

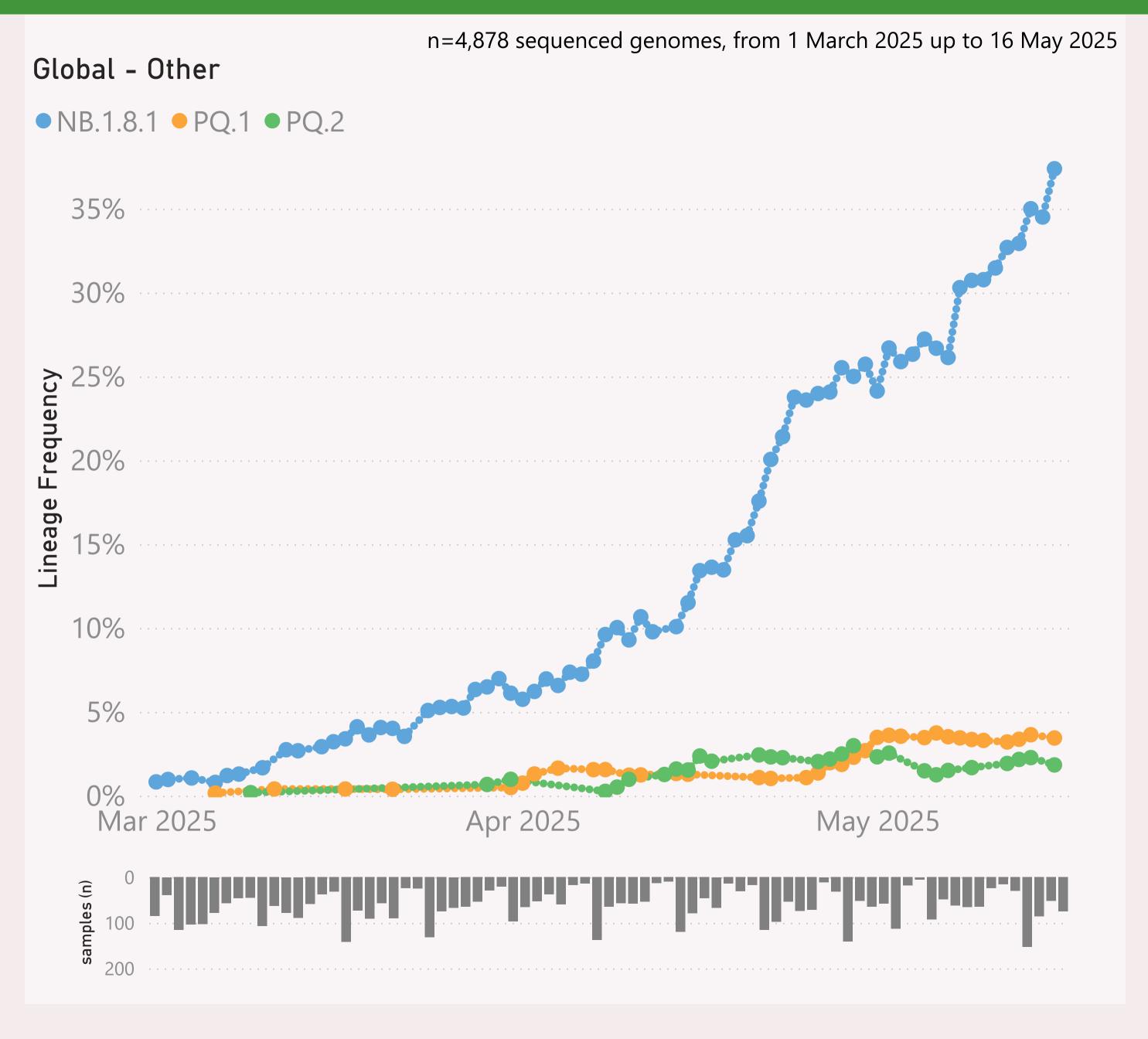
This "Global - Other" report aggregates the available data from countries besides those I regularly report on: Australia, NZ, the US, Canada and Europ.

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.

