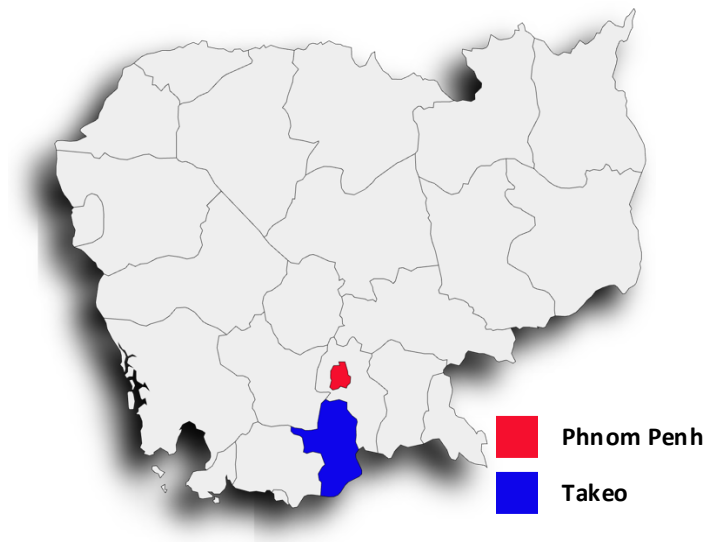
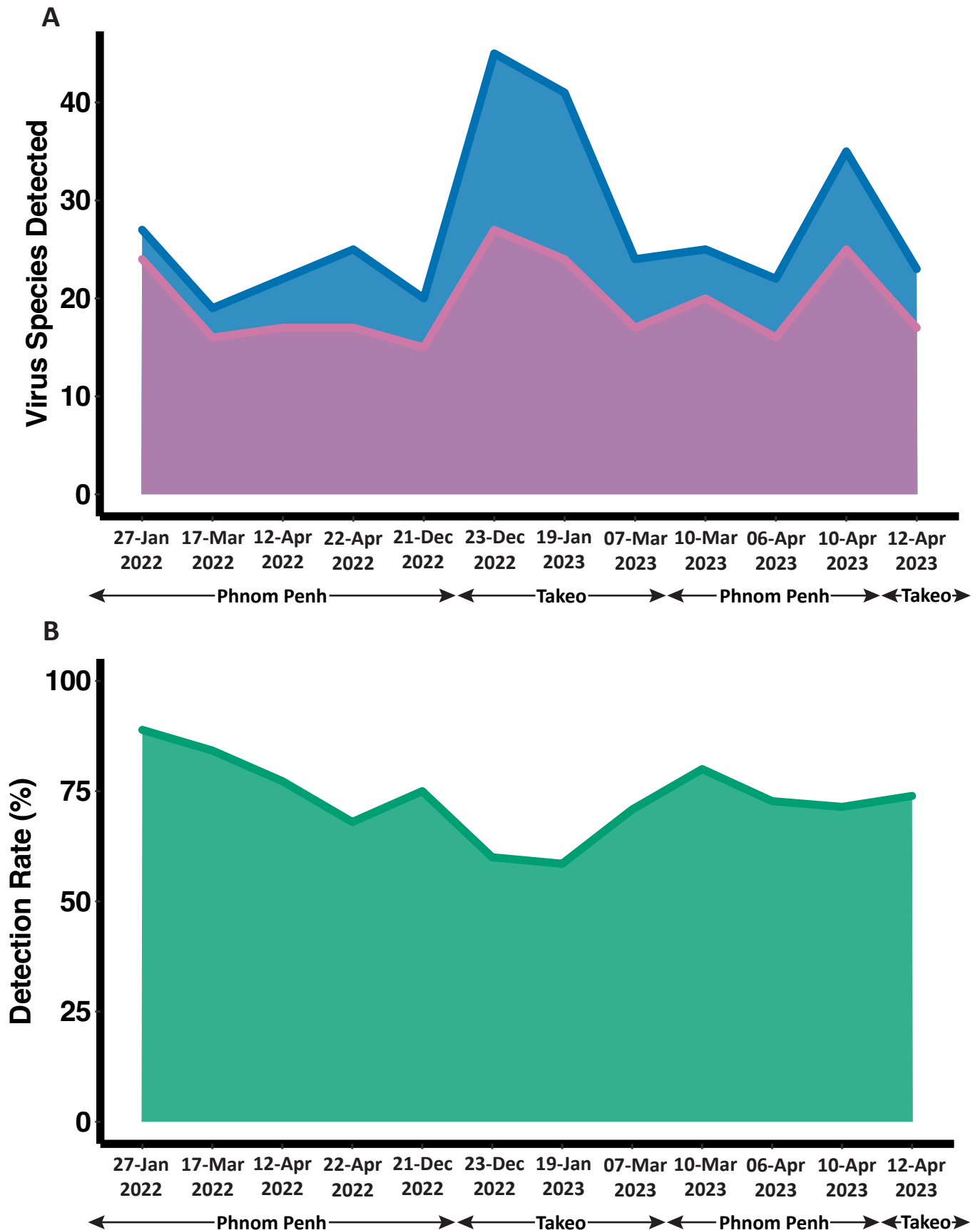
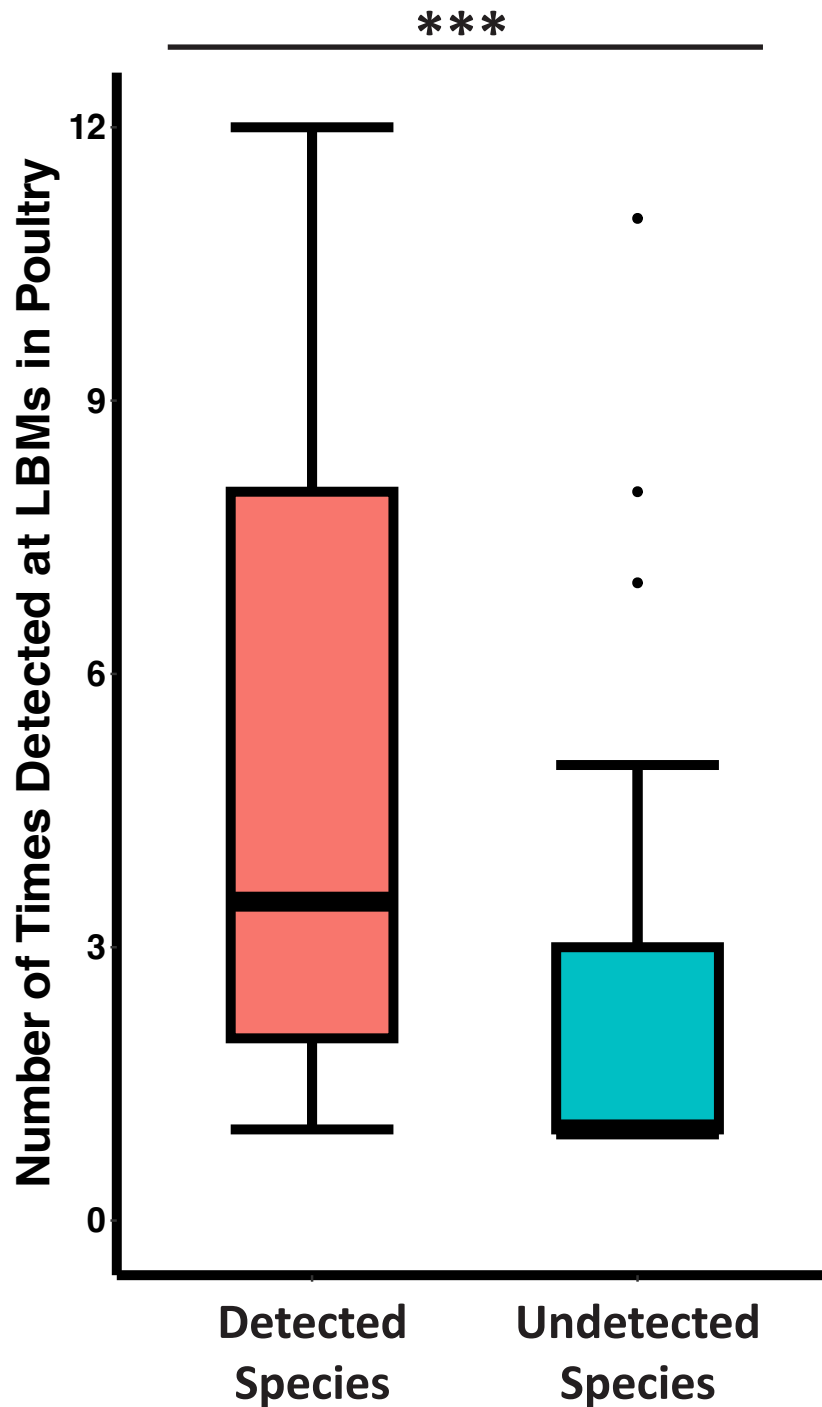




