8 December 2023

COVID-19 Genomics Insights Dashboard (CGID) #44

The COVID-19 genomics insights dashboard (CGID) provides a public and high-level overview of viral genomic surveillance across Aotearoa New Zealand. It aims to explain how whole-genome sequencing (WGS) complements other epidemiological data to support public health decision-making. As SARS-CoV-2, the virus that causes COVID-19, continues to adapt, mutate, and spread, the CGID reports trends and insights gained by our WGS surveillance programme in Aotearoa New Zealand, and abroad.

Summary Infographics & Insights:

Genomes analysed:

1342*

genomes from cases since the last report (2 October)

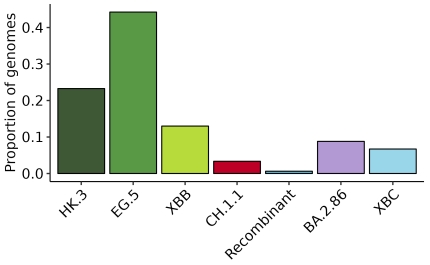
~11,500

genomes reported so far in 2023

* number of successful genomes. Sample no. processed is higher due to failed WGS attempts & cases sequenced multiple times

Variant surveillance:

EG.5 lineages have remained the most prevalent in the past two weeks, comprising 23% for HK.3 and 45% for other EG.5 variants. Another variant, BA.2.86, which is highly divergent, now accounts for 9% of the cases sequenced during this period



Hospital surveillance:

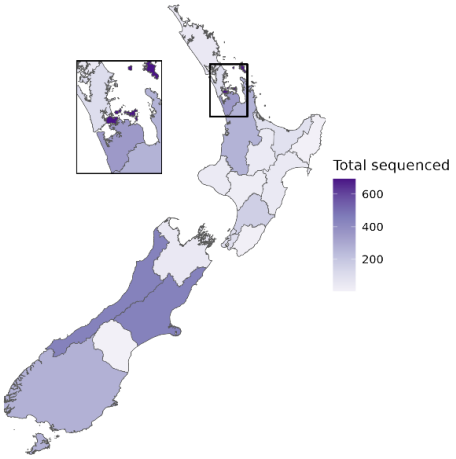
42% (202 of 475*) of PCR-positive cases with a hospital admission date from 17 Nov to 1 Dec successfully produced a genome to date. The approximate composition of hospital cases:

- EG.5: 45%
- HK3: 23 %
- XBB: 12%
- BA.2.86: 9%
- XBC 7%

*The total number of PCR positive admitted cases includes high Ct samples not suitable for sequencing, samples that fail to produce genomes and cases reported late in the reporting period.

Graphical overview showing sample origins

Number of SARS-CoV-2 genomes sequenced



Key Trends & Insights:

- The EG.5 group of variants remains the most common among sequenced cases and has been growing. Among these lineages, HK.3 accounted for 23% of cases in the past two weeks, while other EG.5 variants accounted for 45%.
- The growth of the EG.5 group is partly because of new variants like HK.1.2 and HV.1. These new variants might spread faster than the original EG.5.
- The BA.2.86 variant currently represents 9% of the sequenced cases. It is showing a slightly faster daily growth rate compared to the original EG.5 lineage. This suggests BA.2.86 might continue spreading more in the future.
- The XBB.1.5 and XBB.1.16 lineages are decreasing and are no longer included in the tracked variants for this report.
- Wastewater analysis aligns with clinical samples, reflecting the dominance of EG.5, the rise of HK.3, XBC's stability, and the presence of BA.2.86 at low frequency (demonstrating consistency in results between different data sources).

