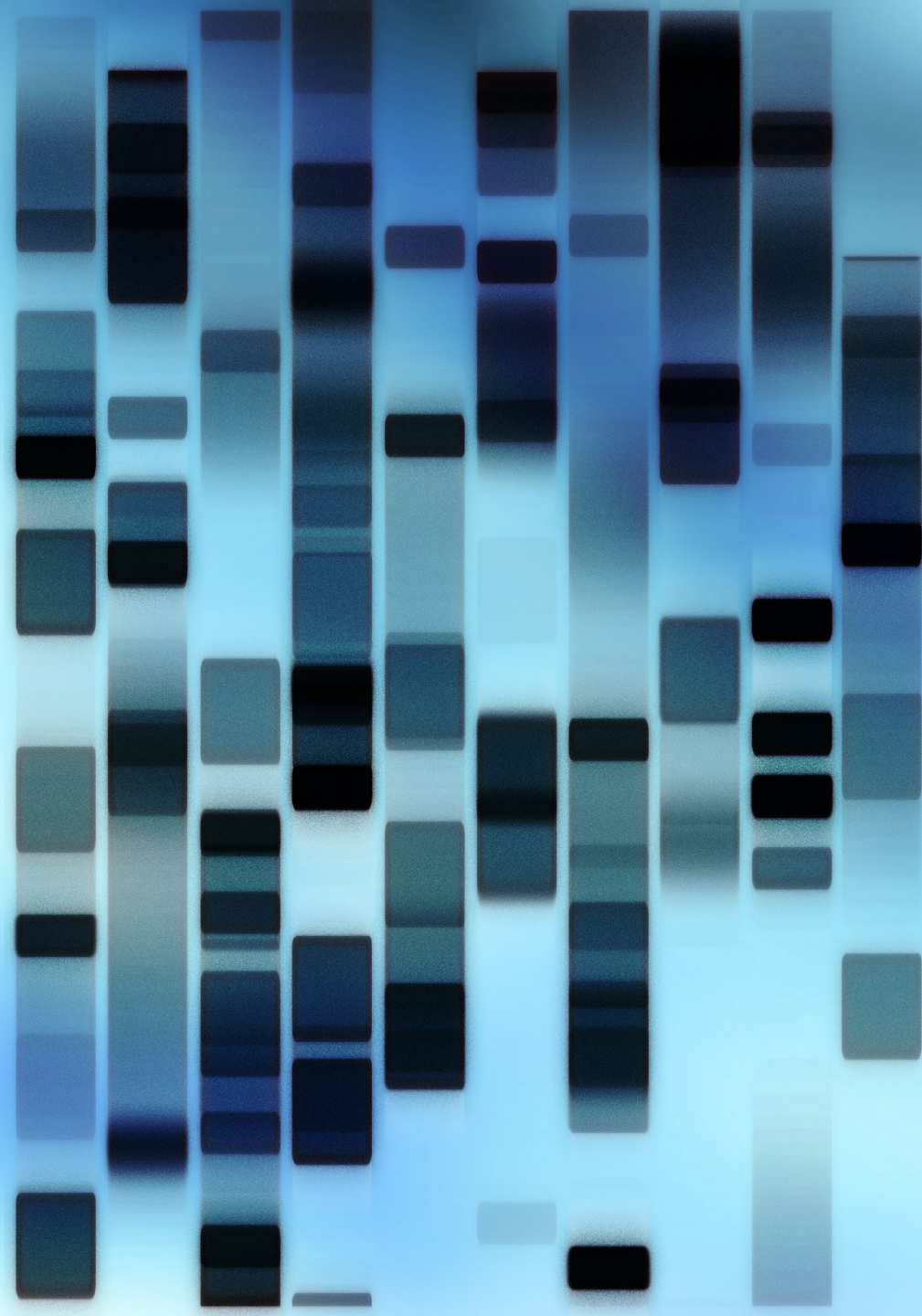


# Genomic epidemiology of the H5N1 AIV outbreak in BC in 2022

**Michelle Coombe, Shannon Russell**

Agatha Jassem, James Zlosnik, Kevin Kuchinski,  
Jessica Caleta, Natalie Prystajeky, Chelsea  
Himsworth