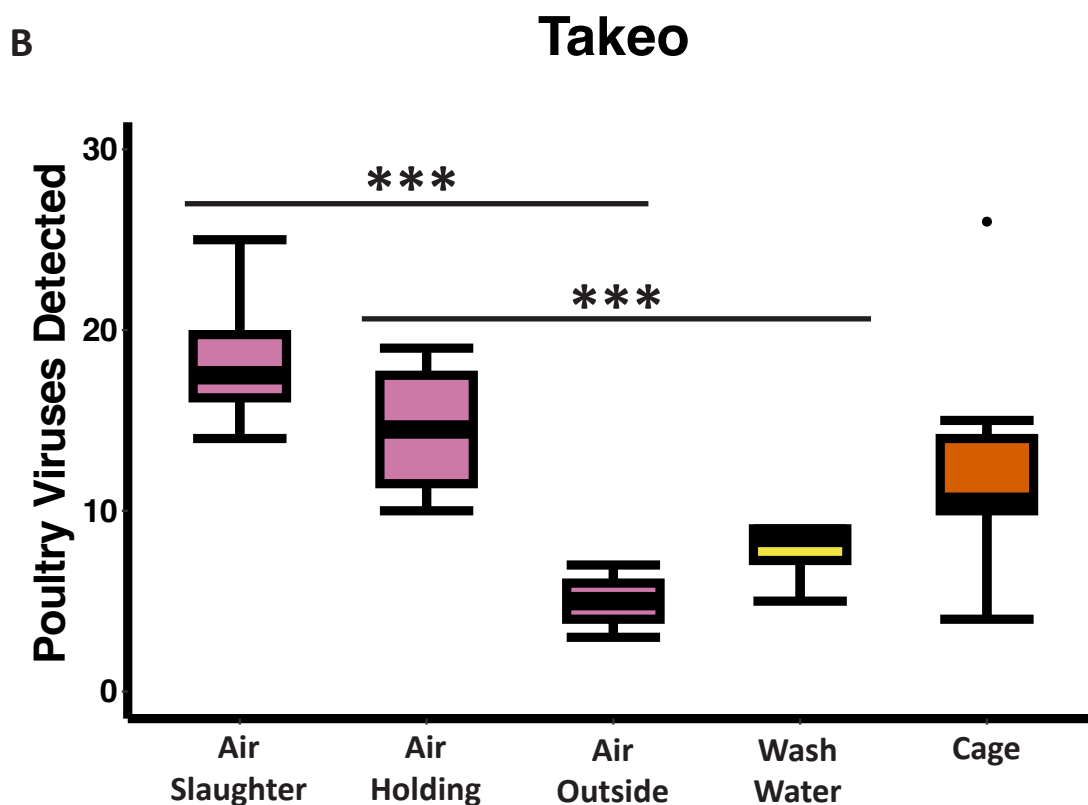
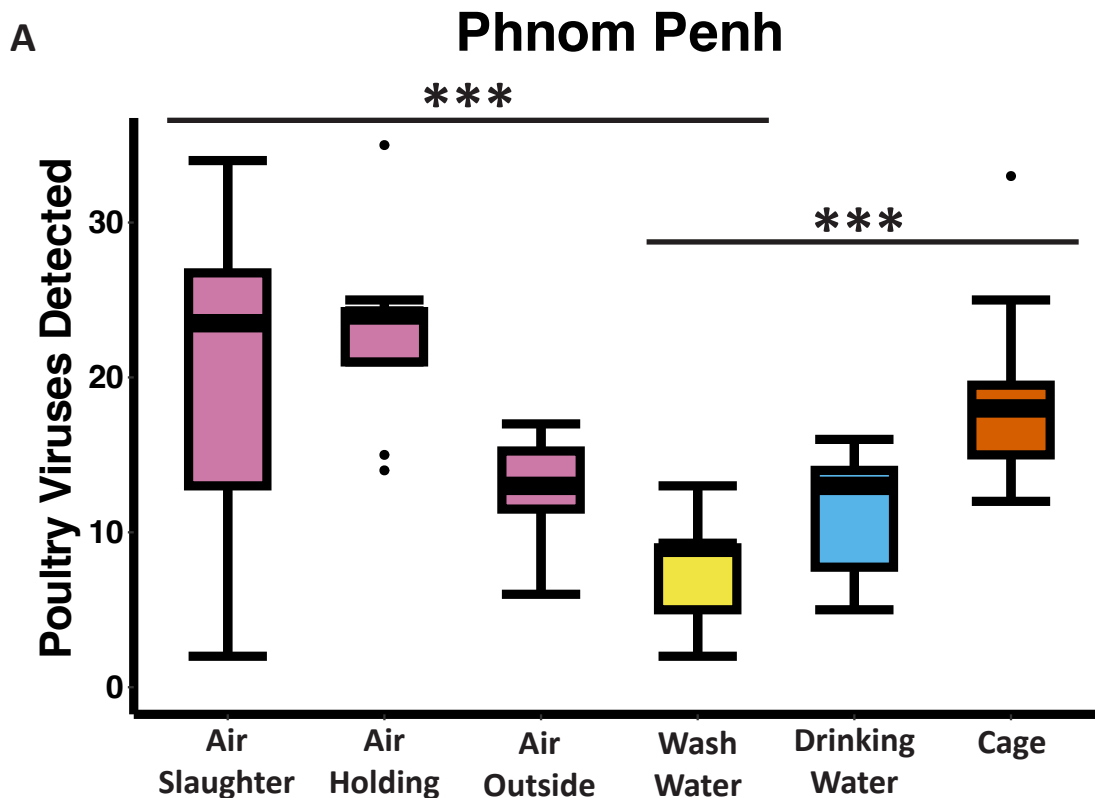
Supplementary Figure 1: Map of Cambodia highlighting the sampling locations at two LBMs in the Takeo and Phnom Penh regions.



Supplementary Figure 2: Detection rate of viruses in environmental samples compared to poultry swabs ranges between 70% and 90%. A) Total number of virus species detected across all environmental samples compared to all poultry swabs at each sampling timepoint. B) Data shown in A) is expressed as a percentage (%) of total virus detection.



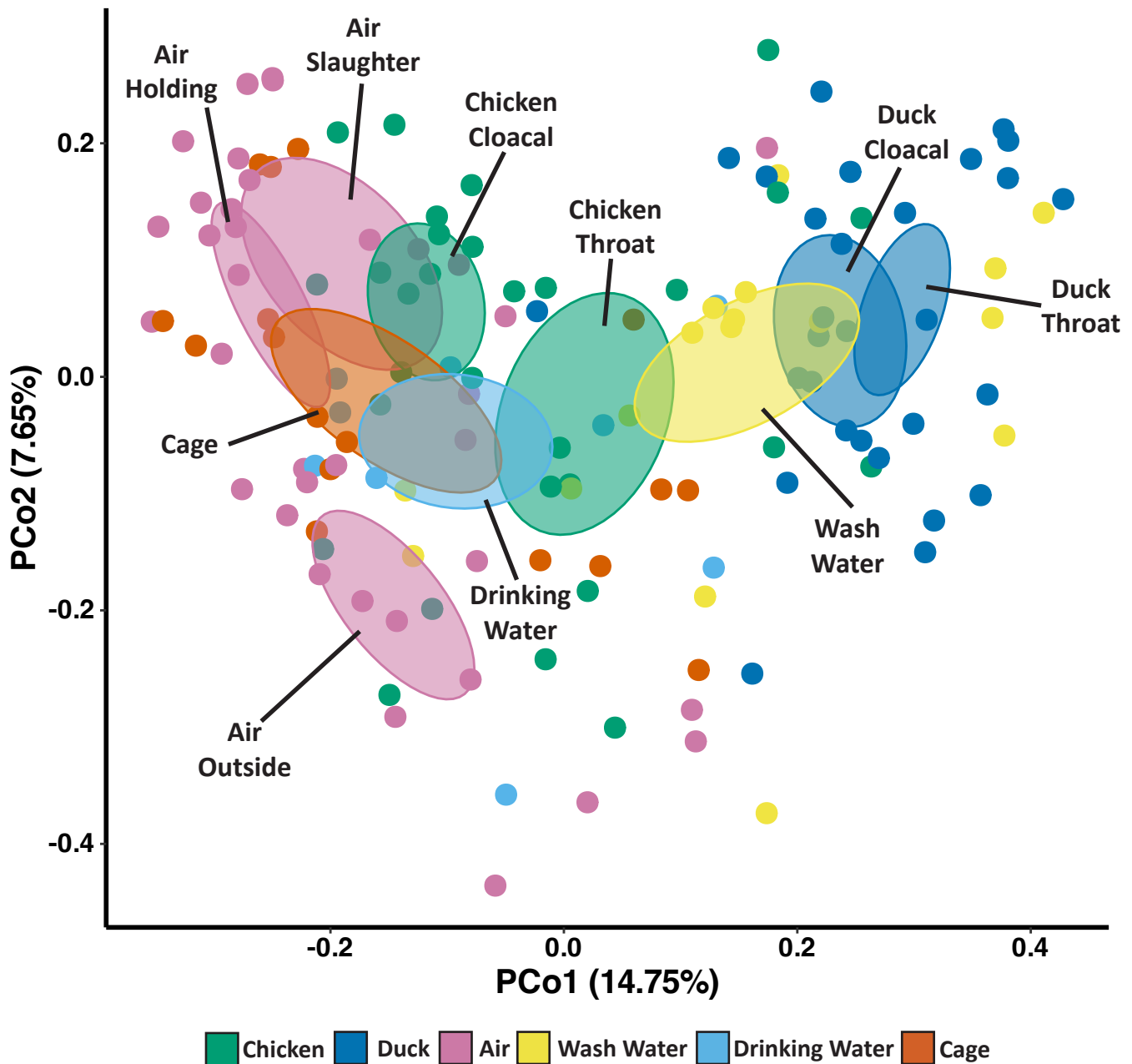
Supplementary Figure 3: Virus species detected in poultry swabs that could not be found in environmental samples (labelled as undetected species on x-axis) were discovered significantly less often at LBMs than viruses successfully detected in both sample types (labelled as detected species on x-axis). Statistical significance was determined using a Wilcoxon Test. P values are annotated as follows: $P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***.



