

This page shows the frequency of the top 6 "L2" lineages, across recent months.

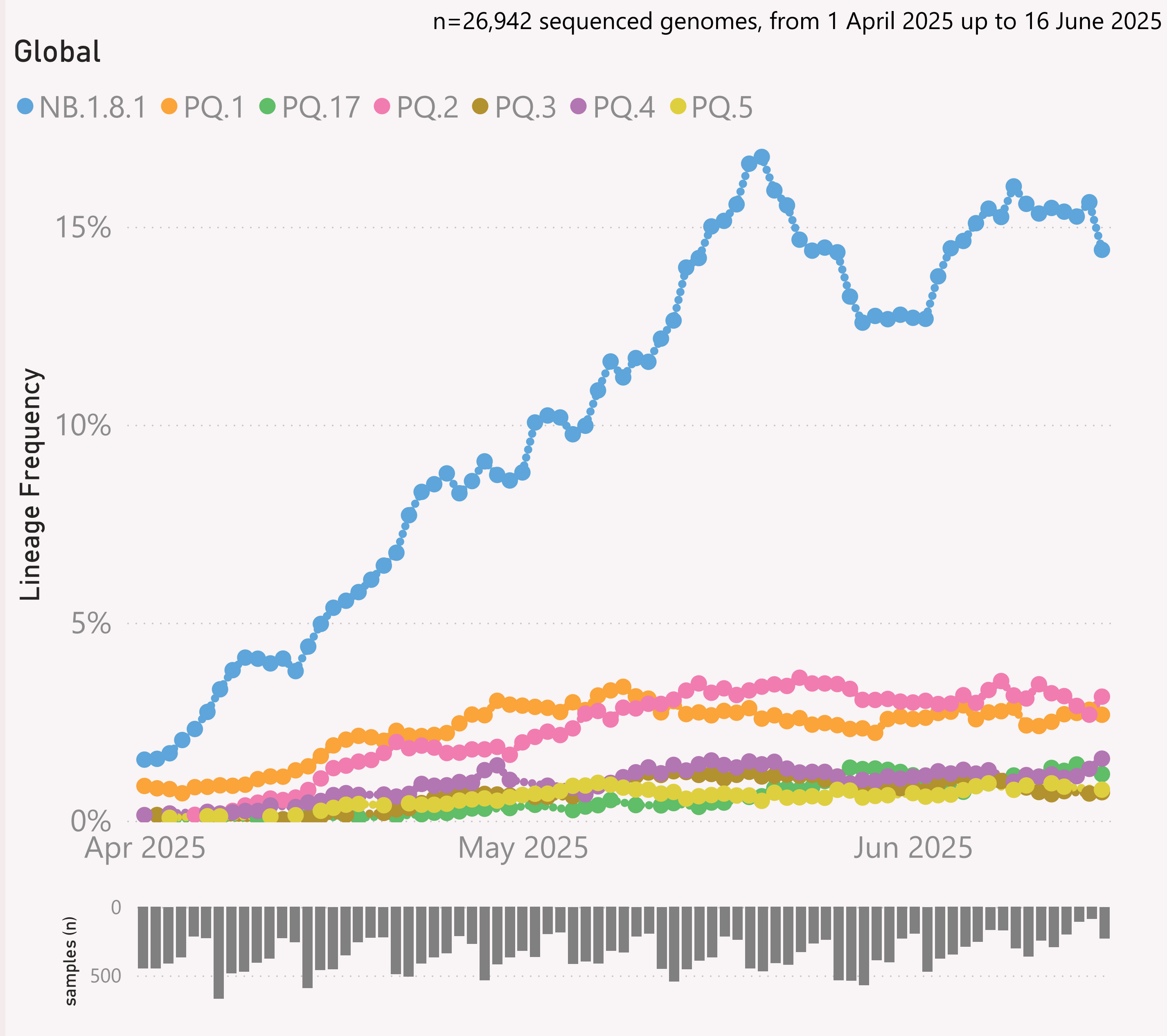
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all it's descendants, e.g. the JN.\* lineages.

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.



