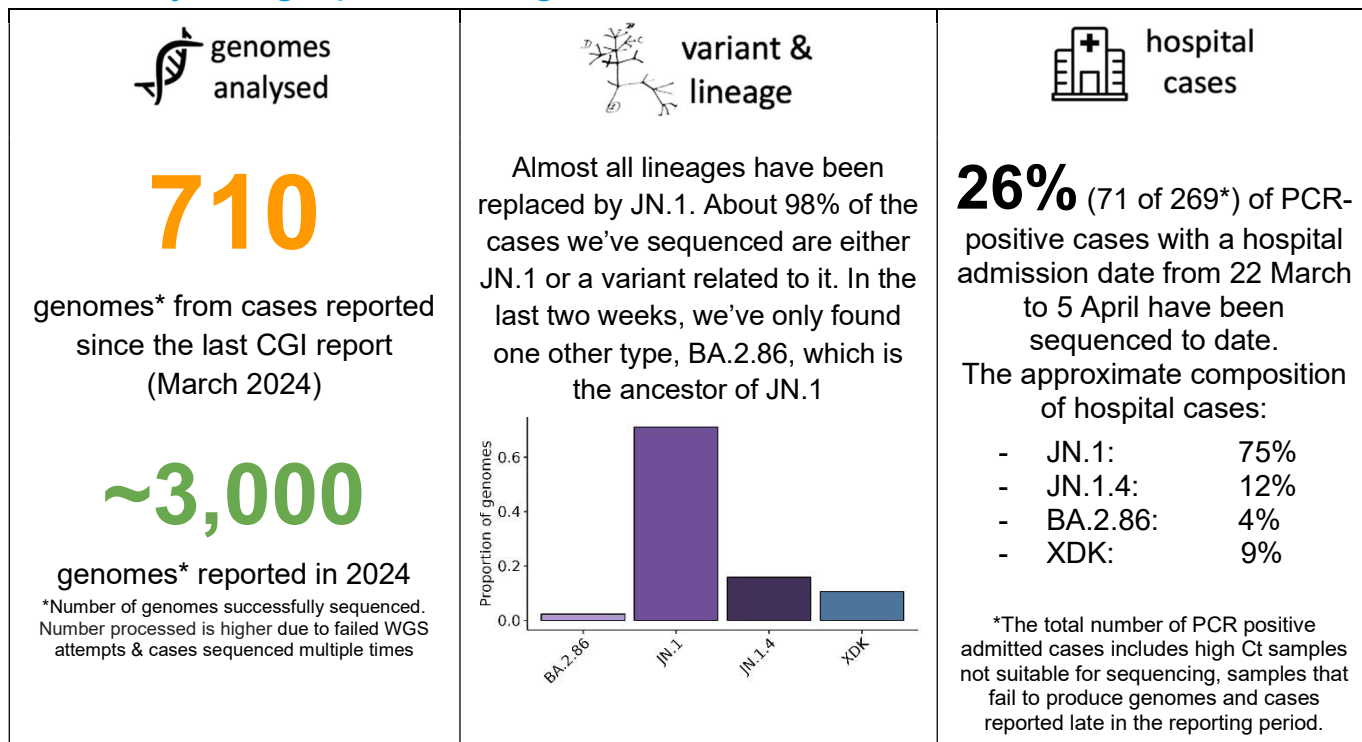


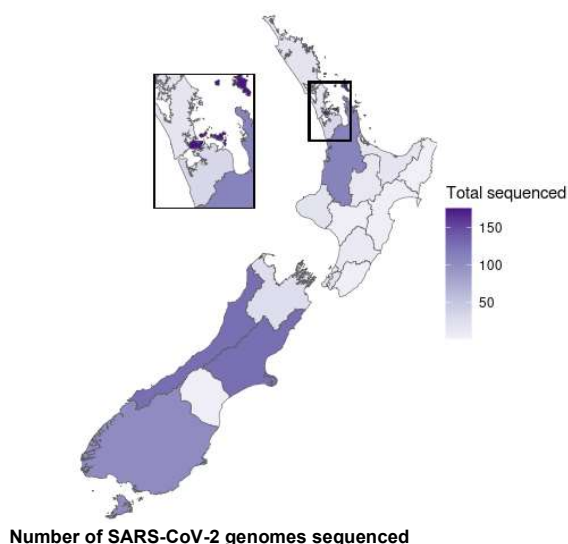
COVID-19 Genomics Insights Dashboard (CGID) Report #47