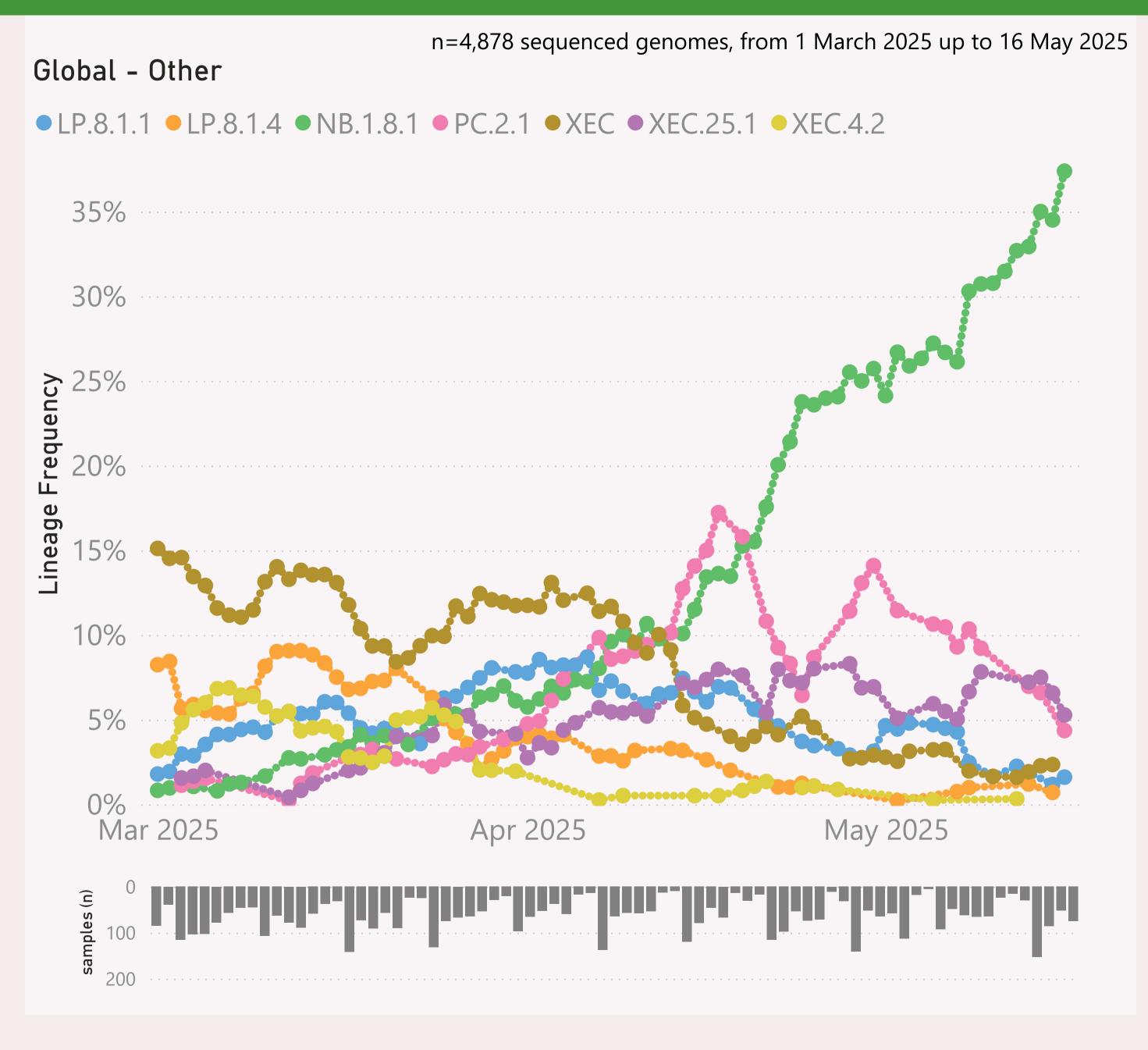


This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.\* Nimbus.

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.

