

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

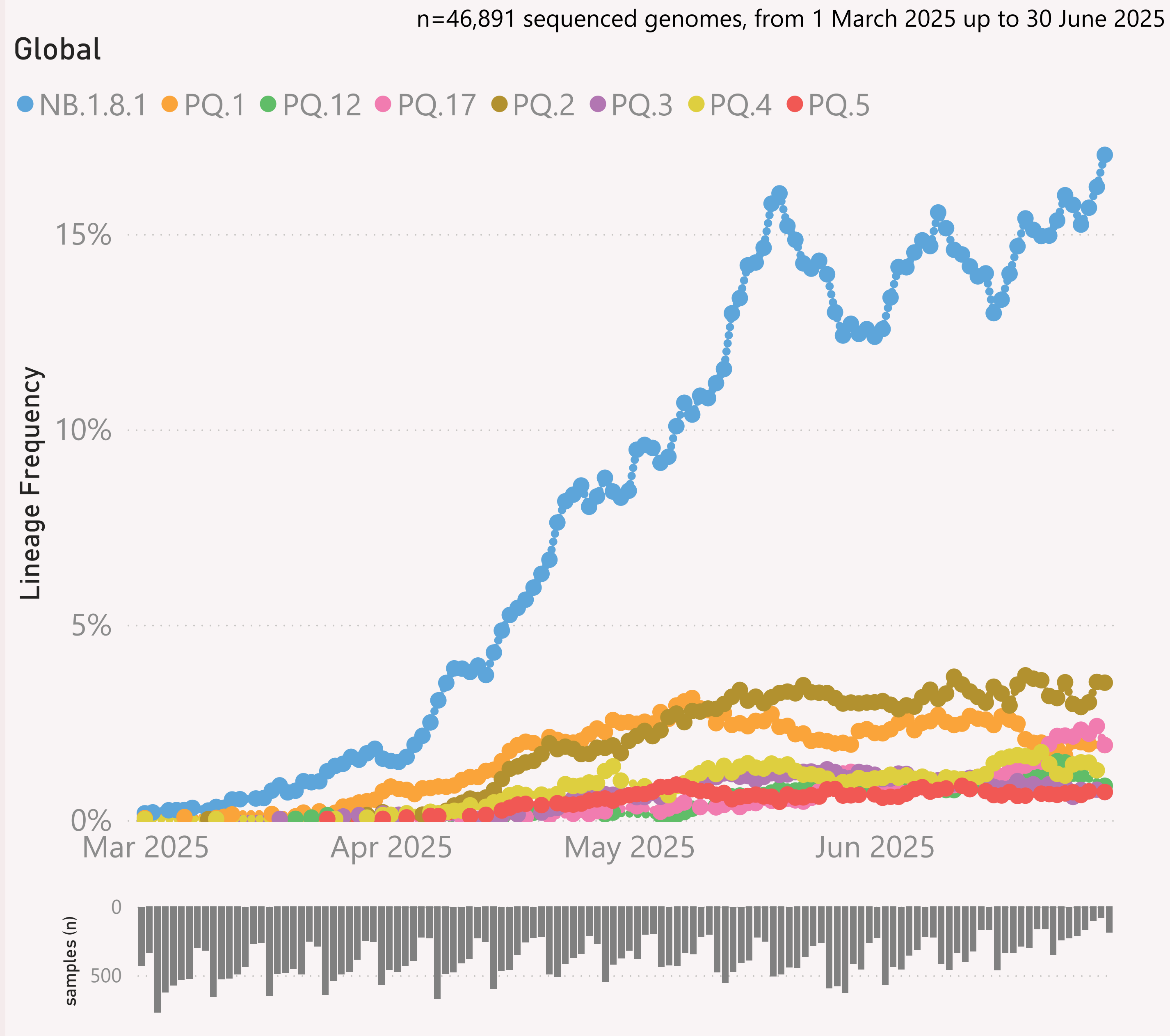
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all it's descendants, e.g. the JN.\* lineages.

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.



