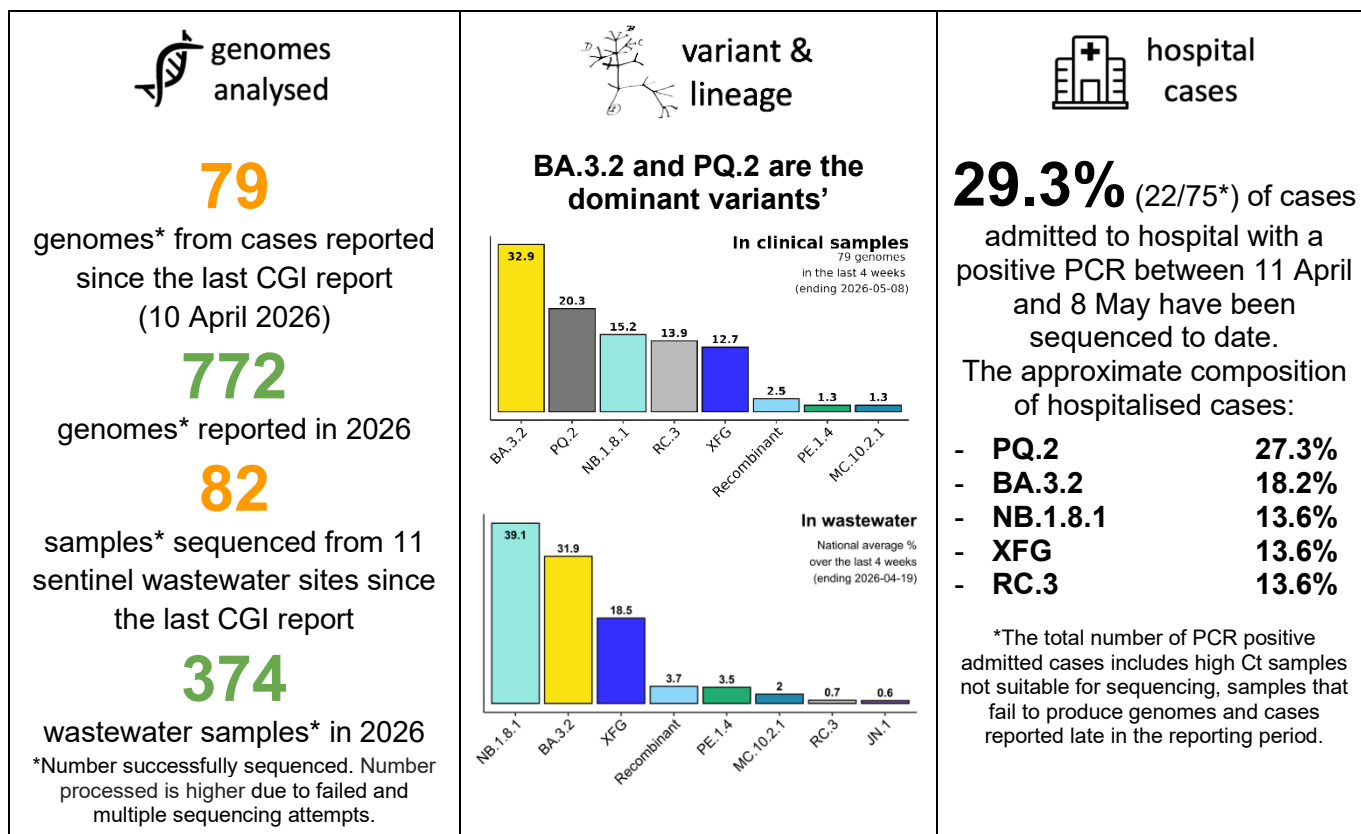


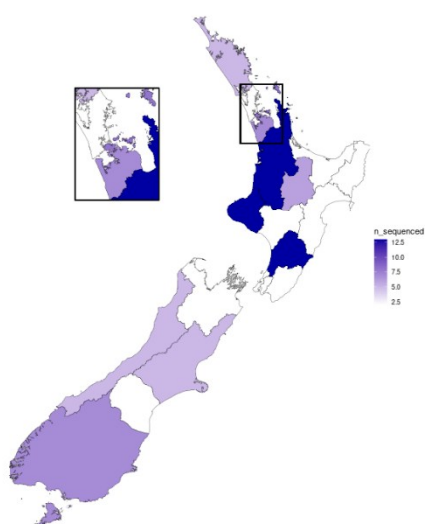
COVID-19 Genomics Insights Dashboard (CGID) Report #70

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 11 April – 8 May 2026

Key trends and insights

- BA.3.2 and PQ.2/NB.1.8.1 are currently the main variants circulating in Aotearoa with broadly similar patterns seen in clinical and wastewater surveillance.
- No other variants show any growth advantage over them.
- Variant patterns in New Zealand broadly match international trends, with BA.3.2, NB.1.8.1 and related lineages dominating in most countries.
- Low circulating SARS-CoV-2 levels and therefore limited samples available for sequencing can impact the accuracy of genomic surveillance.

