

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

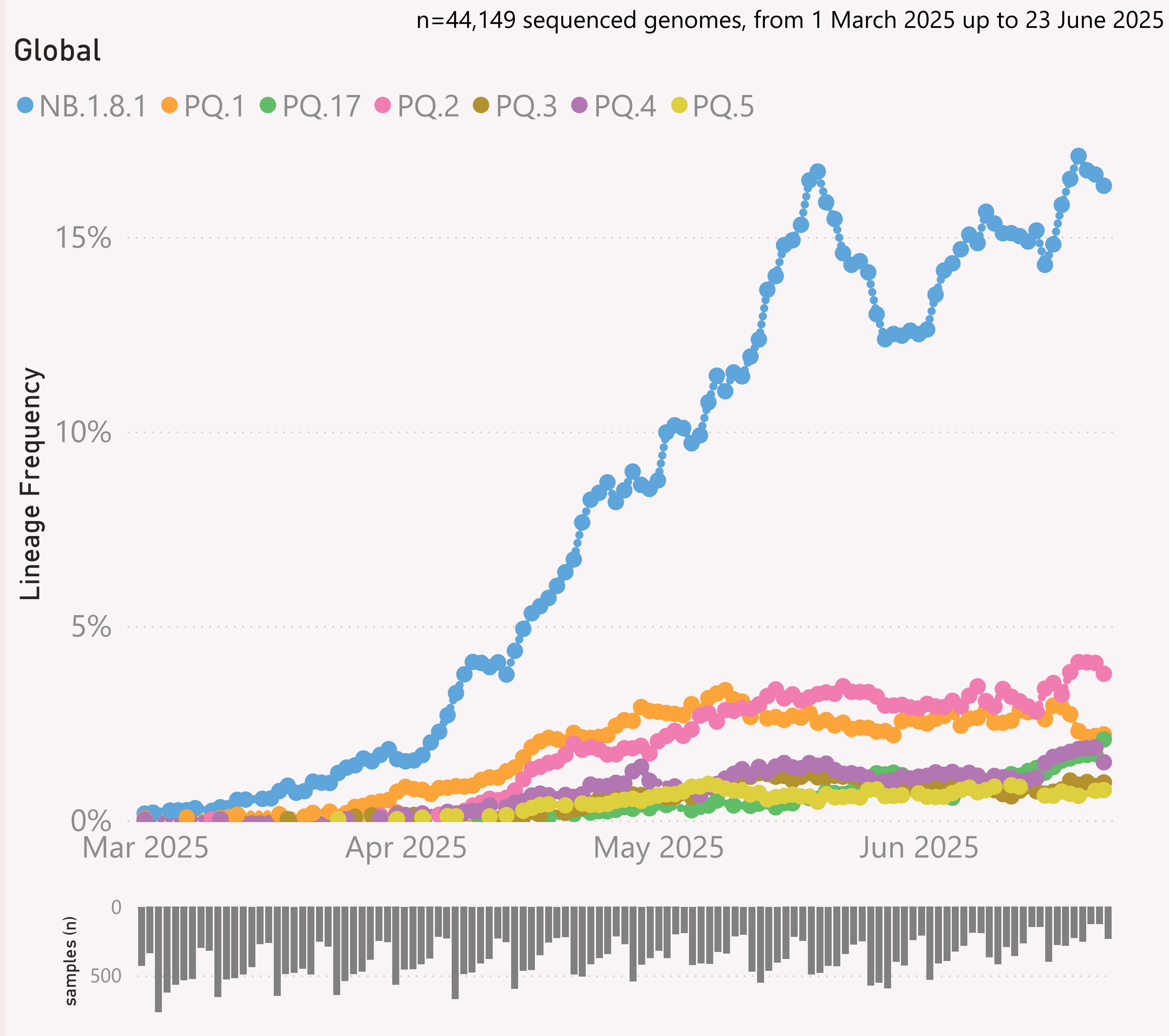
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



