7 August 2026

COVID-19 Genomics Insights Dashboard (CGID) Report #73

The COVID-19 genomics insights dashboard (CGID) provides a public and high-level overview of SARS-CoV-2 genomic surveillance across Aotearoa. It aims to explain how whole-genome sequencing (WGS) of clinical samples and wastewater surveillance 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 genomic surveillance programme in Aotearoa New Zealand and abroad.

Summary Infographic and Insights:

genomes analysed

54

genomes* from cases reported in the last four weeks

1036

genomes* reported in 2026

81

samples* sequenced from 11 sentinel wastewater sites since the last CGI report

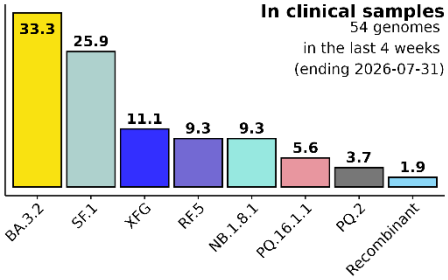
618

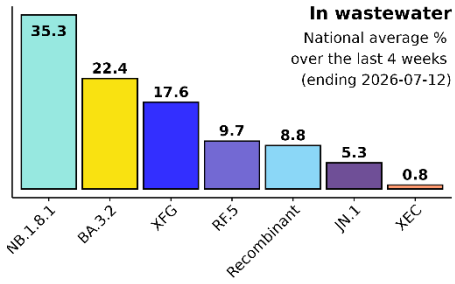
wastewater samples* in 2026

*Number successfully sequenced. Number processed is higher due to failed and multiple sequencing attempts.

variant & lineage

BA.3.2 is dominant in clinical samples, common in wastewater





hospital cases

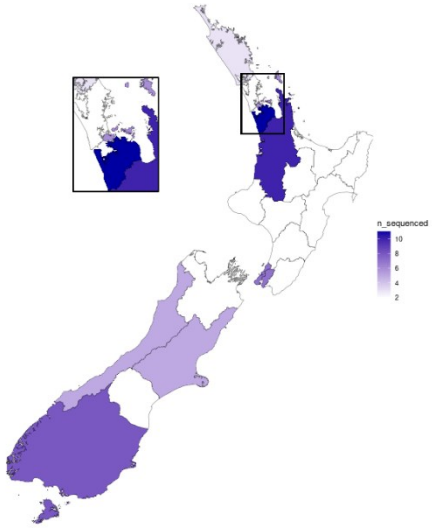
23.4% (11/47*) of cases admitted to hospital with a positive PCR between 4 and 31 July 2026 have been sequenced to date.

The approximate composition of hospitalised cases:

- **XFG** **36.4%**
- **RF.5** **27.3%**
- **SF.1** **18.2%**
- **BA.3.2** **9.1%**
- **PQ.2** **9.1%**

*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.

Origin of sequenced cases



Number of SARS-CoV-2 genomes sequenced for cases reported between 4 and 31 July 2026

Key trends and insights

- Several lineages are emerging while BA.3.2 is declining, representing 33.3% of sequences.
- We started tracking **SF.1, emerging local sublineage of NB.1.8.1**, representing 25.9% of sequences.
- We started tracking **RF.5**, JN.1 sublineage increasing in wastewater, representing 9.3% of clinical sequences.
- The WHO TAG-EV designated on 27 July a **new Variant under monitoring (VUM), PQ.16.1.1.** This NB.1.8.1 sublineage represents 5.6% of sequences in NZ with no growth advantage (note estimates based on a small sample size). It has been associated with an increased test positivity rate in Singapore and Hong Kong.