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

Data Summary and Reporting Period

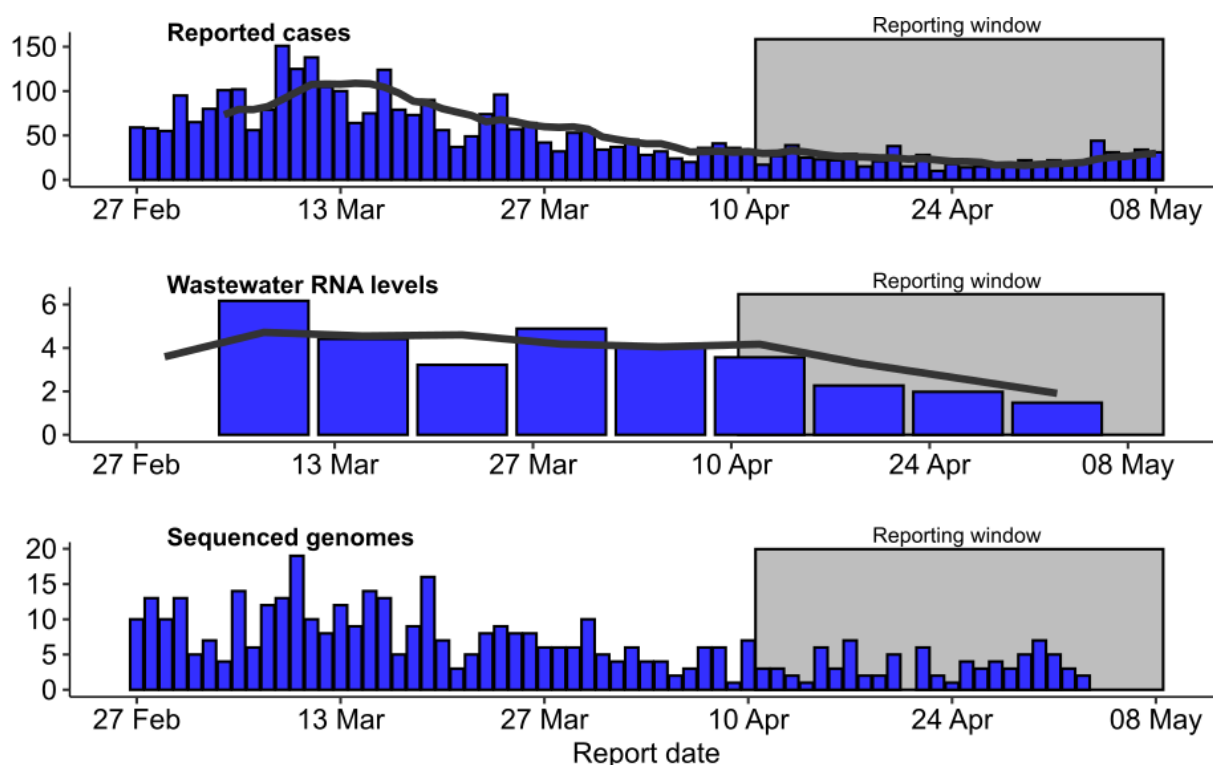


Figure 1. Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater. Bottom: The number of sequenced 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 12 May 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. A fuller description of these variants is provided in the Appendix to this report.

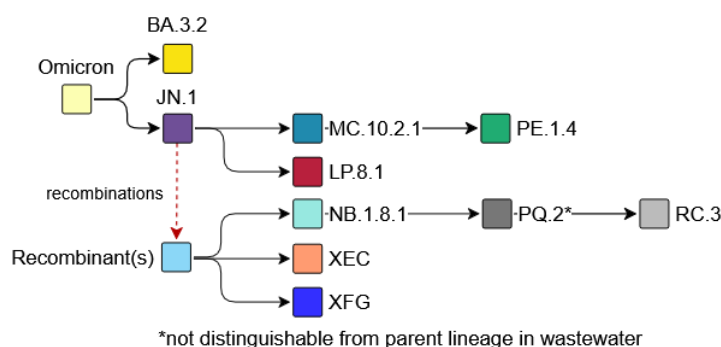


Figure 2. Relationships between the variants tracked in this report.

Changes made since last report

The variants tracked in the CGI reports are frequently updated to reflect trends in SARS-CoV-2 evolution and epidemiology. This month, PQ.43.1.1 and QY.2 that were circulating at low levels were removed from the list of tracked variants and re-integrated into their parent lineages, NB.1.8.1 and XFG, respectively.

