

This "Global - Other" report aggregates the available data from countries besides those I regularly report on: Australia, NZ, the US, Canada and Europ.

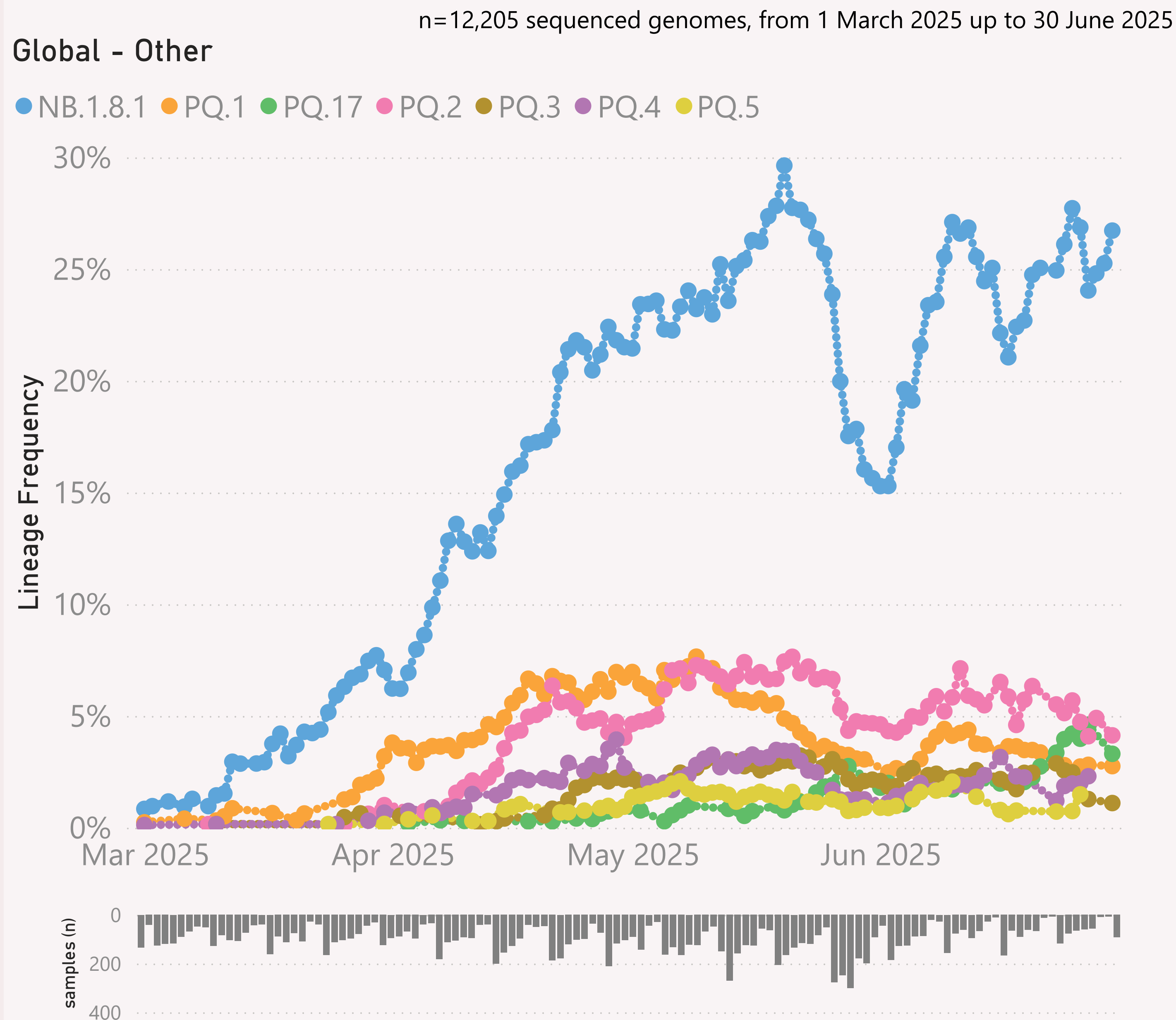
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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 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.