The CGID report is produced 'at pace' by ESR in collaboration with Massey University, University of Auckland, and University of Otago. Data & insights are subject to change and correction

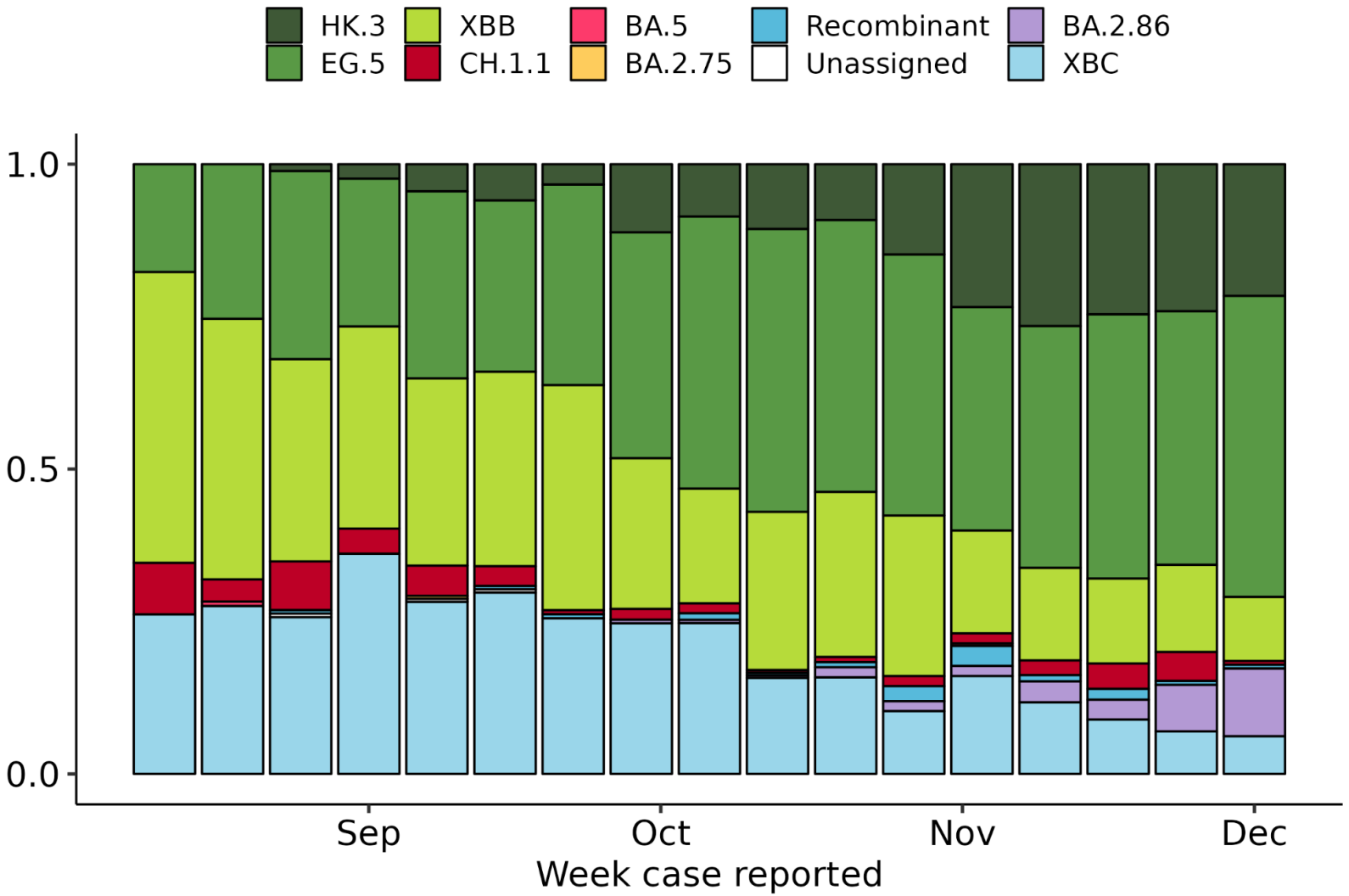


Figure 1: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 17 weeks) as determined by whole-genome sequencing. *Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week is based on a limited number of genomes (162) as data is still being generated for this week. [The category 'unassigned' is typically where a partial genome has been recovered, and a definitive assignment to a variant was not possible].*

