

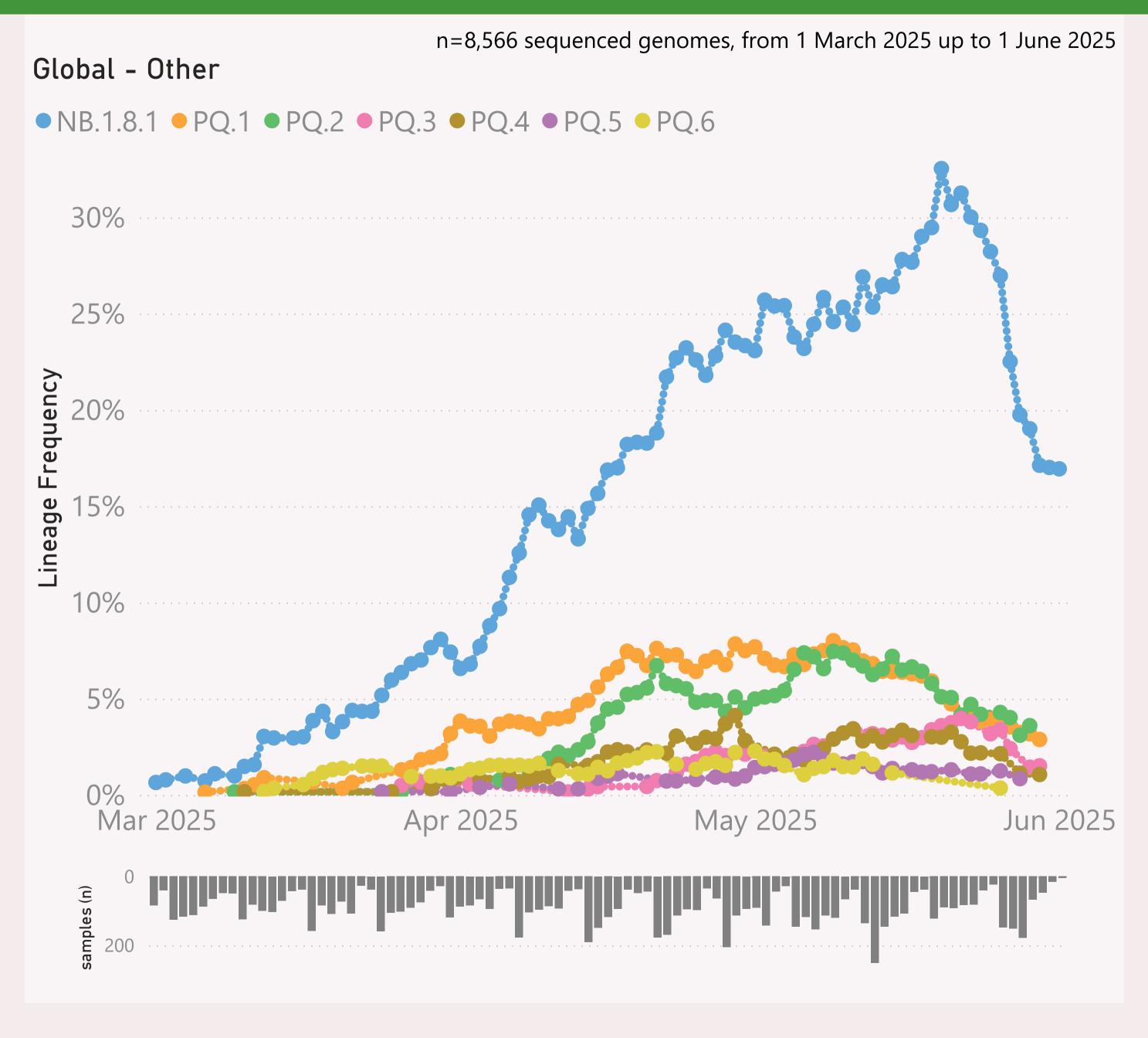
This "Global - Other" report aggregates the available data from countries besides those I regularly report on: Australia, NZ, the US, Canada and Europ.

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.

