20 November 2026

COVID-19 Genomics Insights Dashboard (CGID) Report #76

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 explore and explain how whole-genome sequencing (WGS) of clinical samples and wastewater surveillance support public health decision-making. As SARS-CoV-2 continues to adapt and mutate, the CGID reports trends and insights gained by our WGS surveillance programme in Aotearoa New Zealand, and abroad.

Summary Infographic and Insights:

genomes analysed

26

genomes* from cases reported in the four-week window

1175

genomes* reported in 2026

127

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

894

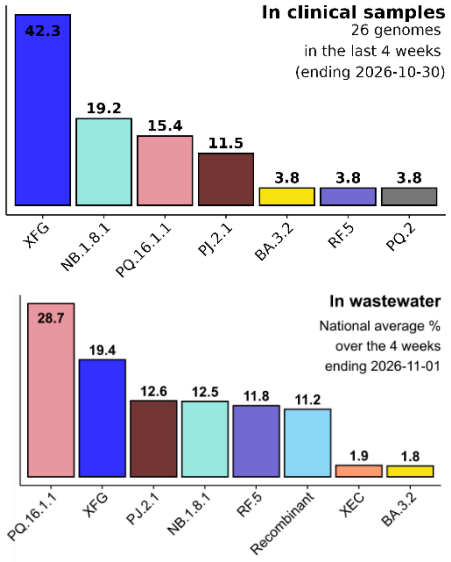
wastewater samples* in 2026

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

variant & lineage

PQ.16.1.1 is the most detected variant in wastewater

(note small sample size for clinical)



hospital cases

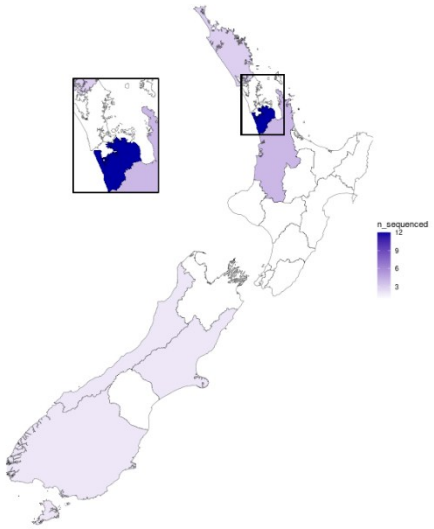
52% (13/25*) of cases admitted to hospital with a positive PCR between 3 and 30 October 2026 have been sequenced to date.

The approximate composition of hospitalised cases:

- **NB.1.8.1 38.5% (5/13)**
- **XFG 30.8% (4/13)**
- **PQ.16.1.1 23.1% (3/13)**
- **PQ.2 7.7% (1/13)**

*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 3 and 30 October 2026

Key trends and insights

- Based on wastewater levels, COVID-19 activity remained low over the period. Low numbers of clinical samples available for sequencing impact the accuracy of clinical genomic surveillance.
- Wastewater surveillance shows that PQ.16.1.1 and XFG are dominant, with PJ.2.1 increasing.
- There is week-on-week variation in the composition of variants in clinical samples, with XFG lineages dominant this month.
- BA.3.2, RF.5 and PQ.2 remain present at low levels
- Hospitalised cases show no clear variant difference.