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 Infographic & Insights:



Origin of sequenced samples



Key trends and insights

- JN.1 and its descendant lineages account for 98% of sequenced cases.
- One JN.1 descendant, JN.1.11 has given rise to a constellation of new sub lineages, each with mutations known to aid in immune evasion. This includes JN.1.11.1, the fastest growing lineage in Aotearoa at present.
- Internationally, there has been a focus on three spike mutations that have arisen in different JN.1 lineages. Very few genomes from New Zealand have more than one of these mutations.
- The latest wastewater results mirror those from whole genome sequencing from clinicals, with almost 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

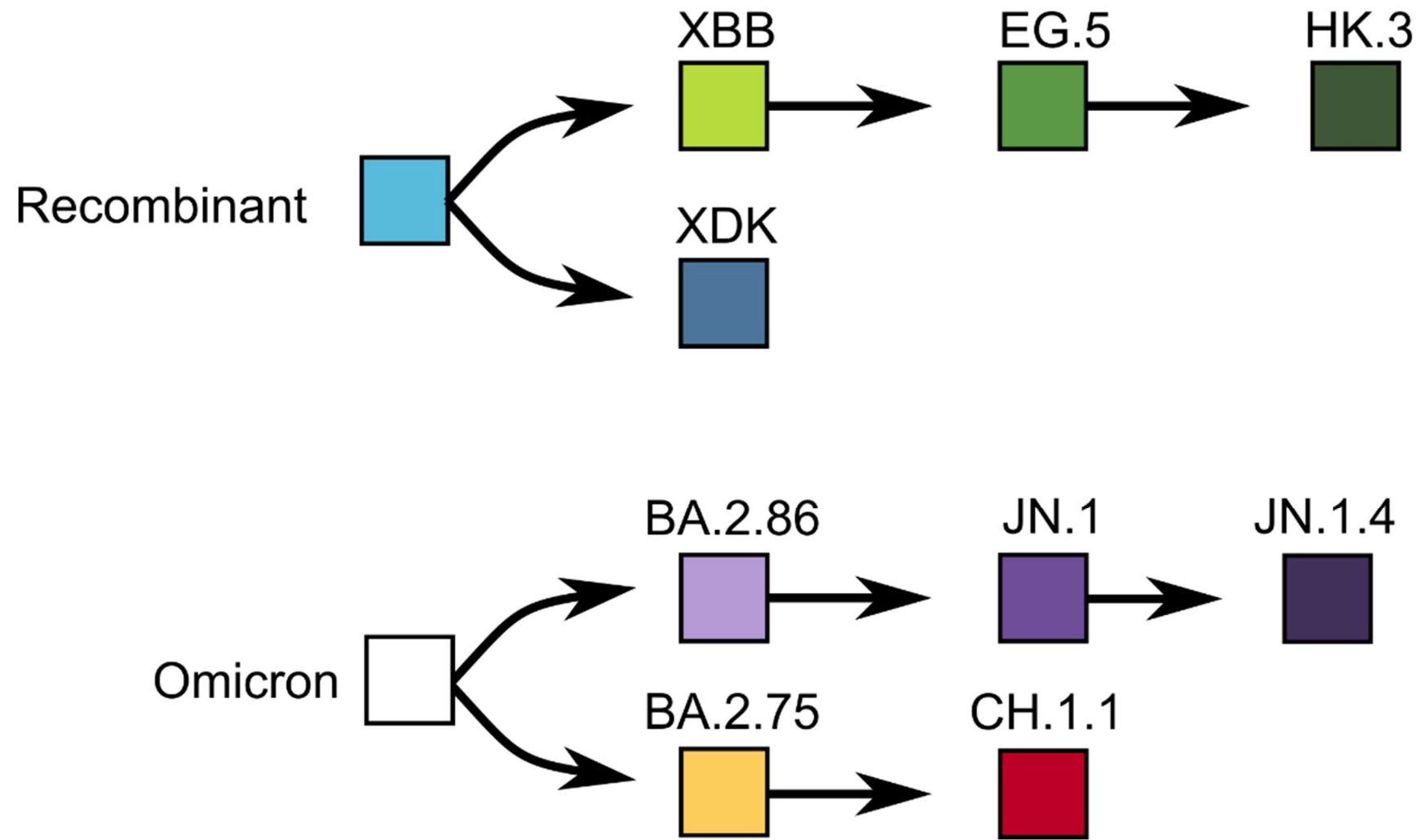


Figure 1. Relationships between the variants tracked in this report.