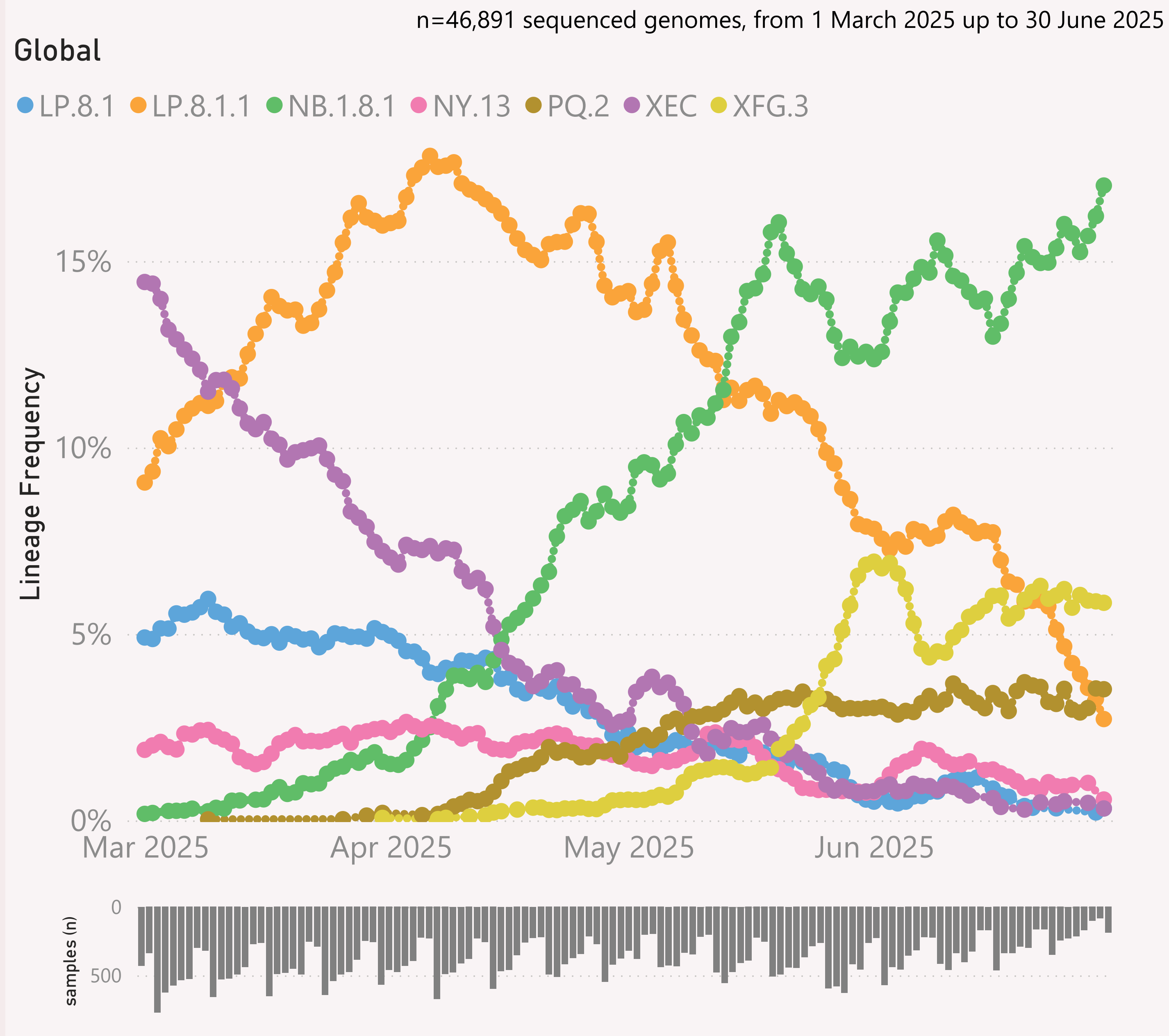
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.\* Nimbus.

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

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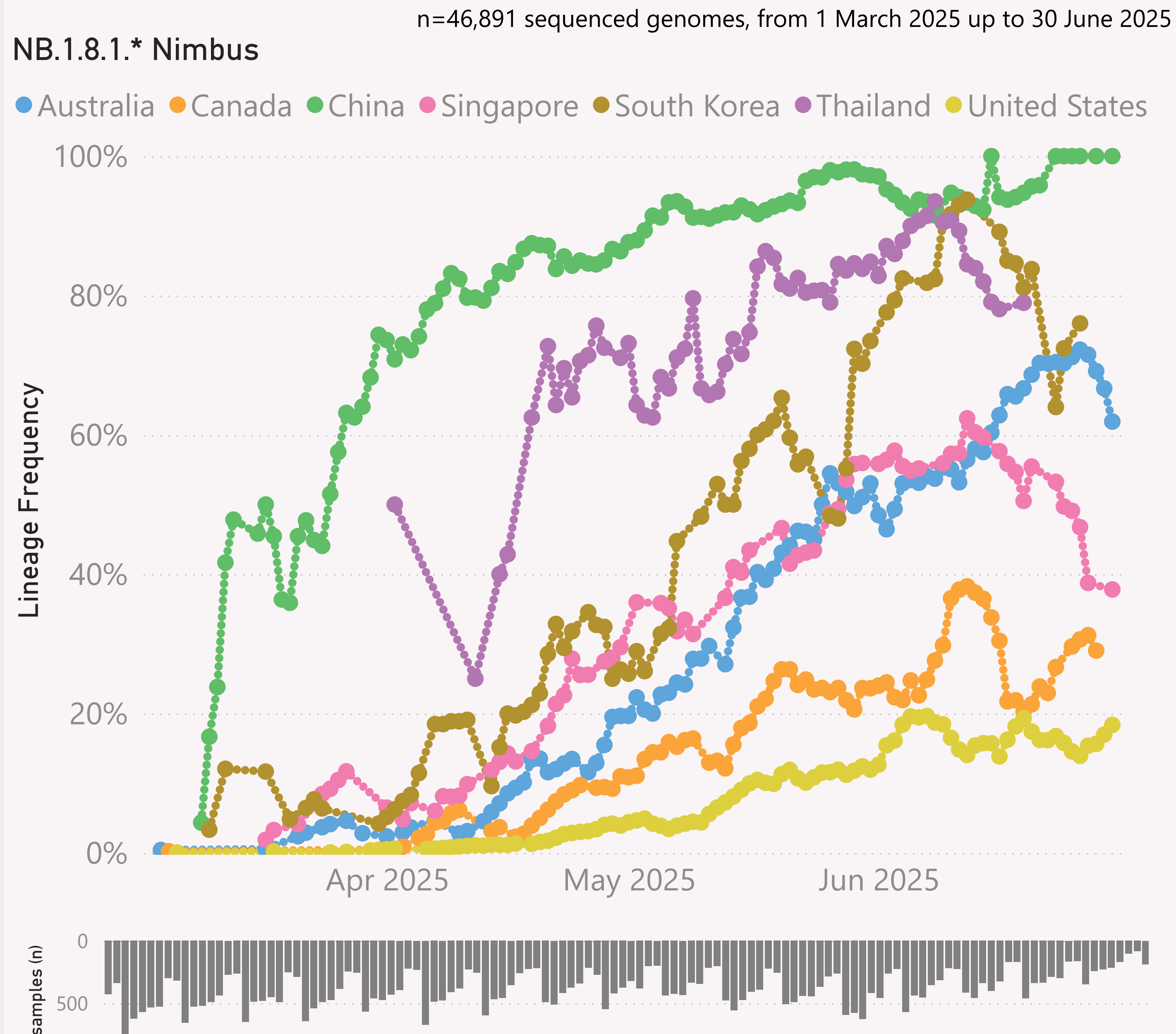
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This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

