5 September 2025

COVID-19 Genomics Insights Dashboard (CGID) Report #63

CGI provides an overview of SARS-CoV-2 genomic surveillance across Aotearoa New Zealand. It aims to explore and explain how whole-genome sequencing (WGS) complements wastewater and other epidemiological data to support public health decision-making. As SARS-CoV-2 continues to adapt and mutate, the CGI will highlight scientific research on viral evolution in New Zealand and overseas.

Summary Infographic and Insights:

genomes analysed

253

genomes* from cases reported since the last CGI report (1 August 2025)

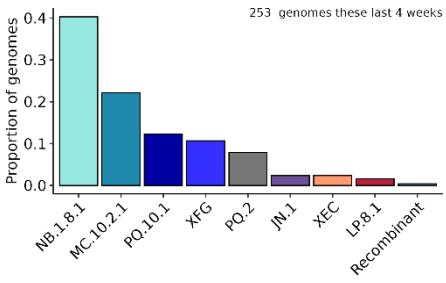
2008

genomes* reported in 2025

*Number of genomes successfully sequenced. Number processed is higher due to failed WGS attempts and cases sequenced multiple times.

variant & lineage

NB.1.8.1 is declining but remains dominant (40%), above MC.10.2.1 (22%) with PQ.10.1 and PQ.2 increasing (12% and 8%), and XFG stable (11%) in the last four weeks



hospital cases

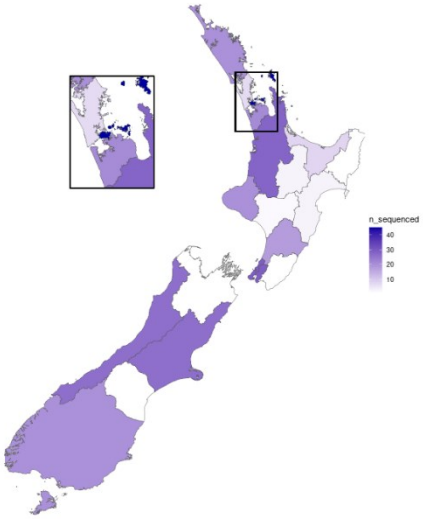
36% (91/253*) of cases admitted to hospital with a positive PCR between 2 and 29 August have been sequenced to date.

The approximate composition of hospital cases:

- **NB.1.8.1 40.7%**
- **XFG 14.3%**
- **MC.10.2.1 13.2%**
- **PQ.10.1 13.2%**
- **PQ.2 8.8%**

*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 samples



Number of SARS-CoV-2 genomes sequenced for cases reported between 2 August – 29 August

Key trends and insights

- NB.1.8.1 remains the dominant variant in the country but has started to decline. In the last four weeks it accounts for 40.3% of cases, with a mean prevalence of 53% in wastewater.
- Two of its many subvariants PQ.10.1 and PQ.2 are showing a growth advantage over NB.1.8.1 and are now tracked separately.
- XFG, the dominant lineage overseas, is stable at low levels in NZ, with 10.7% of sequences and a mean prevalence of 18% in wastewater.
- The highly divergent BA.3.2 lineage that emerged in late 2024 in South Africa and is spreading in Western Australia has not (yet?) been detected in Aotearoa.
- The 'NZ-made' MC.10.2.1 variant remains stable at 22.1%. We provide some insights in this report as to why it has not been replaced by new sublineages.