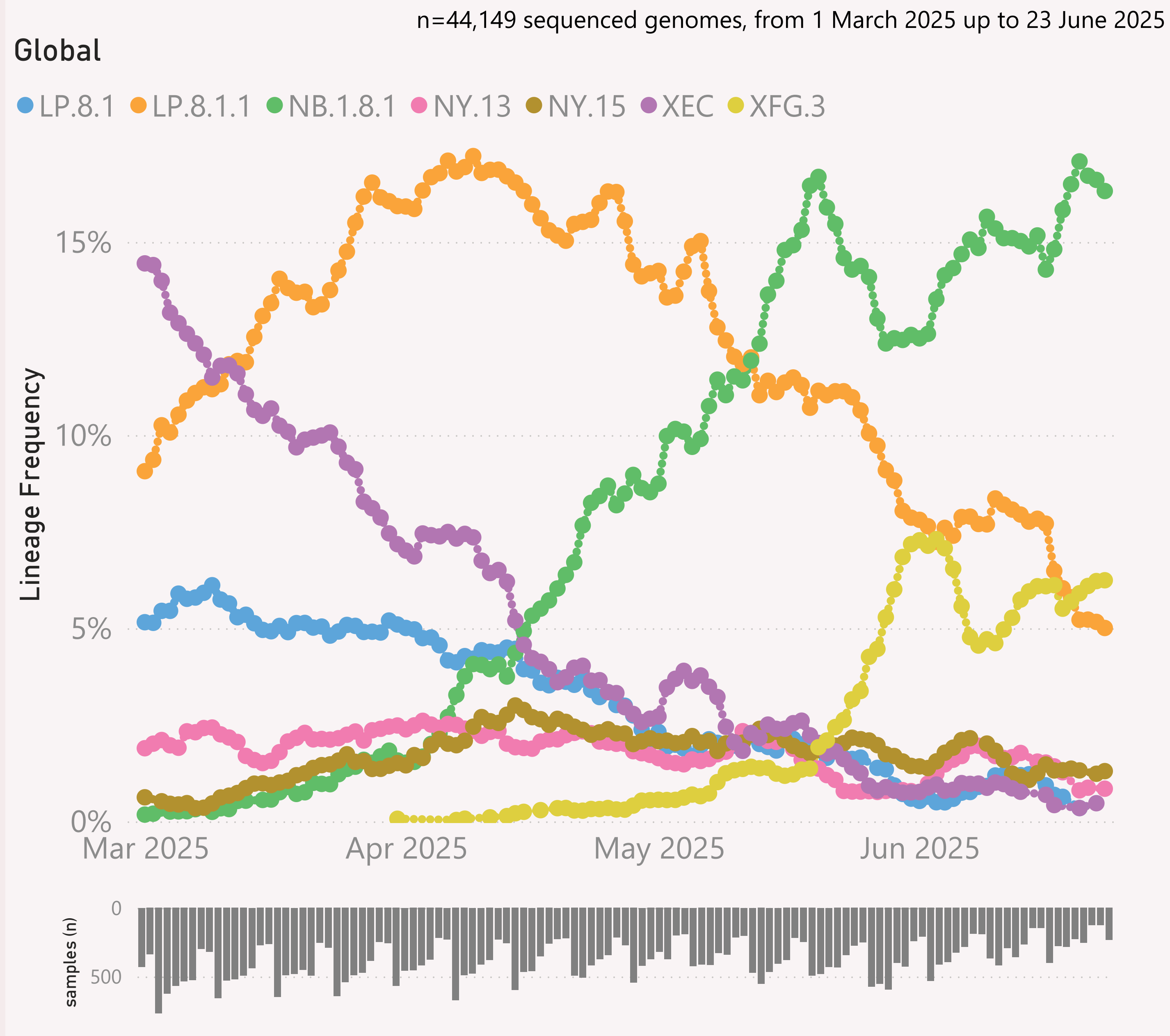
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.* Nimbus.

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

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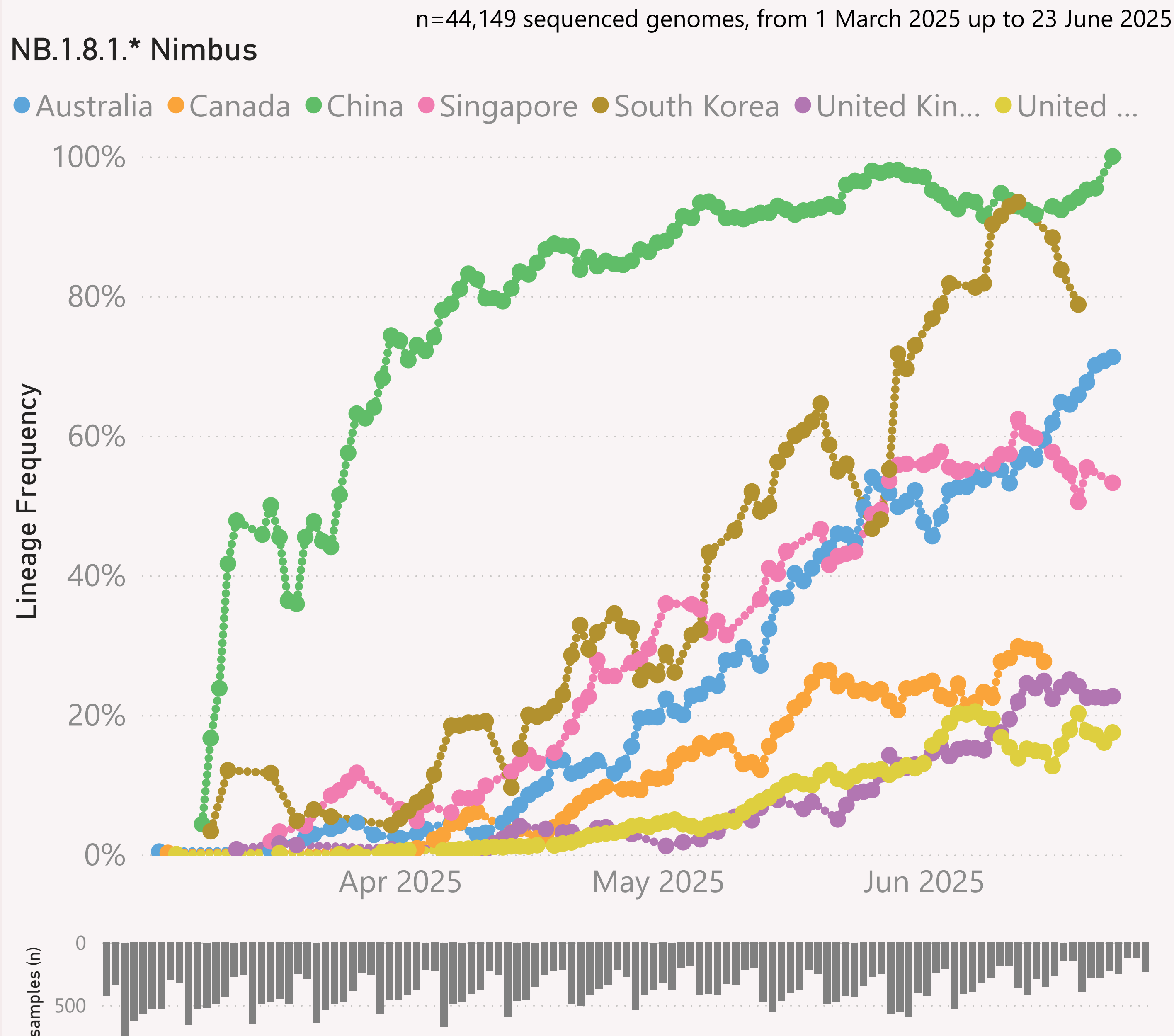
This page shows the frequency of the top 7 lineages, across recent months.

