16 October 2026

COVID-19 Genomics Insights Dashboard (CGID) Report #75

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 CGD reports trends and insights gained by our WGS surveillance programme in Aotearoa New Zealand, and abroad.

Summary Infographic and Insights:

genomes analysed

21

genomes* from cases reported in the four-week window

1145

genomes* reported in 2026

70

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

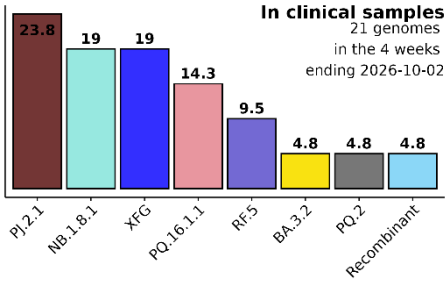
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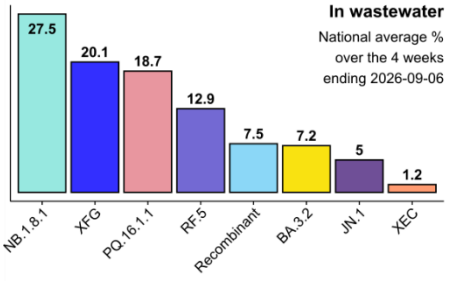
wastewater samples* in 2026

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

variant & lineage

PJ.2.1 is the most detected variant in clinical samples
(note earlier window for wastewater)





hospital cases

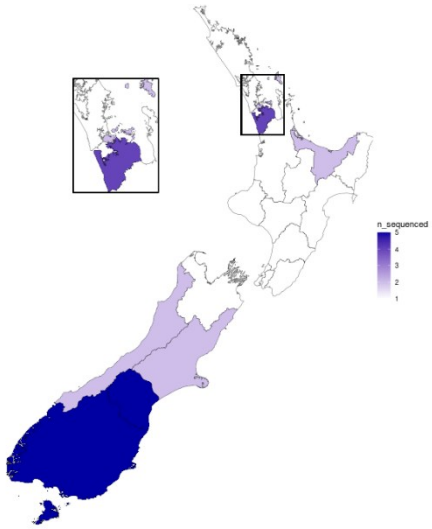
22.2% (4/18*) of cases admitted to hospital with a positive PCR between 5 September and 2 October 2026 have been sequenced to date.

The approximate composition of hospitalised cases:

- **PJ.2.1 75% (3/4)**
- **PQ.16.1.1 25% (1/4)**

*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 5 September and 2 October 2026

Key trends and insights

- Overall COVID-19 activity levels remain low and impact the accuracy of genomic surveillance.
- There is week-on-week variation in the composition of variants, with SF.1 previously dominant not detected this month.
- We started tracking PJ.2.1, a highly divergent JN.1 variant with over 25 Spike mutations that rapidly spread internationally and represents 24% of sequences (5/21).
- BA.3.2 and PQ.2 have declined while NB.1.8.1, XFG, RF.5 and PQ.16.1.1 continue circulating.