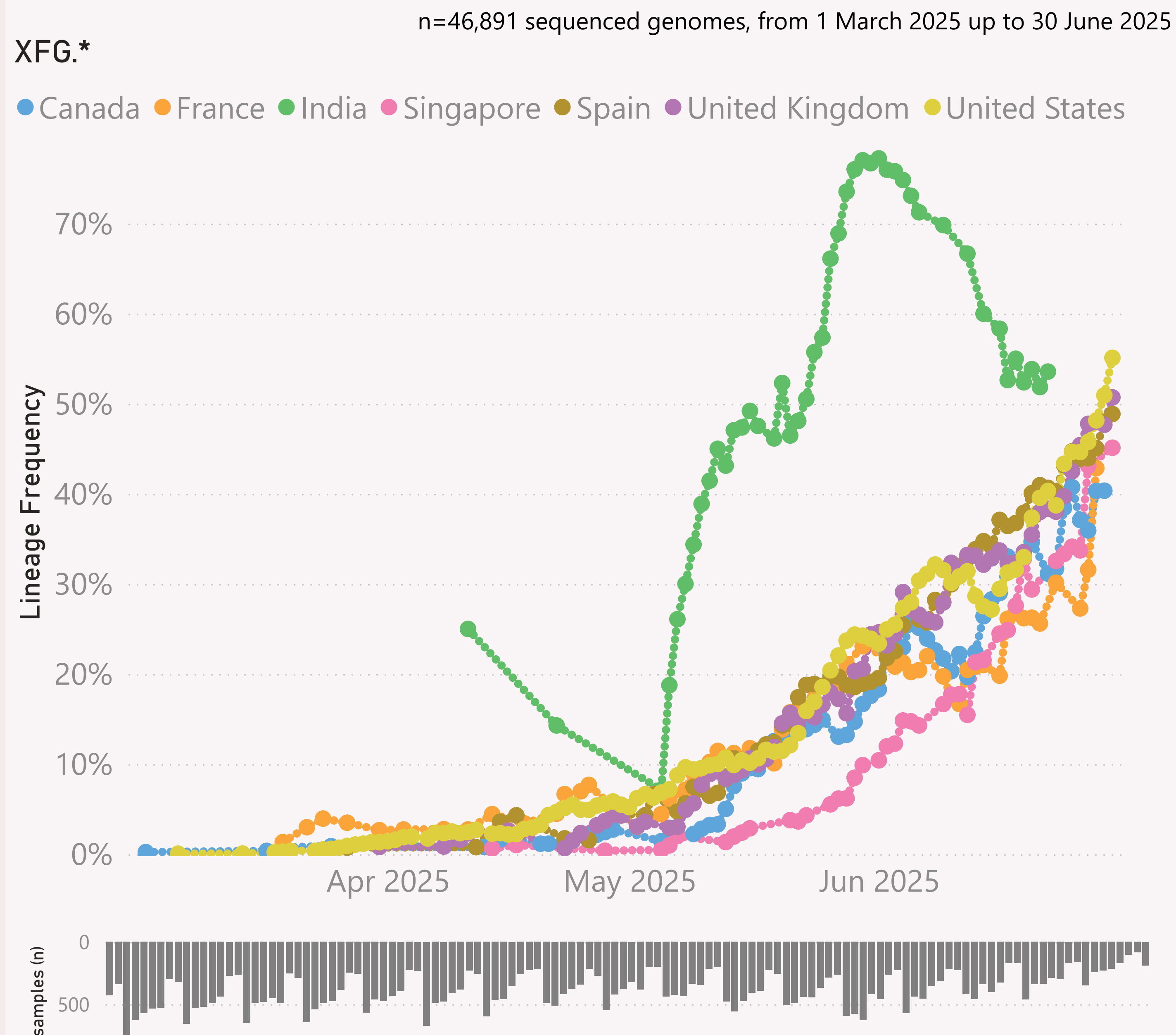
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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.