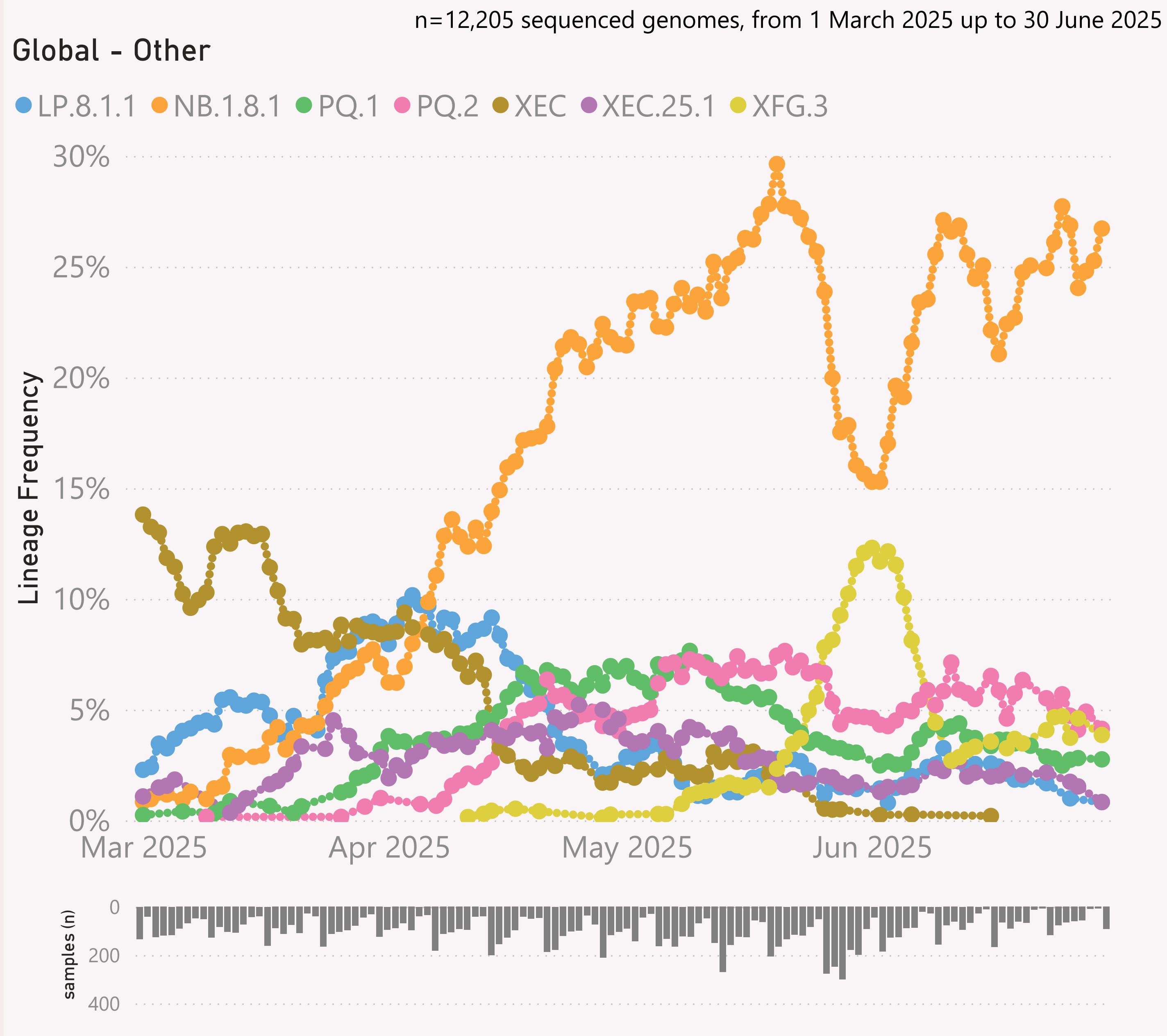
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.* Nimbus.