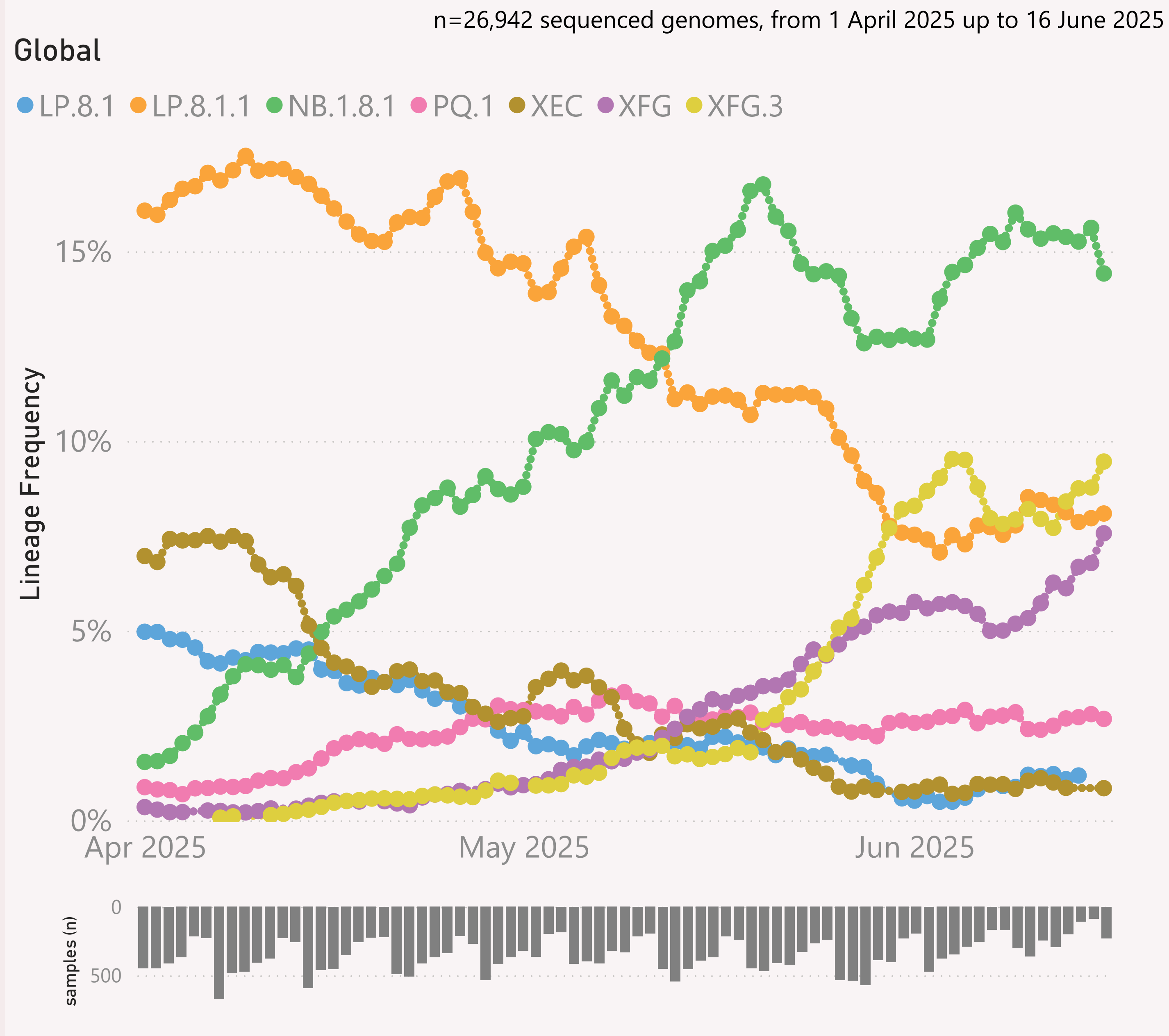
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.\* Nimbus.

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 the top 7 lineages, across recent months.

