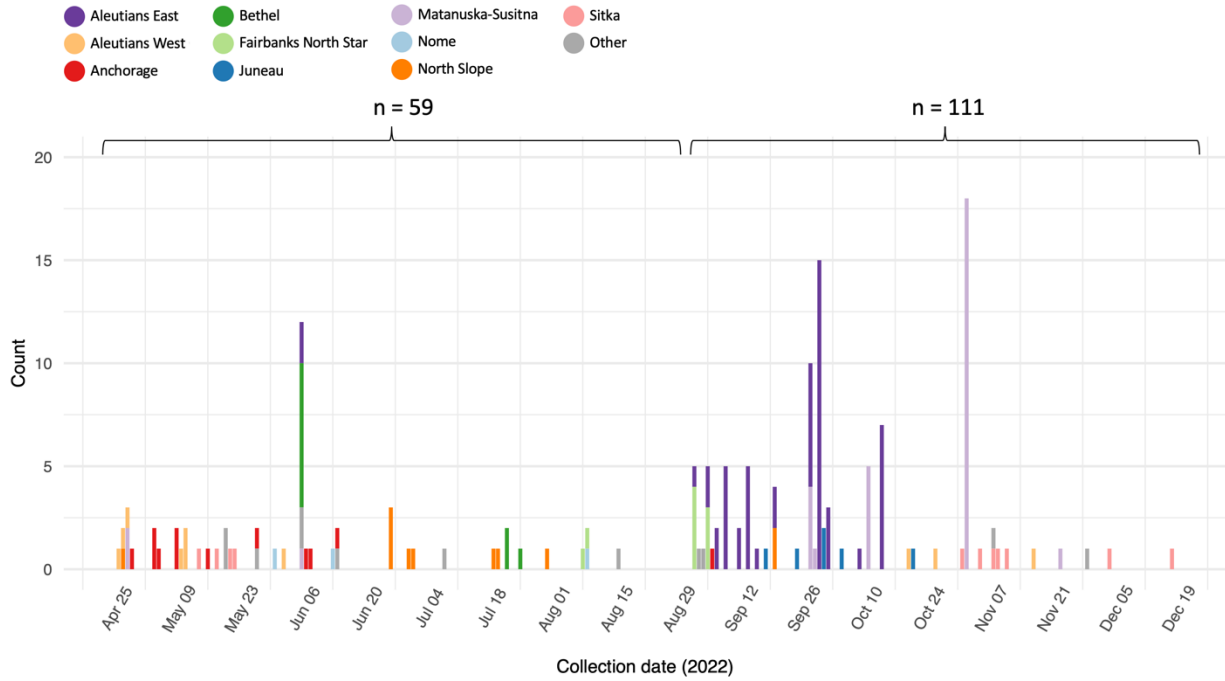
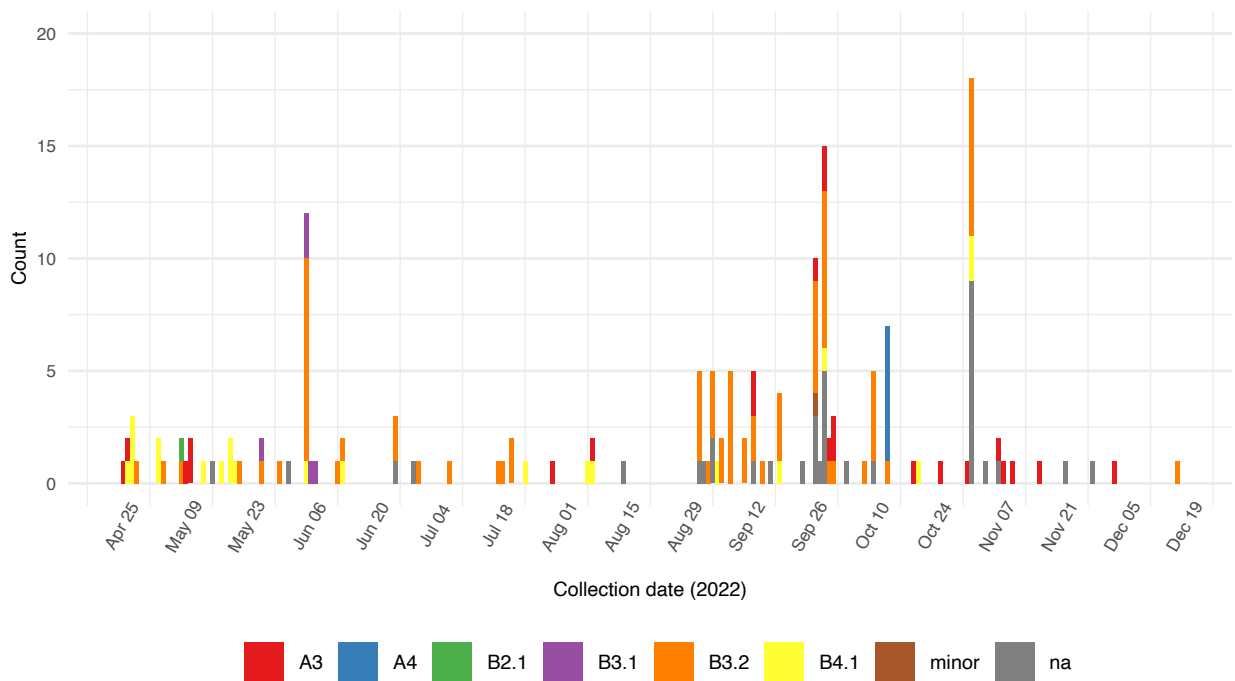