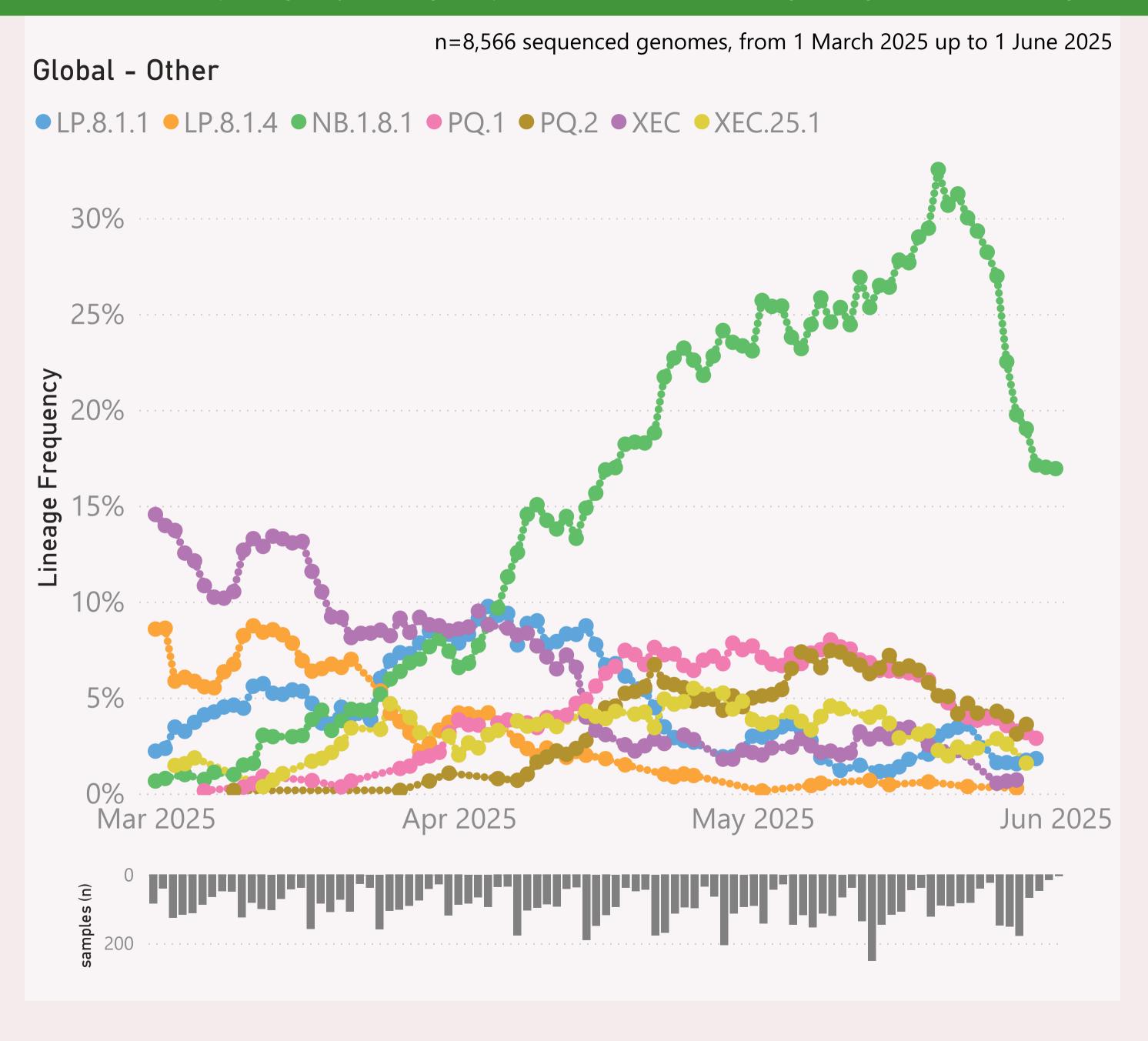


This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.\* Nimbus.

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.