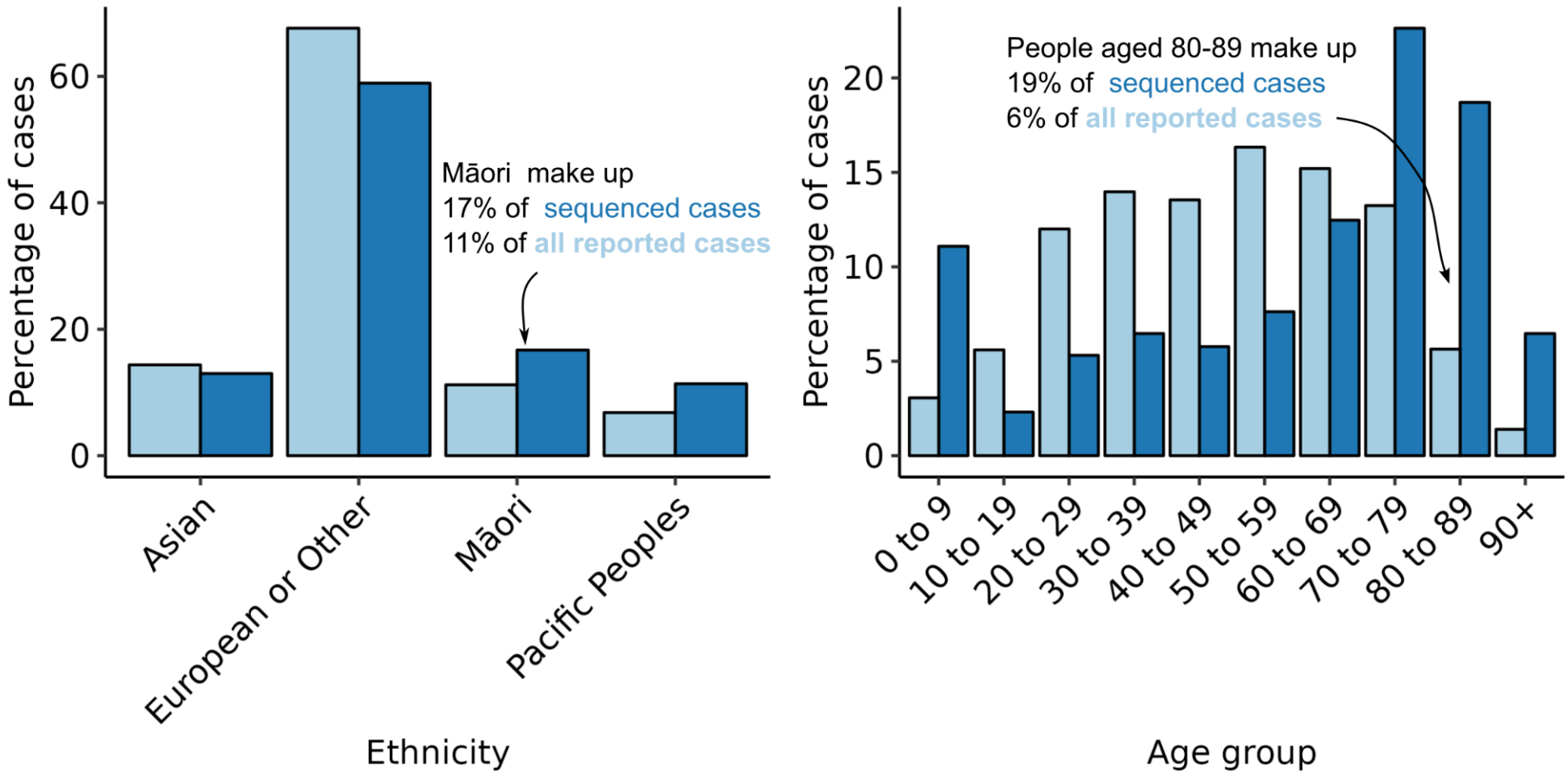


Figure 2: *(**Left**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**Right**) Comparison of age distribution across all reported cases (light blue) and sequenced cases (dark blue).*

