11 September 2026

COVID-19 Genomics Insights Dashboard (CGID) Report #74

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) of clinical samples and wastewater surveillance support public health decision-making. As SARS-CoV-2 continues to adapt and mutate, the CGID reports trends and insights gained by our WGS surveillance programme in Aotearoa New Zealand, and abroad..

Summary Infographic and Insights:

genomes analysed

39

genomes* from cases reported in the last four weeks

1109

genomes* reported in 2026

79

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

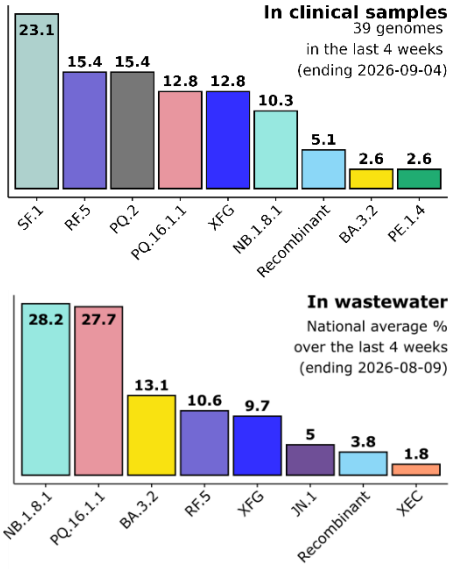
697

wastewater samples* in 2026

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

variant & lineage

SF.1 is dominant in clinical samples, common in wastewater



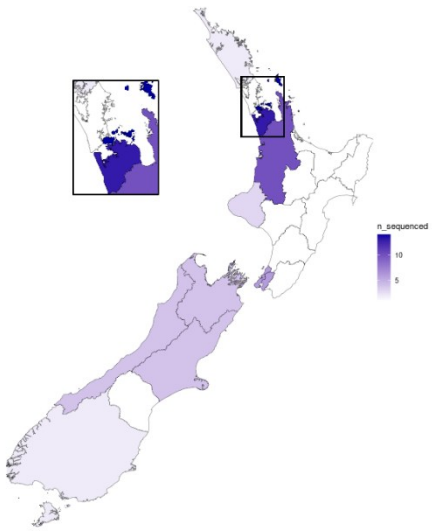
hospital cases

32.1% (18/56*) of cases admitted to hospital with a positive PCR between 1 August and 4 September 2026 have been sequenced to date. The approximate composition of hospitalised cases:

- **PQ.16.1.1** **33.3%**
- **SF.1** **27.8%**
- **NB.1.8.1** **16.7%**
- **BA.3.2** **11.1%**
- **PQ.2** **11.1%**

*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 1 August and 4 September 2026

Key trends and insights

- Overall COVID-19 activity levels remain low.
- SF.1 has replaced BA.3.2 as the dominant variant, representing 23.1% of sequences.
- Other variants circulating at appreciable levels are Variant under Monitoring PQ.16.1.1, RF.5, PQ.2 and XFG.
- PQ.16.1.1 and BA.3.2 are more prevalent in wastewater than clinical cases, representing 28% (vs 13%) and 13% (vs 3%) respectively.
- We describe the closeness of circulating genomes with vaccine strains, including the newly approved XFG vaccine, and review recent data on the relationship between SARS-CoV-2 evolution and vaccine efficacy.