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

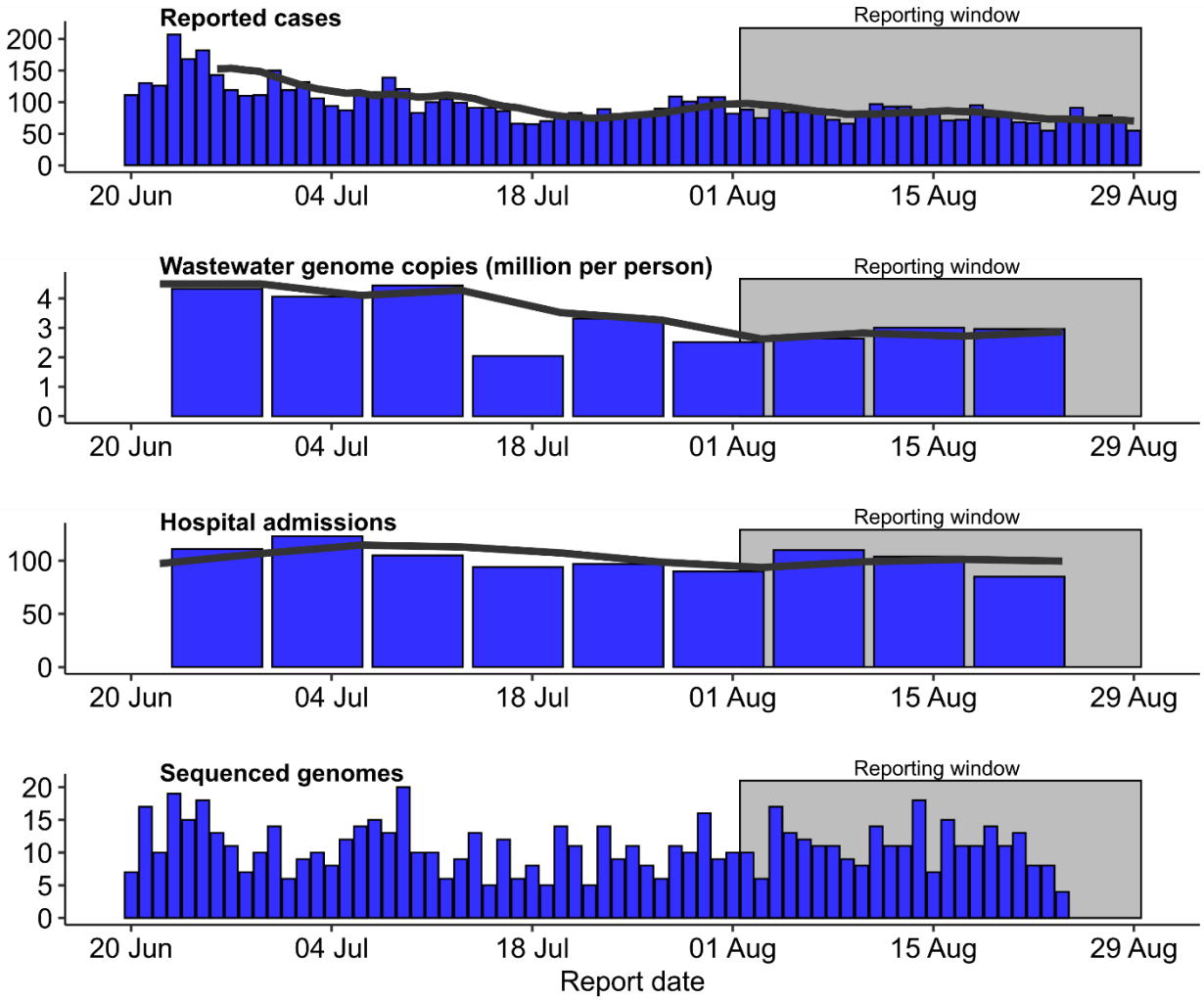


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Top Middle: Trends in wastewater detections. Bottom Middle: Number of patients admitted with COVID-19 per week. Bottom: The number of sequenced genomes from cases reported on a given day. In each subplot, the open rectangle represents the period since the last CGI report and the shaded rectangle is the current reporting window used for summary statistics in this report. Data as of 9am 5 September*

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.

