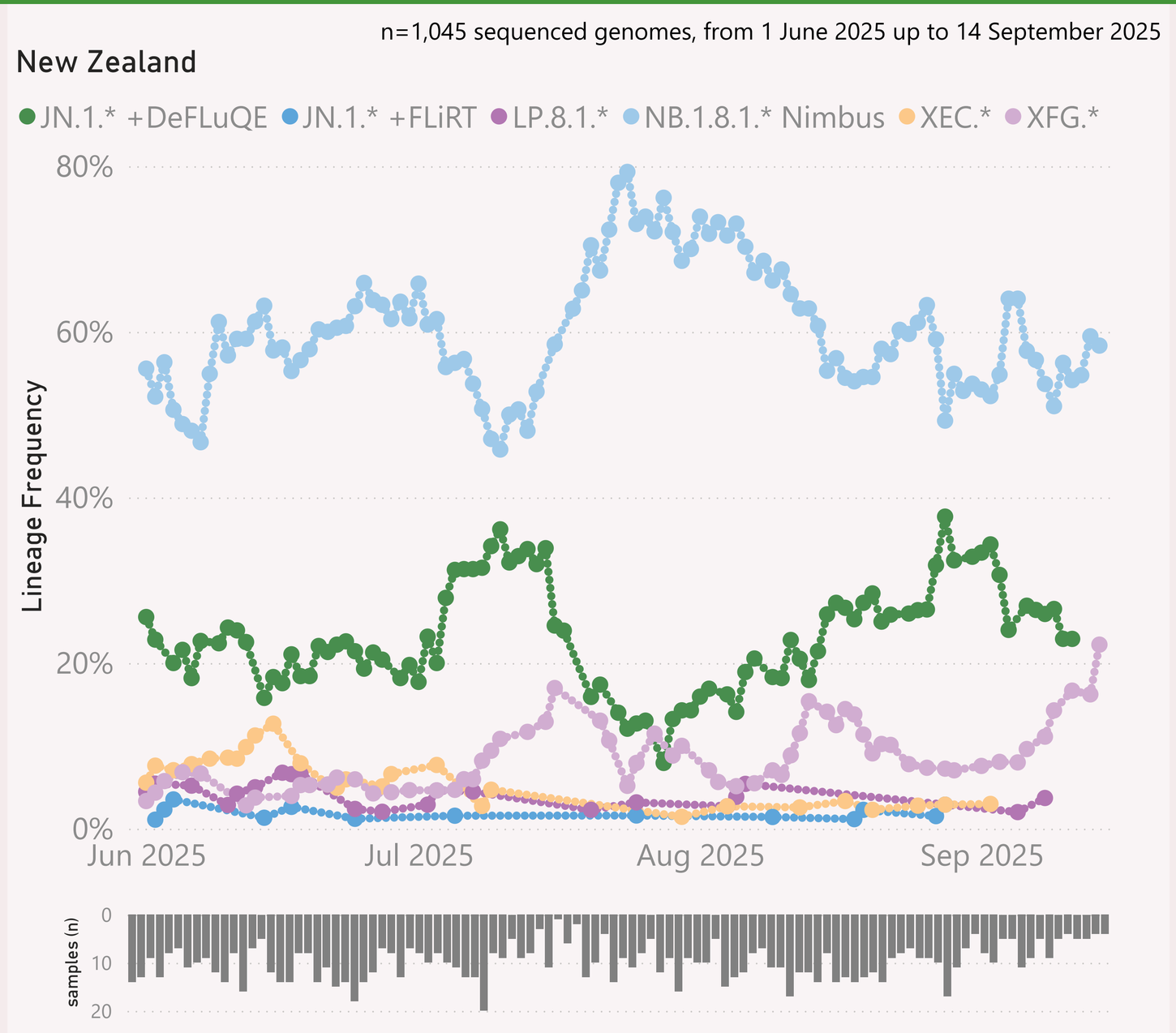
n=1,045 sequenced genomes, from 1 June 2025 up to 14 September 2025



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.