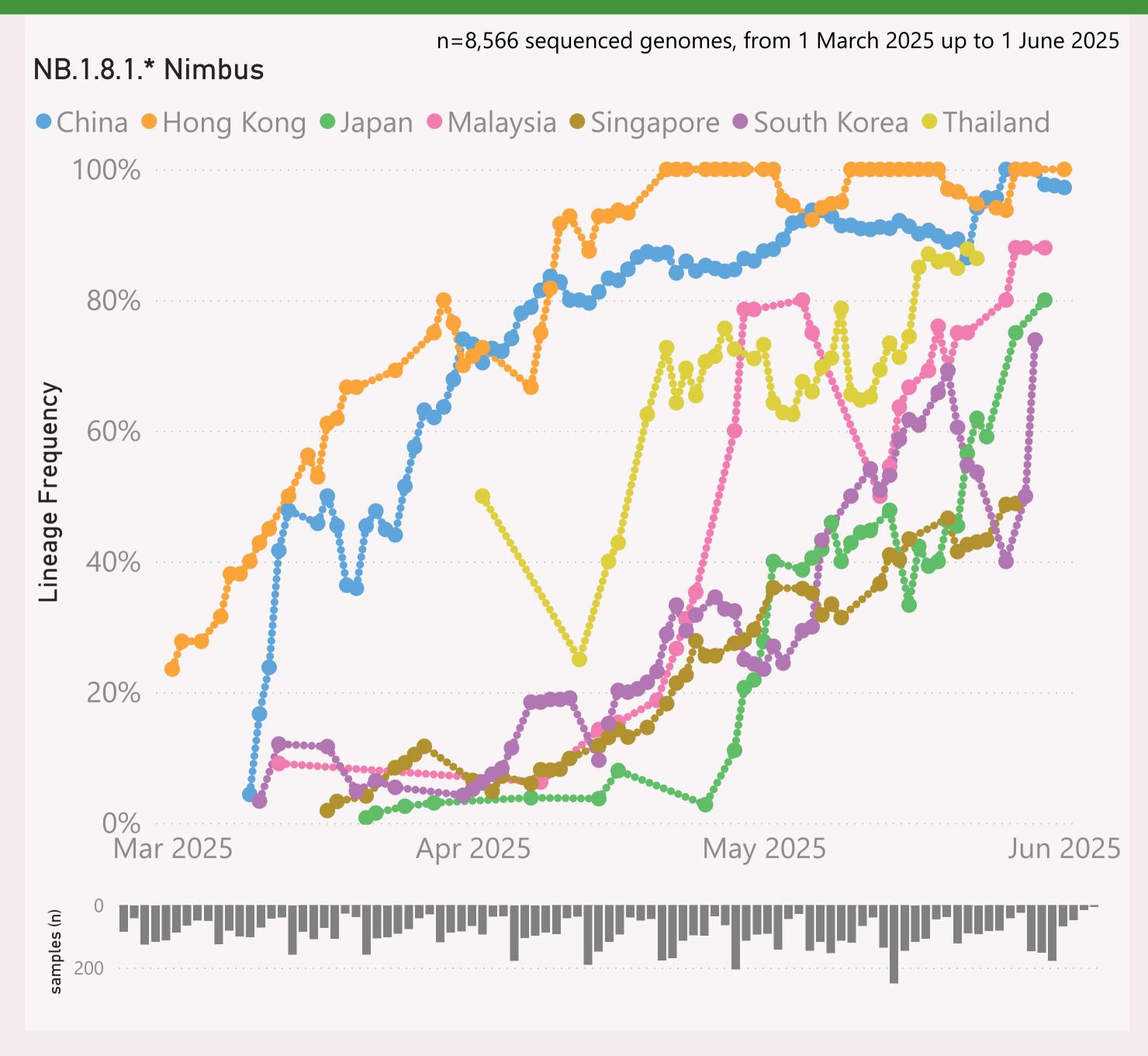


This page shows the frequency of the top 7 lineages, across recent months.

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.