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

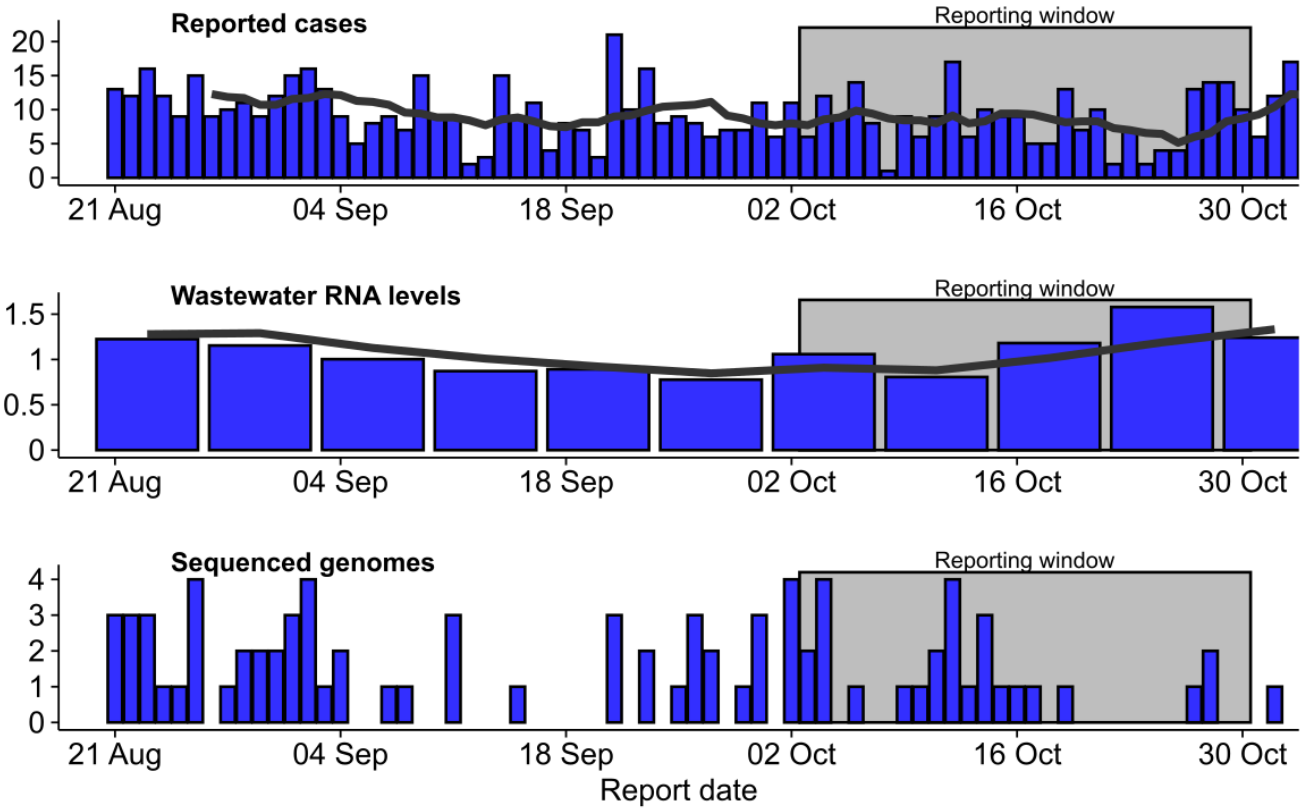


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater and 3-week rolling average (black 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 9 am 10 November 2026.*

Tracked Variants

Tracking the frequency and epidemiological properties of SARS-CoV-2 variants is a key goal of the CGID 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.

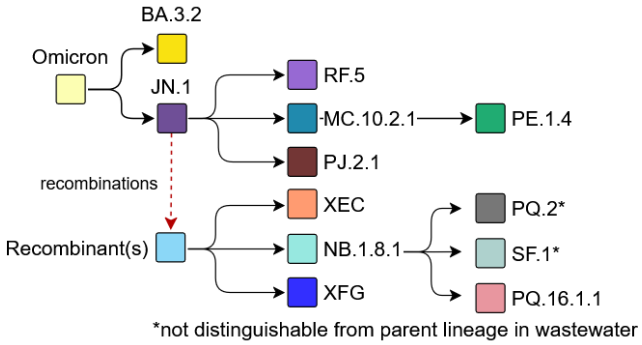


Figure 2. *Relationships between the variants tracked in this report.*

Changes made since last report

No changes were made in tracked lineages this month.