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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.

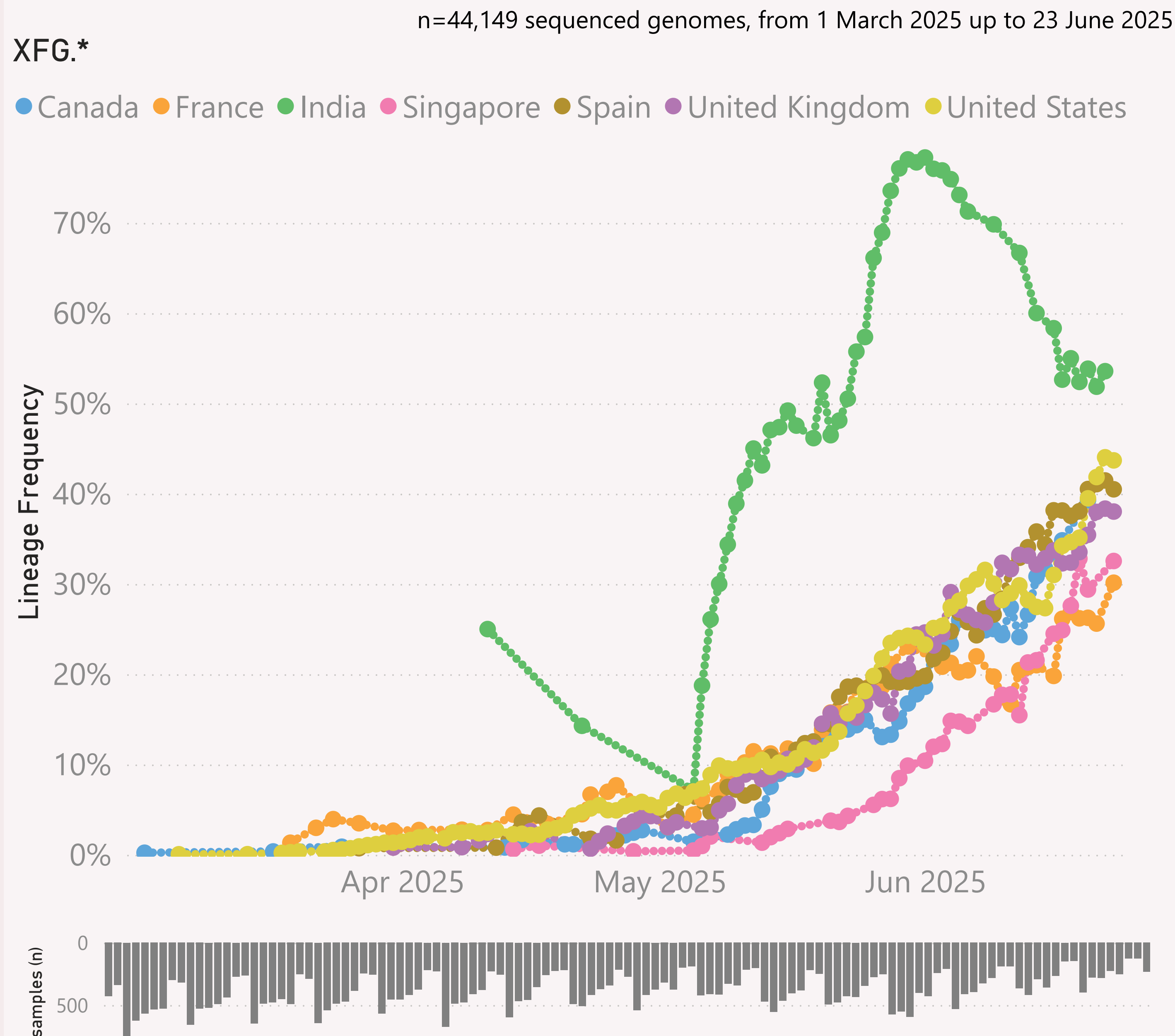
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