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

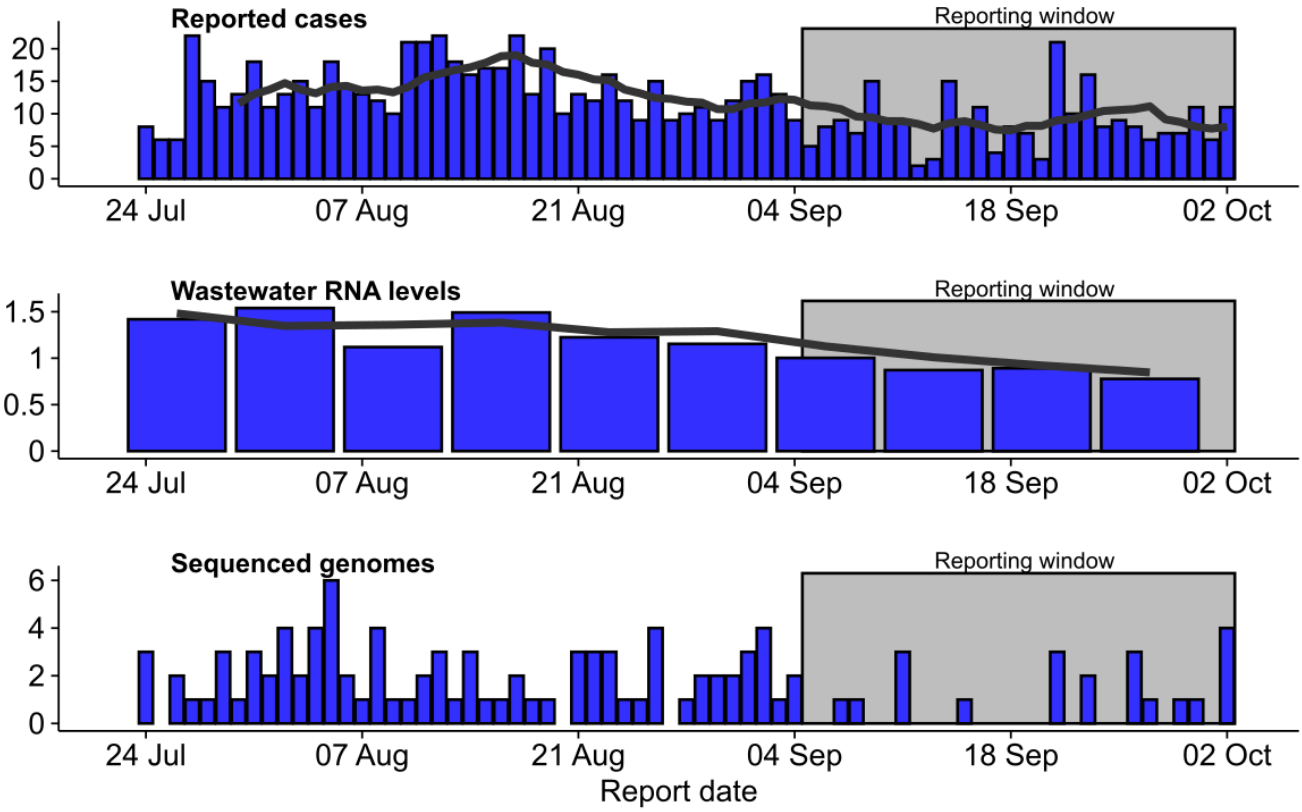


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater and 3-week rolling average (black 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 10 am 13 October 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.

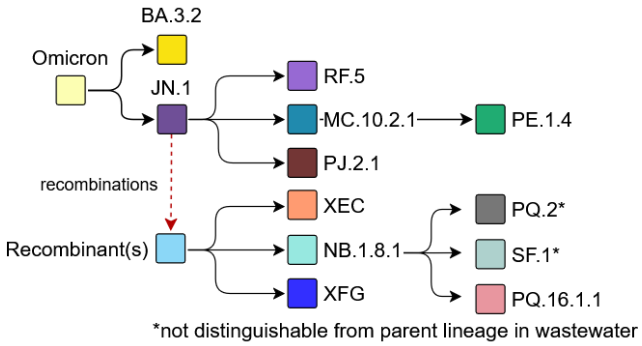


Figure 2. *Relationships between the variants tracked in this report.*

Changes made since last report

This month, we started tracking PJ.2.1, a globally rapidly spreading MC.10.1.7 sublineage. LP.8.1, that has not been detected in Aotearoa since January 2026, was removed from the list of tracked lineages.

