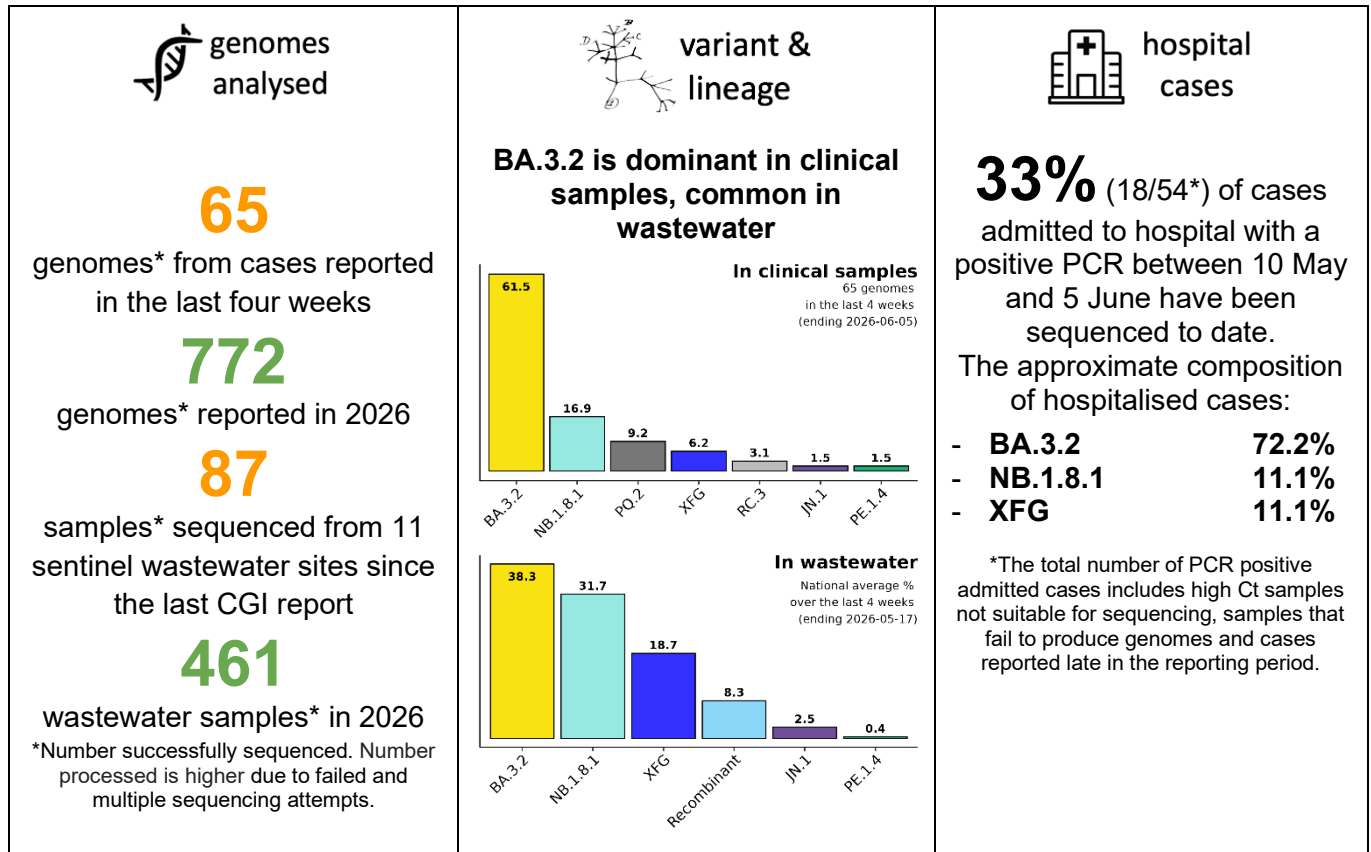


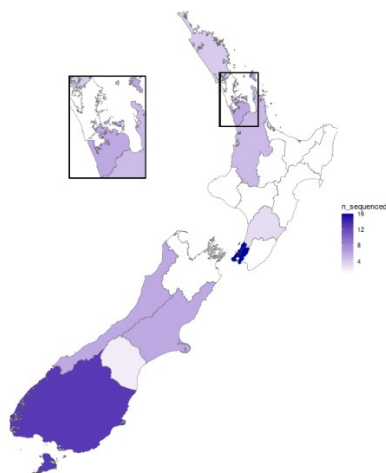
COVID-19 Genomics Insights Dashboard (CGID) Report #71

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 and Insights:



Origin of sequenced cases



Number of SARS-CoV-2 genomes sequenced for cases reported between 9 May to 5 June 2026

Key trends and insights

- BA.3.2 is the dominant variant among clinical cases and the most common in wastewater.
- Although BA.3.2 has been steadily growing as a lineage, no sublineage has a substantial growth advantage at present
- BA.3.2 remains over-represented in young people. We summarise recent research suggesting this may be a result of limited exposure to ancestral SARS-CoV-2 viruses