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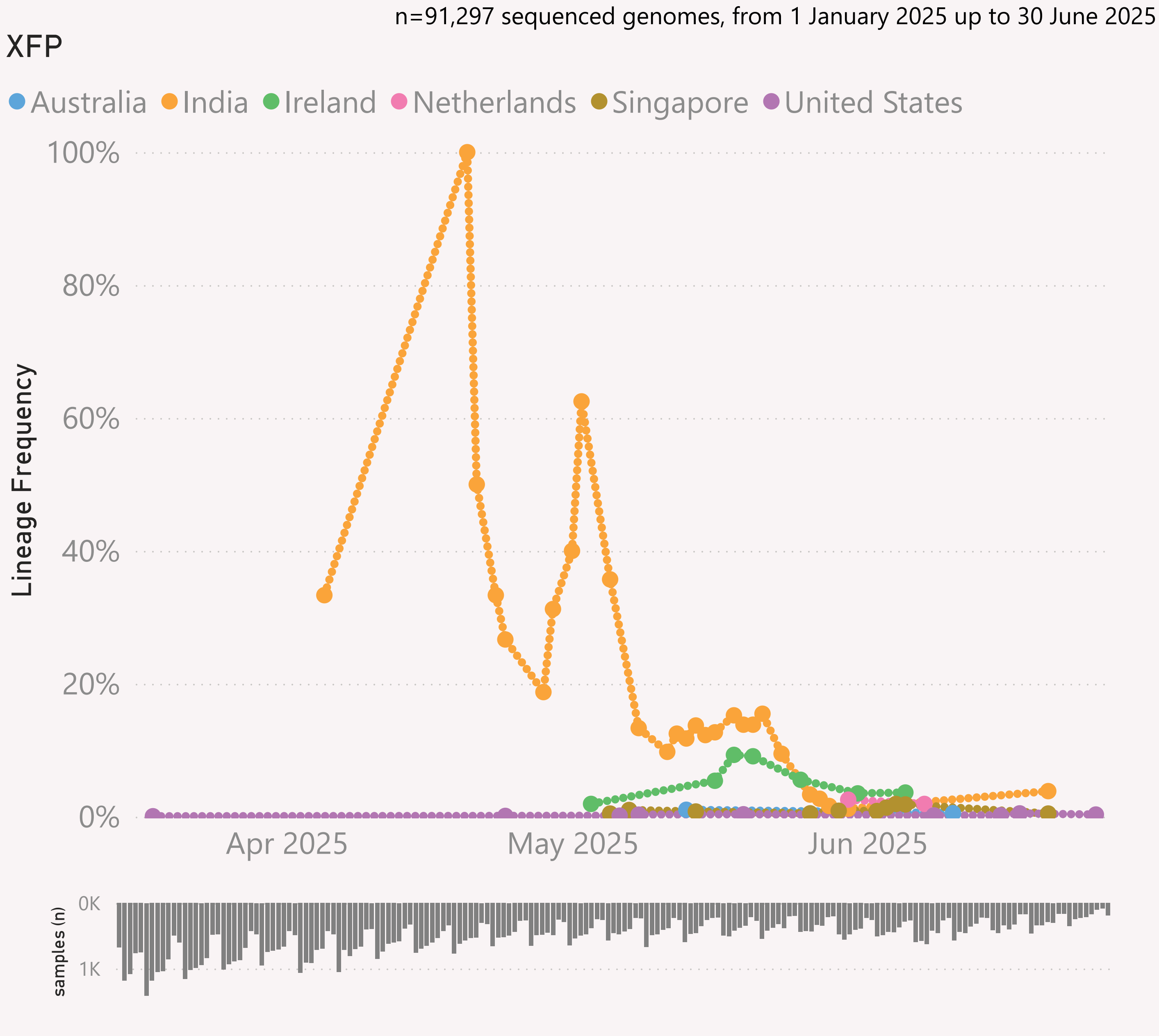
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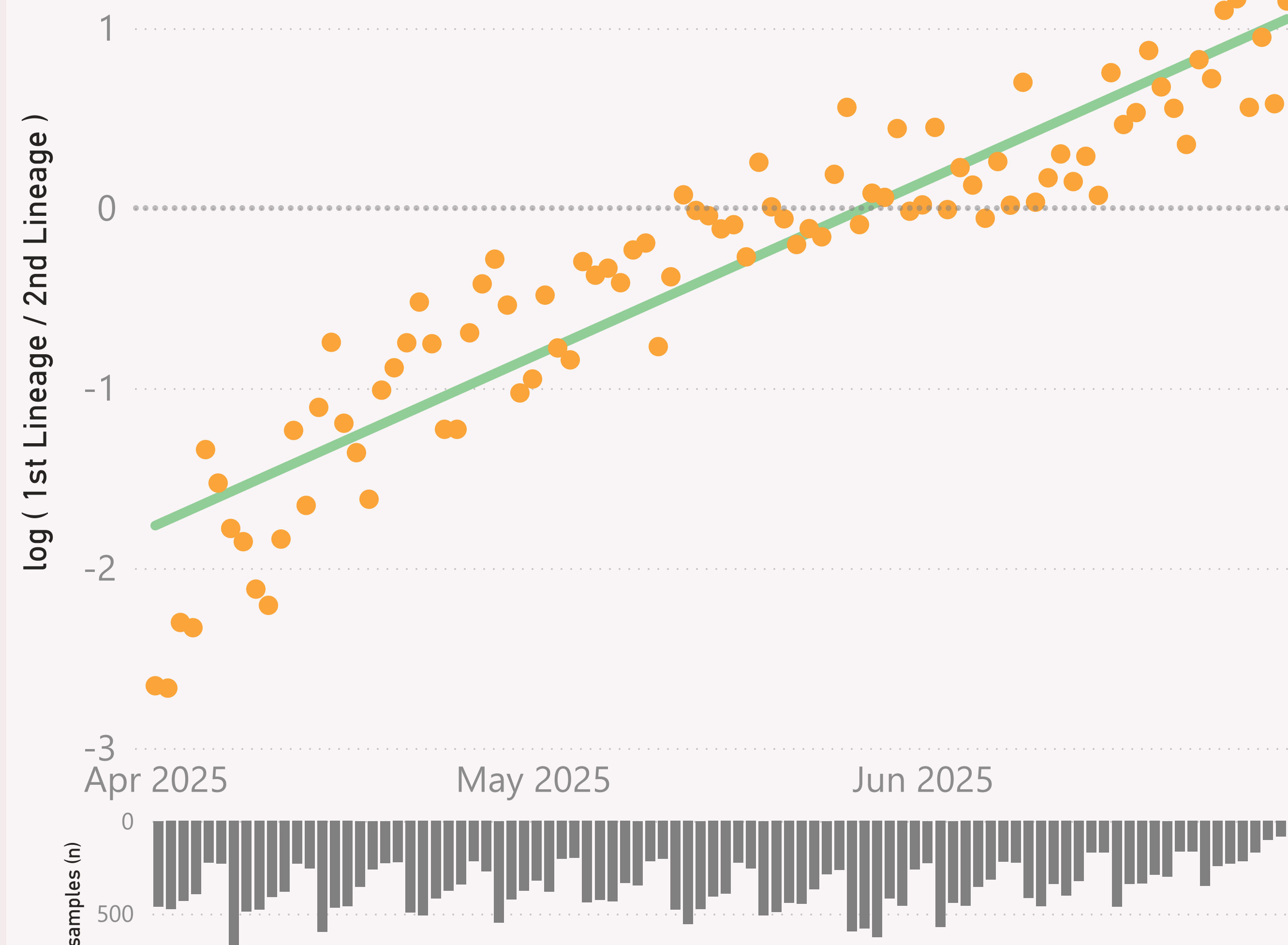


