June 2024

COVID-19 Genomics Insights Dashboard (CGID) #49

CGID provides a public and high-level overview of SARS-CoV-2 genomic surveillance across Aotearoa New Zealand. It aims to explore and explain how whole genome sequencing (WGS) complements other epidemiological data to support public health decision-making.

Summary Infographic & Insights:

genomes analysed

1470

genomes* from cases reported since the last CGI report (May 2024)

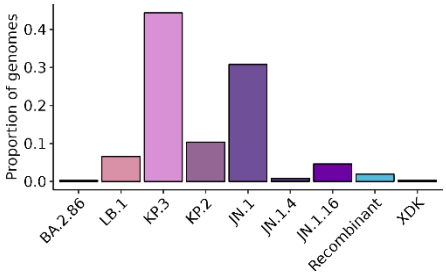
~6000

genomes* reported in 2024

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

variant & lineage

KP.3 has supplanted JN.1 as the main variant (47% vs 29% of genomes), with other variants below 10%: KP.2 (9%), LB.1 (7%) and JN.1.16 (4%)



hospital cases

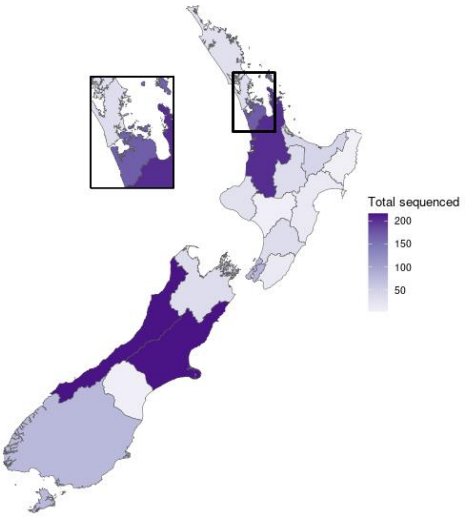
30% (64 of 217*) of PCR-positive cases with a hospital admission date from 31 May to 14 June have been sequenced to date.

The approximate composition of hospital cases:

- **KP.3 40%**
- **JN.1 33%**
- **LB.1 12%**
- **KP.2 6%**
- **JN.1.16 4%**
- **Recombinant 4%**

*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

Key trends and insights

- After a period in which multiple lineages competed to replace JN.1, KP.3 has emerged as most common variant in Aotearoa. Making up 47% of sequenced cases and showing a sustained growth advantage we expect this variant to dominate over the coming weeks.
- No specific sublineage of any of our tracked variants shows a growth rate comparable to that of KP.3. The recombinant XDV.1, which is currently growing rapidly in China, has been detected but is still present only at low levels.
- LB.1, a lineage with three key mutations associated with increased transmission has been added to the list of tracked variants.
- The latest wastewater results mirror those from whole genome sequencing of patient samples.

Data summary and reporting periods

WGS sampling

ESR continues to request PCR-positive samples with PCR Ct values less than 30 (and samples with no recorded Ct) from cases not recently sequenced. Only PCR samples are suitable for WGS, and the COVID-19 Testing Plan prioritises PCR testing for cases in hospital and residential care. For this reason, sequenced cases are not a random or representative sample. As previously reported, the most notable bias is in the age of sequenced cases, which is substantially older than reported cases (**Figure 1**, **Figure 2**). Of note in this report, the bias is apparent from a younger age group (70 to 79) compared to previous reports.

