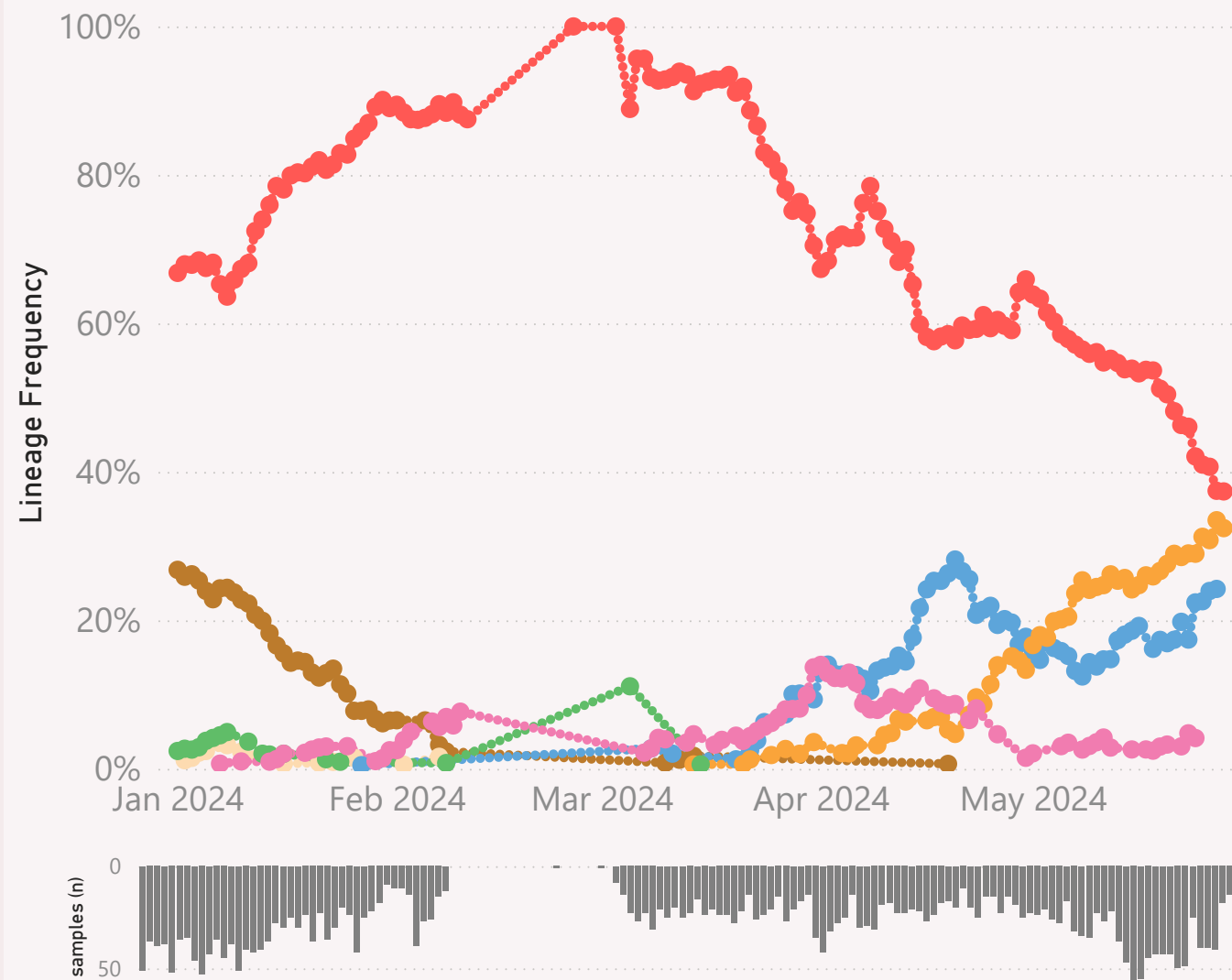


New Zealand

n=3,549 sequenced genomes, up to 28 May 2024

● BA.2.86.* ● EG.5.* ● FL.1.5.1.* ● JN.1.* + FLiRT ● JN.1.* + FLuQE ● XBB.1.5.* ● XDK.*



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 its 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.

