

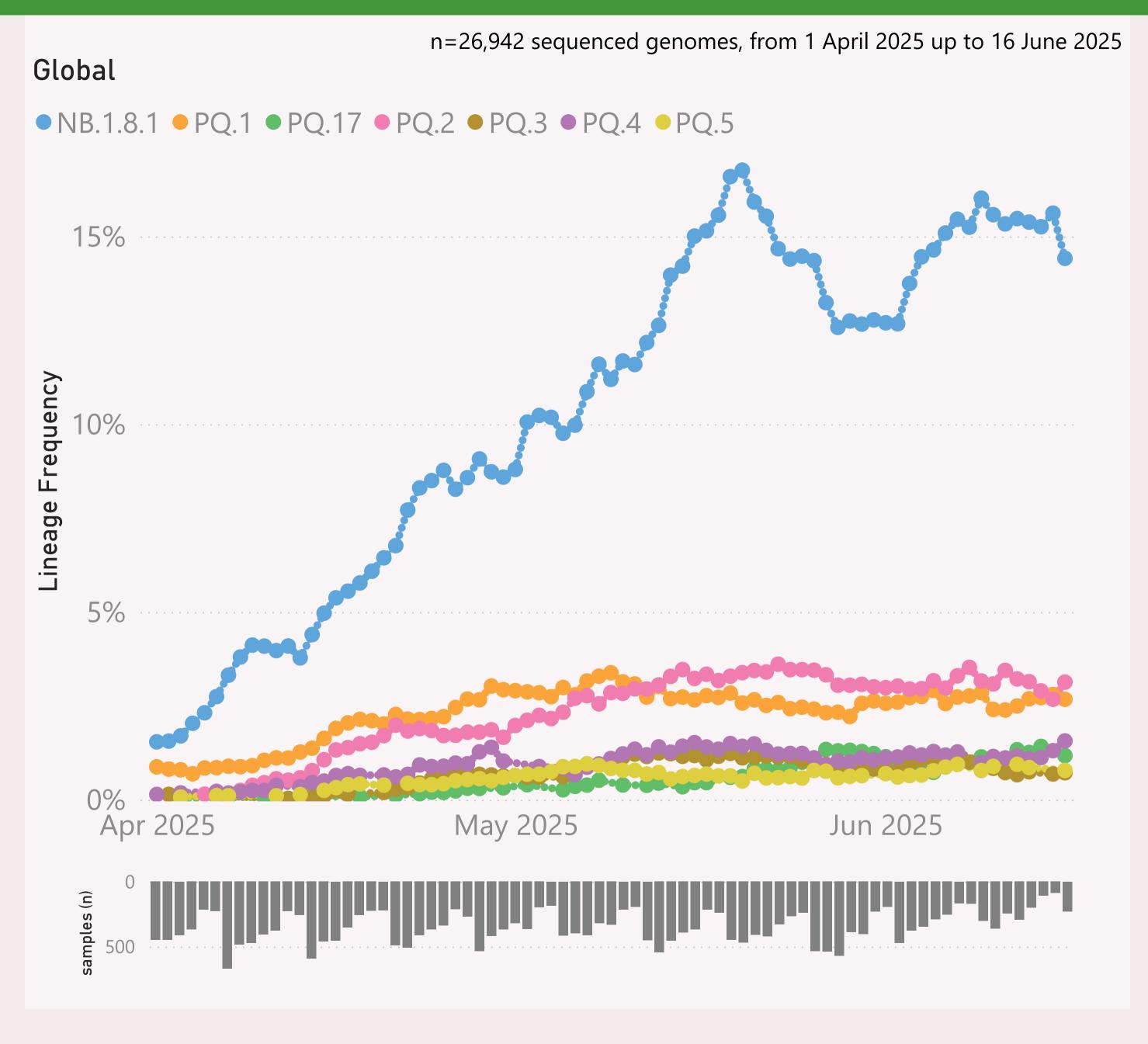
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.