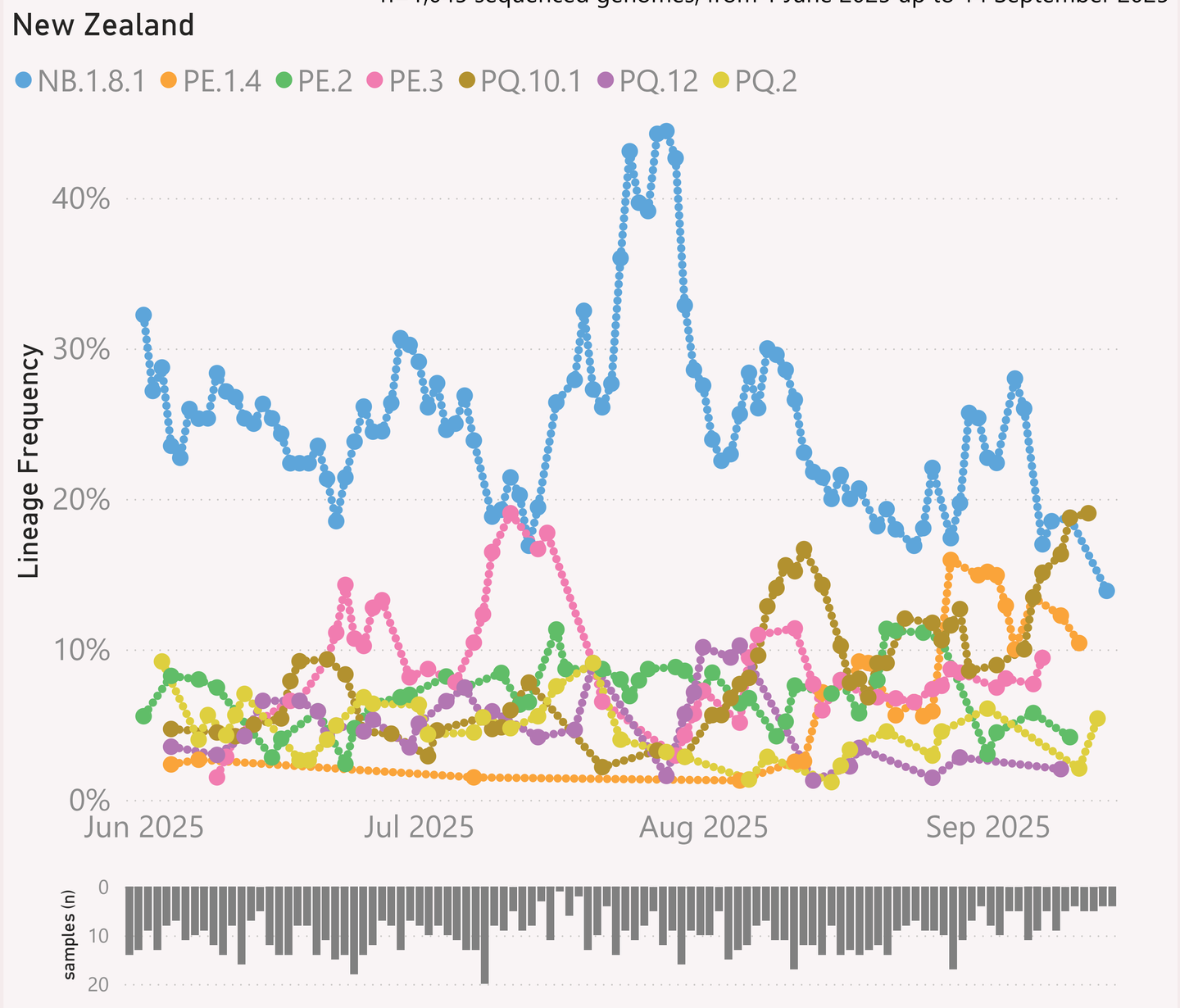
The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

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.