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

PHF Science

Data Summary and Reporting Period

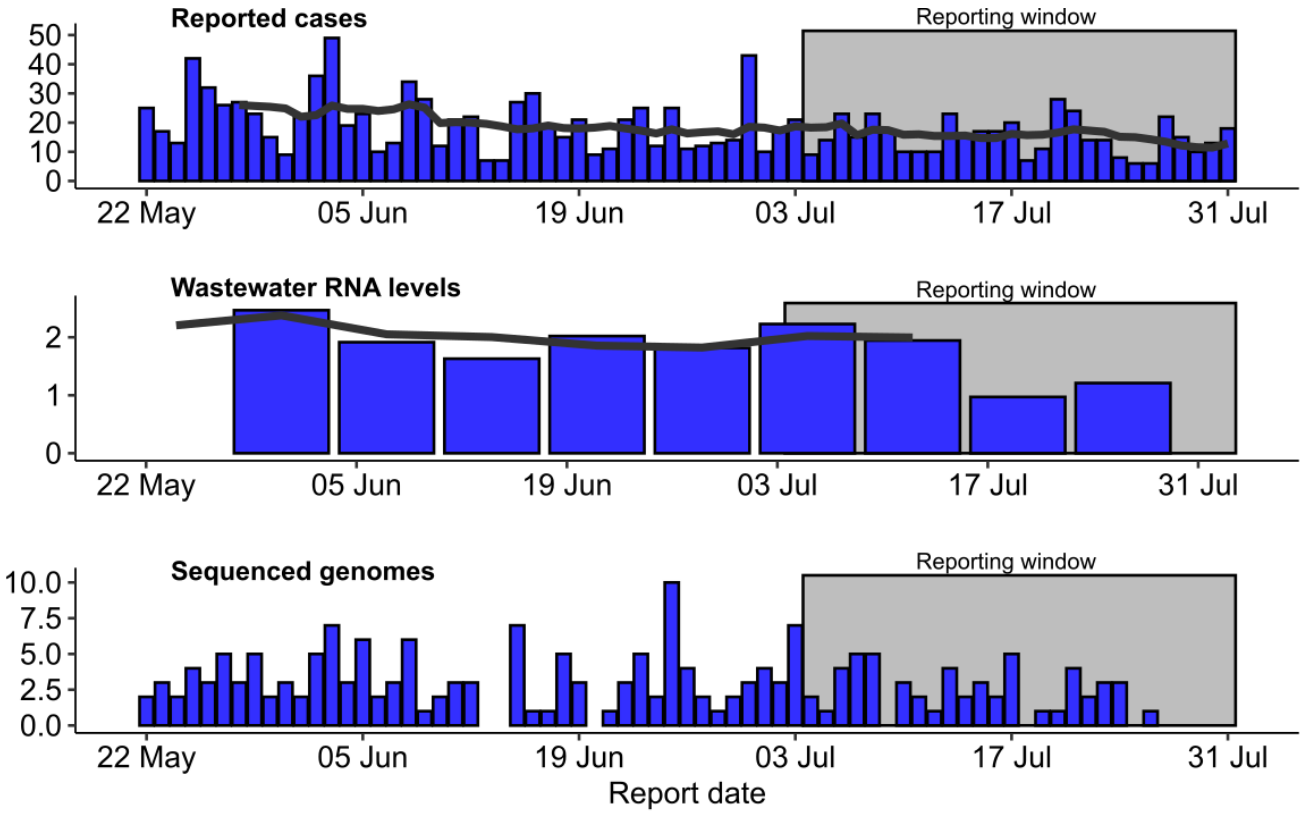


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater and 3-week rolling average (black line). 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 4 August 2026.*

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.

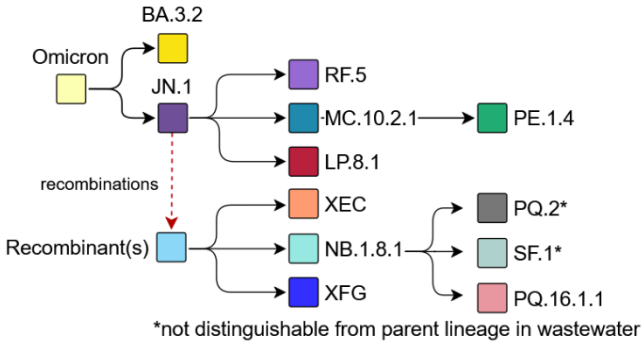


Figure 2. *Relationships between the variants tracked in this report.*

Changes made since last report

This month, we started tracking RF.5, SF.1 and PQ.16.1.1 individually. RC.3 that was circulating at low levels was removed from the list of tracked variants and re-integrated into its parent lineage PQ.2.