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

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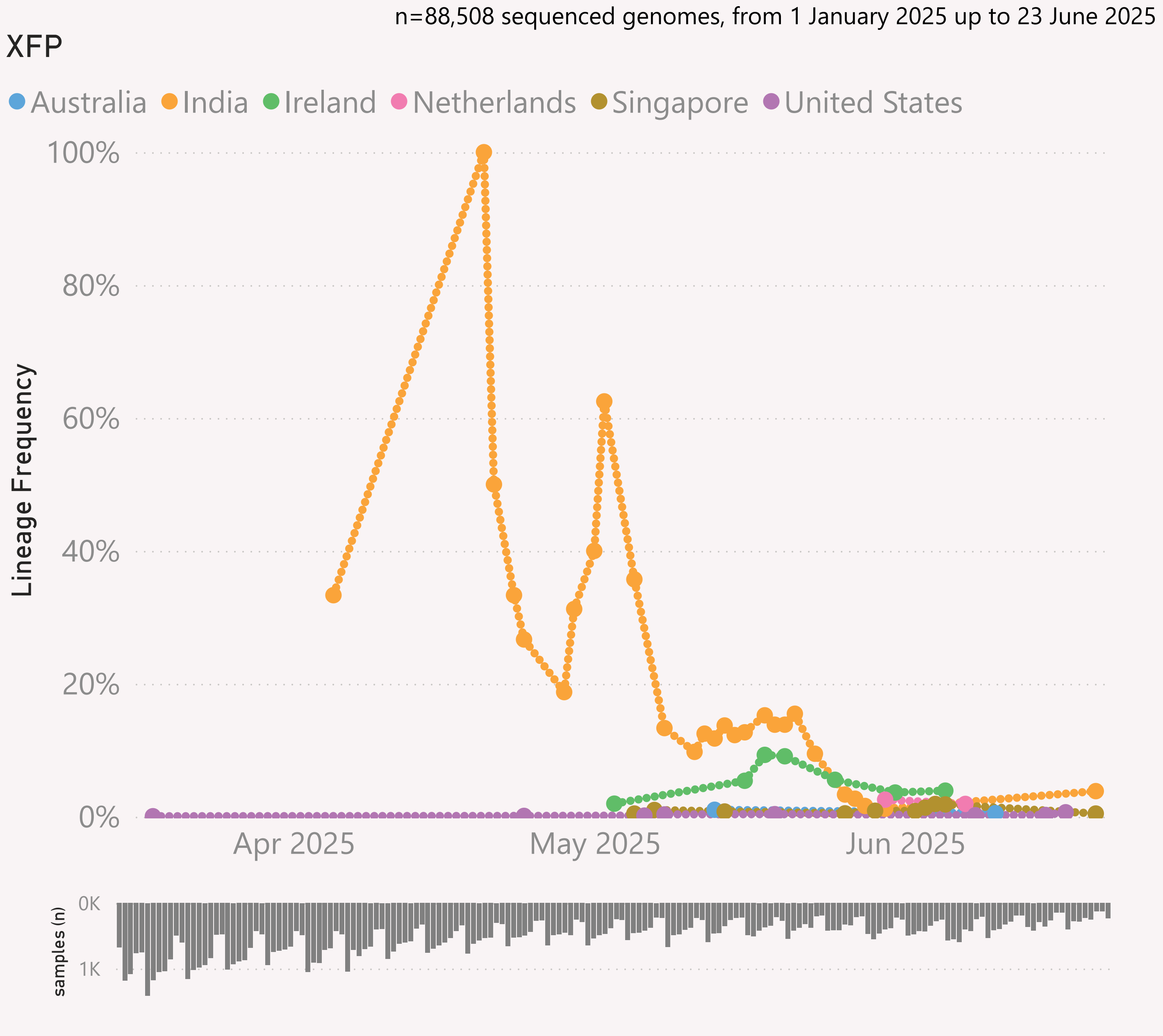
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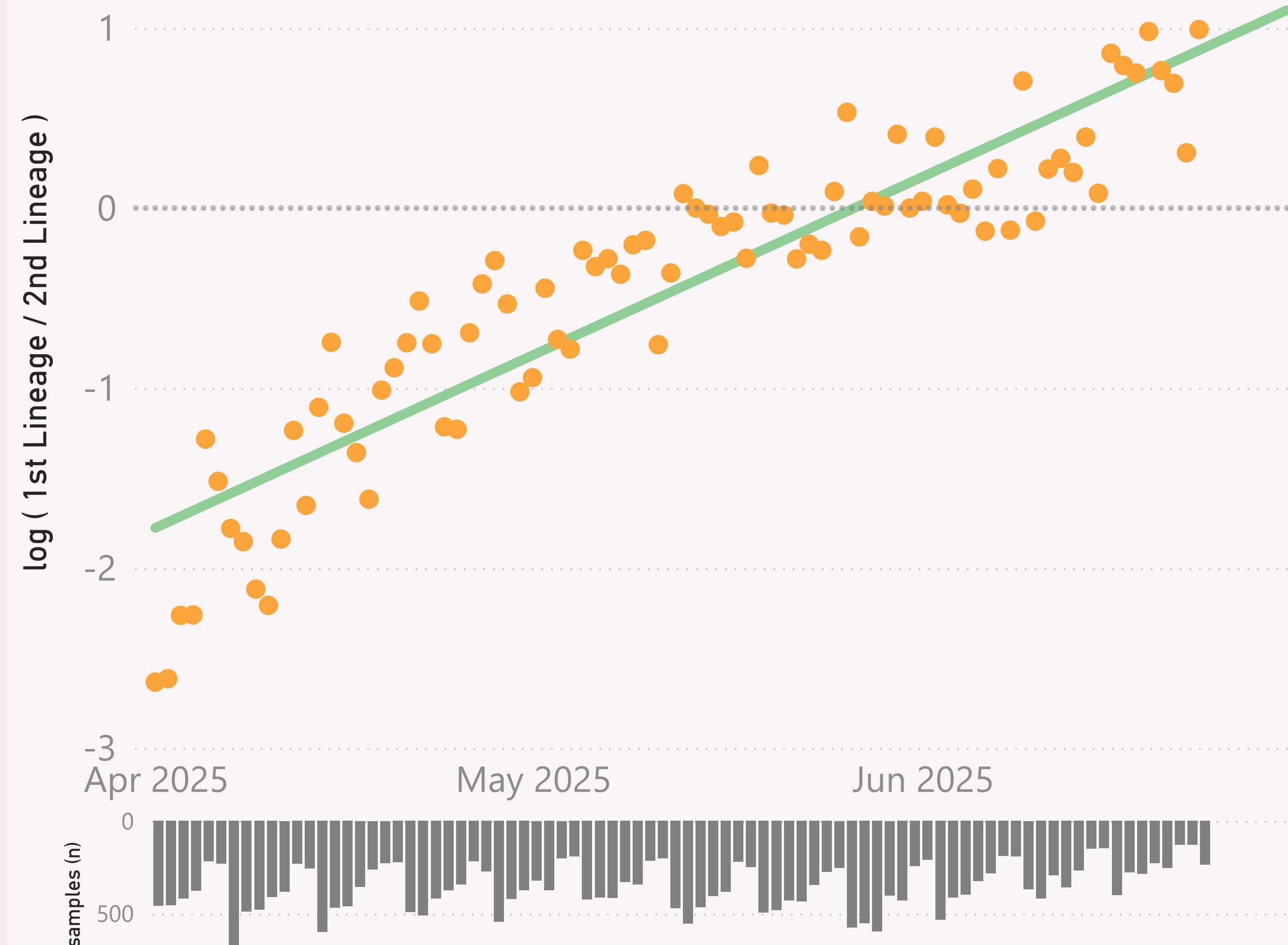