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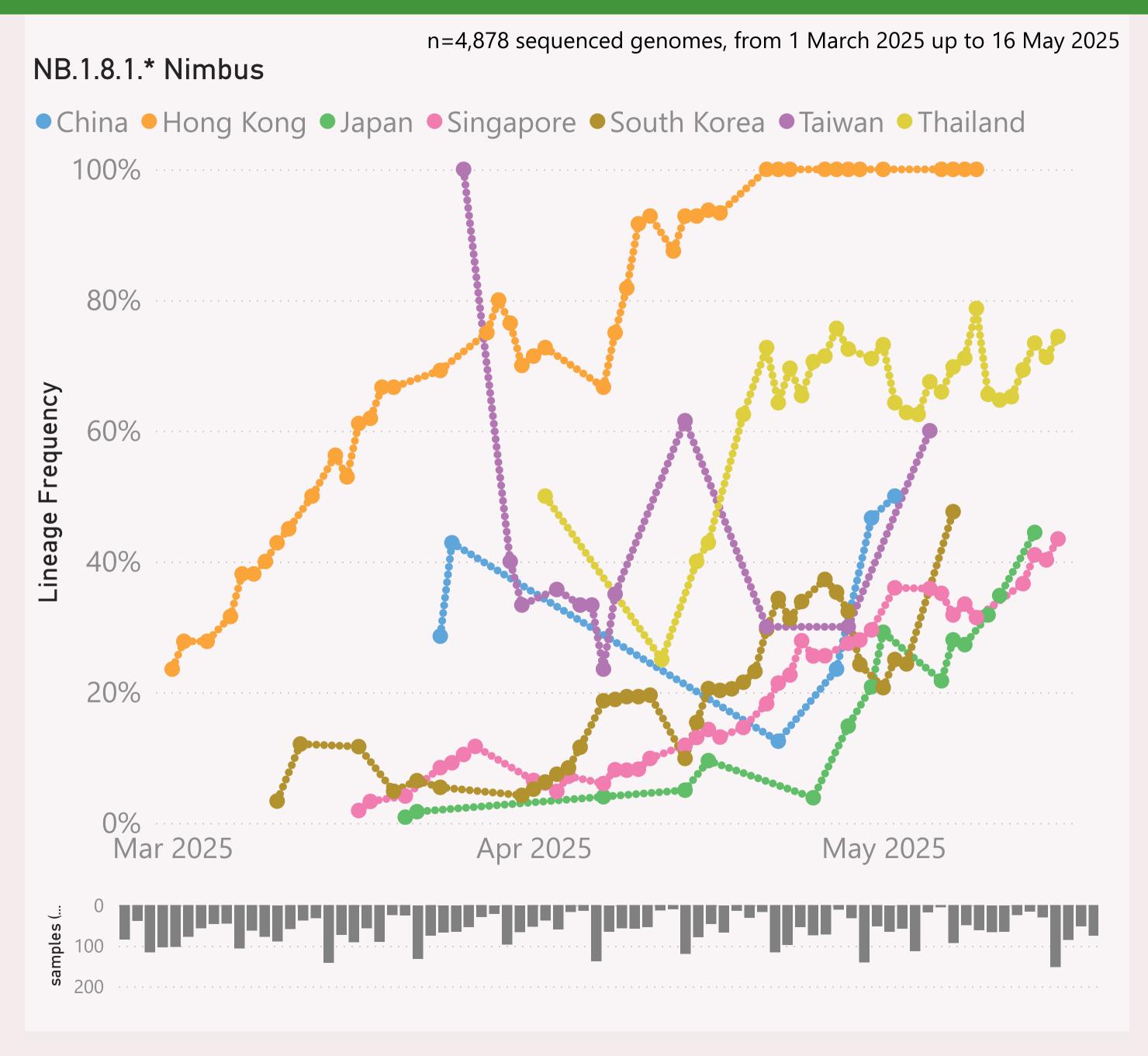


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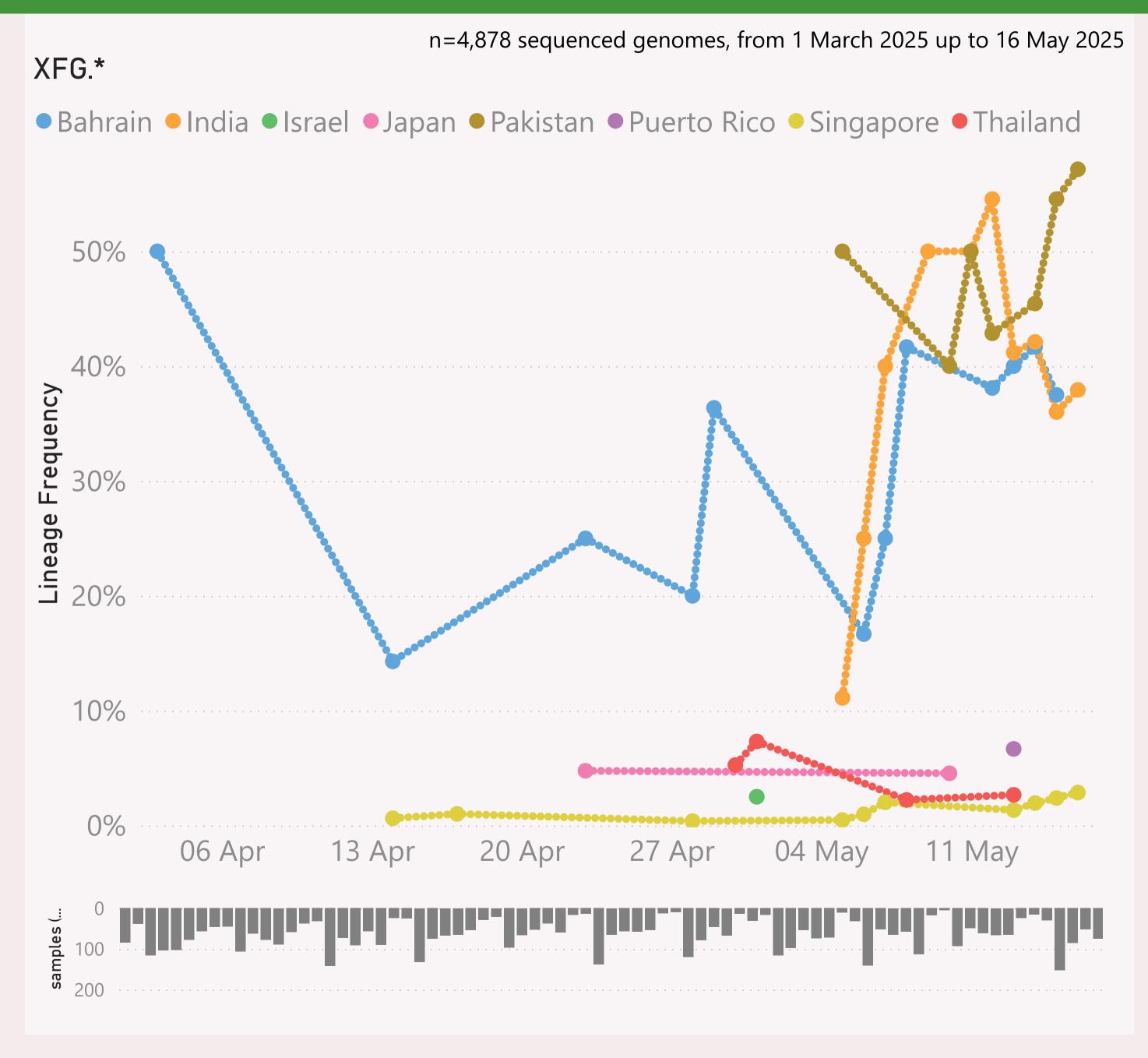
This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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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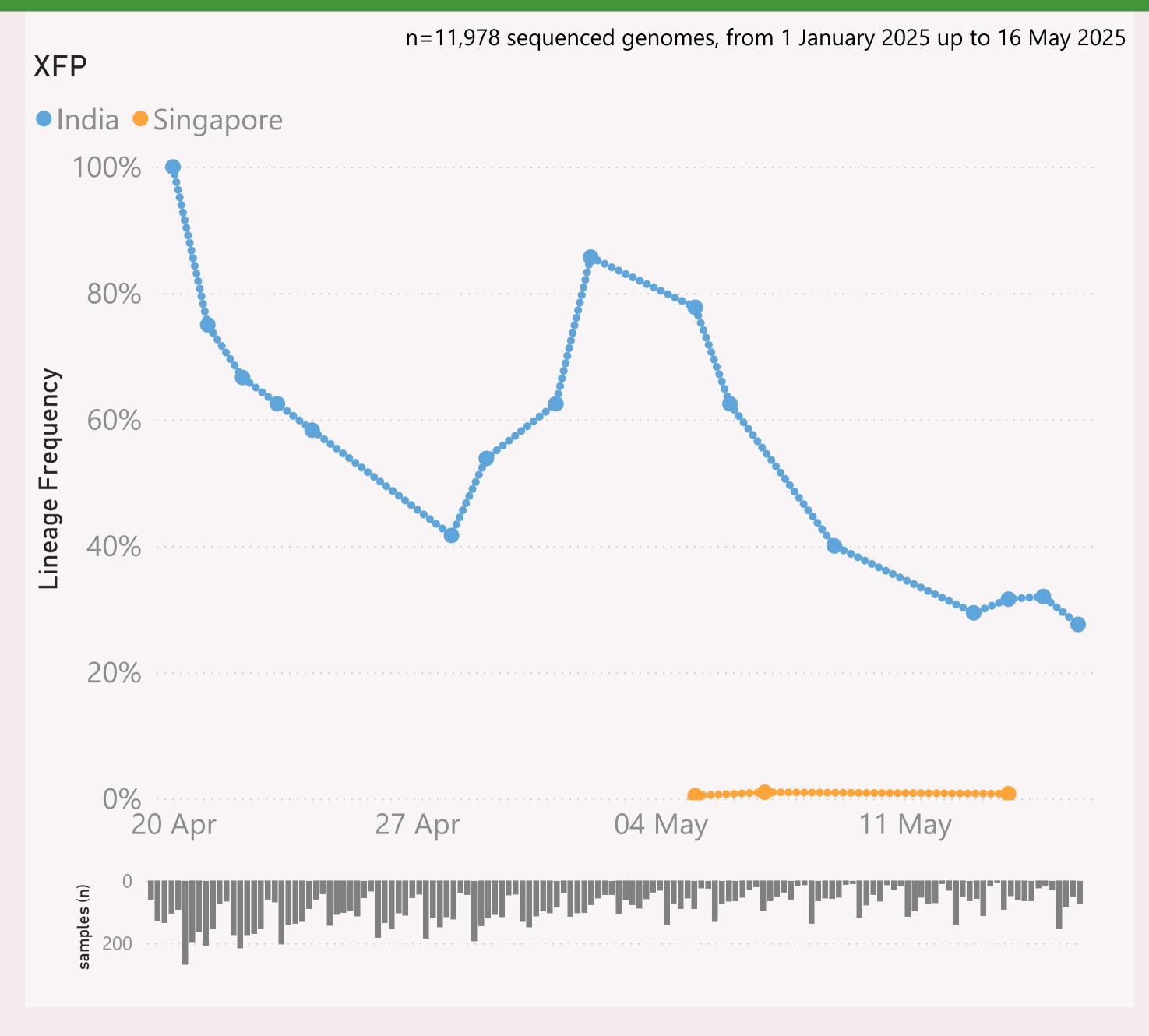
