6 March 2026

COVID-19 Genomics Insights Dashboard (CGID) Report #68

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:

genomes analysed

135

genomes* from cases reported since the last CGI report (30 January 2026)

283

genomes* reported in 2026

70

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

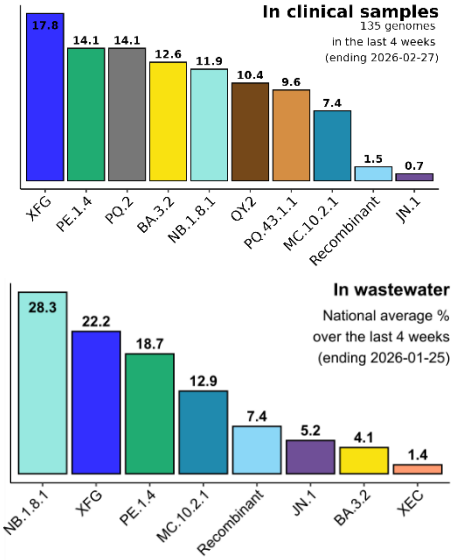
135

samples* in 2026

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

variant & lineage

Several variants are co-circulating



hospital cases

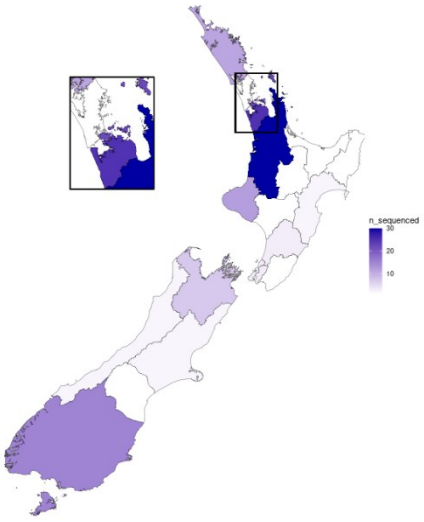
45.5% (55/121*) of cases admitted to hospital with a positive PCR between 31 Jan and 27 Feb have been sequenced to date.

The approximate composition of hospitalised cases:

- **PE.1.4 21.8%**
- **XFG 20.0%**
- **QY.2 14.5%**
- **BA.3.2, MC.10.2.1, PQ.2 each 9.1%**
- **NB.1.8.1 7.5%**
- **PQ.43.1.1 5.5%**

*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 31 January – 27 February 2026

Key trends and insights

- There is currently no dominant variant in either wastewater or clinical data.
- The highly divergent BA.3.2 lineage continues to spread in Aotearoa and represents around 12.6% of sequences in clinical surveillance.
- We started tracking **QY.2*** (XFG child) and **PQ.43.1.1** (NB.1.8.1 child) that are slowly emerging and represent 10.4% and 9.6% of sequences
- We investigated the suggestions that BA.3.2 may be more widespread among children