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

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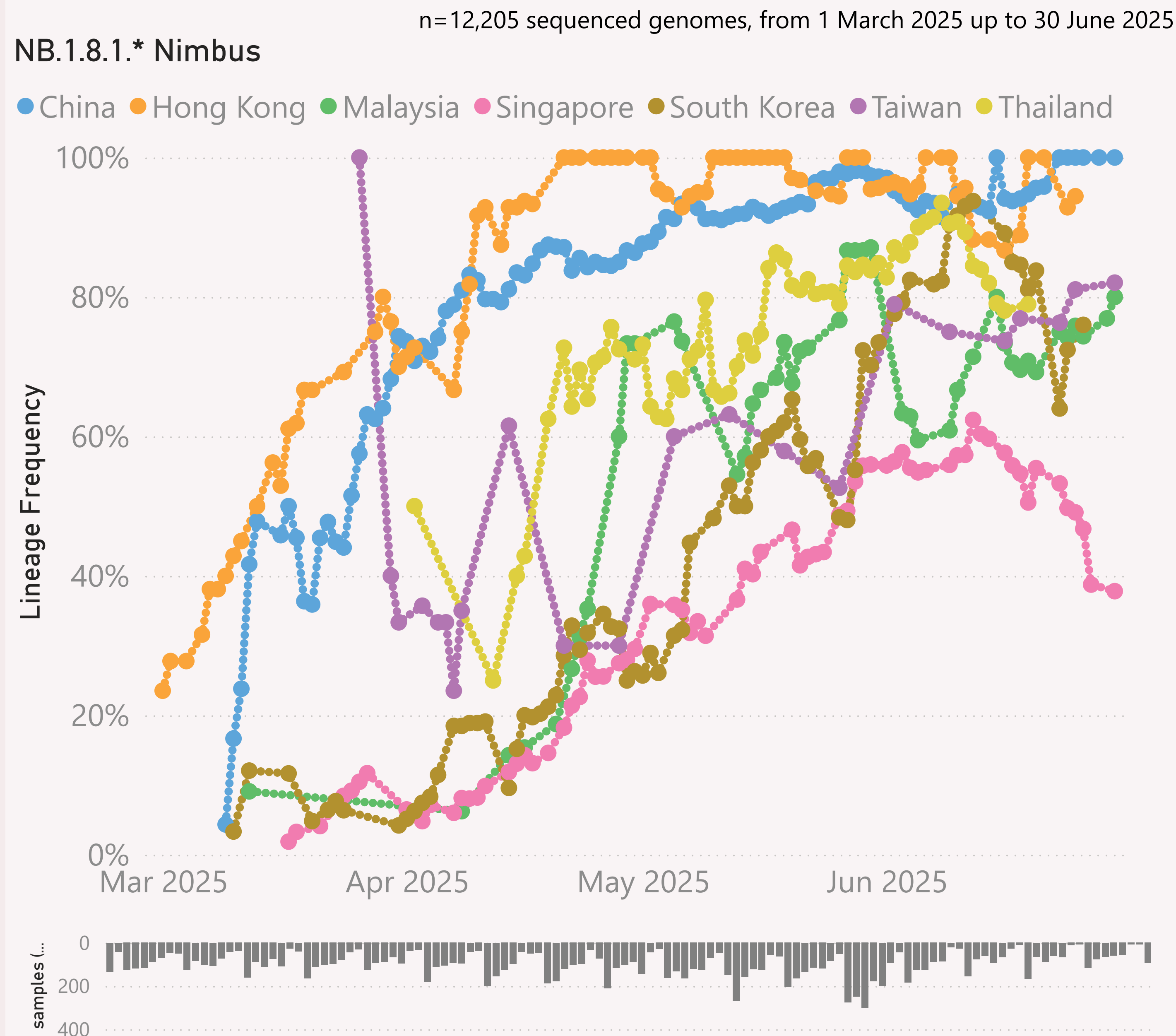
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This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