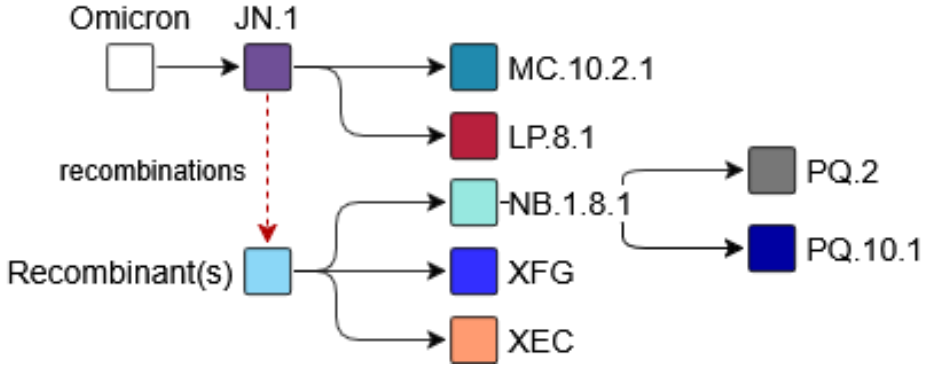


Figure 2. *Relationships between the variants tracked in this report.*

Overview of variants from clinical samples

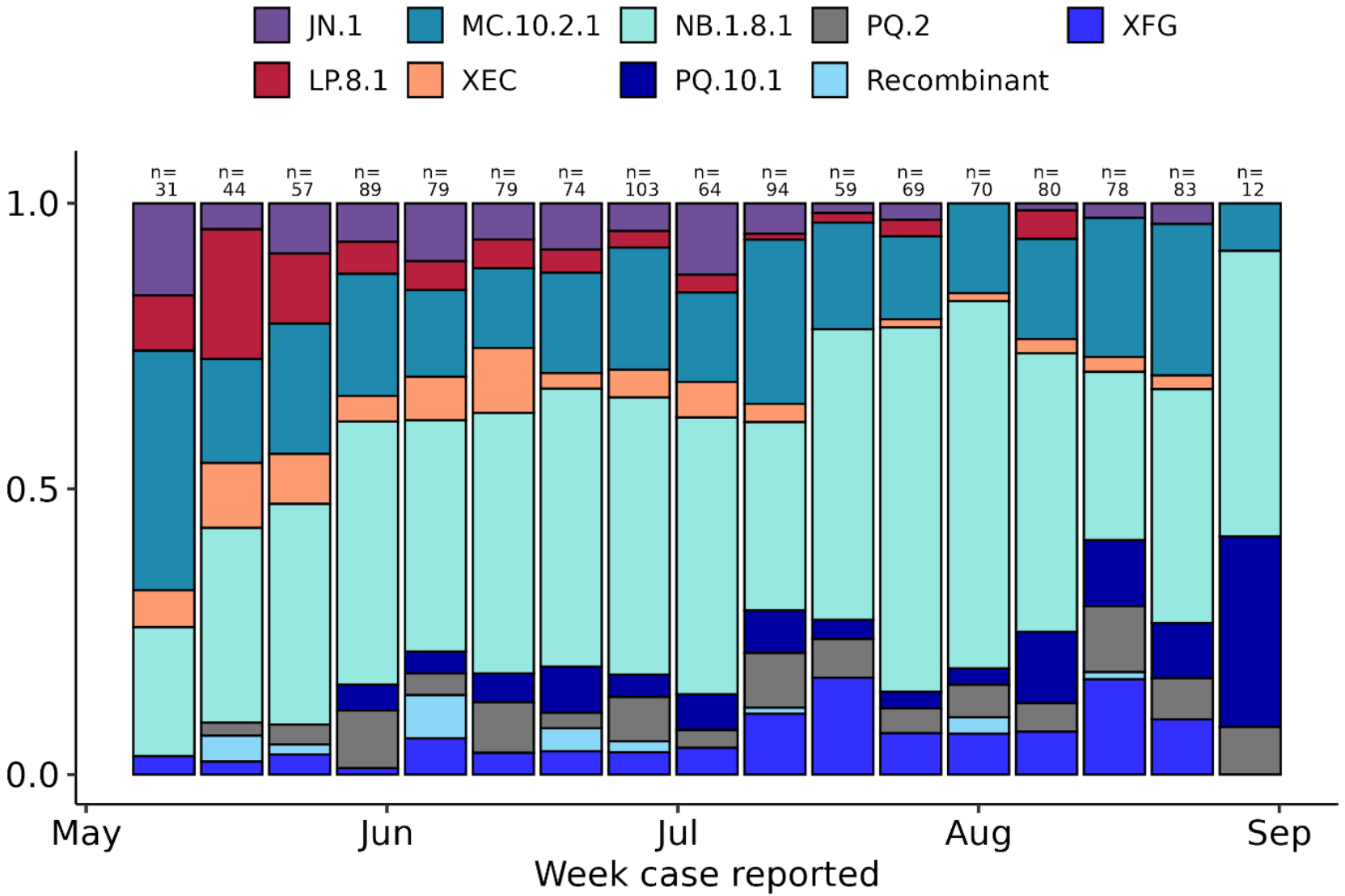


Figure 3. *Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based on the number of genomes indicated above each bar. Tracked lineages are defined in* ***Figure 2****.*

Overview of variants from wastewater samples

Wastewater surveillance data from 11 sentinel sites across New Zealand for the week ending 31 August are available via PHF Science's online dashboard https://poops.nz/ and summarised in **Figure 4**. Due to assay limitations, some lineages tracked in this report are grouped with their parent (e.g., PQ.2 within NB.1.8.1; certain NB.1.8.1 subvariants, including PQ.17, under PQ.10.1). Results broadly align with clinical data, with XFG slightly higher and MC.10.2.1 showing a late-July trough; JN.1 appears elevated as it includes the KP.3 clade circulating at low-level, which is tracked separately on the dashboard.