Overview of variants from clinical samples

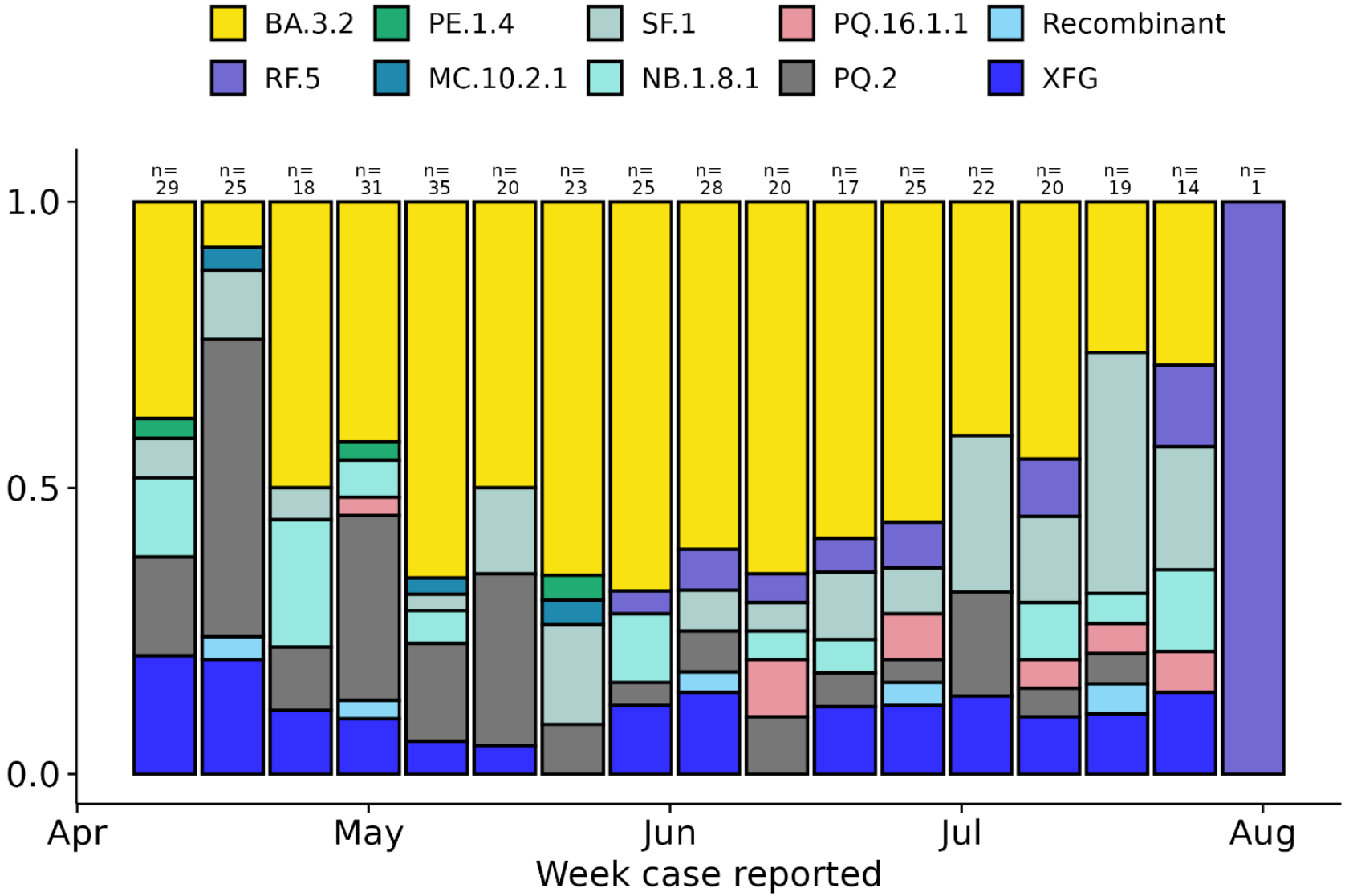


***Figure 3**. Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, **data for the most recent two weeks is preliminary**. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is 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 12 July are available via PHF Science's online dashboard esr-cri.shinyapps.io/wastewater/ and summarised in **Figure 4**. **For the wastewater analysis, PQ.16.1.1, PQ.2 and SF.1 are included in the NB.1.8.1 lineage.** PQ.16.1.1 can be distinguished from other NB.1.8.1 lineages and will be added to wastewater results in future reports. Note that the 4-week window reported in wastewater data is 3 weeks earlier than the reporting window for clinical cases.