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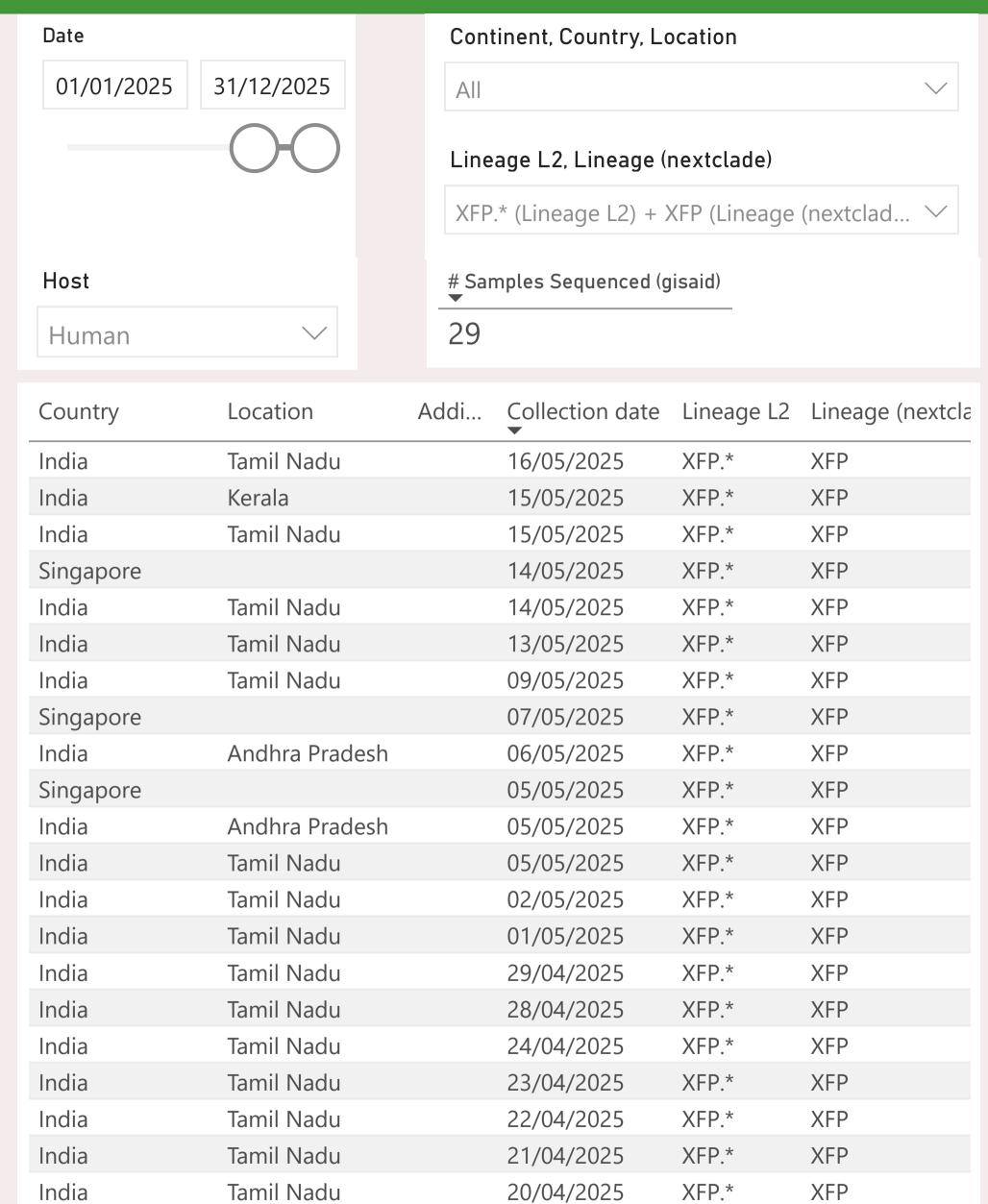
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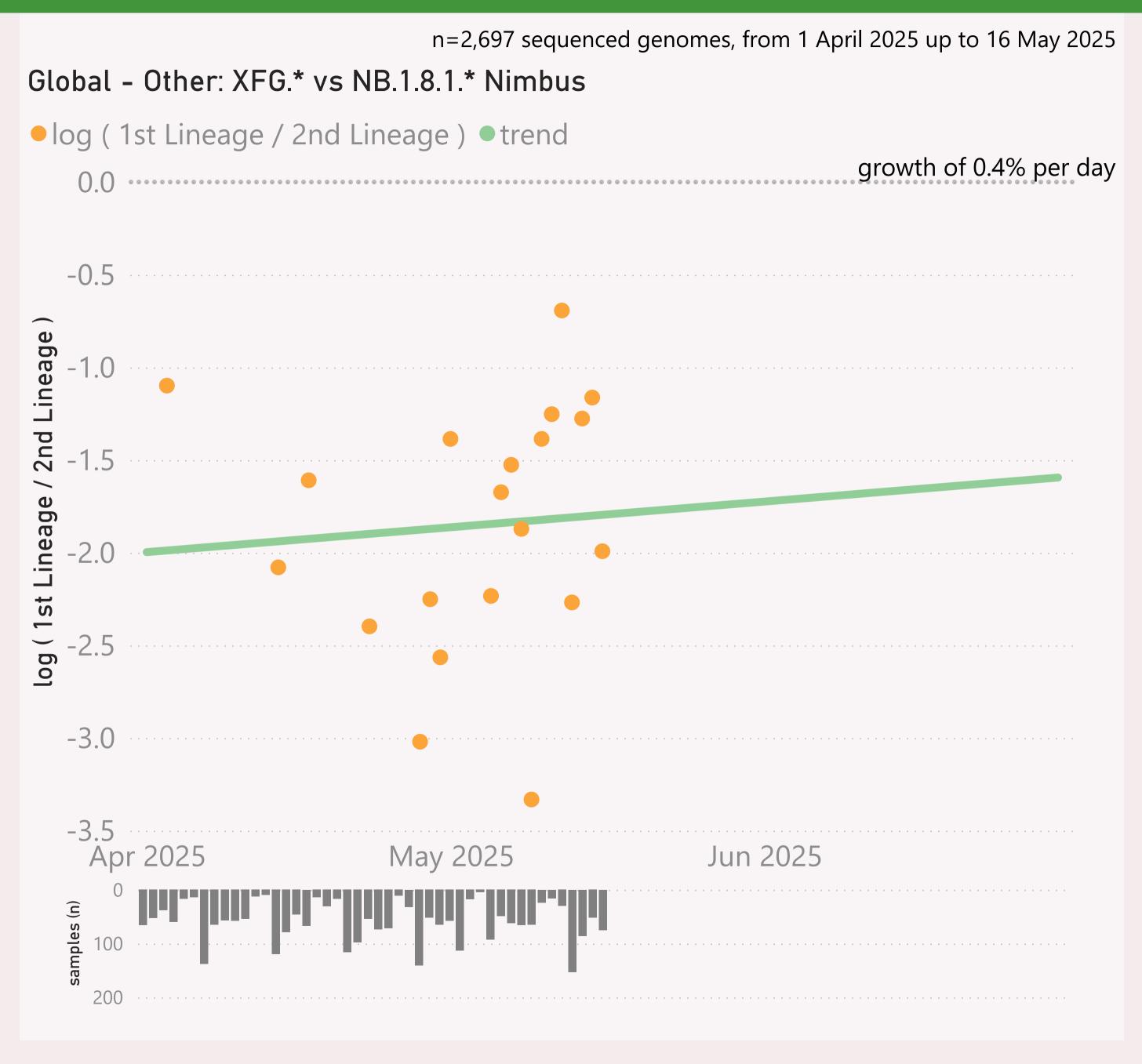
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**Total** 



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.