n=32,554 sequenced genomes, from 1 April 2025 up to 30 June 2025

## Global - NB.1.8.1.\* Nimbus vs LP.8.1.\*

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

growth of 3.1% per day, crossover on 28-May-25

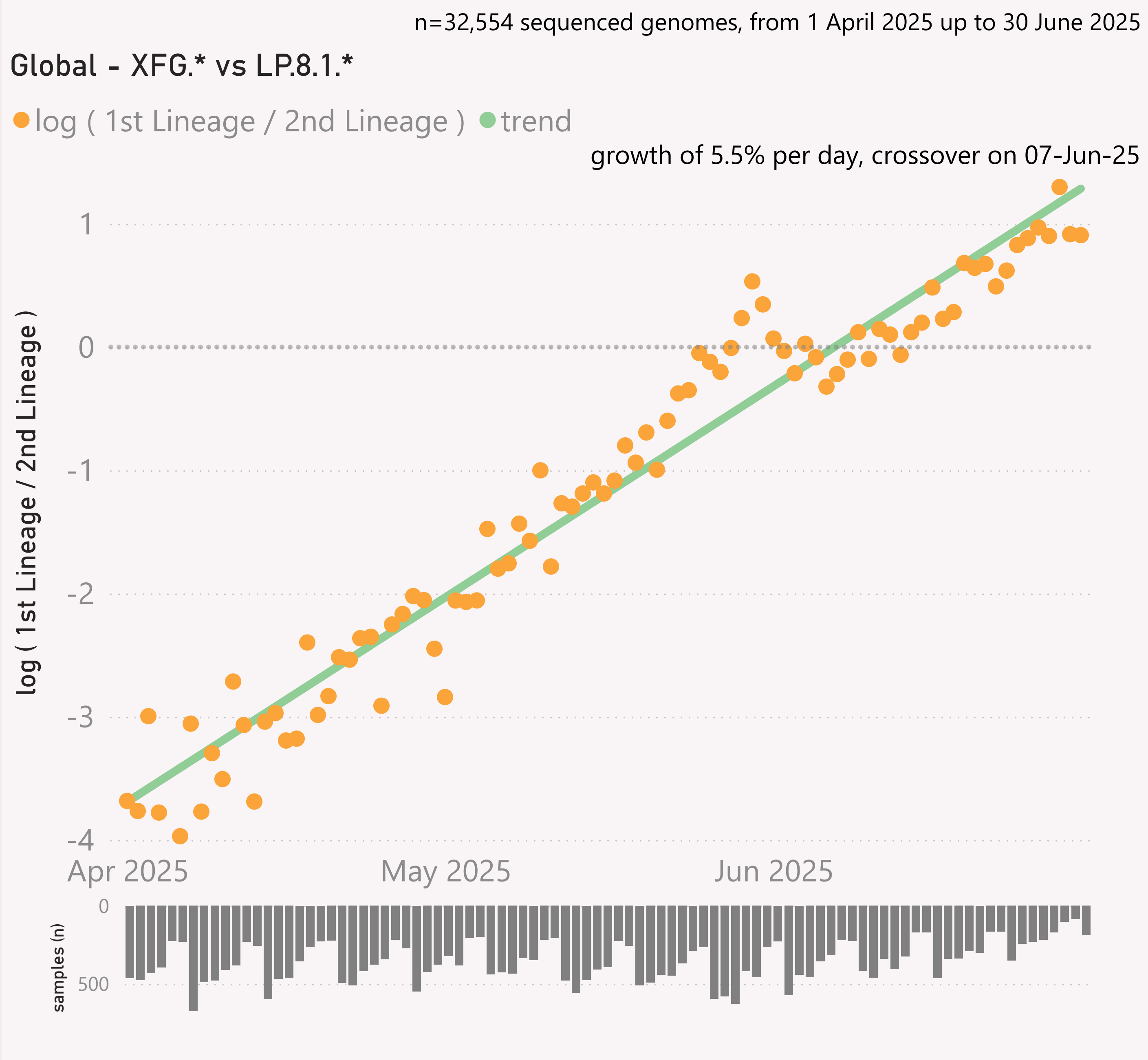