n=1,045 sequenced genomes, from 1 June 2025 up to 14 September 2025



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

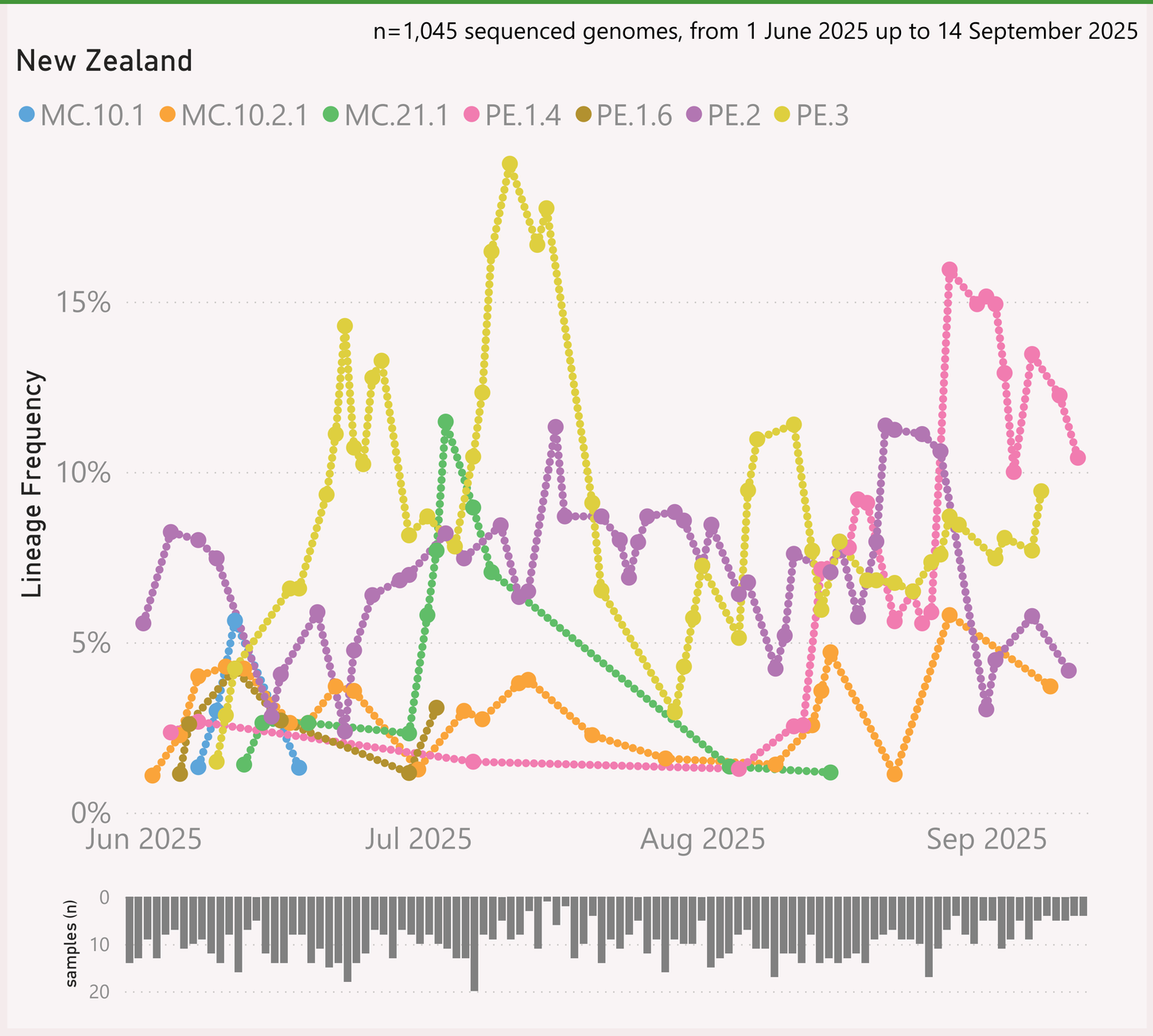
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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.

COVID-19 Genomic Sequencing analysis. Lineage Frequencies. Data from gisaid.org, with nextclade lineages. Source files and more info on github. Last Update: 2025-09-26 22:42 (UTC)



This page shows the frequency of the top 7 lineages for NZ, across recent months, for a selected Lineage L2 group.

