

This page shows the frequency of the top 7 "L2" lineages for NZ, across recent months.

The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all it's descendants, e.g. the JN.\* lineages.

The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

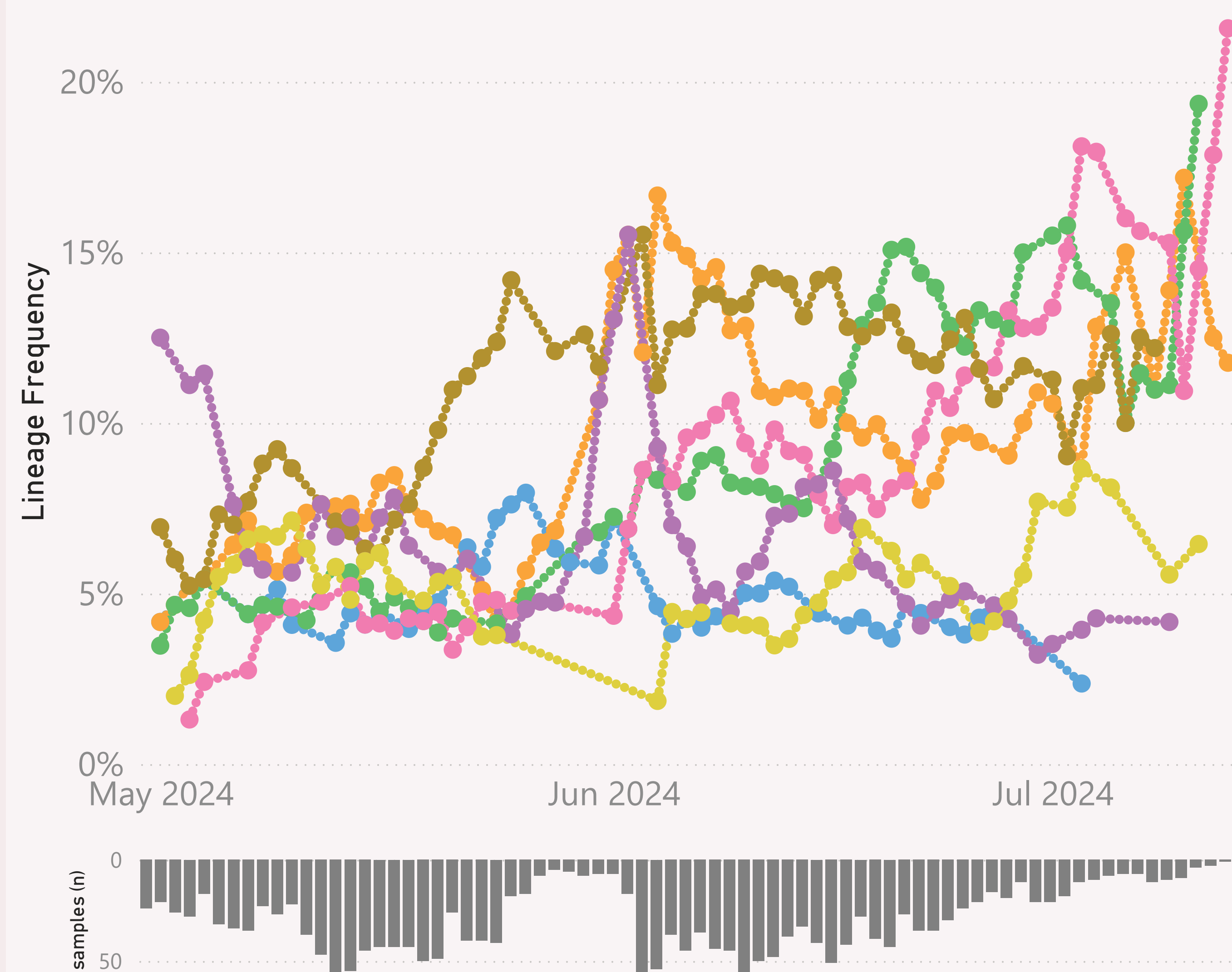
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