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

Data Summary and Reporting Period

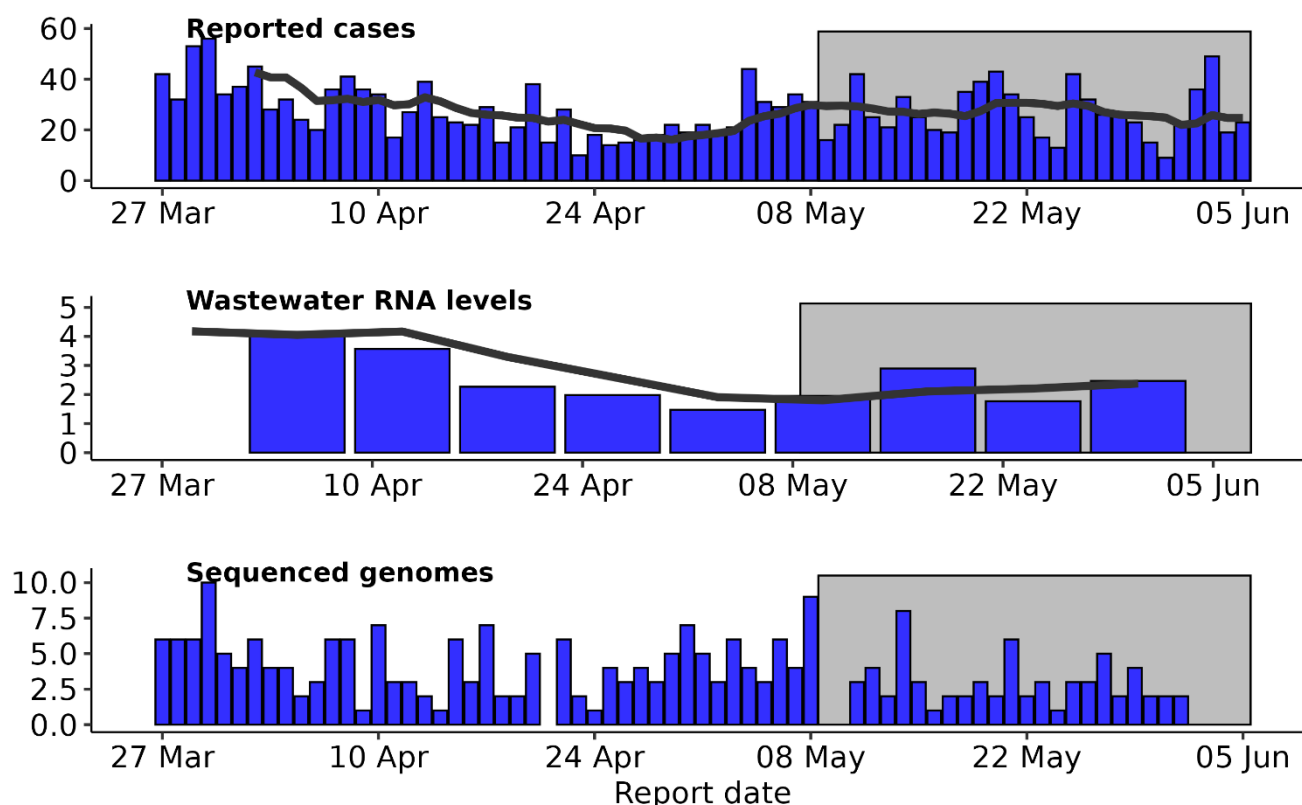


Figure 1. Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater. Bottom: The number of sequenced genomes from cases reported on a given day. In each subplot, the shaded rectangle is the current reporting window used for summary statistics in this report. Data as of 12pm 10 June.

Tracked Variants

Tracking the frequency and epidemiological properties of SARS-CoV-2 variants is a key goal of the CGI report. These reports follow the Pango nomenclature to classify sequences (<https://cov-lineages.org/>). The specific lineages of the sequenced genomes are then grouped into higher-level classifications representing the evolutionary relationships between lineages and potential increases in transmissibility or immune evasiveness. **Figure 2** describes the set of tracked variants used for this report and how they relate to each other.

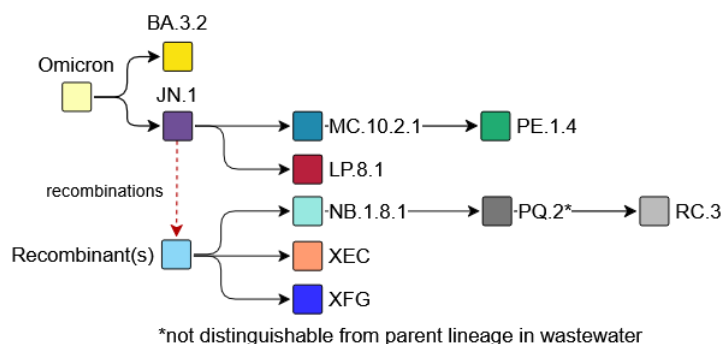


Figure 2. Relationships between the variants tracked in this report.

Changes made since last report

No changes have been made.