n=29,833 sequenced genomes, from 1 April 2025 up to 23 June 2025

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

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

growth of 3.2% per day, crossover on 27-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".

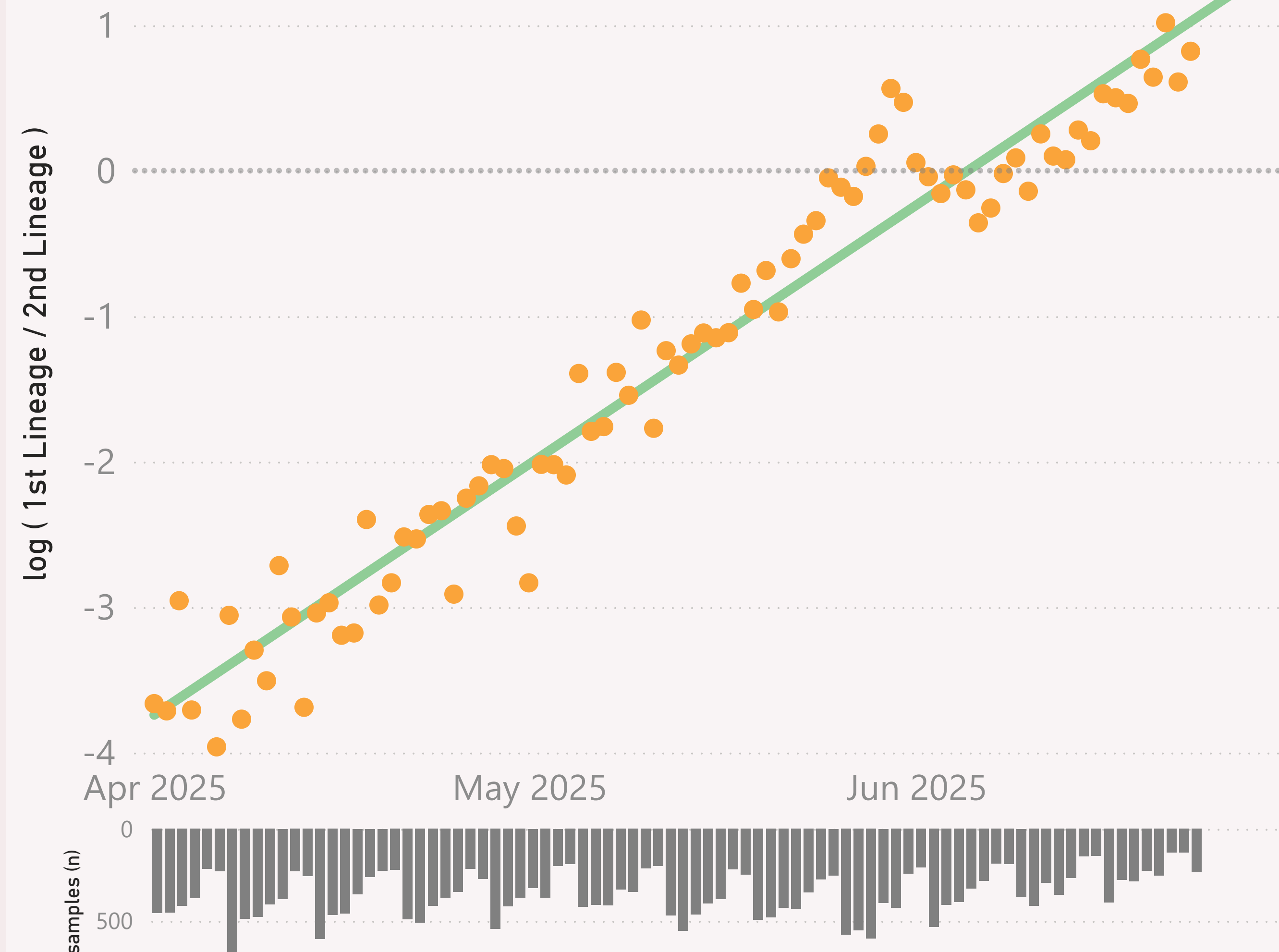
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n=29,833 sequenced genomes, from 1 April 2025 up to 23 June 2025