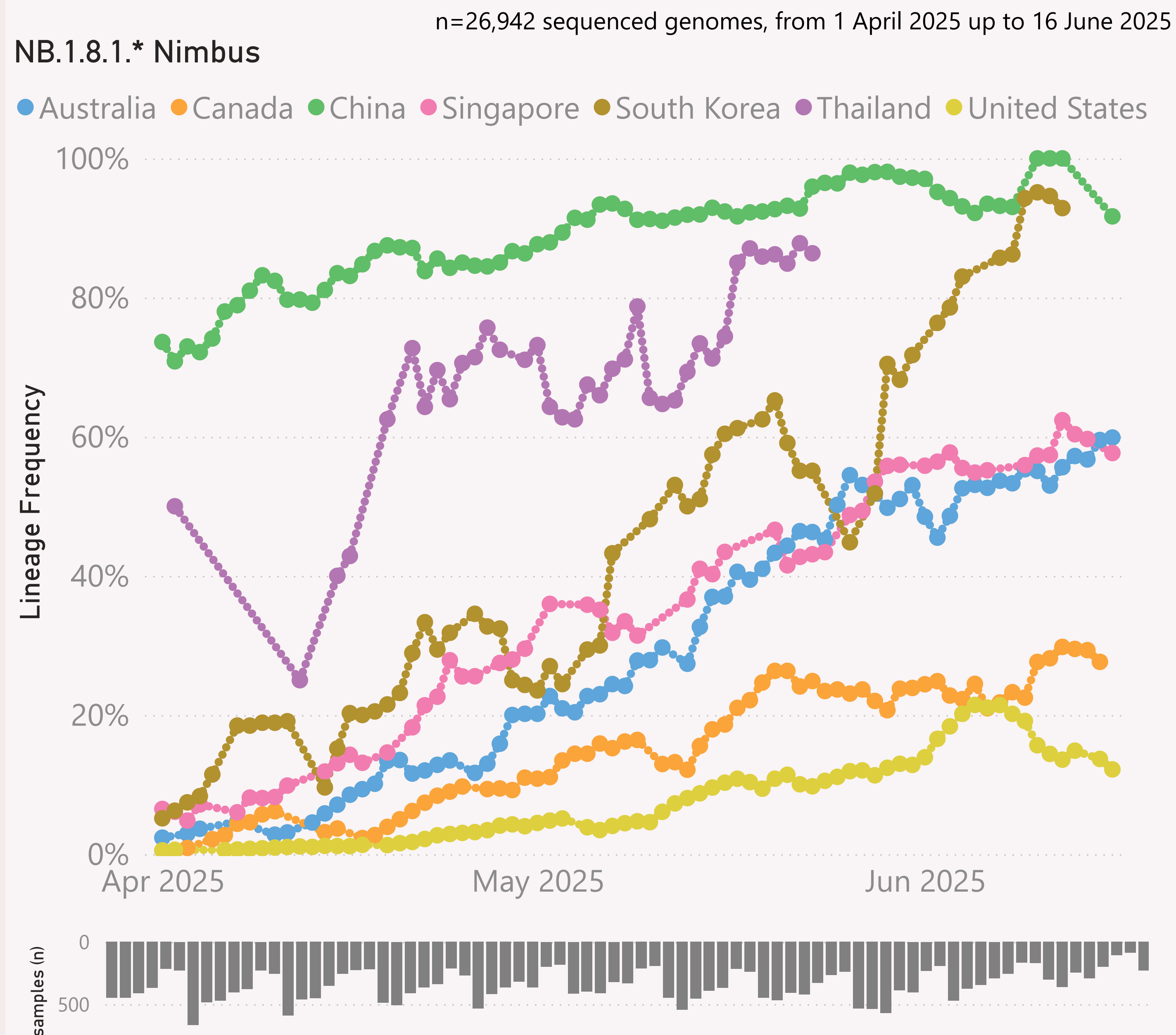
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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 L2" group of interest, for the 7 countries reporting the most samples over recent months.

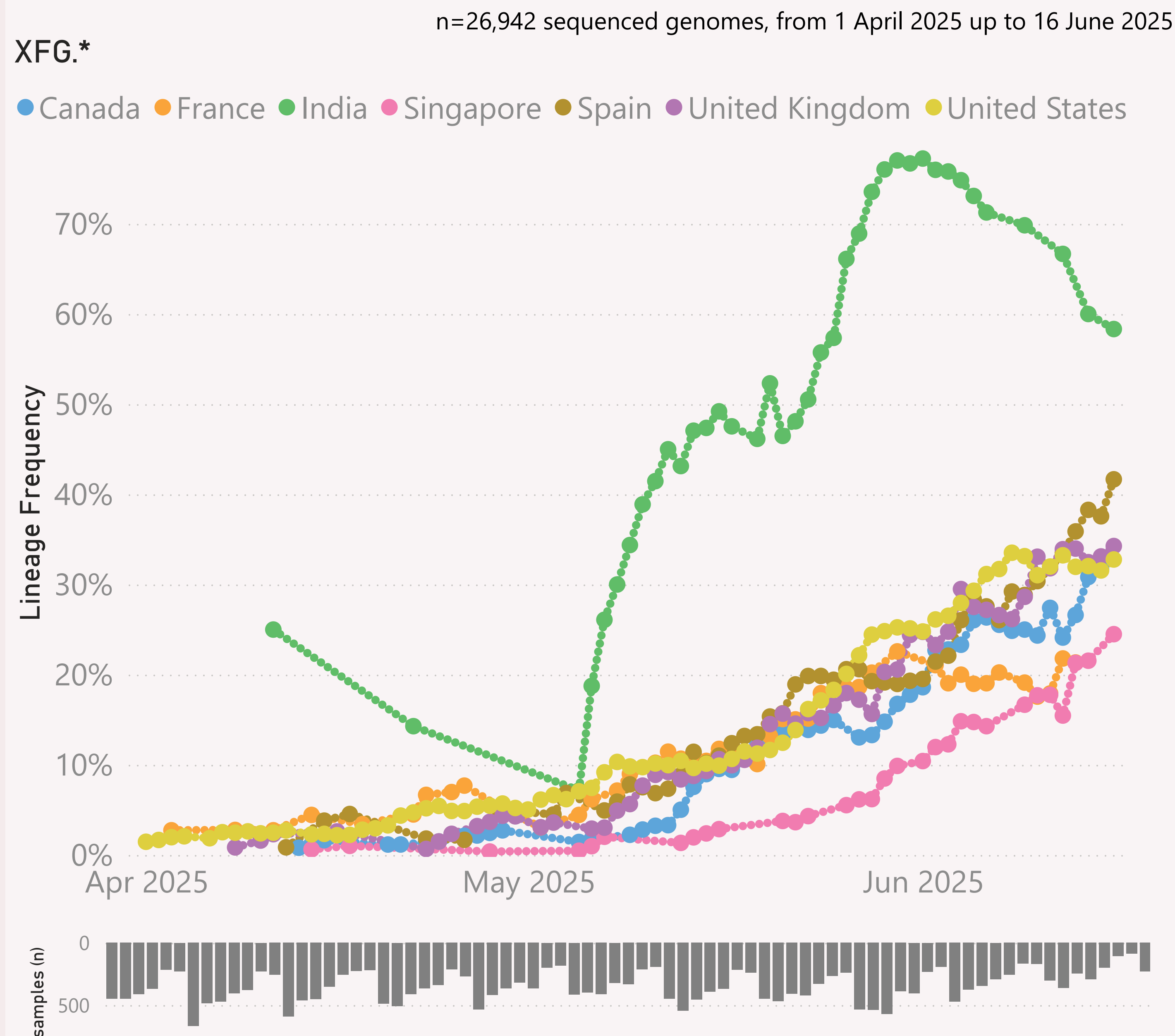
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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, for that country.