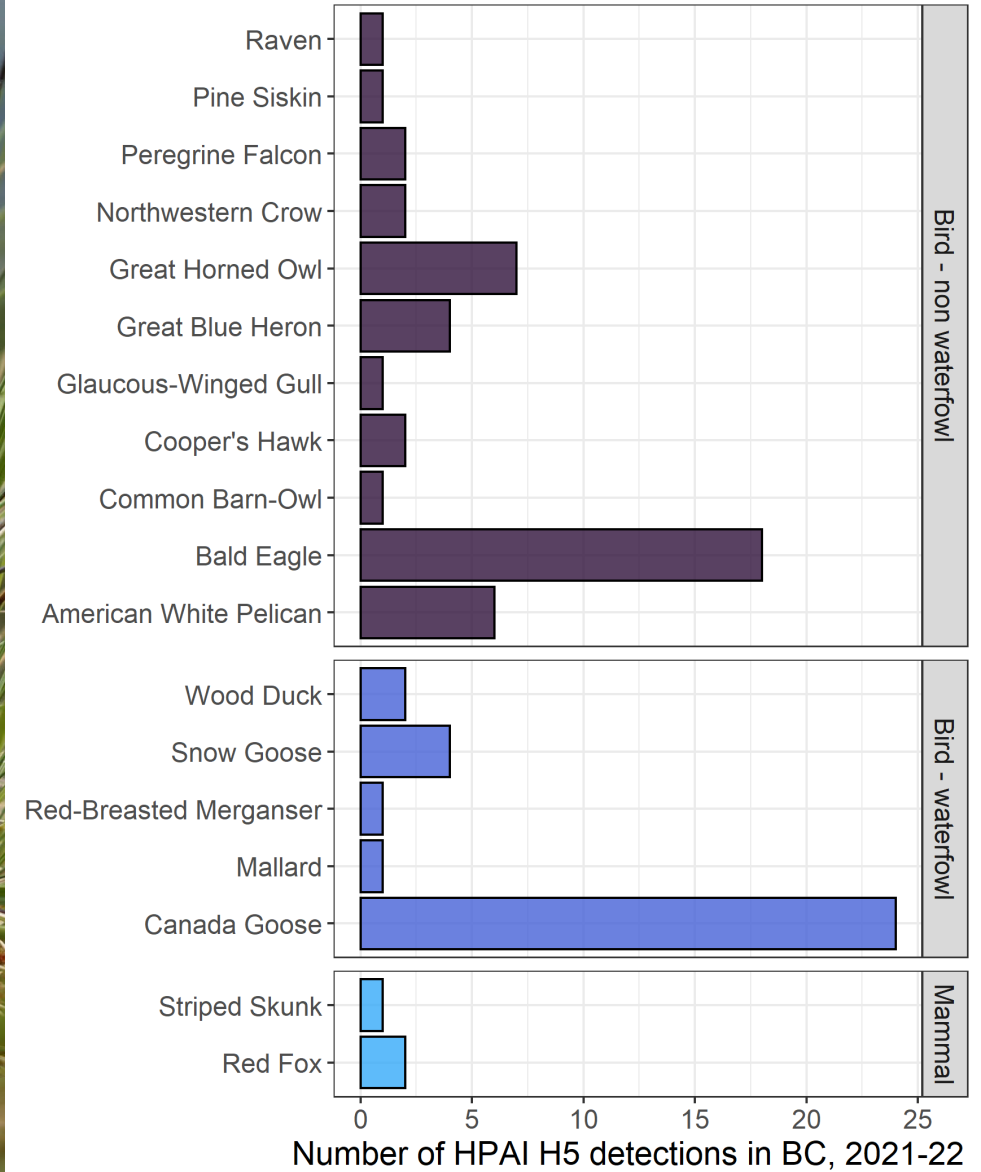
# **HIGHLY PATHOGENIC**

Avian

**INFLUENZA**

&

**One Health**



Number of HPAI H5 detections in BC, 2021-22

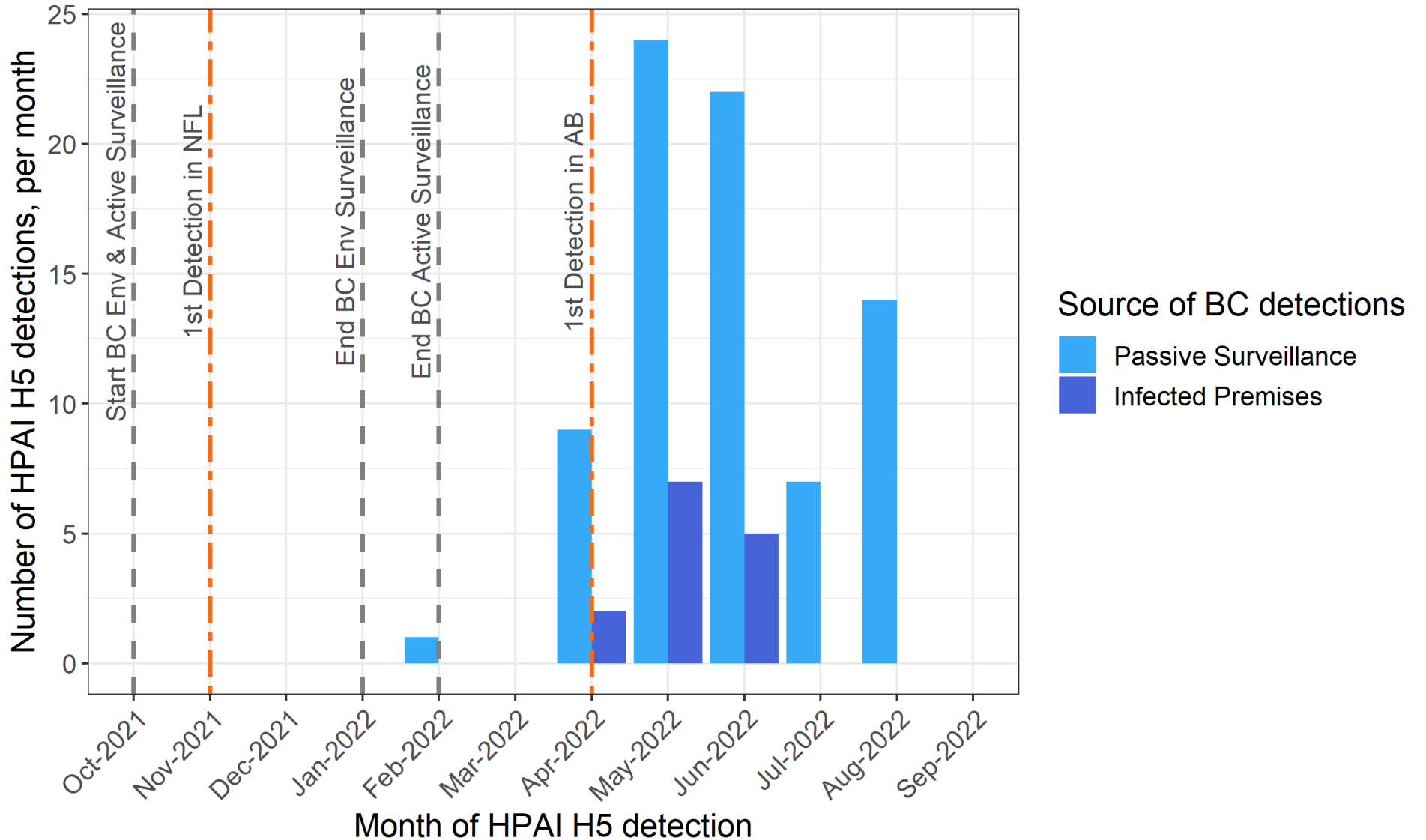
A person wearing a white protective suit, hood, and goggles is holding up their right hand, which is covered in a white glove. The hand is held palm facing forward, with fingers spread. The background is dark. The text "Human Health Risk?" is overlaid on the image in white.

Human Health Risk?