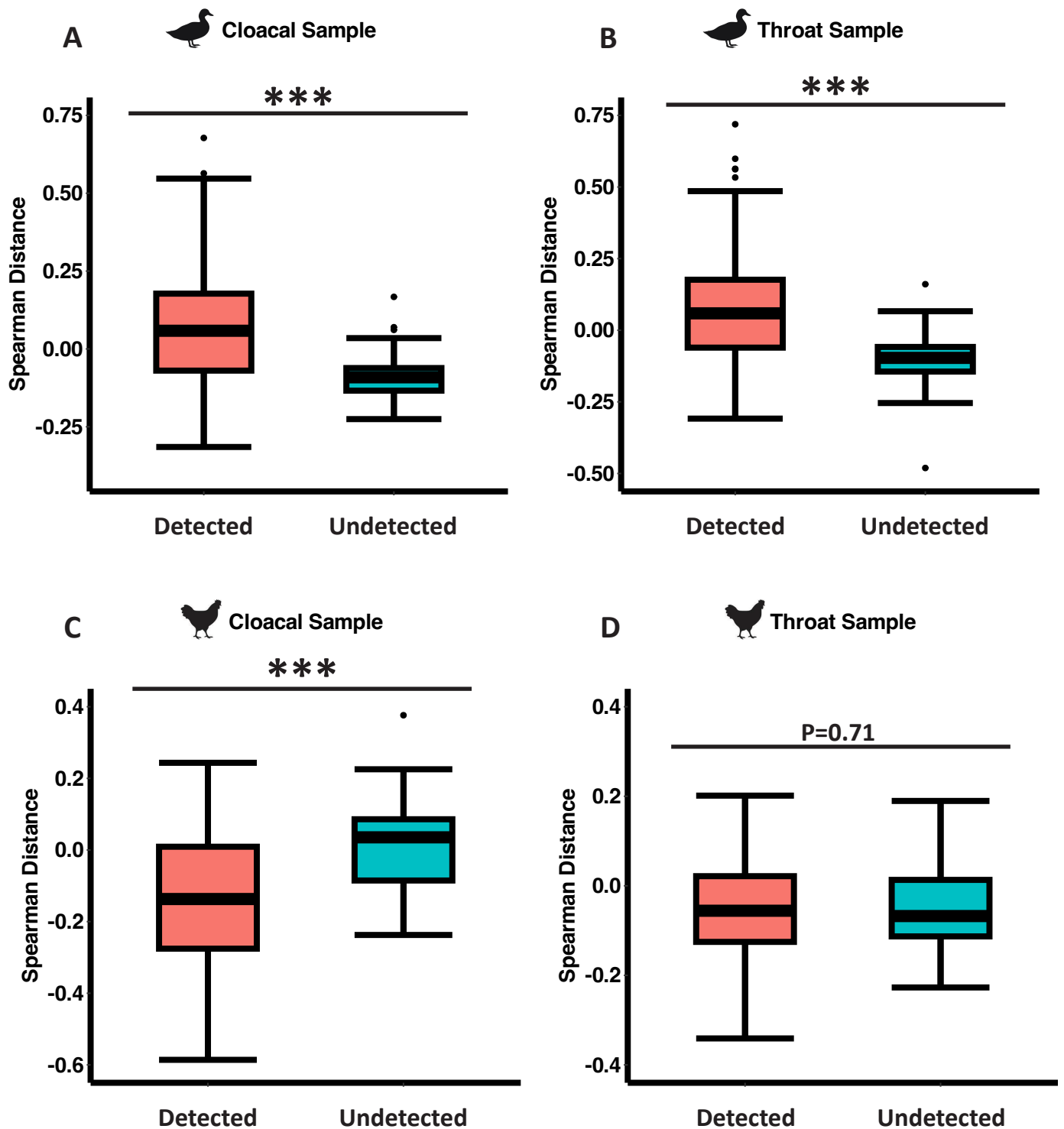
Supplementary Figure 4: Number of poultry virus species detected in each environmental sample at A) Orussey market, Phnom Penh and B) Daun Keo market, Takeo. Air sampling from the slaughter and holding area detected the most poultry viruses at both locations. Statistical significance was calculated using Kruskal-Wallis with Dunns post-hoc test. P values are annotated as follows: $P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***.

Jaccard Index

$P=0.0001^{***}$, $R^2=0.037$



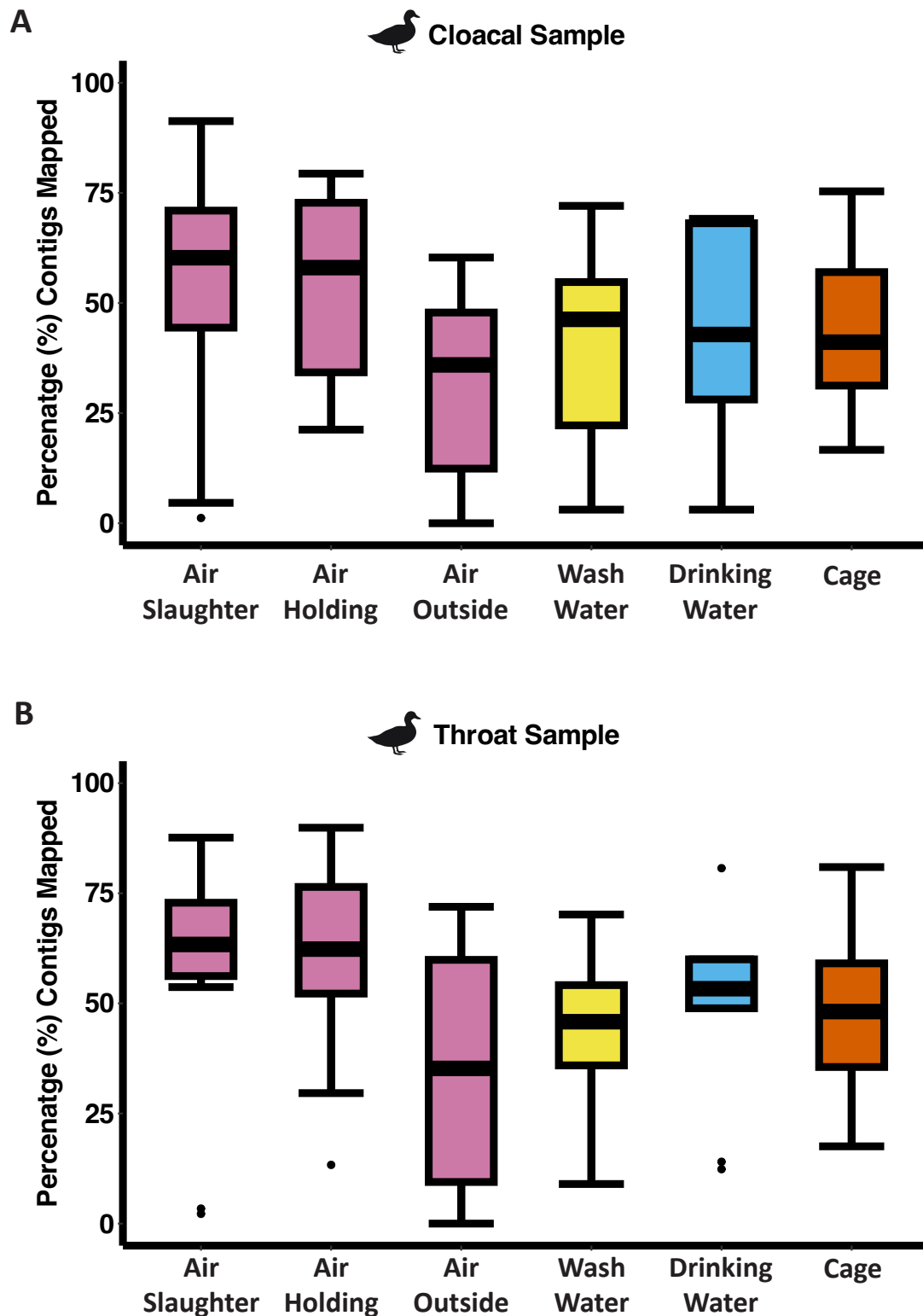
Supplementary Figure 4: Principle coordinate analysis (PCoA) of beta-diversity (Jaccard) of poultry virus species reveal statistically significant separation between the groups. PERMANOVA was calculated adjusting for both location and time as a confounder. The eigen values are also reported which show the variation reported in the X-axis (14.75%) and Y-axis (7.65%) of the PCoA.



Supplementary Figure 6: Poultry viruses which could not be detected in environmental samples associate with ducks but not chickens. Here we conducted Spearman correlations between poultry virus abundance and the distance from the Jaccard median centroid as calculated in Figure 1. Both A) cloacal and B) throat samples collected from ducks had significantly lower Spearman correlations when comparing taxa successfully detected or undetected through environmental sampling (as shown in Figure 1). The opposite finding was reported for C) cloacal samples from chickens while no significant differences were found for D) throat samples (from chickens). Statistical significance was calculated using a Wilcoxon Test. P values are annotated as follows: $P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***.



Supplementary Figure 7: A number of non poultry viruses could be detected in environmental samples at different LBMs. Heatmap showing the abundance of non-poultry viruses detected, represented as reads per million (RPM). Rows represent different viruses, while columns indicate sampling locations and environmental sample types, as annotated.



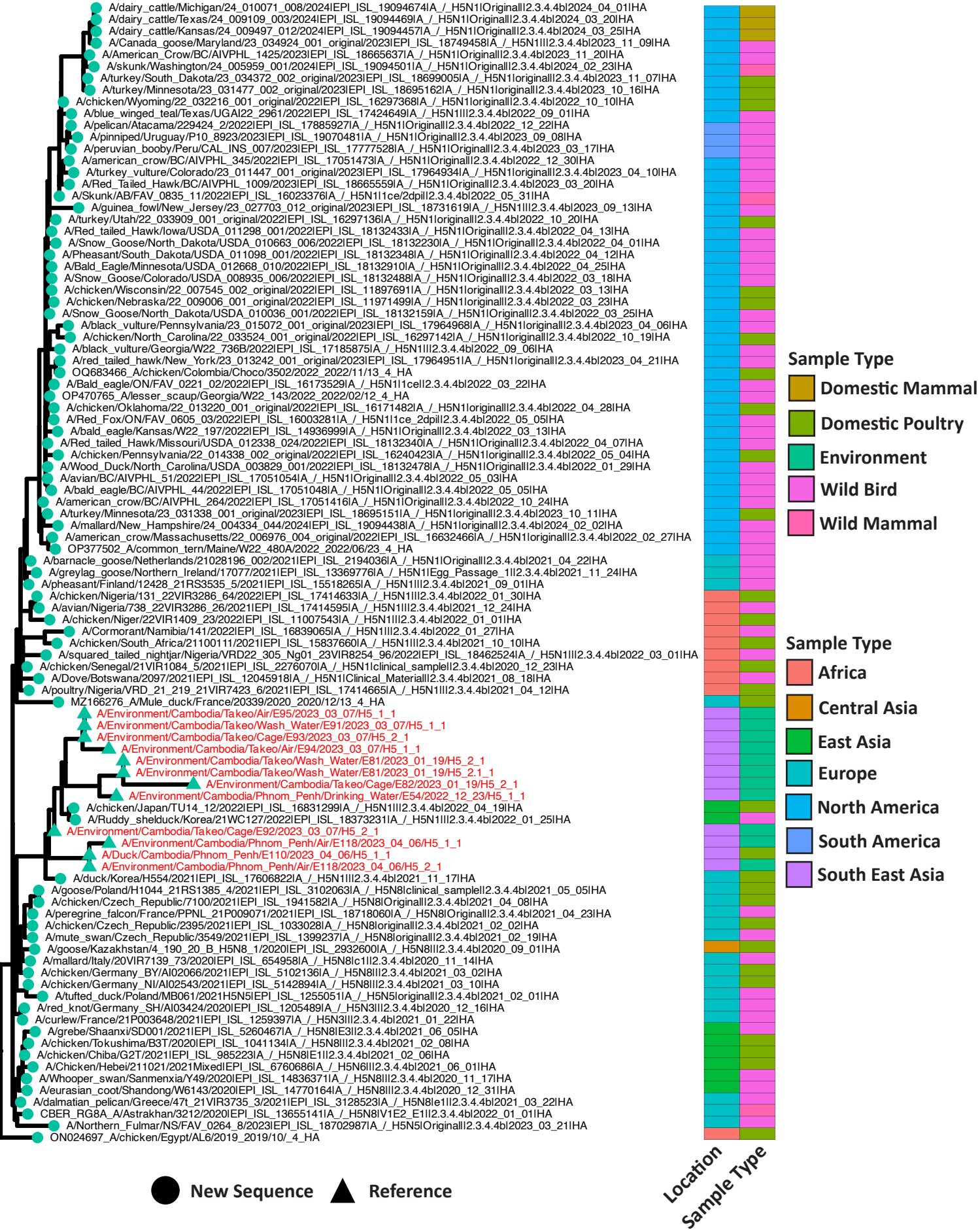
Supplementary Figure 8: Consistent overall alignment rates are observed between duck viral pathogens and environmental sample types. No significant differences could be detected between environmental samples when mapped to A) cloacal samples and B) throat samples obtained from ducks. Statistical significance was calculated using Kruskal-Wallis with Dunns post-hoc test. P values are annotated as follows: $P < 0.05$ *; $P < 0.01$ **; $P < 0.001$ ***.

