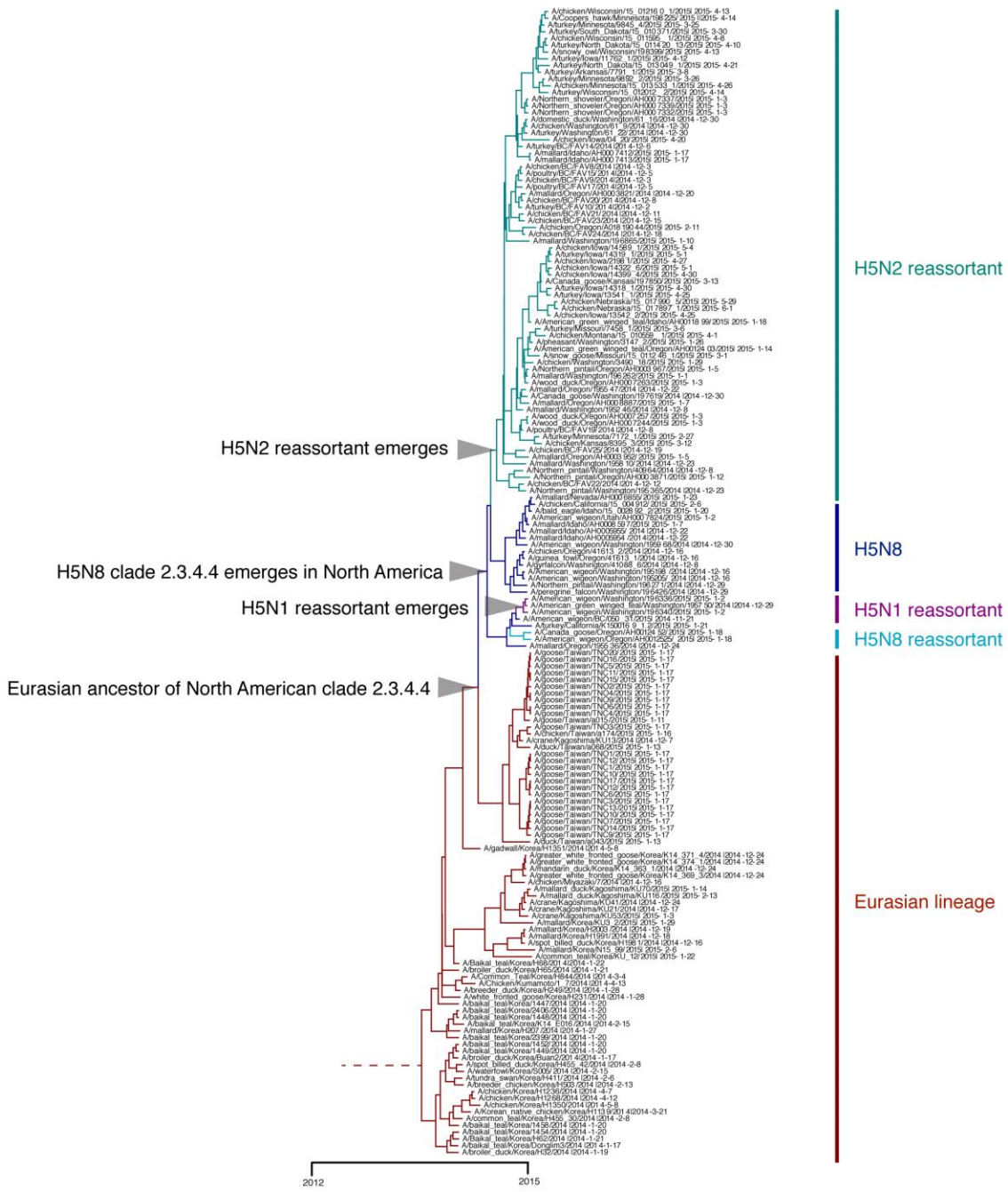
Technical Appendix Figure 4. Bayesian phylogenetic tree for the PB2 segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCAs: posterior probabilities >0.85) are marked with gray arrows.