Overview of variants from clinical samples

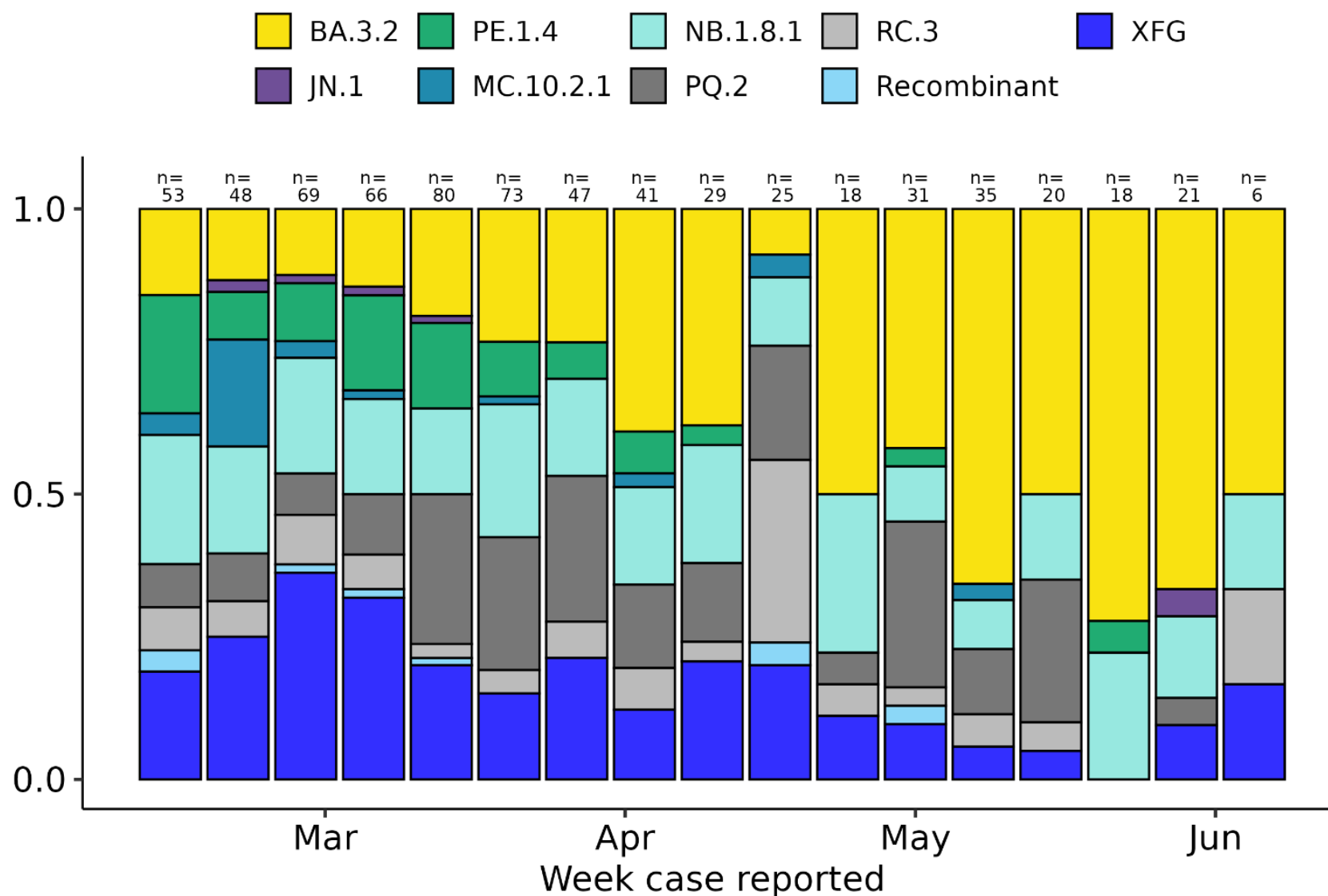
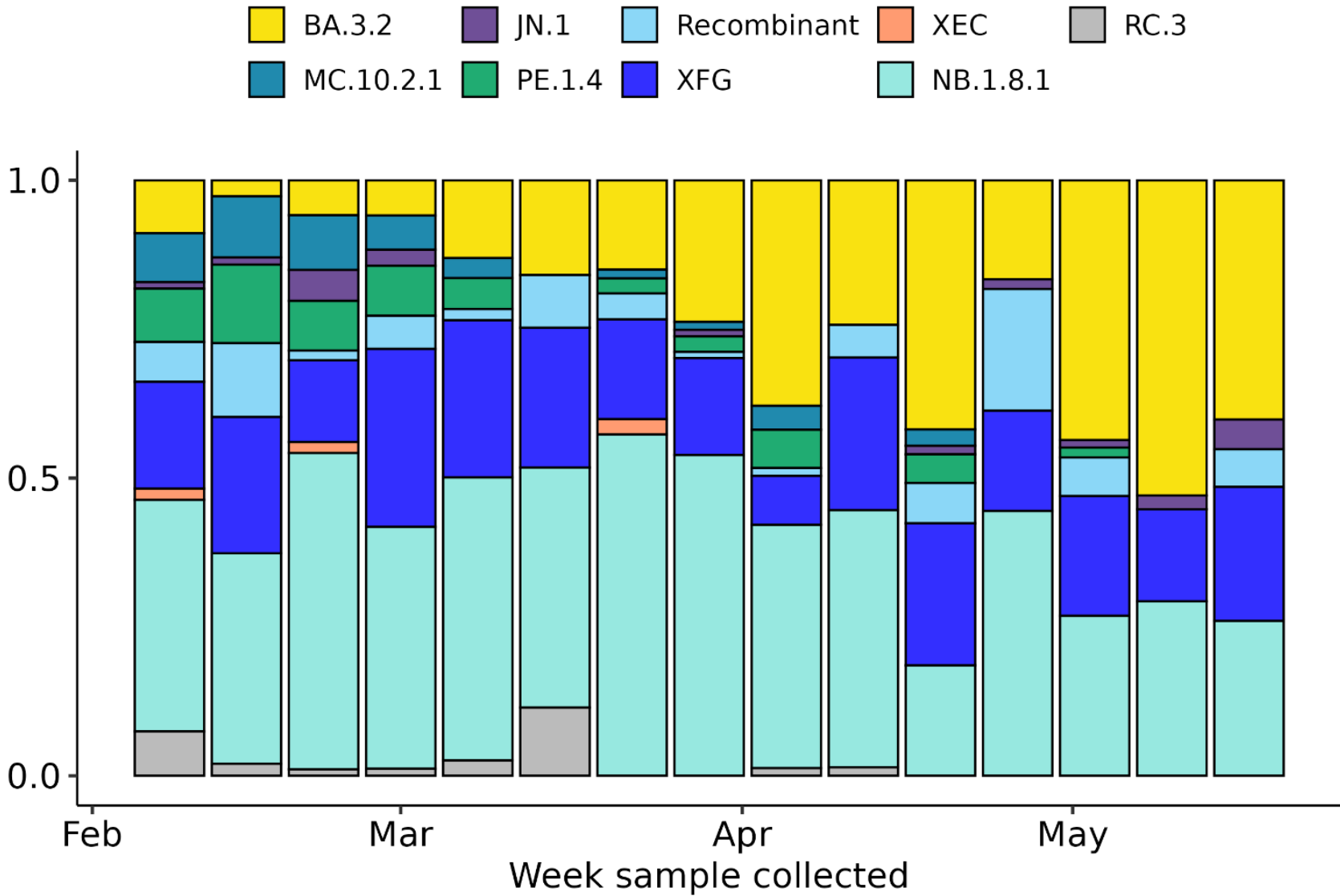


Figure 3. Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based on the number of genomes indicated above each bar. Tracked lineages are defined in [Figure 2](#).

Overview of variants from wastewater samples

Wastewater surveillance data from 11 sentinel sites across New Zealand for the week ending 11 January are available via PHF Science’s online dashboard esr-cri.shinyapps.io/wastewater/ and summarised in **Figure 4**. Due to assays limitations, **for the wastewater analysis, PQ.2 is included in the NB.1.8.1 lineage**. Note that the 4-week window reported in wastewater data is 3 weeks earlier than the reporting window for clinical cases.