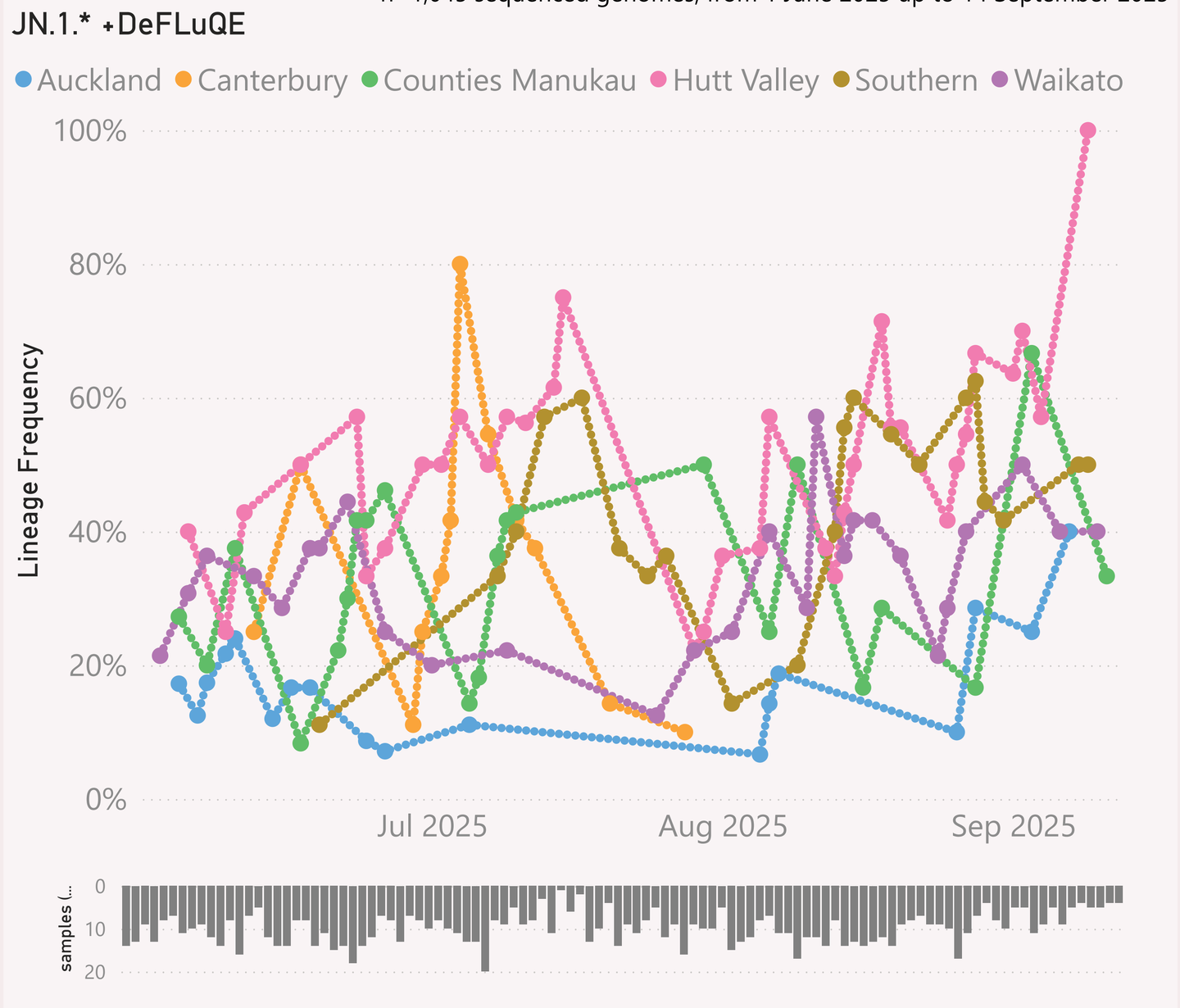
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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=1,045 sequenced genomes, from 1 June 2025 up to 14 September 2025



This page shows the frequency of a selected Lineage L2 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.