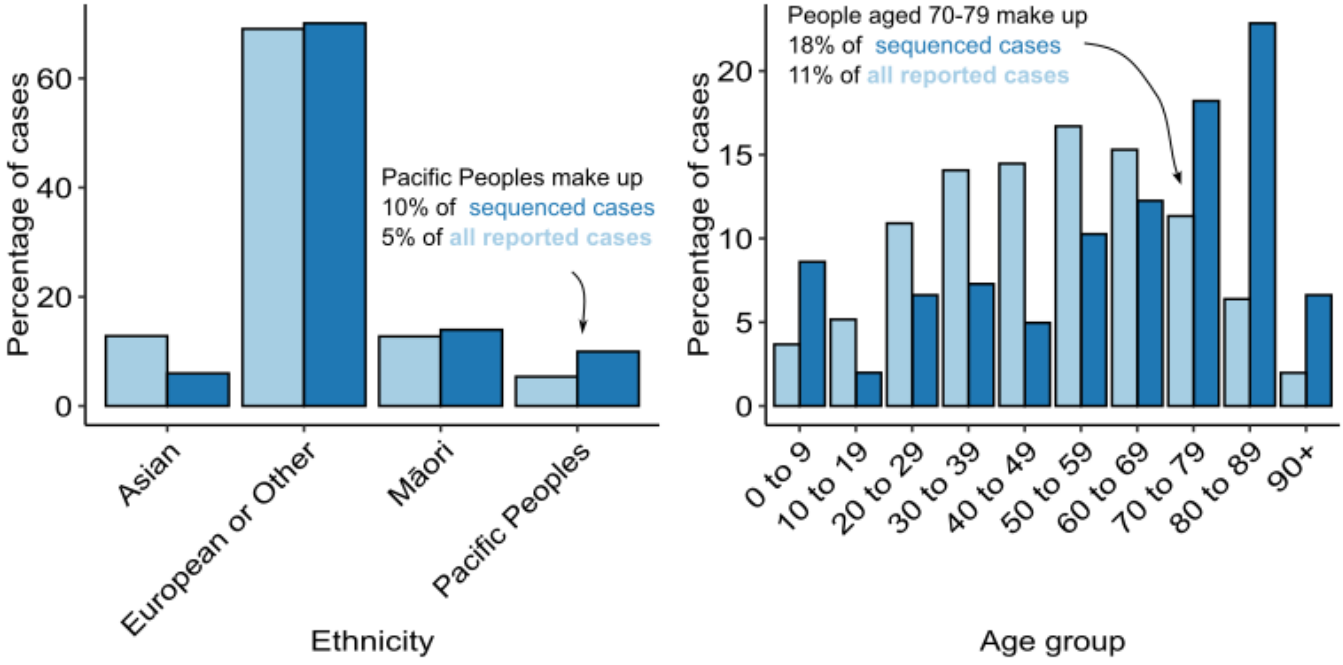


Figure 1. Left: *Distribution of sequenced cases (dark blue) and all reported cases (light blue) by ethnicity. Each case is assigned to a single ethnicity for this analysis, with priority order Māori, Pacific Peoples, Asian, European or Other.* ***Right****: Distribution of reported and sequenced cases by age.*

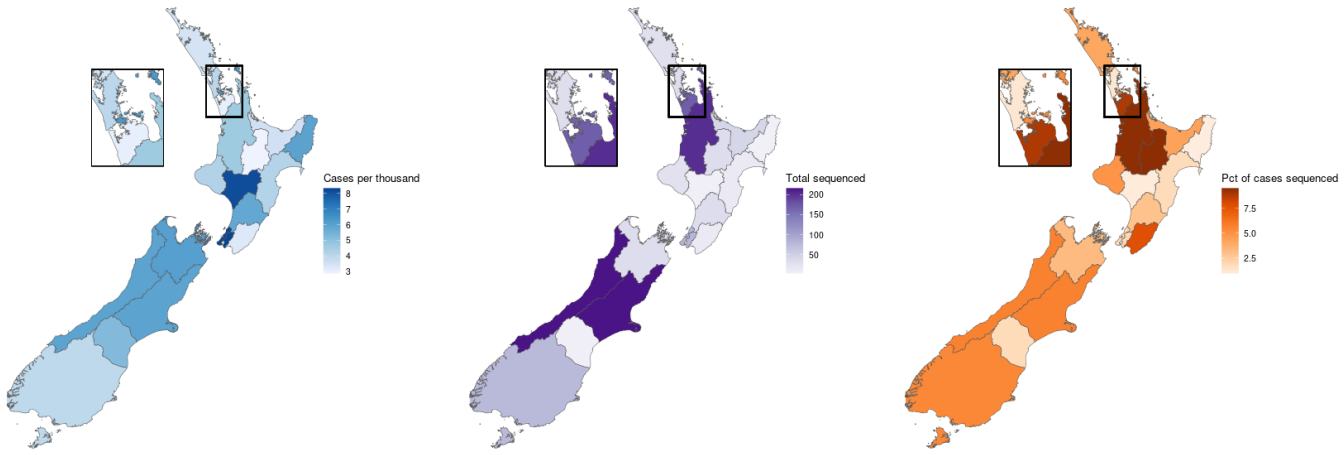


Figure 2. *Geographic sampling of COVID-19 cases and genomes since the last CGI. From left to right, each Health District is shaded by the number of reported COVID-19 cases per thousand, the number of sequences obtained, and the percentage of all reported cases sequenced.*

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 3** describes the set of tracked variants used for this report and how they relate to each other.