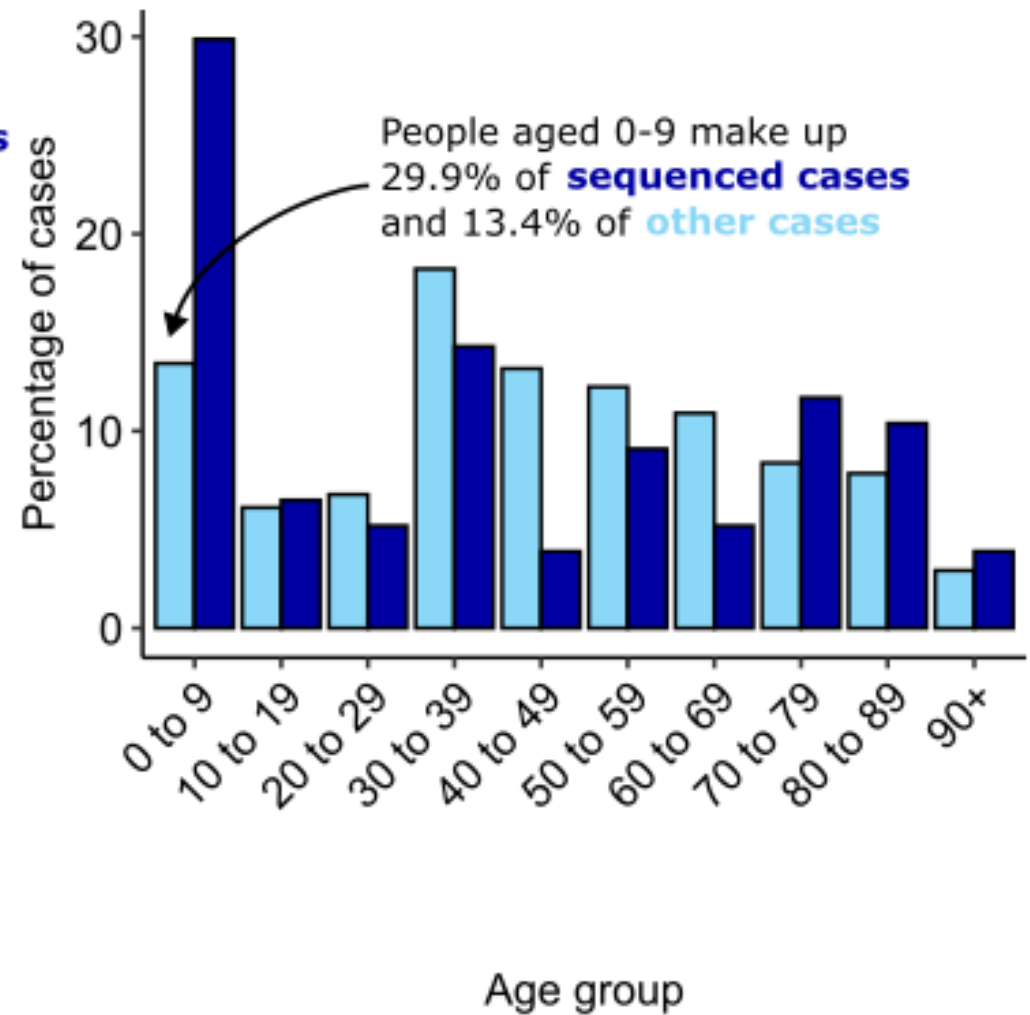
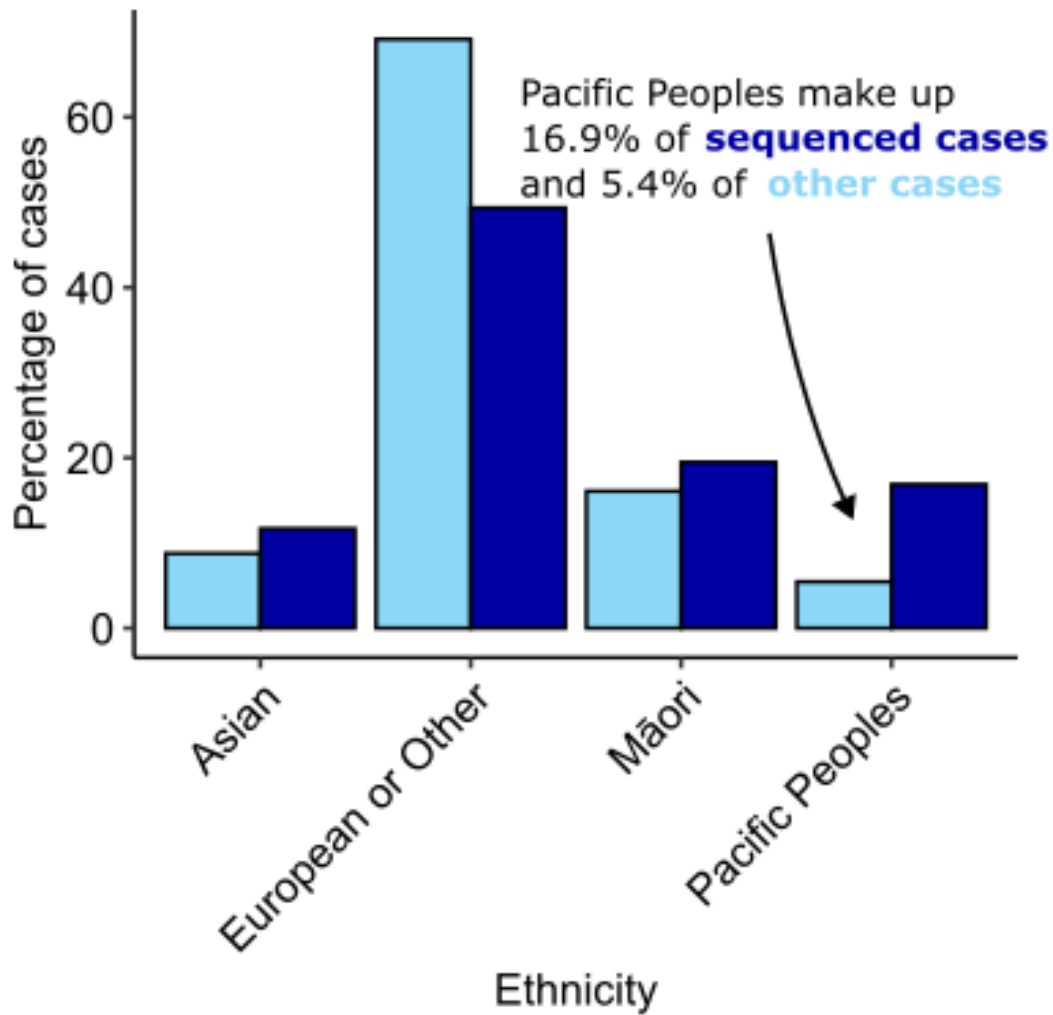


Figure 5. Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported between 9 May – 5 June 2026. **Left:** by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. **Right:** Distribution of reported and sequenced cases by age. Data as of 12 pm 10 June.