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

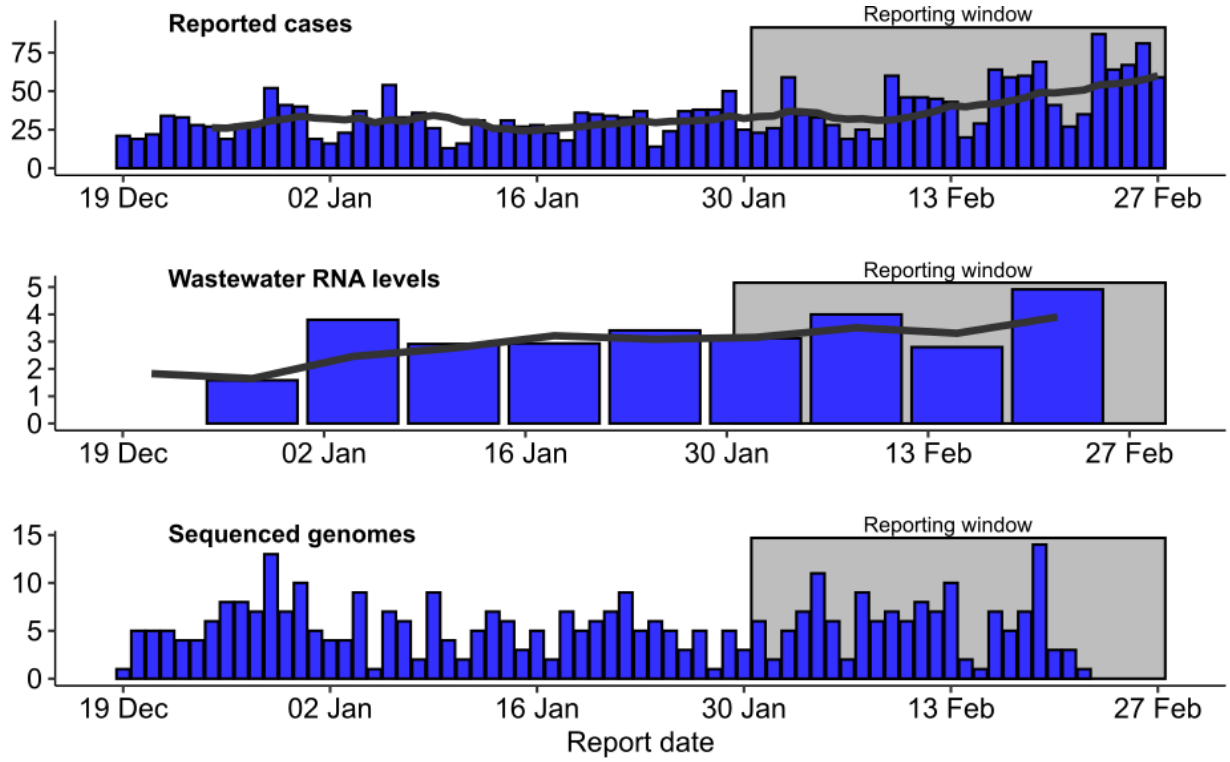


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater. Bottom: The number of sequenced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