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 L2" group of interest, for the 7 countries reporting the most samples over recent months.

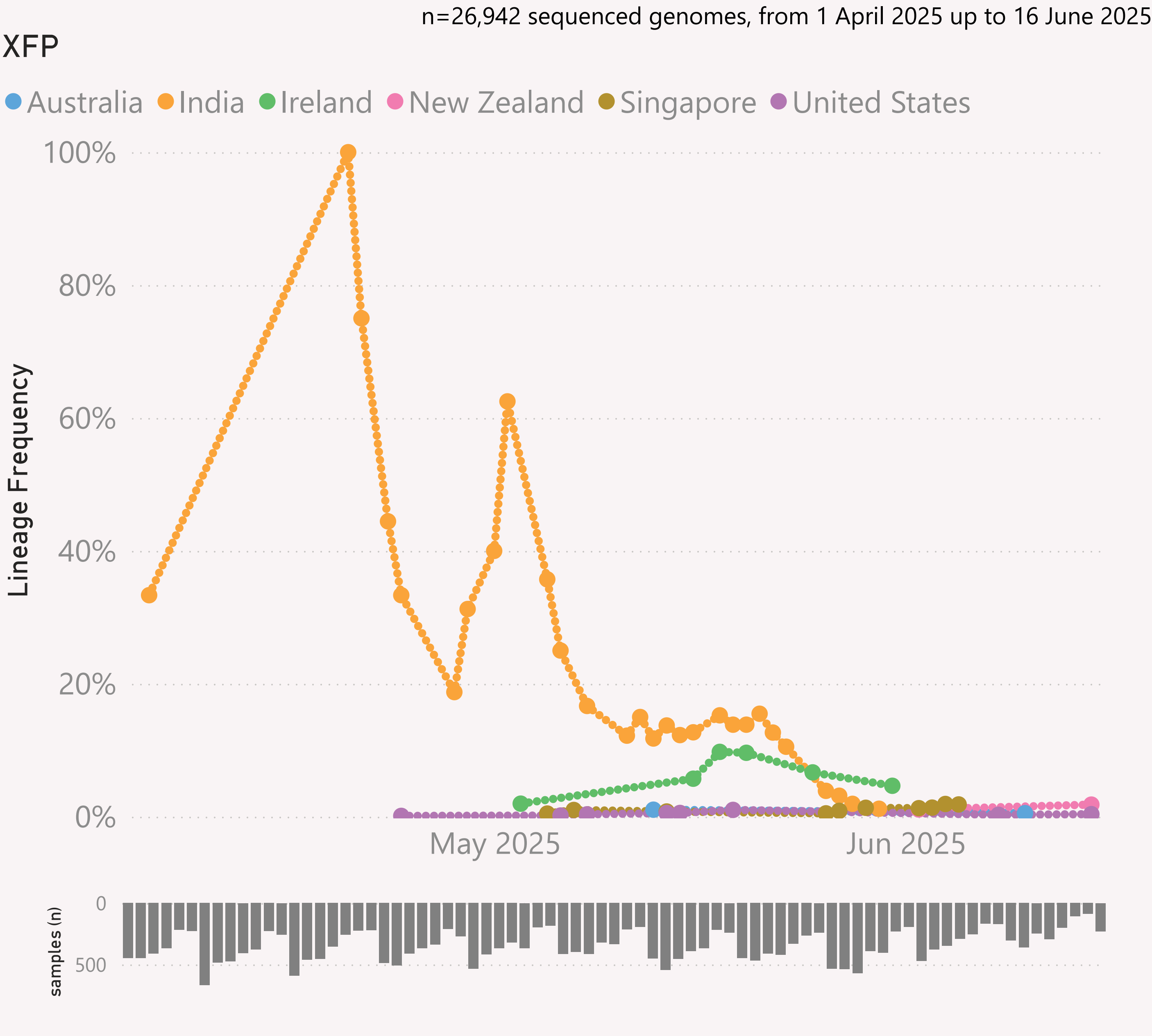
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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.