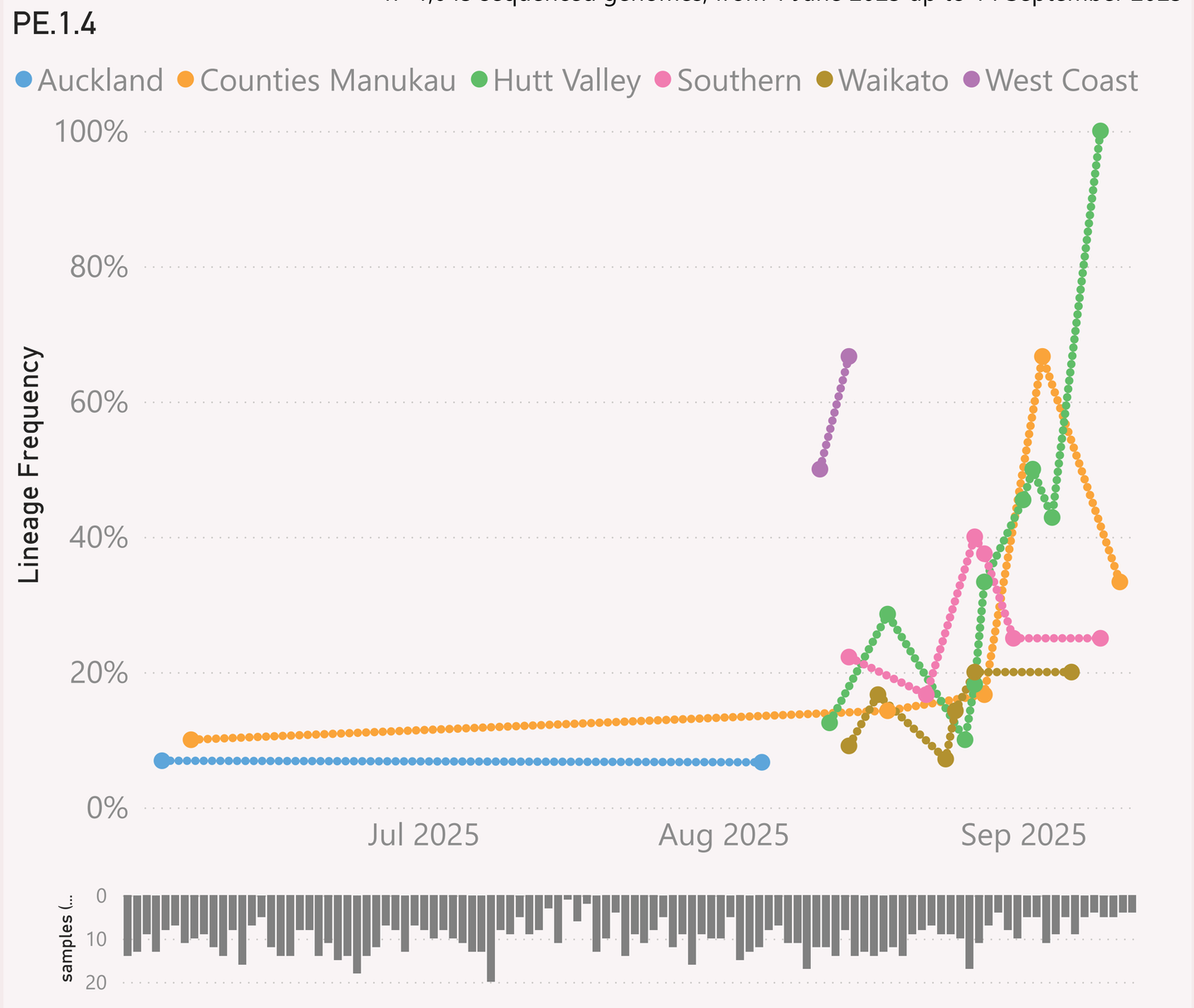
The Lineage classifications are provided by Nextclade.

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

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=1,045 sequenced genomes, from 1 June 2025 up to 14 September 2025



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.