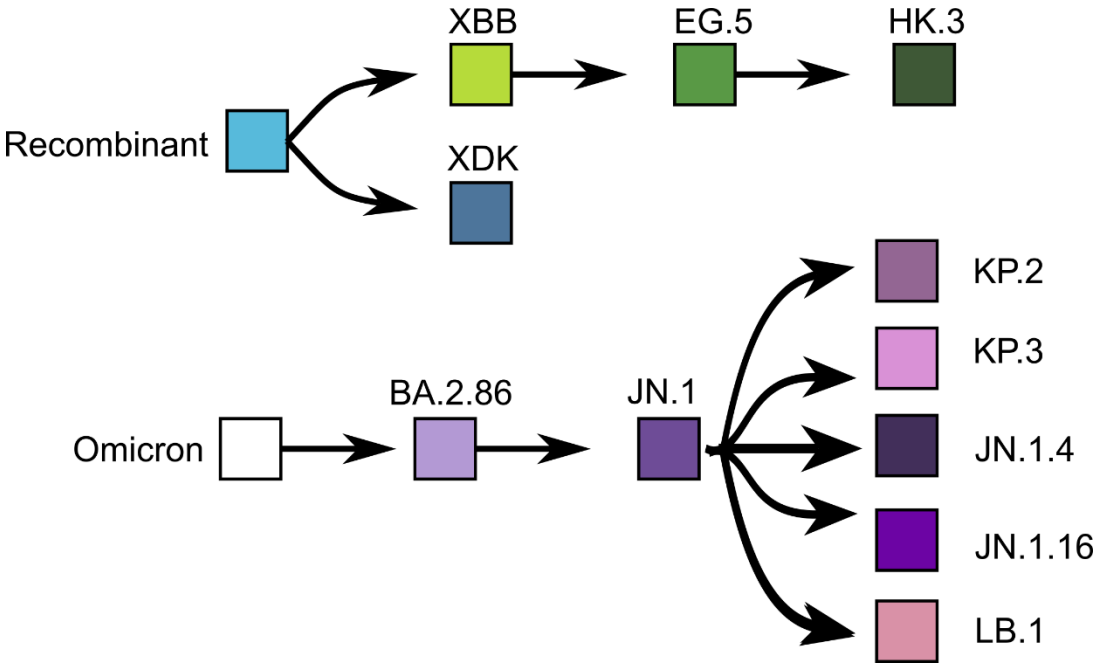


***Figure** 3. Relationships between the variants tracked in this report.*

Changes made since last report

The variants tracked in the CGI reports are frequently updated to reflect trends in SARS-CoV-2 evolution and epidemiology. This month the following changes have been made: BA.2.75 and CH.1.1 have been removed from the list of tracked variants, and LB.1 has been added. The logic for the inclusion/exclusion of these lineages and their properties are described below.