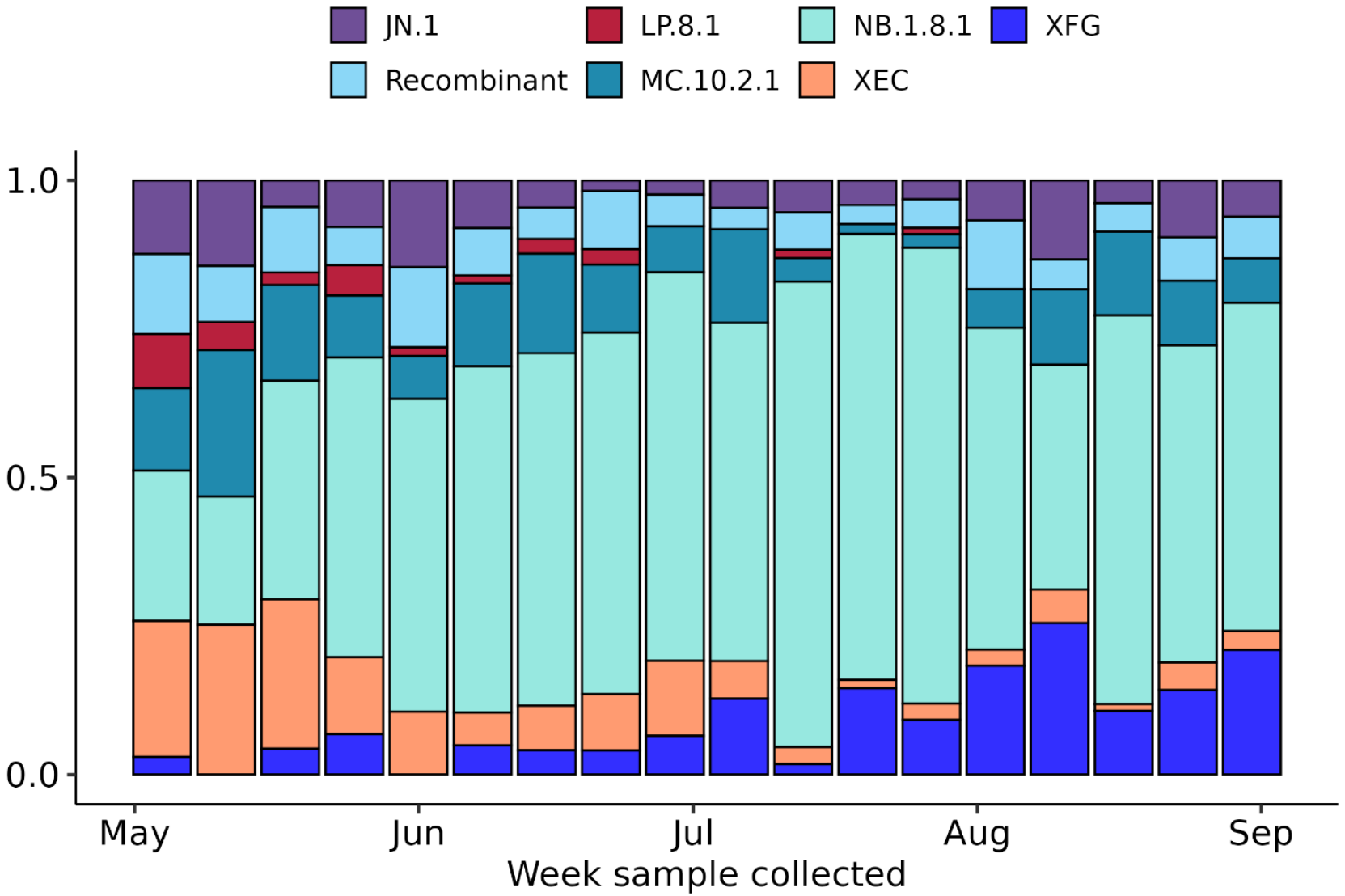


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

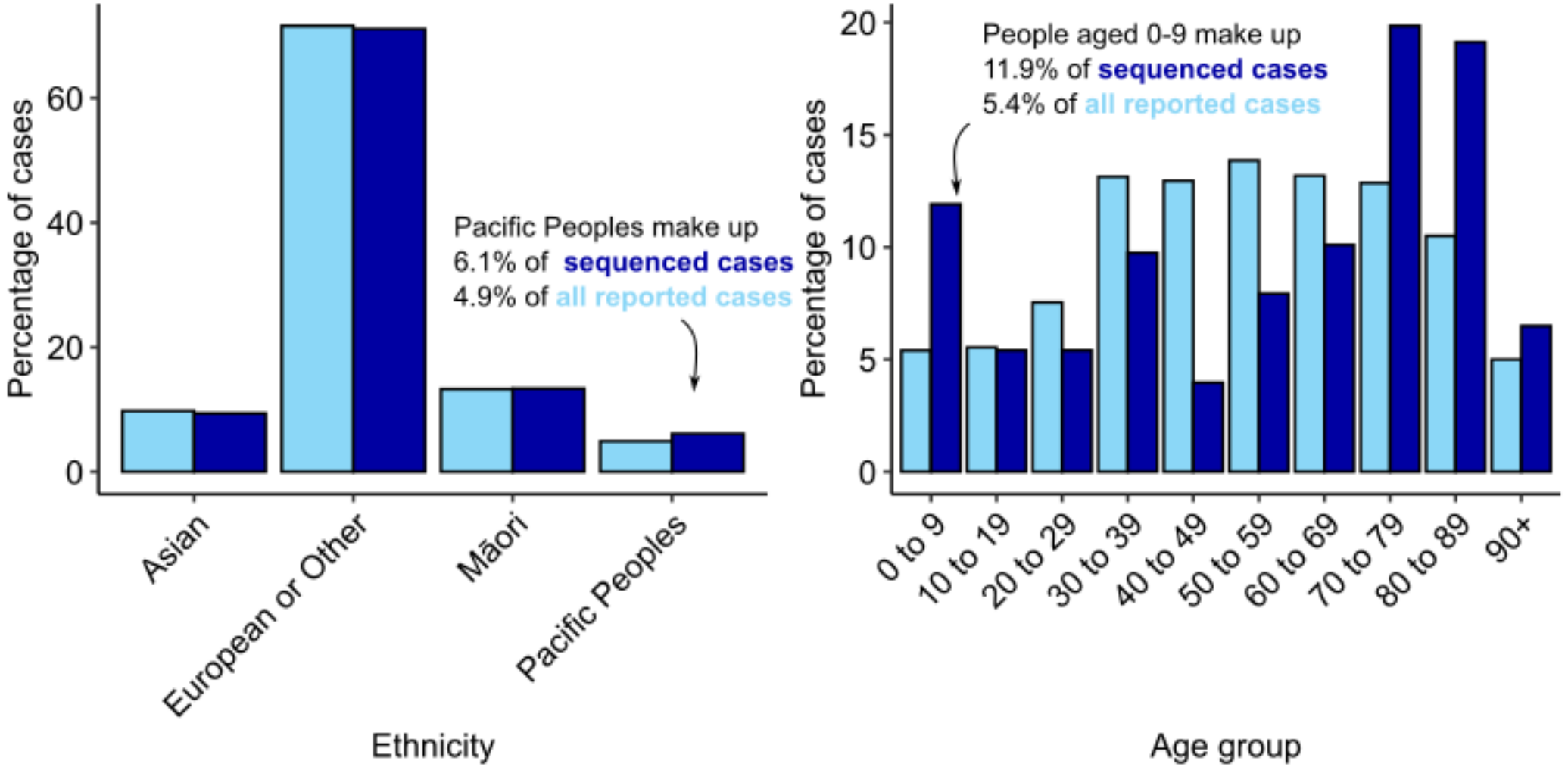


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported between 3 May – 30 May.* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 10am 3 September.*