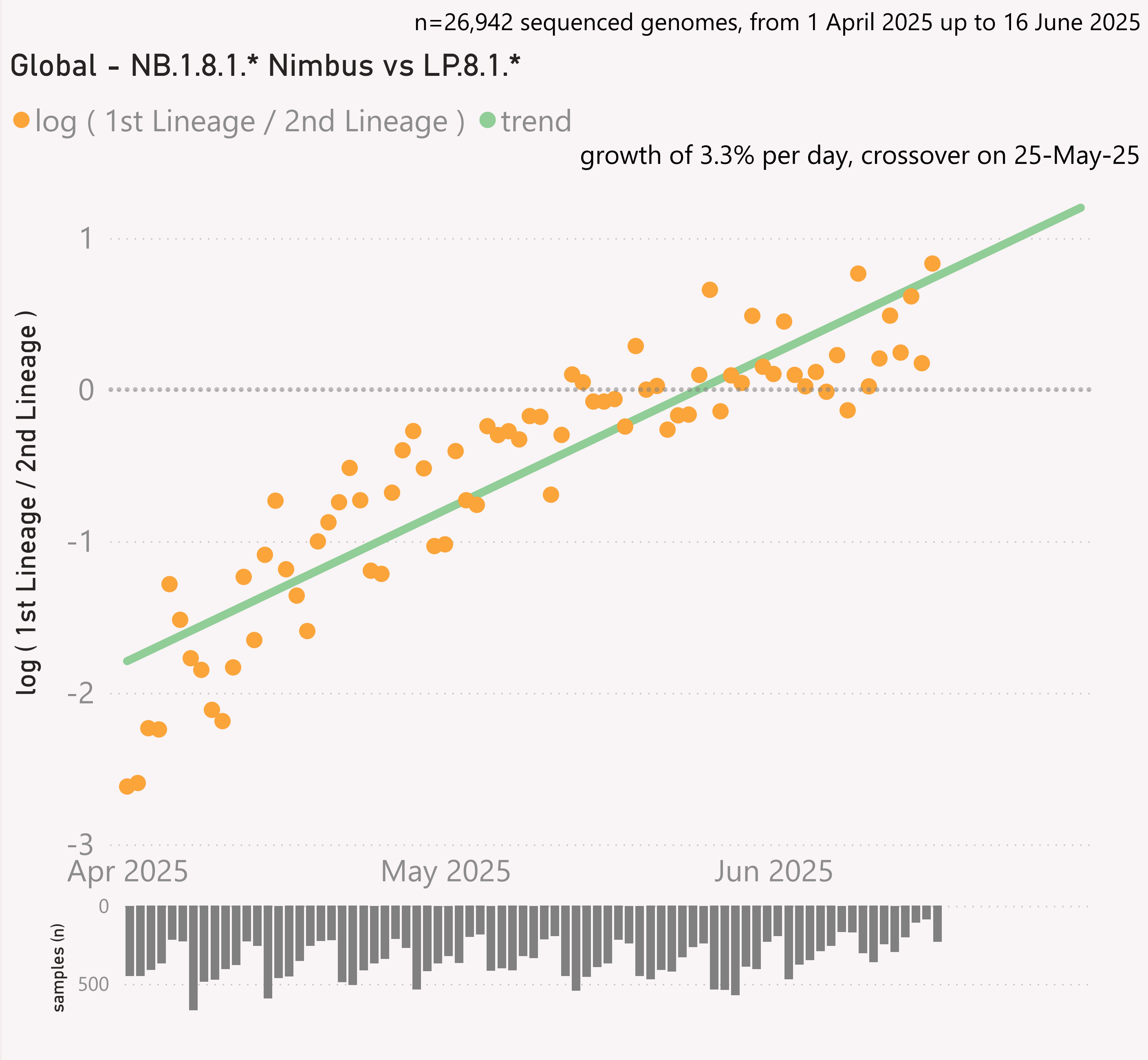
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

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 compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 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 L2 is considered to have "crossed over" or taken over dominance from the incumbent Lineage L2.