HA-H5 (2.3.2.1c)



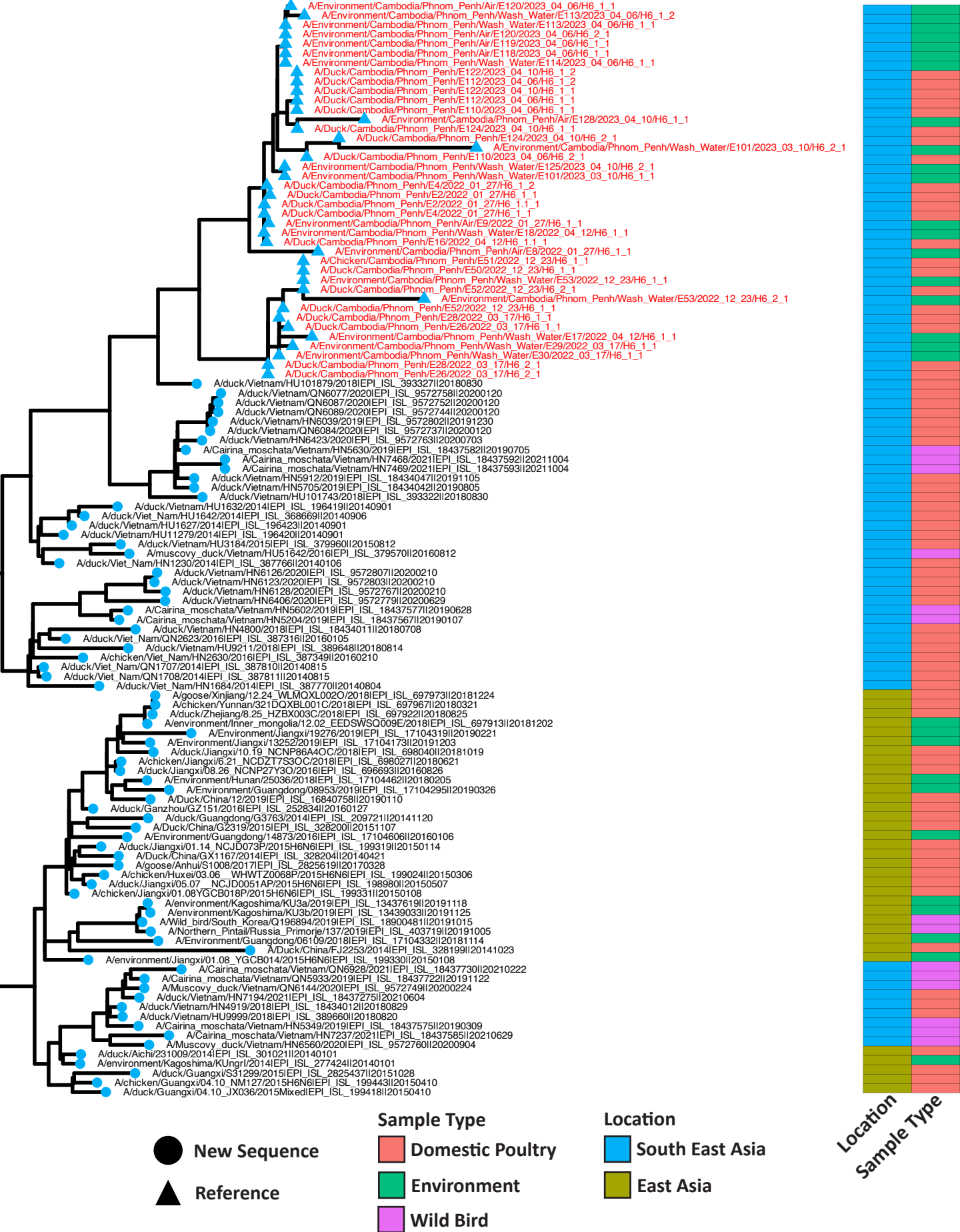
Supplementary Figure 9: HA-H5 sequences of the clade 2.3.2.1c *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

HA-H5 (2.3.4.4b)



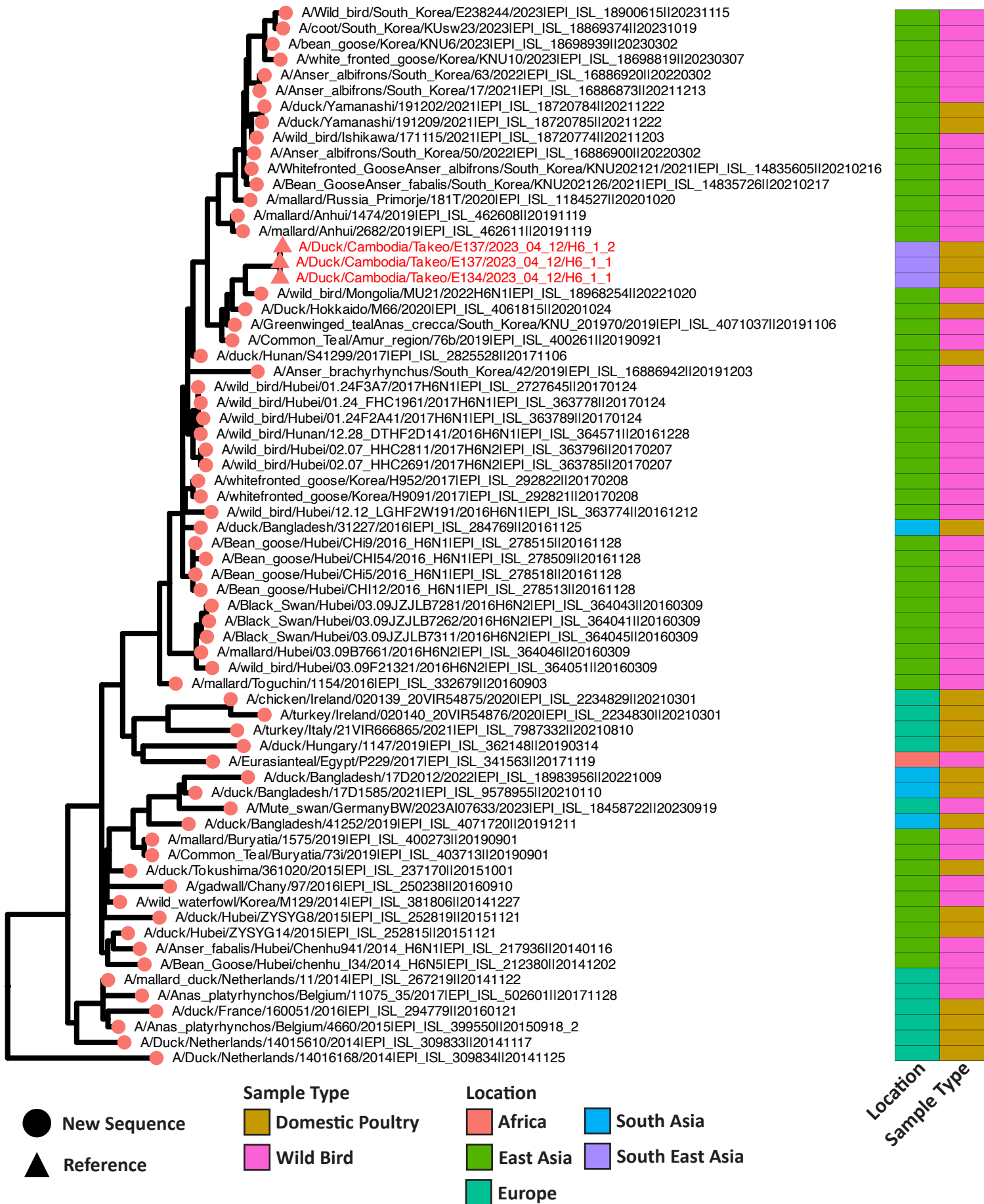
Supplementary Figure 10: HA-H5 sequences of the clade 2.3.4.4b *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

HA-H6 (ST2853-like)