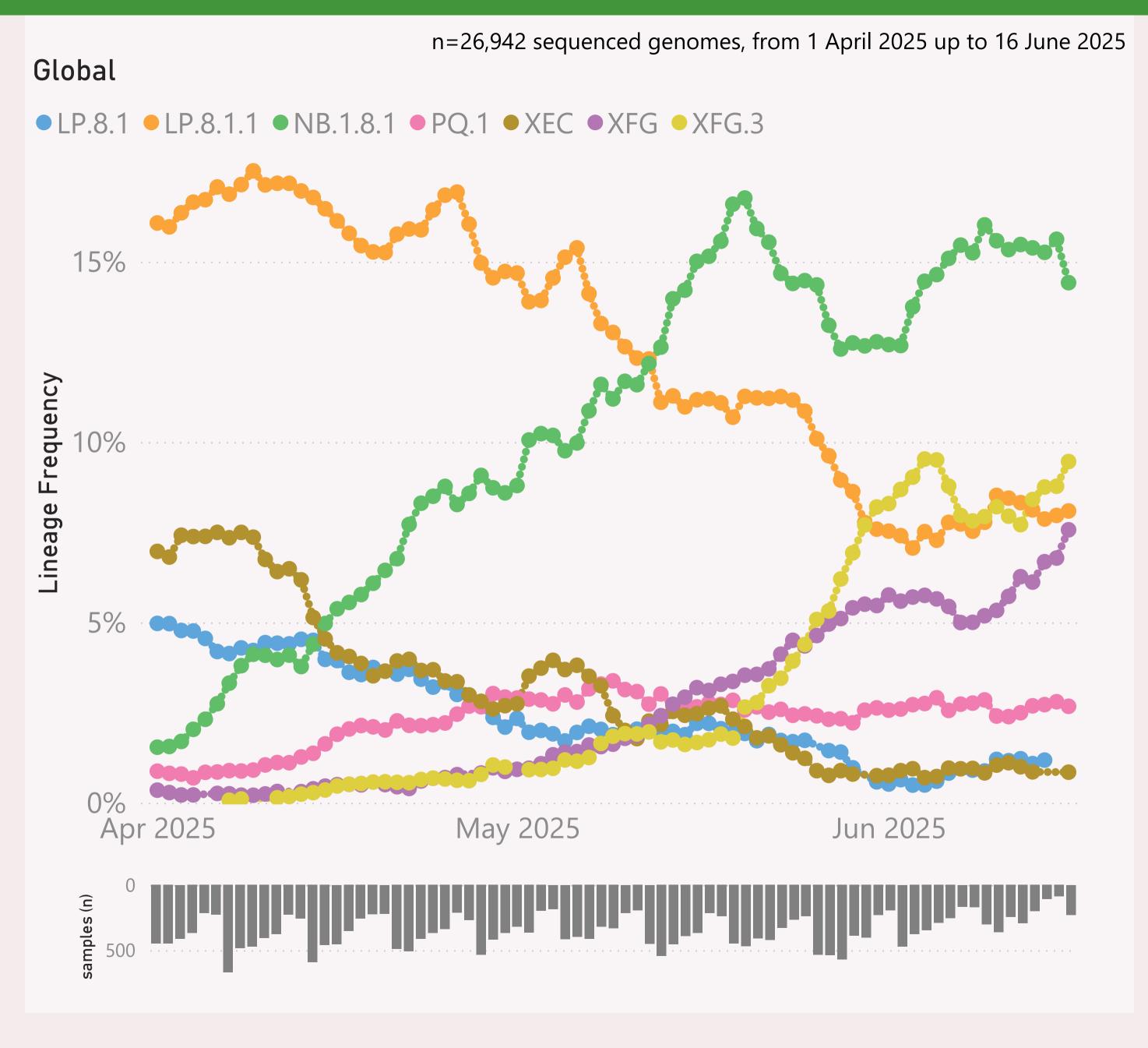


This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.* Nimbus.