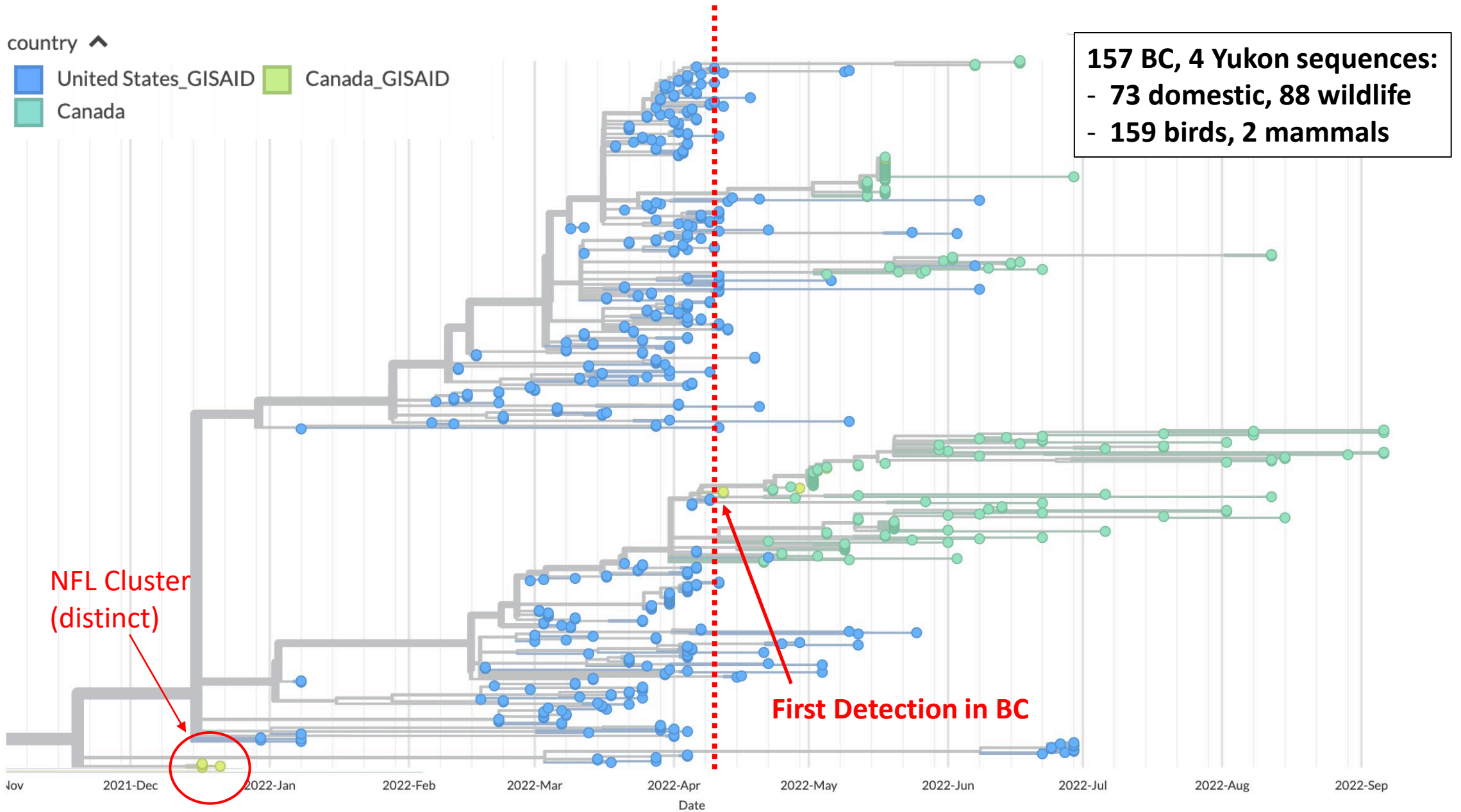


# Sources of WILDLIFE surveillance in BC

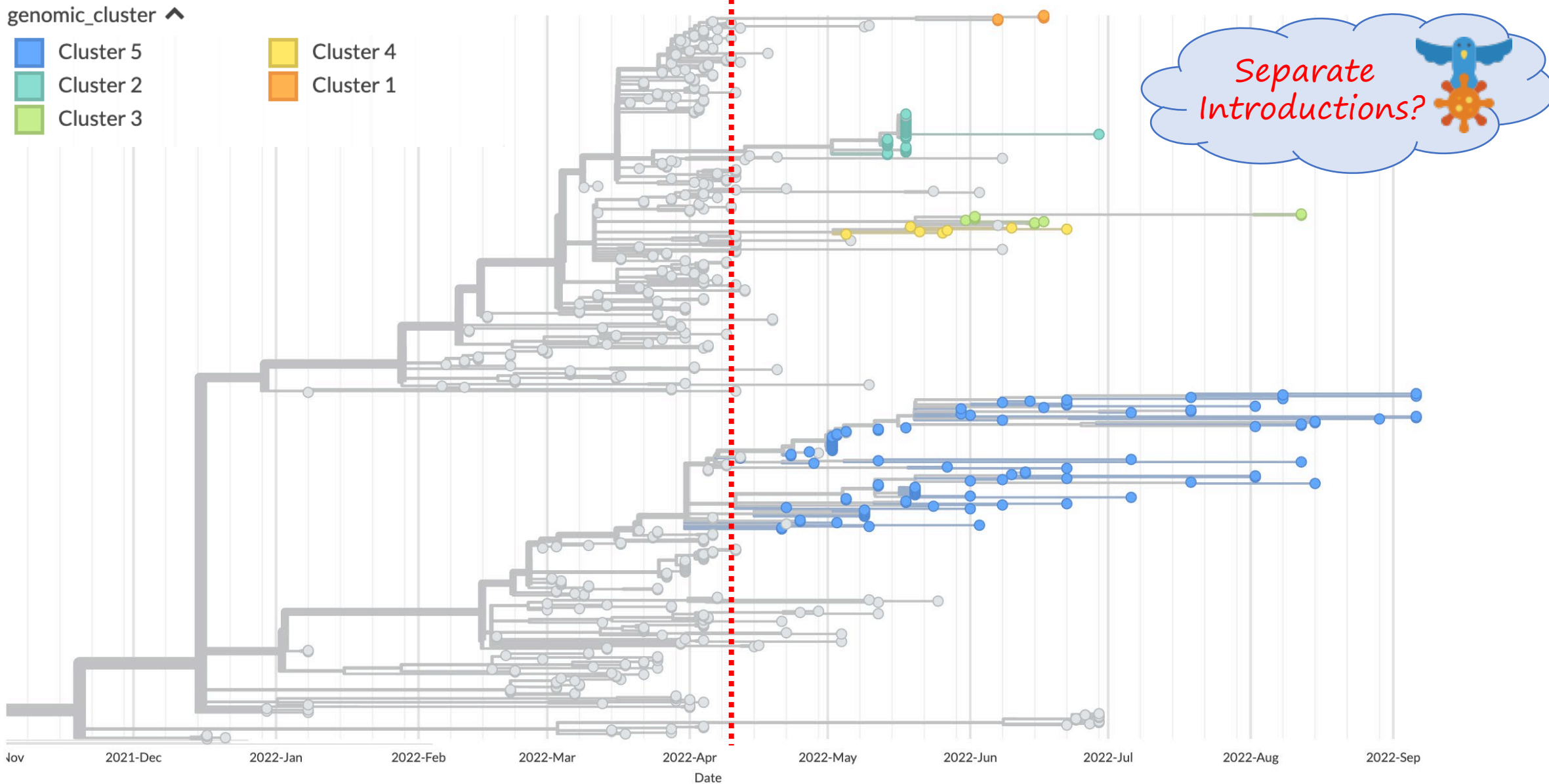
# Epi curve for BC surveillance 2021-22



# Timeline of the HPAI H5N1 outbreak in