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

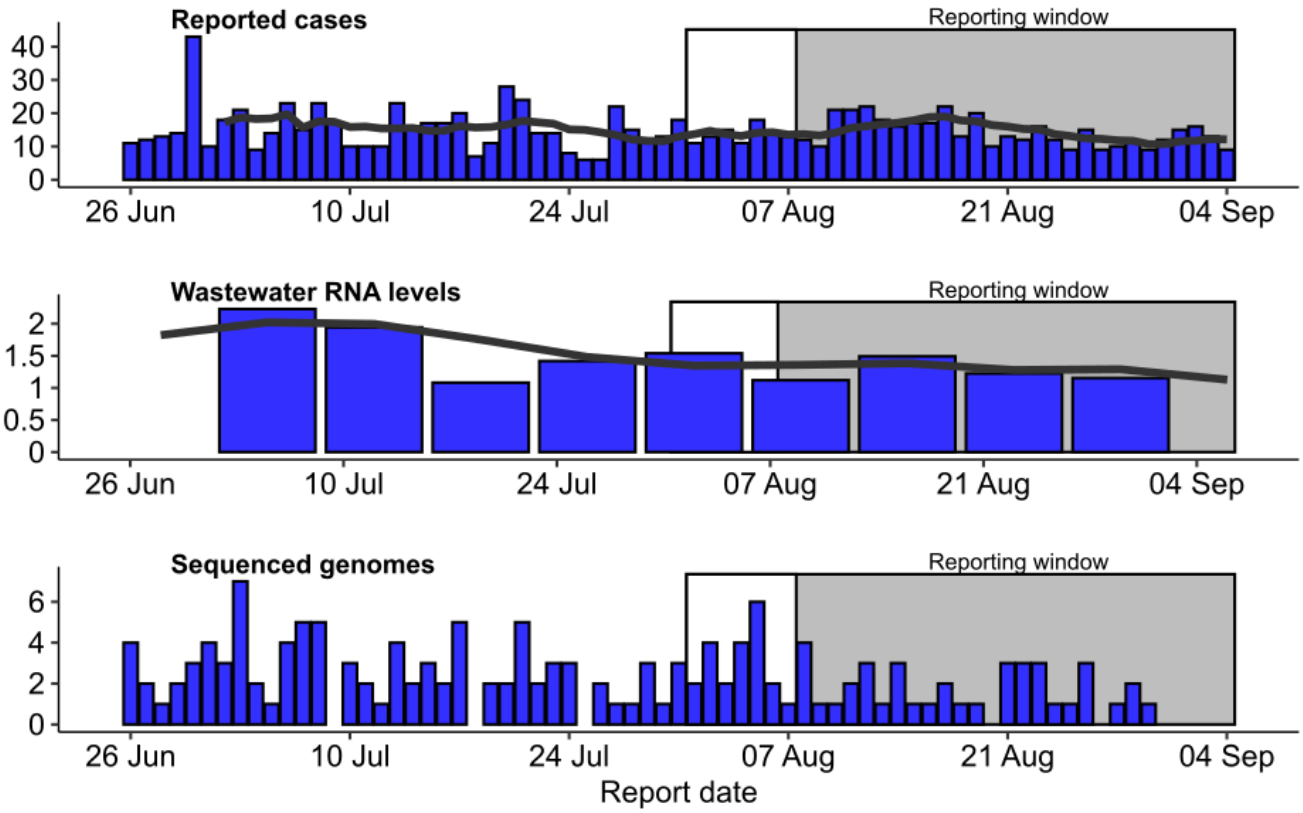


Figure 1. *Reporting windows and epidemiological context of this report. Top: Recent COVID-19 case numbers reported by day (blue bars) and the 7-day rolling average (black line). Middle: Trends in SARS-CoV-2 RNA levels (in million genome copies/person/day) in wastewater and 3-week rolling average (black line). 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 10 am 11 September 2026.*

Tracked Variants

Tracking the frequency and epidemiological properties of SARS-CoV-2 variants is a key goal of the CGID 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.

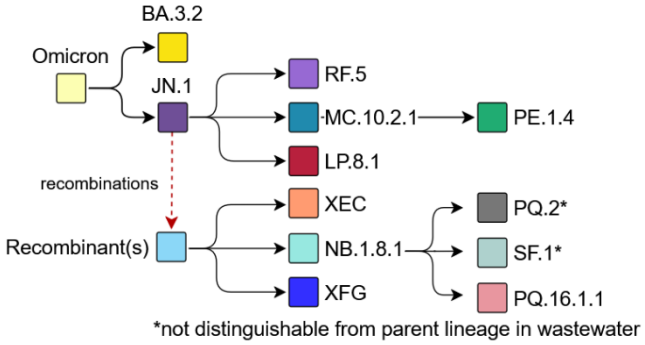


Figure 2. *Relationships between the variants tracked in this report.*

Changes made since last report

No changes were made in tracked lineages this month.