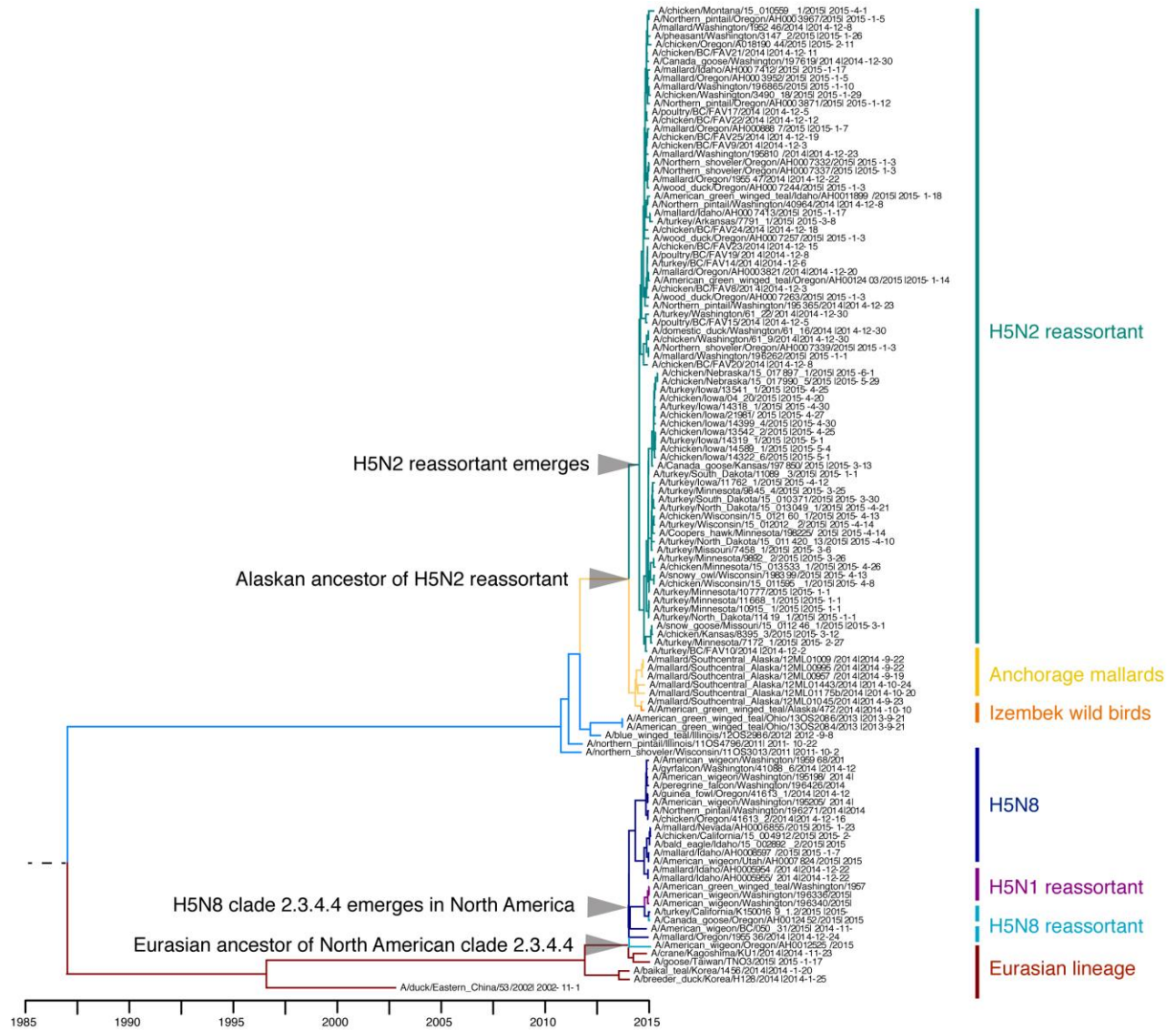
Technical Appendix Figure 5. Bayesian phylogenetic tree for the PB1 segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with gray arrows.



