10 October 2025

COVID-19 Genomics Insights Dashboard (CGID) Report #64

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

182

genomes* from cases reported since the last CGI report (29 August 2025)

2321

genomes* reported in 2025

62

samples* collected from 11 sentinel wastewater sites

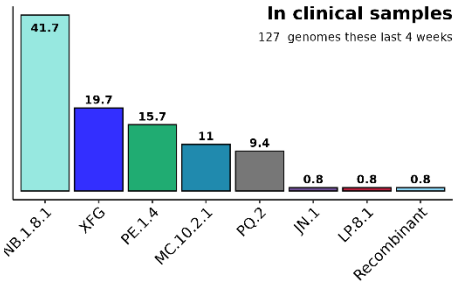
757

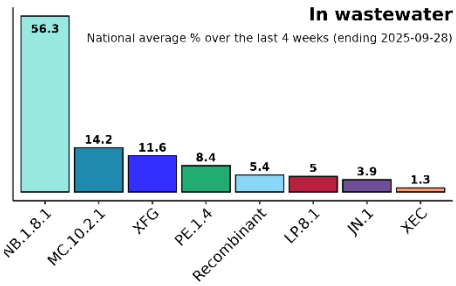
samples* in 2025

*Number of genomes/samples 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





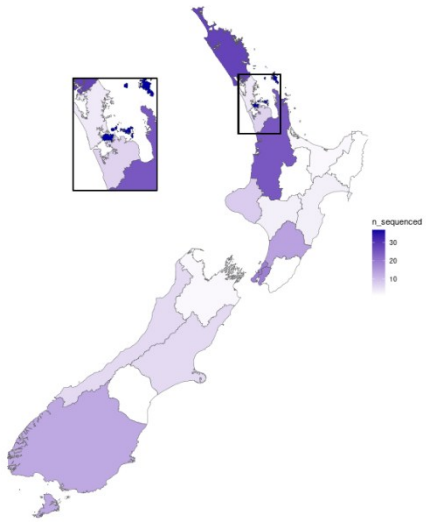
hospital cases

37% (53/142*) of cases admitted to hospital with a positive PCR between 6 September and 3 October have been sequenced to date. The approximate composition of hospital cases:

- **NB.1.8.1 41.5%**
- **XFG 22.6%**
- **MC.10.2.1 15.1%**
- **PE.1.4 11.3%**
- **PQ.2 7.5%**

*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 30 August – 03 October

Key trends and insights

- NB.1.8.1 remains the dominant variant but is continuing to decline, representing 41.7% of cases over the past four weeks. In wastewater, NB.1.8.1 and PQ.2 (which cannot be distinguished in the current assay) combined have a mean frequency of 56%.
- XFG, the dominant lineage in Europe and the Americas, remains stable, with 19.7 % of sequences and a mean prevalence of 12% in wastewater.
- We started tracking PE.1.4 independently from its parent lineage MC.10.2.1, this lineage is showing the highest growth in both clinical (15.7%) and wastewater data (8.4%).
- The highly divergent BA.3.2 lineage that continues spreading in Western Australia has not been detected in Aotearoa.