Overview of variants from clinical samples

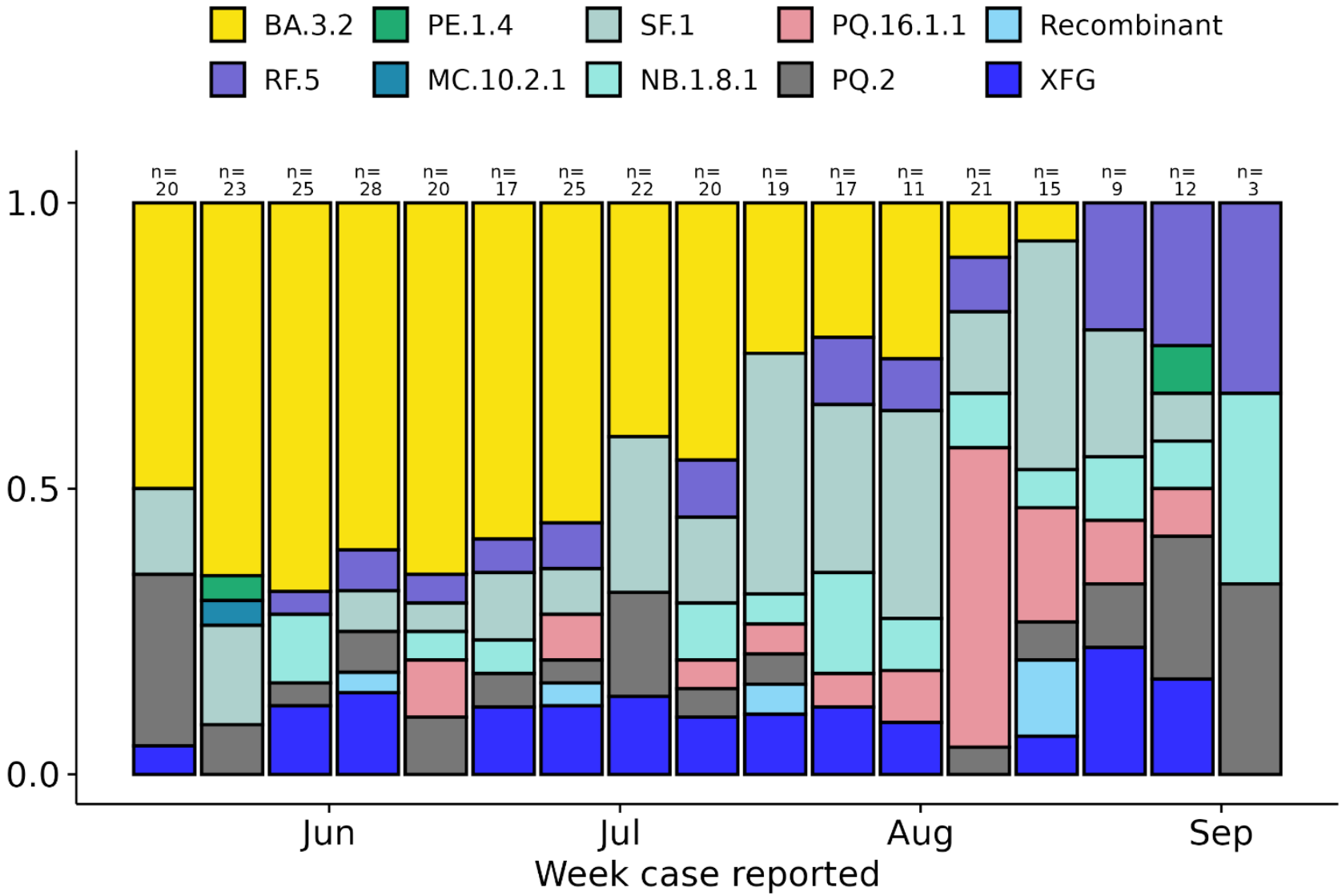


***Figure 3**. Frequency of variants/lineages from clinical cases reported in the past 17 weeks. Note, **data for the most recent two weeks is preliminary**. It will be updated as additional cases reported within these weeks are referred to PHF Science and sequenced. Data from each reporting week is based on the number of genomes indicated above each bar. Tracked lineages are defined in **Figure 2** and in Appendix Error! Reference source not found..*

Overview of variants from wastewater samples

Wastewater surveillance data from 11 sentinel sites across New Zealand for the **week ending 9 August**, are available via PHF Science's online dashboard https://esr-cri.shinyapps.io/wastewater/ and summarised in **Figure 4**. Due to assays limitations, **for the wastewater analysis, PQ.2 and SF.1 are included in the NB.1.8.1 lineage.** Note that the 4-week window reported in wastewater data is 4 weeks earlier than the reporting window for clinical cases.

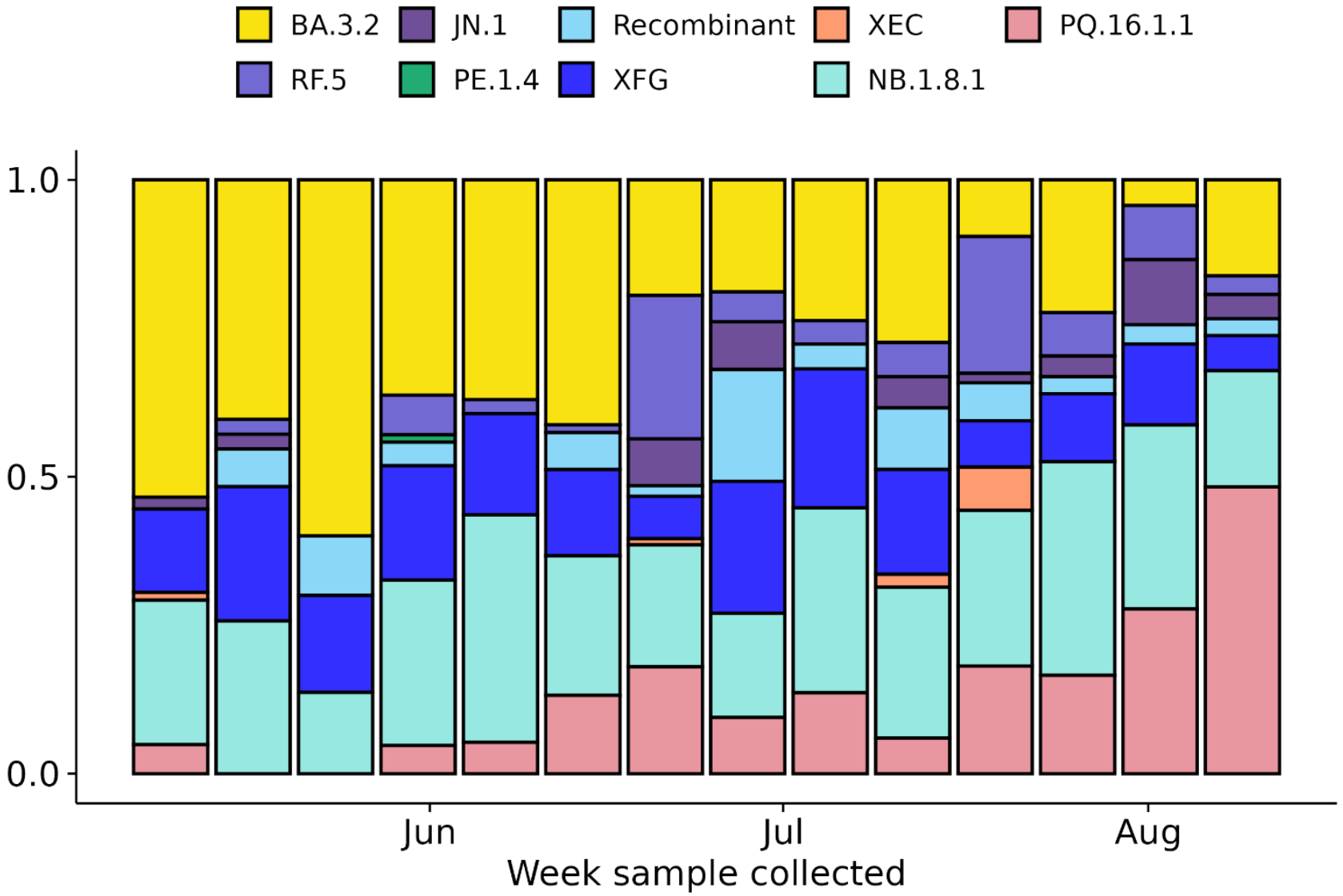


Figure 4. *Estimated variant frequencies from 11 wastewater sites across New Zealand.*