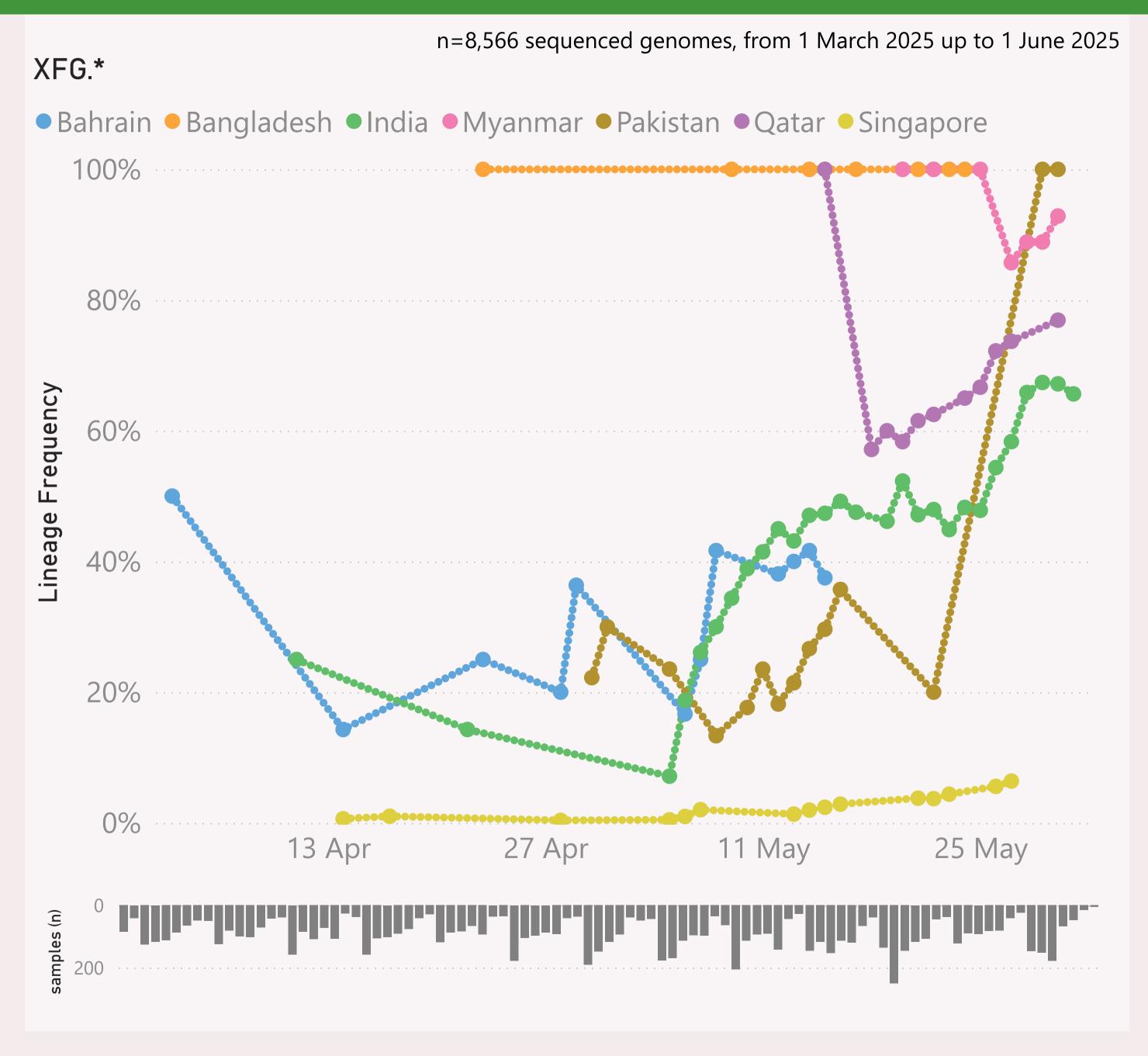
This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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.