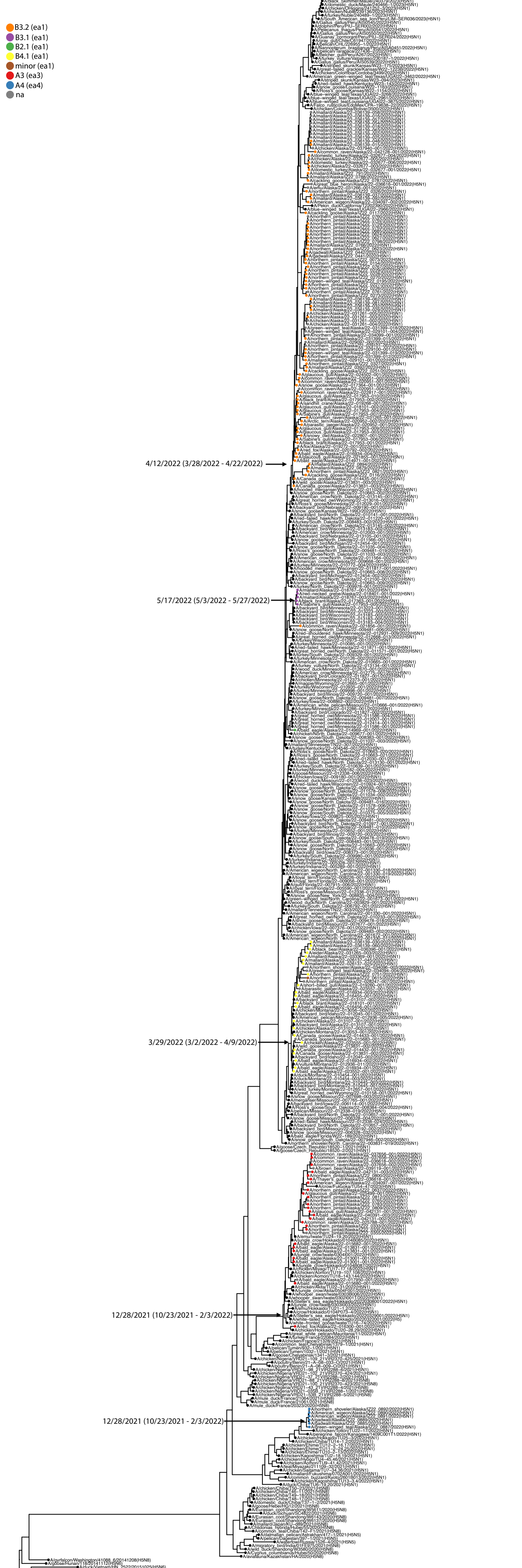
A)