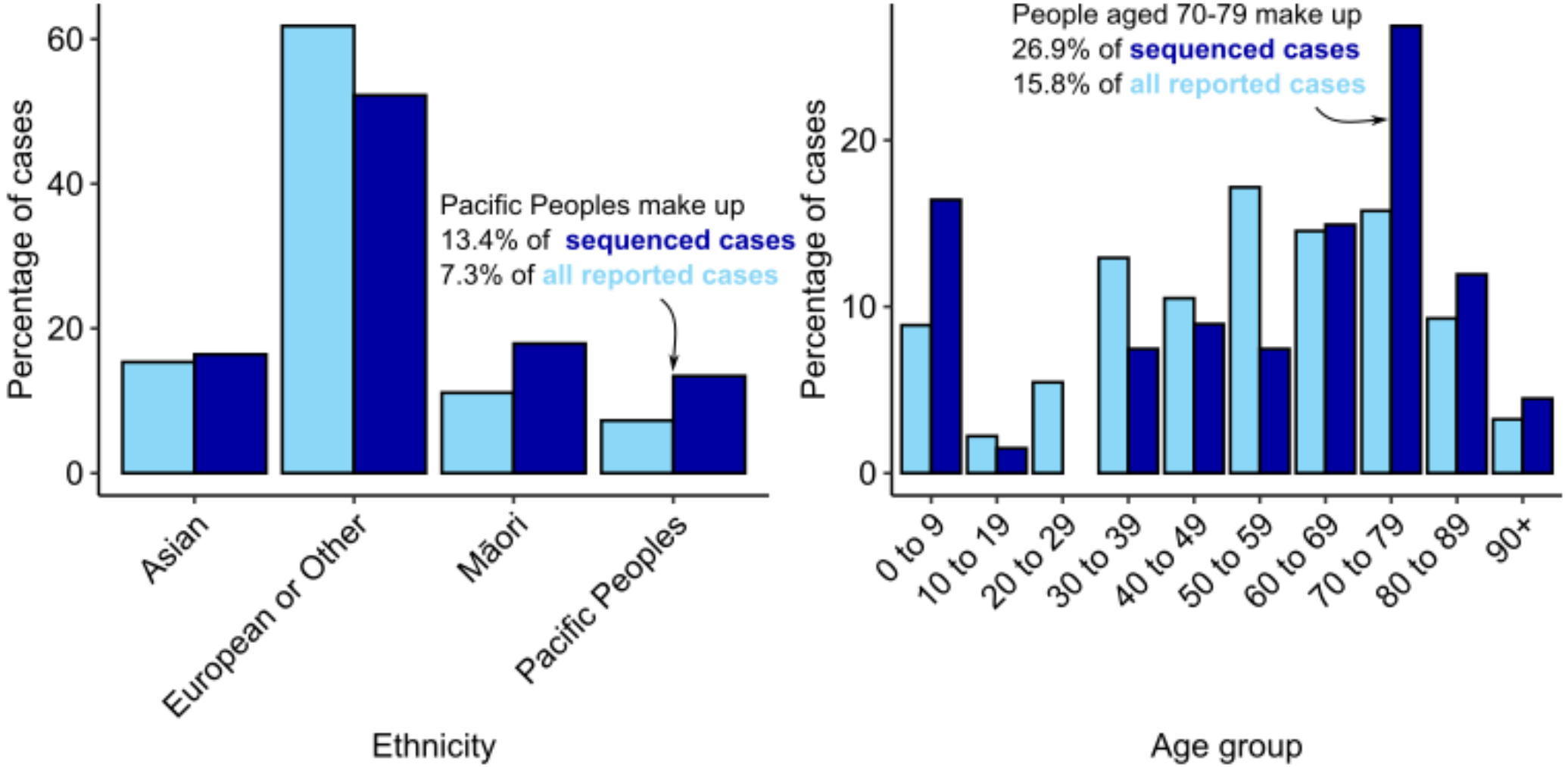


Figure 5. *Distribution of sequenced cases (dark blue) and all reported cases (light blue) reported in this reporting window* ***Left:*** *by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right:*** *Distribution of reported and sequenced cases by age. Data as of 4 pm 8 September 2026.*

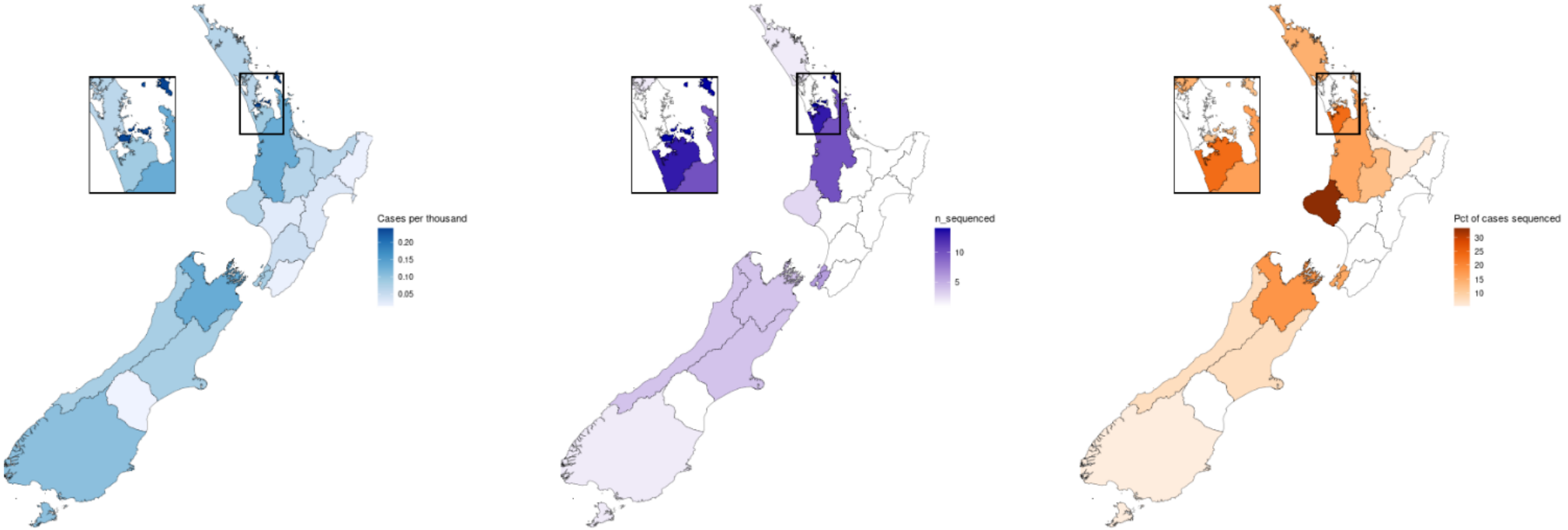


Figure 6. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand (blue), the number of sequences obtained (purple), and the percentage of all reported cases sequenced (orange). Data as of 2 pm 8 September 2026.*