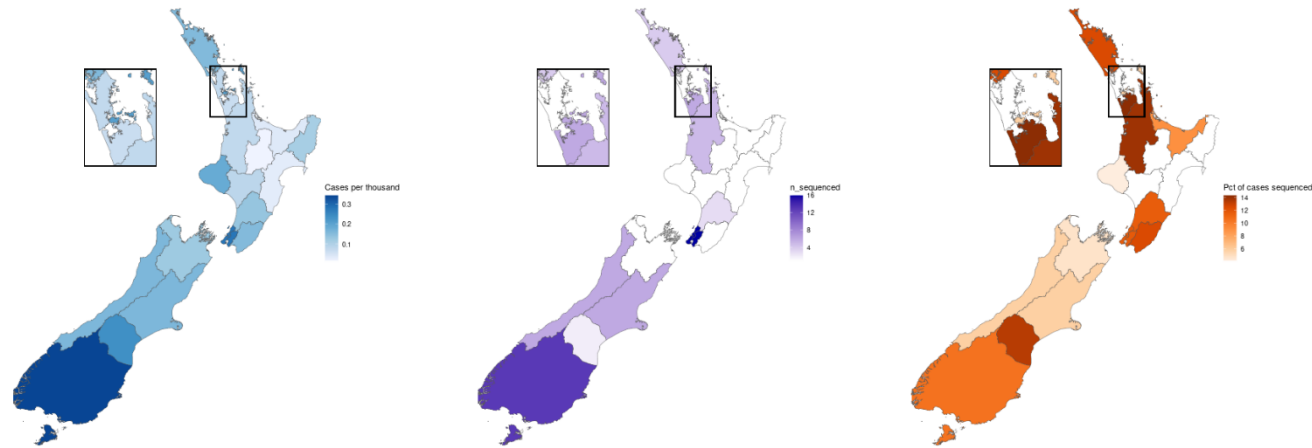


Figure 6. Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 12 pm 10 June 2026.

Emerging lineages

Most of the tracked variants defined in this report contain several distinct named sublineages, each of which descend from the named variant. PHF Science analyses SARS-CoV-2 genomic surveillance data closely to identify any sublineage that may display a growth advantage over the currently tracked lineages. These “emerging lineages” may give an early indication of the arrival or establishment of more transmissible variants in Aotearoa.

No variants show any significant growth advantage over the main circulating variants (Figure 7). No specific BA.3.2 lineage has been responsible for the steady growth of this variant in recent weeks. Among other variants only SF.1 (including its daughter lineage SF.1.1) has shown growth over this period. This lineage has circulated in New Zealand since late 2025 and has not shown a consistent pattern of growth over that period.