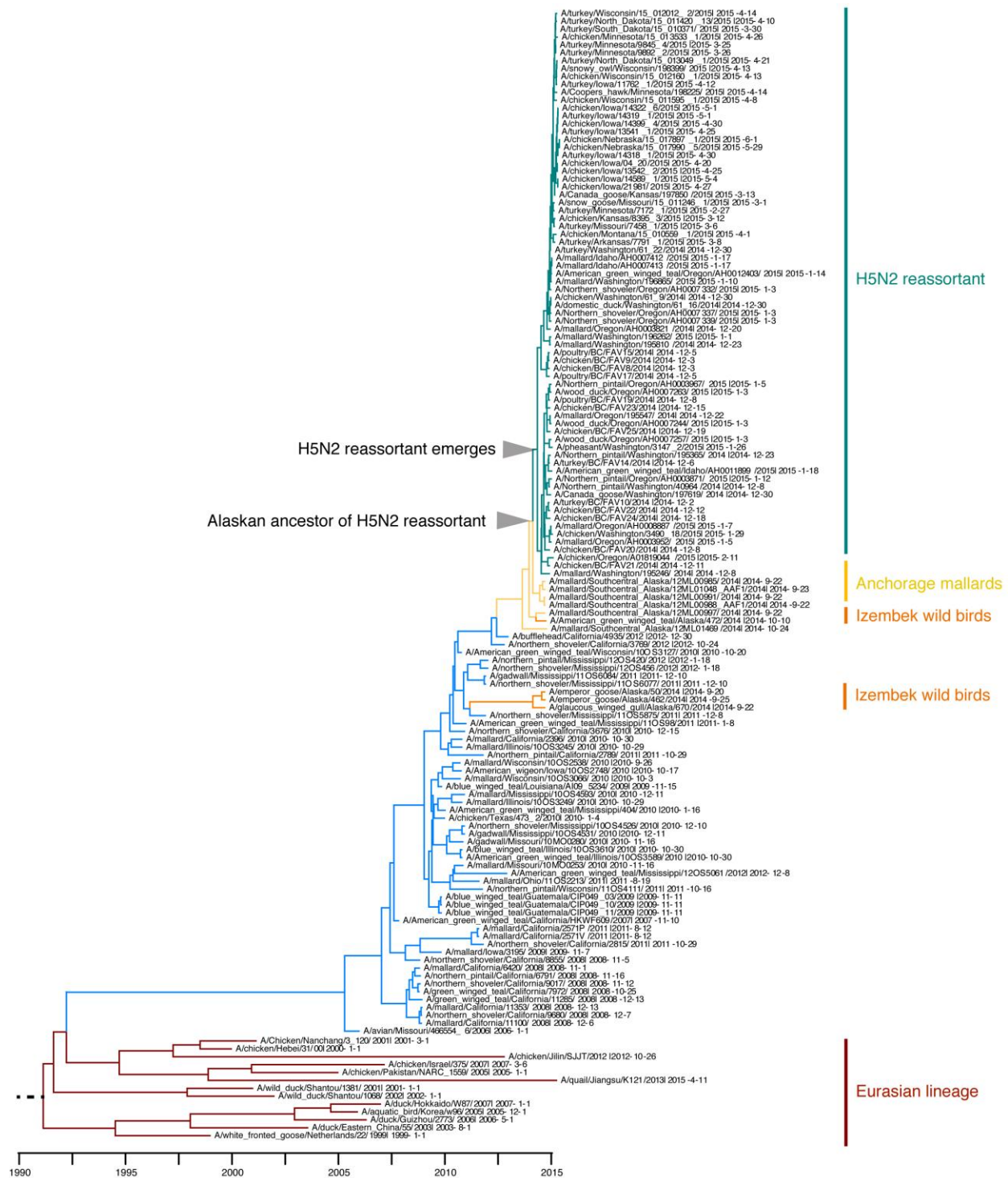
Technical Appendix Figure 6. Bayesian phylogenetic tree for the PA segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with grey arrows.