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

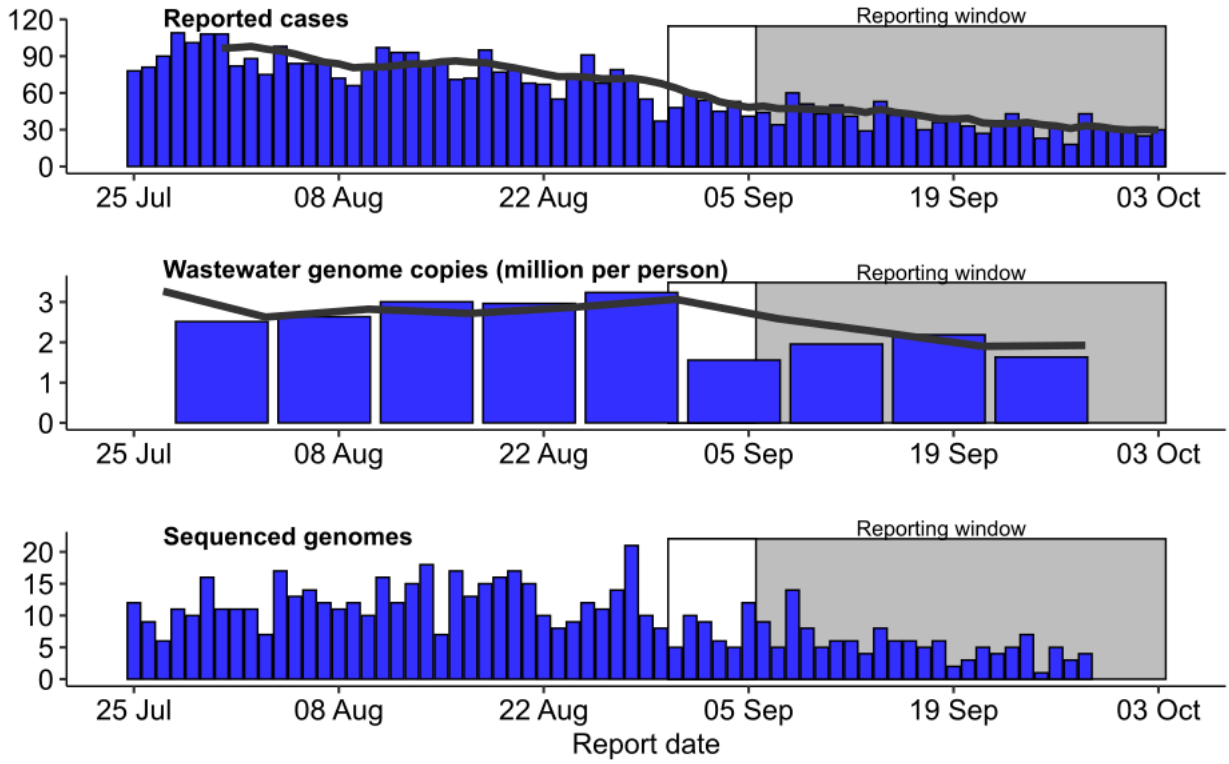


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in wastewater detections. Bottom: The number of sequenced genomes from cases reported on a given day. In each 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 10am 7 October*

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.