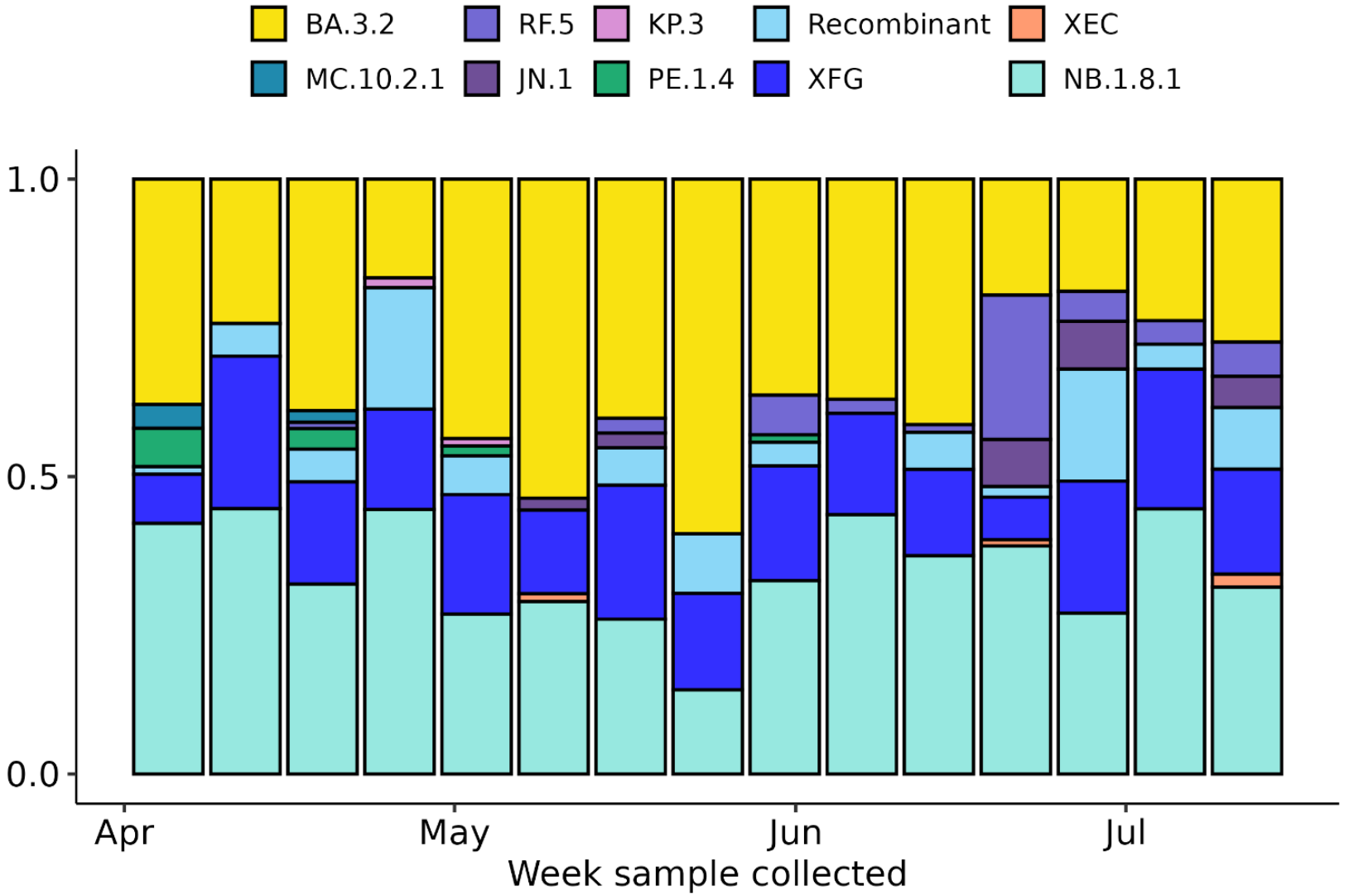


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

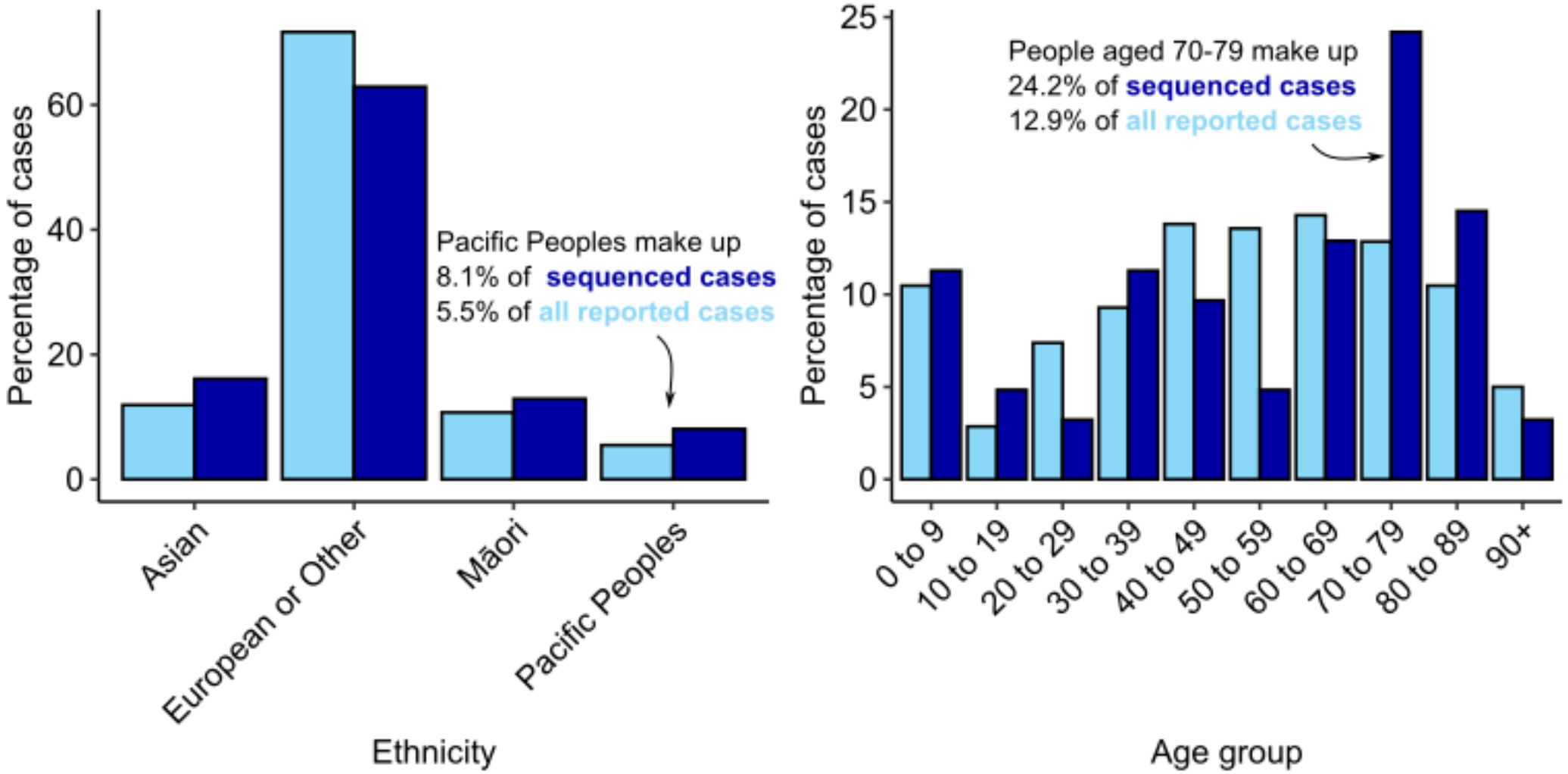


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported in this reporting window* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 12 pm 4 August 2026.*

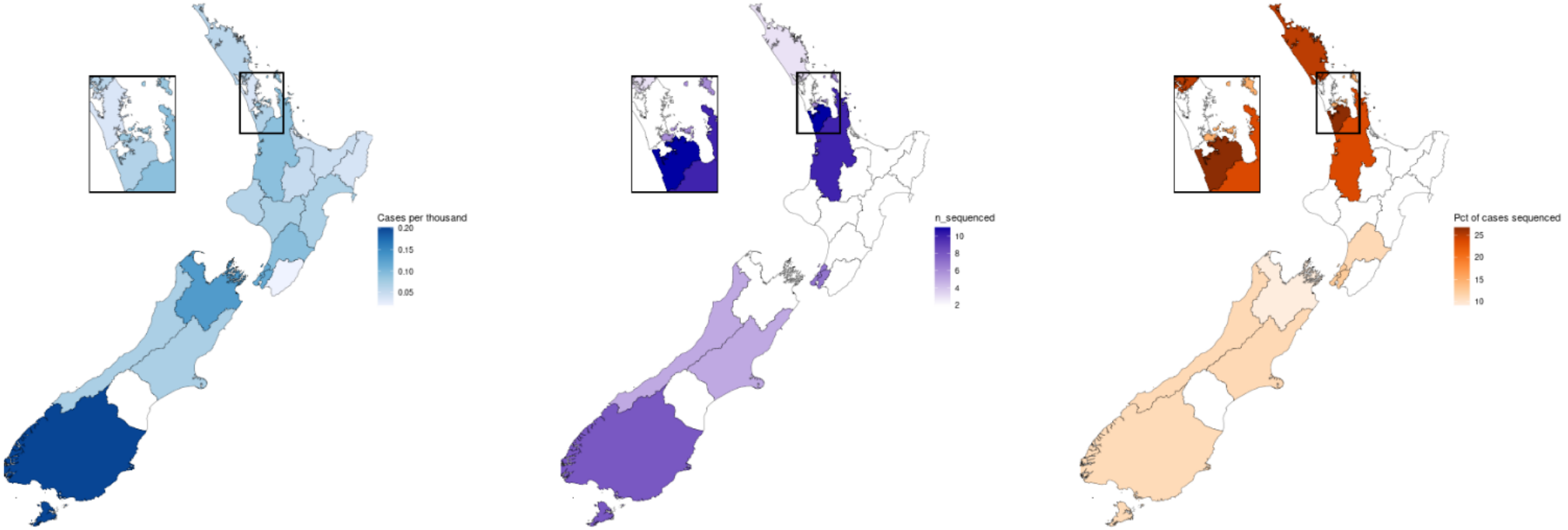


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 12 pm 4 August 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**).