## New Zealand

n=2,149 sequenced genomes, up to 14 July 2024

● KP.2 ● KP.3 ● KP.3.1 ● KP.3.1.6 ● KP.3.2 ● KW.1.1 ● LB.1



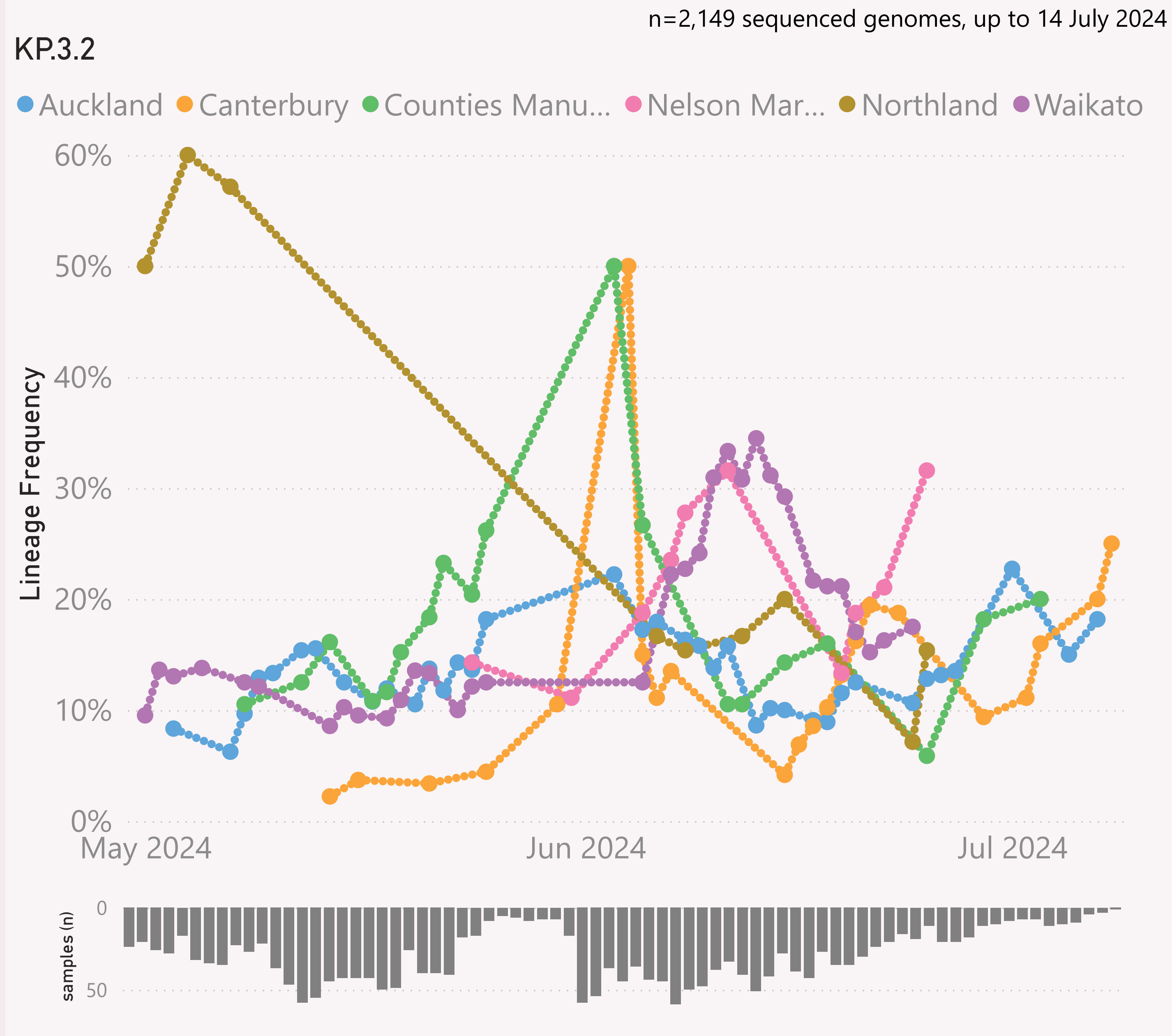
This page shows the frequency of the top 7 lineages for NZ, across recent months.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

The frequency shown at each point is based on the 7-day rolling average across all lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.



This page shows the frequency of a selected Lineage of interest, across the District Health Boards (DHB) of NZ, over recent months. The top 6 locations are shown, based on the volume of samples.

The Lineage classifications are provided by Nextclade.

The frequency shown at each point is based on the 7-day rolling average across all lineages, for that state.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