Global - XFG.* vs LP.8.1.*

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

growth of 5.7% per day, crossover on 06-Jun-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.

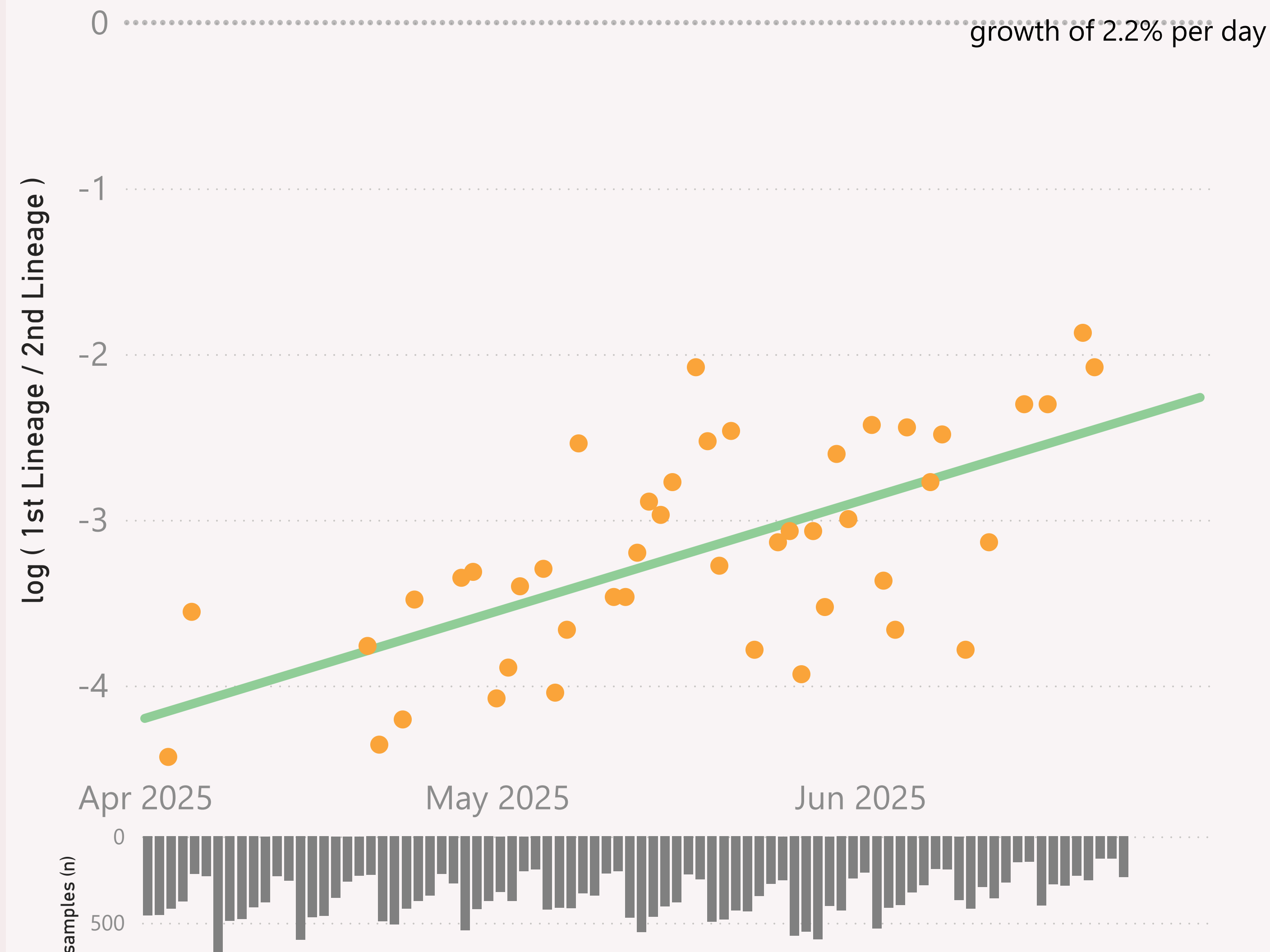
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n=29,833 sequenced genomes, from 1 April 2025 up to 23 June 2025

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.