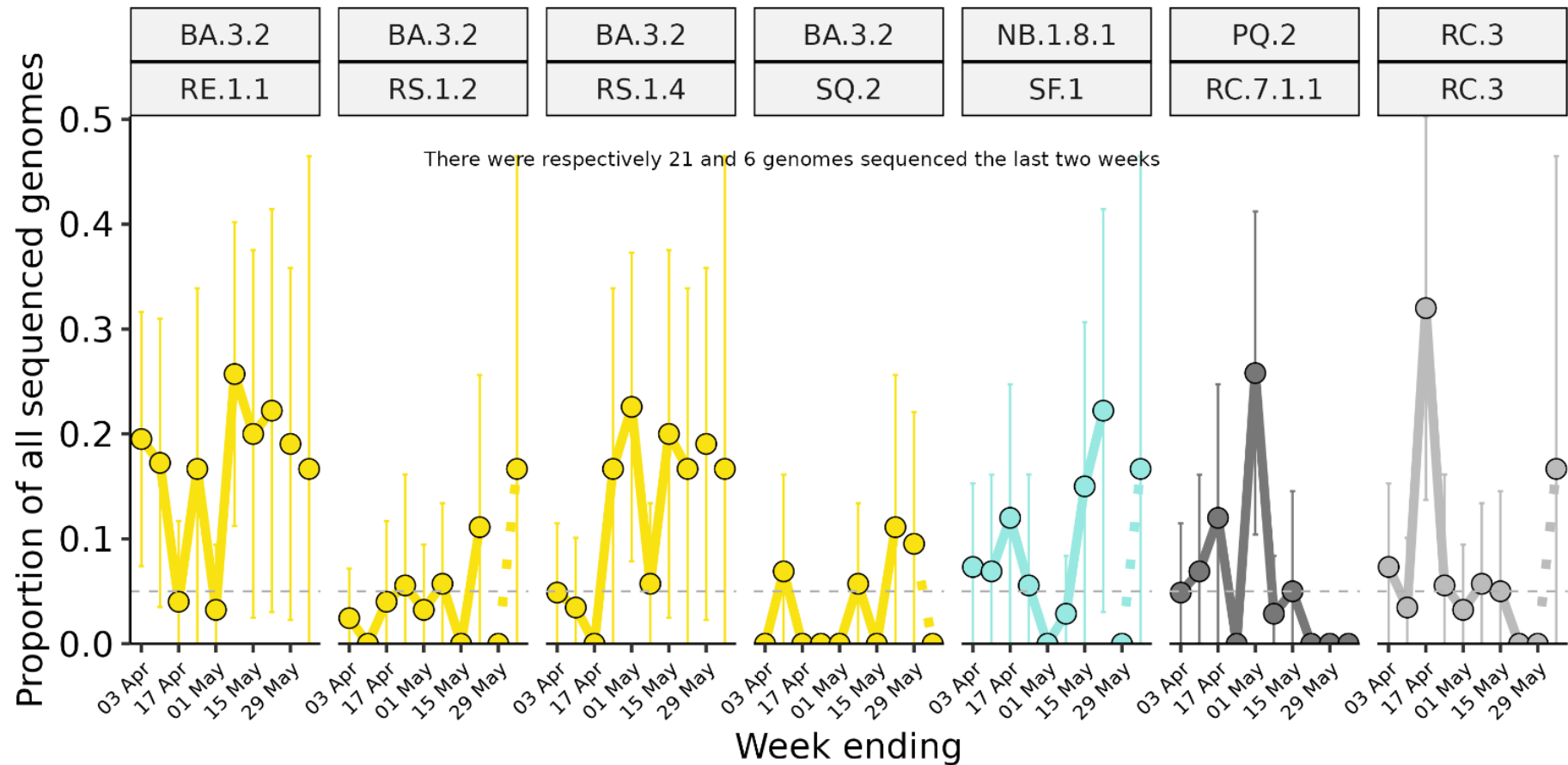


Figure 7. Frequency of specific lineages in clinical surveillance in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the rest of this report. The dashed grey line indicates a 5% proportion. Note, data for the most recent two weeks is preliminary.

Major trends in variants

Low COVID-19 activity levels in Aotearoa

This report covers a period of stable and low COVID-19 activity as measured by reported cases and wastewater concentrations (Figure 1). When considering clinical samples, this period has been associated with a steady growth in the BA.3.2 variant, which now represents 61.5% of clinical samples (Figure 3). This is considerably higher than the frequency of BA.3.2 in the most recent wastewater surveillance data (38.3%, Figure 4), though note the data covers four weeks ending 17 May so does not include the recent period of growth for BA.3.2. The possible reasons for this divergence in the frequency of BA.3.2 are discussed below.

Among other tracked variants, the NB.1.8.1 group remains the second most common with a frequency of 29.2% in clinical cases (including 9.2% in PQ.2 lineage and 3.1% in RC.3) and 31.7% in wastewater. XFG is the only other variant to still be circulating at appreciable frequency with 6% in clinical samples and 19% in wastewater. All samples reported under the generic “recombinant” category during this period are of the XGA.1 lineage.

Low SARS-CoV-2 levels, reduced reporting, and low testing volumes continue to limit PHF Science’s ability to estimate growth advantages precisely. Current data suggest that the BA.3.2 lineages have a moderate daily growth advantage over other tracked variants (Figure 7). This growth advantage comes with a broad confidence interval, underlining the uncertainty caused by a low sample size.

BA.3.2 over-representation in children may be due to lack of exposure to ancestral SARS-CoV-2 lineages

As reported previously, the BA.3.2 variant is seen at a higher frequency in younger people (Figure 8), with cases under 10 six times more likely to be due to BA.3.2 than any other variant (Odds Ratio 6.1 [2.7 – 14.5]).

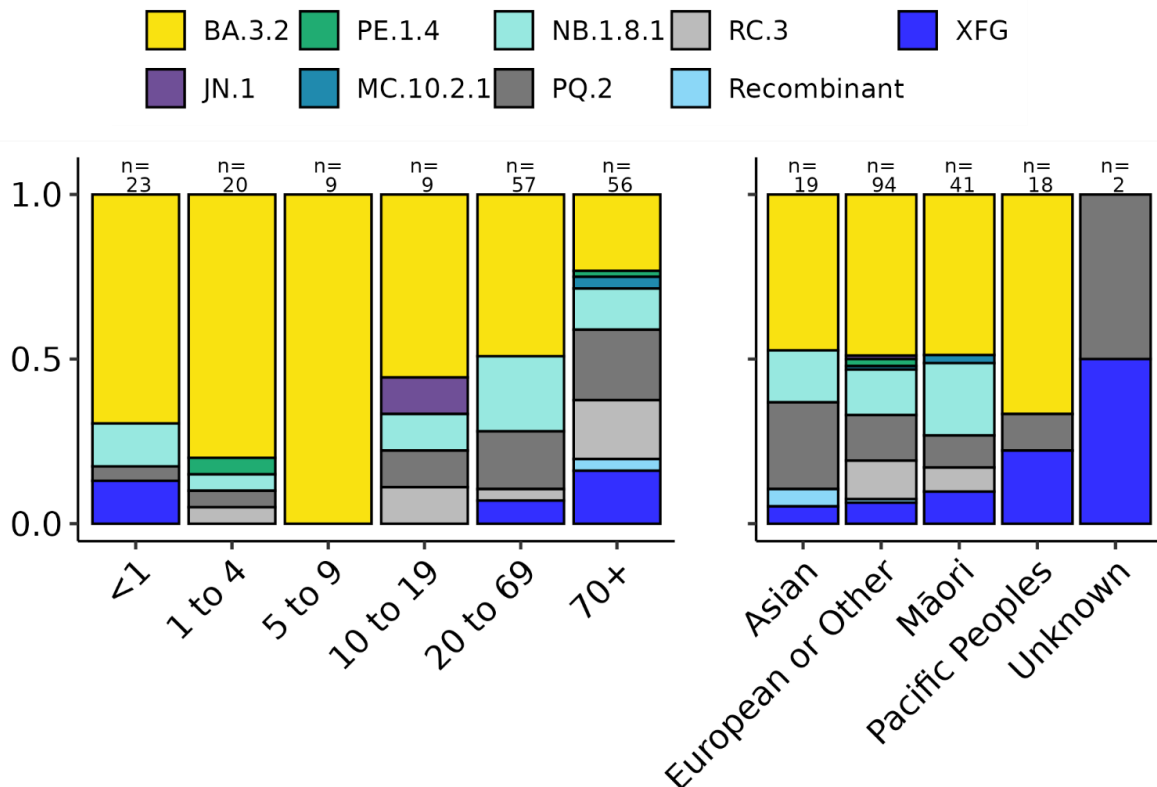


Figure 8. Proportion of tracked variants by age and ethnicity over the last 8 weeks.

