14 July 2025

COVID-19 Genomics Insights Dashboard (CGID) Report #61

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

311

genomes* from cases reported since the last CGI report (30 May 2025)

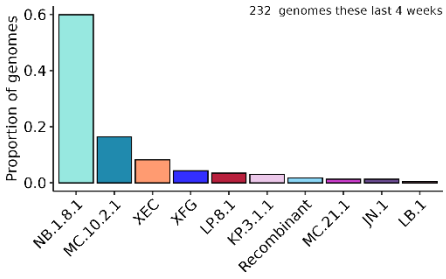
1375

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 remains dominant (60%), above MC.10.2.1 (16%) with XEC stable (8%), XFG (4%) and other variants declining in the last four weeks



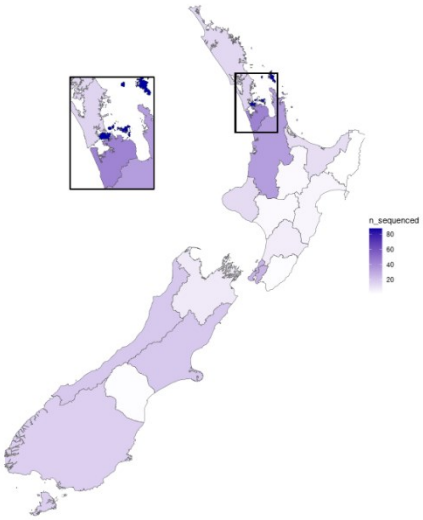
hospital cases

41.7% (136/326*) of cases admitted to hospital with a positive PCR between 31 May and 4 July have been sequenced to date.
The approximate composition of hospital cases:

- **NB.1.8.1 57.4%**
- **MC.10.2.1 12.5%**
- **XEC 8.1%**
- **XFG 5.9%**

*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 3 May – 30 May

Key trends and insights

- NB.1.8.1 remains the dominant variant in the country and accounts for 59.9% of cases in the last four weeks.
- The growth advantage of this lineage has stalled as it stabilizes and as multiple sublineages start to emerge.
- XFG, another recombinant variant (LF.7 x LP.8.1.2), is now growing overseas, particularly India and Spain, and has been classified as Variant under Monitoring by WHO on 25 June. This variant remains rare in NZ.
- There is currently no indication that XFG will cause more severe disease than previously circulating variants.
- Emerging variants and XFG have the potential to further increase caseloads in the coming weeks.