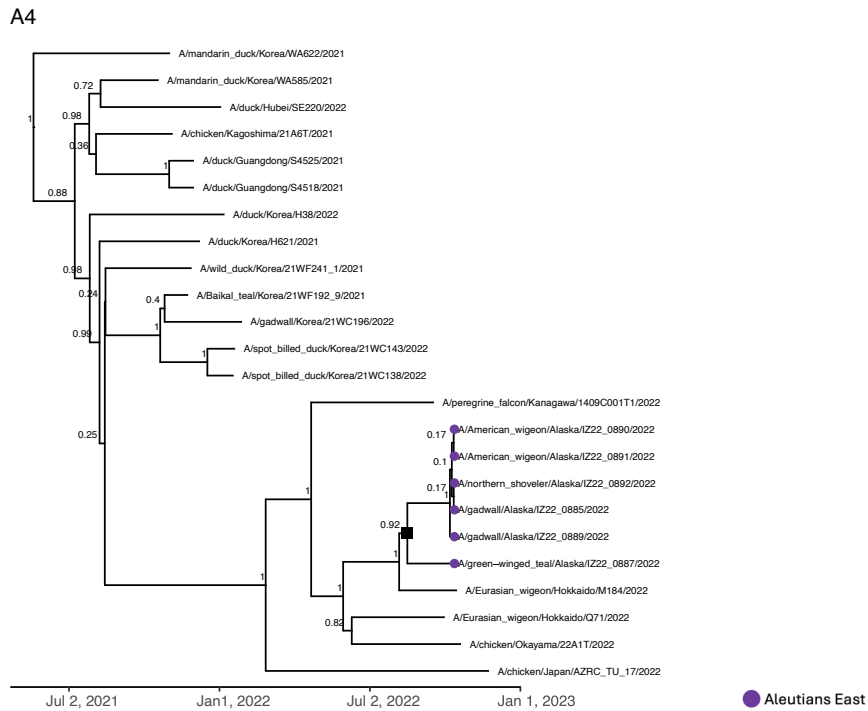
B)



**Supplementary Figure 1** Collection dates in 2022 of samples from which H5 clade 2.3.4.4b highly pathogenic avian influenza virus genomes were obtained. Colors represent A) sampling location (Alaska boroughs) and B) Genotypes (na indicates that a genotype was unable to be assigned).



**Supplementary Figure 2** Maximum credibility tree of H5 clade 2.3.4.4 highly divergent avian influenza virus sequences based on the HA gene segment from Alaska (colored tips) and elsewhere. Tips are colored according to genotype. Time to the most recent common ancestor nodes are indicated for each genotype with an arrow indicating the node from which all Alaska viruses of that genotype diverged. 95% highest posterior density intervals are presented in parenthesis.