Emerging lineages

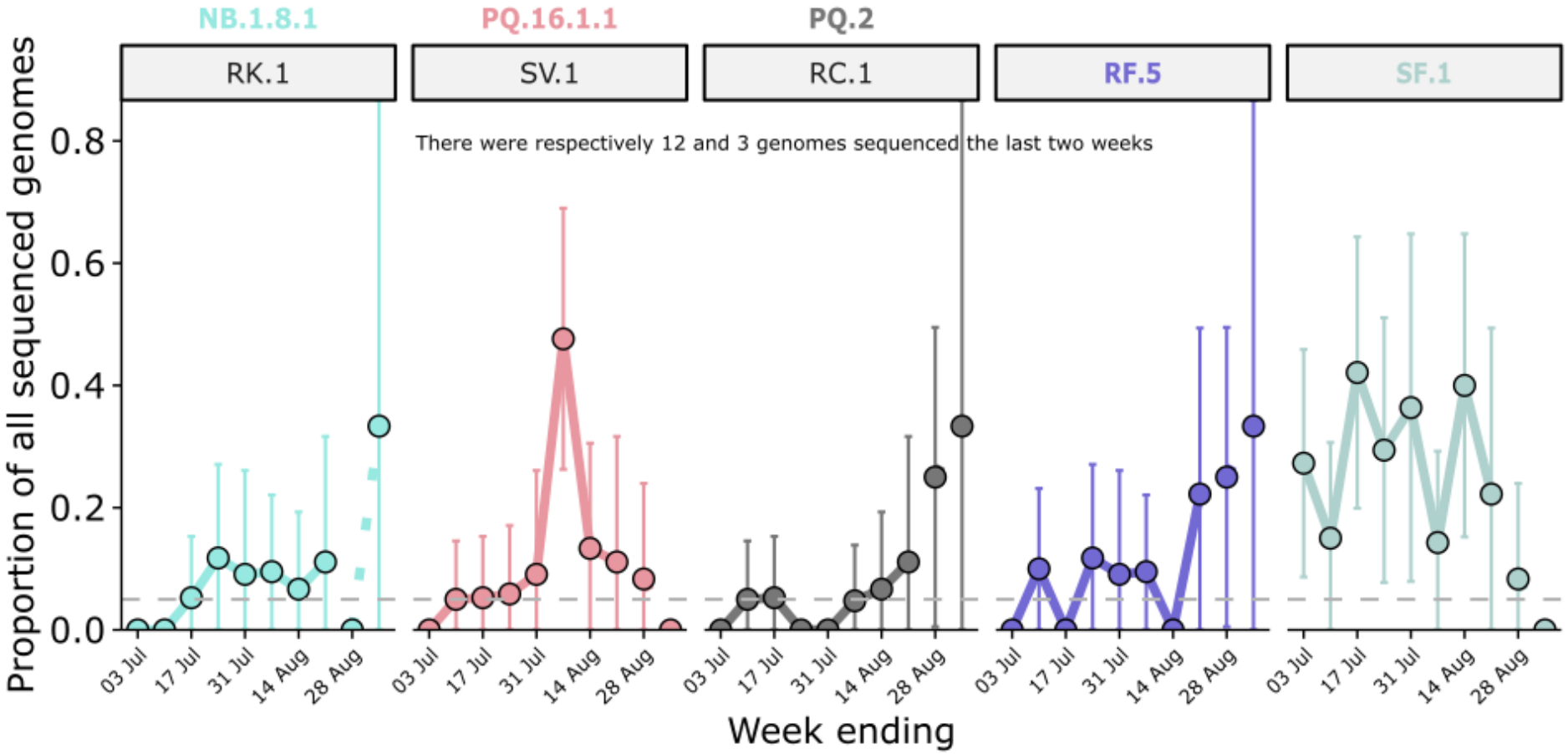


Figure 7. *Frequency of specific lineages in clinical surveillance in recent weeks. Each sub-plot represents data from a single lineage and all its descendant lineages not included elsewhere in this graph. The label above each subplot describes the tracked variant this lineage is reported under for the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

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 (**Error! Reference source not found.**), although RC.1, a PQ.2 sublineage that circulated at the start of 2026, is showing signs of a re-increase. Recent NZ genomes appear on a branch with the D253G Spike mutation alongside recent Australian sequences. The small sample size limits the precision of PHF Science’s daily growth advantage estimates, but we will continue to monitor this variant.

Major trends in variants

COVID-19 activity remains low in Aotearoa

The period of stable and low COVID-19 activity—as measured by reported cases and wastewater concentrations—mentioned in the previous CGID has continued over this reporting period (**Figure 1**). The variants landscape has however completely changed in the interval.