Overview of sequenced cases

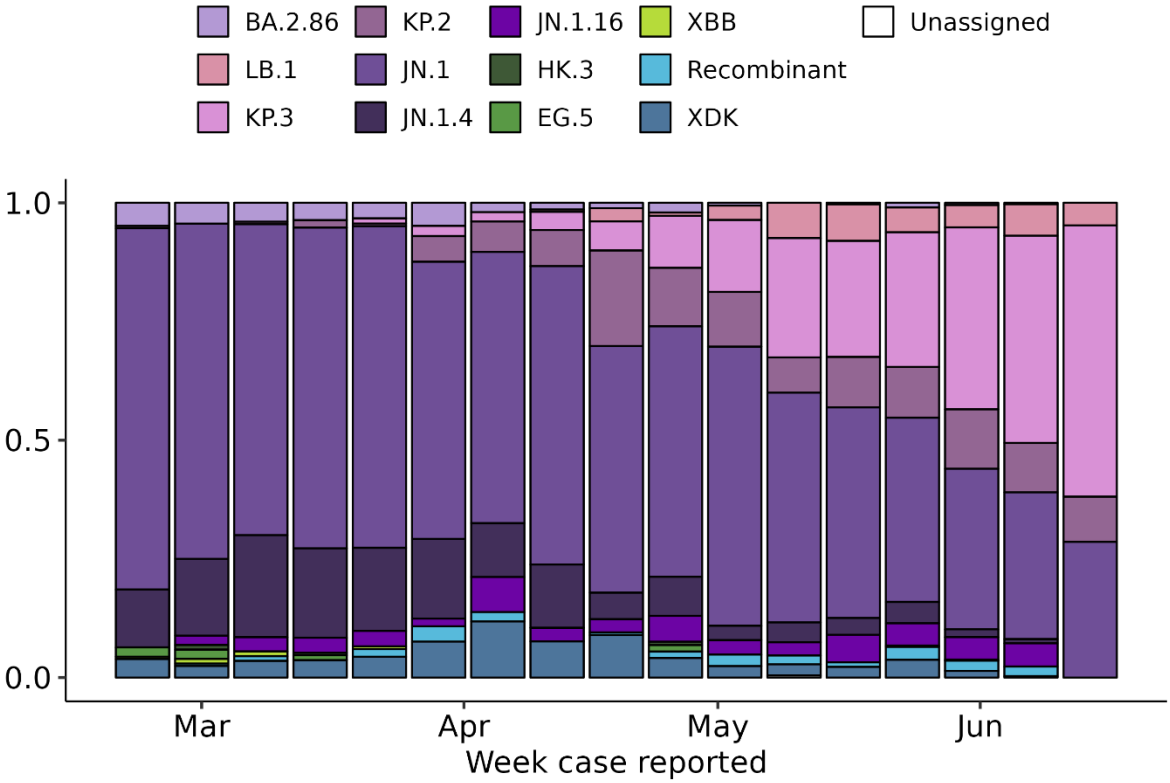


***Figure** 4. Frequency of variants/lineages in the past 17 weeks. Note, data for the most recent two weeks is preliminary. It will be updated as additional cases reported within these weeks are referred to ESR and sequenced. Data from the last reporting week is based on 21 genomes. Tracked lineages are defined in **Figure 3**.*

KP.3 replaces JN.1 as the most common variant in Aotearoa.

Recent CGI reports have focused characterising a set of 'emerging lineages', each of which had acquired mutations that increase the transmissibility of the virus. In this reporting period one of these variants, KP.3, has consistently increased in frequency while other emerging lineages have remained relatively static. As a result, **KP.3 is now the most common tracked variant, being responsible for 47% of sequenced cases** (up from 15% in the last report). Over this period KP.3 has demonstrated an approximately 4% per day growth advantage over the JN.1 category (which includes all descendants of JN.1 not included in another tracked variant).

The growth of KP.3 is consistent with international trends, as KP.3 has consistently grown in genomic surveillance from the USA, Canada, the UK, and Australia. In New Zealand the growth of KP.3 has coincided with a period of elevated case numbers and concentration of the virus in wastewater.

Other variants are static or in decline.

LB.1 has been added to the list of tracked lineages for this report. This lineage was described in detail in the 'emerging lineages' section of the most recent CGI Report (#48) due to its growth rate and the presence of three key mutations (The FLiRT mutations R346T and F456L in addition to a deletion in the spike protein). At the time of last report LB.1 was growing at a rate similar to KP.3 (albeit from a lower base frequency), however that growth has stalled during the current reporting period. LB.1 accounted for 7% of sequenced cases in most recent two-week window but does not exhibit any growth advantage over other JN.1 lineages at present. Give the relatively high frequency of this variant, its previous rapid growth and the presence of these three key mutations LB.1 has been added to the tracked variants to allow close scrutiny of this lineage in future. BA.2.75 and CH.1.1 that have not been detected in New Zealand since February 2024 have been removed from the list of tracked variants.

Emerging Lineages

Most of the tracked variants defined for this report contain several distinct named sublineages, each of which descent from the named variant. ESR analyses SARS-CoV-2 genomic surveillance data closely to identify any sublineage that may display a growth advantage over the currently tracked lineage (**Figure 5**). These so called "emerging lineages" may give an early indication of the arrival or establishment of more transmissible variants in Aotearoa.

