8 March 2024

COVID-19 Genomics Insights Dashboard (CGID) #46

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:

605

genomes from cases since the last report (February 2024)

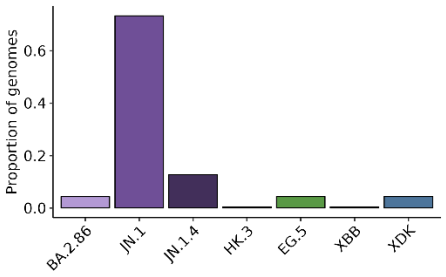
~2,000

genomes reported so far in 2024

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

Variant surveillance:

The most common COVID-19 variant in Aotearoa is still JN.1. Over 90% of recently identified cases in the past two weeks were linked to the JN.1 variant. We've also started watching two related variants, JN.1.4 and a recombinant called XDK



Hospital surveillance:

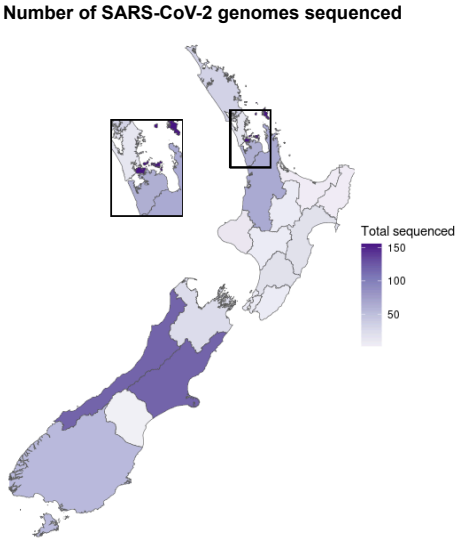
29% (107 of 369*) of PCR-positive cases with a hospital admission date from 16 Feb to 1 Mar have been sequenced to date.

The approximate composition of hospital cases:

-	JN.1	71%
-	JN.1.4	14 %
-	BA.2.86	5%
-	XDK	5%
-	EG.5	5 %

*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



Key Trends & Insights:

- JN.1 is the most common variant in New Zealand, accounting for over 90% of sequenced cases and nearly all wastewater findings.
- Two related sub-lineages, JN.1.4 (with an extra mutation) and XDK (a recombinant), have been added to the list of monitored variants. JN.1.4 and XDK are estimated to grow 1% faster each day compared to other JN.1 lineages.
- No tracked variant is over-represented in hospitalised cases.
- The latest wastewater results mirror those from whole genome sequencing, albeit with an even more complete replacement of older lineages by JN.1

The CGID report is produced 'at pace' by ESR Data & insights are subject to change and correction