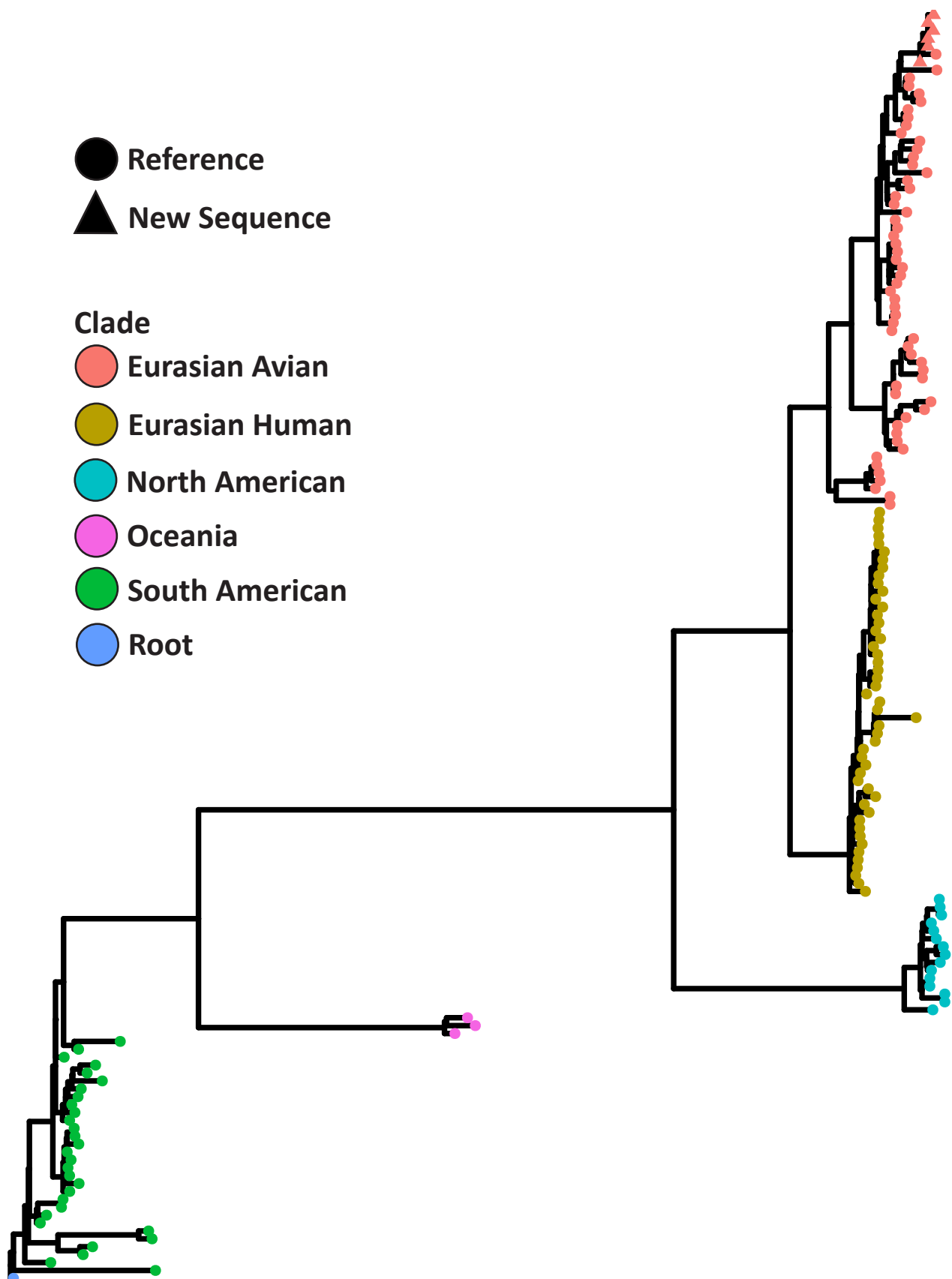
Supplementary Figure 11: HA-H6 sequences of the clade ST2853-like *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

HA-H6 (HN57-like)



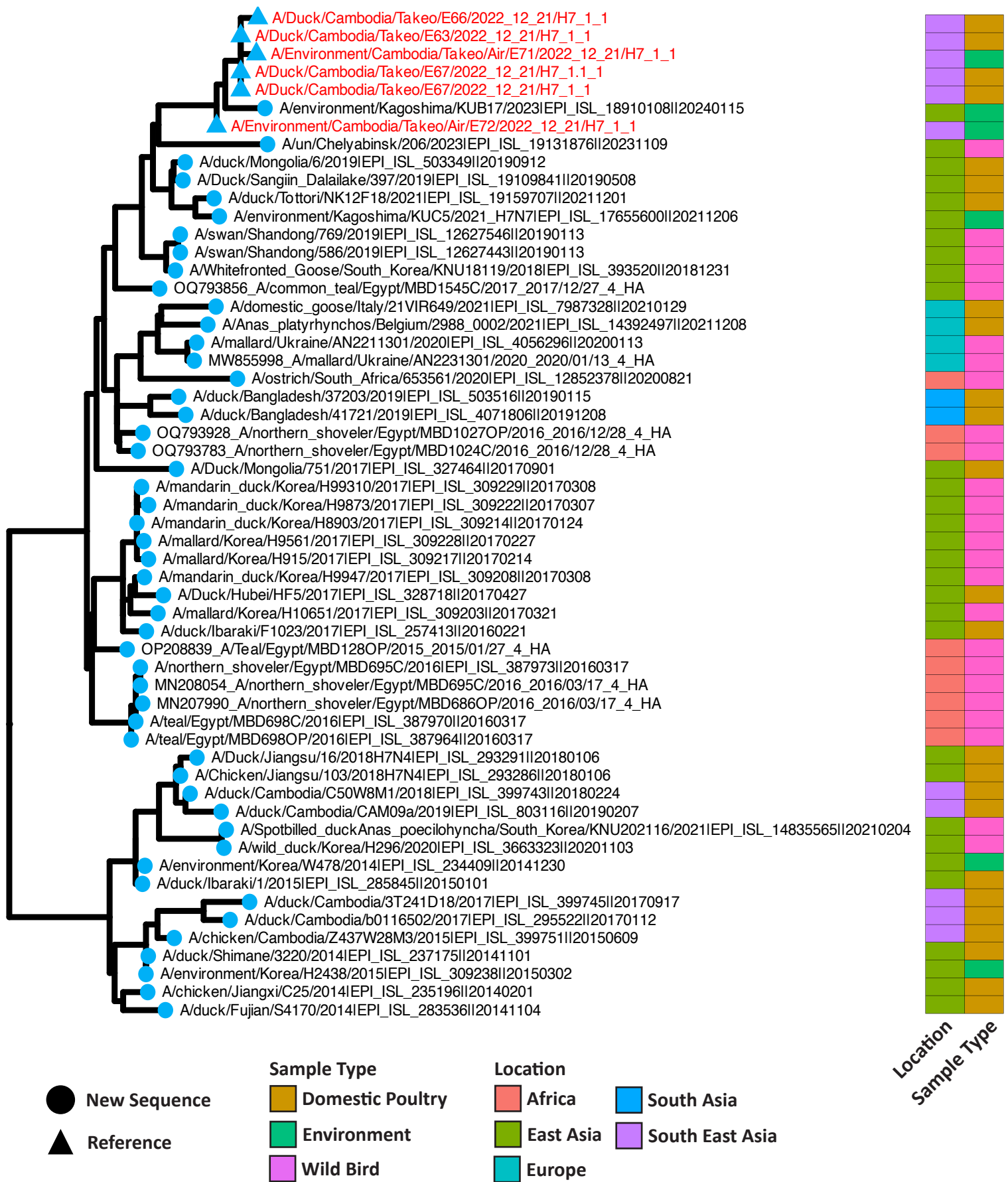
Supplementary Figure 12: HA-H6 sequences of the HN57-like clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

HA-H7



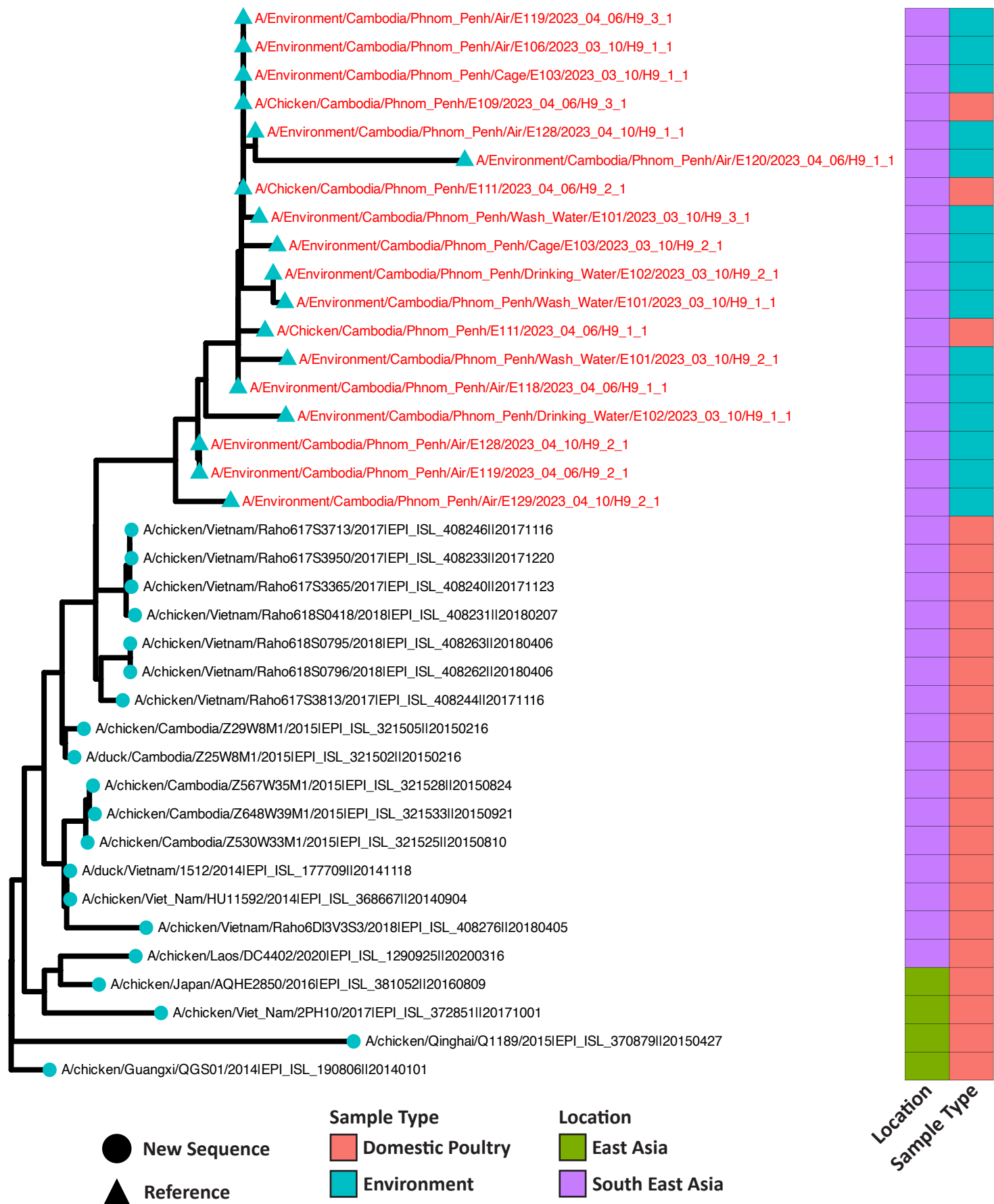
Supplementary Figure 13: HA-H7 phylogenetic tree shows that sequences from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol highlights nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label.