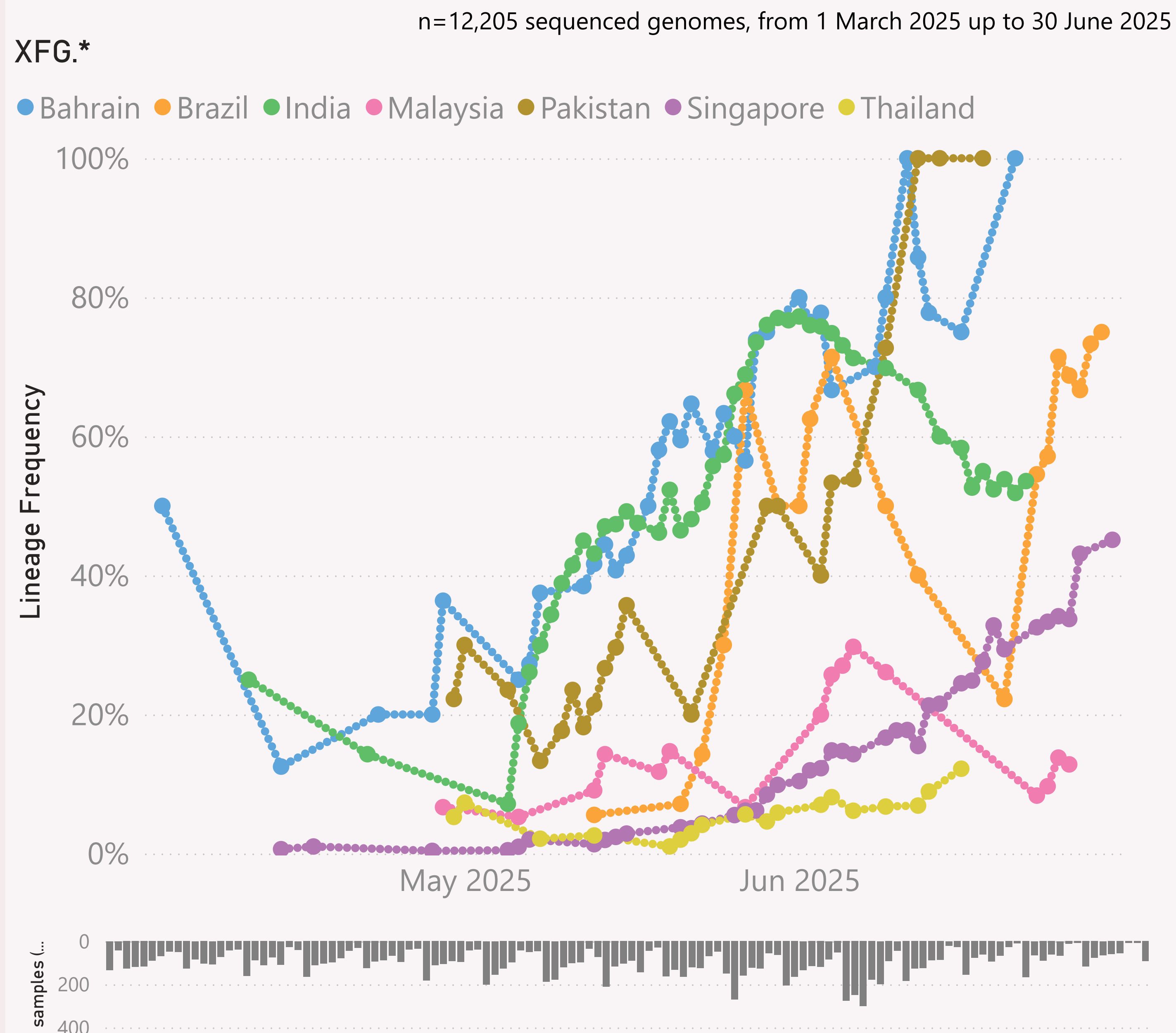
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