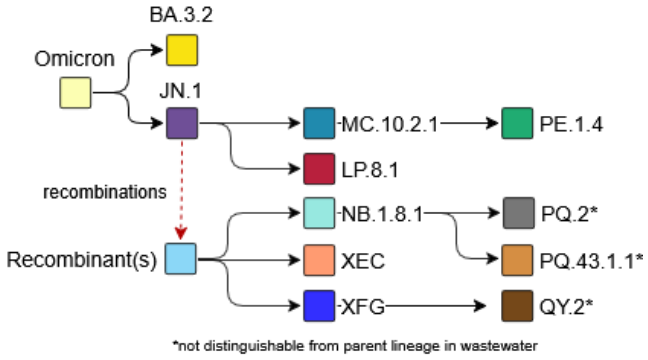


Figure 2. *Relationships between the variants tracked in this report.*

Overview of variants from clinical samples

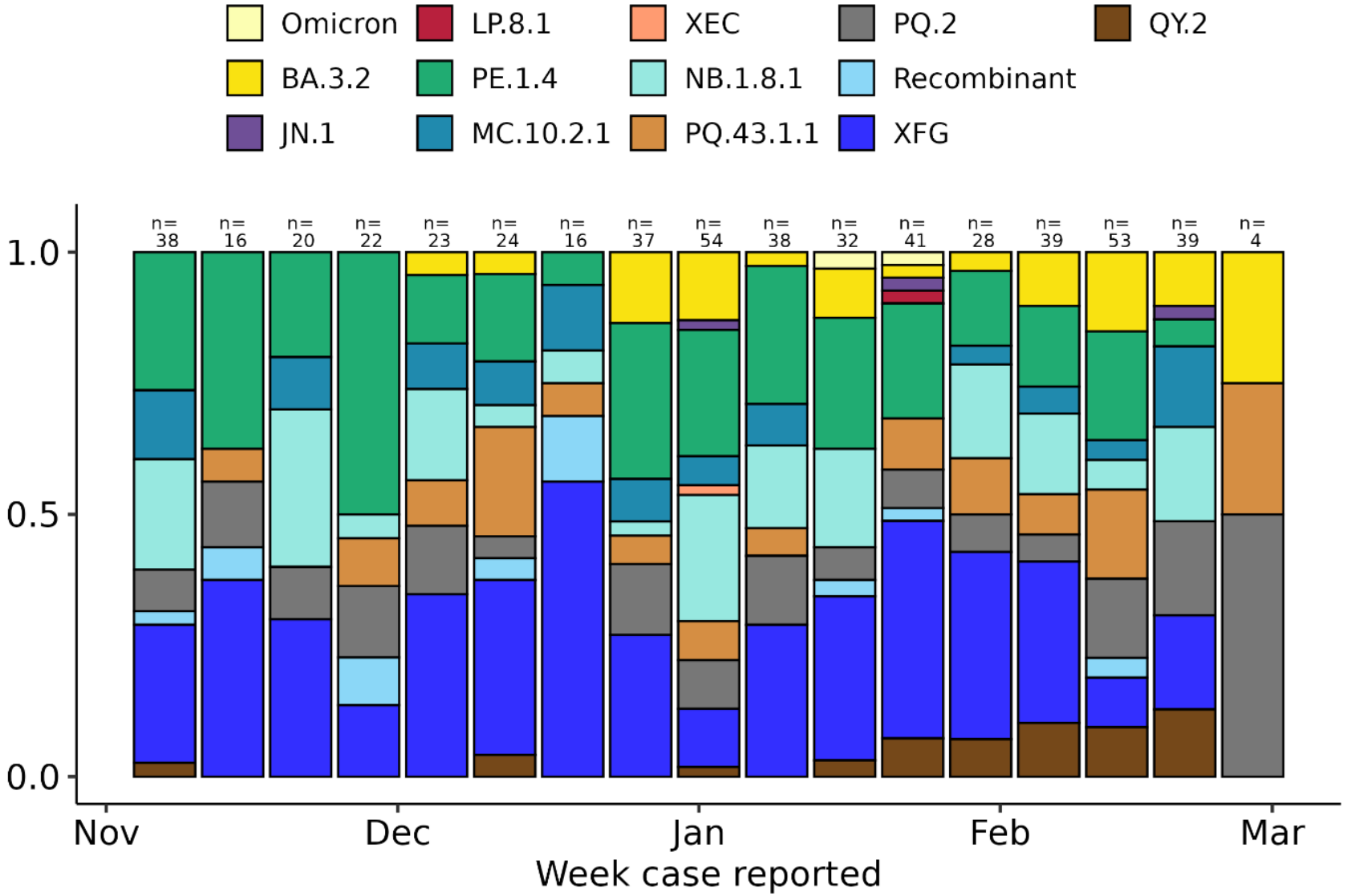


***Figure 3**. Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based 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 https://poops.nz/ and summarised in **Figure 4**. Due to assays limitations, **for the wastewater analysis, PQ.2 and PQ.43.1.1 are included in the NB.1.8.1 lineage and QY.2 in the XFG lineage.** Note the most recent wastewater results include data from weeks prior to the 4 weeks used as a reporting-window for clinical WGS.