A preprint published this week (Niu et al., 2026¹; not yet peer-reviewed) offers a possible explanation for the enrichment of BA.3.2 among children. Using global genomic surveillance data and laboratory neutralisation assays, the authors show that BA.3.2.2 (the parent lineage of most BA.3.2 viruses currently circulating in New Zealand) is over-represented among individuals under 17 years of age across multiple countries and continents. They then demonstrate that serum samples from children have lower neutralising activity against BA.3.2.2 than those from adults, despite producing a strong response to currently circulating SARS-CoV-2 variants. The authors propose that these differences are a result of age-specific exposure histories, with children more likely to have immunity derived exclusively from the Omicron variants that displaced earlier lineages in 2022.

Although relatively few New Zealanders were infected with pre-Omicron SARS-CoV-2 lineages, most adults were vaccinated with ancestral-strain mRNA vaccines during the initial vaccine rollout. In contrast, many children were either unvaccinated or vaccinated after New Zealand adopted monovalent Omicron-based vaccines in March 2024. As a result, a substantial proportion of children may have had no exposure to ancestral SARS-CoV-2 antigens.

The age distribution of BA.3.2 infections may also help explain the higher frequency of this lineage in clinical sequencing compared with wastewater surveillance. Children are both over-represented among sequenced clinical samples (Figure 5) and 6-fold more likely to be infected by BA.3.2 than any other variant. This combined over-representation will inflate the lineage's apparent frequency in clinical datasets relative to wastewater, which more closely reflects transmission across the wider population.

The concentration of BA.3.2 in children warrants ongoing surveillance. The large number of younger people infected by this lineage provides many opportunities for the virus to continue to evolve, and Niu et al. identify several spike mutations that could alter BA.3.2's ability to evade immune responses in those exposed to ancestral SARS-CoV-2 lineages.

Global overview

COVID-19 activity remains low across most comparator countries, with XFG and BA.3.2 lineages dominant in the Americas and Europe and NB.1.8.1 increasingly prominent across the Asia-Pacific region (Table 1). Australia is an exception, with a modest increase in test positive and NB.1.8.1 now accounting for 55% of sequences (Table 1)

Table 1. International trends

Country/Region	Activity	Test positivity	Main variants	Reporting period
Australia ²	Increasing	2.3% (increase)	NB.1.8.1 group (55%),	18 - 31 May
United States ³	Low	0.7% (decrease)	XFG sublineages	week-ending 9 May
Canada ⁴	Low	0.8% (stable)	XFG sublineages	week-ending 23 May
United Kingdom ⁵	Low	1% (stable)	BA.3.2 (50%), XFG (25%)	week-ending 31 May (27 April - 10 May for Variants)
Europe ⁶	Low	2*% (stable)	BA.3.2 and XFG	week-ending 23 May
Hong Kong ⁷	Low	0.99% (stable)	NB.1.8.1	week-ending 6 June
Singapore ⁸	Increased	11-14%** (stable)	Not updated	week-ending 30 May

**pooled over 17 countries; **test positivity rate among patients presenting with acute respiratory infection. Other figures reflect community testing or are not further specified.*

¹ Lack of ancestral SARS-CoV-2 imprinting promotes BA.3.2.2 infection in children (Niu et al). *bioRxiv* 2026.06.05.730251; doi: <https://doi.org/10.64898/2026.06.05.730251>

² [Australian Respiratory Surveillance Report – 18 May to 31 May 2026.](#)

³ [Surveillance and Data Analytics CDC](#) (accessed 10 June)

⁴ [Canadian respiratory virus surveillance report](#) (accessed 10 June)

⁵ [National flu and COVID-19 surveillance report: 4 June 2026 \(week 23\)](#)

⁶ [European Respiratory Virus Surveillance Summary](#) (accessed 10 June)

⁷ [COVID-19 & FLU EXPRESS](#) (accessed 10 June)

⁸ [Weekly Infectious disease bulletin](#)