Overview of variants from clinical samples

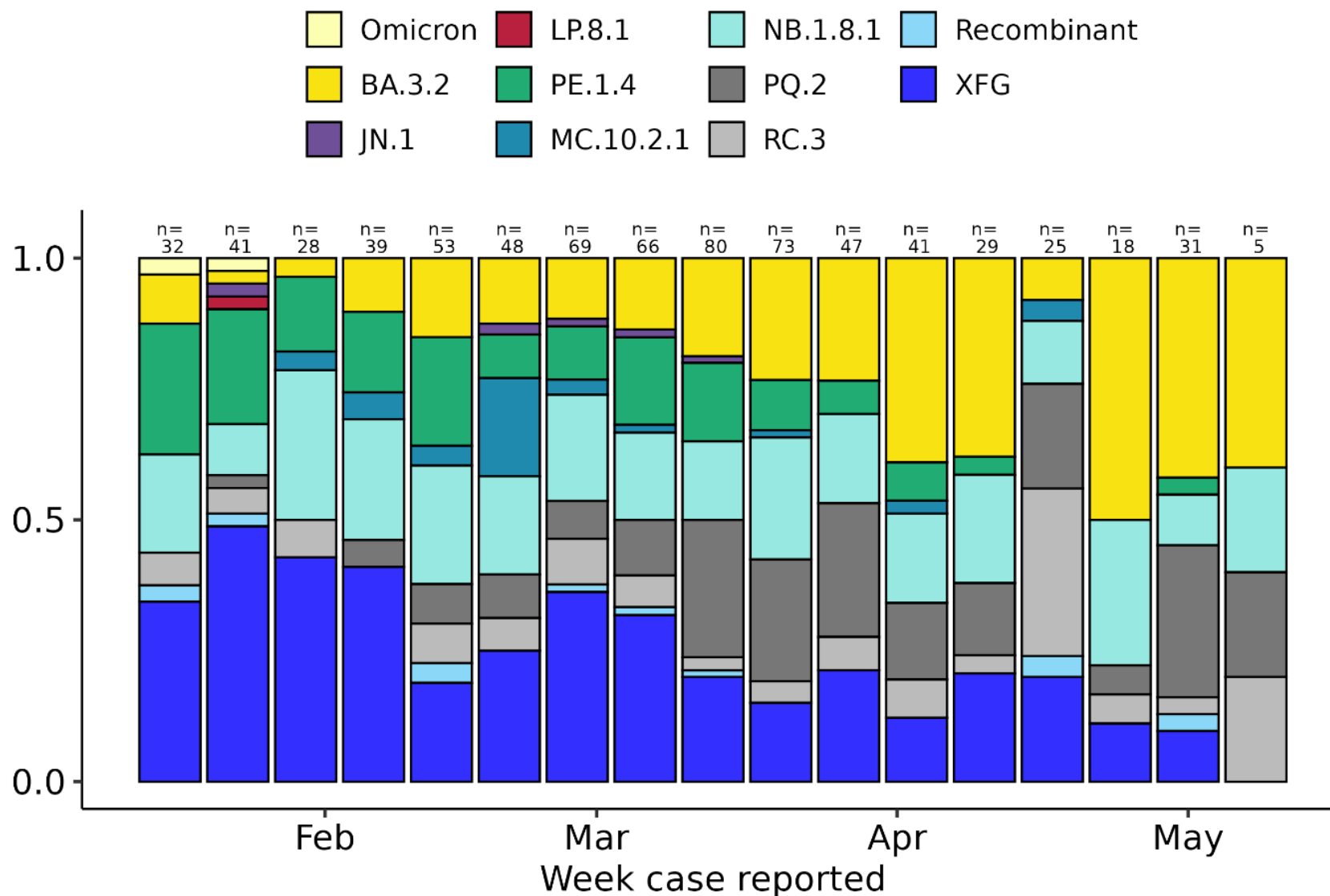


Figure 3. Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based on the number of genomes indicated above each bar. Tracked lineages are defined in [Figure 2](#). The two genomes identified as 'Omicron' are genomes with partial coverage of the Spike protein, which limit the power of the standard bioinformatics tools used by PHF Science to assign a tracked lineage. Based on manual review, both genomes are most consistent with BA.3.2; however, they are retained within the parent "Omicron" category for reporting purposes.

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 esri.shinyapps.io/wastewater/ and summarised in (Figure 4)Error! Reference source not found.. 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.