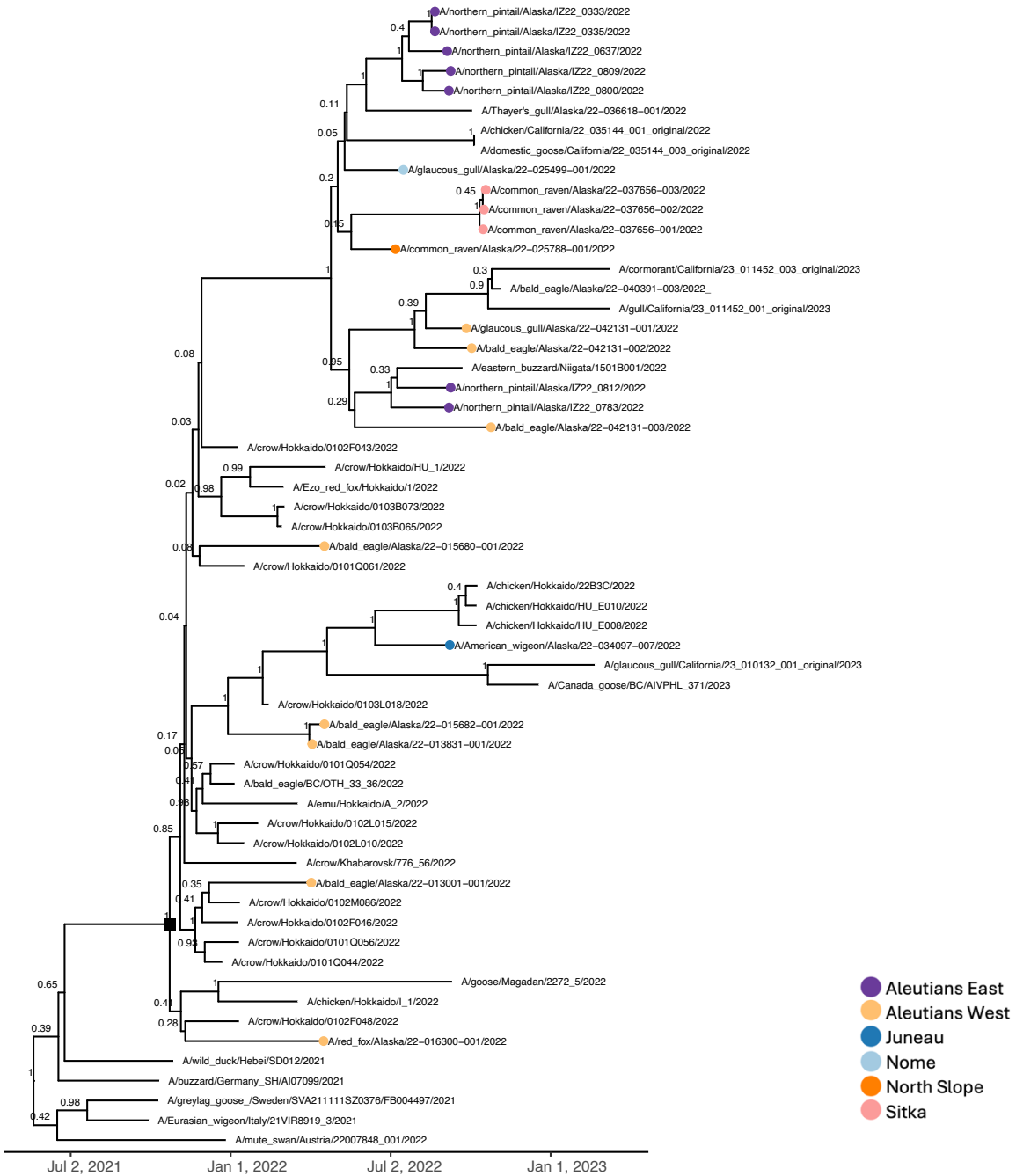


**Supplementary Figure 3** Maximum clade credibility tree of Genotype A4 H5 clade 2.3.4.4b highly pathogenic avian influenza virus whole genomes from Alaska (colored tips) and elsewhere. A black square indicates the node from which the time to most recent common ancestor was estimated. Node labels indicate posterior probabilities.

B3.1



**Supplementary Figure 4** Maximum clade credibility tree of Genotype B3.1 H5 clade 2.3.4.4b highly pathogenic avian influenza virus whole genomes from Alaska (colored tips) and elsewhere. A black square indicates the node from which the time to most recent common ancestor was estimated. Node labels indicate posterior probabilities.