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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".

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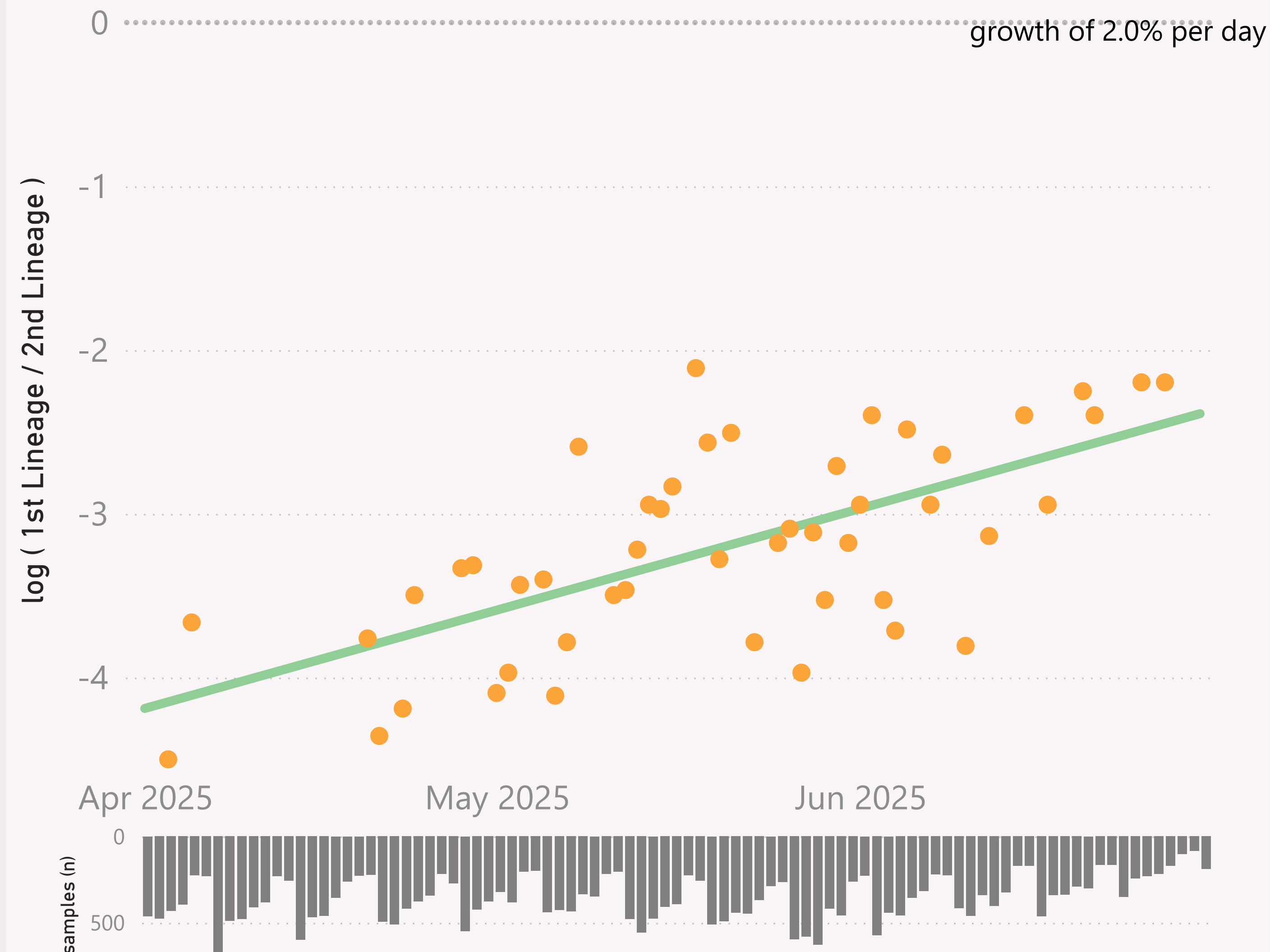
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## Global - XFP vs LP.8.1.1