Overview of variants from clinical samples

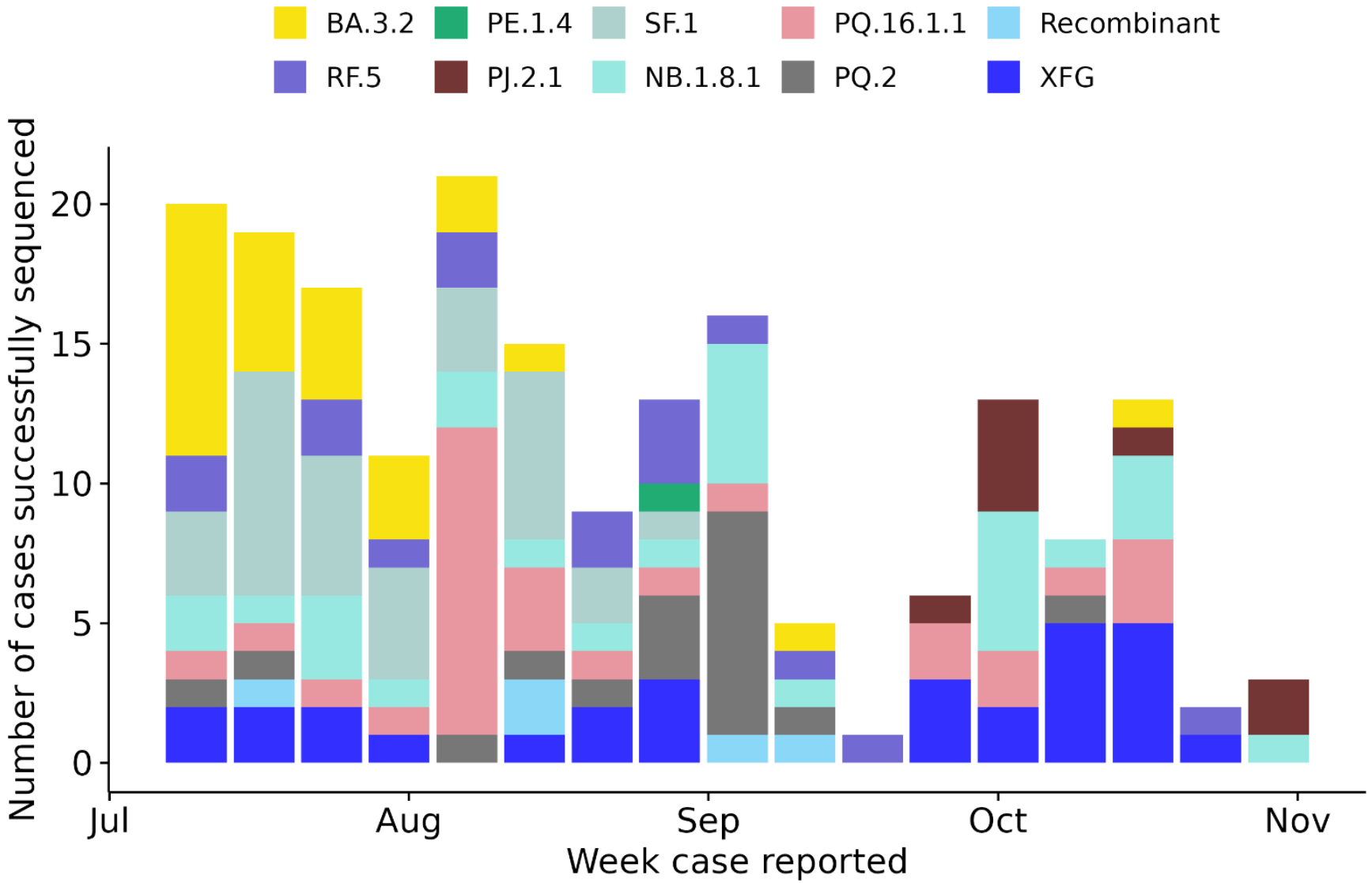


***Figure 3**. Number of variants/lineages sequenced from clinical cases reported in the past 17 weeks. Note, **data for the most recent two weeks is preliminary**. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week 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 1 November**, are available via PHF Science's online dashboard https://esr-cri.shinyapps.io/wastewater/ and summarised in **Figure 4**. Due to assays limitations, **for the wastewater analysis, PQ.2 and SF.1 are included in the NB.1.8.1 lineage.**