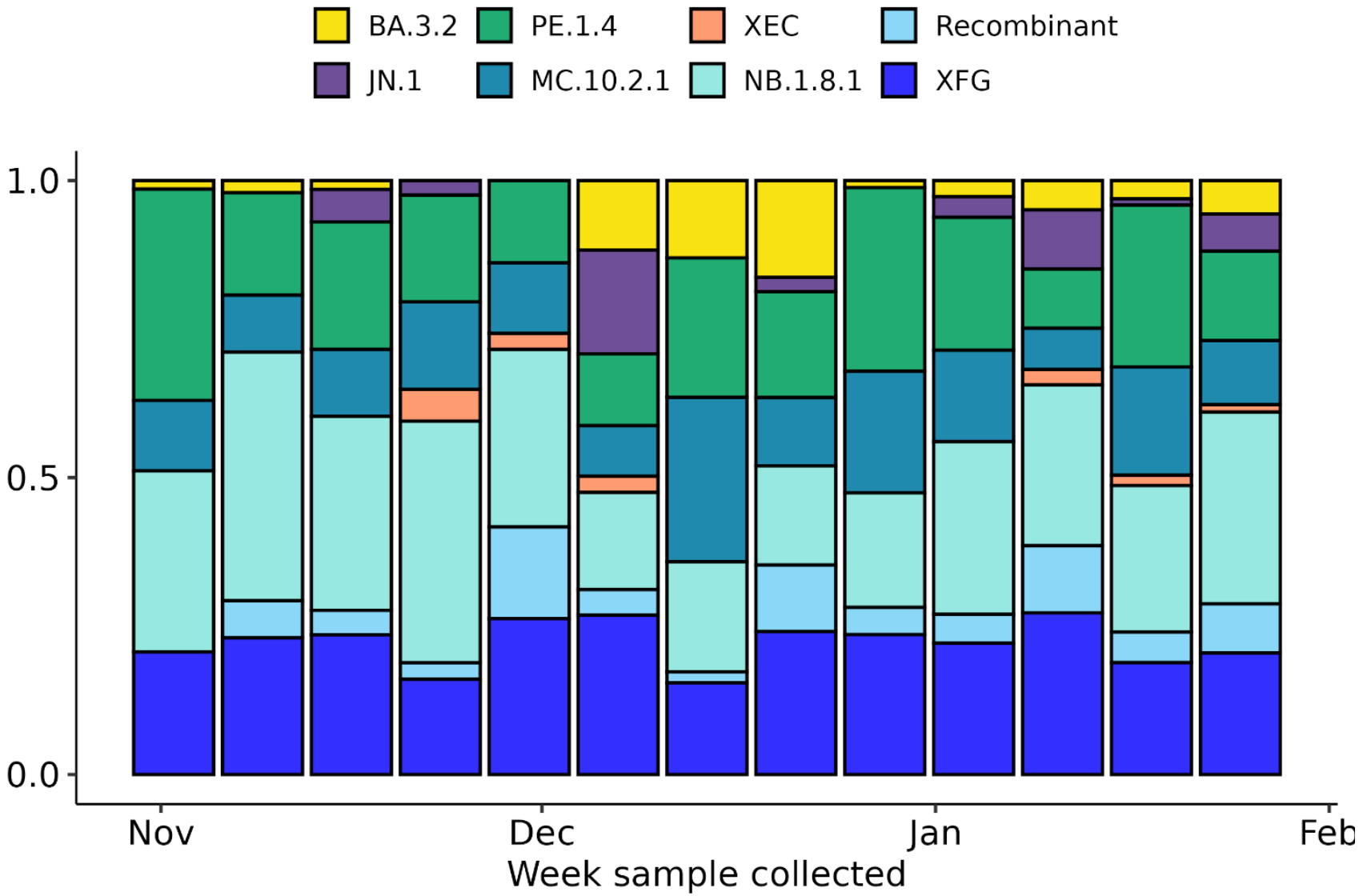


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

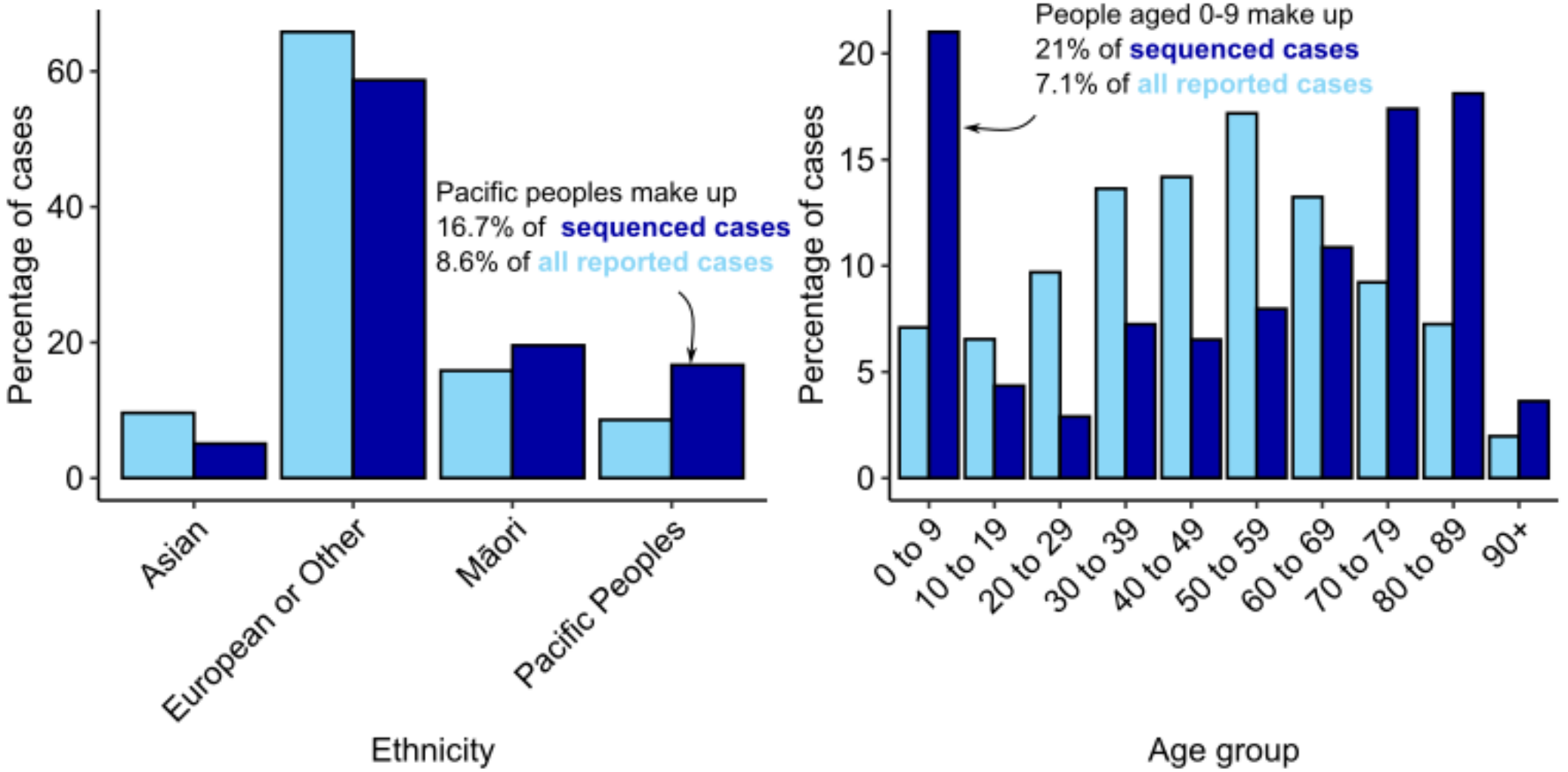


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported between 31 January – 27 February 2026.* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 10am 4 March 2026.*