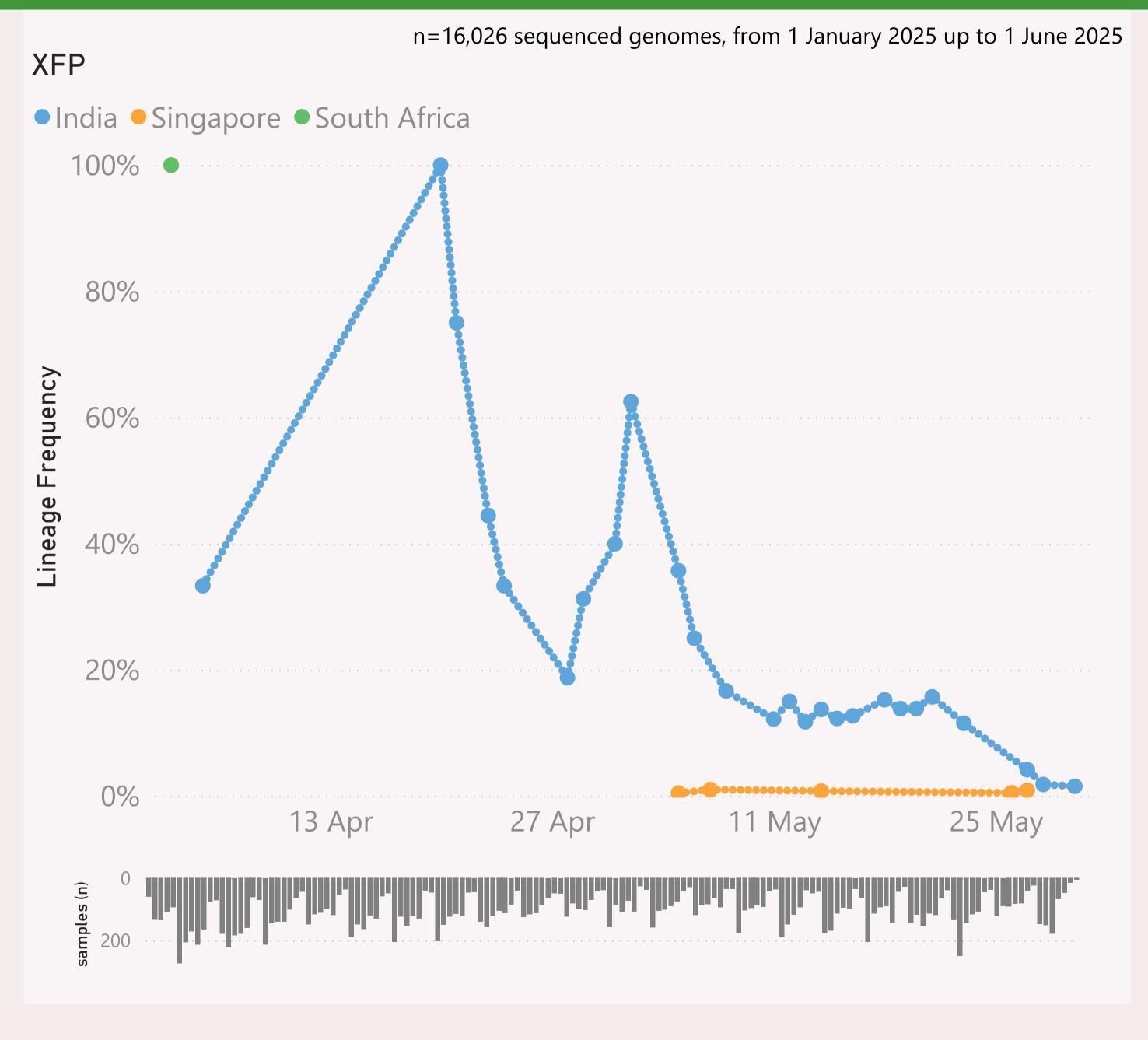
This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