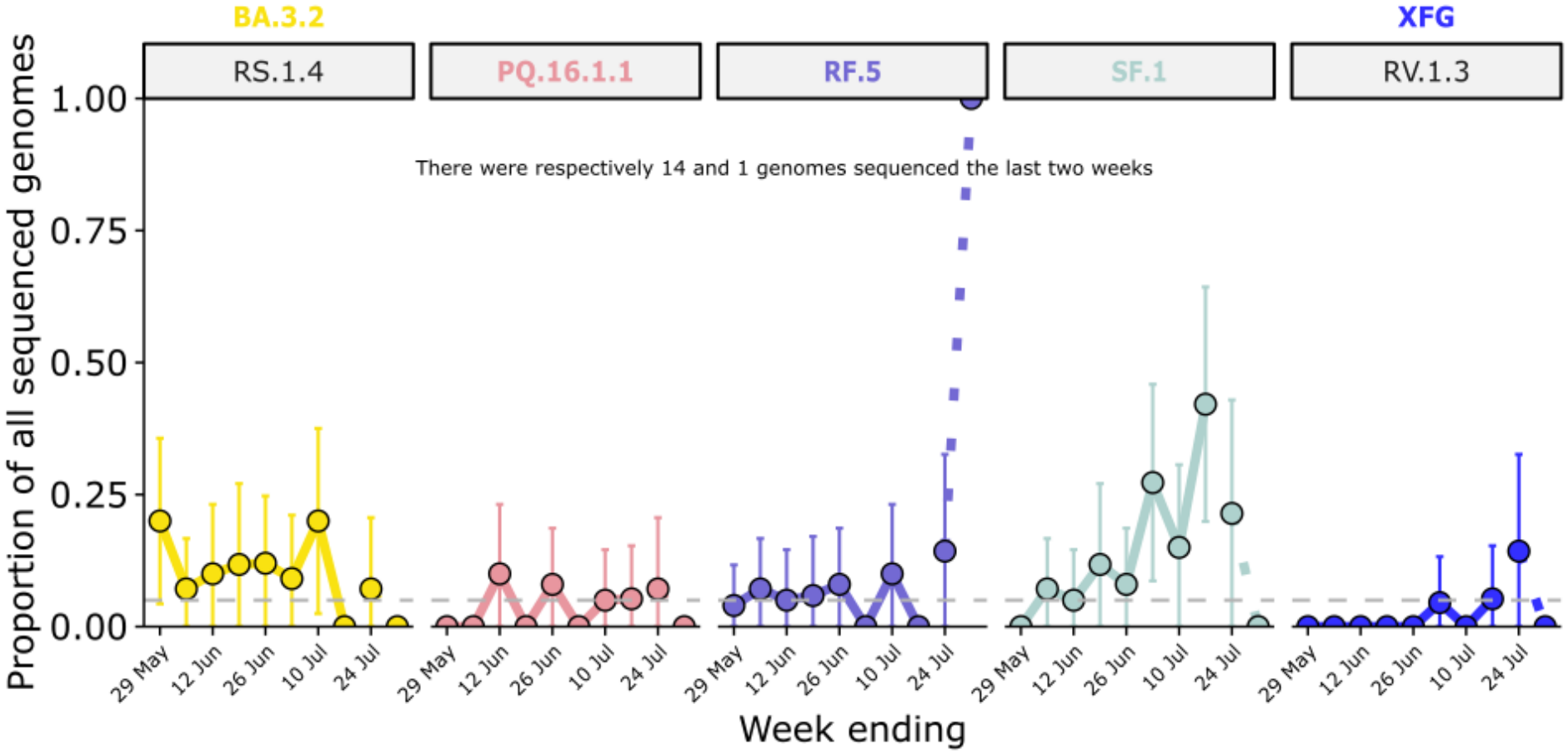


Figure 7. *Frequency of specific lineages in clinical surveillance in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the 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**). The variants landscape is however starting to change.

The BA.3.2 variant remains dominant in clinical samples but is declining (**Figure 3**; 33.3% in the last four weeks, compared to ~61% in the last two reports) and is not the most common variant in wastewater (**Figure 4**; 22,4% in the most recent wastewater data, a decrease from 43.5% in the previous report).

BA.3.2 has mostly declined in favour of SF.1, that represents 25.9% of sequences in clinical samples and presents a significant growth advantage over other variants (albeit in a context of small sample size). SF.1 is not distinguished from its parent lineage in wastewater data, likely explaining why NB.1.8.1 is the main circulating variant in wastewater, representing 35.3% of sequences.

As mentioned in the last CGID (#72), last month saw the emergence of RF.5, a JN.1 sublineage from the LF.7 branch, a branch that peaked last year overseas, especially North America, but that has not circulated widely in New Zealand. RF.5 has been increasing in prevalence overseas, it is the main variant in India.

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.