Overview of variants from clinical samples

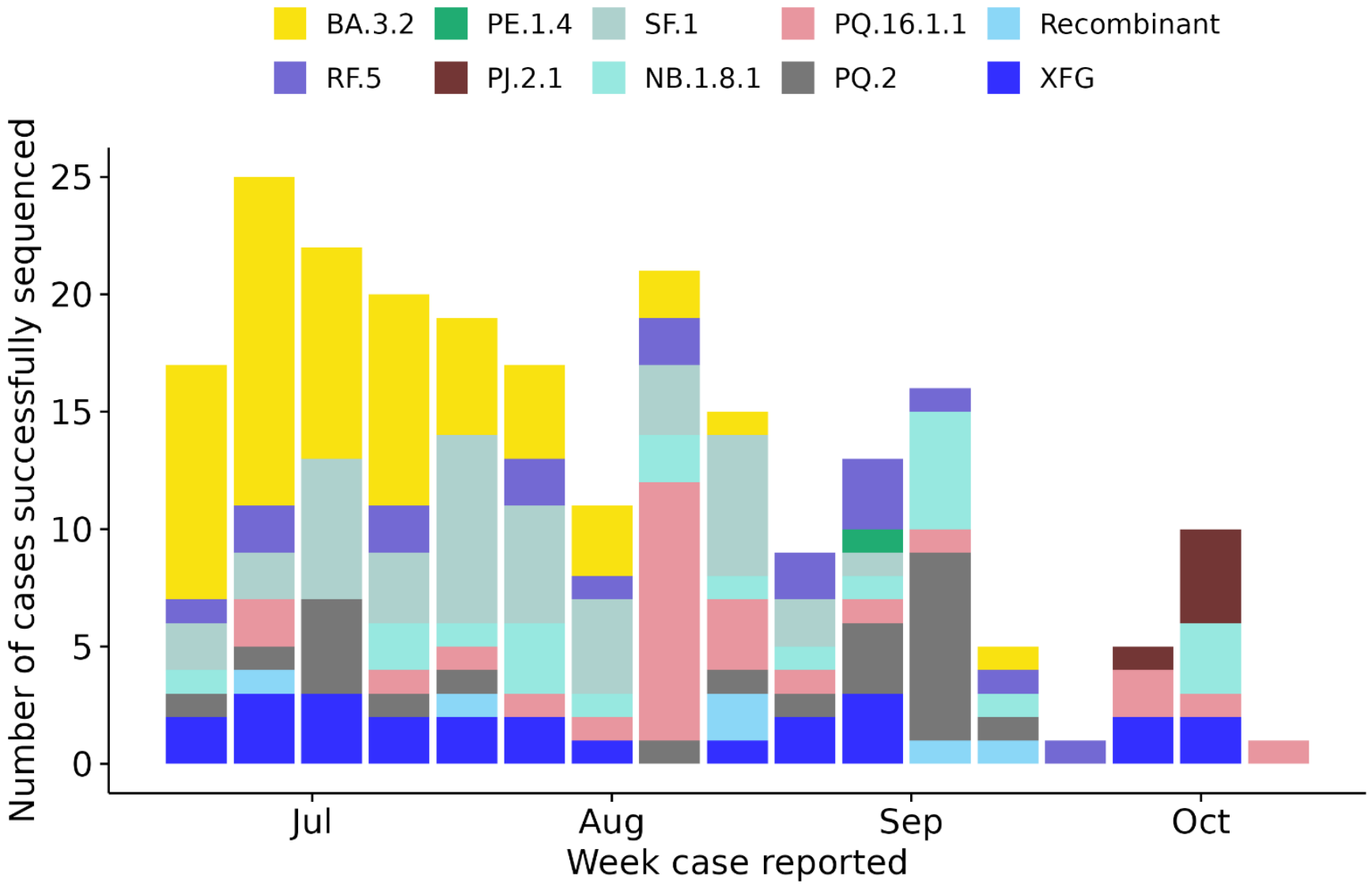


***Figure 3**. Number of variants/lineages sequenced from clinical cases reported in the past 17 weeks. Note, **data for the most recent two weeks is preliminary**. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week 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 across New Zealand for **the week ending 6 September**, 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.** Note that the 4-week window reported in wastewater data is 4 weeks earlier than the reporting window for clinical cases.