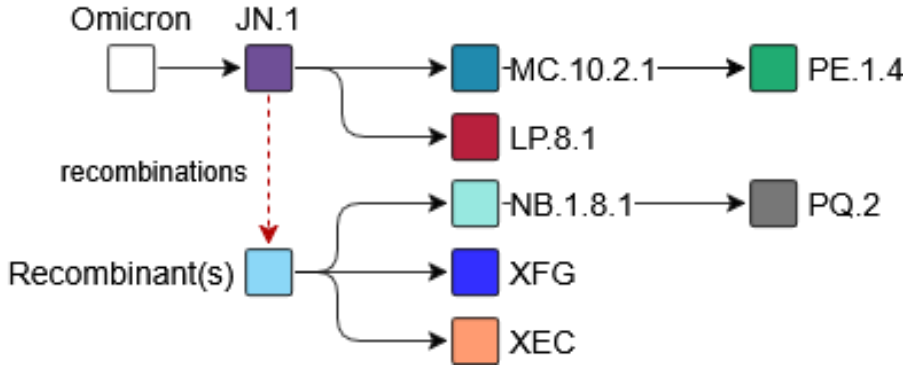


Figure 2. *Relationships between the variants tracked in this report.*

Overview of variants from clinical samples

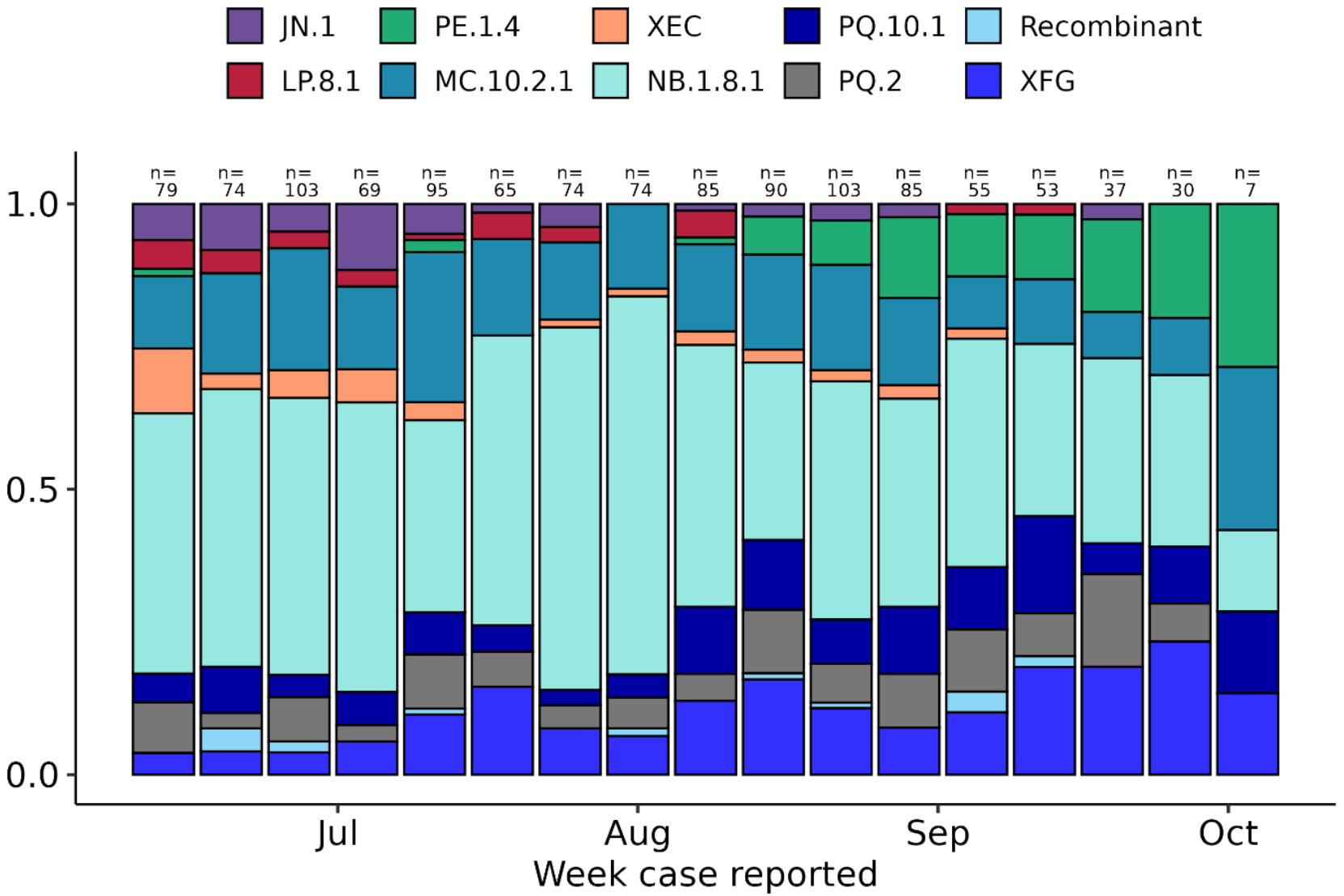


***Figure 3**. Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based 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 assays limitations, **for the wastewater analysis, PQ.2 is included in the NB.1.8.1 category.**