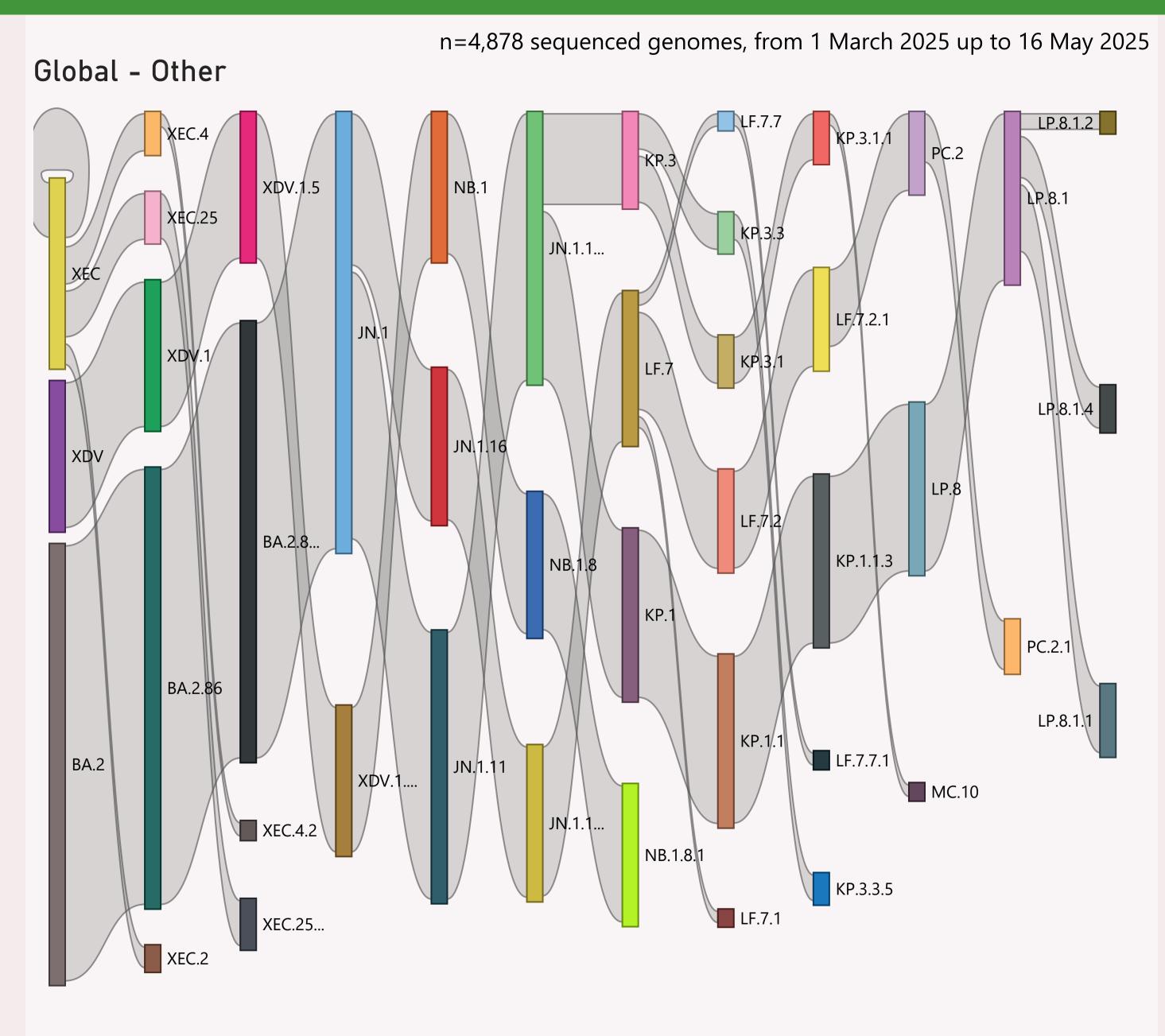


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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
Singapore	1,382	16/05/2025		10/05/2025	
	1,048	15/05/2025	allia annu da la Maria	10/05/2025	and the last the sale
⊕ Brazil	942	13/05/2025		10/05/2025	and the second