At present no emerging lineage has a comparable growth rate to the KP.3 (and no specific KP.3 sublineage appears to be responsible for the growth of this variant). Several lineages currently reported under JN.1 have been singled out for closer examination. KW.1 (which includes KW.1.1, carrying one of the "FLiRT" mutations) an KP.1 represent the (also with one FLiRT mutation) represent most JN.1 genomes and neither are showing a growth advantage at present. JN.1.7 has been the subject of attention overseas but remains rare in New Zealand.

In the last month the XDV.1 lineage has increased rapidly in China and has been detected in Europe, North America and Australia. This variant is a 'multi-recombinant" containing genomic information from the XBB lineage (itself a recombinant) and a JN.1 spike protein (including one FLiRT mutation). Though XDV has been detected in New Zealand it remains at very low levels currently. Given the rapid growth and unique profile XDV this lineage will be watched closely in the coming weeks.

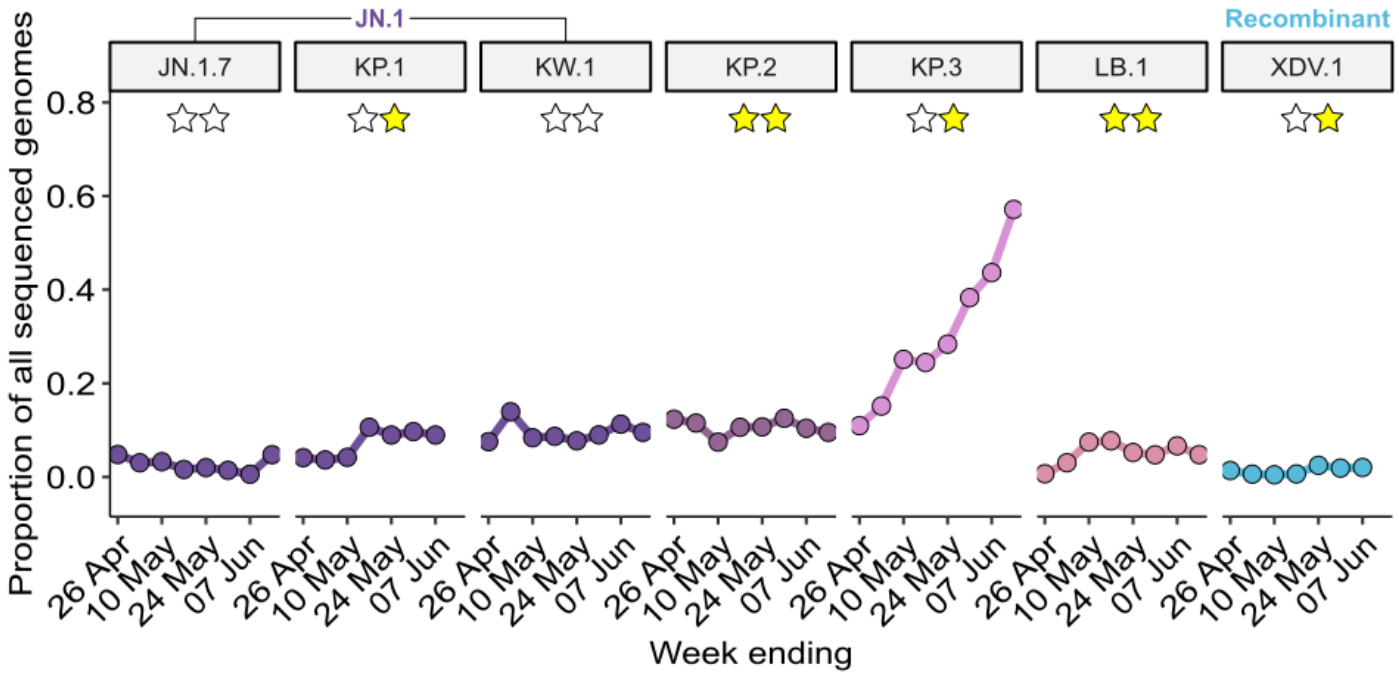


Figure 5. *Frequency of specific lineages in recent weeks. Each sub-plot represents data from a single lineage, and all its descendant lineages not included elsewhere in this graph. The yellow stars above each plot represent the presence of one or both "FLiRT" mutations in each genome. The leftmost three lineages are currently reported within the JN.1 lineage classification*