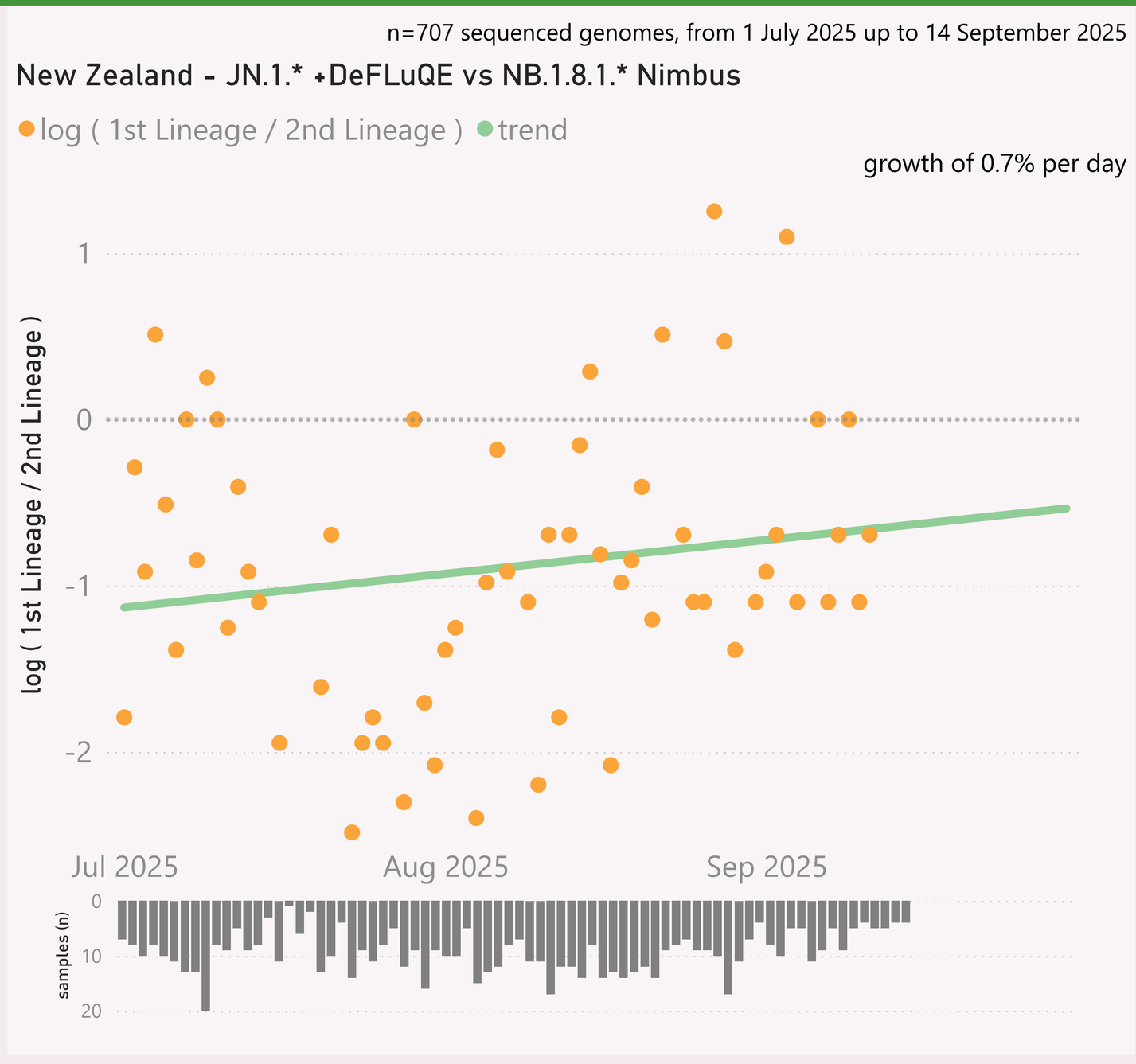
The Lineage classifications are provided by Nextclade.

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=707 sequenced genomes, from 1 July 2025 up to 14 September 2025