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

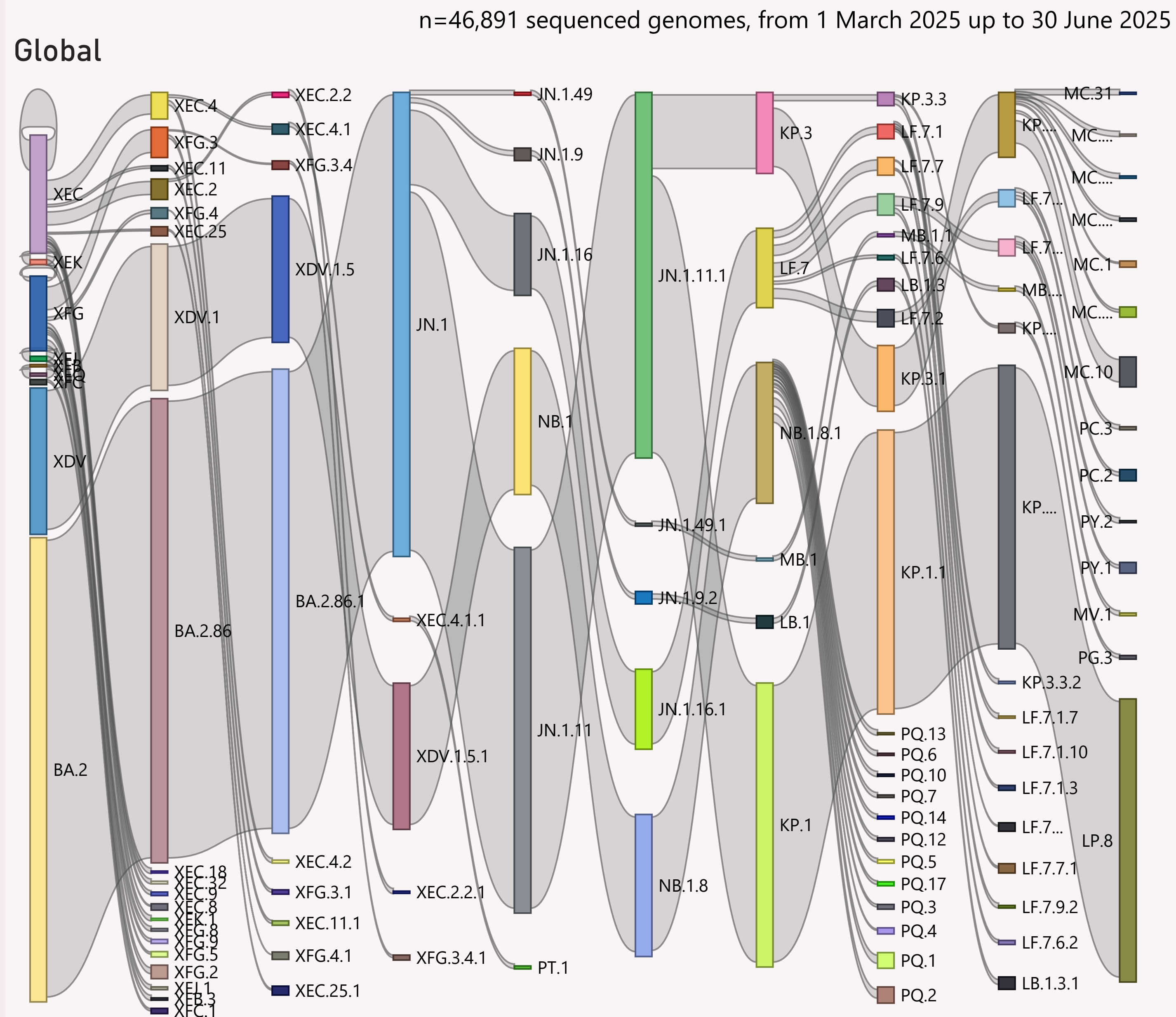


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

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

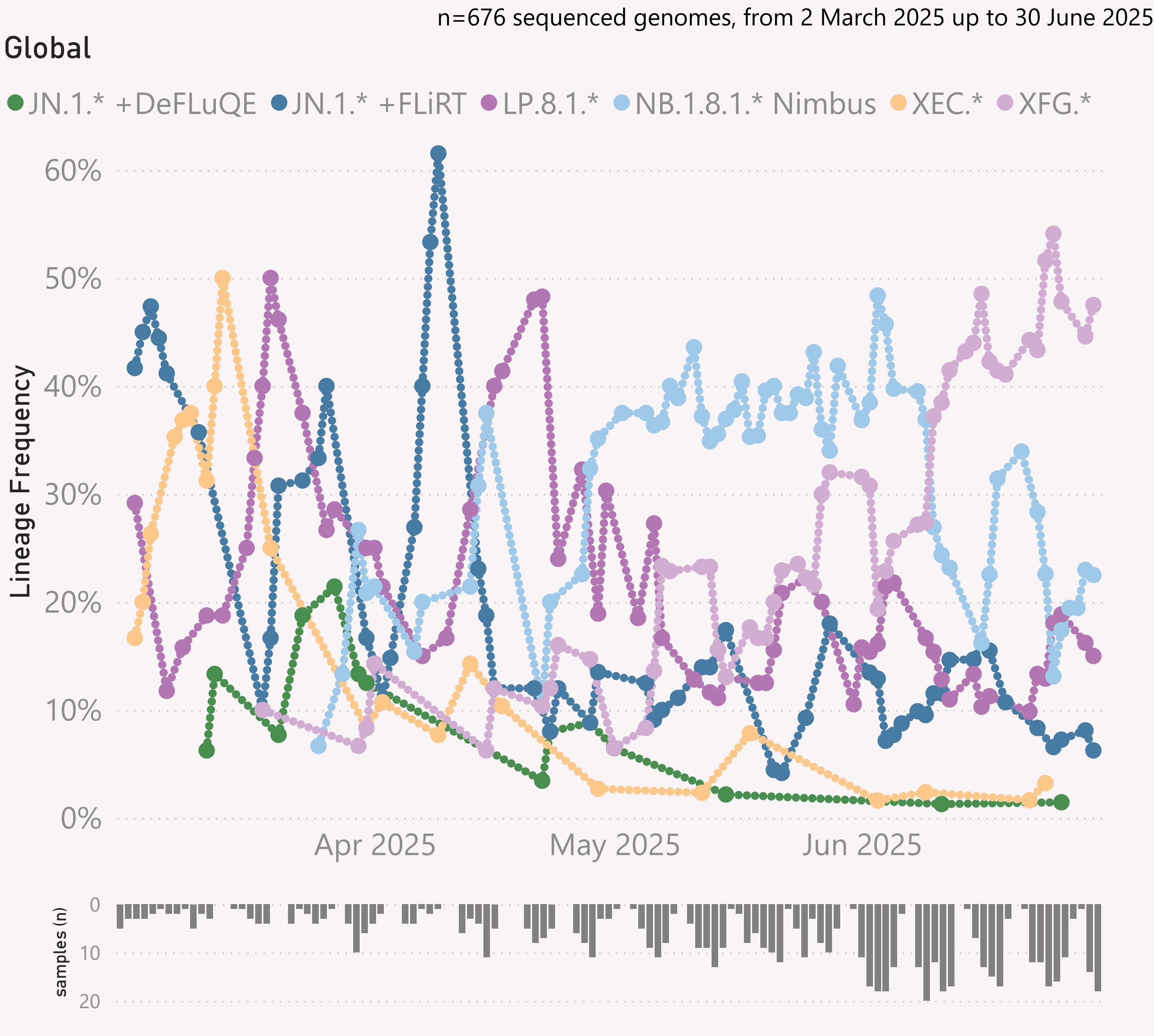
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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.





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>+ Canada</div>	25,031	29/06/2025		02/07/2025	
<div>+ United States</div>	7,288	30/06/2025		02/07/2025	
<div>+ Spain</div>	2,618	30/06/2025		02/07/2025	
<div>+ China</div>	2,082	30/06/2025		02/07/2025	
<div>+ United Kingdom</div>	1,879	30/06/2025		02/07/2025	
<div>+ Australia</div>	1,539	30/06/2025		02/07/2025	
<div>+ Singapore</div>	1,503	30/06/2025		02/07/2025	
<div>+ India</div>	850	22/06/2025		02/07/2025	
<div>+ France</div>	778	28/06/2025		02/07/2025	
<div>+ Mexico</div>	595	18/06/2025		02/07/2025	
<div>+ Brazil</div>	546	29/06/2025		02/07/2025	