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

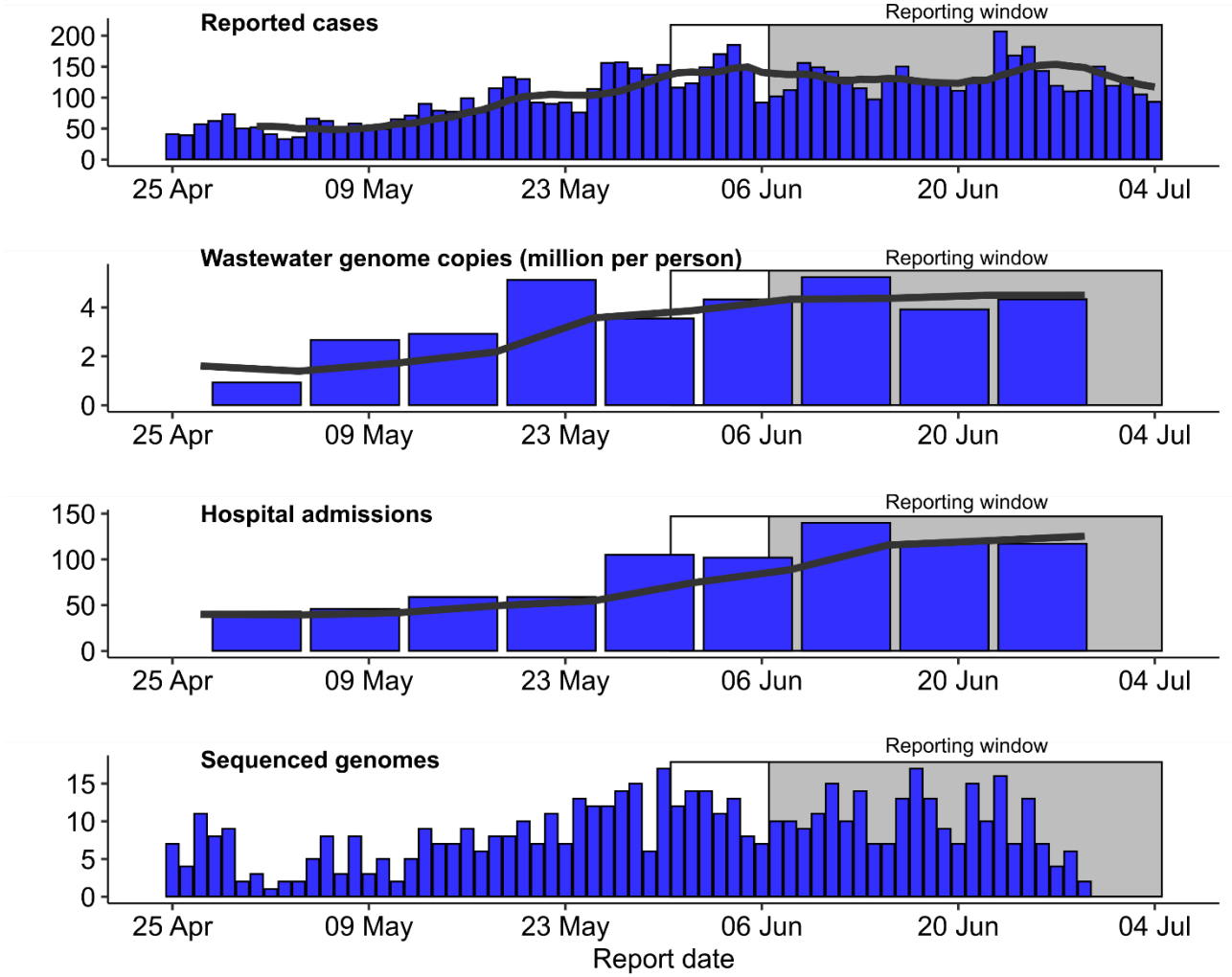


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Top Middle: Trends in wastewater detections. Bottom Middle: Number of patients admitted with COVID-19 per week. Bottom: The 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 11am 11 July*

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.