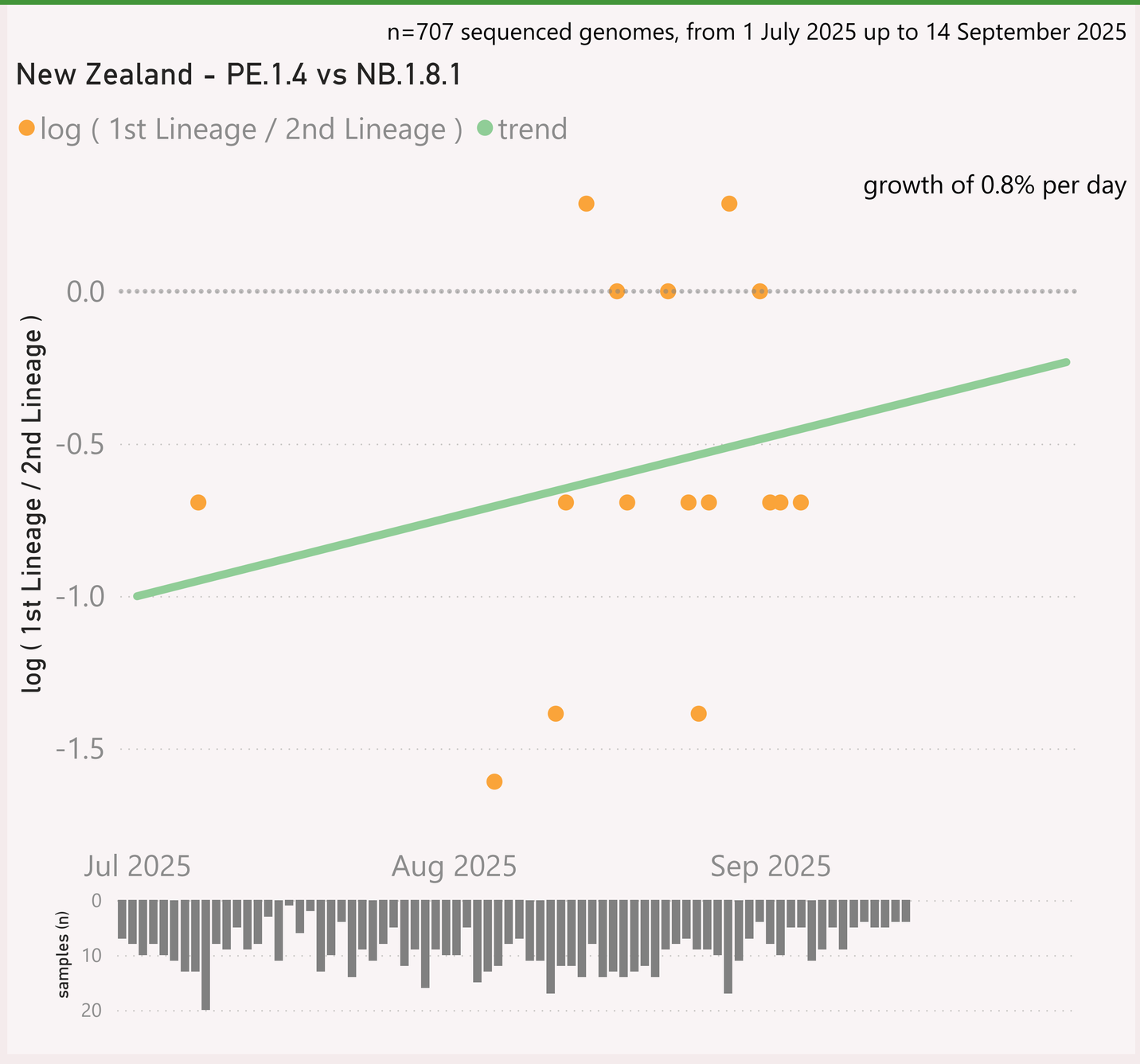


This page compares the relative frequency of 2 selected "L2" Lineages for NZ, over recent months. A challenging "L2" Lineage is selected first, and compared to the incumbent.

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.