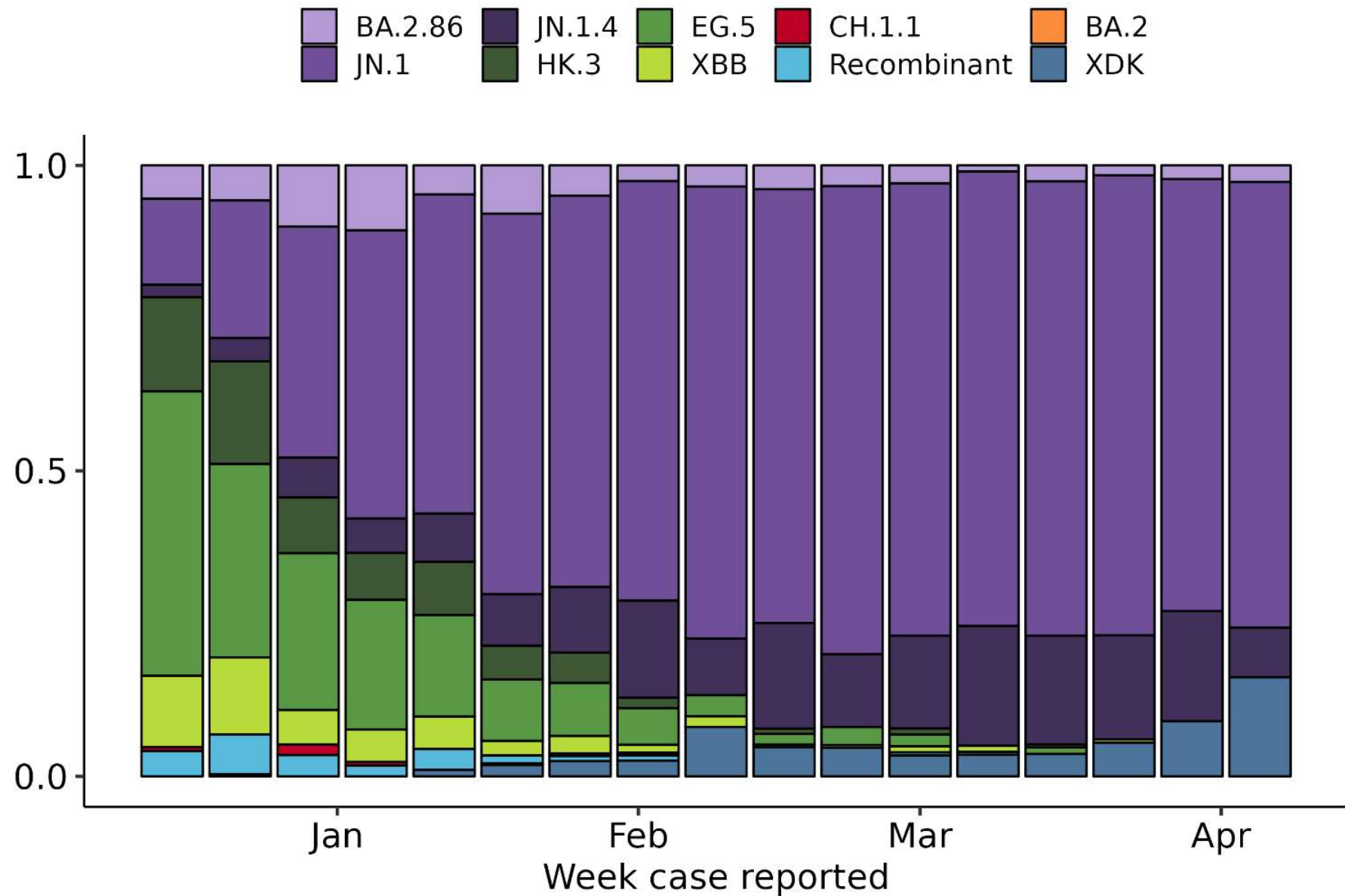


Figure 2. Frequency of SARS-CoV-2 variants in the New Zealand community each week (for the past 17 weeks) as determined by whole-genome sequencing. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to ESR and sequenced. Only variants with a frequency above 1% are shown. Data from the last reporting week is based on 37 genomes. Tracked lineages are defined in [Figure 1](#).