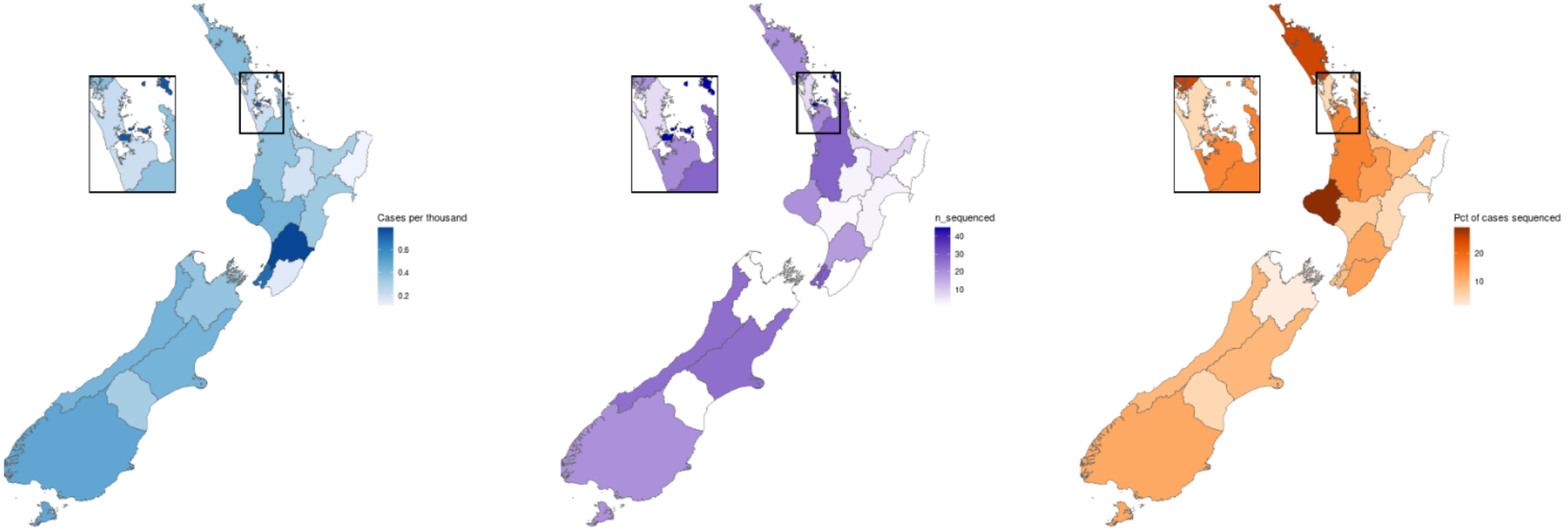


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data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