HA-H7 (Eurasian Avian)



Supplementary Figure 14: HA-H7 sequences of the Eurasian Avian clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

HA-H9 (Y280)



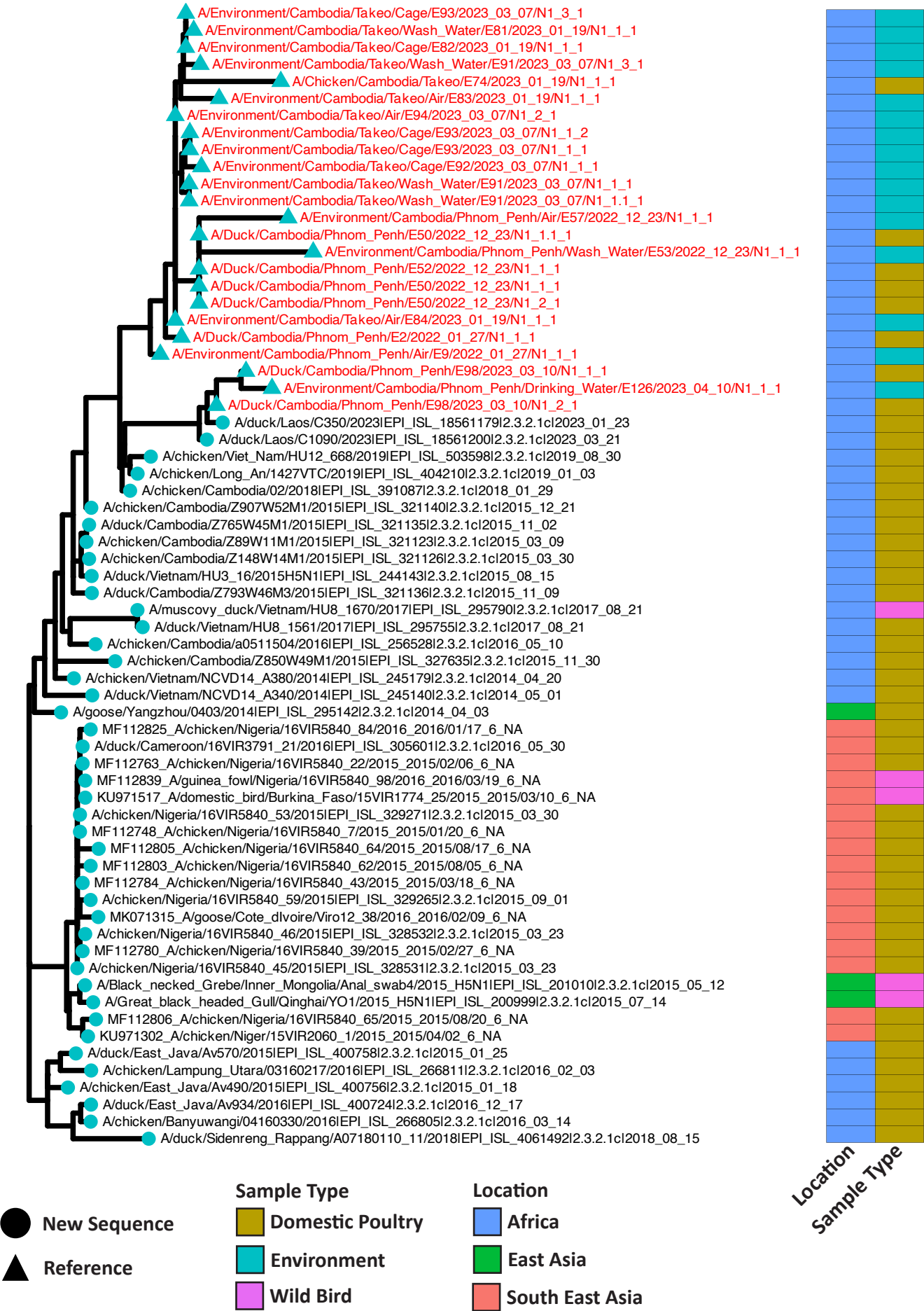
Supplementary Figure 15: HA-H9 sequences of the clade Y280 *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographhic location and sample type of all sequences are shown on the right of the plot.

HA-H9 (Y280)



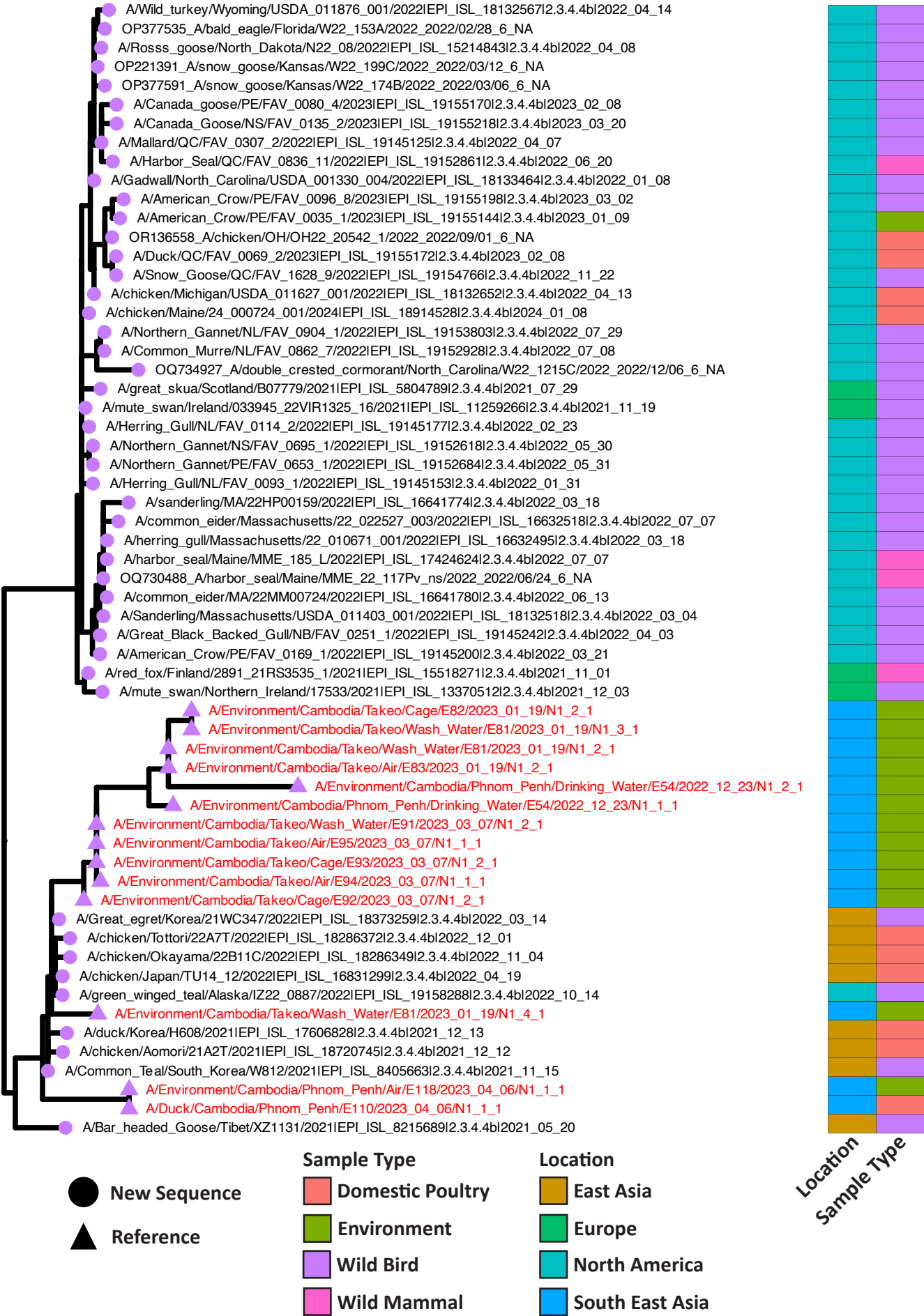
Supplementary Figure 16: HA-H9 sequences of the clade Y280 *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geograpghic location and sample type of all sequences are shown on the right of the plot.

NA-N1 (2.3.2.1c)



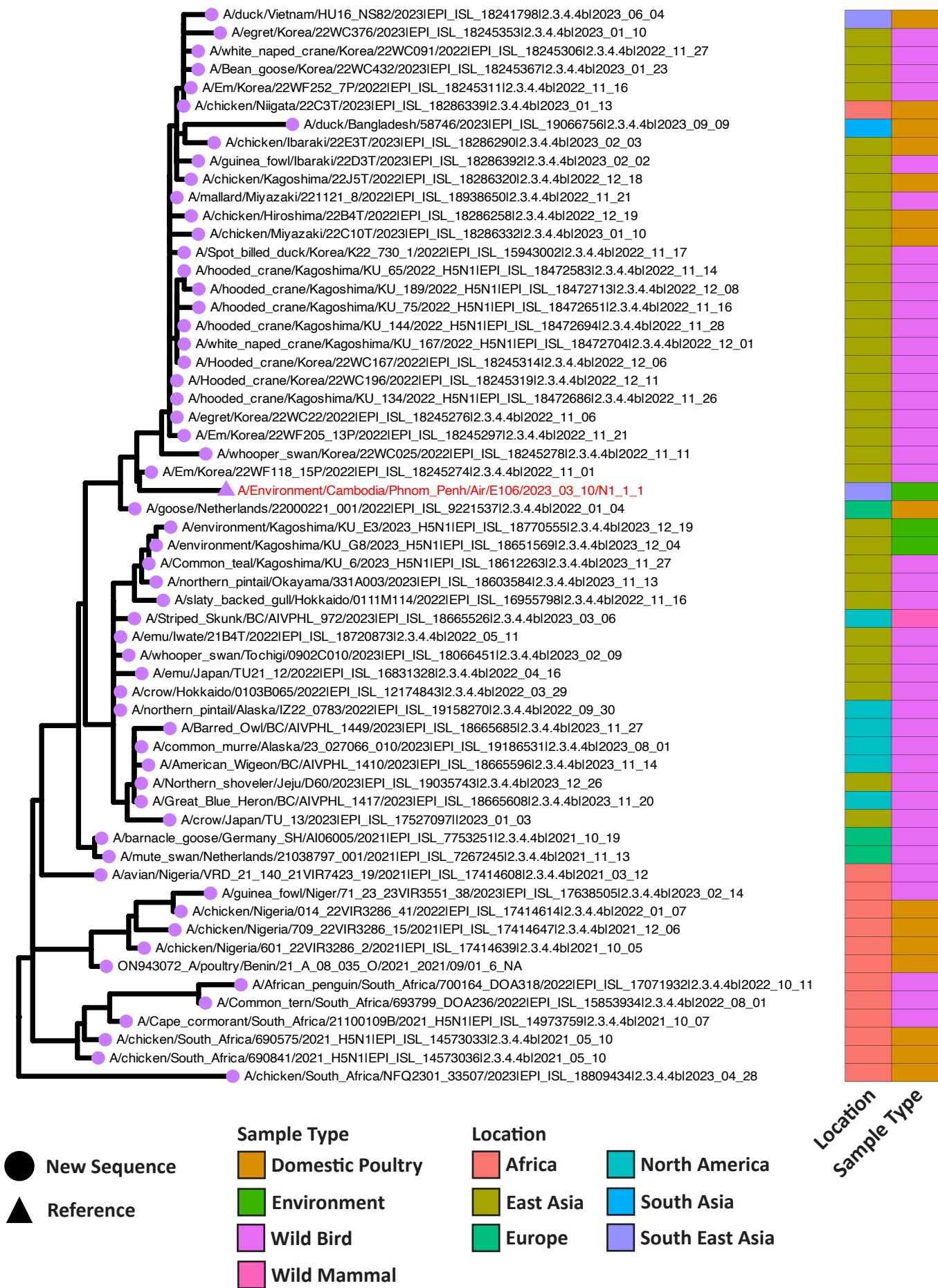
Supplementary Figure 17: NA-N1 sequences from the 2.3.2.1c clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

NA-N1 (2.3.4.4b)



Supplementary Figure 18: NA-N1 sequences from the 2.3.4.b clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographhic location and sample type of all sequences are shown on the right of the plot.