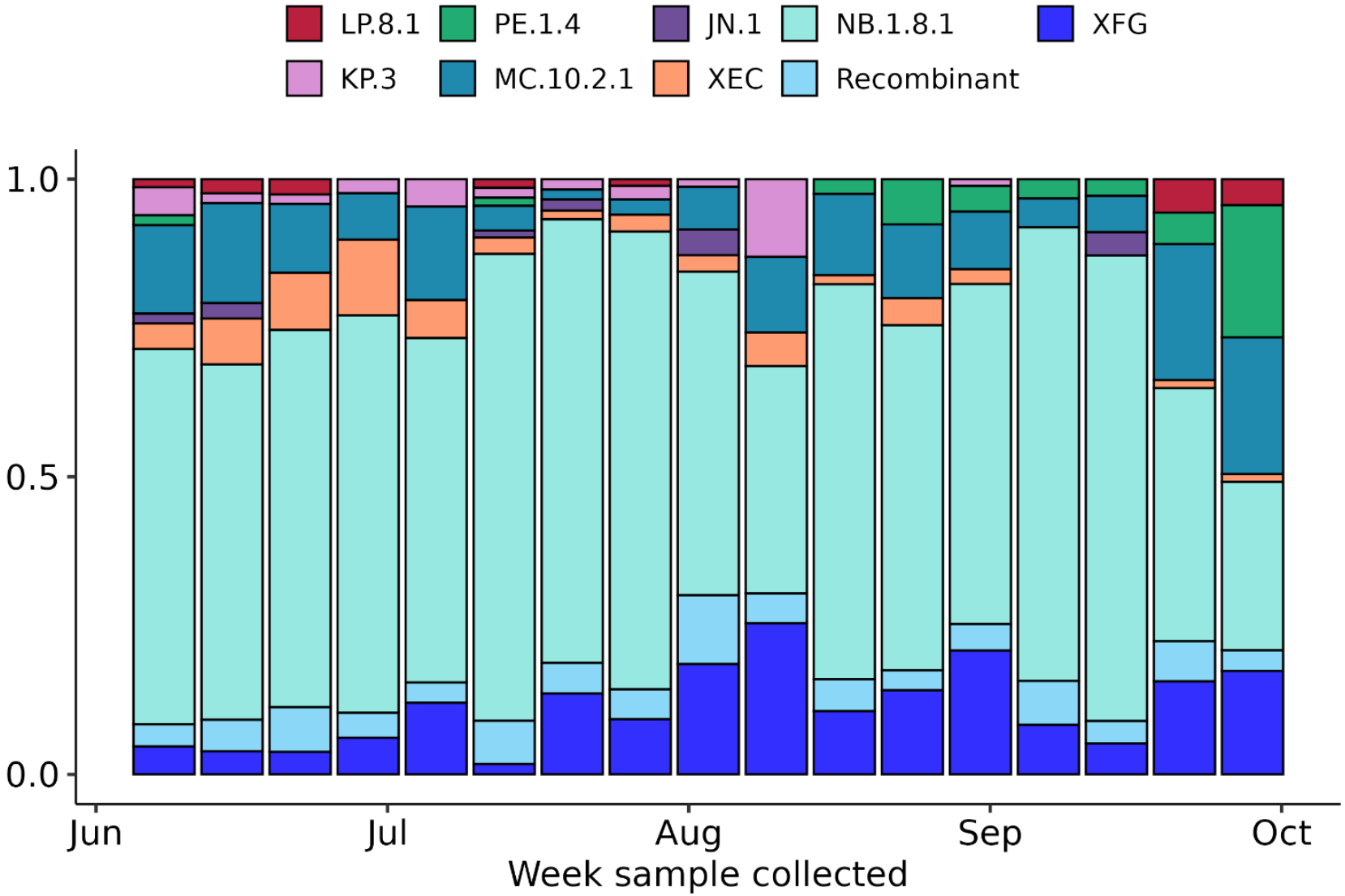


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

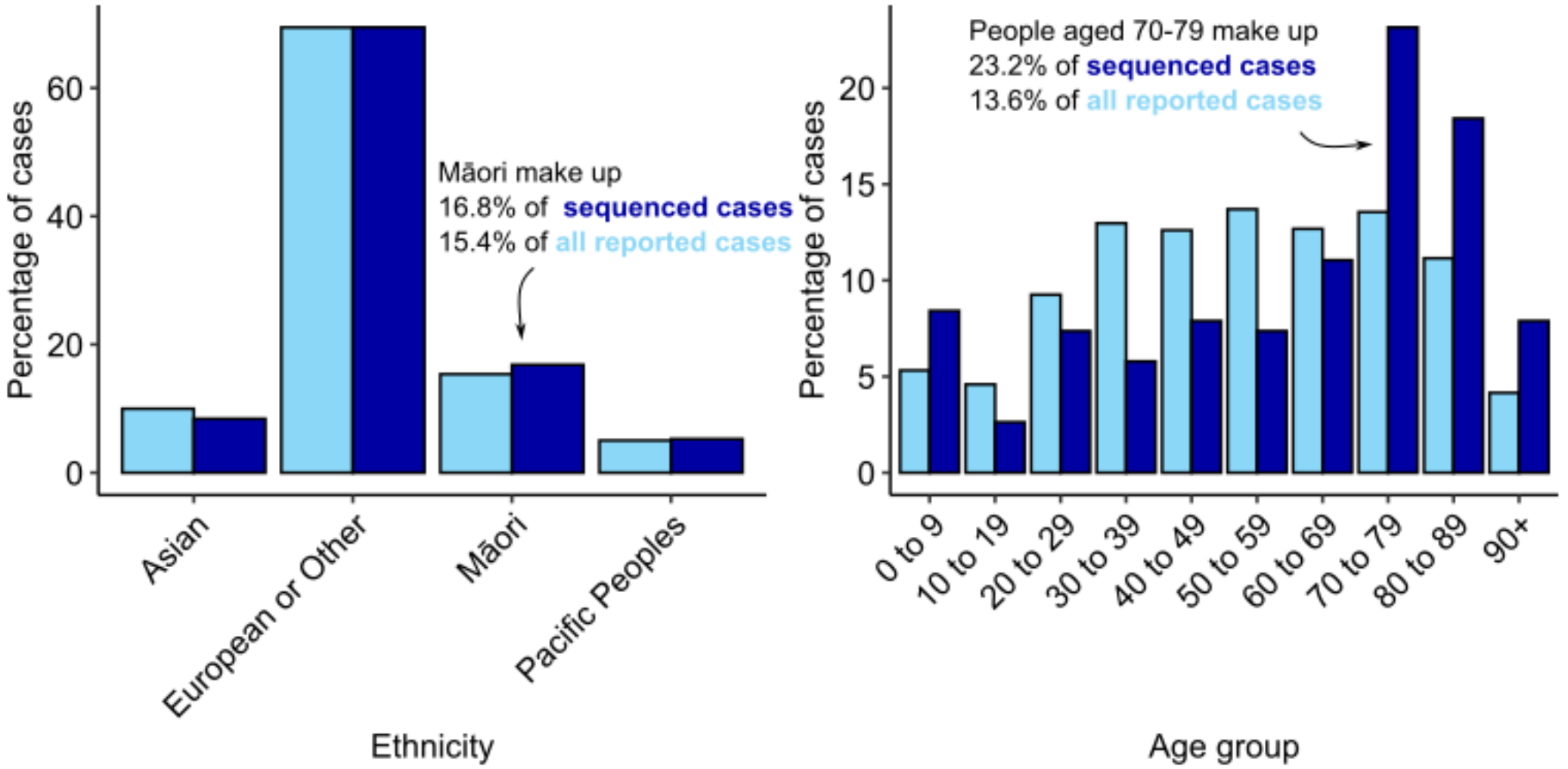


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported between 30 August – 3 October.* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 10am 7 October.*