North America using phylogenetics



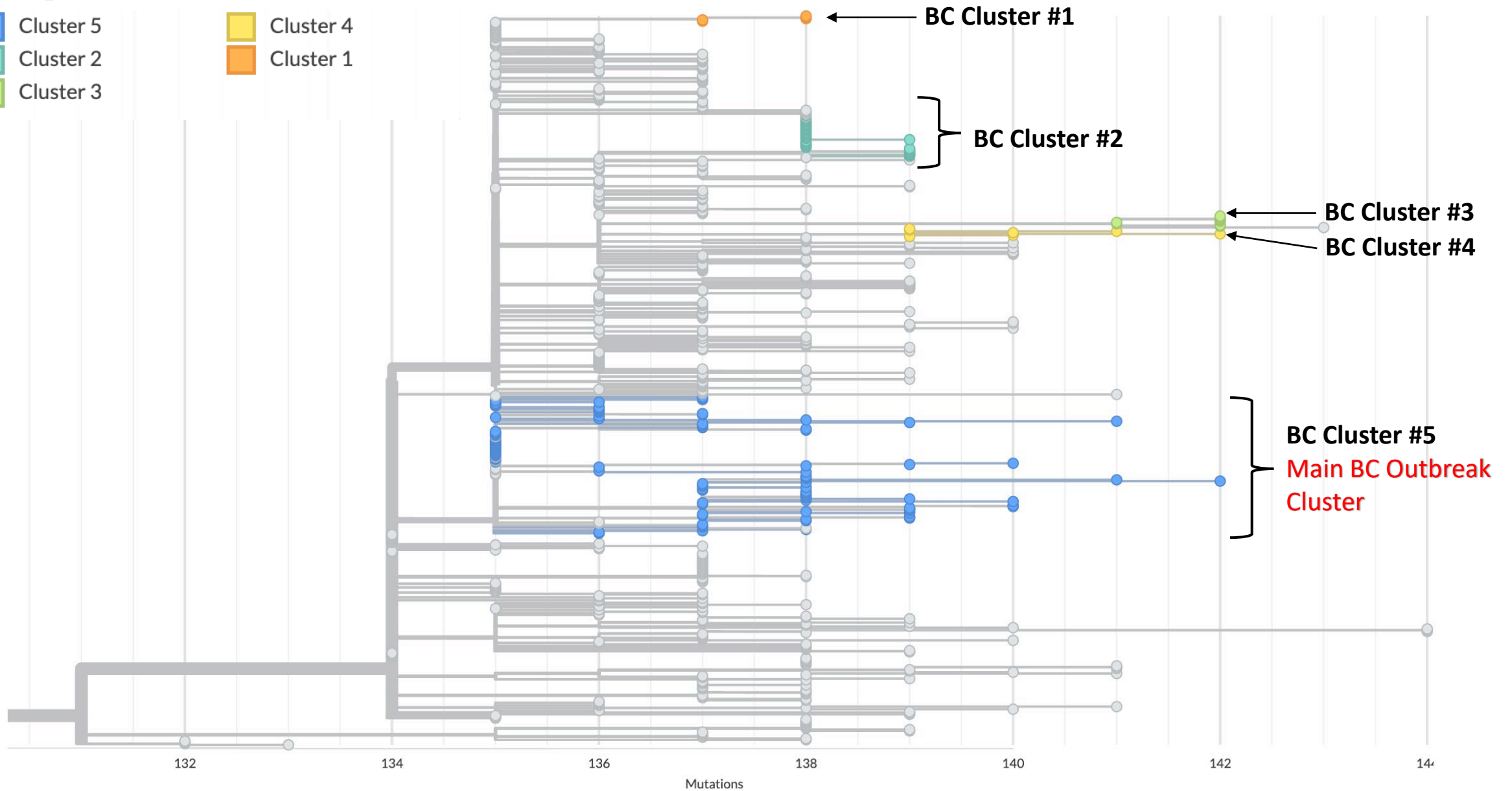
# Five distinct BC genomic clusters appear: more closely related to US sequences than other BC sequences in the same outbreak