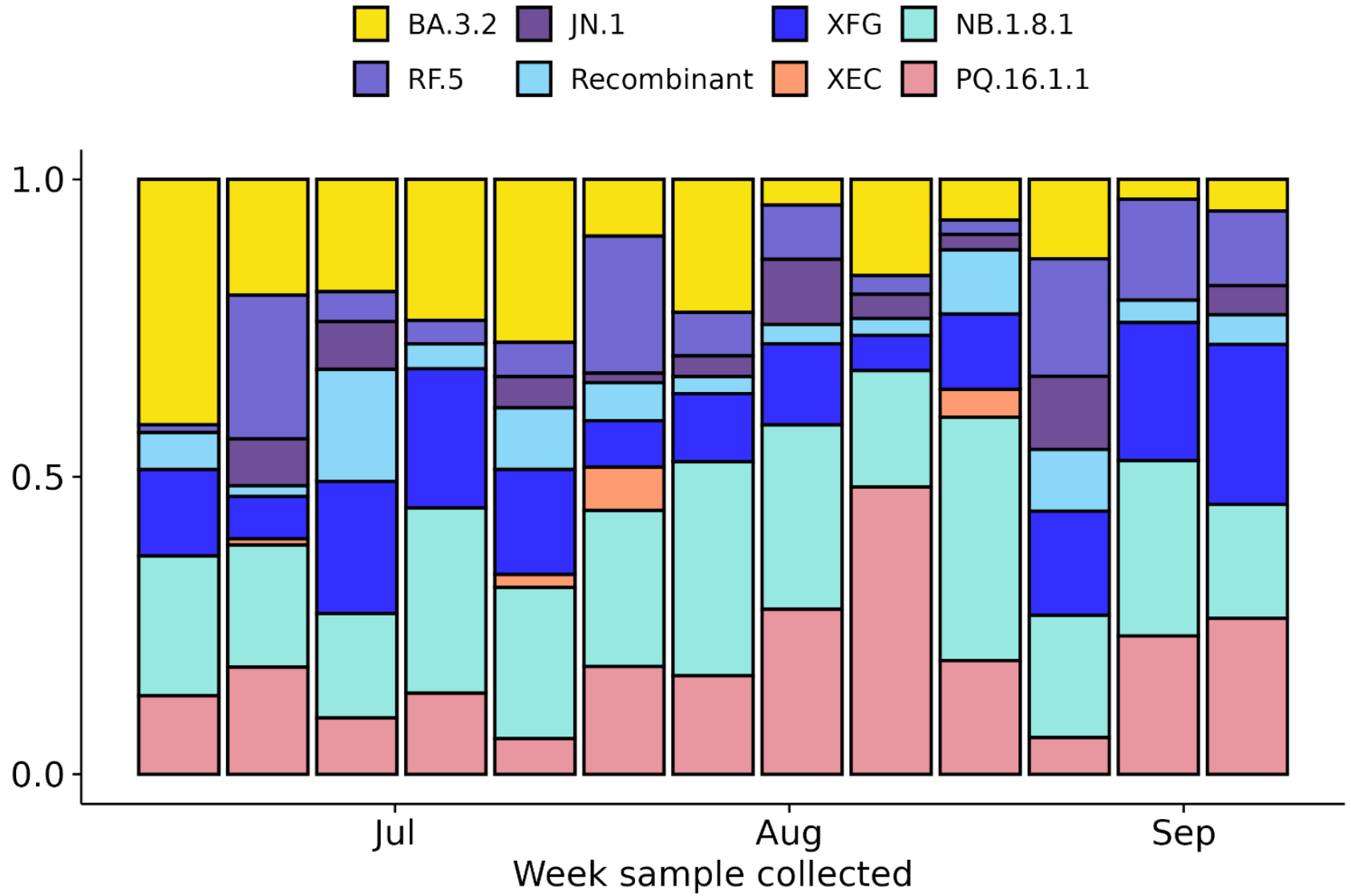


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

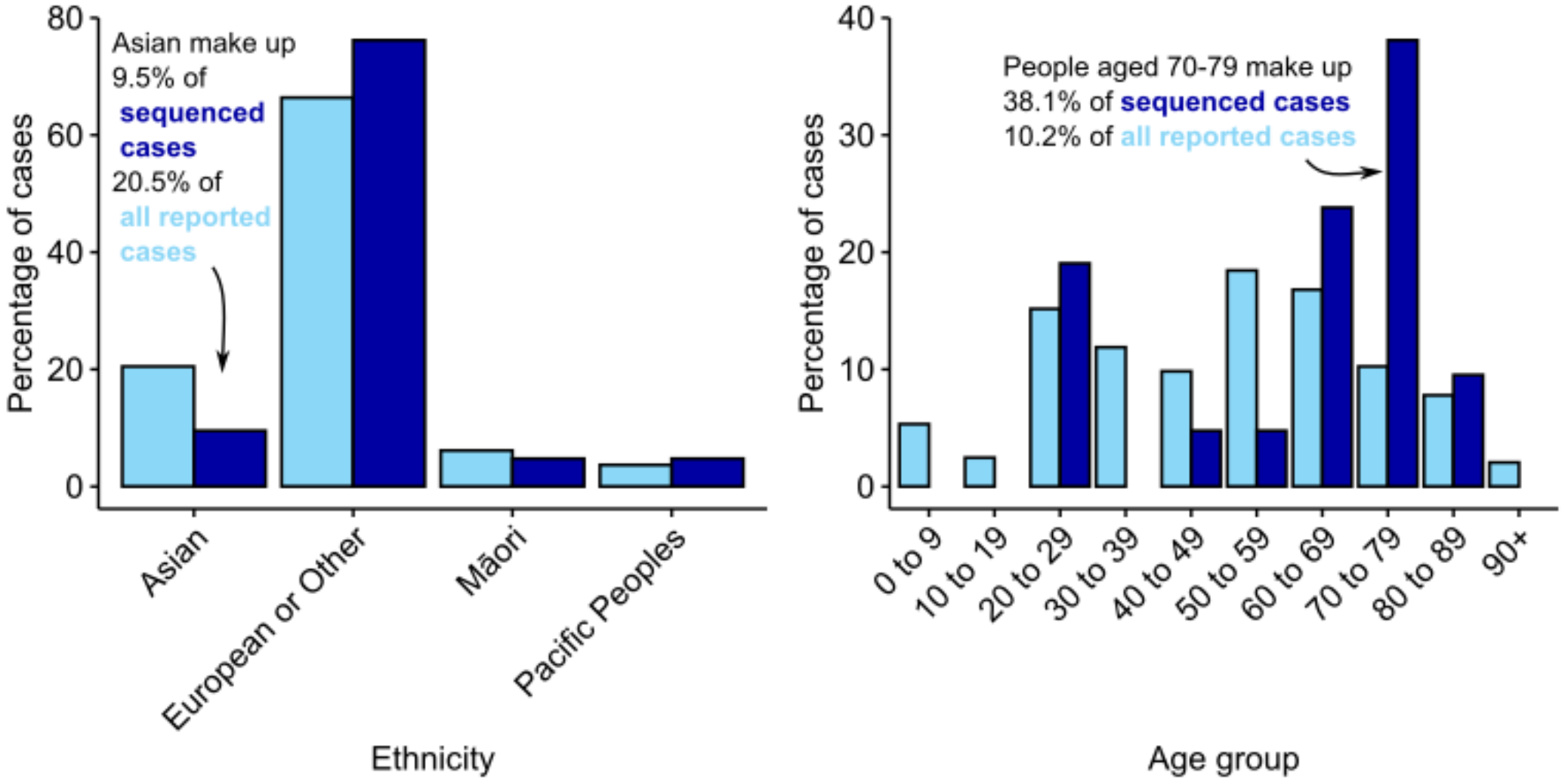


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported in this reporting window* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 10 am 13 October 2026.*