BA.3.2, previously the dominant variant, was only detected once in this reporting window (**Figure 3**; 2.6% in the last four weeks, compared to 33.3% in the last report and ~61% in the two previous-to-last reports). In clinical samples, this variant has been replaced by SF.1 a local NB.1.8.1 sub lineage (see CGID #73) that now accounts for 23.1% of sequences). This sub lineage has a significant growth advantage over other variants (albeit in a context of small sample size). Neither SF.1 or PQ.2 can be distinguished from their parent lineage in wastewater data, so they are included in the NB.1.8.1 variant in this dataset. NB.1.8.1 is consequently the most common variant in wastewater with a frequency of 28.1% (*vs.* 48.8% overall in clinical cases). Other variants circulating at appreciable level include PQ.16.1.1, the recently designated Variant Under Monitoring and RF.5 (respectively 12.8% and 15.4% over the reporting period).

Low number of genomes sequenced mean more volatility in proportions over weeks. Proportions calculated over the four weeks excluding the latest—incomplete—week (for cases reported between 1st and 28 August) show PQ.16.1.1 dominant with 28.1% of sequences, followed by SF.1 (21%), RF.5 (12.3%), PQ.2 (10.5%), NB.1.8.1 and XFG (8.8% each). Low SARS-CoV-2 levels, reduced reporting, and low testing volumes continue to limit PHF Science's ability to estimate growth advantages precisely.

WGS Hospital Reporting

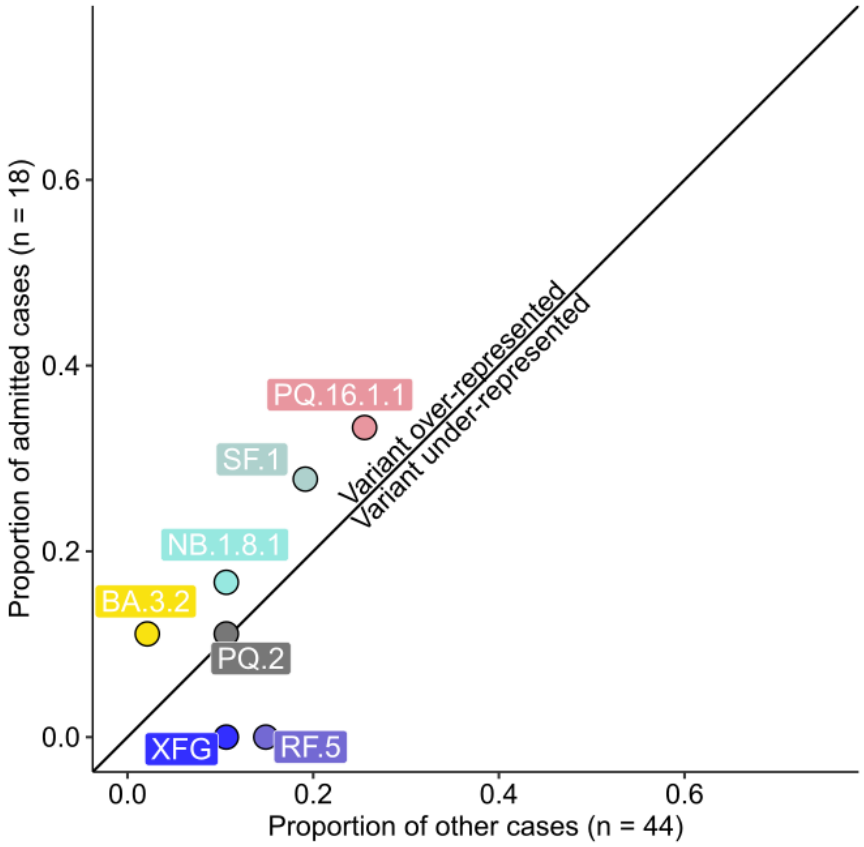


Figure 8. *Frequency of variants among cases not associated with hospital admission (x-axis) and those hospitalised for any reason in the 7 days before or after the reporting date (y-axis). Variants overrepresented in hospitalised cases will appear above the diagonal line. Variants representing less than 5% of cases are omitted*

A total of 18 genomes have been sequenced since the last report and within the reporting period from patients admitted to hospital with a positive COVID-19 PCR result. 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 = 0.206; **Figure 8**). However, the small sample size limits the precision of these estimates, and the current data are insufficient to draw firm conclusions about differences in variant frequencies between the two groups.

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.

The evolution of SARS-CoV-2 and vaccine strains

The recent approval of an updated Comirnaty mRNA vaccine for New Zealand provides an opportunity to review how COVID-19 vaccines kept pace with the evolution of the virus, and where the newest vaccine fits among the variants currently circulating in Aotearoa.

The original COVID-19 vaccines developed in the midst of the pandemic were first introduced in December 2020 internationally and started to be rolled out at the start of 2021 in Aotearoa. They include mRNA vaccines (Pfizer and Moderna), protein subunit vaccines (Novavax), and viral vector vaccines (AstraZeneca and Janssen (Johnson & Johnson); **Table 1**). These initial vaccines all worked by exposing the recipient's immune system to all or part of the spike protein from the ancestral SARS-CoV-2 virus. The original vaccines have been updated with five and soon six generations of "booster" containing spike proteins from emerging Omicron lineages:

- In 2022, bivalent vaccines targeted both the original virus and Omicron variants BA.1 or the original virus and BA.4/BA.5.
- In 2023, a monovalent vaccine targeted the XBB.1.5 lineage.
- In 2025, a monovalent vaccine targeted the JN.1 lineage.
- Since the start of 2026, the current monovalent vaccine targets the LP.8.1 lineage.
- The new vaccine approved on 3 September[1] and soon available will be a monovalent vaccine targeting the XFG lineage (LF.7 x LP.8.1.2 recombinant).

Vaccines targeting KP.2 (JN.1 sublineage) available overseas in 2025 were not rolled-out in New Zealand.