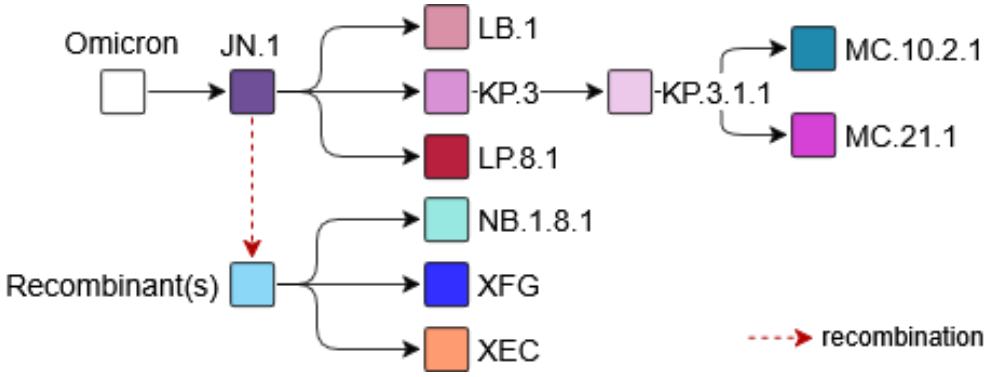


Figure 2. *Relationships between the variants tracked in this report.*

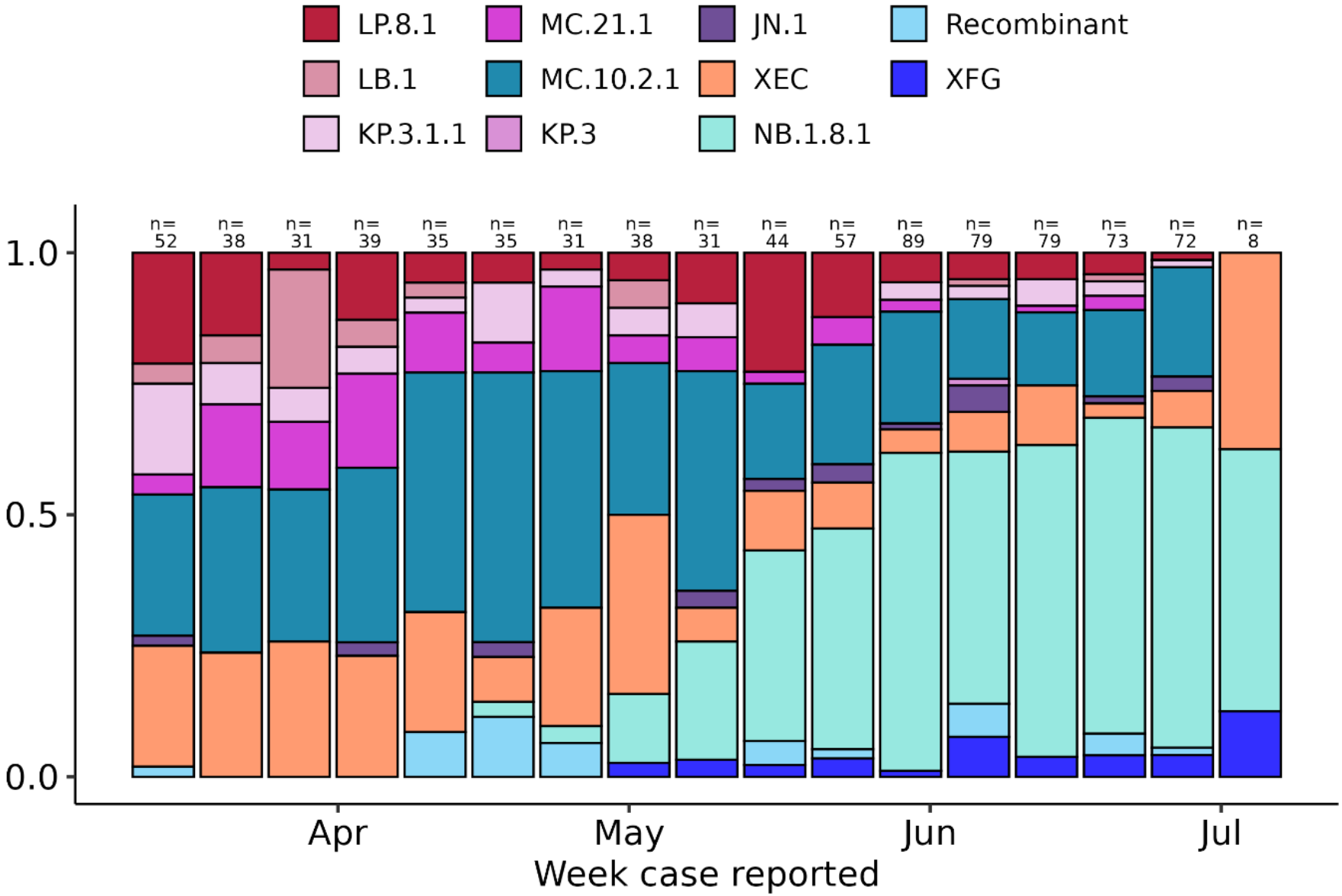


Figure 3. *Frequency of variants/lineages in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based on the number of genomes indicated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