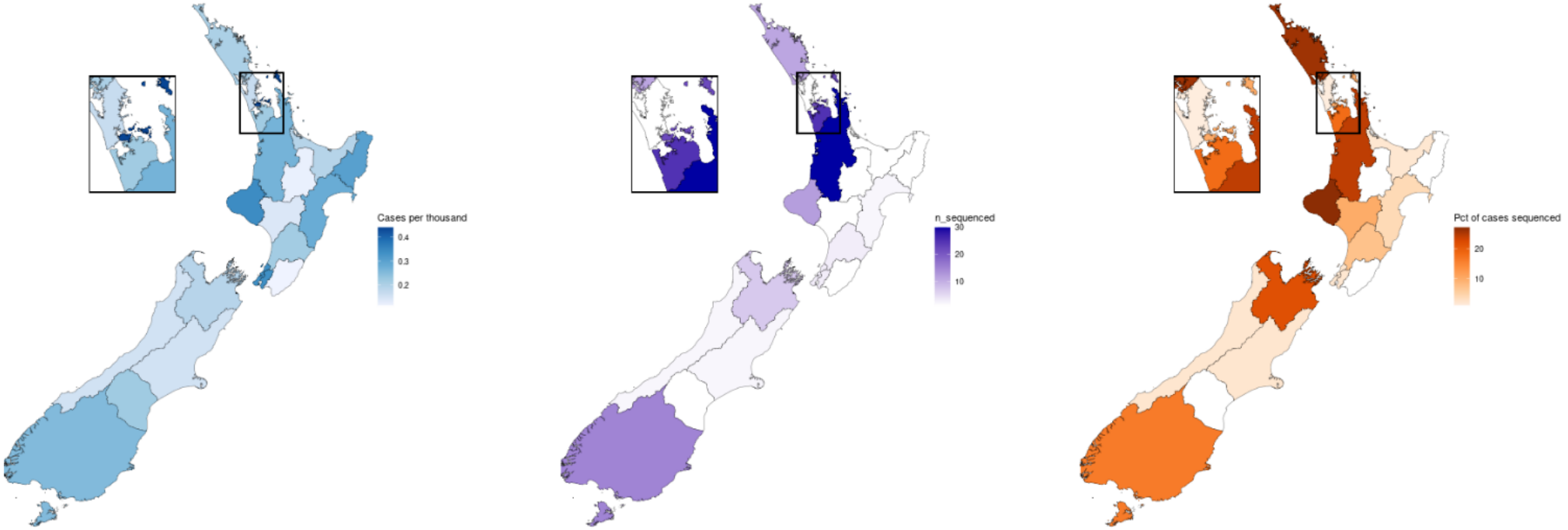


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 10am 3 March 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.

Alongside PQ.43.1.1 and QY.2 that we started to track individually from NB.1.8.1 and XFG respectively, RC.3 (PQ.2 child) and PE.1.7 (MC.10.2.1 child) are worth mentioning (**Figure 7**). PHF Science will continue to closely monitor those variants.