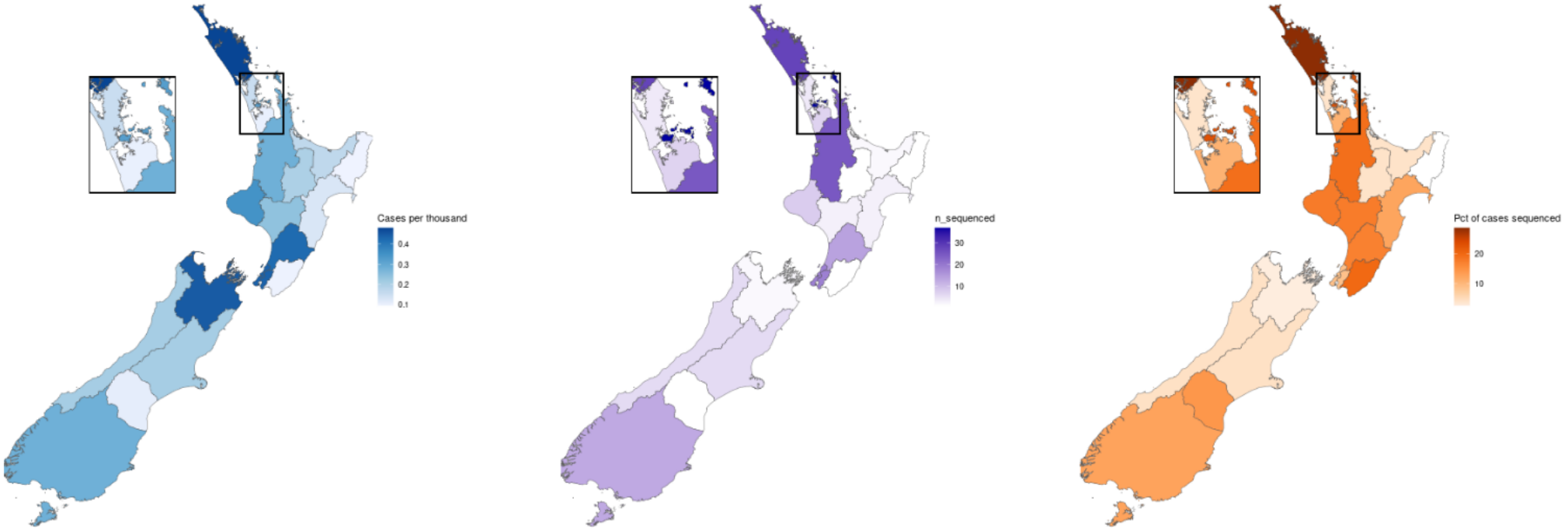


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 10am 7 October.*

Emerging lineages

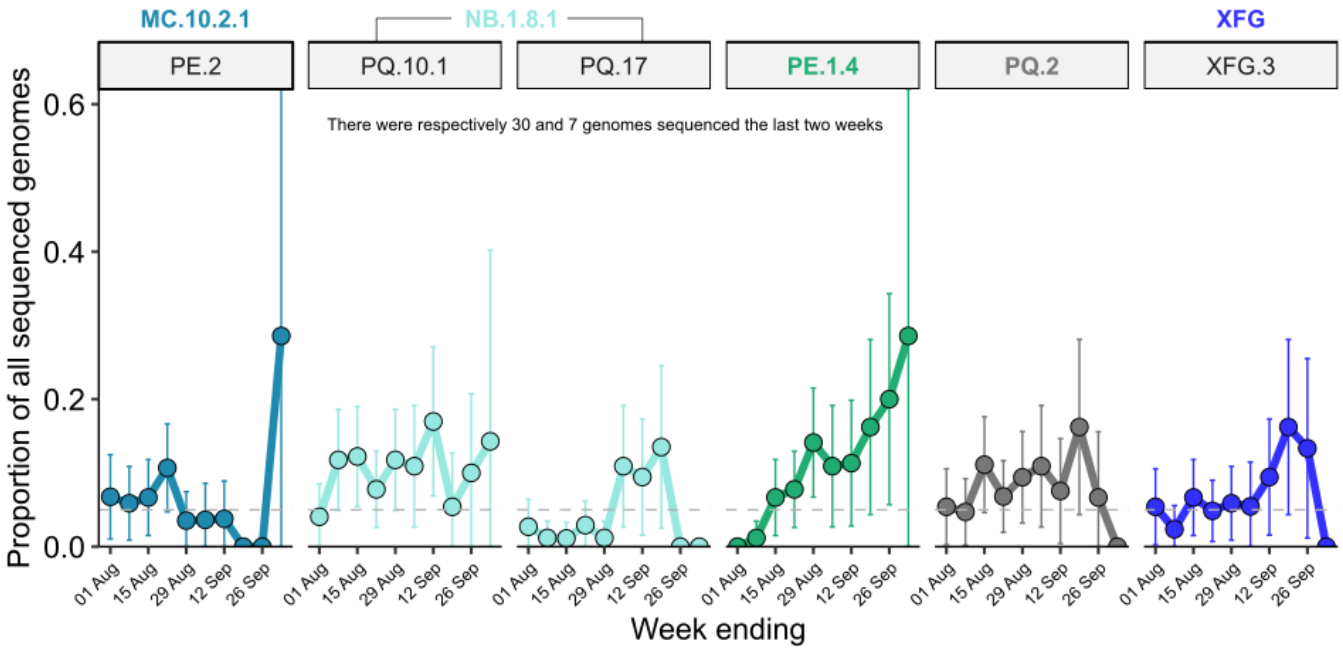


Figure 7. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the rest of this report. The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