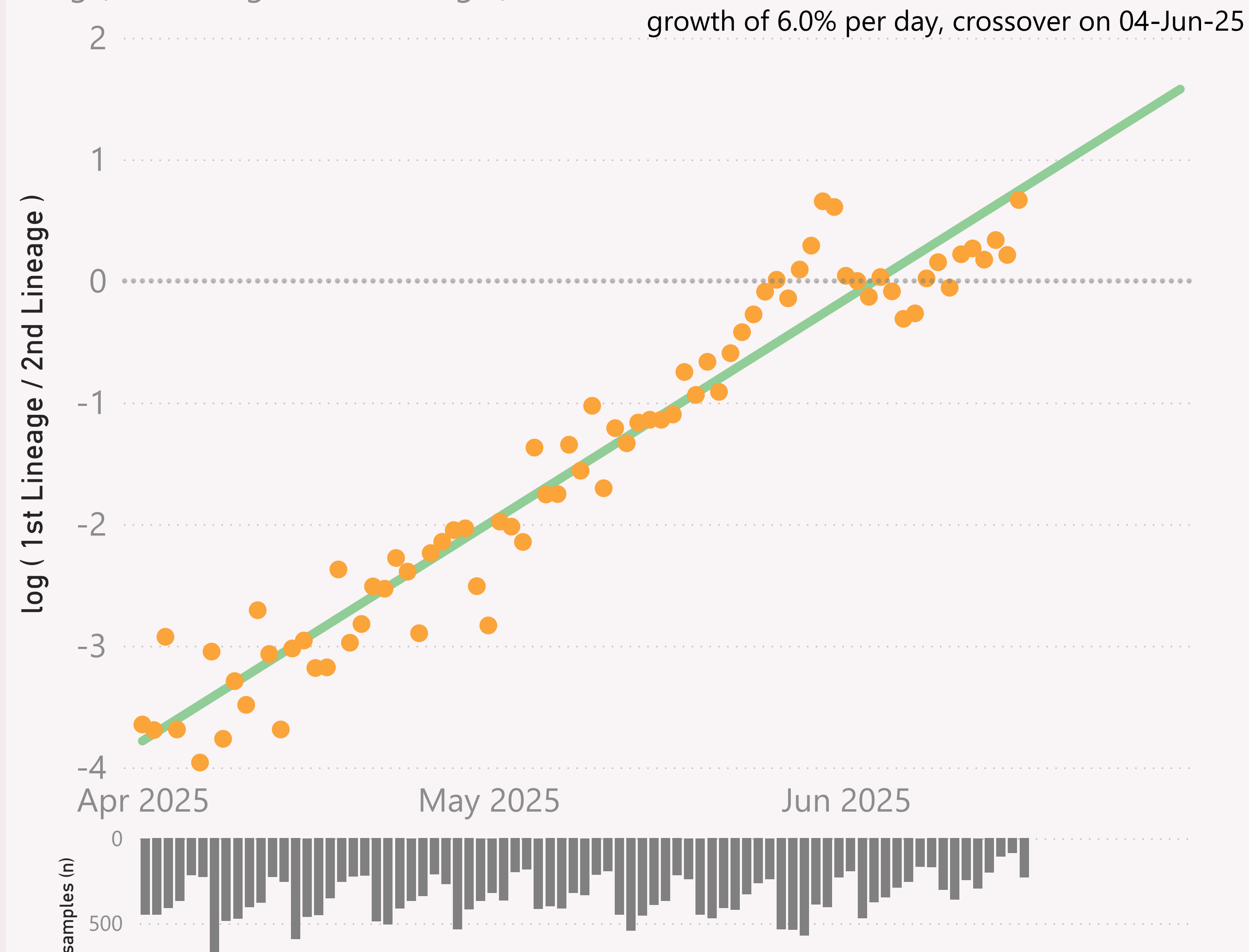
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=26,942 sequenced genomes, from 1 April 2025 up to 16 June 2025

## Global - XFG.\* vs LP.8.1.\*

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



This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 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 L2 is considered to have "crossed over" or taken over dominance from the incumbent Lineage L2.