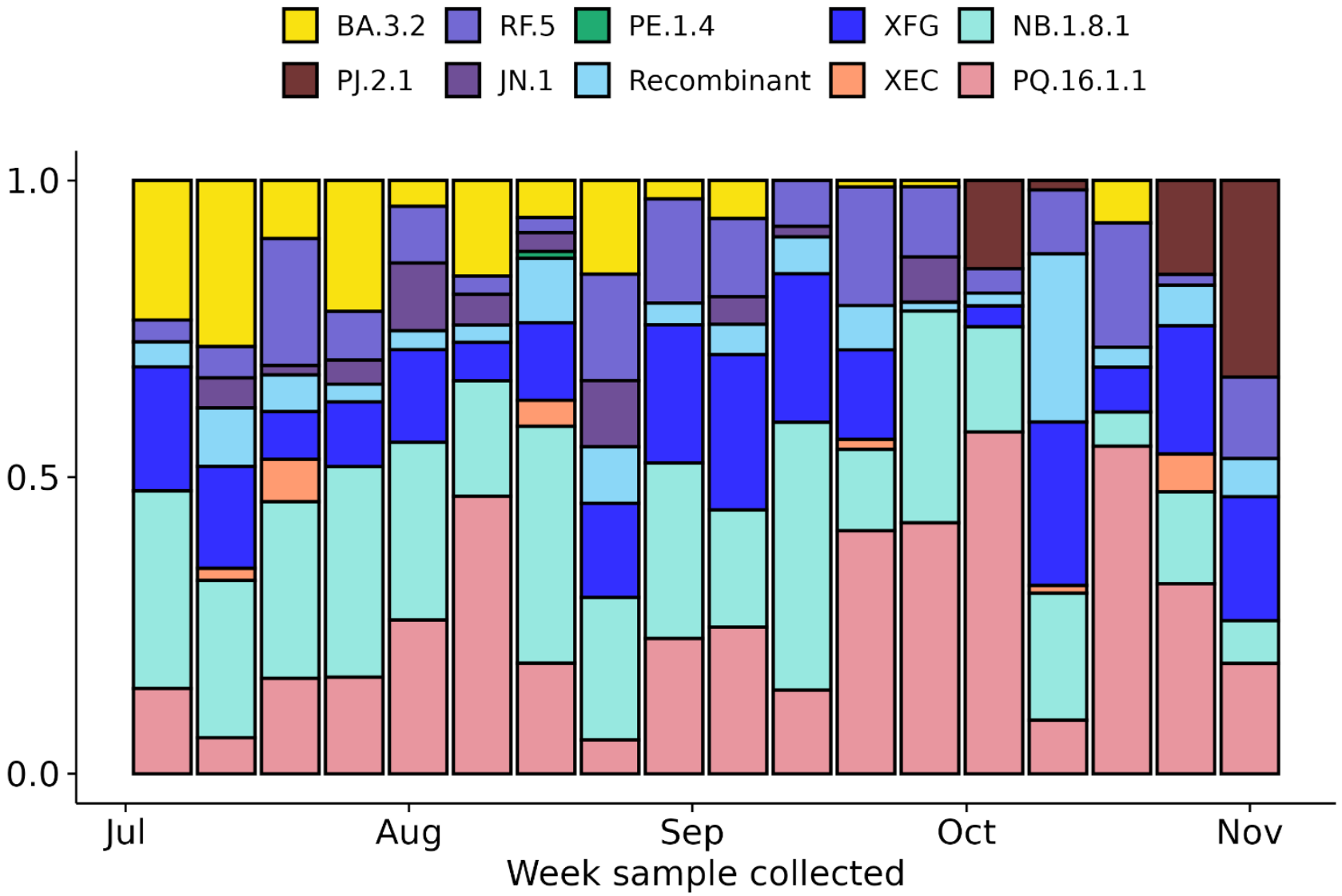


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

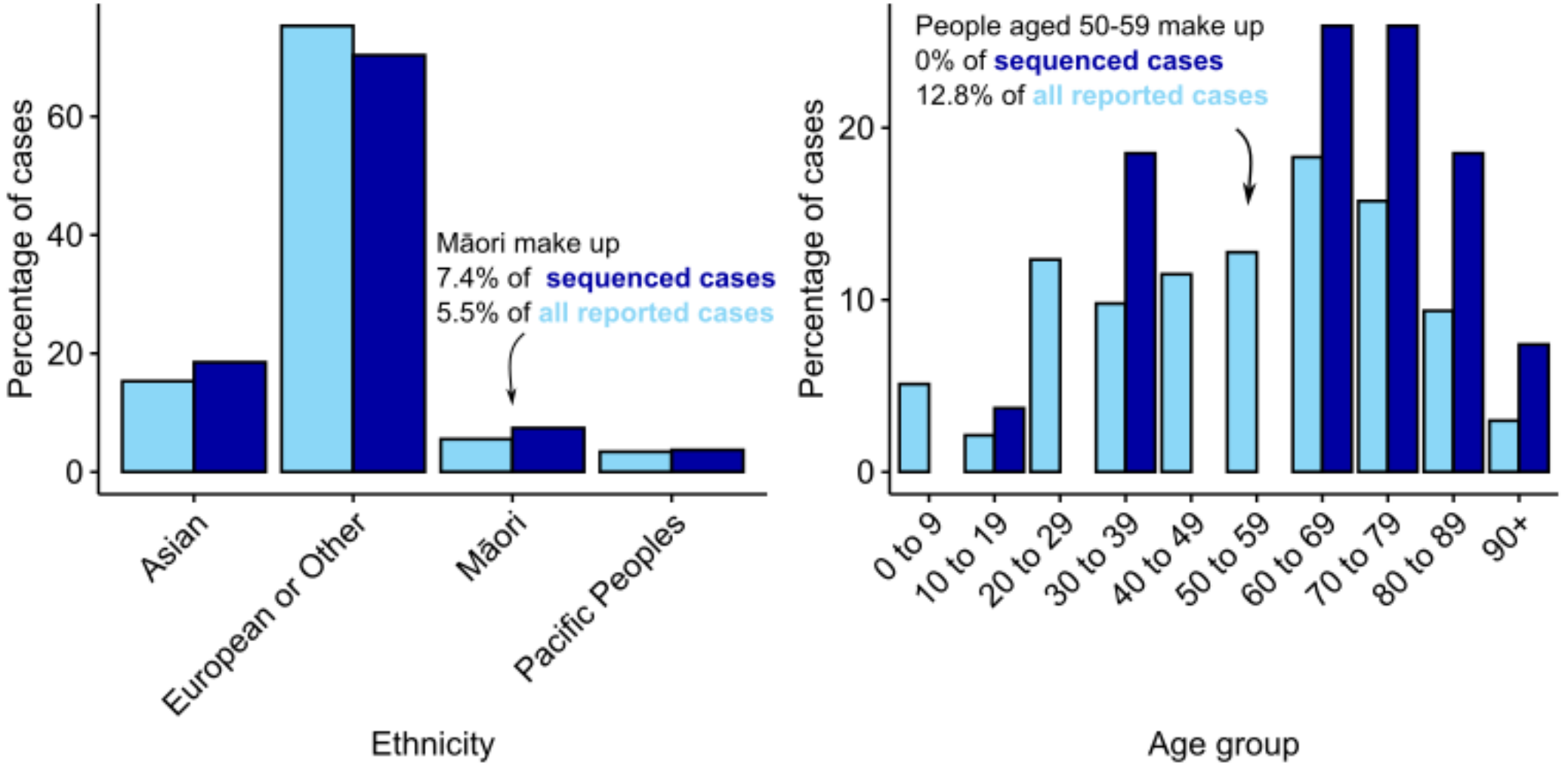


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported in this reporting window* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution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