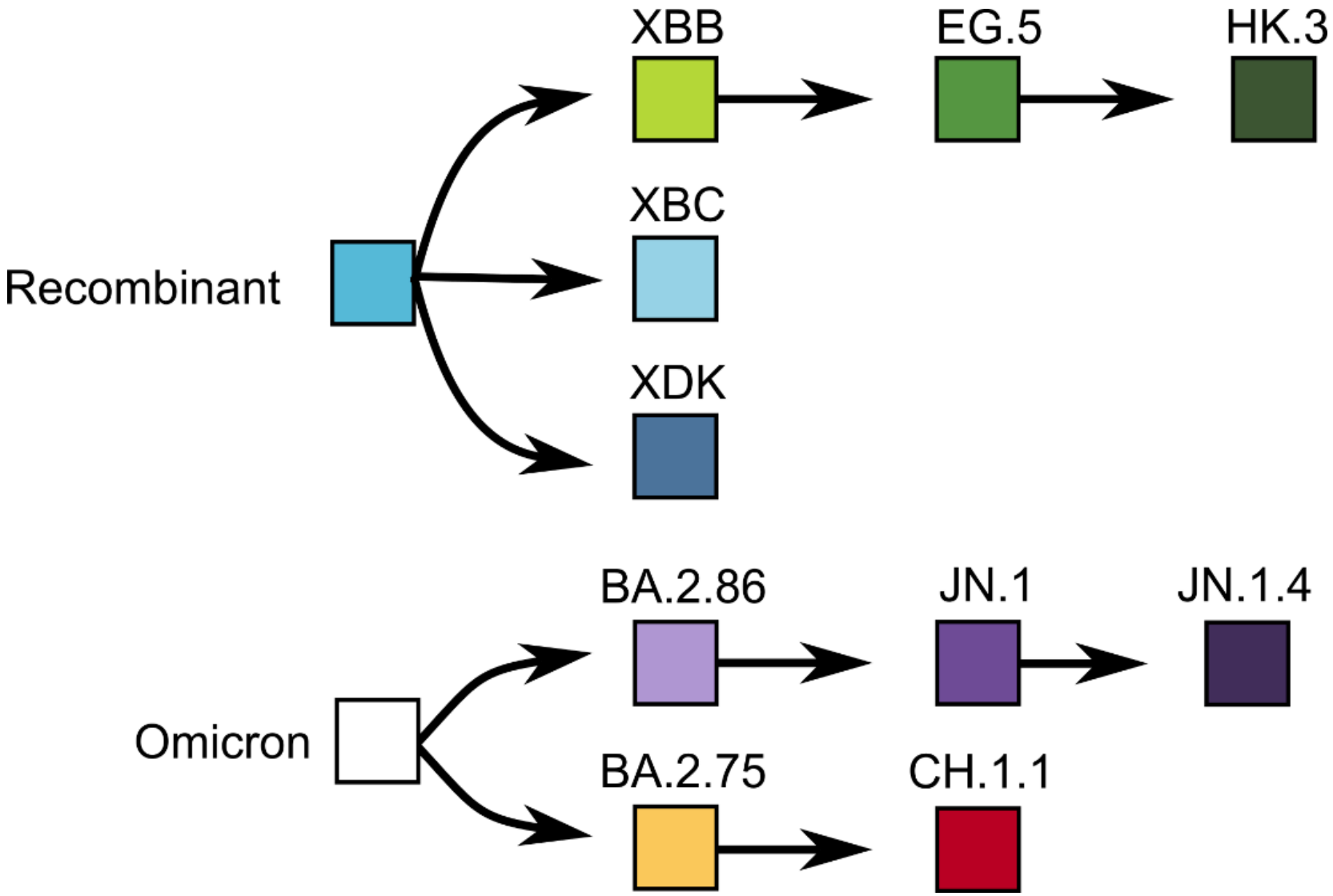


Figure 1: Relationships between the variants tracked in this report.