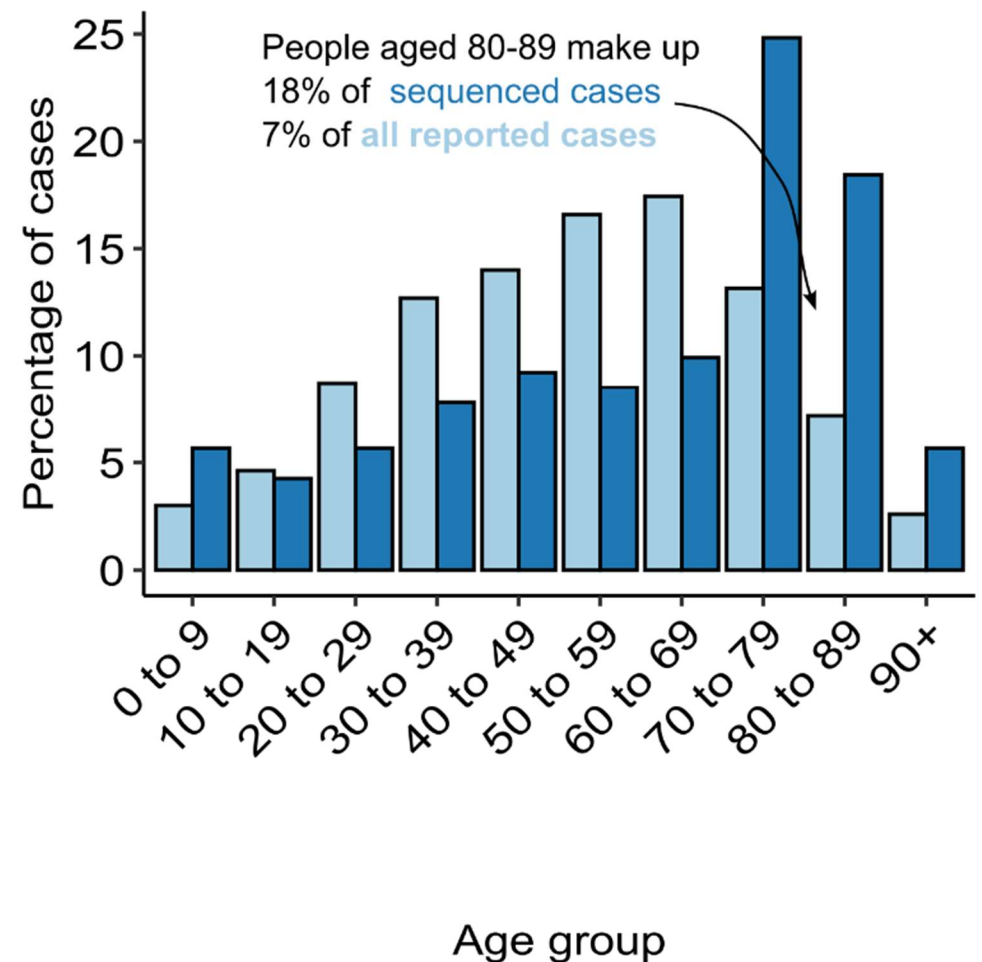
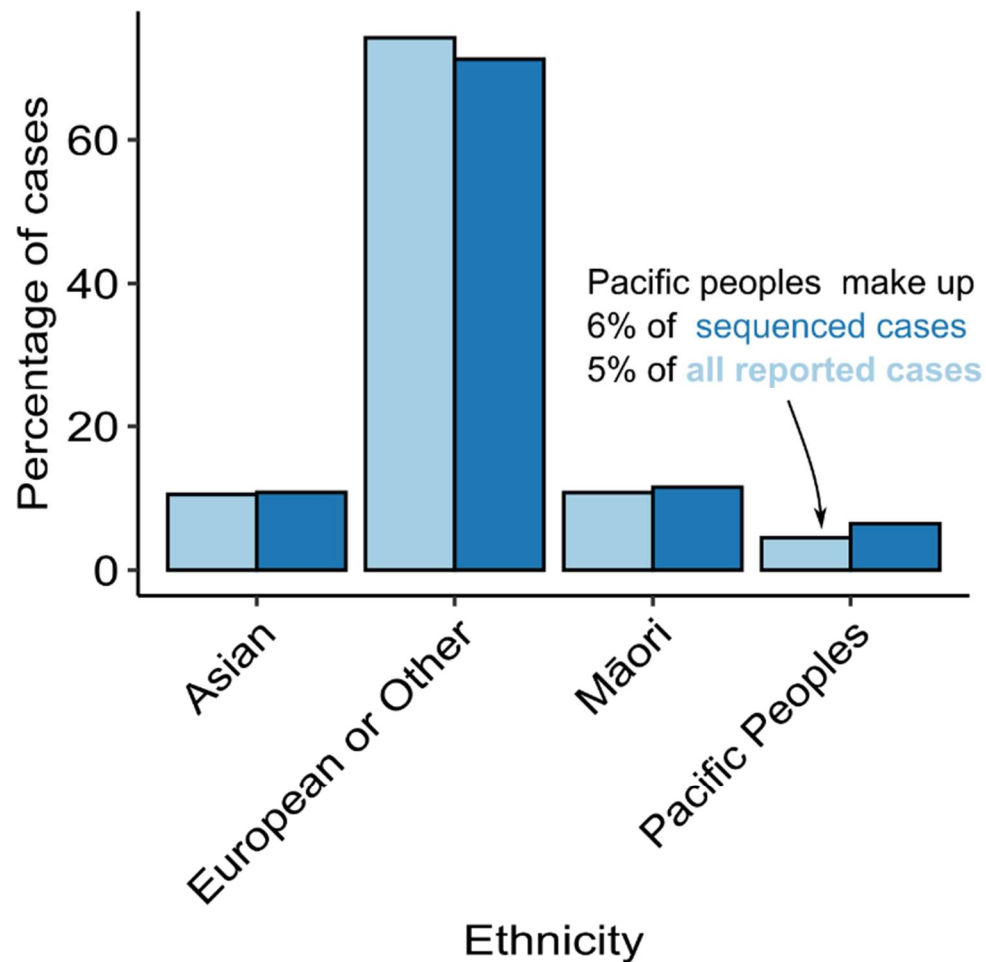


Figure 3. (Left) Composition of sequenced and reported cases by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. **(Right)** Comparison of age distribution across all reported cases (light blue) and sequenced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