# Five BC genomic clusters: relatedness based on HA mutations (no time)

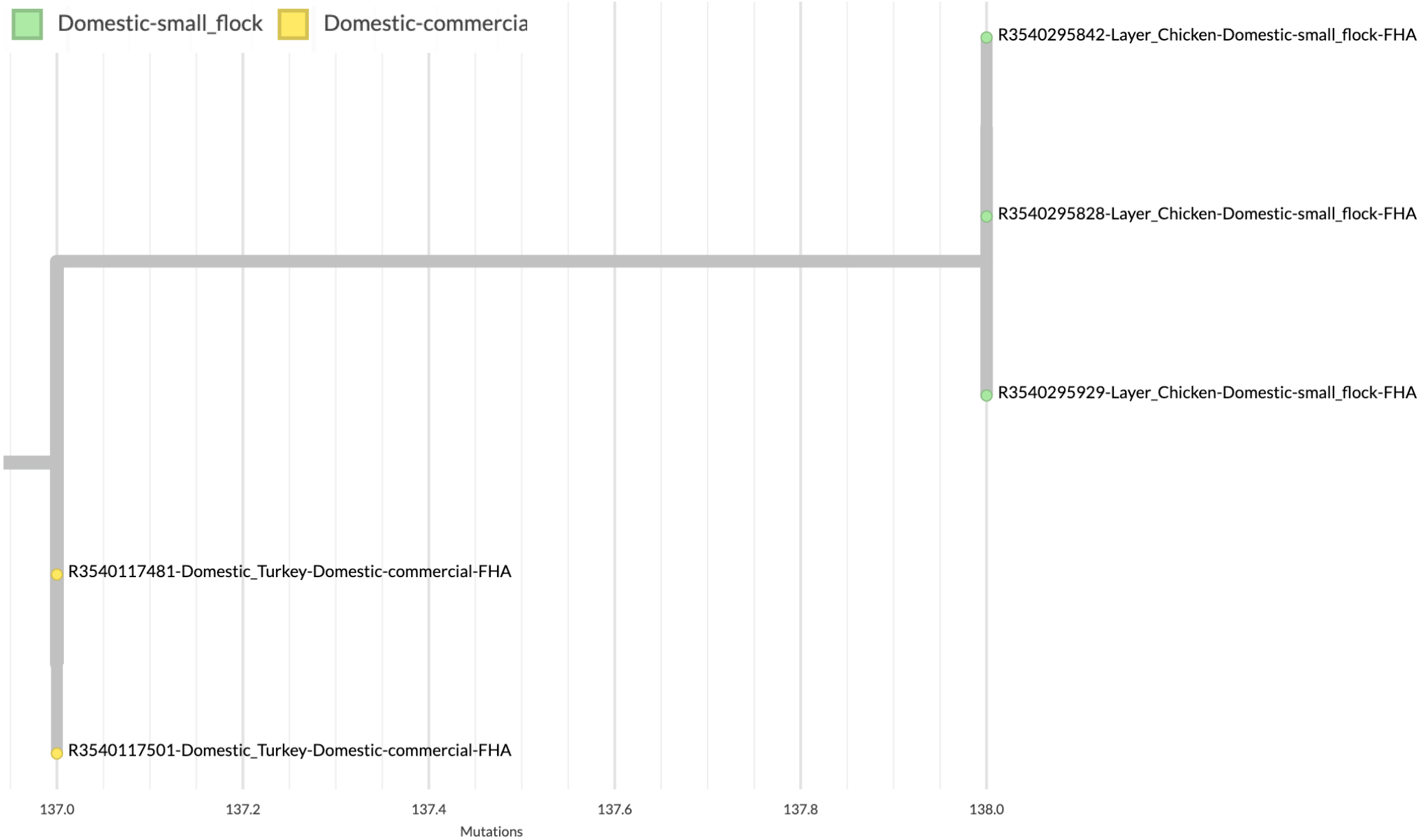
genomic\_cluster ^



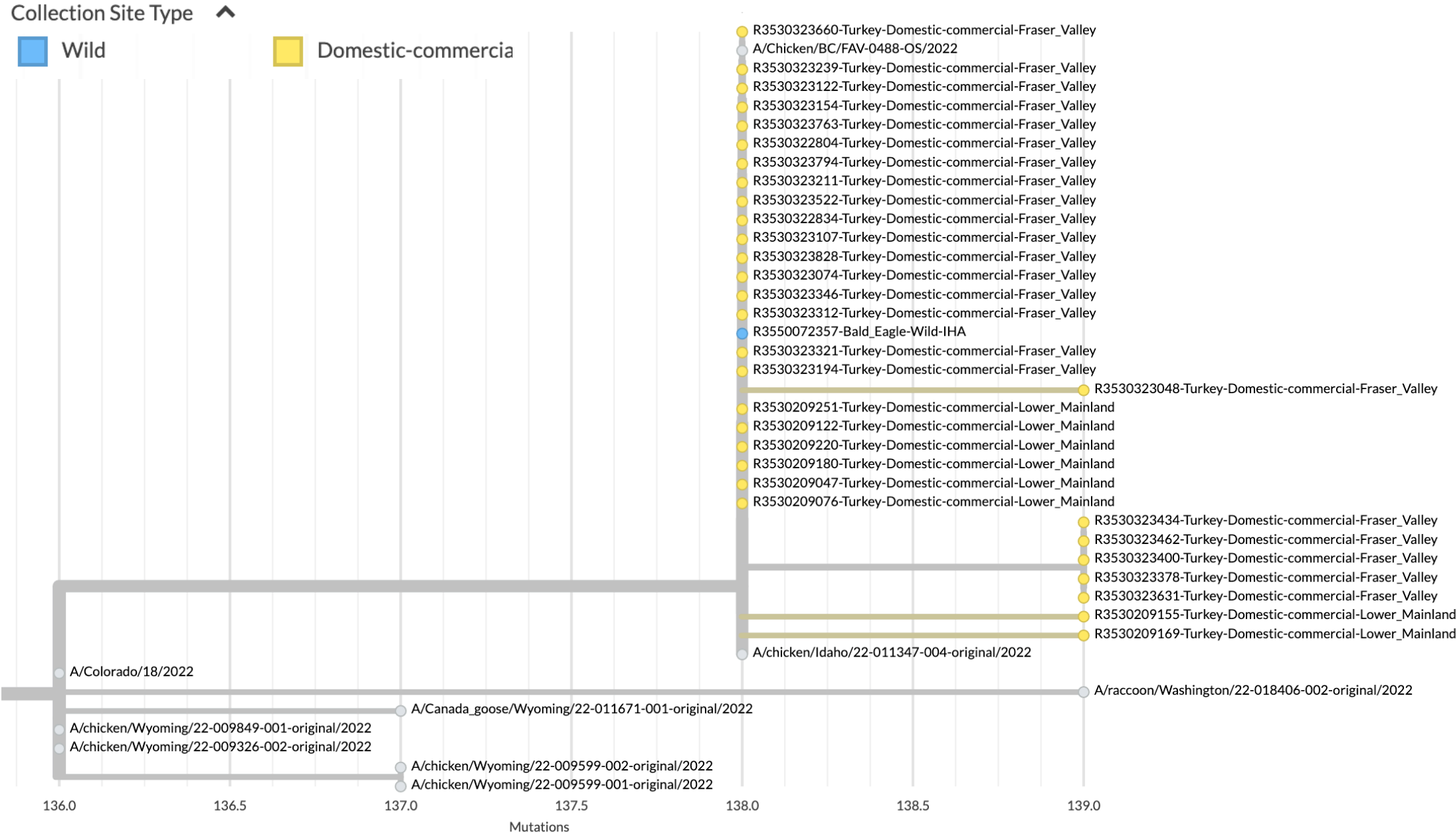
# BC Cluster #1: Domestic only

Collection Site Type ^