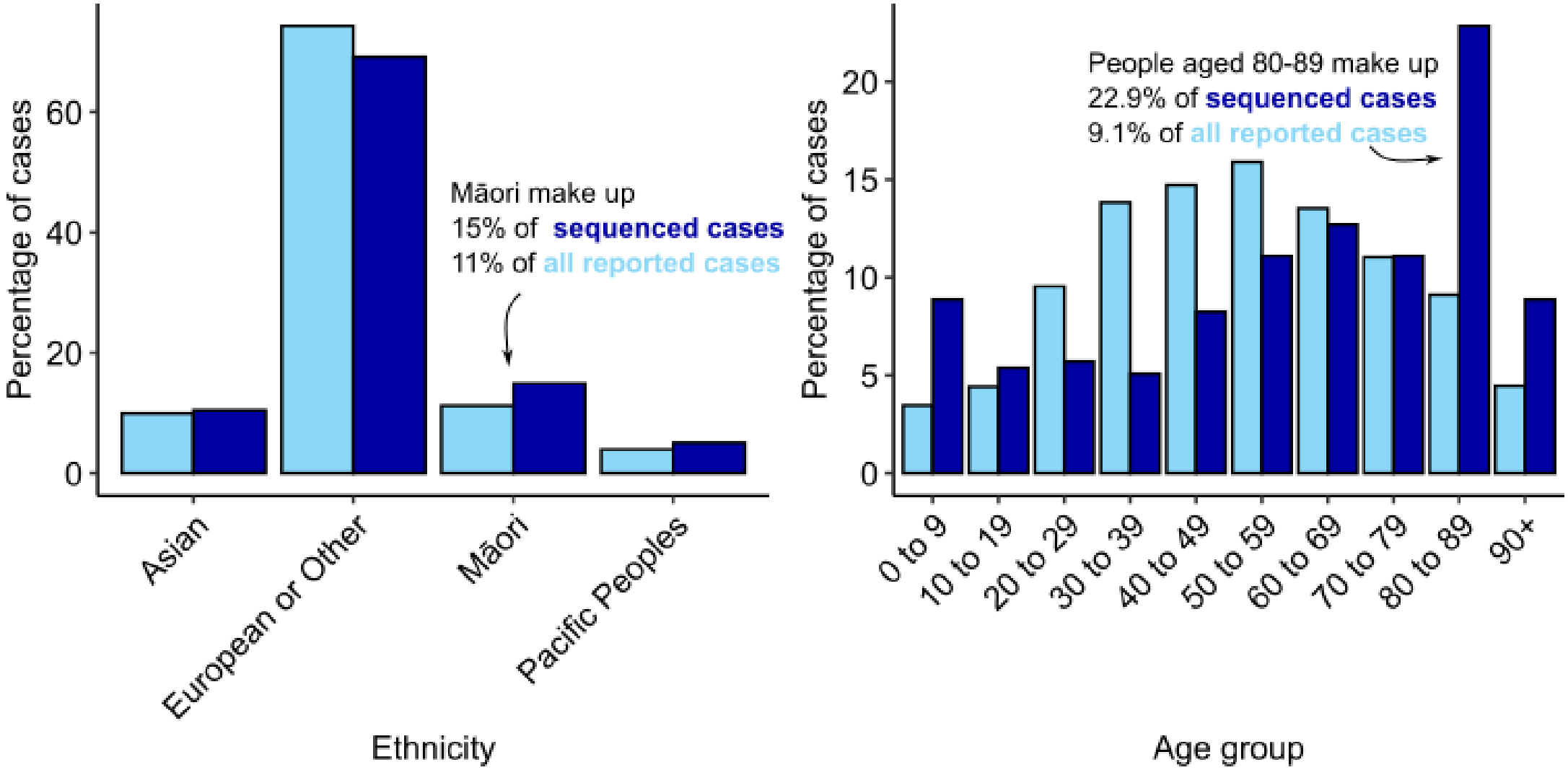


Figure 4. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported between 3 May – 30 May.* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 12pm 8 July.*