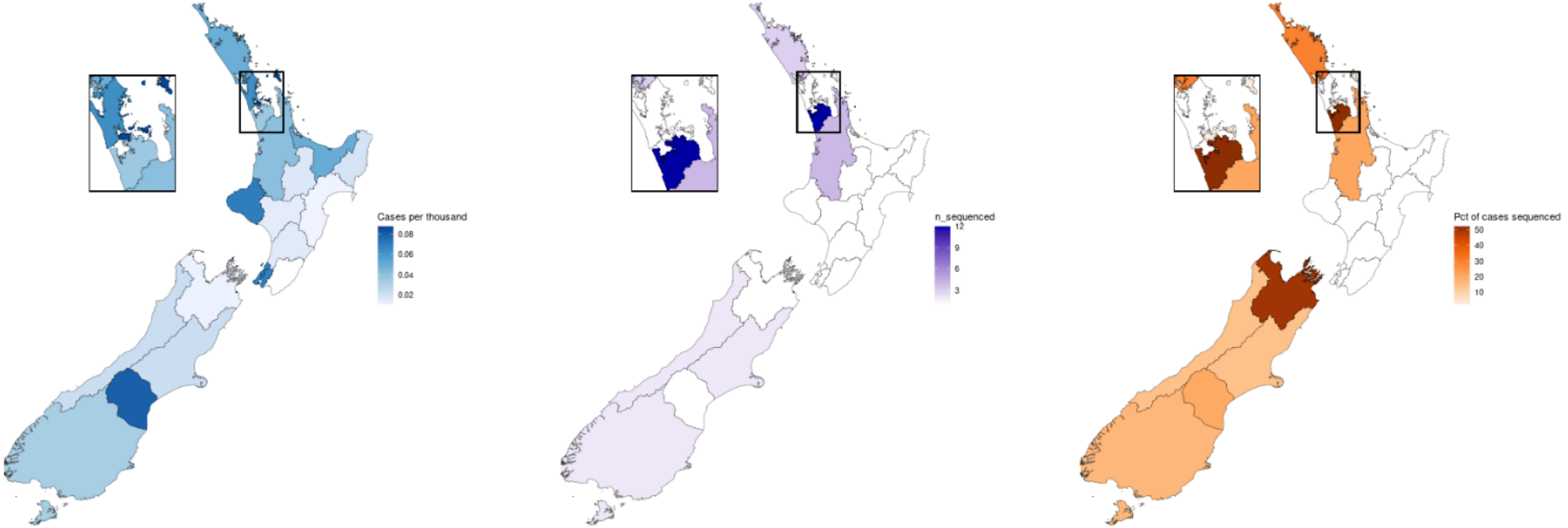


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGID. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 9am 10 November 2026.*

Emerging lineages

Growth estimates for new variants were not estimated due to the low number of cases sequenced at PHF Science over the reporting window

Major trends in variants

Near the end of a trough in COVID-19 activity in Aotearoa?

COVID-19 activity, as measured by reported cases and wastewater concentrations, has remained low over this reporting period, with signs of an increase at the very end of the reporting window (**Figure 1**). The volatility in variants landscape noted in the last CGID has also persisted. In this period, PJ.2.1, which was the dominant variant in the last CGID has been superseded by XFG in clinical surveillance (**Figure 3**).

The number of positive PCR samples available for sequencing over the reporting window is insufficient to provide reliable estimates of variant frequencies or growth rates of emerging subvariants. XFG contains ST.1 and TA.1, two variants increasing in Europe.