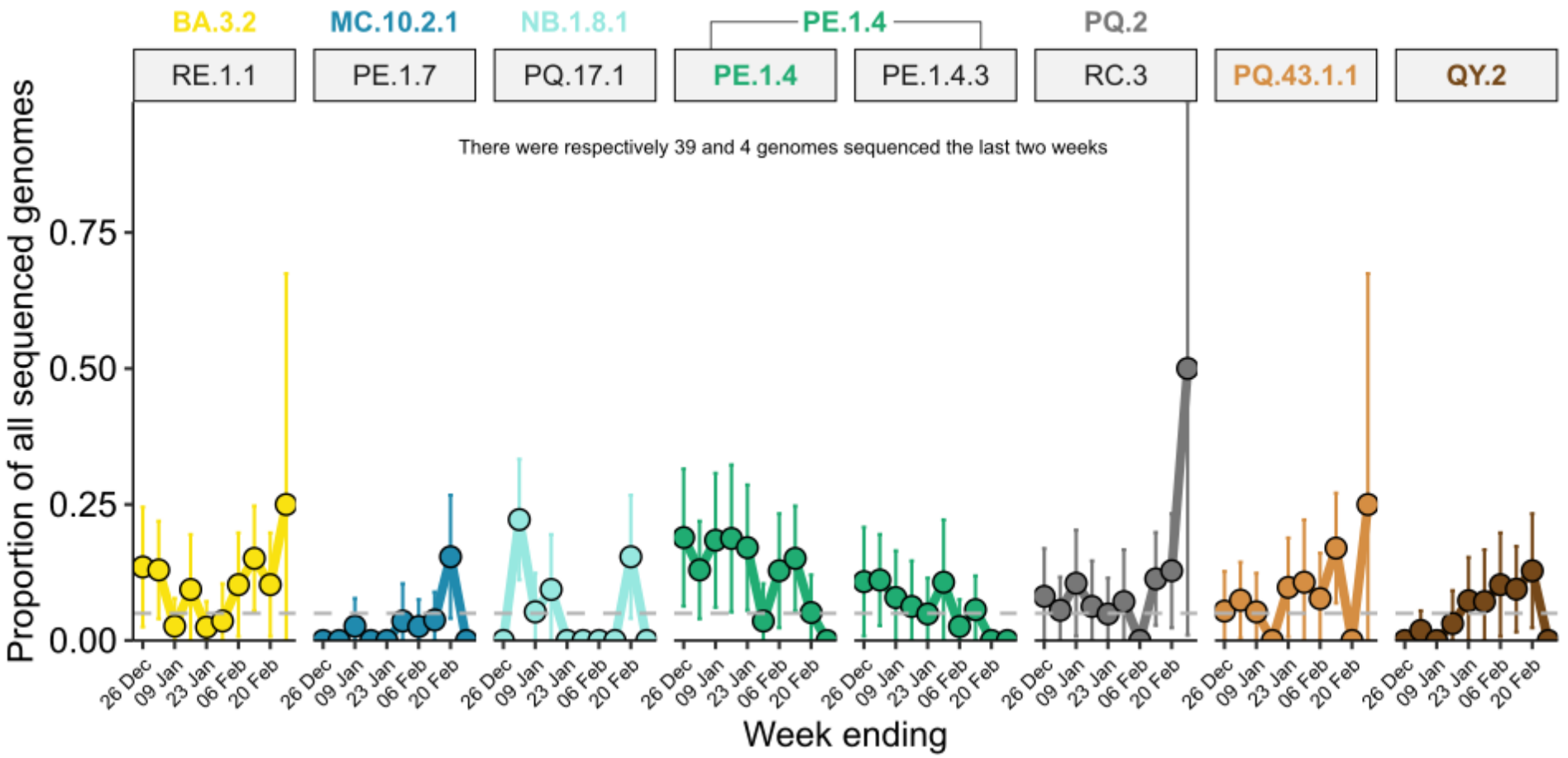


Figure 7. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the rest of this report. The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