Emerging lineages

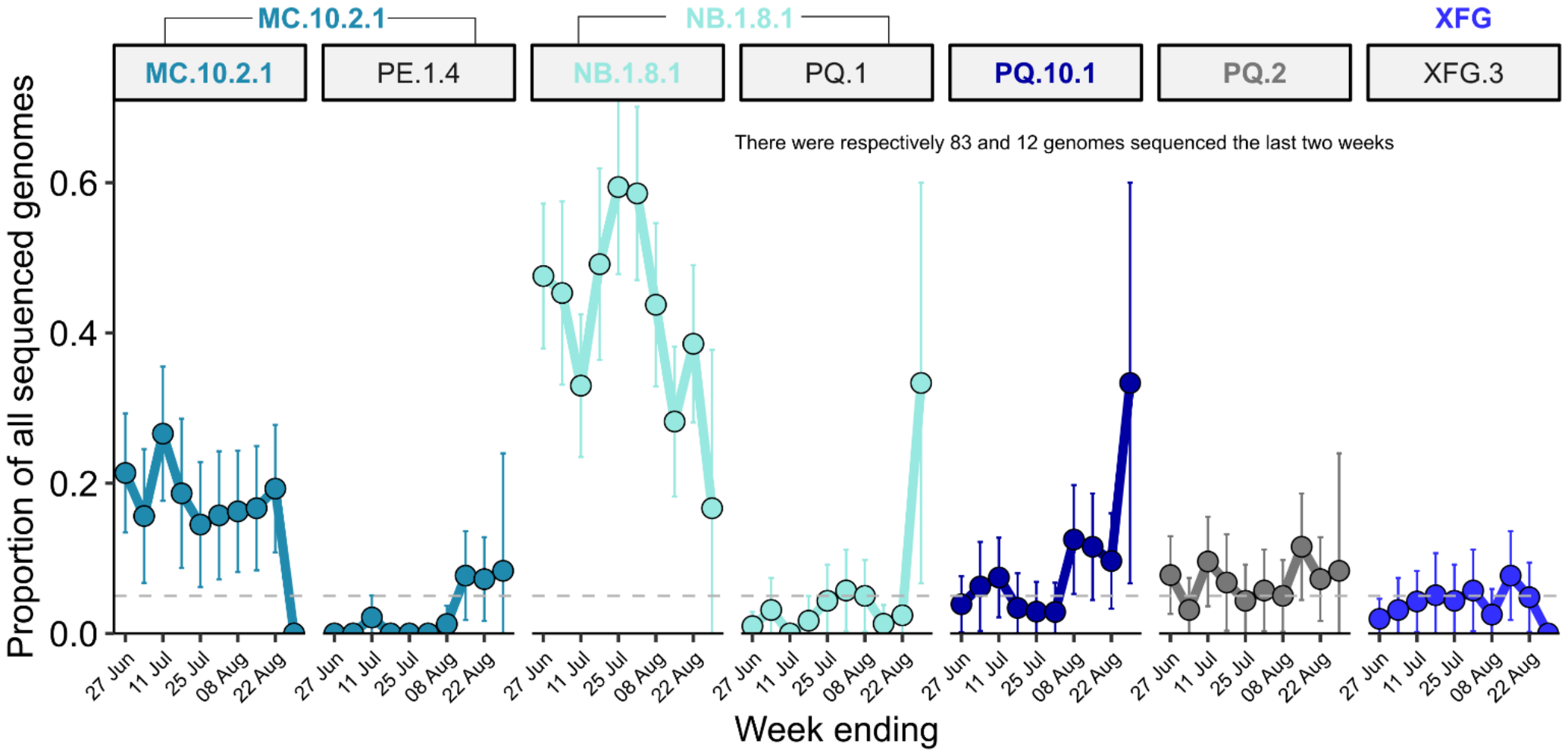


Figure 7. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the rest of this report. The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

Geographical differences in sampling and prevalence

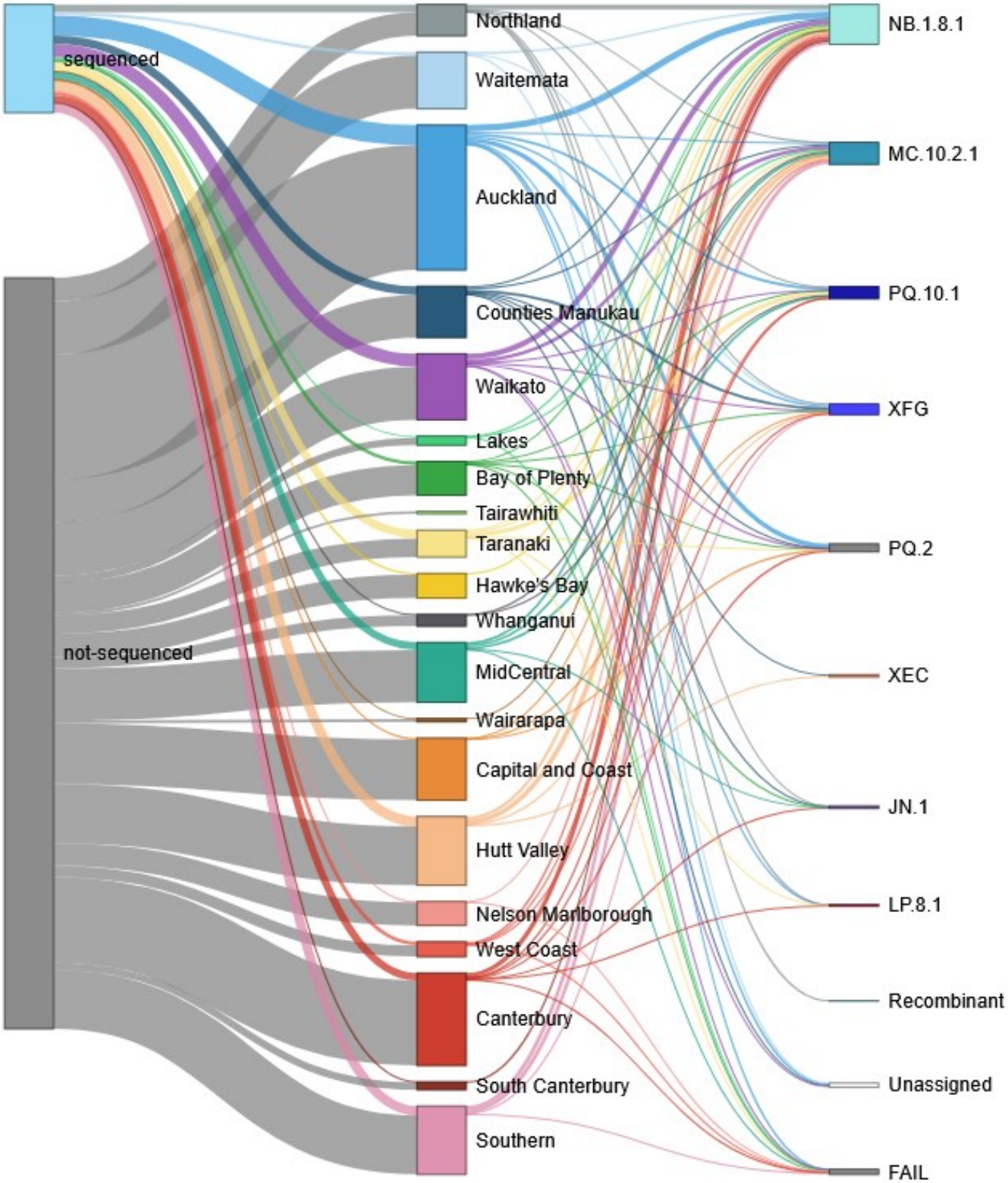


Figure 8. *Origin and sequencing results of the 2200 cases reported between 2 August – 29 August per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a lineage (Unassigned). Data as of 9am 3 September.*

WGS Hospital Reporting

A total of 91 genomes have been sequenced from patients admitted to hospital with COVID-19 infection **since the last report and** within the reporting period. Despite XFG appearing slightly over-represented and MC.10.2.1 under-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.