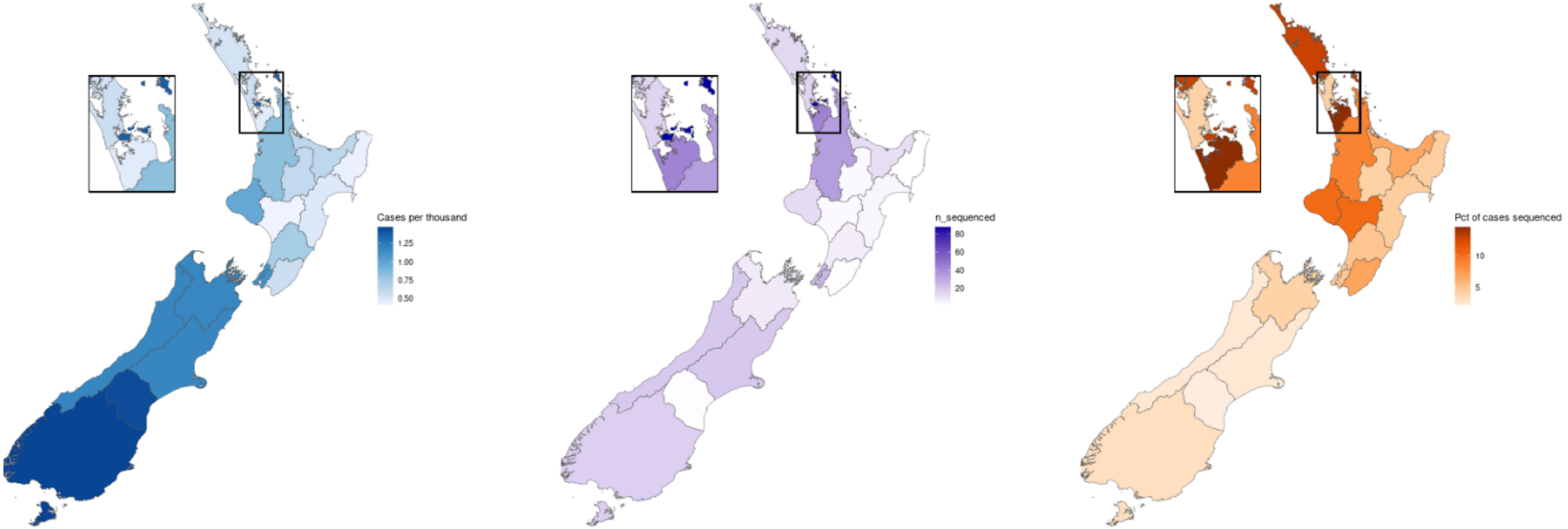


Figure 5. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 12pm 8 July.*

Emerging lineages

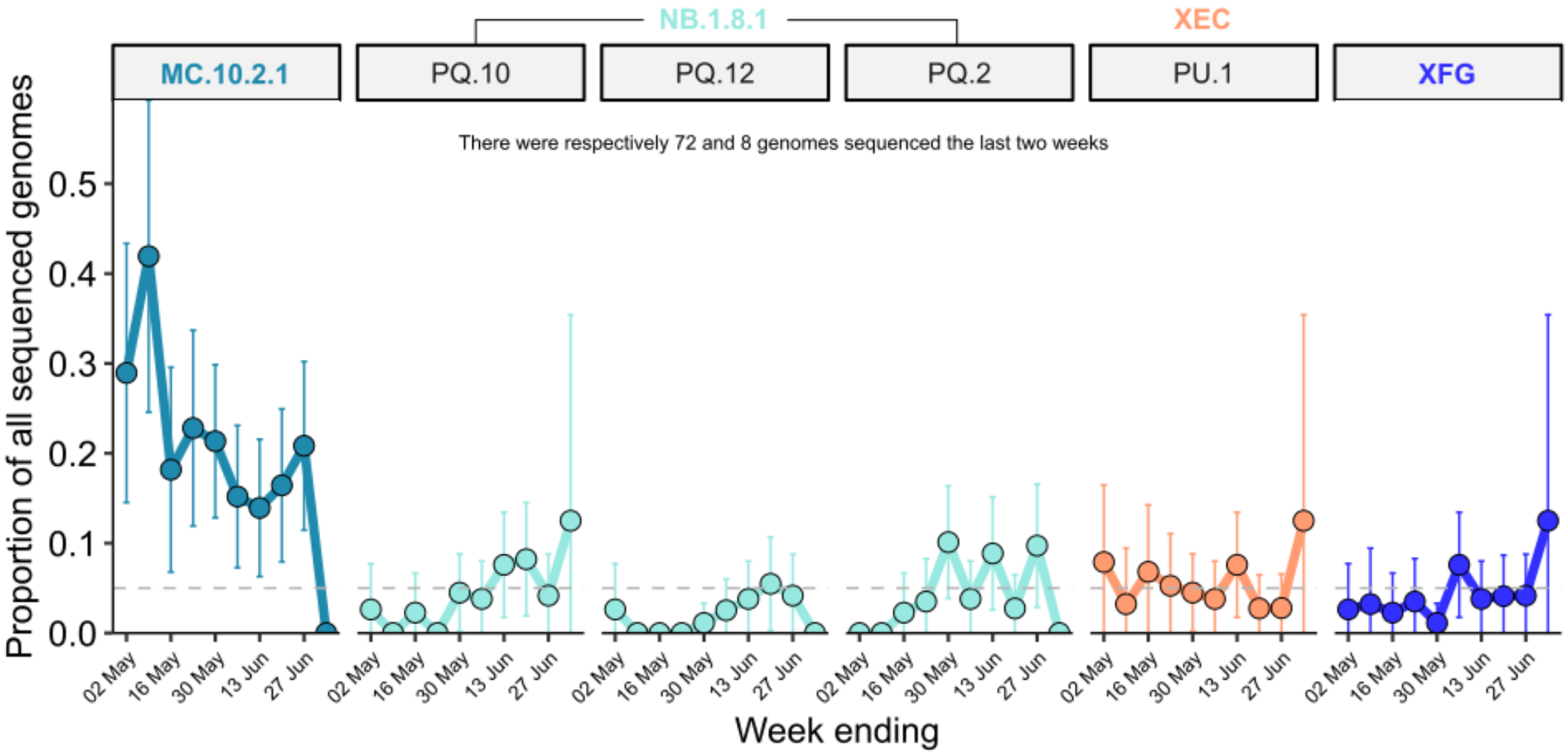


Figure 6. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the rest of this report. The dashed grey line indicates a 5% proportion.*

WGS Hospital Reporting

A total of 136 genomes have been sequenced from patients admitted to hospital with COVID-19 infection **since the last report and** within the reporting period. 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 7**). 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.

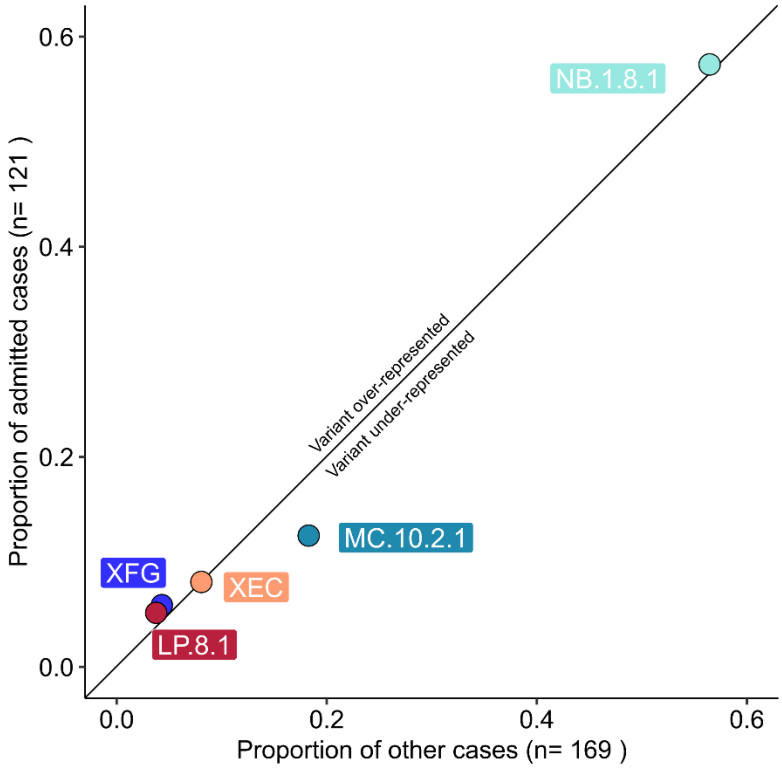


Figure 7. *Frequency of variants among cases reported between 3 May – 30 May not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted from the graph and numbers on the margins.*

Wastewater Variant Analysis

Results from 11 sentinel wastewater sites across New Zealand, with the most recent results from samples collected in the week ending 6 July, are summarised in **Figure 8**. Some lineages described in this report are not distinguishable from their parent lineage using PHF Science's CoVarSeq assay (which amplifies a key region of the Spike protein). For the wastewater analysis, KP.3.1.1 is included in the KP.3 category and LB.1 is included in the JN.1 category.