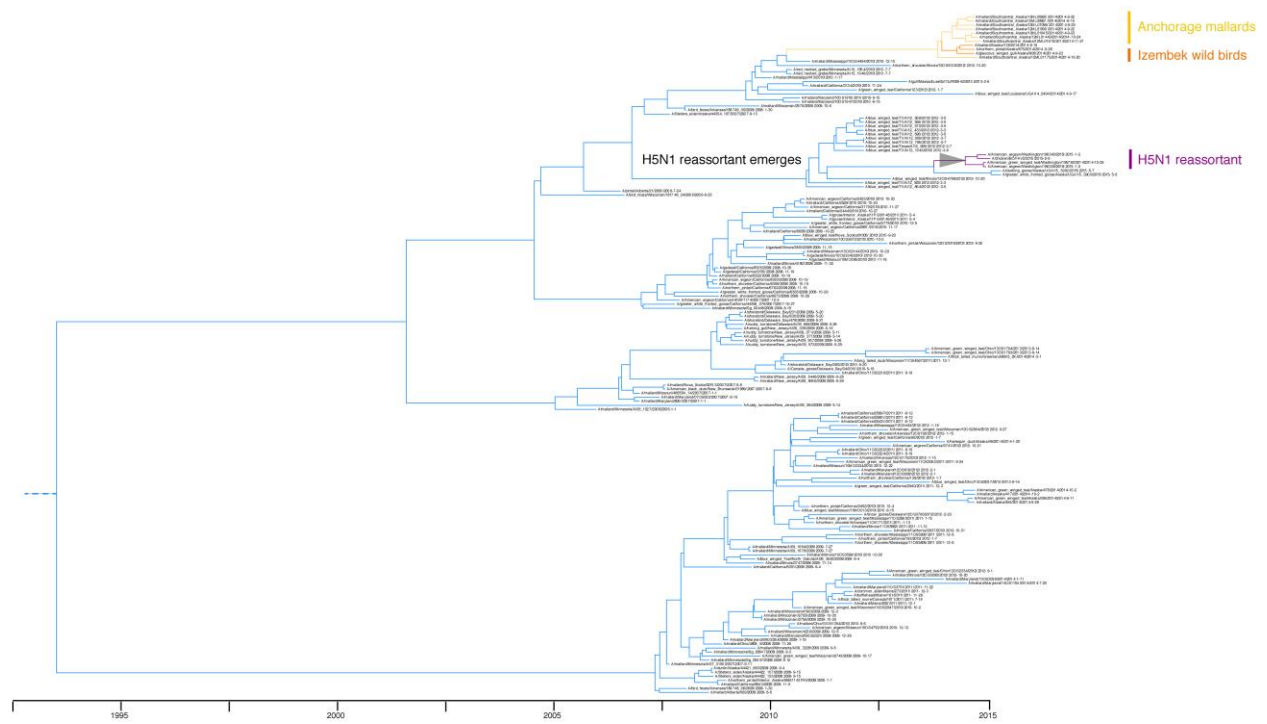
Technical Appendix Figure 7. Bayesian phylogenetic tree for the H5 segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with gray arrows.



Technical Appendix Figure 8. Bayesian phylogenetic tree for the NP segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with gray arrows.