Tracking Specific Mutations

As previously described in the CGI, the growth of lineages such as KP.3 is part of a wider trend in which key mutations in the spike protein have been observed to provide growth advantages in multiple different JN.1 lineages. As different JN.1 lineages converge on the same set of advantageous mutations, we have begun to track the frequency of these mutations independently of the specific lineages carrying them.The

two FLiRT mutations (R346T and F456L) as well as the deletion found in LB.1 and a substitution labelled T572I were defined as key mutations for tracking.

As KP.3 contains only one of the FLiRT mutations and neither of the other tracked mutations, the rise of KP.3 during this reporting period has led to a decrease in the proportion of genomes containing two or more of these mutations. (**Figure 6**). Tracking these mutations is nevertheless useful, as careful analysis of this data will allow ESR to identify any KP.3 lineage acquiring additional mutations prior to a formal designation of that lineage. ESR will continue monitor the frequency of these mutations and review the inclusion of this analysis for future reports.

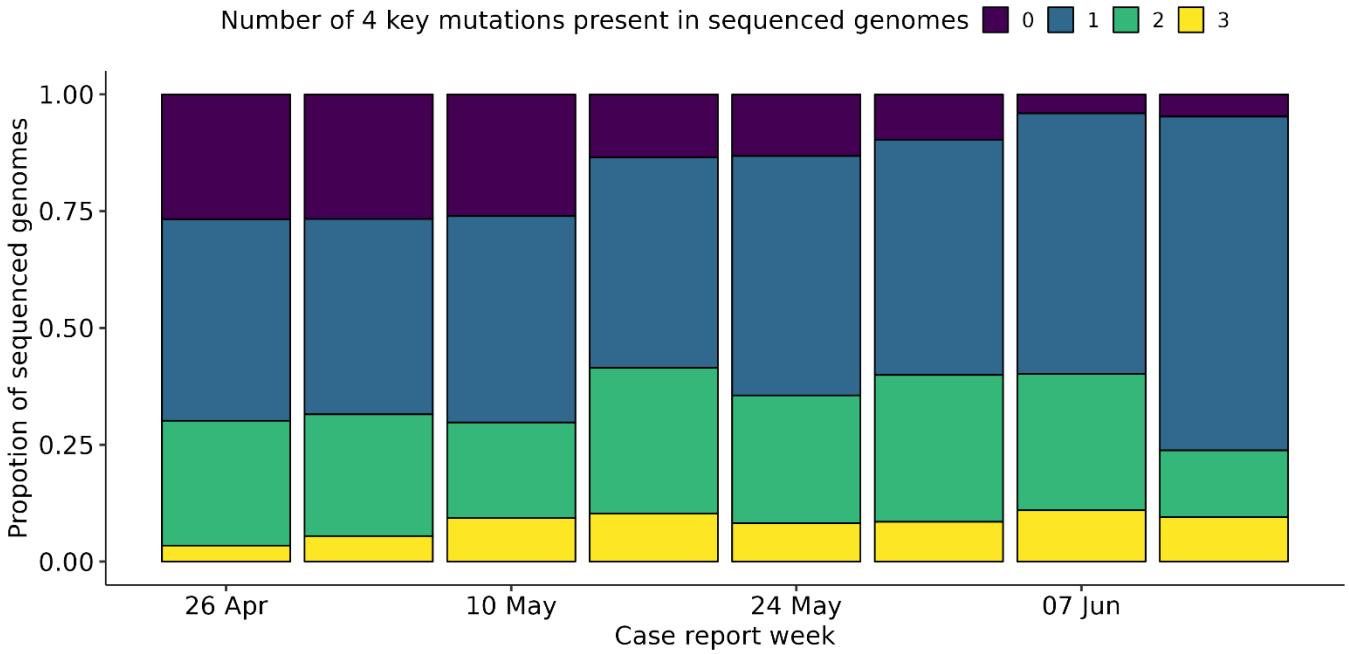


Figure 6. *Frequency of genomes containing between zero and 4 of a set of specific spike protein mutations (R346T, F456L T572I and S31Del) potentially associated with increased transmissibility.*