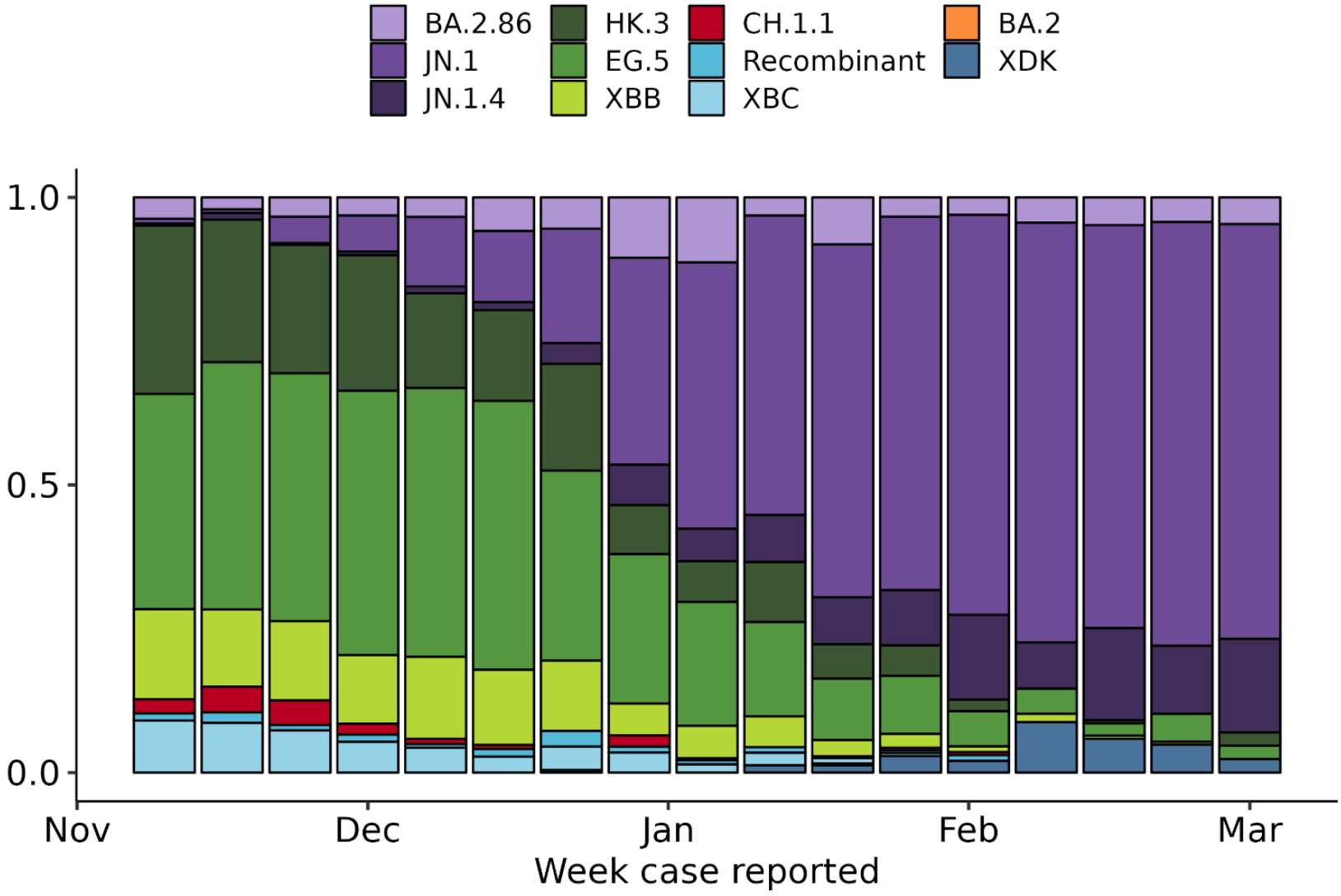


Figure 2: Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 17 weeks) as determined by whole-genome sequencing. *Only variants with a frequency above 1% are shown. Data is subject to change as samples will still be added to the most recent two-week period.* In this case d*ata from the last reporting week is based on a limited number of genomes (43) as data is still being generated for this week.*

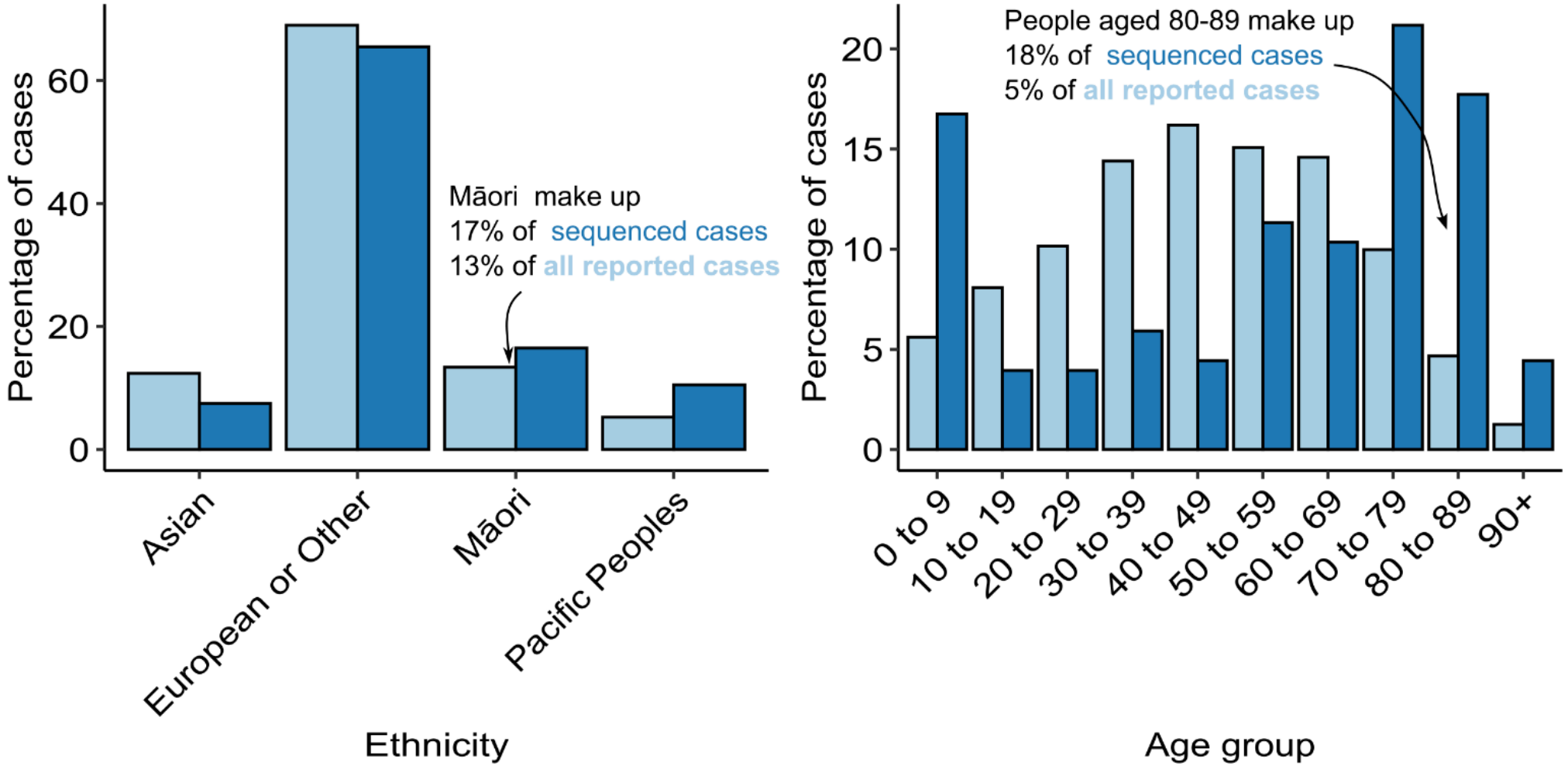


Figure 3: *(**Left**) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. (**Right**) Comparison of age distribution across all reported cases (light blue) and sequenced cases (dark blue).*