[1] https://www.medsafe.govt.nz/DbSearch/ProductDetail?Product_id=28661

***Table 1**: COVID vaccines approved by Medsafe for use in New Zealand and the strain they target. Vaccines with a lapsed approval appear in grey.*

Vaccine	Manufacturer	Active ingredient(s)	Type of vaccine	Strain targeted
Comirnaty	Pfizer-BioNTech	tozinameran	mRNA	Original
Spikevax	Moderna	elasomeran	mRNA	Original*
Vaxzevria	AstraZeneca	ChAdOx1-S	viral vector	Original
*Nuvaxovid***	Novavax	SARS-CoV-2 rS	protein subunit	Original*
COVID-19 Vaccine Janssen	Janssen (Johnson & Johnson)	Ad26.COV2.S	viral vector	Original
Comirnaty Original / Omicron BA.1	Pfizer-BioNTech	Tozinameran and riltozinameran	mRNA	Original / BA.1
Comirnaty Original / Omicron BA.4/5	Pfizer-BioNTech	tozinameran and famtozinameran	mRNA	Original / BA.4/5
Comirnaty XBB 1.5	Pfizer-BioNTech	raxtozinameran	mRNA	XBB 1.5
Comirnaty JN.1	Pfizer-BioNTech	bretovameran	mRNA	JN.1
Comirnaty LP.8.1	Pfizer-BioNTech	*SARS-CoV-2 spike protein (mRNA) LP.8.1*	mRNA	*LP.8.1*
Comirnaty XFG	Pfizer-BioNTech	SARS-CoV-2 spike protein (mRNA) XFG	mRNA	XFG

Several iterations targeting different strains have been released globally over time without a name change (the latest targeting XFG), but only the original was approved in New Zealand;Approval not yet expired but vaccine not available (https://www.medsafe.govt.nz/regulatory/DbSearch.asp)*

Genomic surveillance can help illustrate how the changes in the virus over time have moved the circulating lineages away from those present in the vaccine. We summarise below the genetic relatedness between the strains used in the past and present vaccines and the variants currently circulating (**Figure 9**).

Except the highly divergent BA.3.2 lineage, all currently circulating lineages are descendants of JN.1, including NB.1.8.1 (JN.1 x XBB.1 recombinant), The new XFG vaccine is closer to the main lineages circulating globally that encompass a variety of XFG sublineages,

In Pfizer-BioNTech's supportive data for the 2026-2027 formula[2], both LP.8.1 and XFG vaccines elicited similar neutralising responses in naive mice, with strong immune responses against currently circulating JN.1 sublineages (including XFG.1.1, NB.1.8.1, PQ.17, PQ.2.8.1), and diminished responses against BA.3.2.2. The diminished response against BA.3.2.2 was present but to a lower extent in 'vaccine-experienced' mice (that had received the Original and BA.4/5 vaccines beforehand). This pattern is aligned with observations shared in previous CGID reports that BA.3.2 was more frequent in children, a population not exposed to ancestral strains. This new XFG vaccine appears beneficial from a New Zealand perspective, in a national context where a small BA.3.2 wave seems to have already passed our shores and where the XFG lineage has not circulated at high prevalence.

[2] Vaccines and Related Biological Products Advisory Committee. Meeting Presentation - 2026-2027 COVID-19 Vaccine Formula: Pfizer/BioNTech Supportive Data. May 28, 2026. Accessed 11 September 2026. https://www.fda.gov/media/192765/download