Wastewater variant data currently provides a better understanding of circulating variants, with the caveat that the CoVarSeq assay is not able to differentiate some variants. In the last available wastewater variant data (4-week period ending November 1), the **PQ.16.1.1** lineage was dominant (28.7%), with **XFG** representing 19.4% of sequences, **NB.1.8.1** (including SF.1 and PQ.2), **PJ.2.1** and **RF.5** around 12% each and. **PJ.2.1 has been increasing** since the last CGID, it represented 3.7% of sequences over the previous 4-week window (ending October 4), and 33% over the last week.

WGS Hospital Reporting

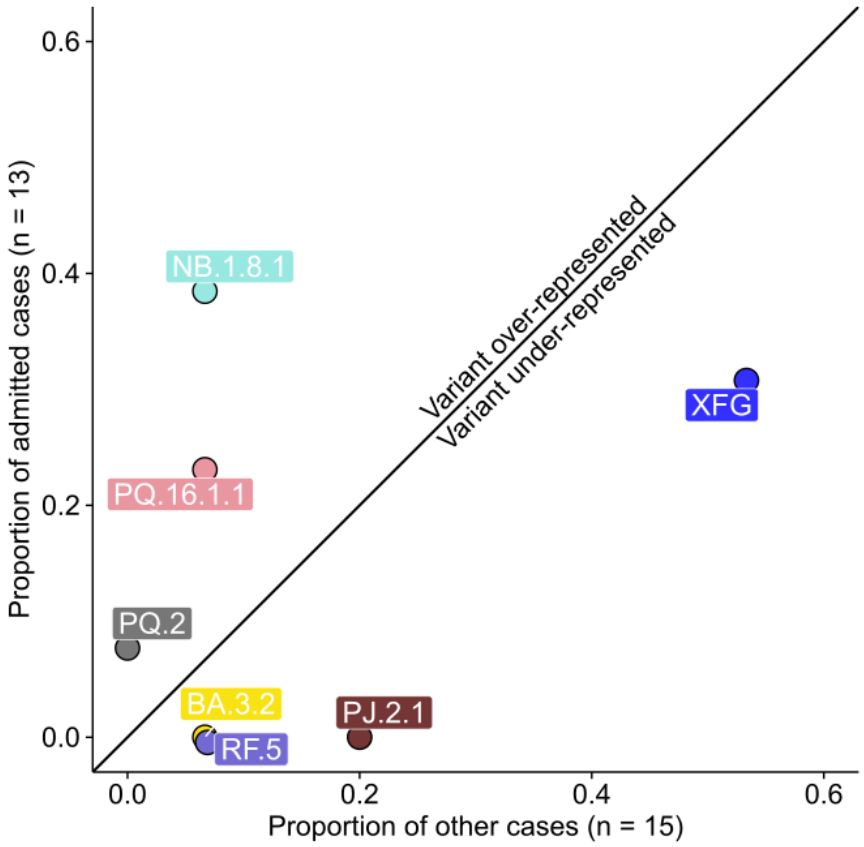


Figure 7. *Frequency of variants among cases not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after a positive PCR test date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted. This graph includes cases with a positive PCR in the reporting window, so may include cases first reported before this reporting window and not included elsewhere in this report.*

A total of 13 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. There is no statistically significant difference in the frequency of tracked variants between hospitalised cases and other cases reported in this window (Fisher's exact test, p-value = 0.054; **Figure 7**). However, the small sample size limits the precision of these estimates, and the current data are insufficient to draw conclusions about differences in variant frequencies between the two groups.