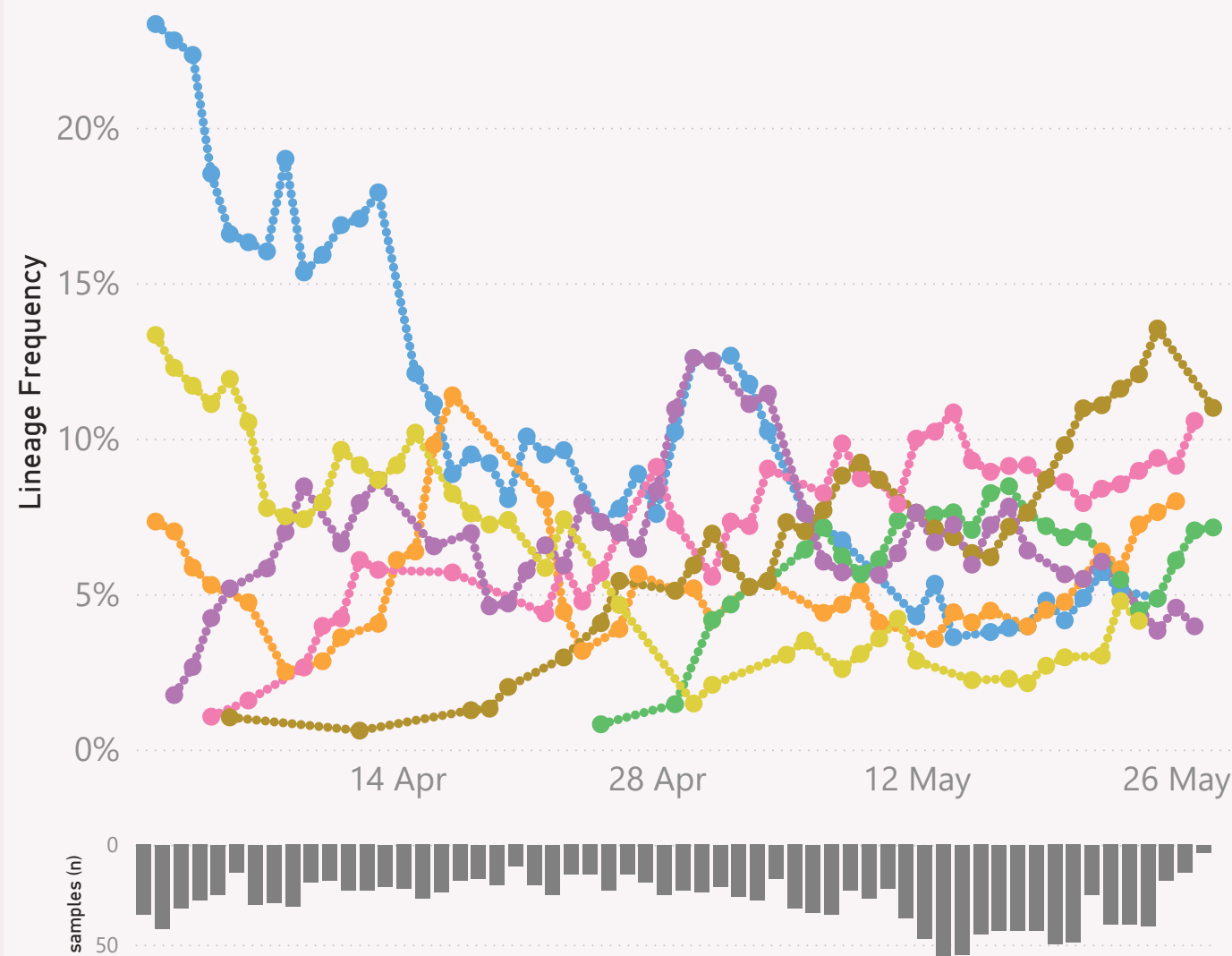
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=1,630 sequenced genomes, up to 28 May 2024

New Zealand

● JN.1 ● KP.2 ● KP.3 ● KP.3.1 ● KP.3.2 ● KW.1.1 ● XDK



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.