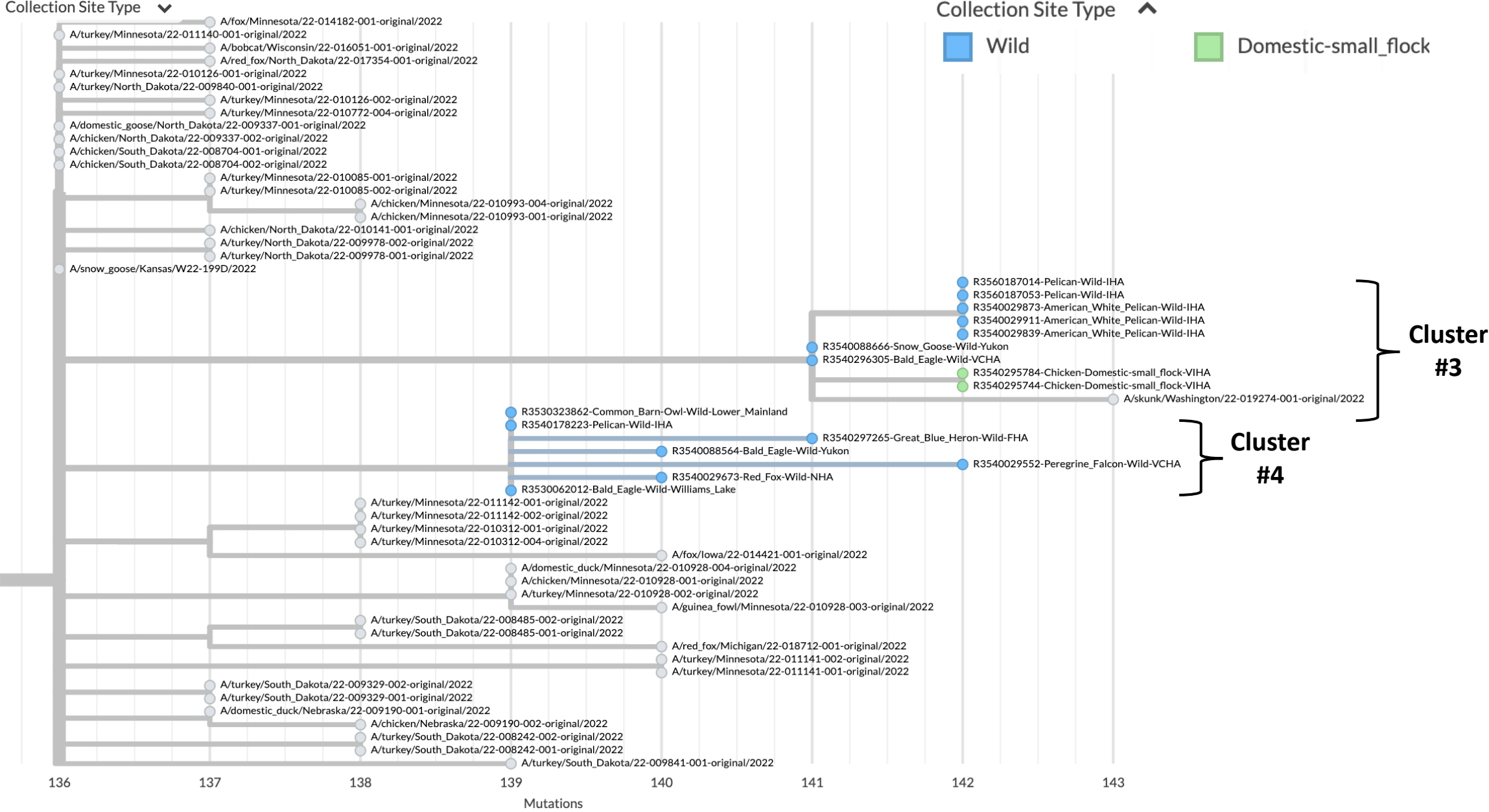
- Domestic-small\_flock
- Domestic-commercial



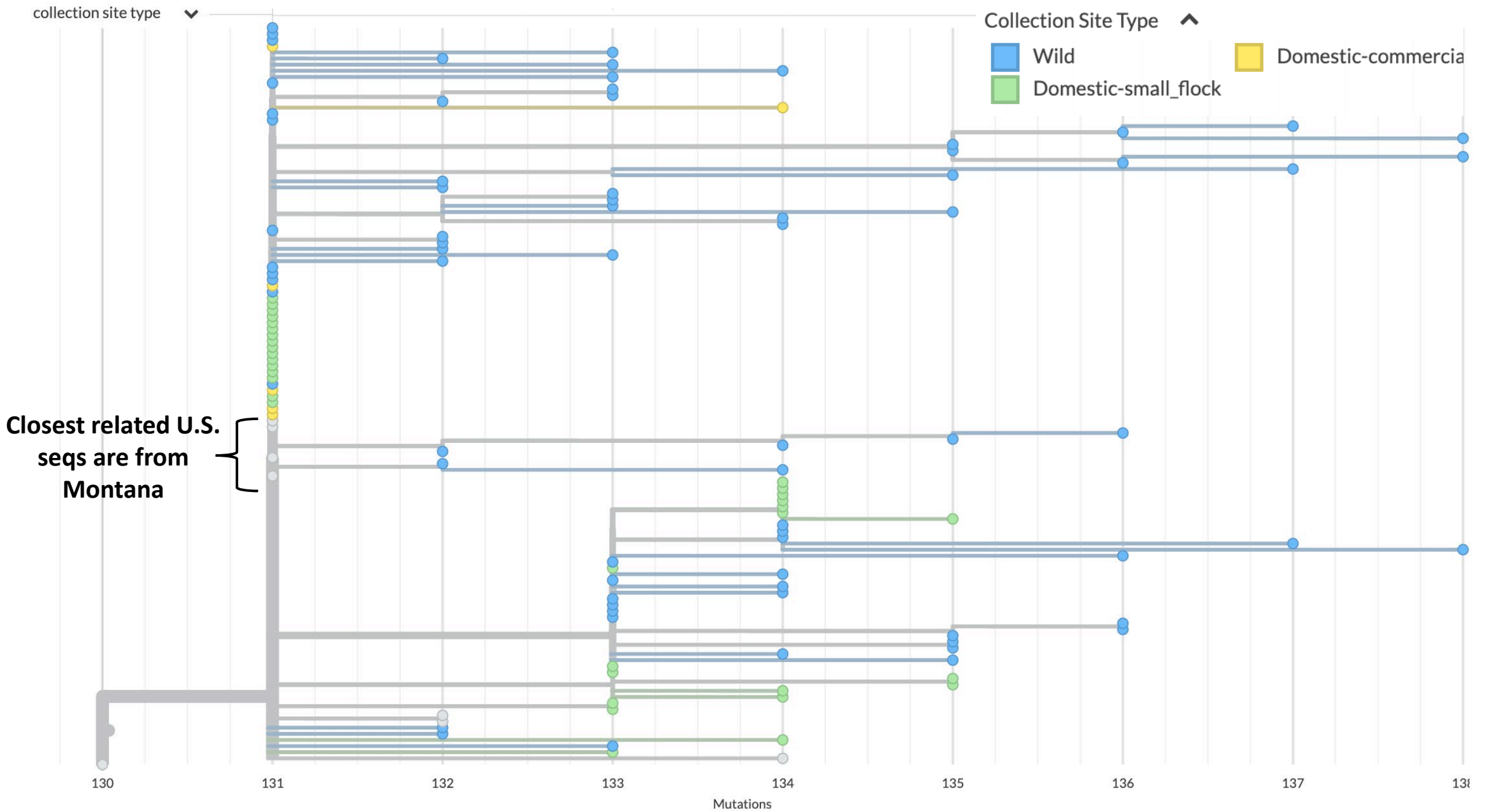
# BC Cluster #2: Primarily domestic, one wild bird detected