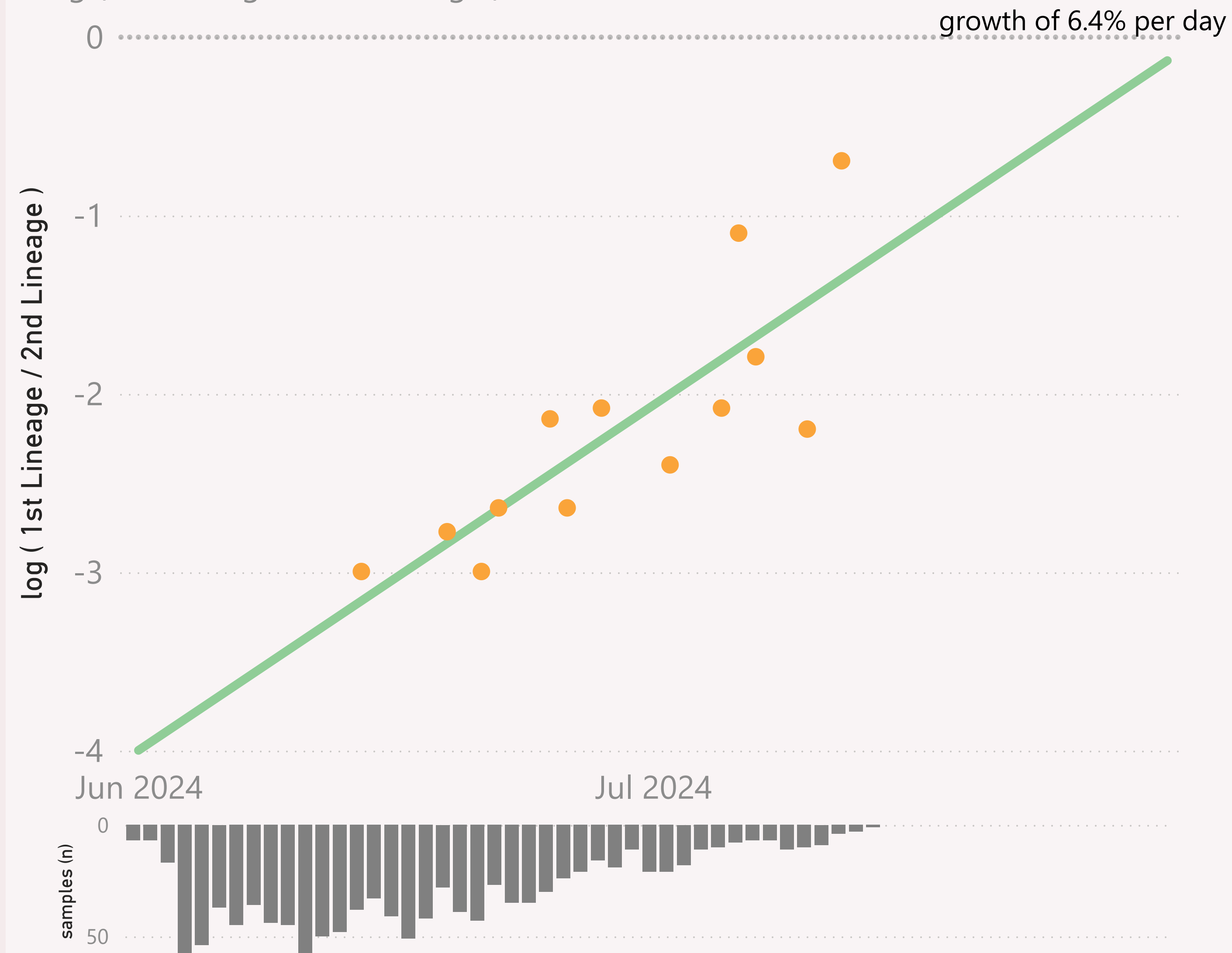
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.



n=1,181 sequenced genomes, up to 14 July 2024

## New Zealand - JN.1.\* +DeFLuQE vs JN.1.\* +FLuQE

●  $\log ( 1st \text{ Lineage} / 2nd \text{ Lineage} )$  ● trend



This page compares the relative frequency of 2 selected "L2" Lineages for NZ, over recent months. A challenging "L2" Lineage is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging "L2" Lineage is considered to have "crossed over" or taken over dominance from the incumbent Lineage