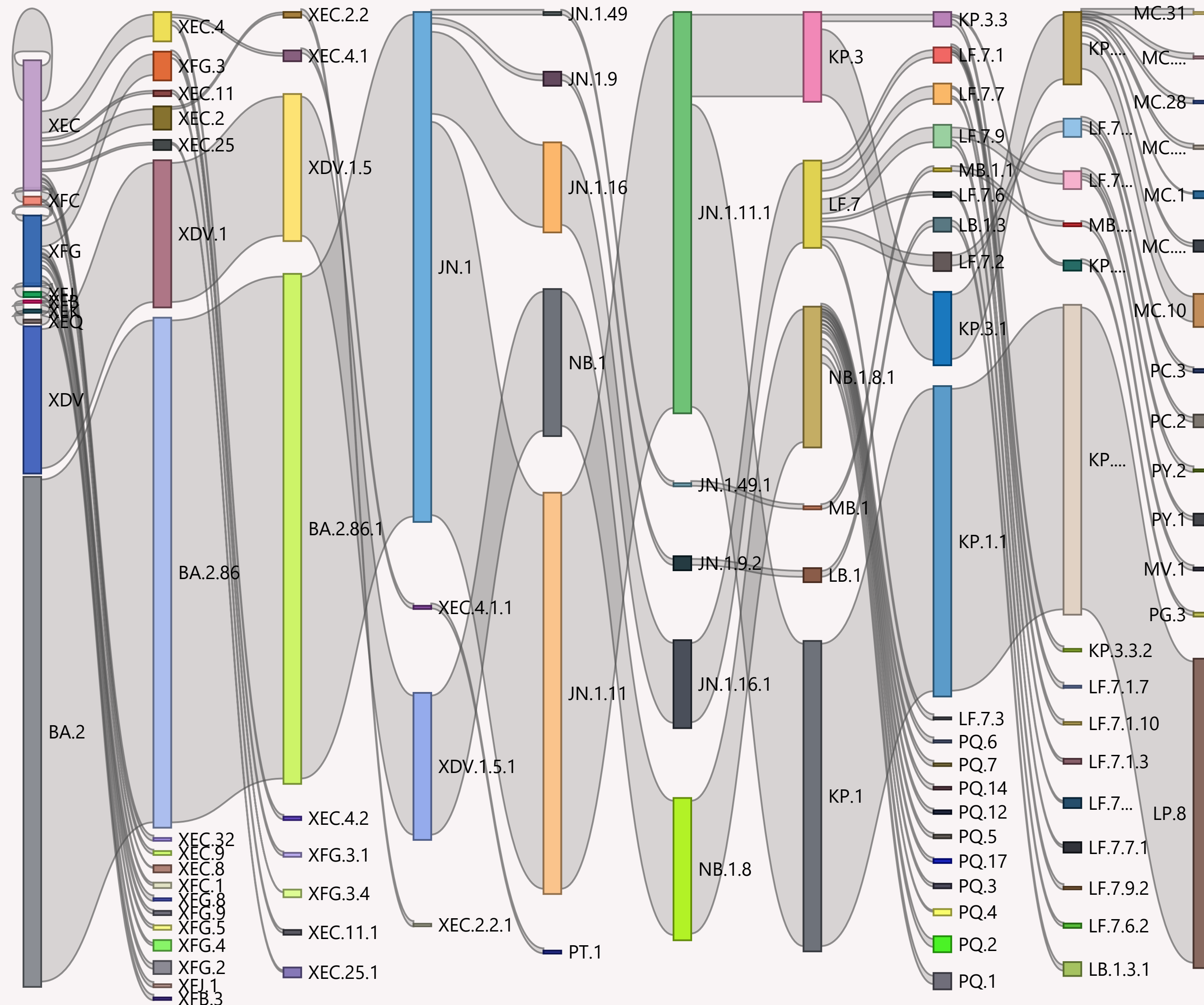
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

The Lineage classifications are provided by Nextclade.