Geographical differences in sampling and prevalence

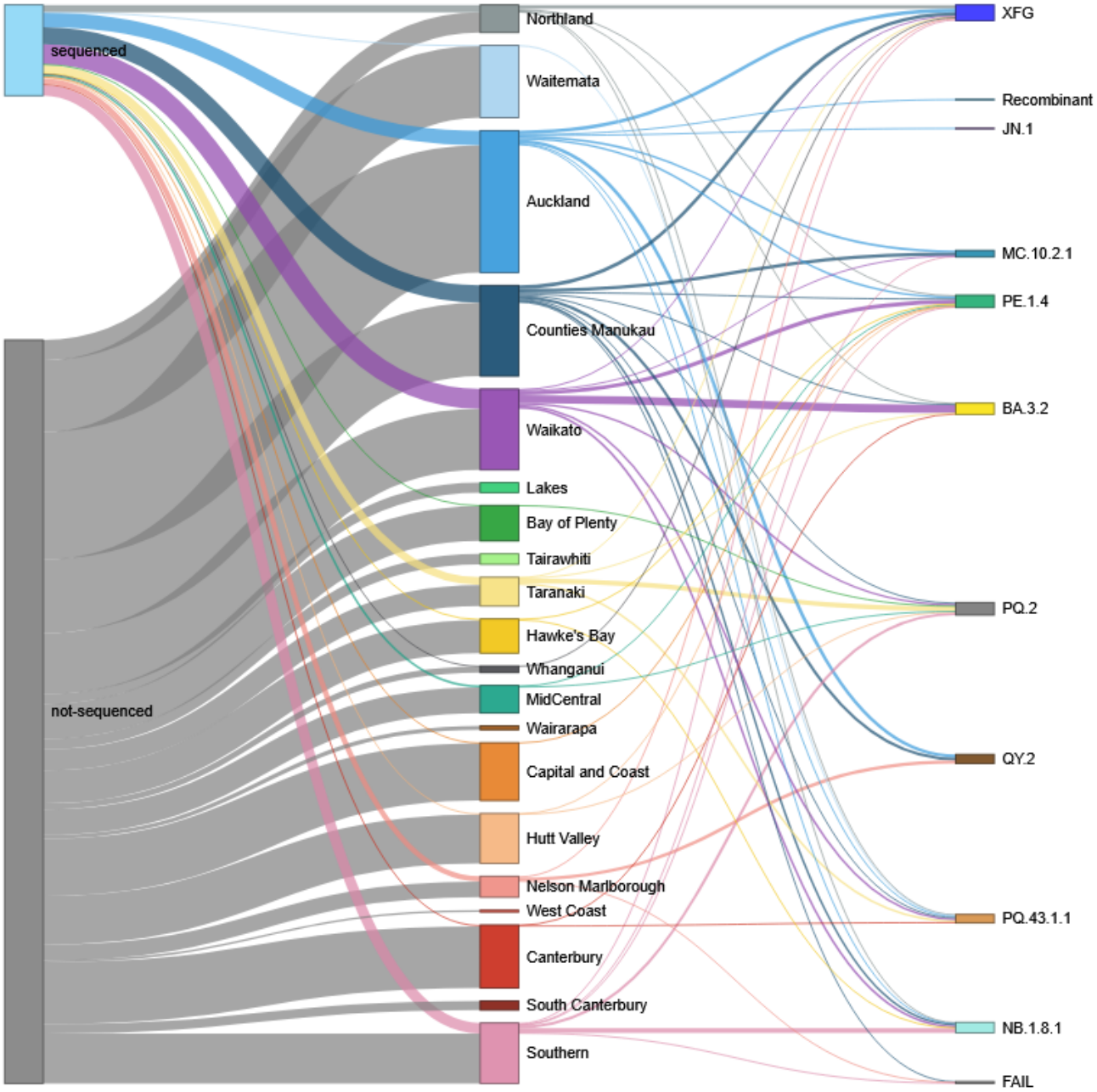


Figure 8. *Origin and sequencing results of the 1269 cases reported between 31 January – 27 February 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned, Omicron). Data as of 10am 4 March.*

WGS Hospital Reporting

A total of 55 genomes have been sequenced from patients admitted to hospital with COVID-19 infection **since the last report and** within the reporting period. Despite PE.1.4 appearing slightly over-represented in hospitalised cases, 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 = 1;**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.

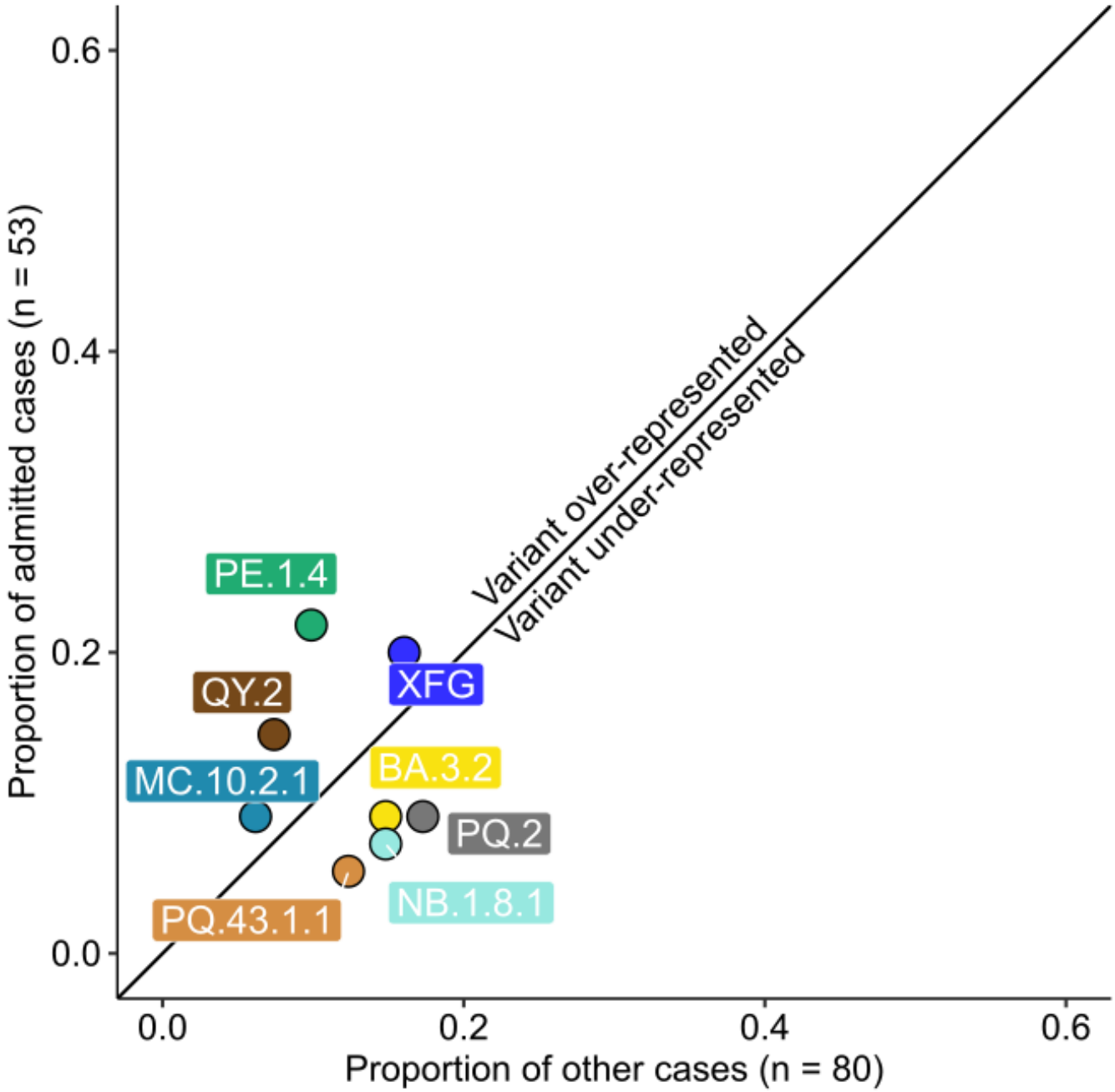


Figure 9. *Frequency of variants among cases reported between 31 January – 27 February not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted from the graph and numbers on the margins.*

Are cases due to BA.3.2 more frequent in children?