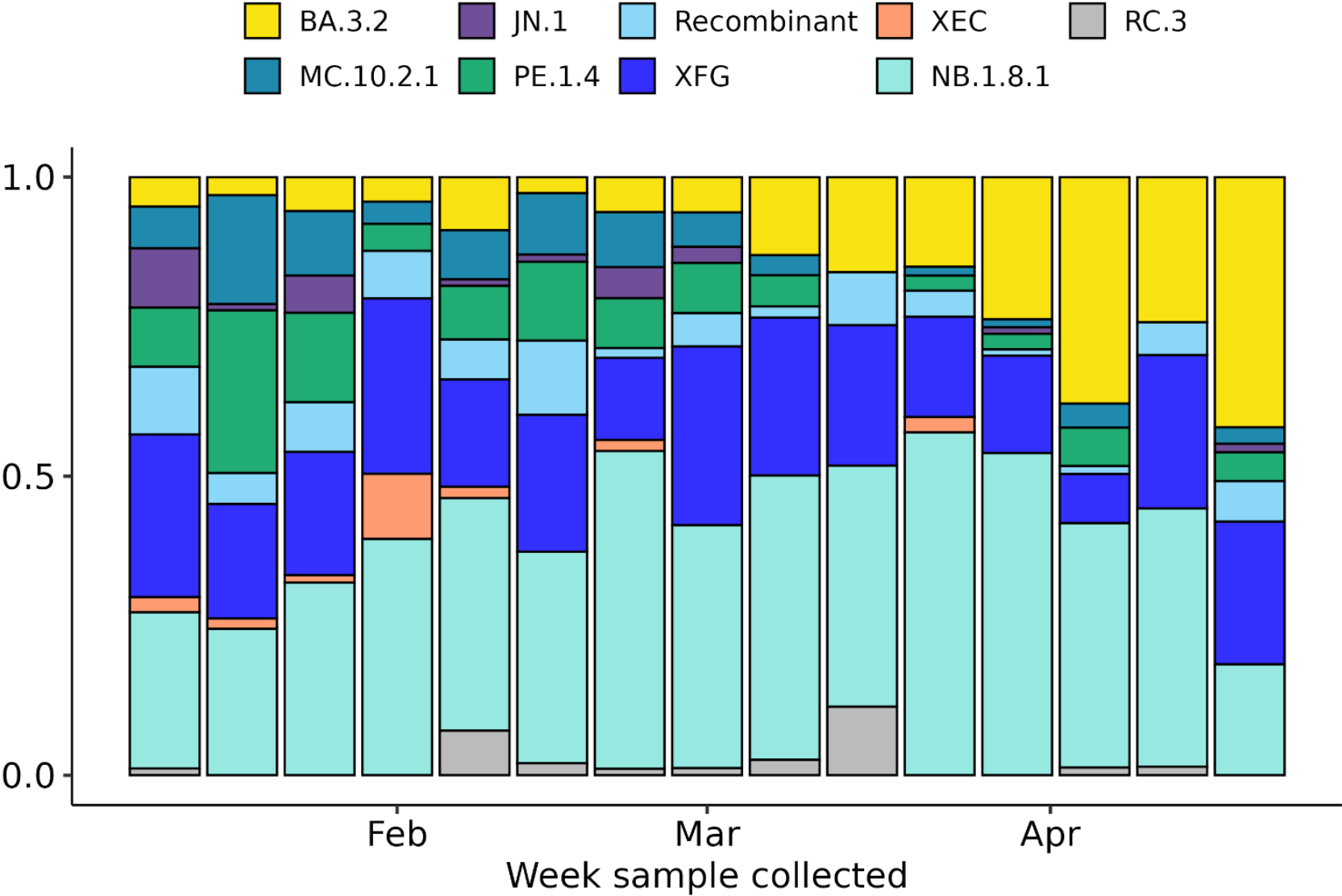


Figure 4. Estimated variant frequencies from 11 wastewater sites across New Zealand.

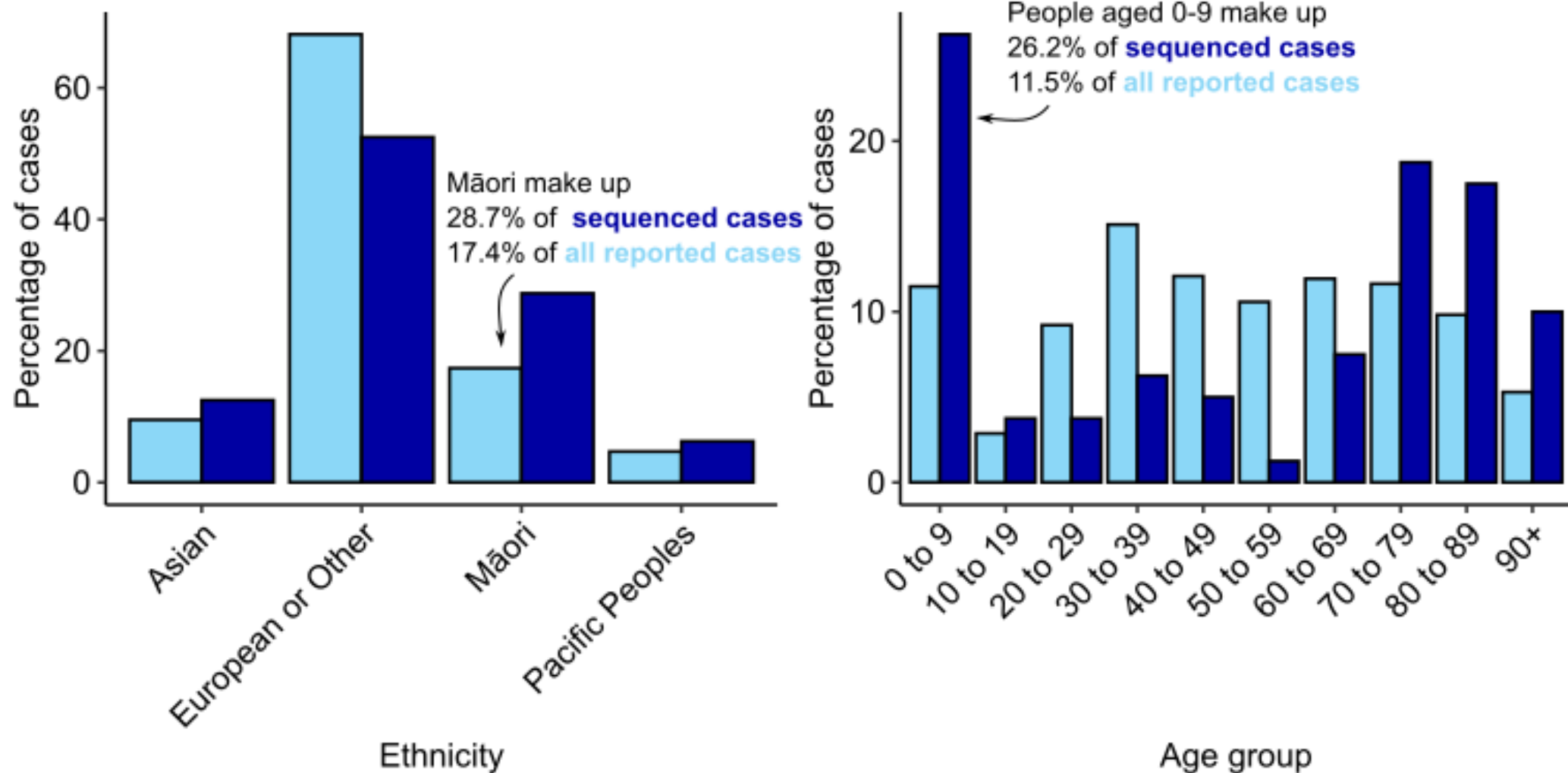


Figure 5. Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported between 11 April – 8 May 2026. **Left:** by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other. **Right:** Distribution of reported and sequenced cases by age. Data as of 12 pm 12 May 2026.