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

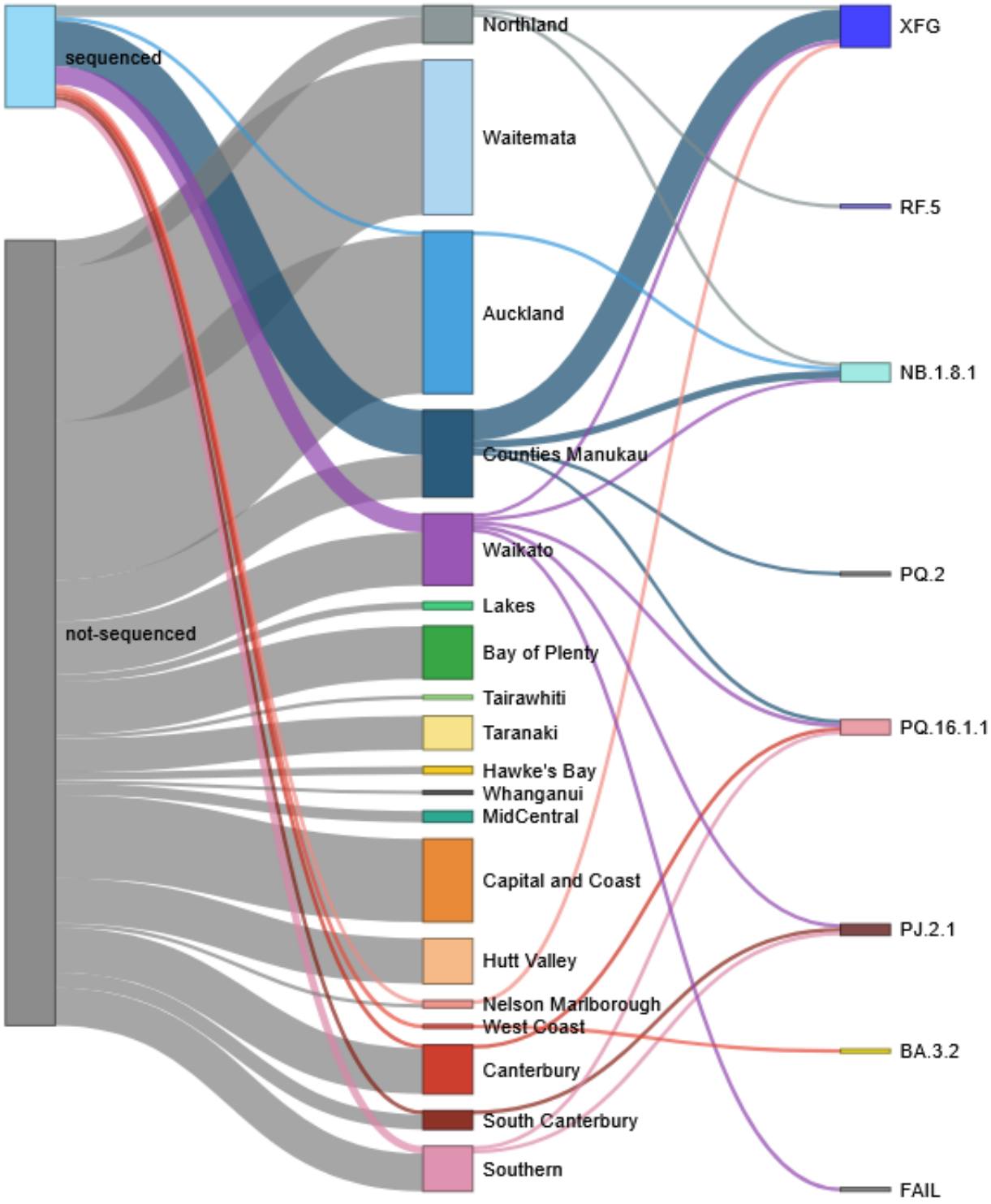


Figure 8. Origin and sequencing results of the 235 cases reported between 3 to 30 October 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned). Data as of 9am 10 November 2026.

Software versions

Lineage assignment done using `pangolin 4.4, pangolin-data 1.41 and nextclade 3.21.0` (2026-10-28--15-04-26Z).