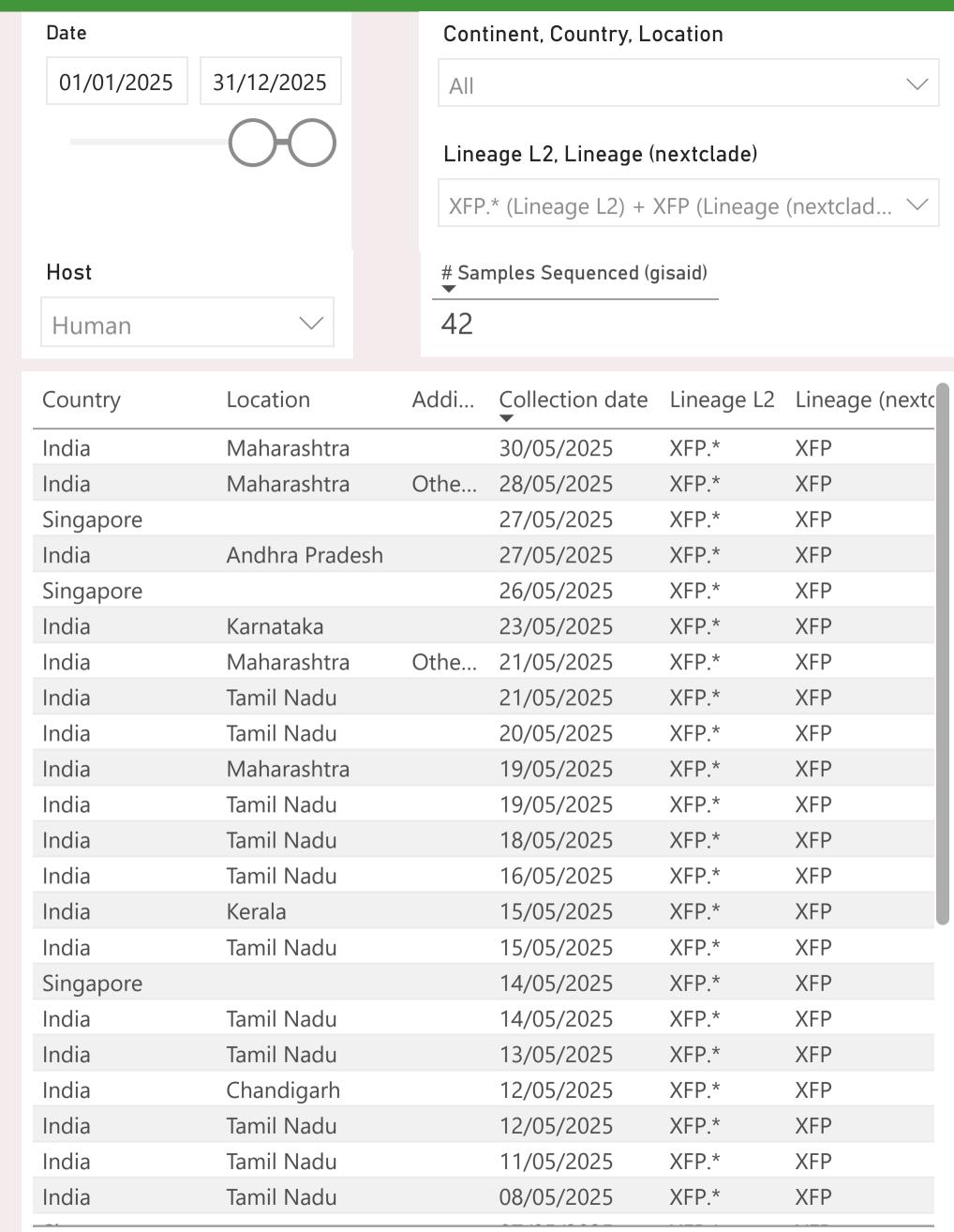
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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.