Geographical differences in sampling and prevalence

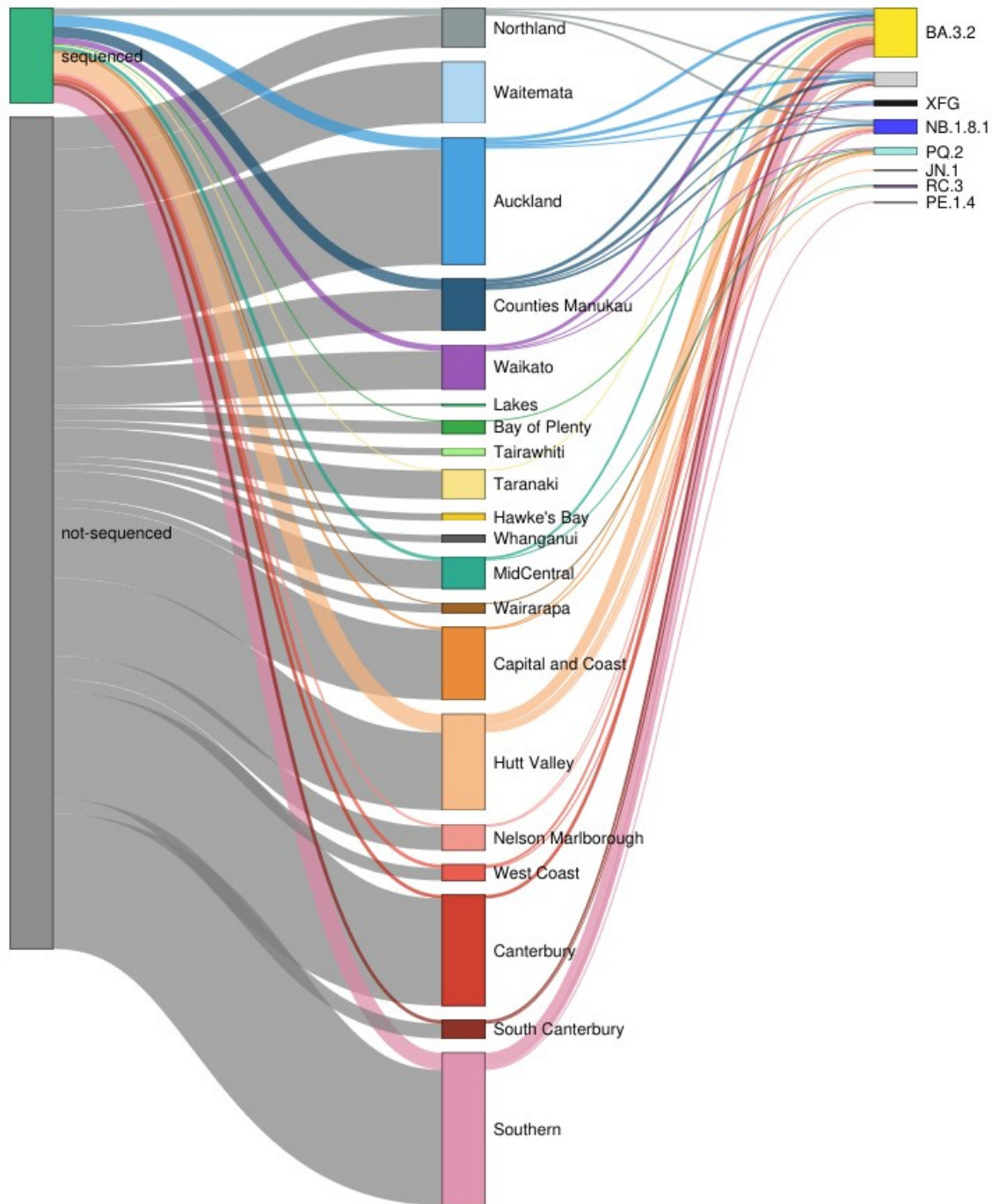


Figure 9. Origin and sequencing results of the 662 cases reported between 9 May to 5 June 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned). Data as of 12pm 10 June 2026.

WGS Hospital Reporting

A total of 18 genomes have been sequenced from patients admitted to hospital with COVID-19 infection since the last report and within the reporting period. While BA.3.2 appears over-represented in hospitalised cases (72% of hospitalised cases vs. 59 % of non-hospitalised cases), there is **no statistically significant difference in the frequency of tracked variants between hospitalised cases and other cases** reported in this window (Chi-squared = 1.9, df = 1, p-value = 0.58; **Figure 10**).

This analysis is based on hospitalisation data as supplied to PHF Science. This data does not include the reason for hospital admission, rather it reflects whether an individual tested positive for COVID-19 during the above-mentioned period.

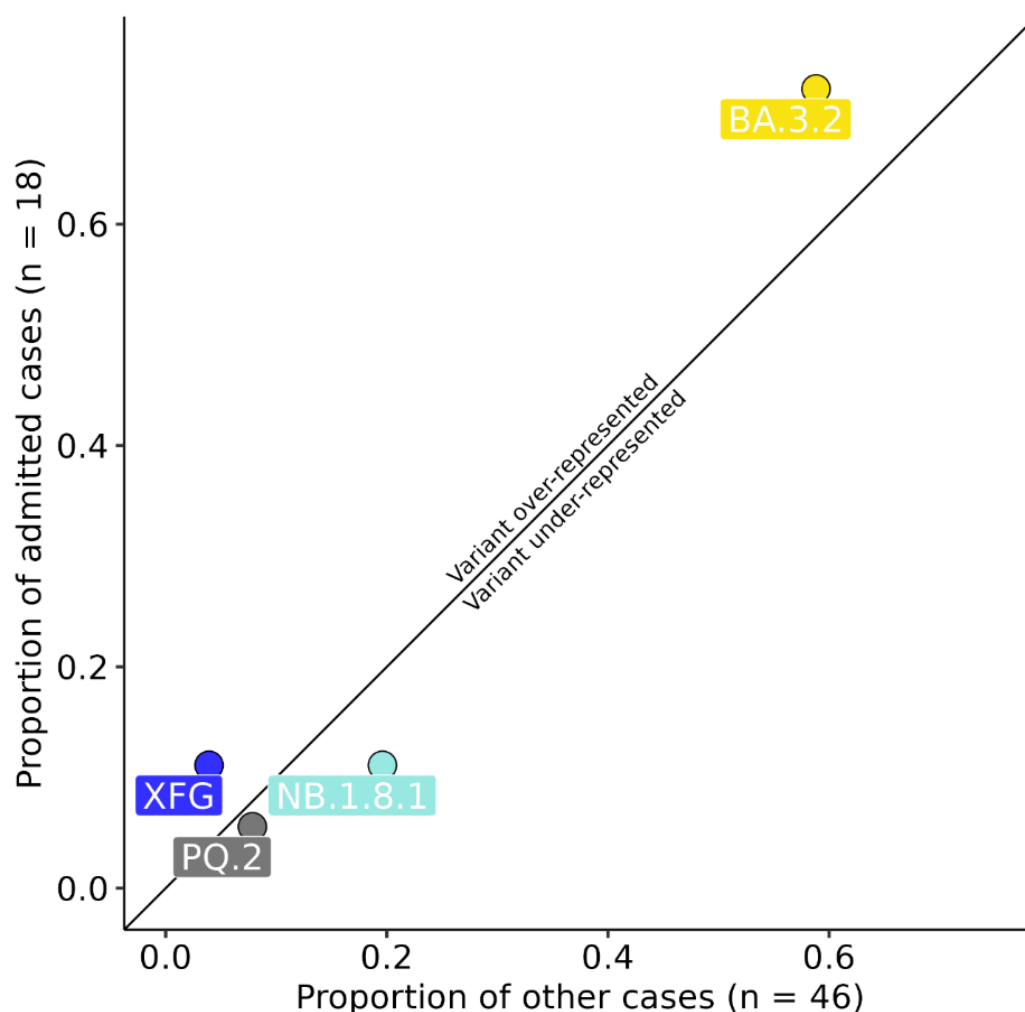


Figure 10. Frequency of variants among cases reported between 11 April – 8 May not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted from the graph and numbers on the margins.