The wastewater qualitative results largely align with clinical samples (**Figure 3**) with the proportion of NB.1.8.1 increasing from late March and XFG consistently detected at a low level. PHF Science's Wastewater COVID-19 Surveillance dashboard that includes variant analysis results is available online at https://esr-cri.shinyapps.io/wastewater https://poops.nz/). The dashboard contains virus levels and variant data for the week ending 6 July. The next update of wastewater quantification results will be on Friday 25 July and the next complete update of wastewater surveillance results (including variant analysis data for the last 4 weeks) will be on Thursday, 7 August.

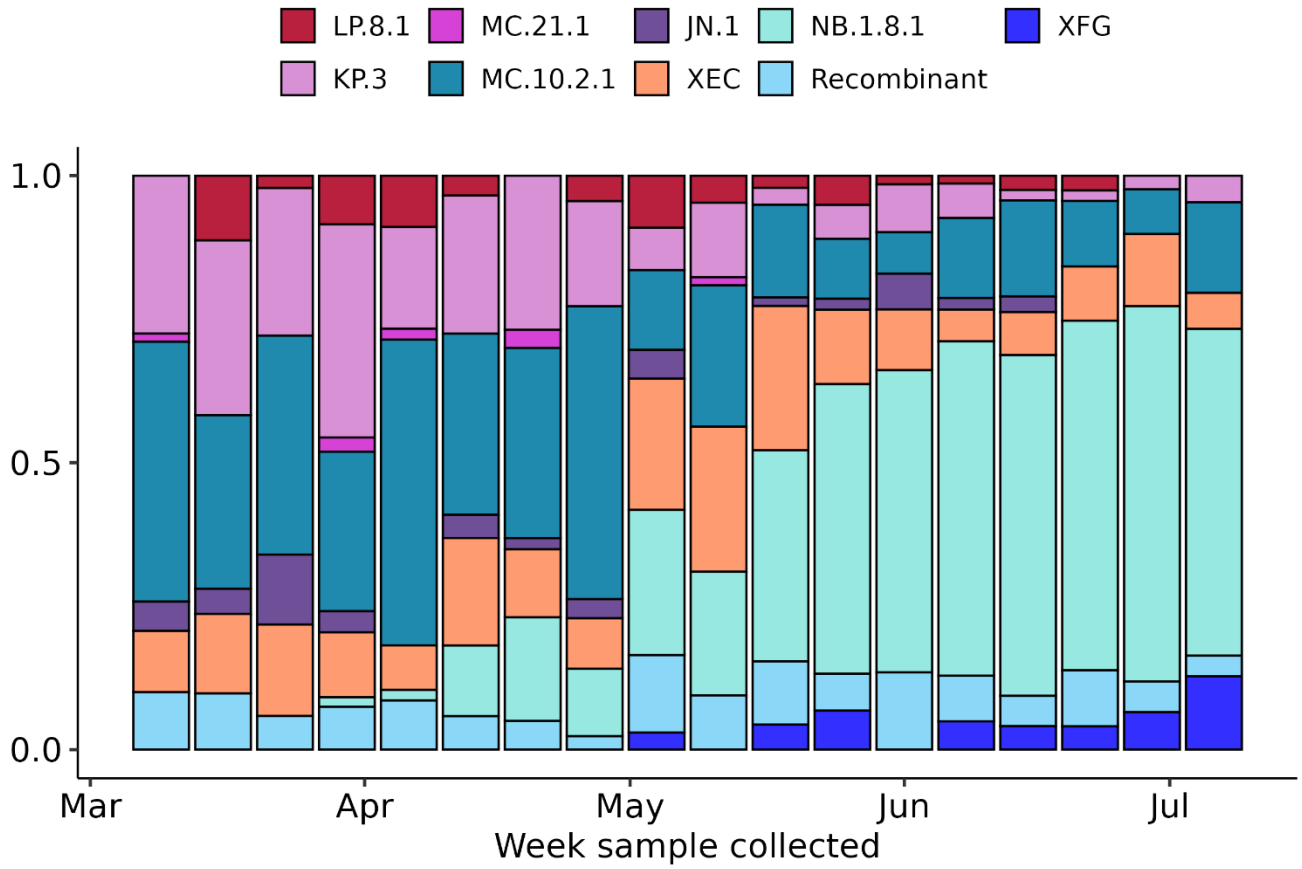


Figure 8. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*