**Total** 

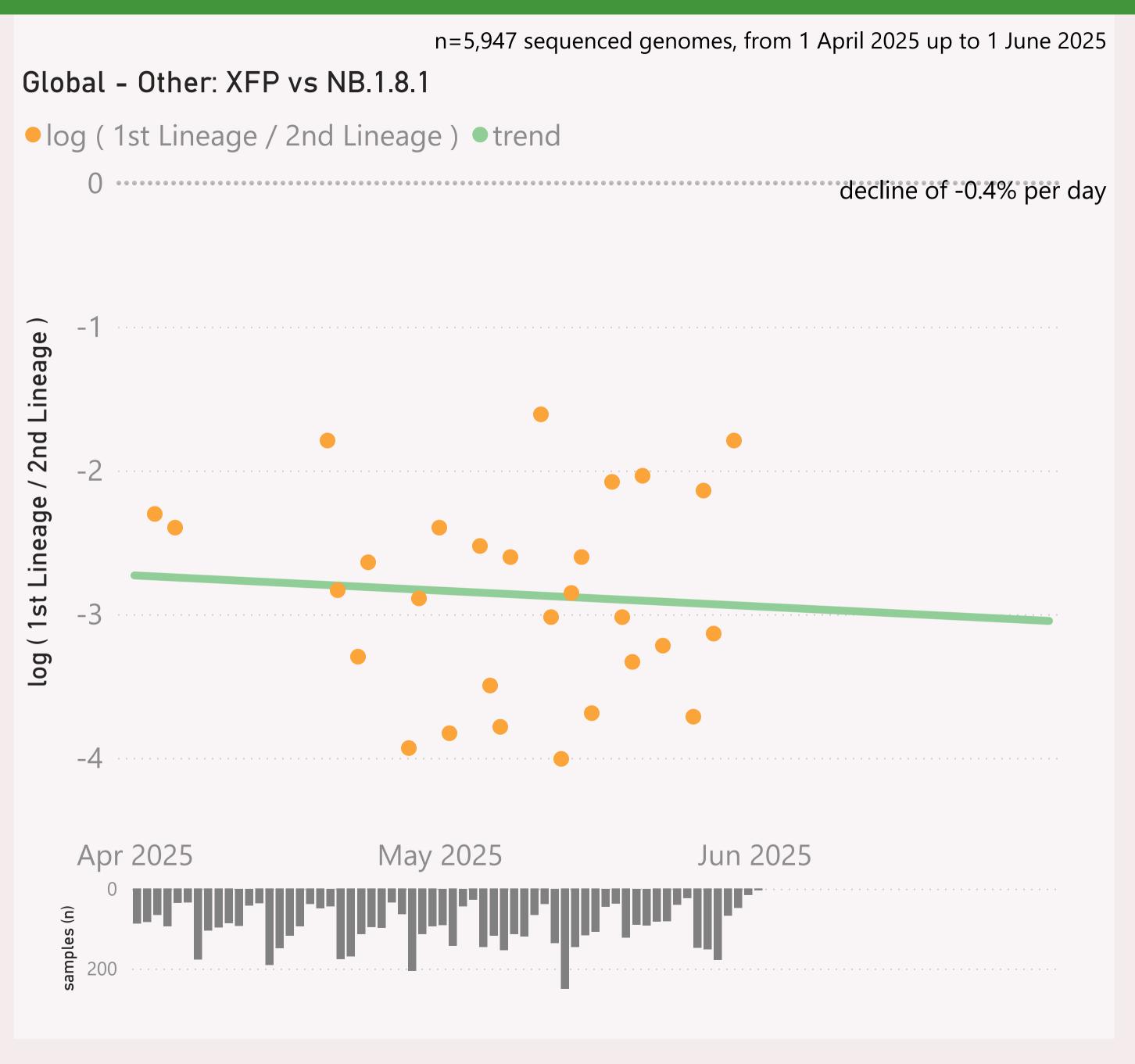
n=5,947 sequenced genomes, from 1 April 2025 up to 1 June 2025 Global - Other: XFG.\* vs NB.1.8.1.\* Nimbus ● log (1st Lineage / 2nd Lineage ) ● trend growth of 6.6% per day, crossover on 07-Jun-25 May 2025 Jun 2025

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.