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

n=44,149 sequenced genomes, from 1 March 2025 up to 23 June 2025



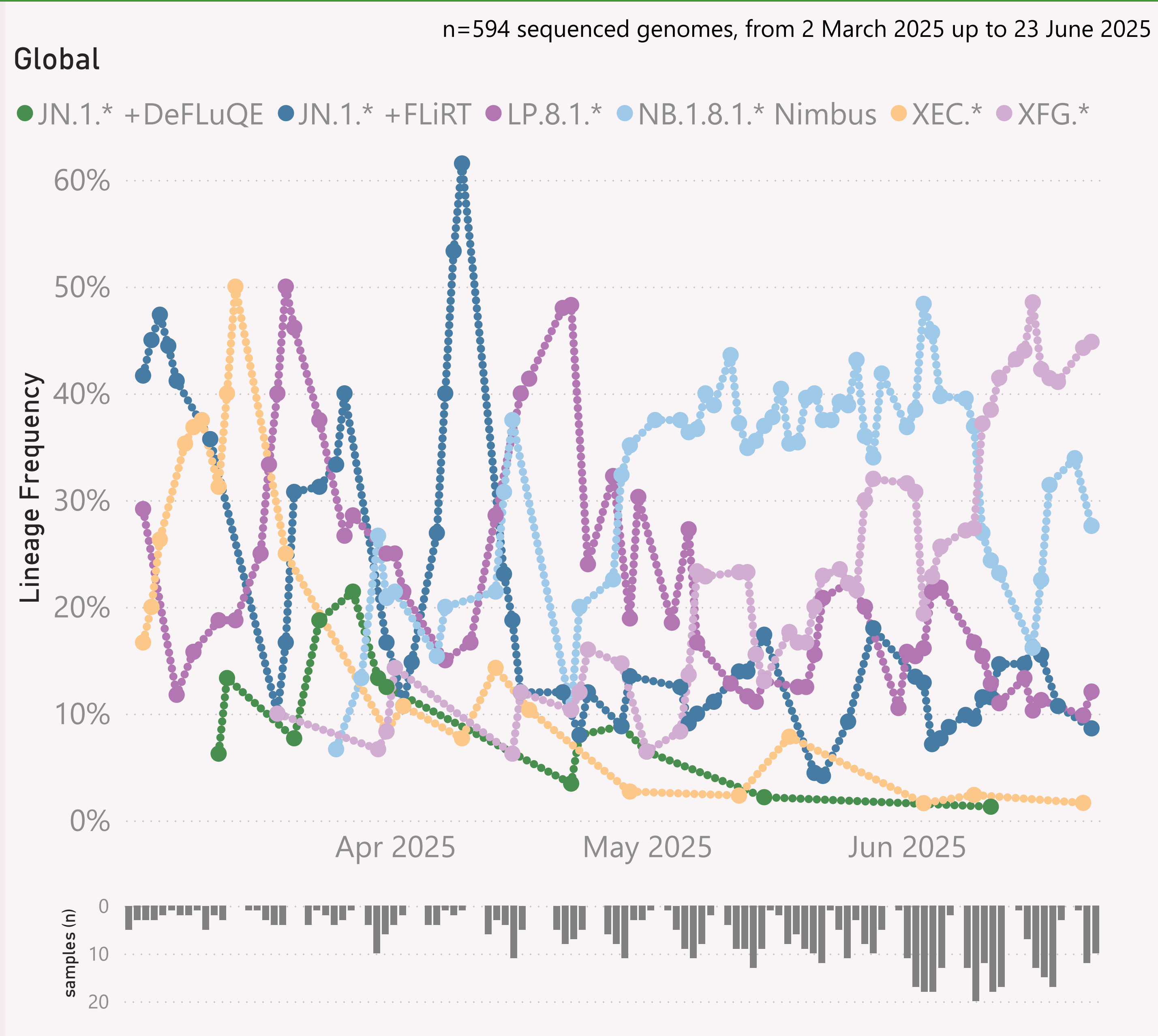
This page shows the hierarchy of the significant Lineages, over recent months.

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>	25,020	20/06/2025		27/06/2025	
<div>+ United States</div>	7,841	23/06/2025		27/06/2025	
<div>+ Spain</div>	2,413	23/06/2025		27/06/2025	
<div>+ China</div>	2,064	23/06/2025		27/06/2025	
<div>+ United Kingdom</div>	1,887	23/06/2025		27/06/2025	
<div>+ Singapore</div>	1,789	23/06/2025		27/06/2025	
<div>+ Australia</div>	1,363	23/06/2025		27/06/2025	
<div>+ India</div>	866	22/06/2025		27/06/2025	
<div>+ France</div>	836	23/06/2025		27/06/2025	
<div>+ Japan</div>	697	23/06/2025		27/06/2025	
<div>+ Brazil</div>	691	23/06/2025		27/06/2025	
<div>+ Mexico</div>	627	18/06/2025		27/06/2025	
<div>+ Netherlands</div>	528	22/06/2025		27/06/2025	
<div>+ New Zealand</div>	481	23/06/2025		27/06/2025	
<div>+ Russia</div>	462	14/06/2025		27/06/2025	
<div>+ Ireland</div>	395	23/06/2025		27/06/2025	
<div>+ Malaysia</div>	395	23/06/2025		27/06/2025	
<div>+ South Korea</div>	377	23/06/2025		27/06/2025	
<div>+ Kenya</div>	375	28/01/2025		27/06/2025	
<div>+ Thailand</div>	281	23/05/2025		30/05/2025	
<div>+ Kazakhstan</div>	218	28/05/2025		27/06/2025	
<div>+ Germany</div>	198	23/06/2025		27/06/2025	
<div>+ Costa Rica</div>	182	14/06/2025		27/06/2025	
<div>+ Luxembourg</div>	171	02/06/2025		19/06/2025	
<div>+ Denmark</div>	166	16/06/2025		27/06/2025	
<div>+ Hong Kong</div>	164	19/06/2025		27/06/2025	
<div>+ Bahrain</div>	163	21/06/2025		27/06/2025	
<div>+ Norway</div>	163	12/06/2025		26/06/2025	
<div>- Total</div>	52,787	23/06/2025		27/06/2025	

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.