The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

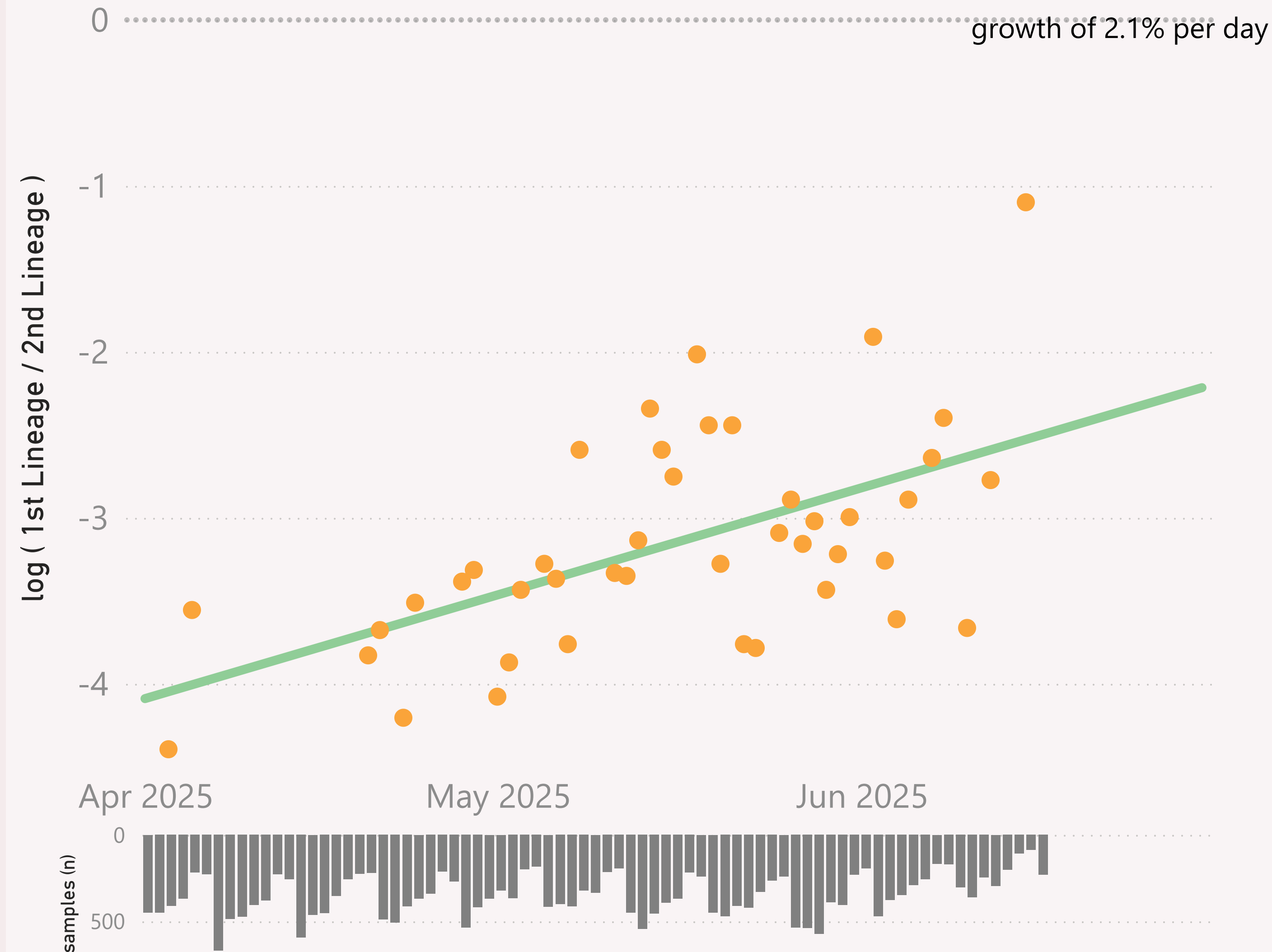
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.



n=26,942 sequenced genomes, from 1 April 2025 up to 16 June 2025

## Global - XFP vs LP.8.1.1

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



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

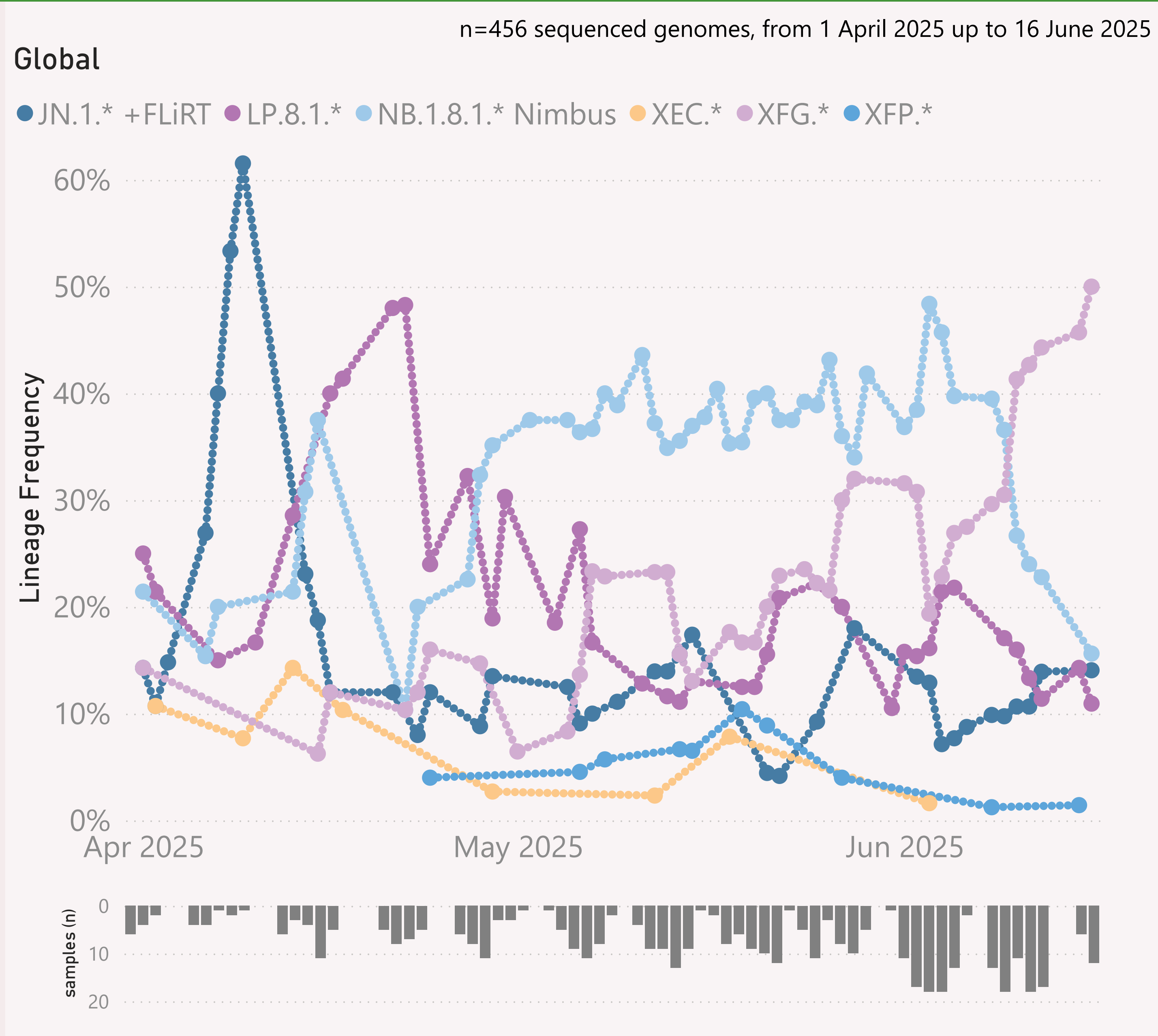
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