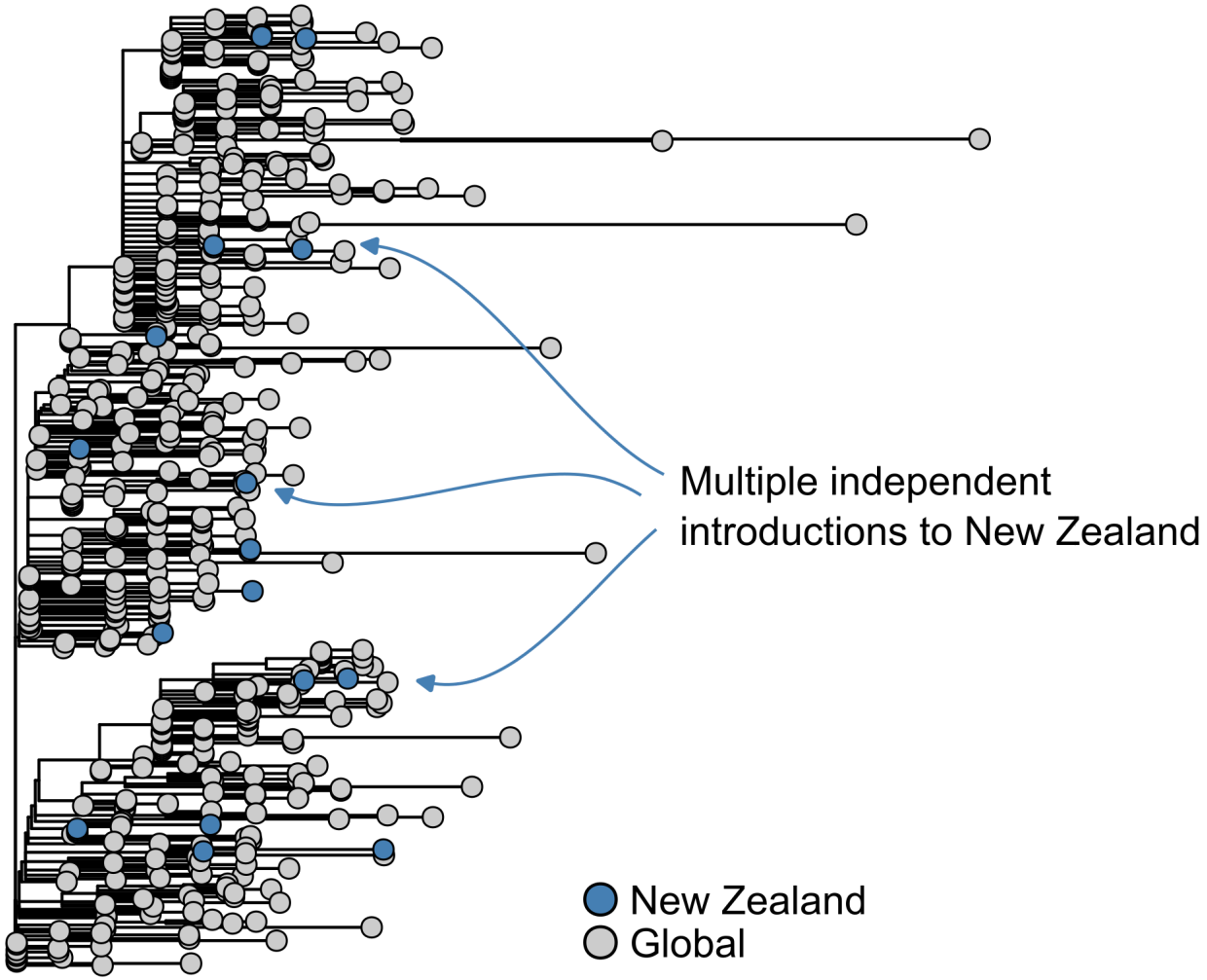


Figure 3: *Evolutionary relationships between New Zealand (blue) and Global (grey) JN.1 genomes. The fact that New Zealand genomes are not clustered in one part of the tree suggests that the recent rise of JN.1 is not the result of specific mutations acquired within New Zealand.*