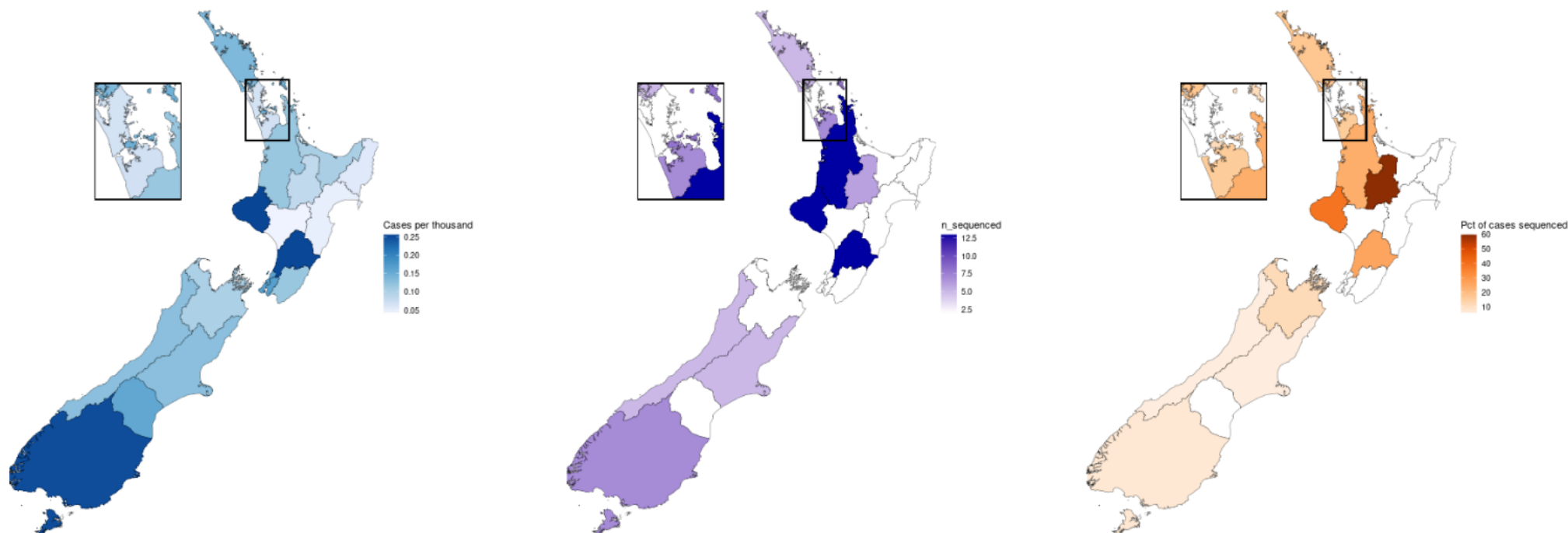


Figure 6. Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 12 pm 12 May 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. RS.1.2 and RS.1.4 are the 2 main sublineages reported under BA.3.2, both with a modest growth advantage over other lineages ([Figure 7](#)).