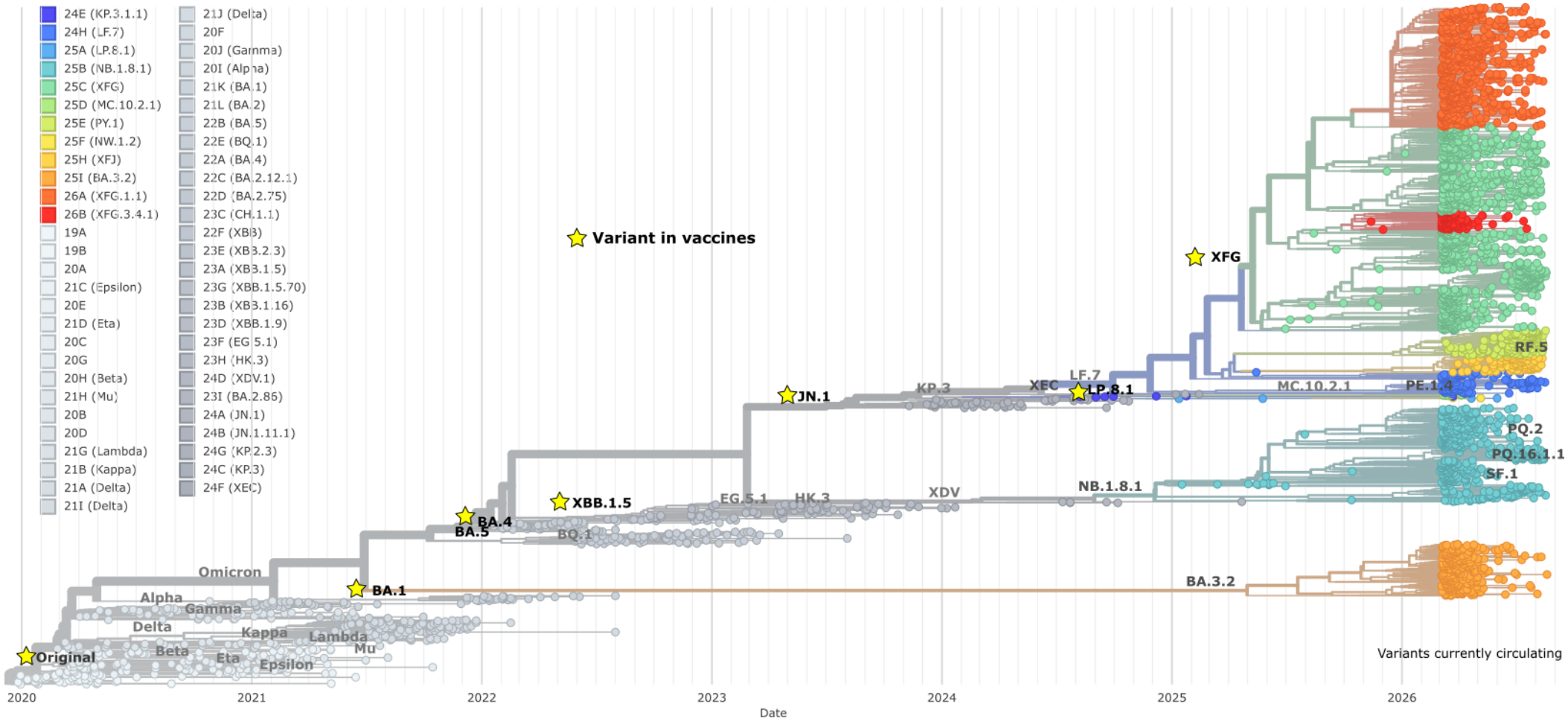


***Figure 9**. Global evolution of SARS-CoV-2 viruses showing (yellow star) the strains targeted in vaccines over time. Phylogenetic tree adapted from nextstrain/ncov with a subsample of 3659 genomes sampled between Dec 2019 and August 2026 and available in NCBI. Recent sequences (<6 months) are oversampled. The Nextstrain clade and WHO designation (Greek letters) are other (coarser) classification methods for SARS=CoV-2 viruses.*

Geographical differences in sampling and prevalence

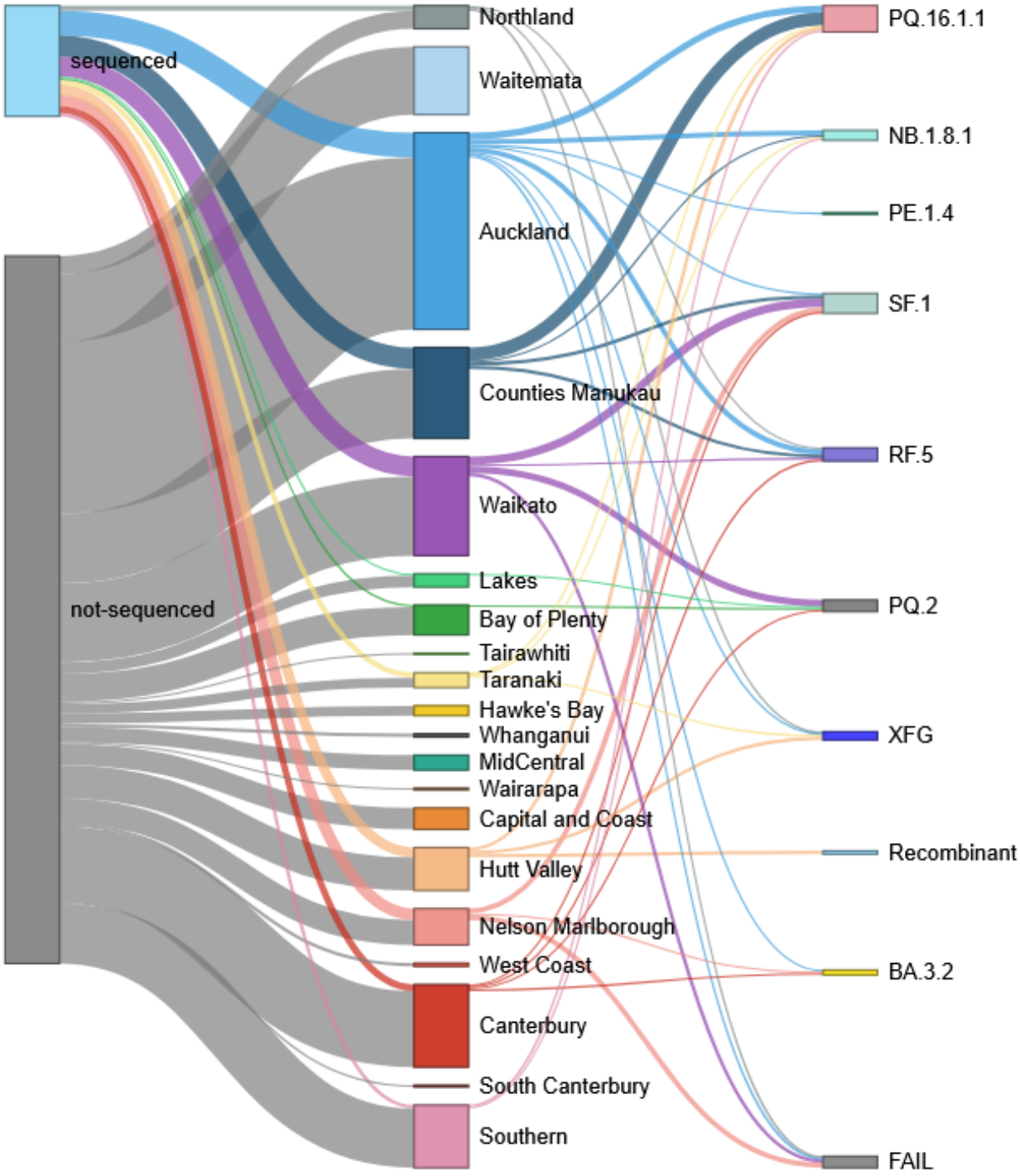


Figure 10. *Origin and sequencing results of the 495 cases reported between 1 August to 4 September 2026 per Health District and lineage. Samples with low viral concentration may provide no sequencing data (FAIL) or partial genomes with insufficient coverage to assign a tracked lineage (Unassigned). Data as of 4pm 8 September 2026.*

Software versions

Lineage assignment done using `pangolin 4.4, pangolin-data 1.40 and nextclade 3.21.0`.