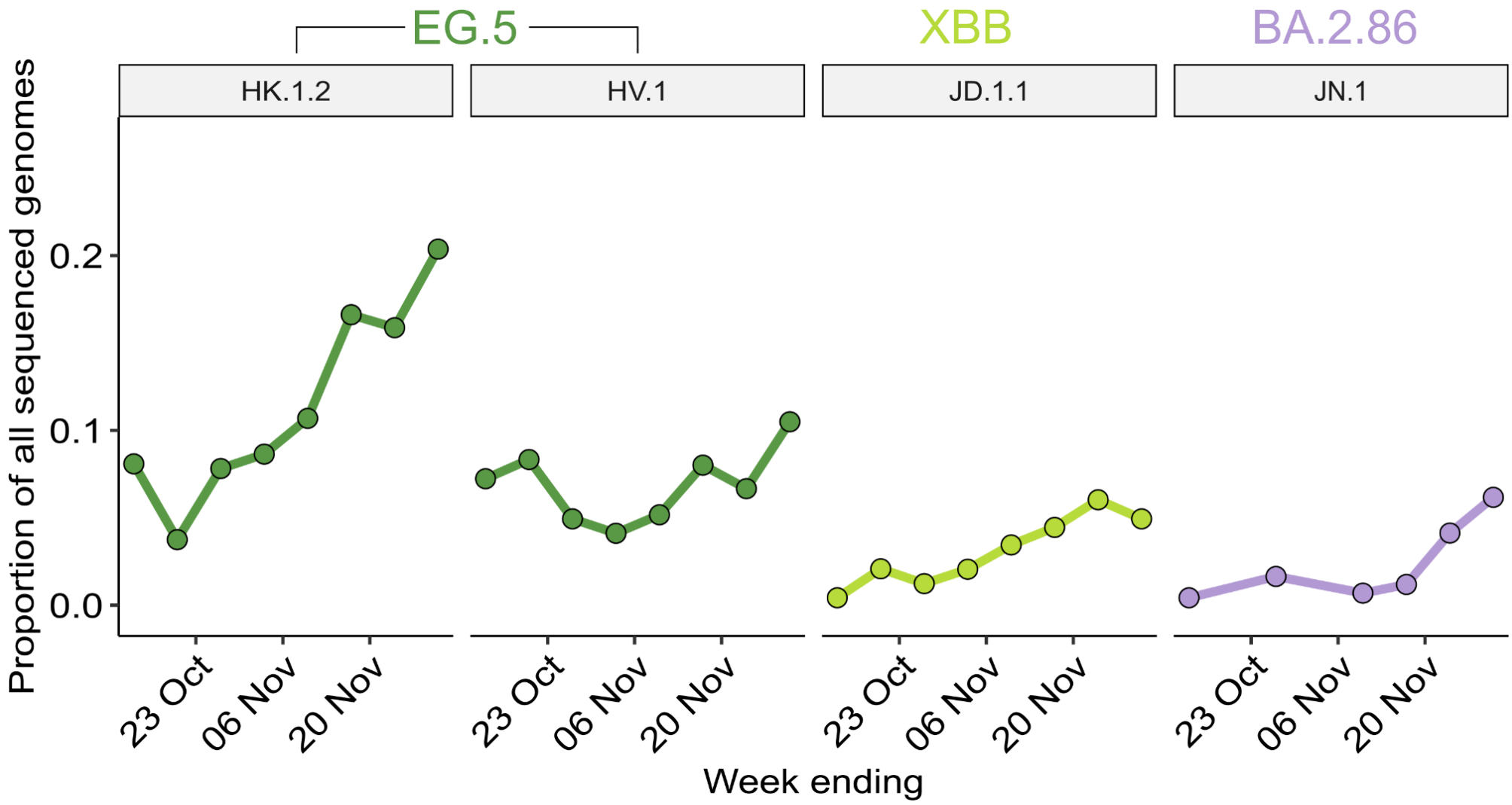


Figure 4: The trajectory of specific sub-lineages in recent weeks*. Each subplot represents a single tracked lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.* The labels above the subplot describe which variant each lineage is reported under in Figure 1.