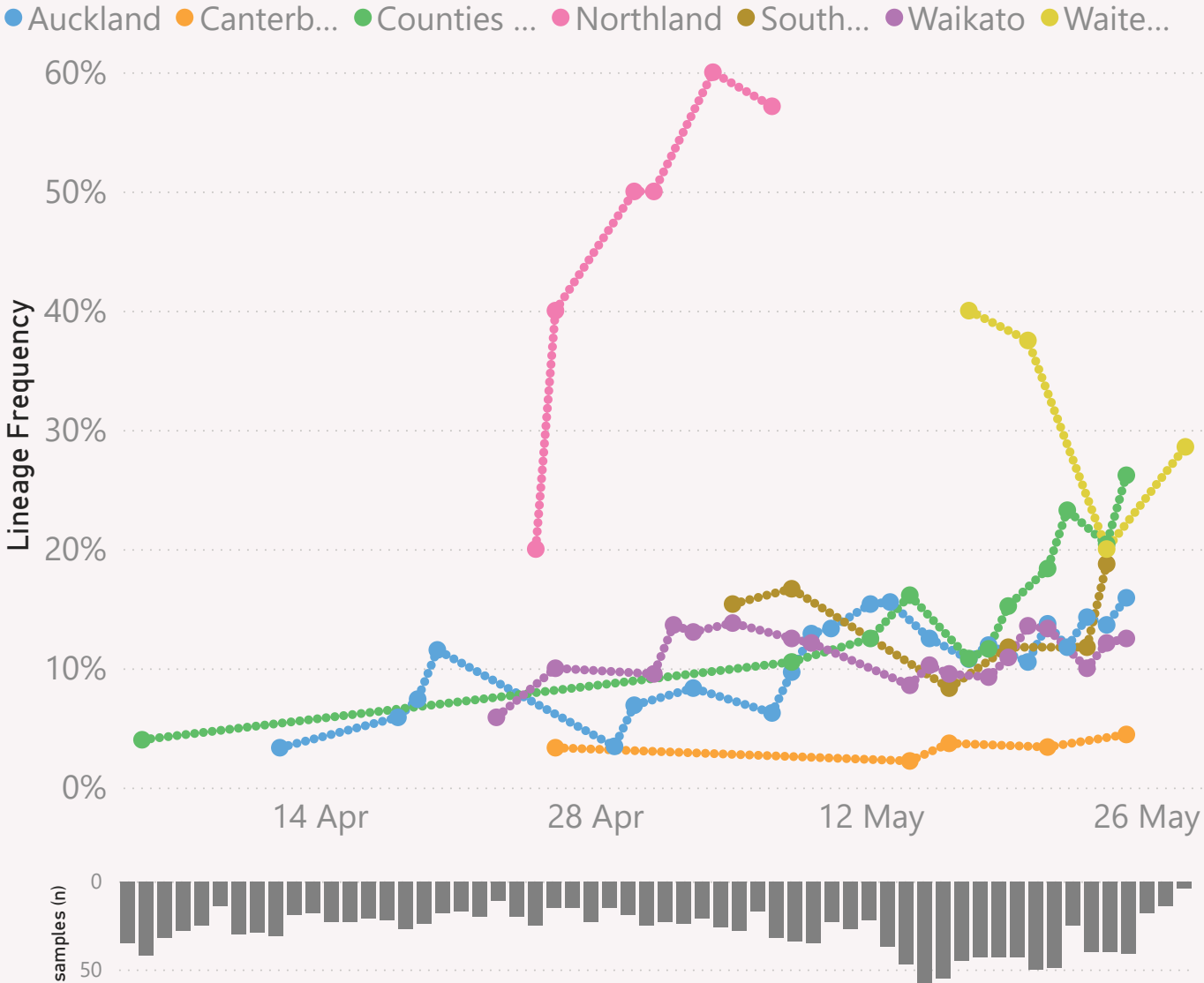
The frequency shown at each point is based on the 7-day rolling average across all lineages.

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.

n=1,630 sequenced genomes, up to 28 May 2024

KP.3.2



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.