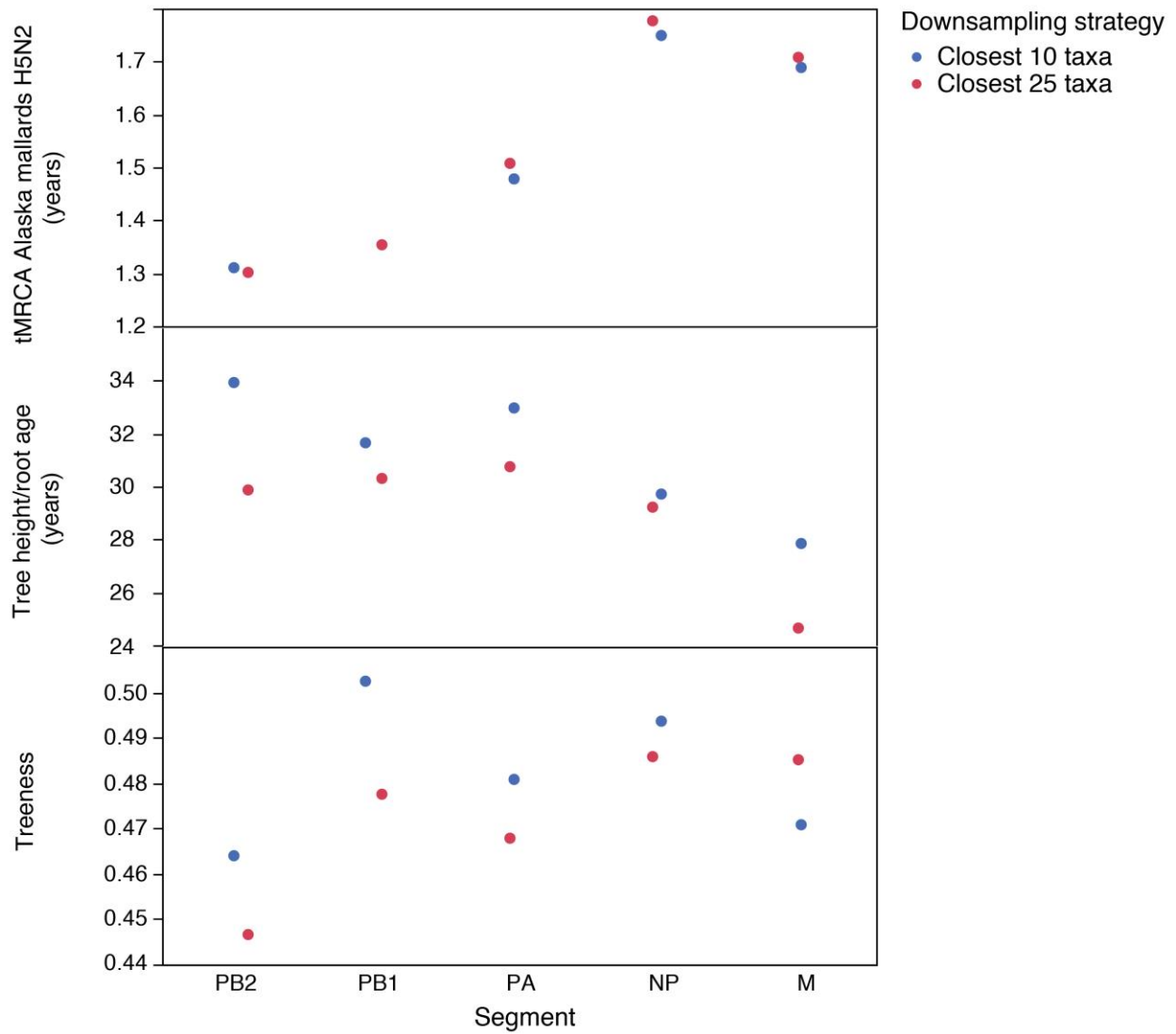
Technical Appendix Figure 9. Bayesian phylogenetic tree for the N2 segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with gray arrows.



Technical Appendix Figure 10. Bayesian phylogenetic tree for the N1 segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with gray arrows.



Technical Appendix Figure 11. Bayesian phylogenetic tree for the M segment constructed using sequences from clade 2.3.4.4 North American outbreaks. The tree has been time-calibrated using a relaxed molecular clock and branch lengths represent years. Nodes used to calculate time of most recent common ancestry (tMRCA: posterior probabilities >0.85) are marked with gray arrows.



Technical Appendix Figure 13. The optimal down-sampling strategy for internal segments was determined using Bayesian tree statistics to compare the reliability of trees generated with the closest 10 or 25 relatives to the in-group (i.e., H5N8 clade 2.3.4.4 and Alaskan isolates from Anchorage and Izembek). The non-structural gene (NS) was not included due to allelic divergence.