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

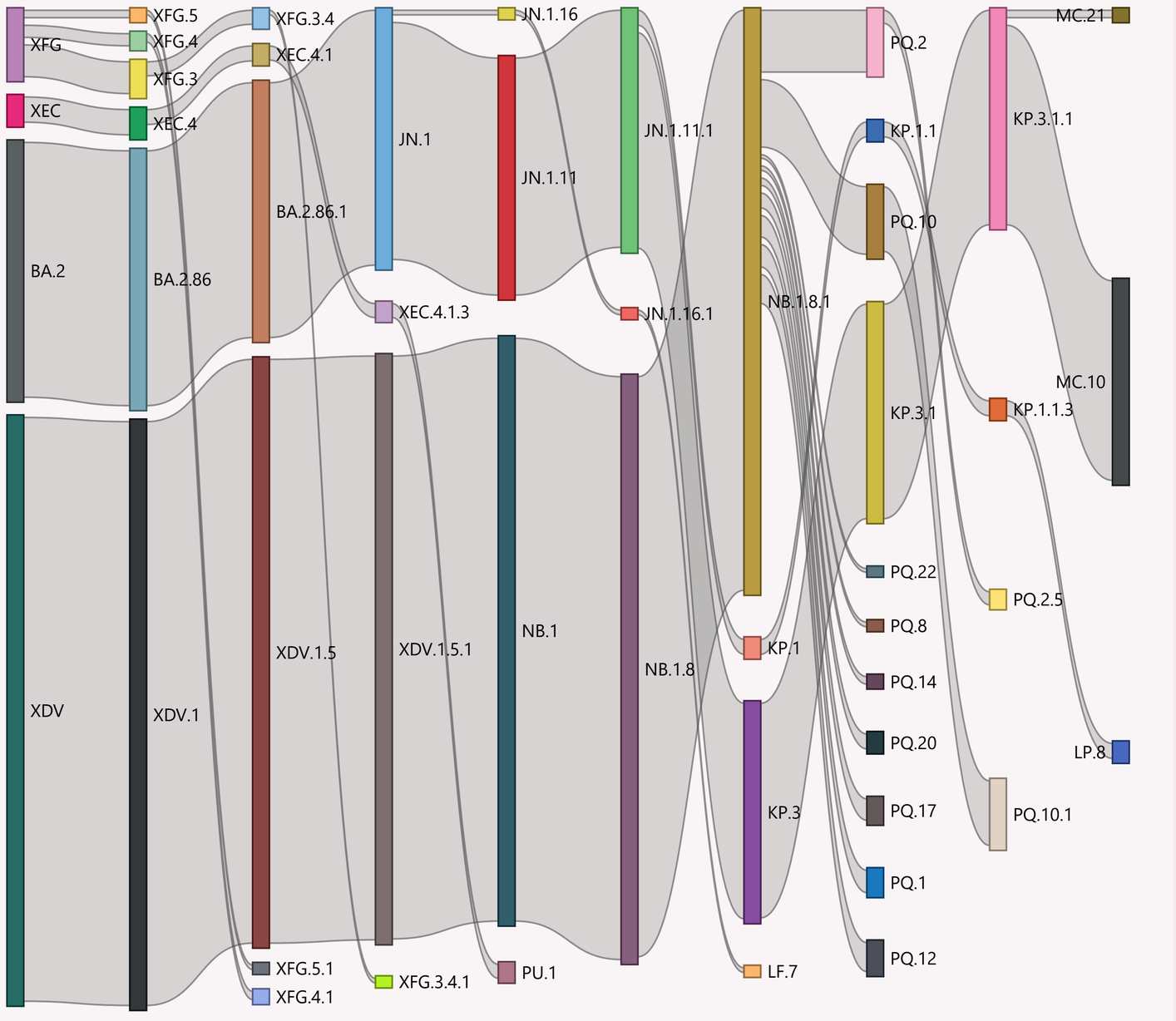
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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=1,045 sequenced genomes, from 1 June 2025 up to 14 September 2025

New Zealand



This page shows the hierarchy of the significant Lineages for NZ, over recent months.

The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

The full picture is typically quite busy, so insignificant Lineages (with few samples, or at the extreme top or bottom of the hierarchy) are not shown.

The Lineage classifications are provided by Nextclade.

COVID-19 Genomic Sequencing analysis - Data Currency. Data from gisaid.org. Source files and info on github.

Last Update: 2025-09-26 22:42 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
New Zealand	**564**	**14/09/2025**		**17/09/2025**	
Auckland	98	14/09/2025		17/09/2025	
Waikato	79	13/09/2025		17/09/2025	
Hutt Valley	60	10/09/2025		17/09/2025	
Southern	58	09/09/2025		17/09/2025	
Northland	48	14/09/2025		17/09/2025	
Canterbury	39	10/09/2025		17/09/2025	
Counties Manukau	38	11/09/2025		17/09/2025	
MidCentral	37	09/09/2025		17/09/2025	
Taranaki	33	12/09/2025		17/09/2025	
Waitemata	14	14/09/2025		17/09/2025	
Bay of Plenty	12	07/09/2025		16/09/2025	
Hawkes Bay	11	05/09/2025		16/09/2025	
West Coast	9	23/08/2025		01/09/2025	
Capital and Coast	7	05/09/2025		16/09/2025	
Nelson Marlborough	7	02/09/2025		16/09/2025	
Whanganui	7	06/09/2025		16/09/2025	
Lakes	4	24/08/2025		08/09/2025	
Wairarapa	2	11/09/2025		17/09/2025	
South Canterbury	1	06/09/2025		16/09/2025	
Total	**564**	**14/09/2025**		**17/09/2025**	

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.