NA-N1 (2.3.4.4b)



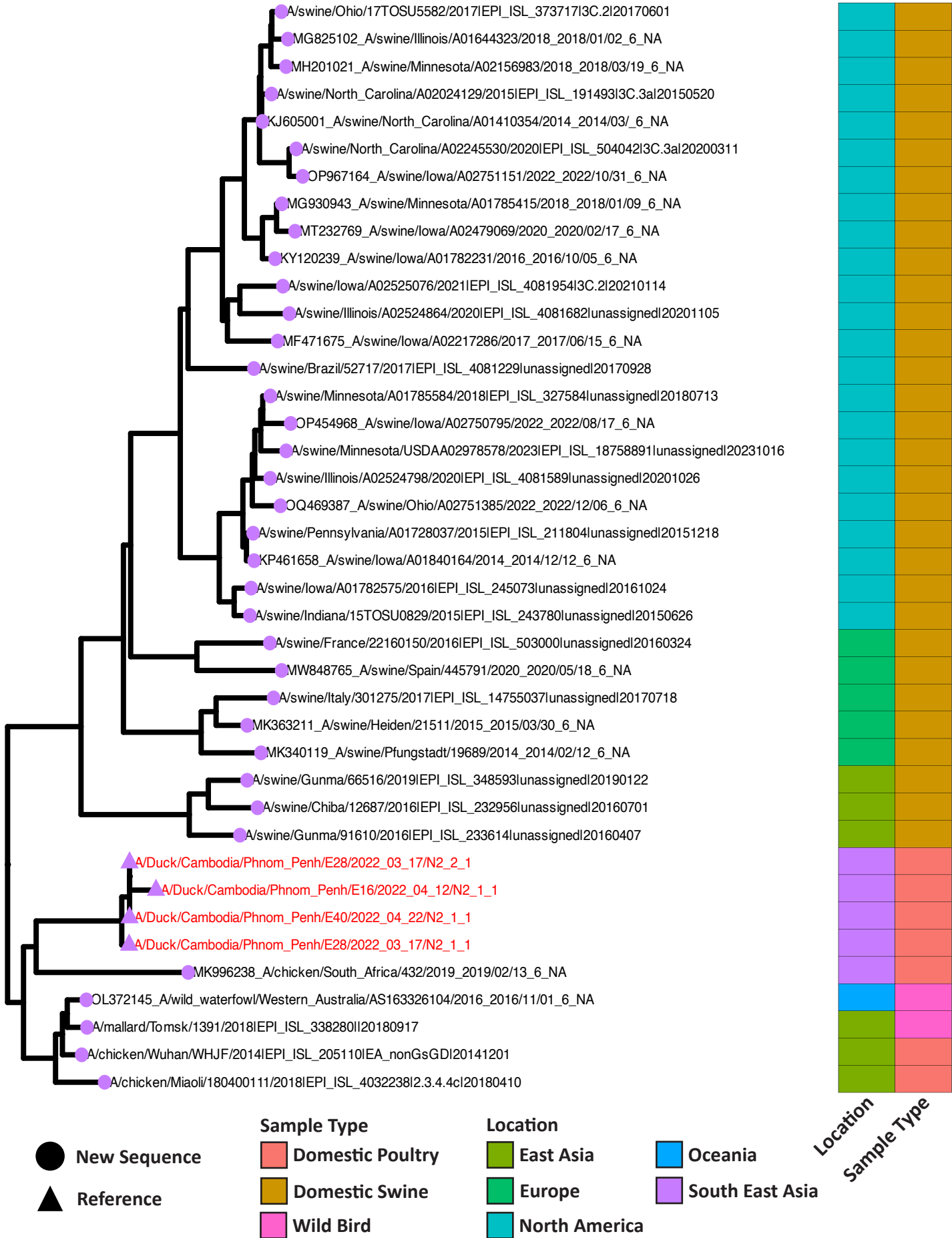
Supplementary Figure 19: NA-N1 sequences from the 2.3.4.b clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are shown with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

NA-N2 (Avian)



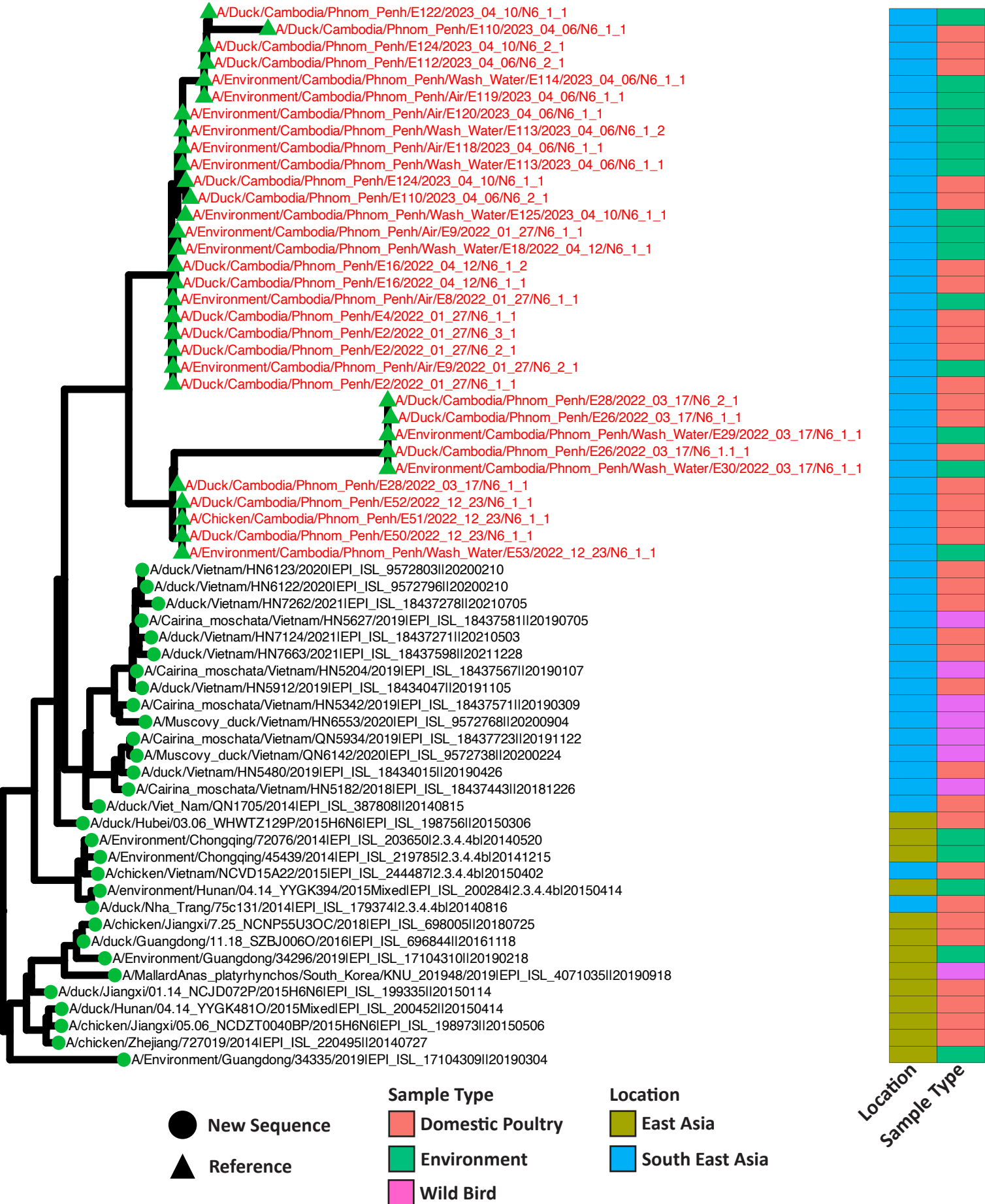
Supplementary Figure 20: NA-N2 sequences from the avian clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographhic location and sample type of all sequences are shown on the right of the plot.