# BC Clusters #3 and #4: Wildlife only, and domestic/wildlife



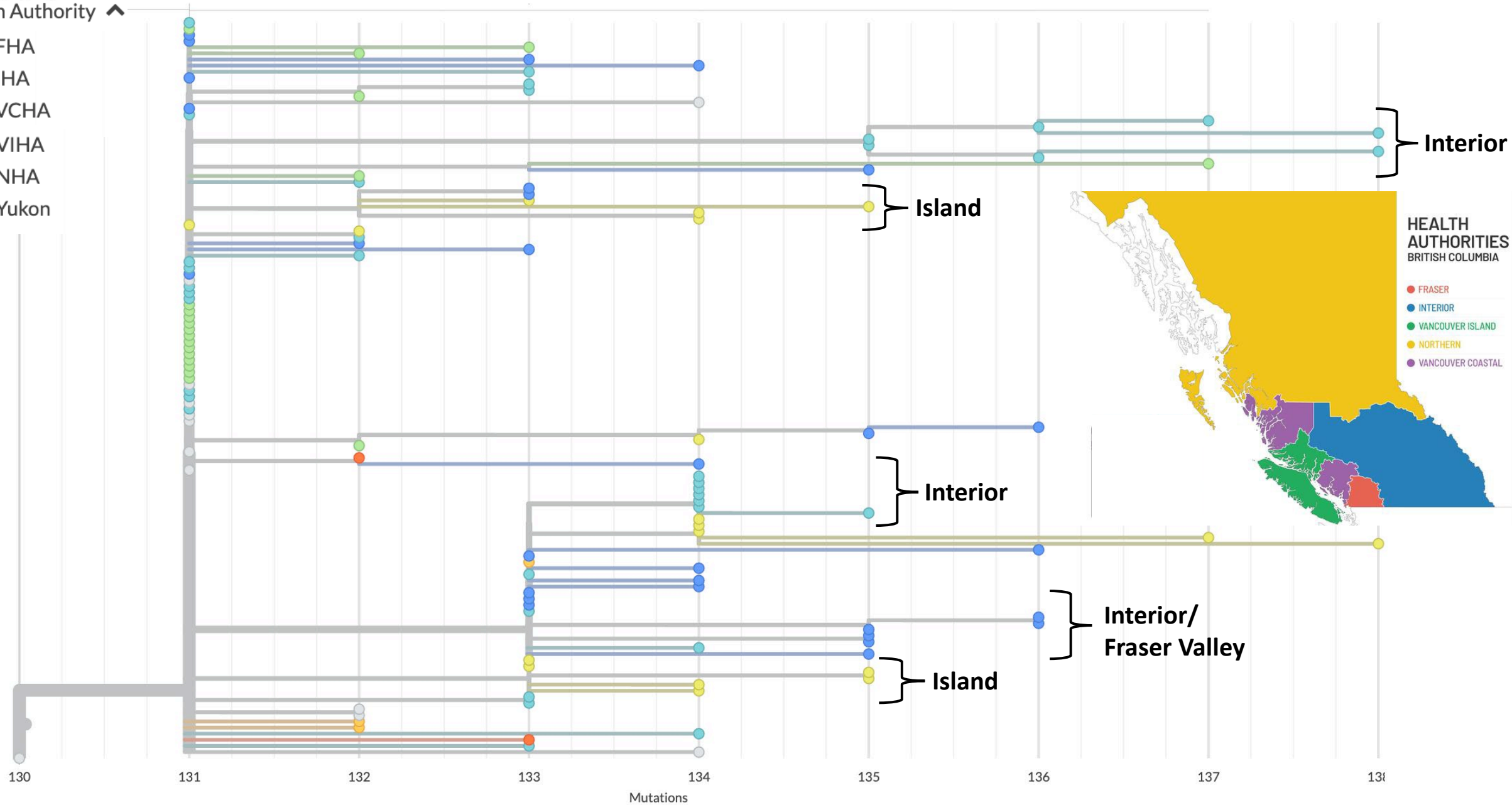
# BC Cluster #5: Main BC Outbreak Cluster, contains domestic and wildlife