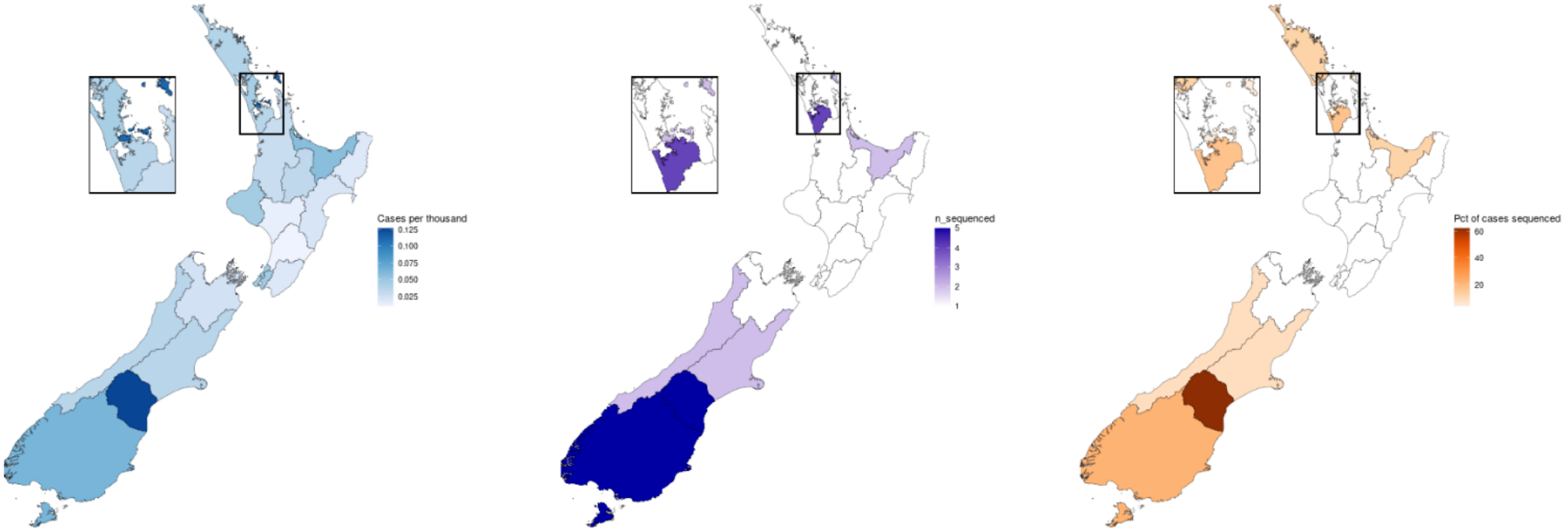


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGID. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 10am 13 October 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

COVID-19 activity remains low in Aotearoa

This reporting period contains the lowest number of sequences since routine SARS-CoV-2 Genomic surveillance started in Aotearoa New Zealand, with a resulting increased week-on-week variability in the composition of variants in clinical samples.

The period of stable and low COVID-19 activity, as measured by reported cases and wastewater concentrations, has continued over this reporting period (**Figure 1**). The volatility in variants landscape noted in the last has also persisted. In this period, SF.1, which was the dominant variant in August has not been detected in clinical surveillance (**Figure 3**). In contrast, the previously undetected PJ.2.1 has been detected more frequently than older circulating variants (23.8%, 5/21).

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. PHF Science are undertaking a limited technical validation of direct sequencing of material from positive rapid antigen tests (RATs)[1], with promising preliminary results.

Wastewater variant data currently provides a better understanding of circulating variants, with the caveat of a CoVarSeq assay not able to differentiate some variants. In the last available wastewater variant data (4-week period ending September 6), the **NB.1.8.1** lineage (including SF.1 and PQ.2) was still dominant (27.5%), with **XFG** and **PQ.16.1.1** representing around 20% of sequences and **RF.5** 13%. PJ.2.1 had not been detected in that period.

Highly divergent PJ.2.1 detected in New Zealand

The PJ.2.1 variant was first detected in May 2026 in Ontario (Canada) and subsequently emerged in New York (USA) in July. It has acquired over 25 Spike mutations compared to its parent lineage, MC.10.1.7, that was last detected a year prior, at the start of May 2025 (Canada, GISAID data).

It has since spread to Europe and other parts of the world, with sequences published in GISAID and NCBI from Australia, Spain, UK, Israel, Singapore and France. In Canada, it is particularly present in Ontario, British Columbia, and Alberta, and in the USA in California, Florida, New York and New Jersey (and detected in 8 other States). Airport surveillance data from the CDC (in GISAID as of 15 Oct) further mention PJ.2.1 cases with travel history to Cuba, Colombia, Costa Rica, United Kingdom, Brazil, Ecuador, Belgium, Turkey, Spain, Italy, Dominican Republic, Mexico, Peru and Guatemala, with 26/128 (20.3%) of genomes collected for Airport screening in the reporting window being PJ.2.1, suggesting broader circulation for this variant, especially in South America.

Recent preprints (non-peer reviewed) comparing this lineage with other currently circulating variants in pseudovirus models point towards augmented ACE2 affinity (not antibody evasion) to explain the observed growth advantage of this variant[2,3]. It remains antigenically close to its JN.1 ancestral lineage and current vaccines are expected to provide a similar level of protection.