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

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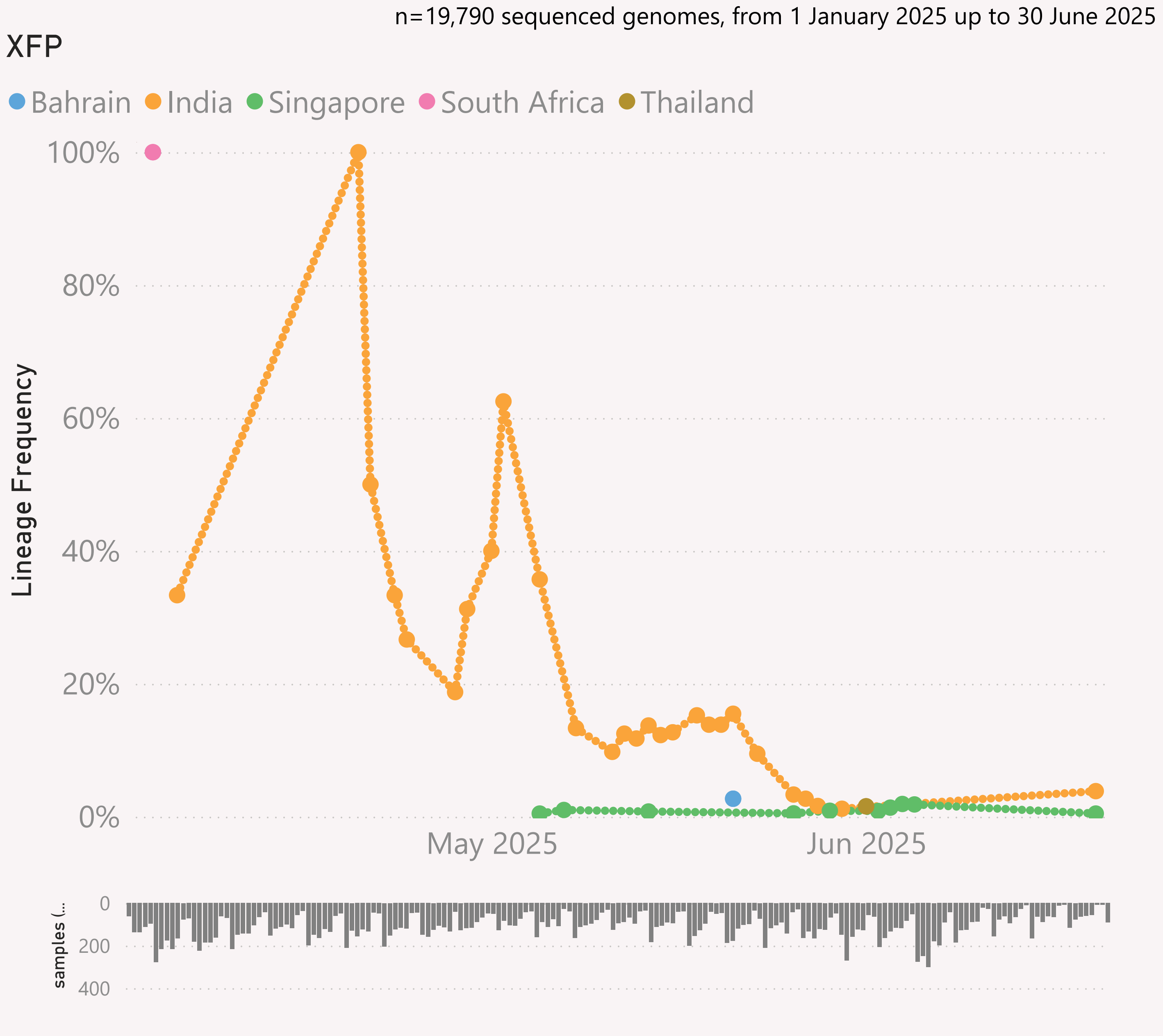
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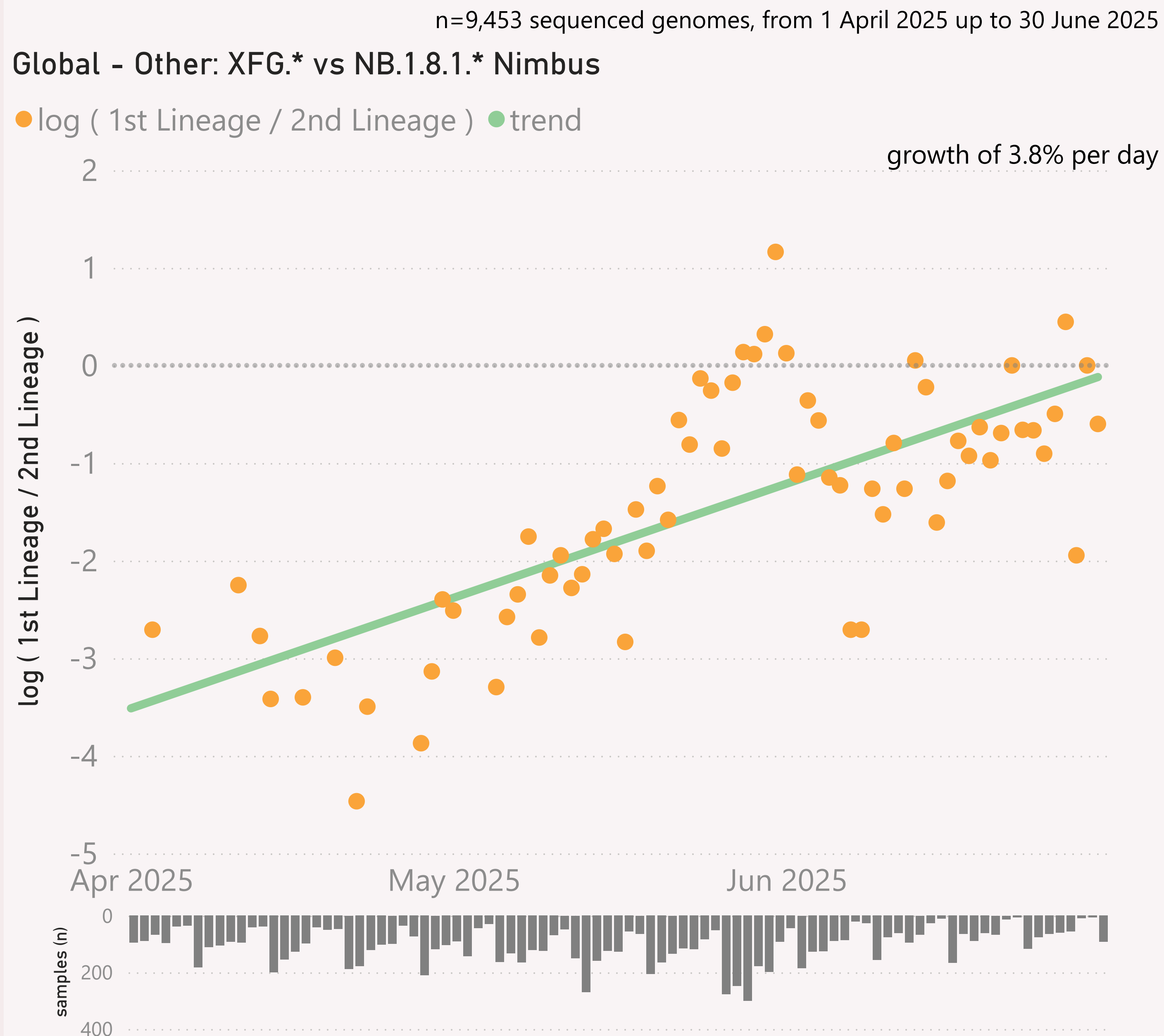
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This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