# BC Cluster #5: Main BC Outbreak Cluster, by region

Health Authority ^

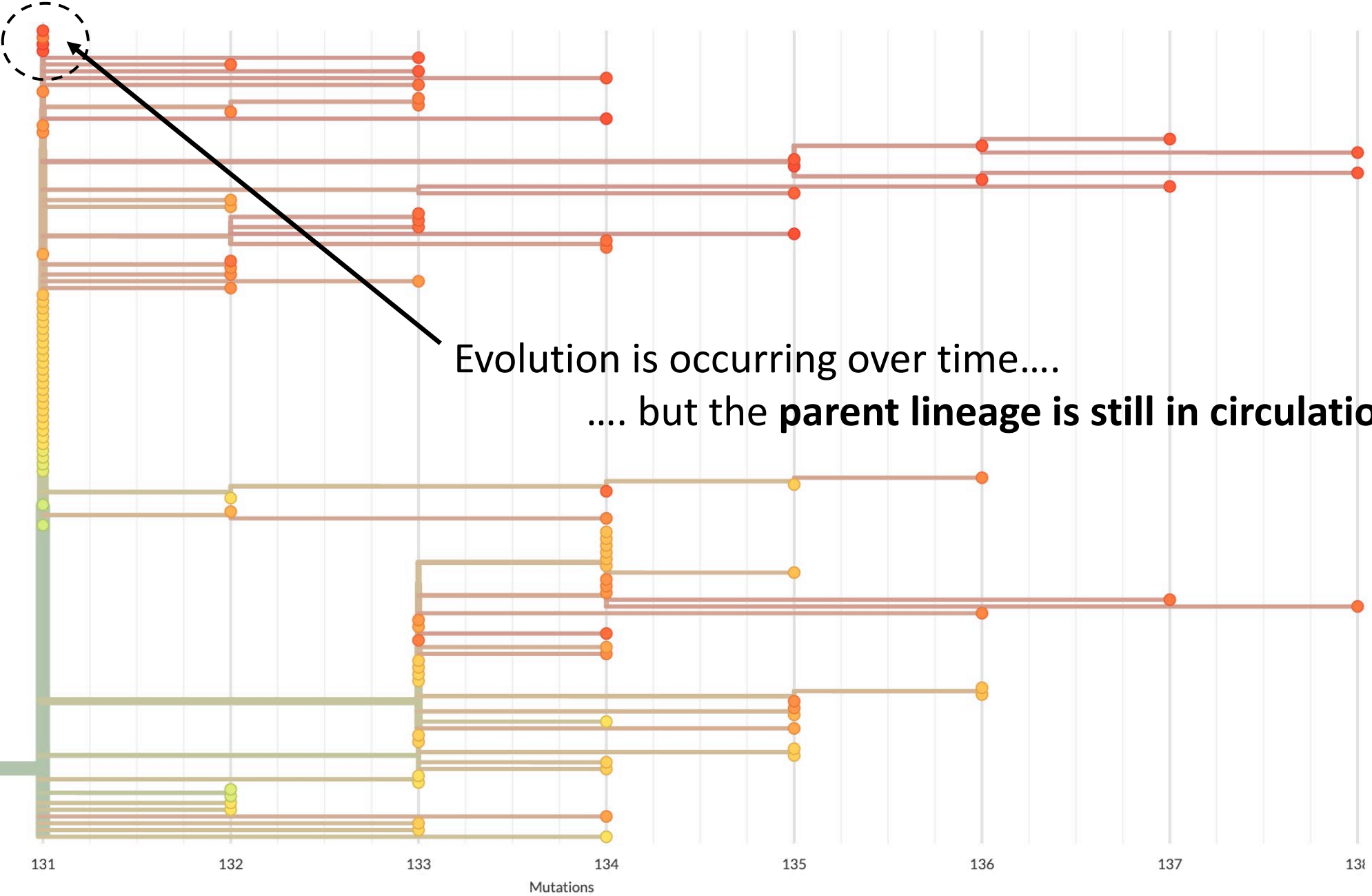
- FHA
- IHA
- VCHA
- VIHA
- NHA
- Yukon



# BC Cluster #5: Main BC Outbreak Cluster, by collection date

Sampling date ^

- Mar 2022
- Mar 2022
- Mar 2022
- Apr 2022
- Apr 2022
- May 2022
- Jun 2022
- Sep 2022

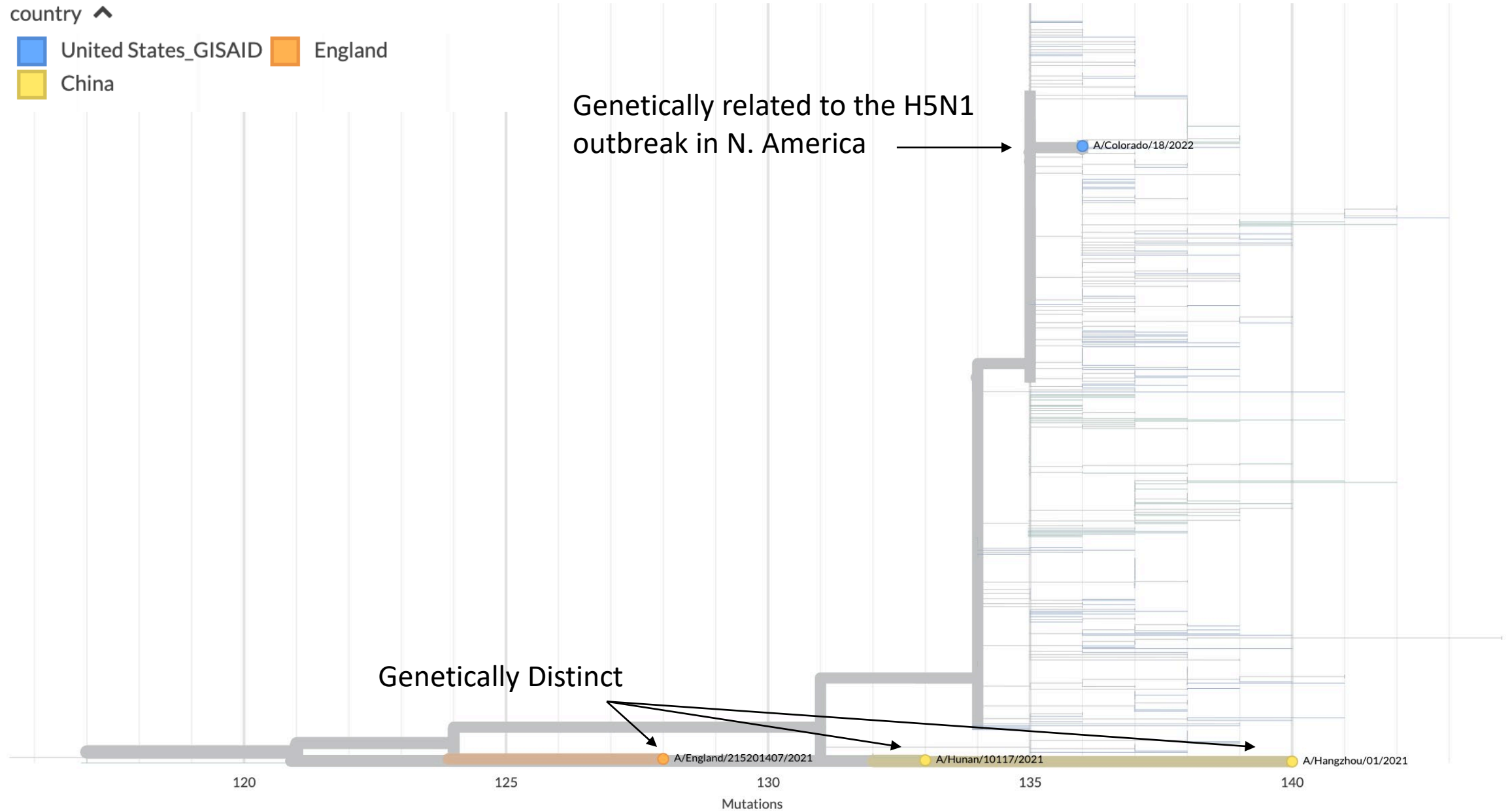


130 131 132 133 134 135 136 137 138

Mutations

# Impact of HPAI H5 on human risk assessment: phylogenetic inferences

country ^





# What have we learned from WGS of H5N1 in BC?

- BC detections are spread amongst 5 genetically distinct clusters, suggesting **multiple variants were circulating**
- Based on the membership of these clusters:
  - Transmission is occurring mostly between wildlife and domestic flocks
  - Some transmission may have occurred between domestic flocks
- The majority of BC detections reside in one large genetic cluster
  - Variants are widely distributed across the regions, some regional clusters
  - Evidence of viral evolution over time
  - But also persistence of parent lineage, why?
    - Fitness advantage? Reservoir host?
- We plan to look at whether these clusters are maintained for other segments of the virus (e.g. NA, etc.), and build a pipeline to detect/monitor reassortment.

# Conclusions – Risks and Surveillance

## of HPAI H5N1 clade 2.3.4.4b



# Acknowledgements

*So many important contributors to this work!*



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Agencies

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Rob Azana



BRITISH  
COLUMBIA



BC Centre for Disease Control



Canadian Food  
Inspection Agency



# BC Bald Eagle detected in February 2022 unrelated to the BC outbreak

Phylogeny

country ^

- United States\_GISAID
- Canada
- Canada\_GISAID
- China
- England



ZOOM TO SELECTED

RESET LAYOUT