Geographical differences in sampling and prevalence

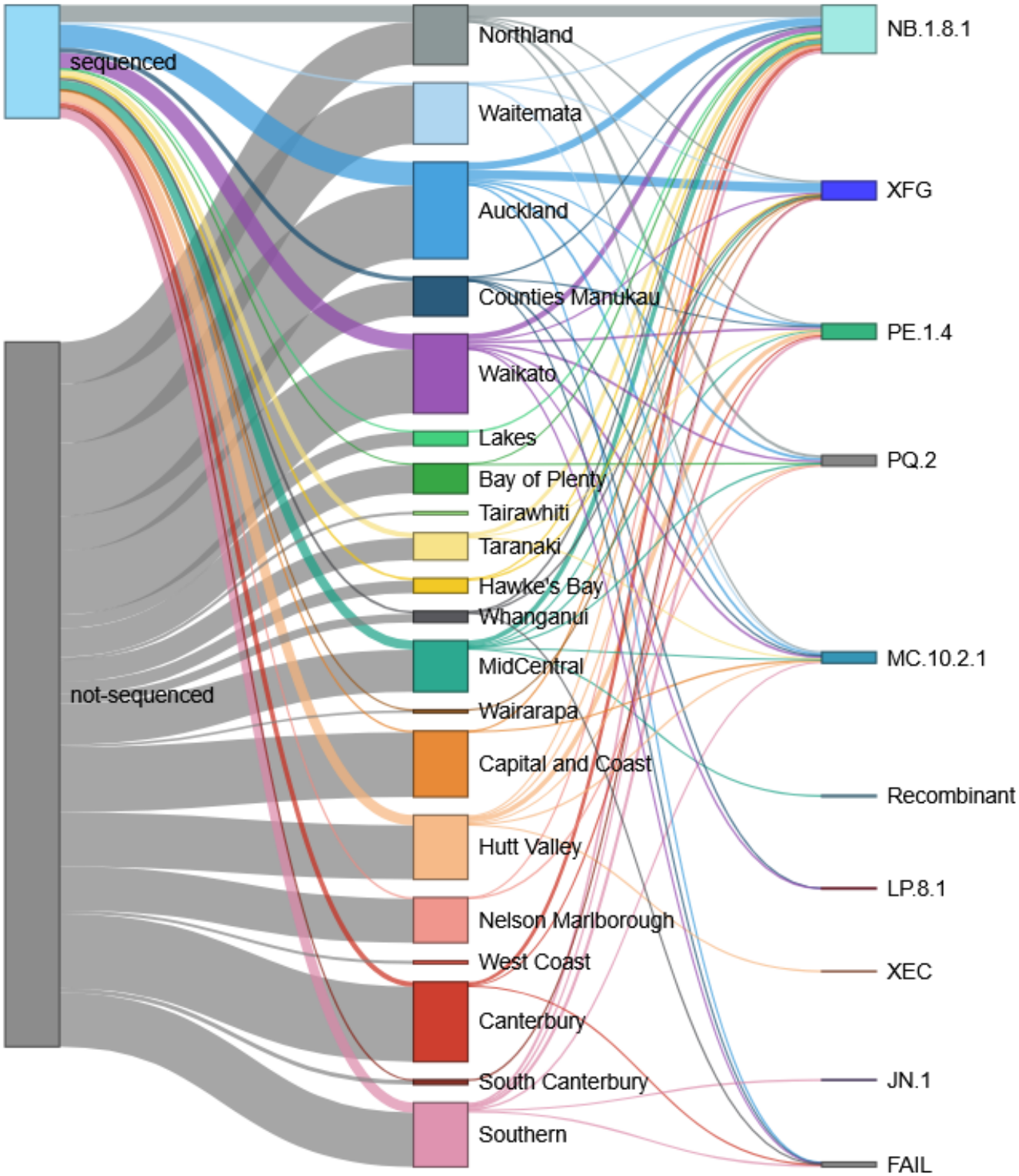


Figure 8. *Origin and sequencing results of the 1375 cases reported between 30 August – 3 October per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a lineage (Unassigned). Data as of 12pm 8 October.*

WGS Hospital Reporting

A total of 56 genomes have been sequenced from patients admitted to hospital with COVID-19 infection **since the last report and** within the reporting period. Despite XFG and MC.10.2.1 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.