## Global



























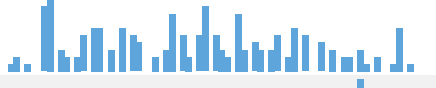







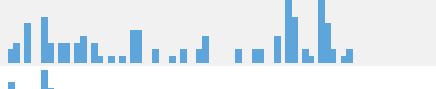






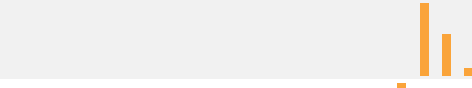








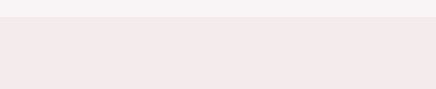
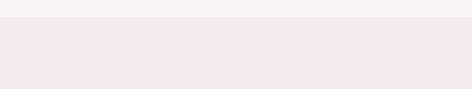
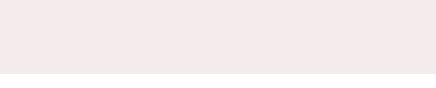
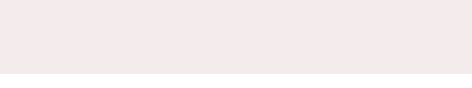
This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

This is probably a more randomised sample than the "Global" aggregate of all samples submitted to GISAID, as those are dominated by the US and Canada

These samples are mainly collected from arrivals into the US and Japan.



Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
<div>+ United States</div>	5,038	16/06/2025		22/06/2025	
<div>+ Canada</div>	1,901	16/06/2025		22/06/2025	
<div>+ Spain</div>	1,868	16/06/2025		22/06/2025	
<div>+ China</div>	1,826	16/06/2025		22/06/2025	
<div>+ United Kingdom</div>	1,623	16/06/2025		22/06/2025	
<div>+ Singapore</div>	1,615	16/06/2025		22/06/2025	
<div>+ Australia</div>	1,407	16/06/2025		22/06/2025	
<div>+ France</div>	867	16/06/2025		22/06/2025	
<div>+ India</div>	828	16/06/2025		22/06/2025	
<div>+ New Zealand</div>	401	15/06/2025		22/06/2025	
<div>+ South Korea</div>	389	12/06/2025		22/06/2025	
<div>+ Ireland</div>	325	16/06/2025		22/06/2025	
<div>+ Mexico</div>	277	16/06/2025		22/06/2025	
<div>+ Thailand</div>	275	23/05/2025		30/05/2025	
<div>+ Japan</div>	266	12/06/2025		22/06/2025	
<div>+ Malaysia</div>	187	16/06/2025		22/06/2025	
<div>+ Costa Rica</div>	182	14/06/2025		22/06/2025	
<div>+ Germany</div>	178	12/06/2025		22/06/2025	
<div>+ Netherlands</div>	174	09/06/2025		22/06/2025	
<div>+ Luxembourg</div>	170	02/06/2025		19/06/2025	
<div>+ Brazil</div>	158	04/06/2025		22/06/2025	
<div>+ Hong Kong</div>	154	14/06/2025		22/06/2025	
<div>+ Bahrain</div>	152	16/06/2025		22/06/2025	
<div>+ Kazakhstan</div>	146	28/05/2025		22/06/2025	
<div>+ Puerto Rico</div>	138	16/06/2025		22/06/2025	
<div>+ Portugal</div>	137	03/06/2025		22/06/2025	
<div>+ Taiwan</div>	115	16/06/2025		22/06/2025	
<div>+ Italy</div>	102	07/06/2025		22/06/2025	
<div>+ Total</div>	21,909	16/06/2025		22/06/2025	

This page shows the volume and currency/timeliness of the genomic sequencing data shared via GISAID, over the last 8 weeks, for the countries sharing the most samples.

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.