This variant does not appear more frequent in a specific age group in international data, unlike what was observed with BA.3.2. It has (to date) not received any WHO designation. It is unclear whether the observed increase in COVID-19 activity observed in North America and Europe reflects a surge caused

[1] Moso et al. Non-SARS-CoV-2 respiratory viral detection and whole genome sequencing from COVID-19 rapid antigen test devices: a laboratory evaluation study, The Lancet Microbe, Volume 5, Issue 4, 2024, https://doi.org/10.1016/S2666-5247(23)00375-0.

[2] He et al. Increased receptor binding capability of the SARS-CoV-2 saltational variant PJ.2.1, bioRxiv 2026.09.03.749172; https://doi.org/10.64898/2026.09.03.749172

[3] Hoffmann et al. Epidemiology and virological characteristics of the emerging SARS-CoV-2 variant PJ.2.1. bioRxiv 2026.10.08.757354; https://doi.org/10.64898/2026.10.08.757354

by this variant or a seasonal pattern (see below). PHF Science will continue monitoring this variant and the potential impact to caseloads.

Global overview

Trends in Aotearoa New Zealand as we are coming into summer are similar to Australia but not the North hemisphere, especially in North America and Europe (Spain) where indicators point to an autumnal increase. Activity levels in Asia are declining after a moderate increase due to PQ.16.1.1, with the exception of Japan where more cases are due to BA.3.2.

Country/Region	Activity	Test positivity	Main variant(s)	Reporting period
Australia[4]	Decreasing	1%†	NB.1.8.1	21 Sept-4 Oct
USA	Increasing	4%[5]†	SW.2[6]	Week ending 3 Oct 2 to 29 Aug 2026 for variants
Canada[7]	Increasing	4.1%†	RF* and PJ*	Week ending 3 Oct
United Kingdom[8]	Increasing	11%†	TA.1 (25.8%)	Week ending 8 Oct 31 Aug – 13 Sept for variants
Europe[9] (21 countries)	Increasing	13%† (0%–23%)	ST.1 (25%)	Week ending 4 Oct September month for variants
Spain[10]	Increasing	27%†	ST.1	Week ending 4 Oct
Hong Kong[11]	Low	0.3%†	PQ.16.1.1 (89%)	Week ending 3 Oct
Singapore[12]	Low	2%†	SV.1 / RK.1.2	Week ending 10 Oct
China[13]	Moderate decreasing	15.8%‡	PQ.16.1.1 (89%)	Week ending 24 Aug
Japan[14]	Decreasing	\	BA.3.2	Week ending 4 Oct
South Africa[15]	Low	0.9%†	\	Week ending 4 Oct

† Primary care; ‡ ILI hospital sentinel surveillance; \ not available

[4] https://www.cdc.gov.au/resources/publications/australian-respiratory-surveillance-report-21-september-4-october-2026
[5] https://www.cdc.gov/nrevss/php/dashboard/index.html
[6] https://www.cdc.gov/covid/php/variants/variants-and-genomic-surveillance.html
[7] https://health-infobase.canada.ca/respiratory-virus-surveillance/covid-19.html
[8] https://www.gov.uk/government/statistics/national-flu-and-covid-19-surveillance-reports-2026-to-2027-season
[9] https://erviss.org/ (WHO region)
[10] https://docsivira.isciii.es/Informe_semanal_SiVIRA_202640.html
[11] https://www.chp.gov.hk/en/resources/29/100148.html
[12] https://www.cda.gov.sg/resources/weekly-infectious-diseases-bulletin-2026/
[13] https://www.chinacdc.cn/jksj/xgbdyq/202609/t20260918_1840296.html
[14] https://www.mhlw.go.jp/stf/seisakunitsuite/bunya/0000121431_00485.html
[15] https://www.nicd.ac.za/diseases-a-z-index/disease-index-covid-19/surveillance-reports/weekly-respiratory-pathogens-surveillance-report-week/

WGS Hospital Reporting

A total of 4 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 in the seven days before or after admission. Three were PJ.2.1 and one belonged to the PQ.16.1.1 lineage. 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 = 0.391; **Error! Reference source not found.**). 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.