Emergence of a new local variant

SF.1 is a sublineage of NB.1.8.1 that has been present in Aotearoa since the end of 2025, in particular SF.1.1. The genomes reported as SF.1 since June 2026 form **a well-defined genetic cluster characterized by mutations T572I in Spike**, A65V in ORF8, T49I in the Nucleocapsid, and Q57H in ORF3a. Of these, Spike T572I is the most biologically interesting, being located just upstream of the S1/S2 cleavage region. This mutation was frequently seen alongside the recurrent 'FLiRT' mutations observed in the JN.1 lineage and considered advantageous[1]. This mutation may explain the growth seen in this yet-to-be-designated variant[2]. The majority of recent SF.1 genomes come from Waikato and Counties Manukau. While a few sequences from Australia dating back to November 2025 – February 2026 share half of the mutations listed above, this genetic cluster appears to be a local variant. It is not carrying any known high-impact fitness mutations but will be closely monitored by PHF Science.

A new Variant Under Monitoring designated but still rare in Aotearoa

On July 27, the WHO Technical advisory Group on SARS-CoV-2 Virus Evolution released a risk evaluation report for **PQ.16.1.1, a newly designated Variant Under Monitoring** (VUM)[3]. PQ.16.1.1 is a NB.1.8.1 subvariant that has acquired the D253G, N417T, D420N and I478T mutations in Spike, together with T135I in the Nucleocapsid and G8E on ORF8. This variant has rapidly become the dominant variant in Hong Kong and Singapore where its emergence has been associated with an increase in test positivity rates. It has also been detected in Australia, Canada, across the USA,

This variant or its subvariants (SV.1 and SV.2) have been detected seven times in seven different health districts across Aotearoa since April 2026. These detections appear to reflect cases imported from overseas rather than local transmission, with sequences closer to genomes from Singapore, Hong Kong and other Asian countries.

[1] https://doi.org/10.1080/22221751.2024.2402880
[2] https://github.com/sars-cov-2-variants/lineage-proposals/issues/3477
[3] https://www.who.int/activities/tracking-SARS-CoV-2-variants

The executive summary of the risk evaluation[3] is reproduced below:

> *"PQ.16.1.1, an NB.1.8.1-descendent SARS-CoV-2 lineage, has been designated a variant under monitoring (VUM) with increasing proportions globally, driven largely by detections in the Western Pacific Region, particularly Singapore. Considering the available evidence, the additional public health risk posed by PQ.16.1.1 is evaluated as low at the global level. Its mutation profile may confer additional immune escape, although direct phenotypic evidence is currently limited. Available surveillance does not indicate increased clinical severity compared with other circulating variants, and existing vaccines are expected to continue providing protection against severe disease."*

WGS Hospital Reporting

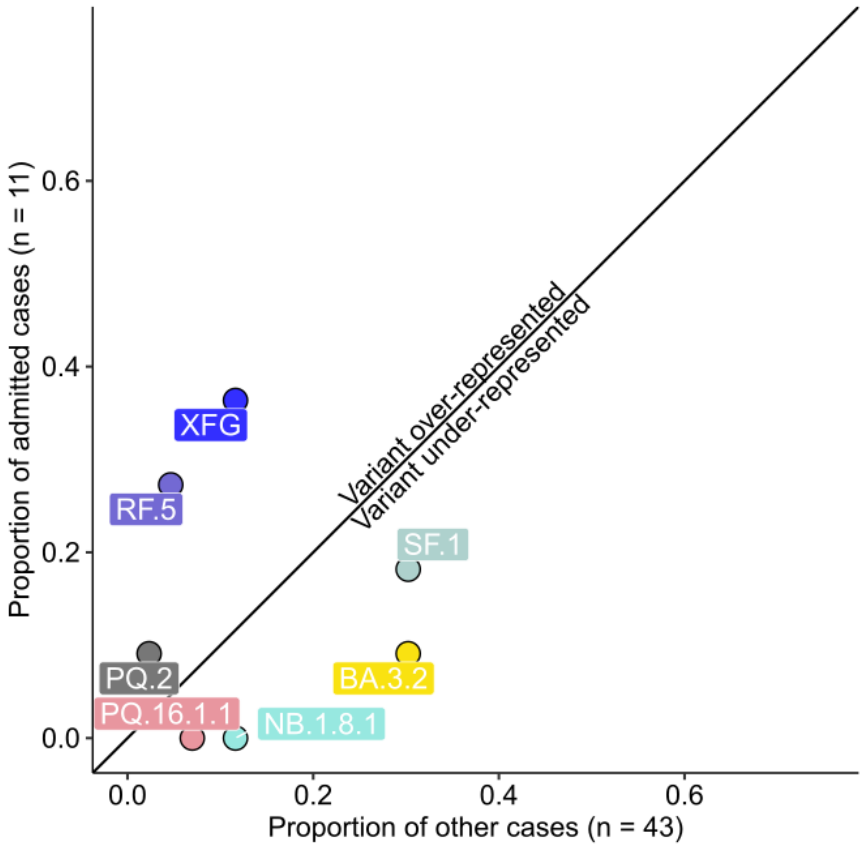


Figure 8 *Frequency of variants among cases not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted*

A total of 11 genomes have been sequenced since the last report and within the reporting period from patients admitted to hospital with a positive COVID-19 PCR result. For this period the **RF.5 and XFG variants were observed more frequently among admitted cases, whereas BA.3.2 was observed more frequently among cases without an admission**. The distribution of tracked variants appeared to differ between hospitalised cases and other cases reported in this window (Fisher's exact test, p-value = 0.060;**Figure 8**). However, the small sample size limits the precision of these estimates, and the current data are insufficient to draw firm conclusions about differences in variant frequencies between the two groups. These patterns will continue to be monitored closely as further data accrue.