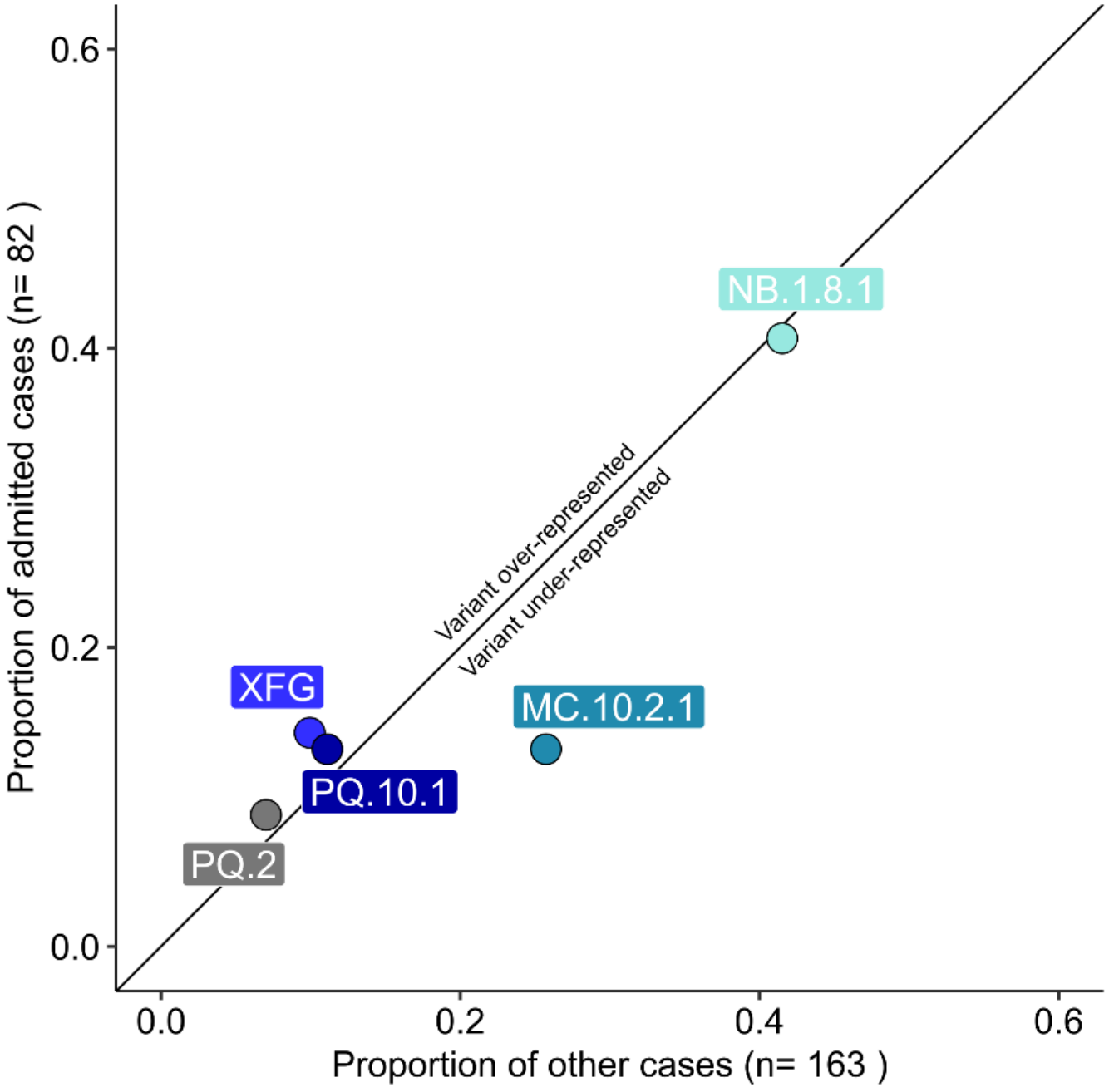


Figure 9. *Frequency of variants among cases reported between 2 August – 29 August not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted from the graph and numbers on the margins.*