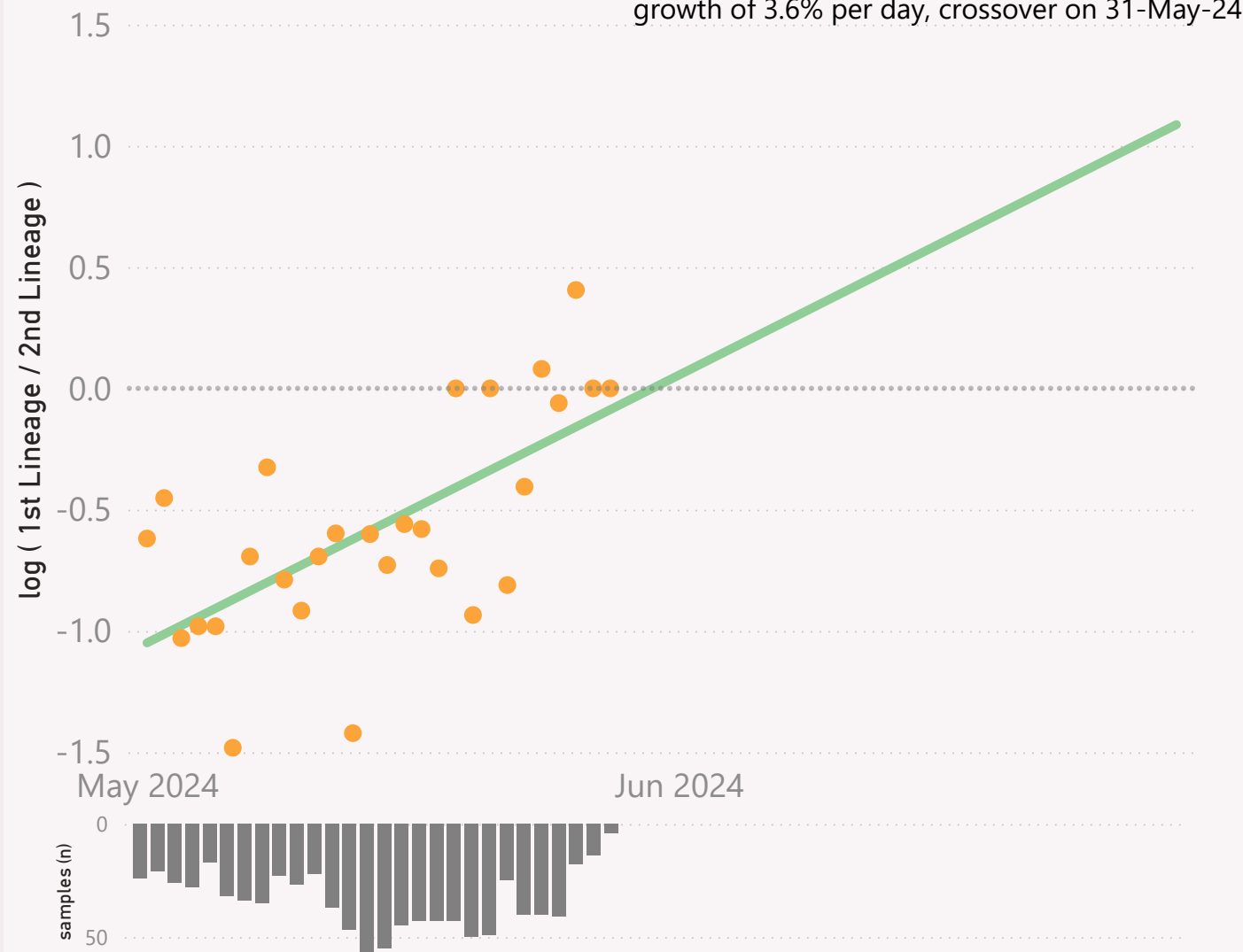
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=941 sequenced genomes, up to 28 May 2024

New Zealand - JN.1.* +FLuQE vs BA.2.86.*

● log (1st Lineage / 2nd Lineage) ● trend

growth of 3.6% per day, crossover on 31-May-24



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.