NA-N2 (Swine)



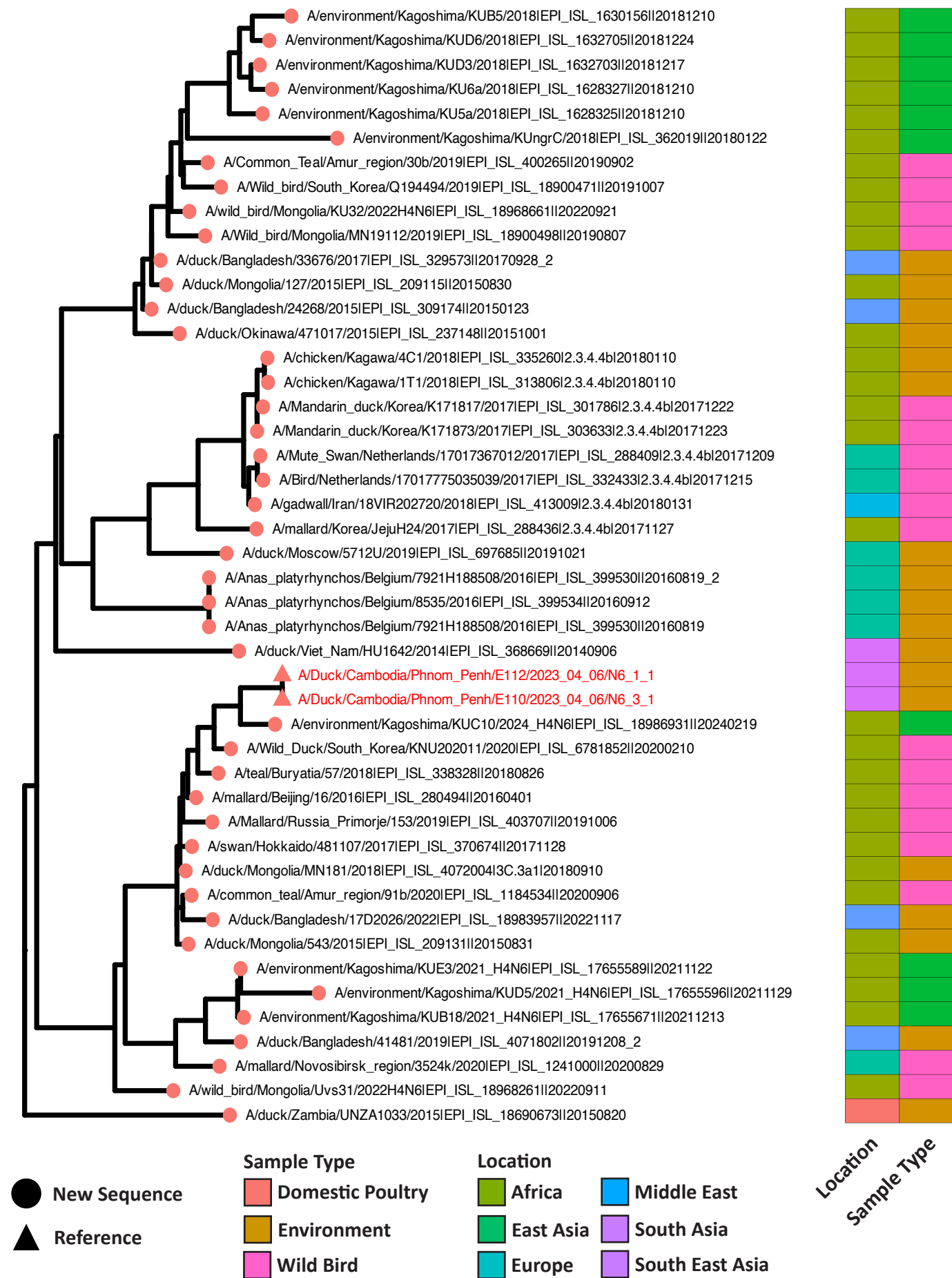
Supplementary Figure 21: NA-N2 sequences from the swine clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geograpghic location and sample type of all sequences are shown on the right of the plot.

NA-N6 (Eurasian H5)



Supplementary Figure 22: NA-N6 sequences from the Eurasian H5 clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographhic location and sample type of all sequences are shown on the right of the plot.

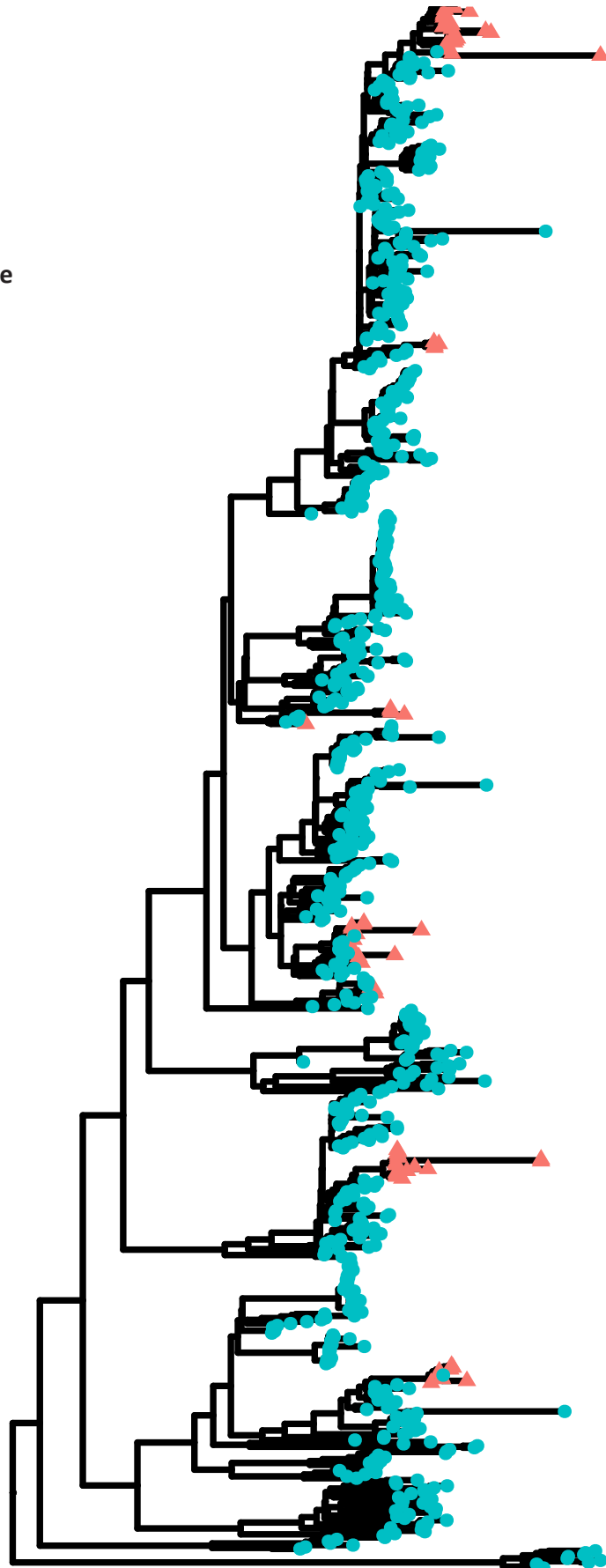
NA-N6 (Eurasian)



Supplementary Figure 23: NA-N6 sequences from the Eurasian clade *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

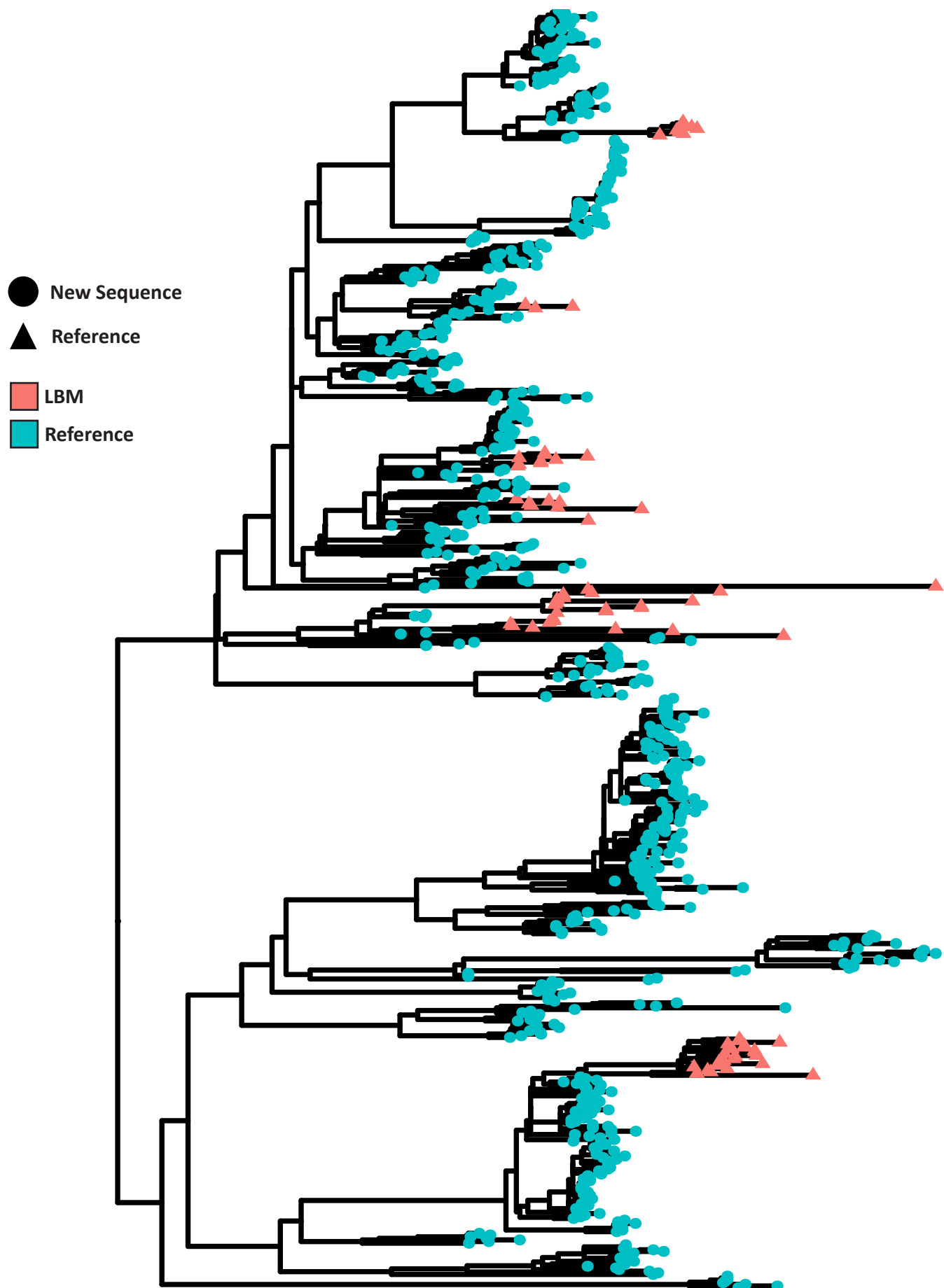
PB2 (Avian)

- New Sequence
- ▲ Reference
- LBM
- Reference



Supplementary Figure 24: PB2 avian sequences *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.

PA (Avian)



Supplementary Figure 25: PA avian sequences *de novo* assembled from environmental samples are a short phylogenetic distance from those found in poultry swabs. The triangle symbol and red text highlight nodes representing new sequences from the current study. Reference sequences are show with a circle symbol and black text for the node label. The geographic location and sample type of all sequences are shown on the right of the plot.