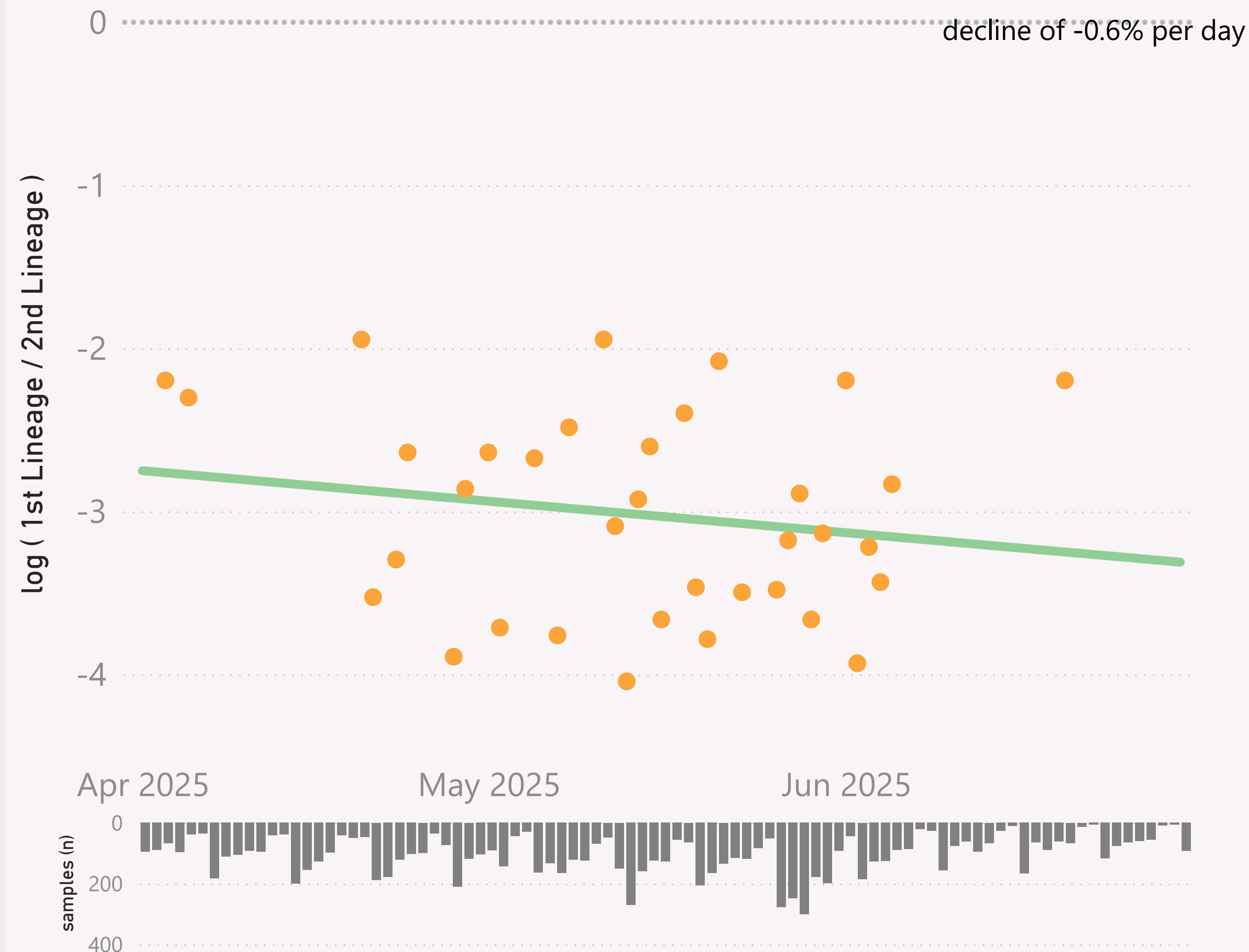
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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n=9,453 sequenced genomes, from 1 April 2025 up to 30 June 2025