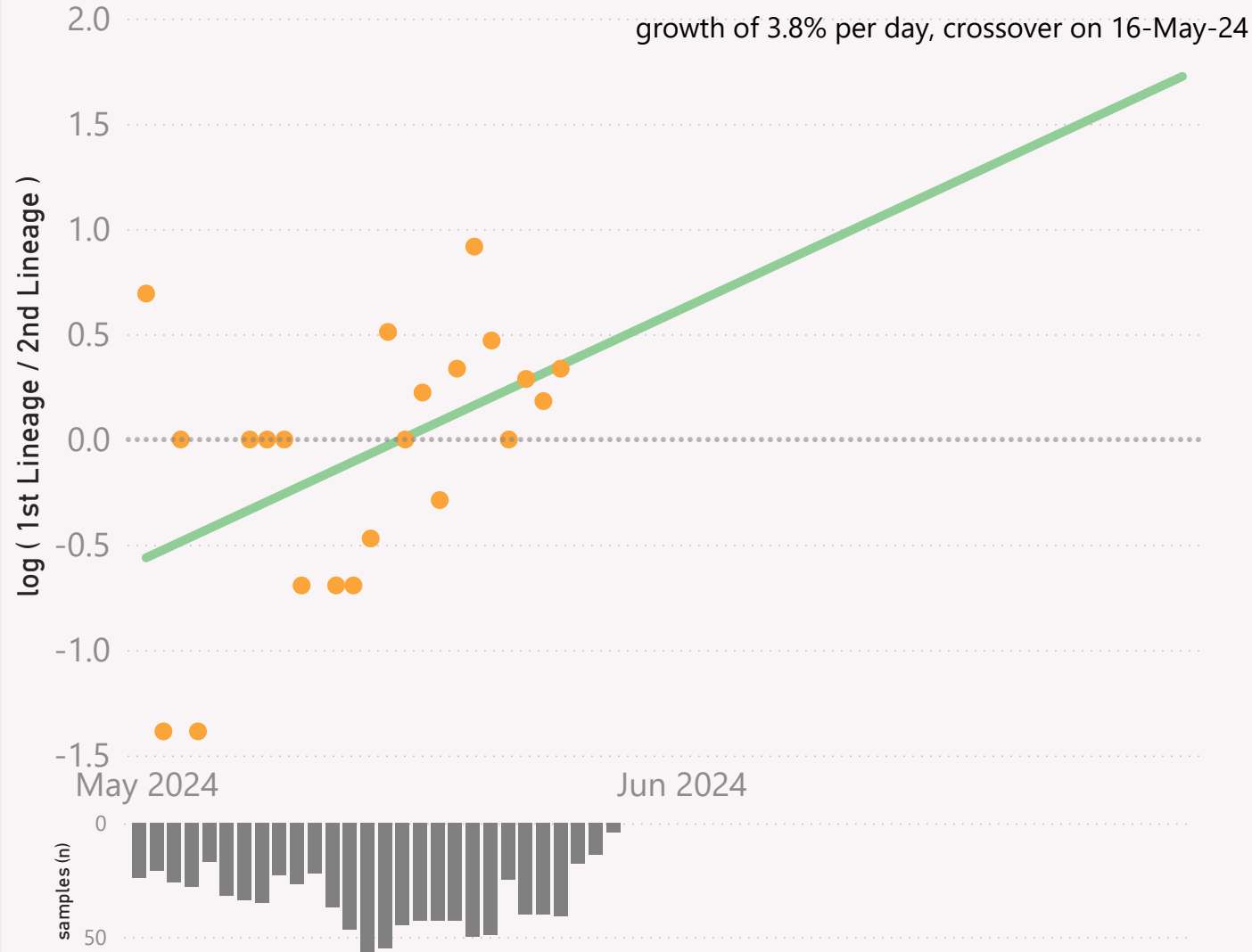
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=941 sequenced genomes, up to 28 May 2024