Data from other countries hints at a possible link between the growth of BA.3.2 lineages and an increased incidence of COVID-19 in children and younger people. In Aotearoa, BA.3.2 appears somewhat more frequent in children under 10 (8 of 28 genomes) compared to older cases (9 of 107 genomes, **Figure 10**). However, the number of sequenced genomes in the reporting period is not sufficient to draw conclusions.

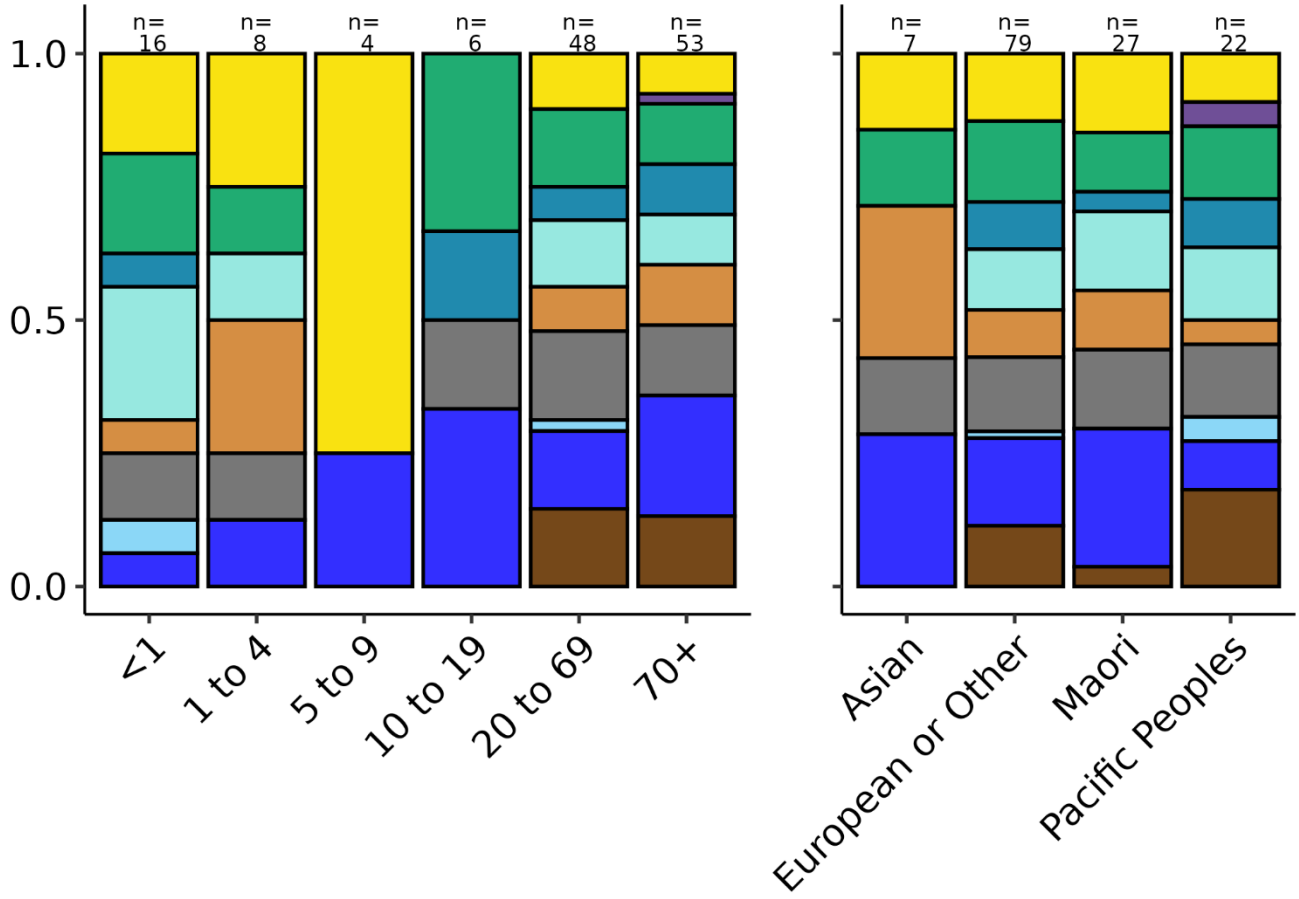


Figure 10. *Proportion of tracked variants by age and ethnicity over the reporting period.*