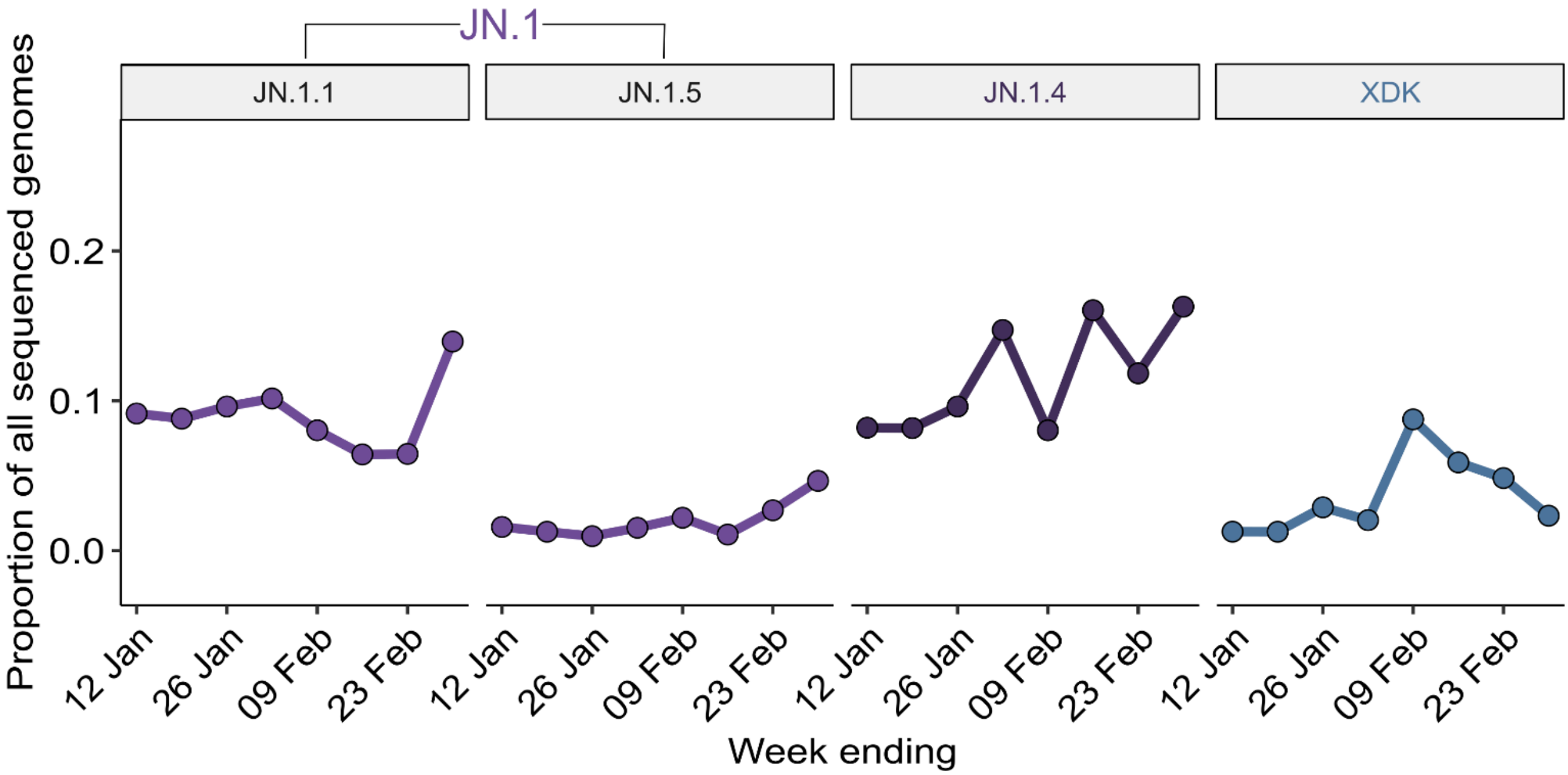


Figure 4: The trajectory of specific sub-lineages in recent weeks*. Each subplot represents a single-tracked lineage (and all of its descendants not covered by another category), with points representing the proportion of all sequenced cases falling to that lineage in a given reporting week.* The labels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