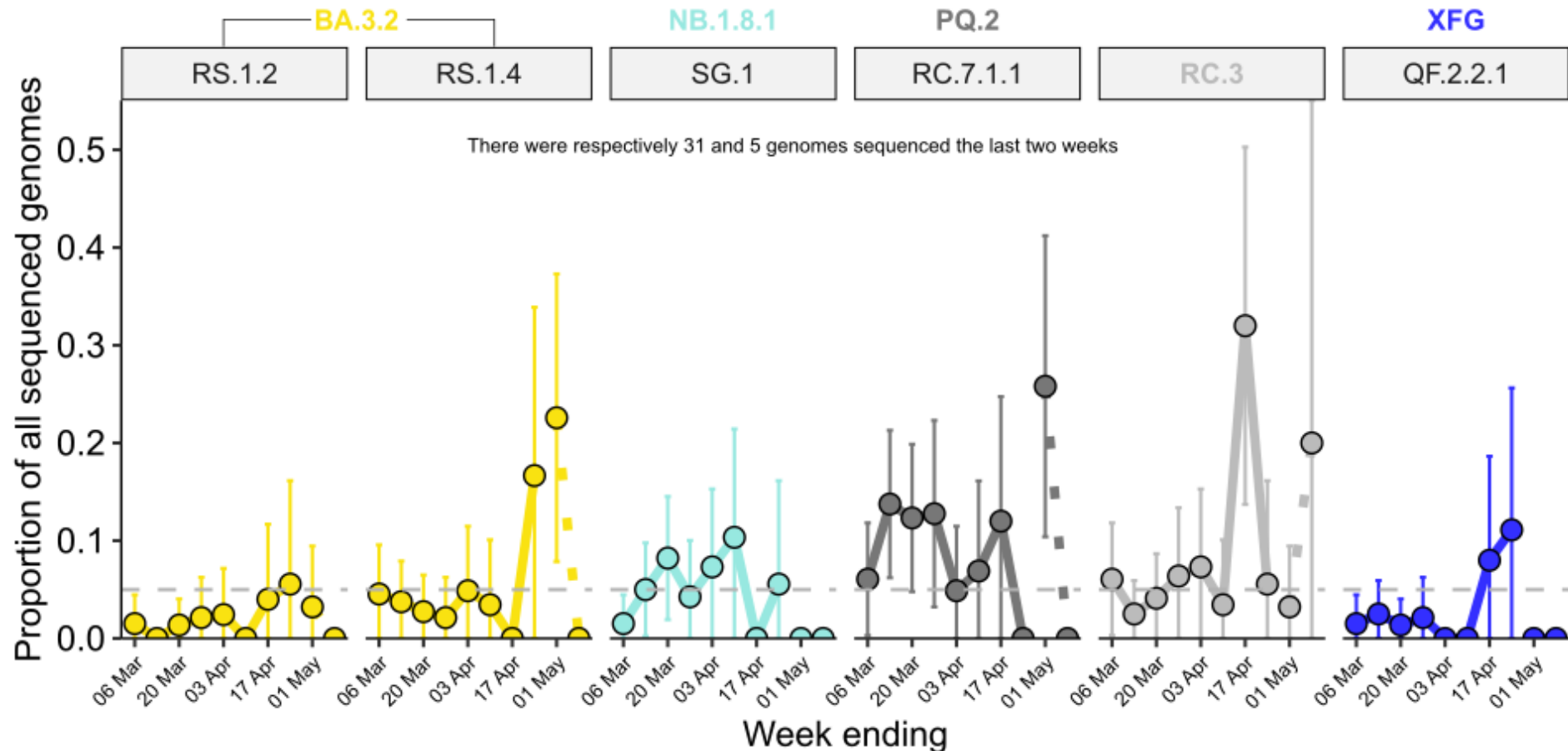


Figure 7. Frequency of specific lineages in clinical surveillance in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the 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 low COVID-19 activity as measured by reported cases and wastewater concentrations ([Figure 1](#)). This relatively low level of activity has been associated with a stable mixture of circulating SARS-CoV-2 lineages ([Figure 3](#); [Figure 4](#)). The BA.3.2 lineage has slowly risen to a frequency of 32.9% among clinical samples and 31.9% in wastewater. NB.1.8.1 (20.3%) and its separately tracked daughter lineage PQ.2 (15.2%) combine for a frequency of 35.5% in clinical samples and 39.1% in wastewater (where these lineages cannot be separated).

The one notable divergence between clinical and wastewater frequencies is RC.3, at 13.9% in clinical samples but only 0.7% in wastewater. The majority of RC.3 samples came from a single region not covered by wastewater surveillance ([Figure 10](#)) suggesting this divergence may reflect a localised geographic cluster rather than a wider trend.

As reported previously the BA.3.2 is seen at a higher frequency in younger people ([Figure 8](#)), with cases <20 almost 9 times more likely to be due to BA.3.2 than any other variant (OR 8.7 [2.7 – 31.0]). BA.3.2 is also more often identified in adult Māori (7 of the 10 BA.3.2 cases reported among Māori in the reporting window are over 20).

Low SARS-CoV-2 levels, reduced reporting and low testing volumes all have an impact on PHF Science's ability to estimate precise growth advantages. Currently, the BA.3.2 lineages shows signs of a moderate daily growth advantage over other tracked variants ([Figure 7](#)[Error! Reference source not found.](#)). This growth advantage comes with a broad confidence interval, underlining the uncertainty caused by a low sample size.