	560	07/05/2025	<u>. de</u>	10/05/2025	and the first state
	291	16/05/2025	u.,	10/05/2025	
	246	22/04/2025	in the second second	05/05/2025	- I - 1 - 1 - 1 - 1
⊕ Peru	198	01/04/2025	l ul	10/05/2025	
	187	13/05/2025	an atalan	10/05/2025	- 1
	171	31/03/2025	A	10/05/2025	
⊕ Costa Rica	124	27/04/2025	111	10/05/2025	I
⊕ Puerto Rico	113	16/05/2025	di	10/05/2025	1 1
	99	09/05/2025	$\Gamma_{i}$	10/05/2025	1 11
	95	07/02/2024		08/05/2025	
<b>Taiwan</b>	85	05/05/2025		09/05/2025	J
⊕ China	82	02/05/2025		10/05/2025	. 1.1
<b>H</b> Guatemala	76	25/04/2025		10/05/2025	. 1
⊕ Malaysia	74	11/02/2025		10/05/2025	
⊞ Bahrain	71	15/05/2025		10/05/2025	
⊞ Israel	71	01/05/2025		10/05/2025	1 1
<b>India</b>	63	16/05/2025		10/05/2025	
⊞ Bhutan	37	16/12/2024		15/04/2025	
⊕ Oman	36	15/02/2025		13/04/2025	
⊕ Ecuador	31	07/04/2025		30/04/2025	
	31	13/04/2025		25/04/2025	
⊕ Pakistan	25	16/05/2025		10/05/2025	1
	24	30/05/2024		23/04/2025	
	22	09/04/2025		02/05/2025	
⊕ Ghana	18	30/04/2025		10/05/2025	
Total	6,263	16/05/2025		10/05/2025	

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.