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 7**).

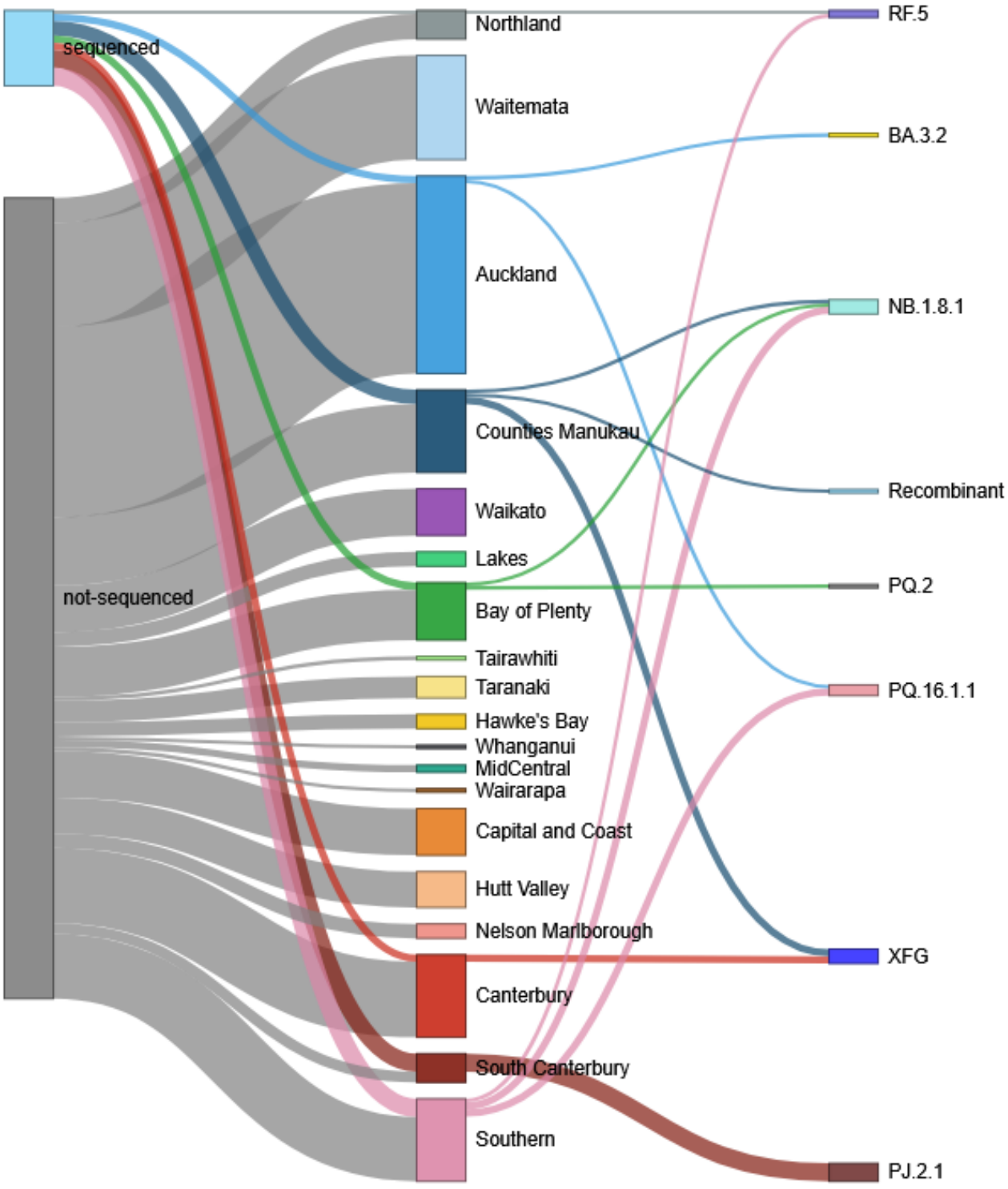


Figure 7. *Origin and sequencing results of the 244 cases reported between 5 September to 2 October 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned). Data as of 10am 13 October 2026.*

Software versions

Lineage assignment done using `pangolin 4.4, pangolin-data 1.41 and nextclade 3.21.0`.