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.

Geographical differences in sampling and prevalence

Differences in testing strategies across regions are reflected in the number of clinical samples available and suitable for sequencing, and we can observe geographical disparities in both surveillance and prevalence of variants (**Figure 9**).

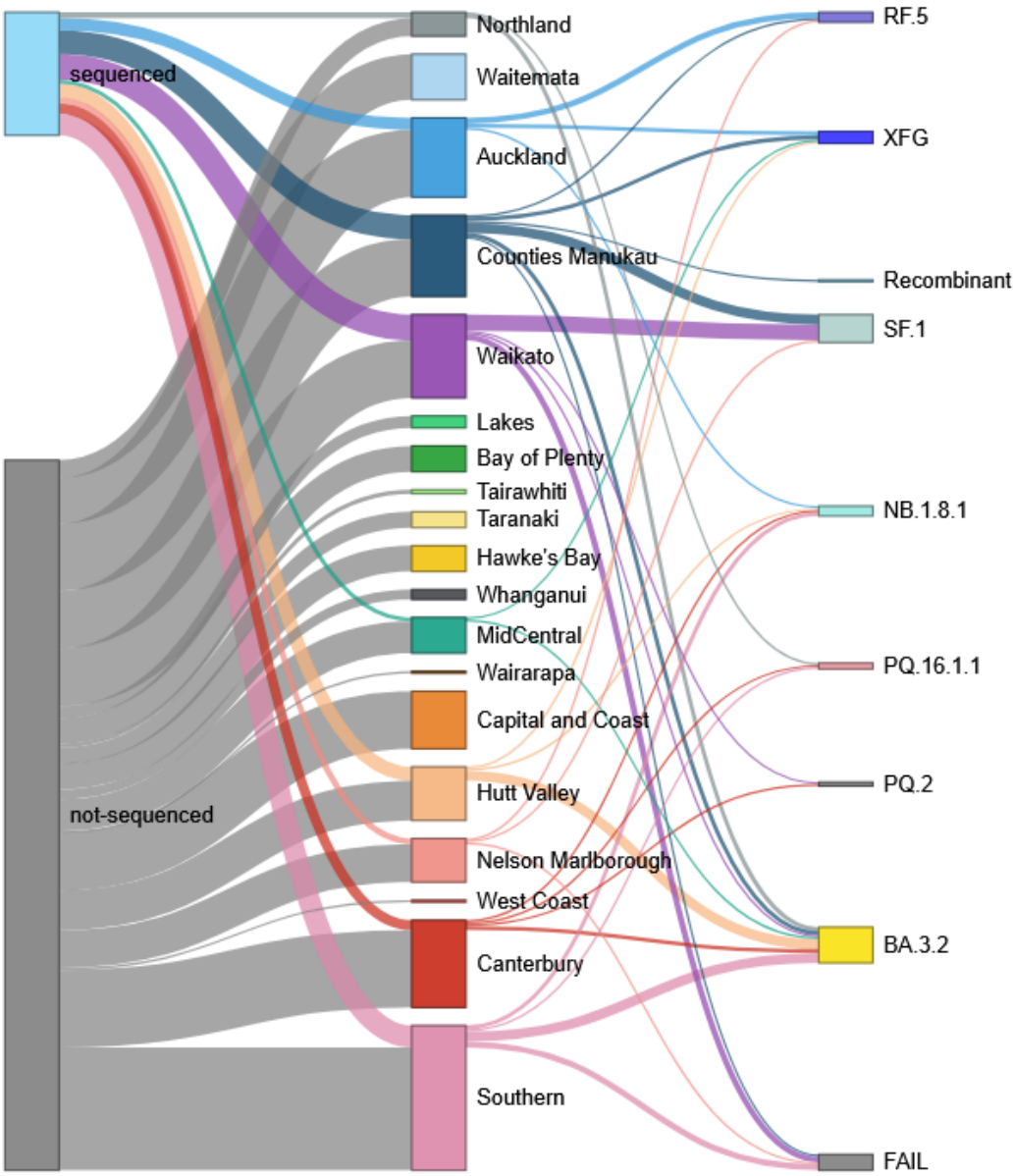


Figure 9. *Origin and sequencing results of the 420 cases reported between 4 to 31 July 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned). Data as of 2pm 6 August 2026.*