<div>+ Netherlands</div>	535	24/06/2025		02/07/2025	
<div>+ New Zealand</div>	531	30/06/2025		02/07/2025	
<div>+ Thailand</div>	516	19/06/2025		02/07/2025	
<div>+ Japan</div>	462	30/06/2025		02/07/2025	
<div>+ Russia</div>	462	14/06/2025		02/07/2025	
<div>+ Malaysia</div>	397	30/06/2025		02/07/2025	
<div>+ South Korea</div>	382	26/06/2025		02/07/2025	
<div>+ Ireland</div>	375	30/06/2025		02/07/2025	
<div>+ Kenya</div>	375	28/01/2025		02/07/2025	
<div>+ Luxembourg</div>	330	30/06/2025		02/07/2025	
<div>+ Costa Rica</div>	246	19/06/2025		02/07/2025	
<div>+ Kazakhstan</div>	218	28/05/2025		02/07/2025	
<div>+ Germany</div>	199	25/06/2025		02/07/2025	
<div>+ Taiwan</div>	192	30/06/2025		02/07/2025	
<div>+ Puerto Rico</div>	182	30/06/2025		02/07/2025	
<div>+ Denmark</div>	164	30/06/2025		02/07/2025	
<div>+ Bahrain</div>	163	21/06/2025		29/06/2025	
<div>— Total</div>	52,488	30/06/2025		02/07/2025	

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.