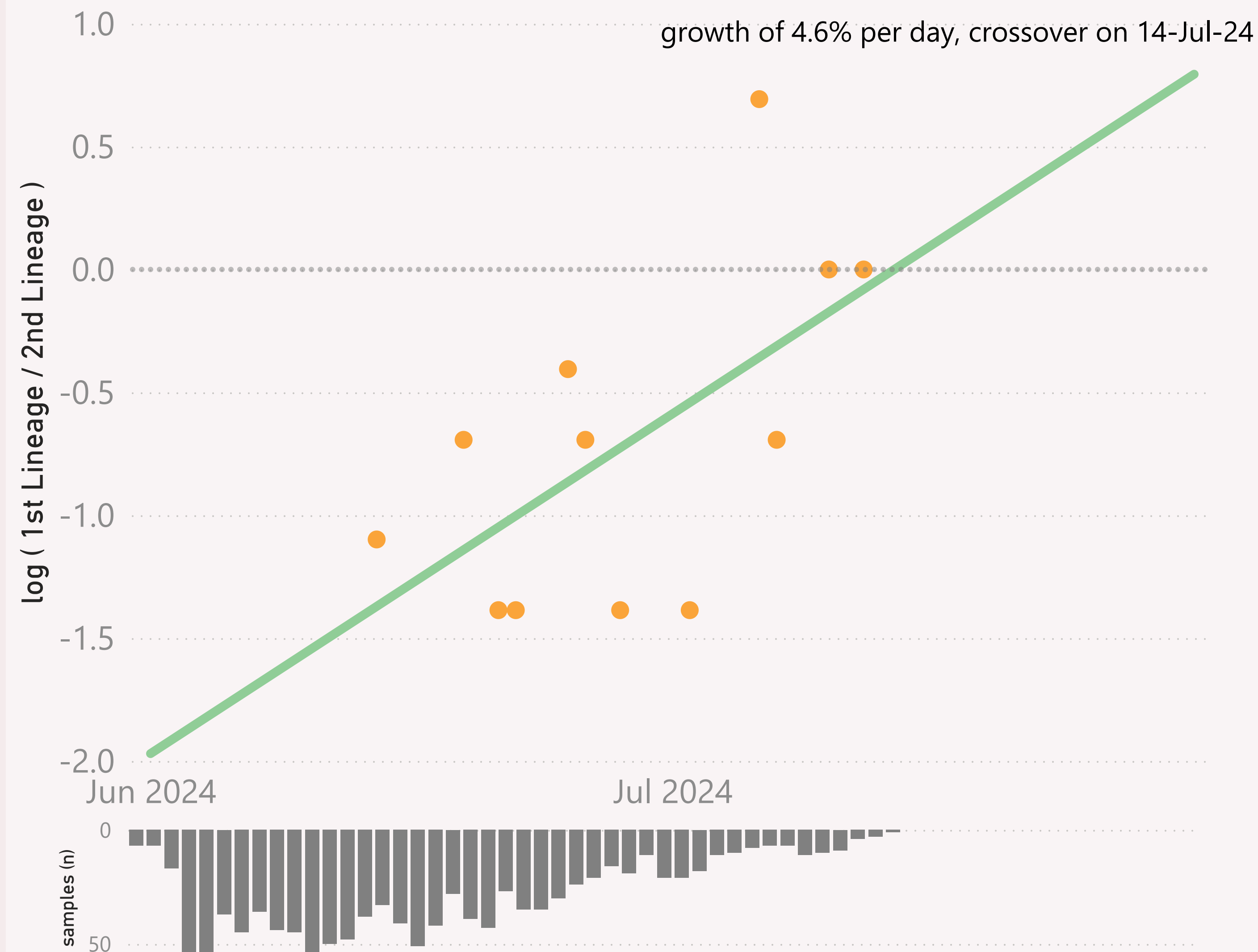
The Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all it's descendants, e.g. the JN.\* lineages.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=1,181 sequenced genomes, up to 14 July 2024

## New Zealand - KP.3.1.1 vs KP.3.1.6

●  $\log ( 1\text{st Lineage} / 2\text{nd Lineage} )$  ● trend



This page compares the relative frequency of 2 selected Lineages for Australia, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the incumbent Lineage

The Lineage classifications are provided by Nextclade.

The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

## New Zealand



## Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
<div><div></div>New Zealand</div>	2,016	7/14/2024		7/22/2024	
Auckland	375	7/12/2024		7/22/2024	
Waikato	296	7/8/2024		7/22/2024	
Canterbury	289	7/14/2024		7/22/2024	
Counties Manukau	201	7/12/2024		7/22/2024	
Southern	180	7/11/2024		7/22/2024	
Hutt Valley	97	7/6/2024		7/22/2024	
Nelson Marlborough	89	7/8/2024		7/22/2024	
Northland	74	7/6/2024		7/22/2024	
Taranaki	74	7/7/2024		7/22/2024	
Bay of Plenty	65	7/11/2024		7/22/2024	
Capital and Coast	57	7/10/2024		7/22/2024	
Waitemata	51	7/11/2024		7/22/2024	
MidCentral	46	7/11/2024		7/22/2024	
Hawkes Bay	45	7/10/2024		7/22/2024	
Lakes	28	7/13/2024		7/22/2024	
Wairarapa	14	7/1/2024		7/22/2024	
West Coast	14	6/18/2024		7/22/2024	
South Canterbury	11	6/24/2024		7/22/2024	
Tairāwhiti	5	6/18/2024		7/22/2024	
Whanganui	5	5/21/2024		6/10/2024	
Total	2,016	7/14/2024		7/22/2024	

This page shows the volume and currency/timeliness of the genomic sequencing data shared for NZ via GISAID, over the last 8 weeks. A breakdown by location is also shown.

Each sample shared comes with a Collection date - when the PCR test for that sample was collected. The GISAID system also records a Submission date for each sample, which is typically the date that sample was uploaded.

The latest date of each type is shown, along with "sparkline"-style mini charts to give a flavour for the spread of recent data by Collection date and by Submission date.