Global - Other: XFP vs NB.1.8.1

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

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Global - Other



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.

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
<div>+ </div> China	2,082	30/06/2025		02/07/2025	
<div>+ </div> Singapore	1,503	30/06/2025		02/07/2025	
<div>+ </div> India	850	22/06/2025		02/07/2025	
<div>+ </div> Mexico	595	18/06/2025		02/07/2025	
<div>+ </div> Brazil	546	29/06/2025		02/07/2025	
<div>+ </div> Thailand	516	19/06/2025		02/07/2025	
<div>+ </div> Japan	462	30/06/2025		02/07/2025	
<div>+ </div> Malaysia	397	30/06/2025		02/07/2025	
<div>+ </div> South Korea	382	26/06/2025		02/07/2025	
<div>+ </div> Kenya	375	28/01/2025		02/07/2025	
<div>+ </div> Costa Rica	246	19/06/2025		02/07/2025	
<div>+ </div> Kazakhstan	218	28/05/2025		02/07/2025	
<div>+ </div> Taiwan	192	30/06/2025		02/07/2025	
<div>+ </div> Puerto Rico	182	30/06/2025		02/07/2025	
<div>+ </div> Bahrain	163	21/06/2025		29/06/2025	
<div>+ </div> Hong Kong	153	26/06/2025		02/07/2025	
<div>+ </div> South Africa	132	24/06/2025		02/07/2025	
<div>+ </div> Ghana	99	27/06/2025		02/07/2025	
<div>+ </div> Vietnam	91	27/06/2025		02/07/2025	
<div>+ </div> Pakistan	80	18/06/2025		30/06/2025	
<div>+ </div> Israel	48	01/03/2025		02/07/2025	
<div>+ </div> Cambodia	40	31/05/2025		02/07/2025	
<div>+ </div> Qatar	40	30/05/2025		16/06/2025	
<div>+ </div> Guatemala	39	26/06/2025		02/07/2025	
<div>+ </div> Paraguay	36	13/01/2025		26/06/2025	
<div>+ </div> French Guiana	34	11/06/2025		23/06/2025	
<div>+ </div> Egypt	31	27/04/2025		19/06/2025	
<div>+ </div> Senegal	23	28/04/2025		02/07/2025	
<div>- </div> Total	9,779	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.