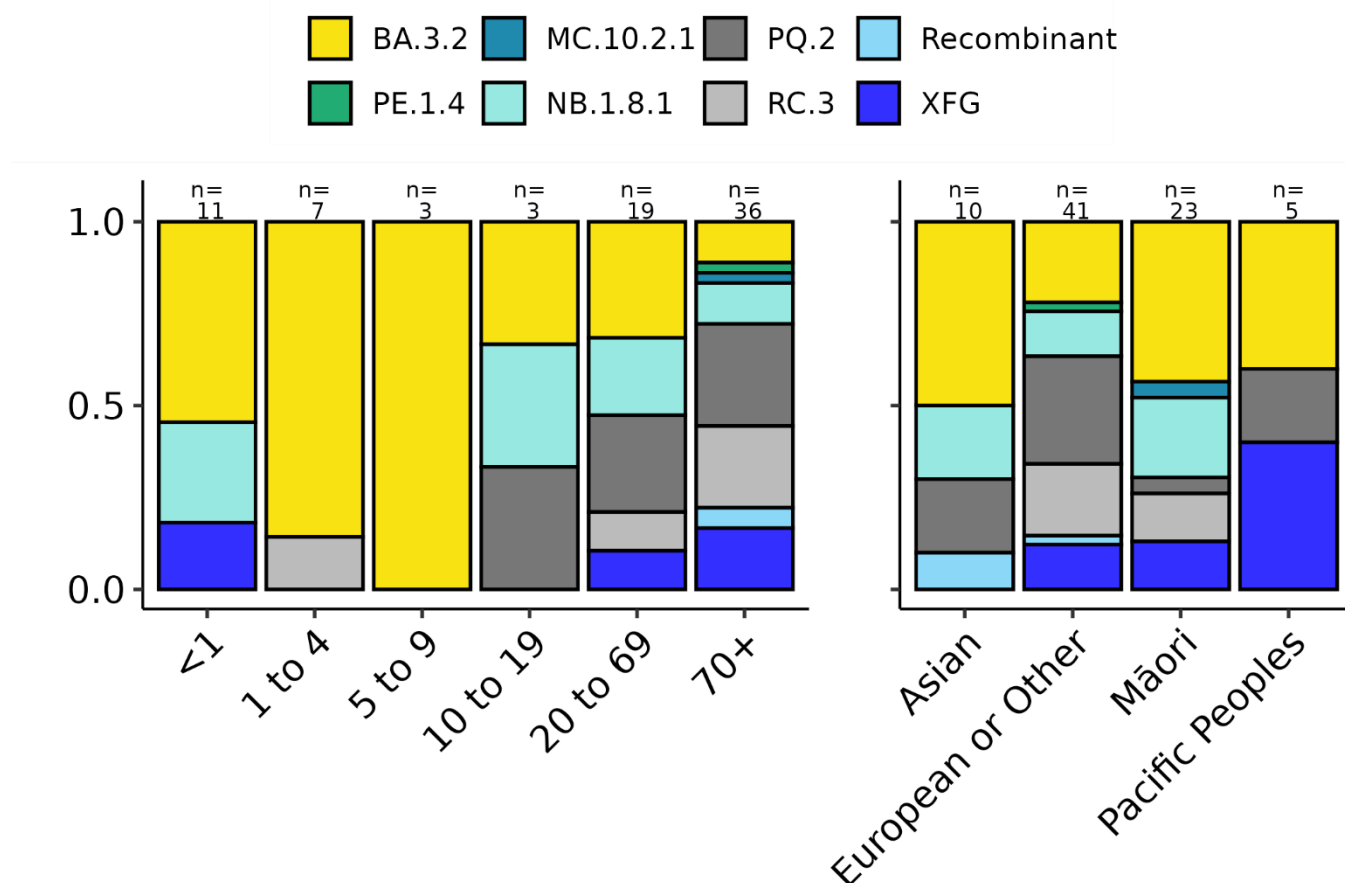


Figure 8. Proportion of tracked variants by age and ethnicity over the reporting period.

Global overview

Trends in Aotearoa New Zealand are broadly consistent with global patterns: low and declining COVID-19 activity, with NB.1.8.1, BA.3.2, and XFG lineages dominant across most comparator countries ([Table 1](#)). Singapore is a notable exception with elevated COVID-19 activity and RF.5 (a lineage that would be reported as JN.1 in this report) dominant. RF.5 has only been sporadically detected in New Zealand to date.

Table 1. International trends

Country/Region	Activity	Test positivity	Main variants	Reporting period
Australia ¹	Decreasing	2.0%	NB.1.8.1 group (33.7%), BA.3.2 (31.4%)	20 Apr–3 May 4 weeks ending 19 April for variants
United States	Low	1.0% ²	XFG sublineages ³	week-ending 2 May
Canada ⁴	Low	1.4%	PQ.2 sublineages	week-ending 2 May
United Kingdom ⁵	Low	~1%	BA.3.2 (50%), XFG (25%)	week-ending 7 May 2 weeks ending 12 April for variants
Europe ⁶	Low	2.1%*	BA.3.2	week-ending 2 May
Hong Kong ⁷	Low	0.45%	NB.1.8.1	week-ending 9 May
China ⁸	Low	1.1%	PQ.2, NB.1.8.1	week-ending 3 May
Singapore ⁹	Increased	14%**	RF.5	week-ending 9 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.

In addition, European data shows early signals of sustained transmission in primary care, though overall burden remains low. Variant data from Africa and South America are based on limited sequences from Ghana and Brazil respectively, all belonging to the XFG lineage.

¹ <https://www.cdc.gov.au/resources/publications/australian-respiratory-surveillance-report-20-april-3-may-2026>

² Surveillance and Data Analytics | Covid | CDC

³ Wastewater Data for COVID-19 Variants | Wastewater Monitoring | CDC

⁴ <https://health-infobase.canada.ca/respiratory-virus-surveillance/covid-19.html>

⁵ National flu and COVID-19 surveillance report: 7 May 2026 (week 19) - GOV.UK

⁶ [erviss.org](https://www.erviss.org) visited 13 May 2026

⁷ COVID-19 & Flu Express (Volume 4), Number 19 (Week 19, 2026)

⁸ https://www.chinacdc.cn/jksj/xgbdyq/202605/t20260512_1835734.html

⁹ <https://www.cda.gov.sg/resources/weekly-infectious-diseases-bulletin-2026>

WGS Hospital Reporting

A total of 79 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 under-represented in hospitalised cases (18.2% of hospitalised cases vs. 38.1% 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 = 2.1, df = 1, p-value = 0.15; [Figure 9](#)).

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.