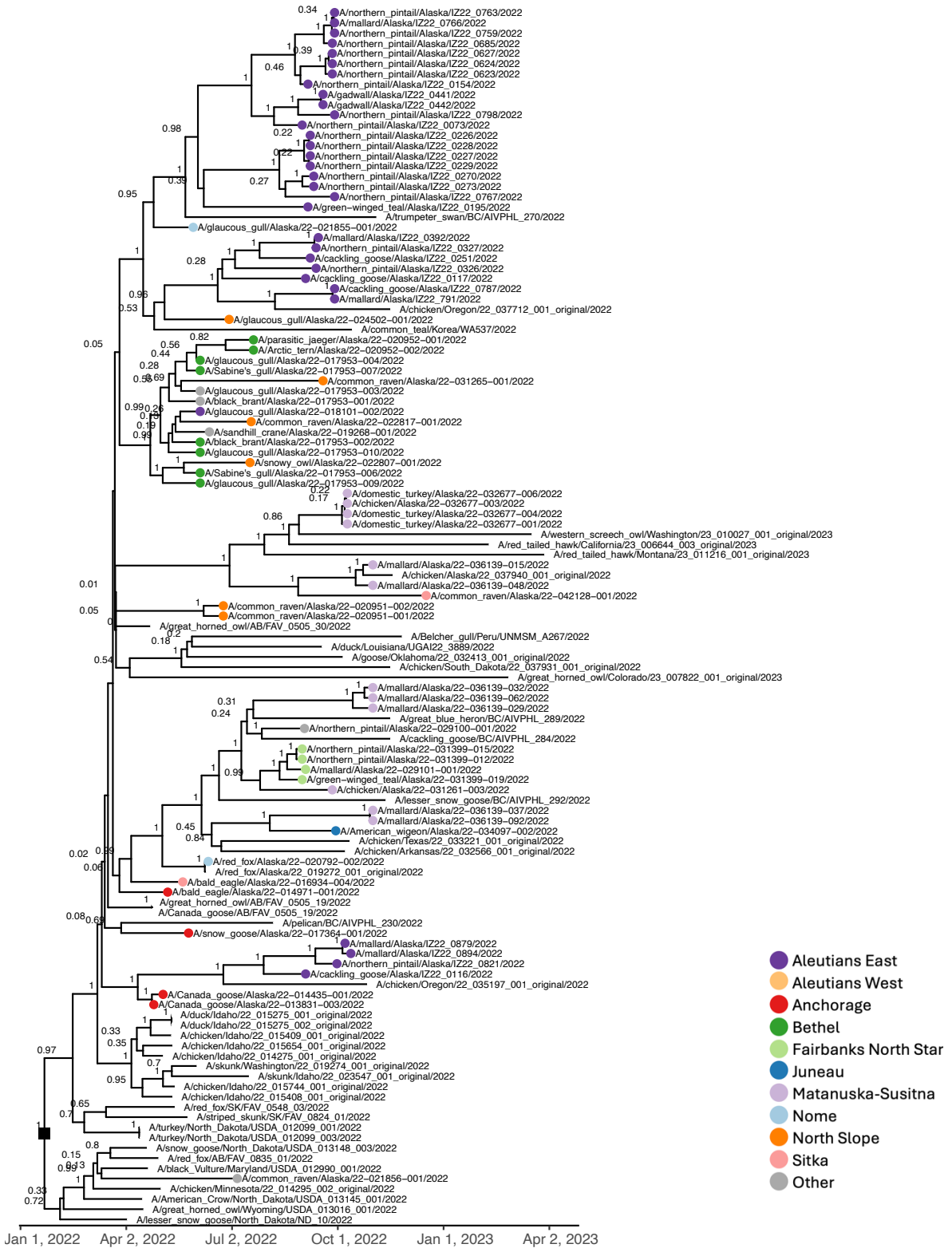
**Supplementary Figure 5** Maximum clade credibility tree of Genotype A3 H5 clade 2.3.4.4b highly pathogenic avian influenza virus whole genomes from Alaska (colored tips) and elsewhere. A black square indicates the node from which the time to most recent common ancestor was estimated. Node labels indicate posterior probabilities.

B4.1



**Supplementary Figure 6** Maximum clade credibility tree of Genotype B4.1 H5 clade 2.3.4.4b highly pathogenic avian influenza virus whole genomes from Alaska (colored tips) and elsewhere. A black square indicates the node from which the time to most recent common ancestor was estimated. Node labels indicate posterior probabilities.

B3.2



**Supplementary Figure 7** Maximum clade credibility tree of Genotype B3.2 H5 clade 2.3.4.4b highly pathogenic avian influenza virus whole genomes from Alaska (colored tips)

and elsewhere. A black square indicates the node from which the time to most recent common ancestor was estimated. Node labels indicate posterior probabilities.