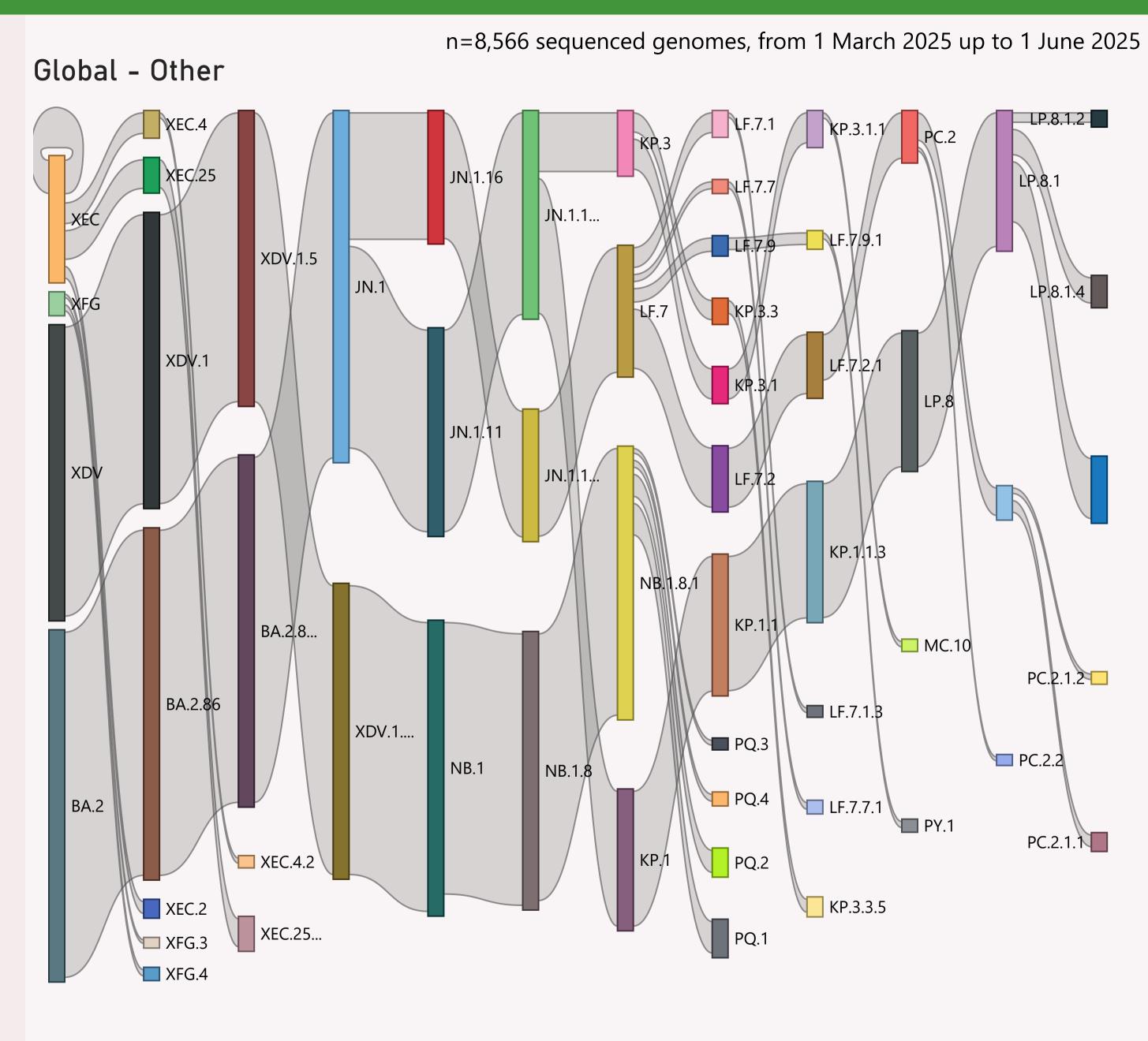


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.



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.

## Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊕ China	1,705	01/06/2025	🚜	18/06/2025	
<b>±</b> Singapore	1,221	27/05/2025		02/06/2025	a litta
⊞ Japan	786	30/05/2025	مامام الله المستحد	20/06/2025	The action of the Control
⊕ Brazil	762	01/06/2025		18/06/2025	1
± Mexico	549	19/05/2025	4	12/06/2025	
	468	29/05/2025	and a	20/06/2025	ald the ratio
⊞ India	421	31/05/2025		18/06/2025	. Industria
	315	30/05/2025	and the second	20/06/2025	I i.∭
	303	28/05/2025	1	20/06/2025	1
	297	23/05/2025		30/05/2025	
⊕ Peru	214	01/04/2025		19/06/2025	
	143	01/06/2025	A.	18/06/2025	and the first
⊞ Taiwan	114	26/05/2025		02/06/2025	
⊕ Puerto Rico	111	30/05/2025		16/06/2025	at a second
	94	20/05/2025	1	11/06/2025	
	81	31/03/2025	dde k	22/05/2025	
<b>H</b> Guatemala	78	15/05/2025	all and the	05/06/2025	
⊕ Pakistan	77	30/05/2025		05/06/2025	a radi
	73	04/04/2025	41.0	05/06/2025	
⊞ Bahrain	71	15/05/2025		26/05/2025	
± Israel	71	01/05/2025		21/05/2025	
	51	30/05/2025		18/06/2025	
⊕ Qatar	40	30/05/2025		16/06/2025	
<b>Egypt</b>	31	27/04/2025		19/06/2025	
⊕ Cambodia	27	19/05/2025		25/05/2025	
<b>E</b> Colombia	22	23/05/2025		06/06/2025	
⊞ Ghana	18	30/04/2025		29/05/2025	
⊞ Bangladesh	17	24/05/2025		05/06/2025	
Total	8,293	01/06/2025		20/06/2025	Tis an amhadar daaran

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.