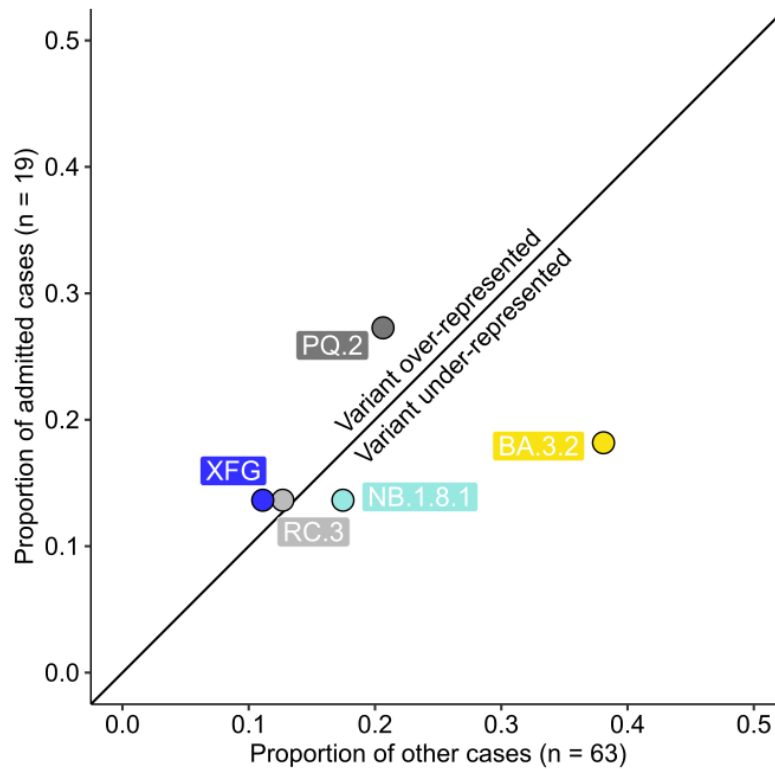


Figure 9. Frequency of variants among cases reported between 11 April – 8 May not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted from the graph and numbers on the margins.

2- Geographical differences in sampling and prevalence

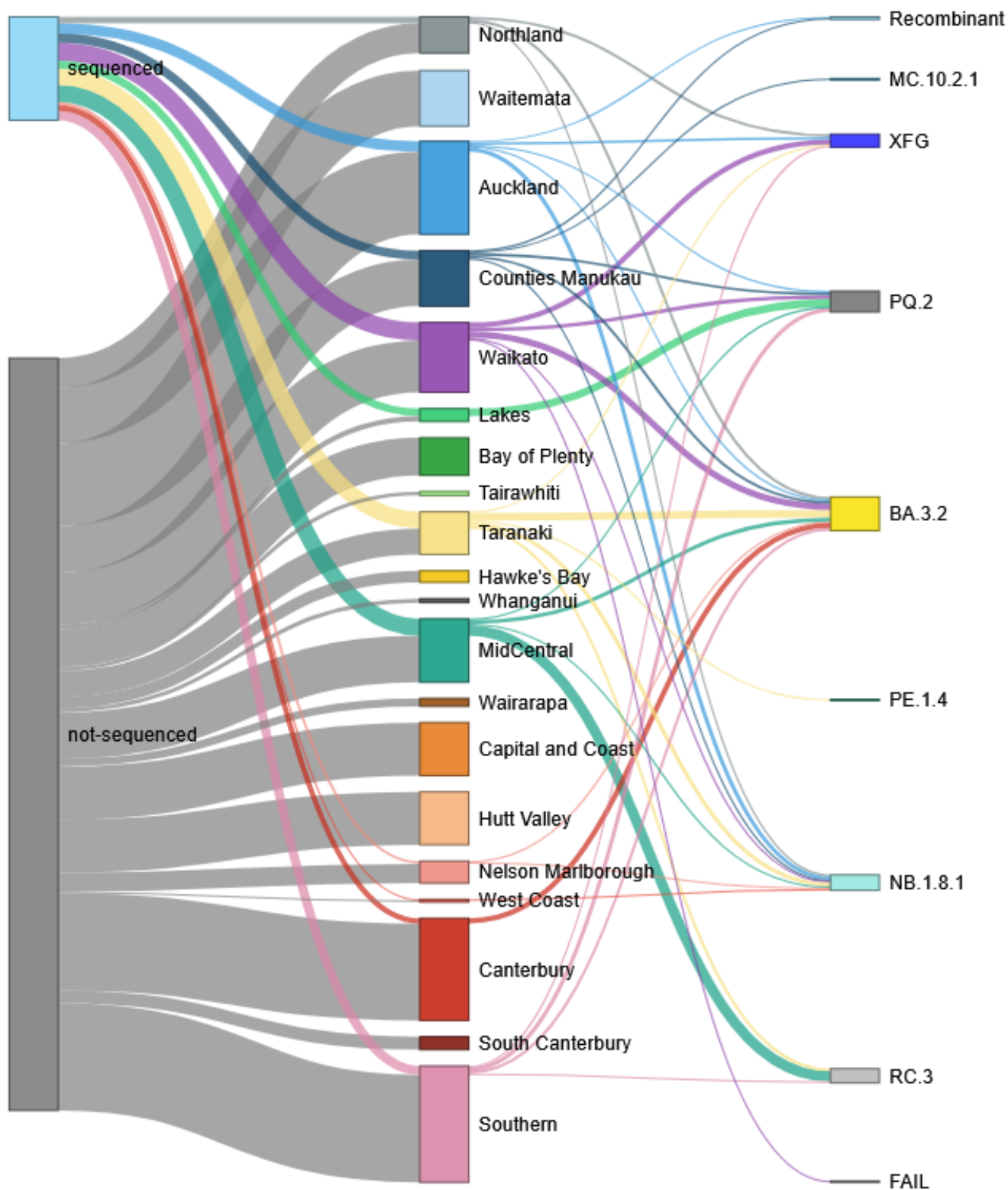


Figure 10. Origin and sequencing results of the 662 cases reported between 11 April – 8 May 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned). Data as of 12pm 12 May 2026.