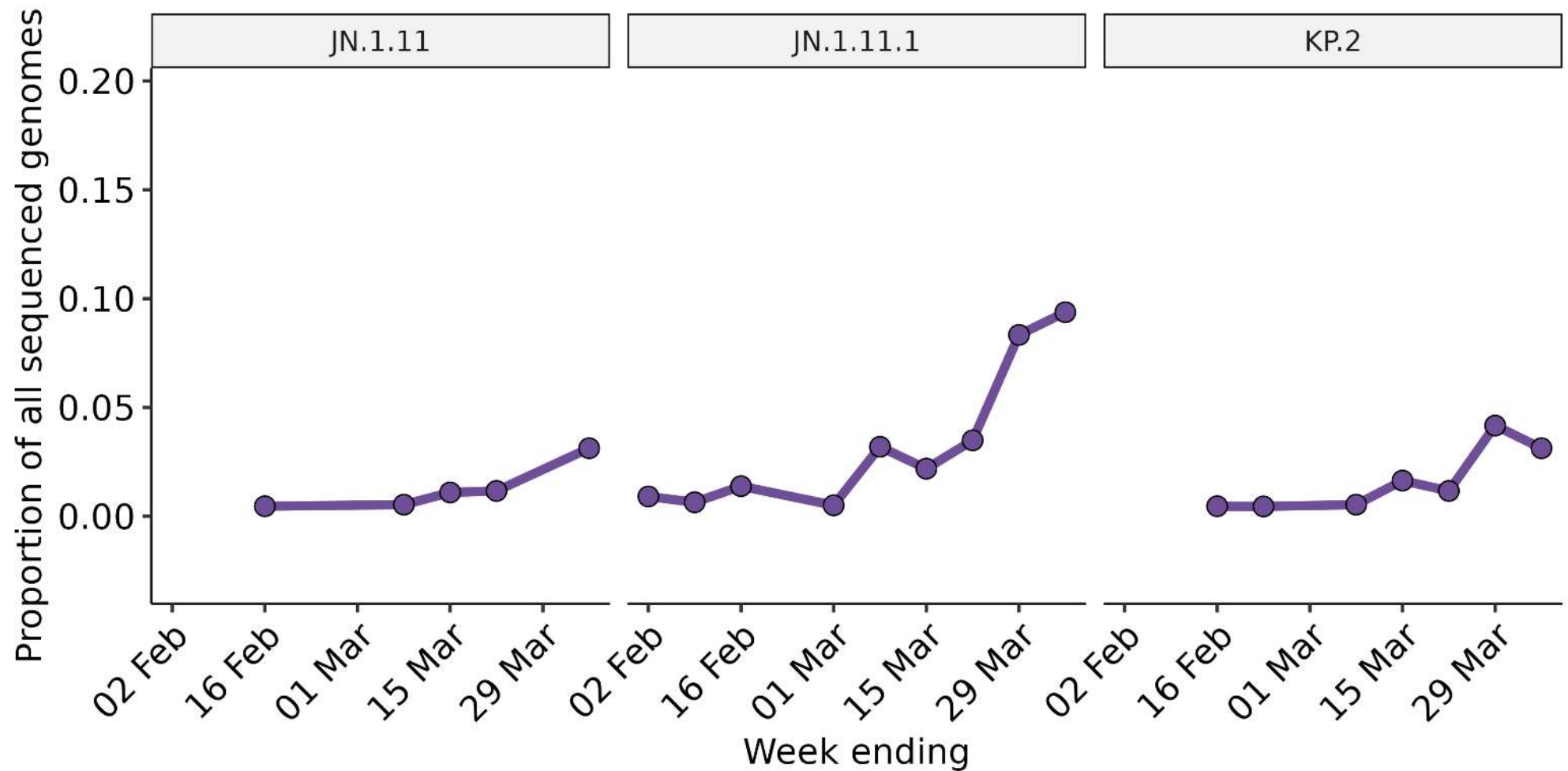


Figure 4. Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single-tracked lineage, and all of its descendant lineages not included elsewhere in this graph.