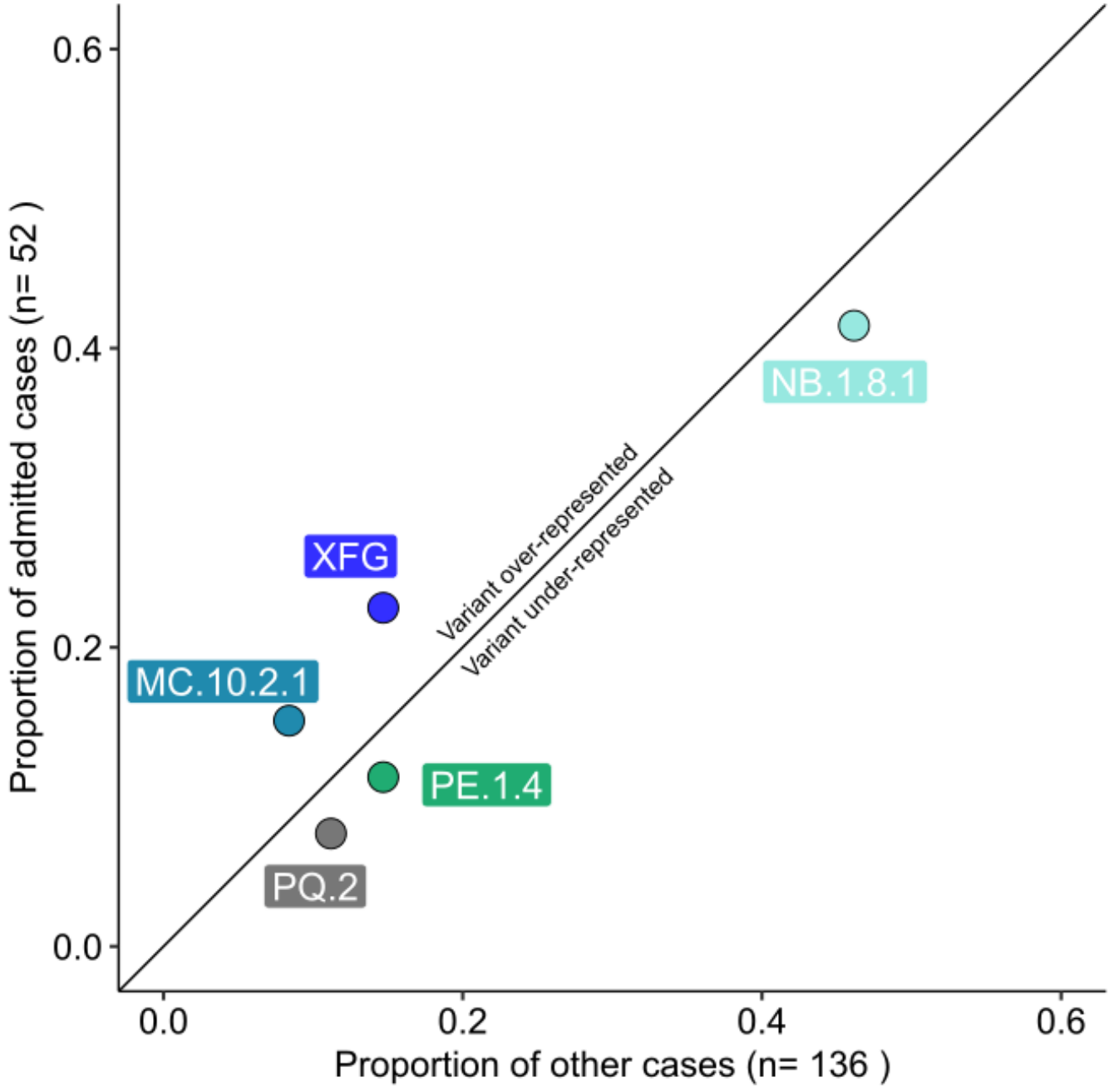


Figure 9. *Frequency of variants among cases reported between 6 September – 3 October not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted from the graph and numbers on the margins.*