New Zealand - KP.3.2 vs KP.3.1

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

growth of 3.8% per day, crossover on 16-May-24



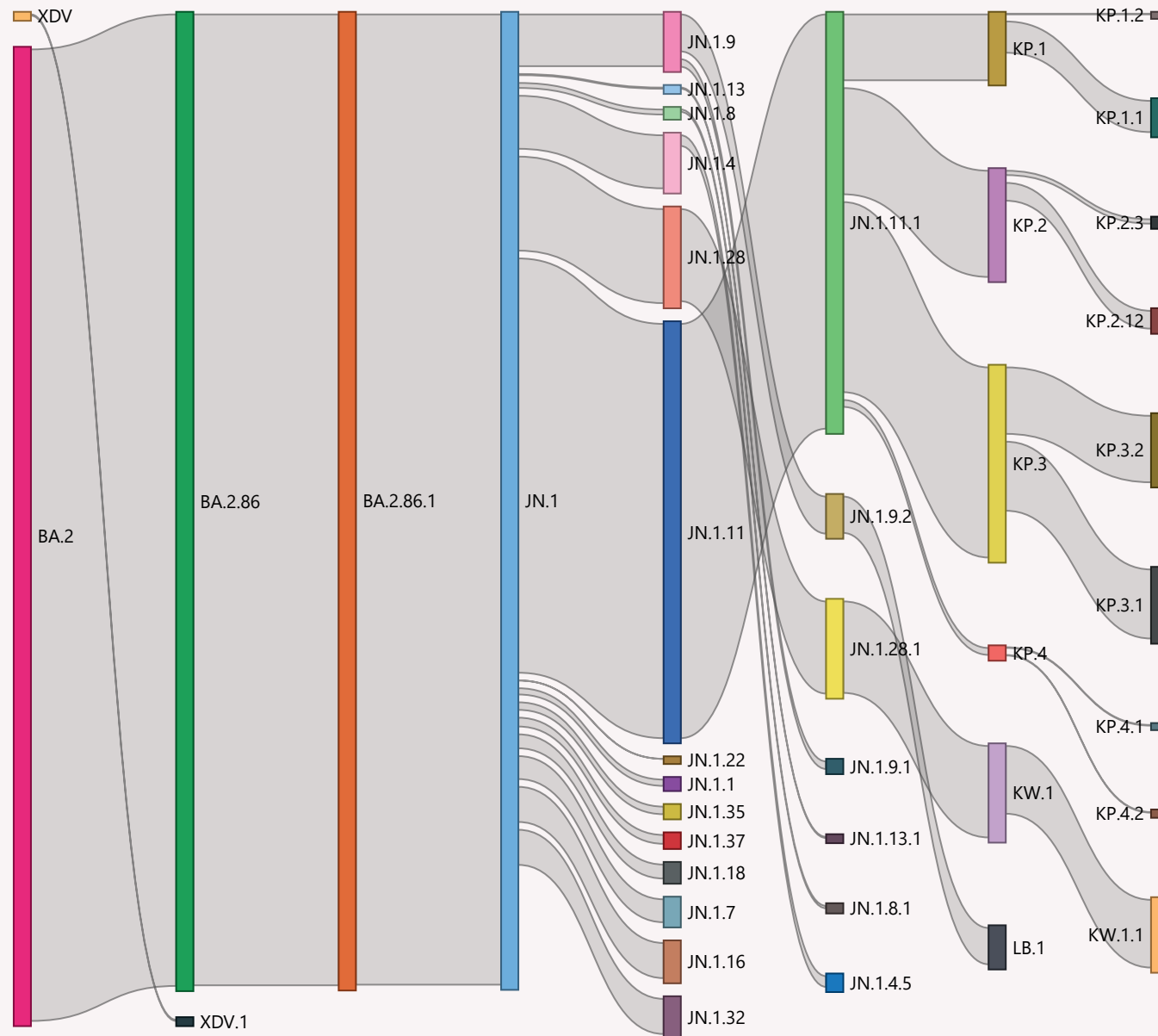
This page compares the relative frequency of 2 selected Lineages for Australia, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

n=1,630 sequenced genomes, up to 28 May 2024



The Lineage classifications are provided by Nextclade.

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
<input checked="" type="checkbox"/> New Zealand	2,210	28/05/2024		10/06/2024	
Auckland	443	28/05/2024		10/06/2024	
Canterbury	417	26/05/2024		10/06/2024	
Waikato	346	26/05/2024		10/06/2024	
Counties Manukau	222	26/05/2024		10/06/2024	
Southern	195	25/05/2024		10/06/2024	
Northland	70	28/05/2024		10/06/2024	
Bay of Plenty	67	21/05/2024		10/06/2024	
Nelson Marlborough	65	27/05/2024		10/06/2024	
Taranaki	62	25/05/2024		10/06/2024	
Hutt Valley	53	25/05/2024		10/06/2024	
Waitemata	52	28/05/2024		10/06/2024	
Lakes	43	25/05/2024		10/06/2024	
Capital and Coast	39	25/05/2024		10/06/2024	
Wairarapa	33	24/05/2024		10/06/2024	
Hawkes Bay	31	28/05/2024		10/06/2024	
MidCentral	31	27/05/2024		10/06/2024	
South Canterbury	15	24/05/2024		10/06/2024	
West Coast	15	20/05/2024		10/06/2024	
Whanganui	8	21/05/2024		10/06/2024	
Tairāwhiti	3	20/05/2024		10/06/2024	
Total	2,210	28/05/2024		10/06/2024	

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.