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

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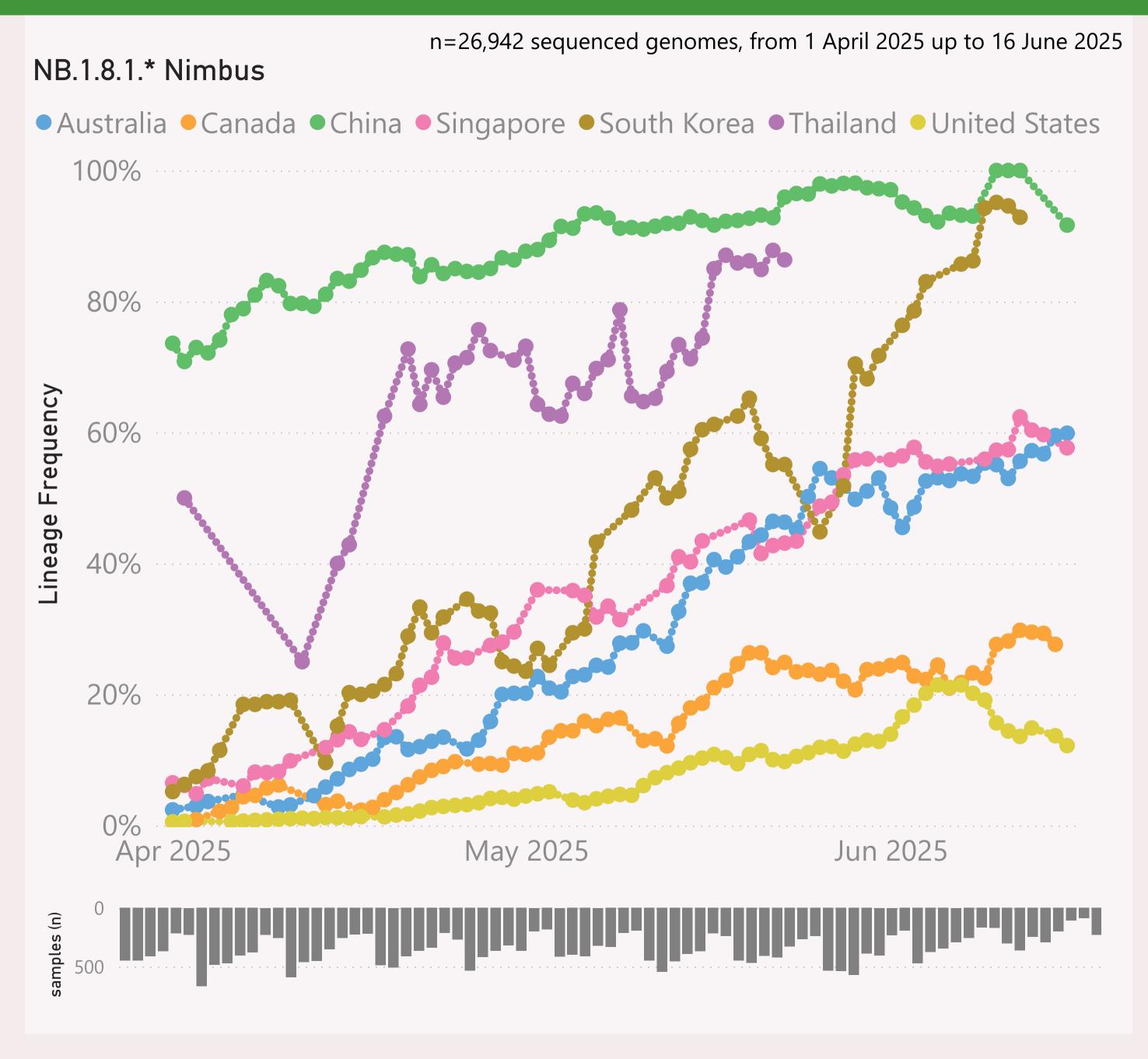


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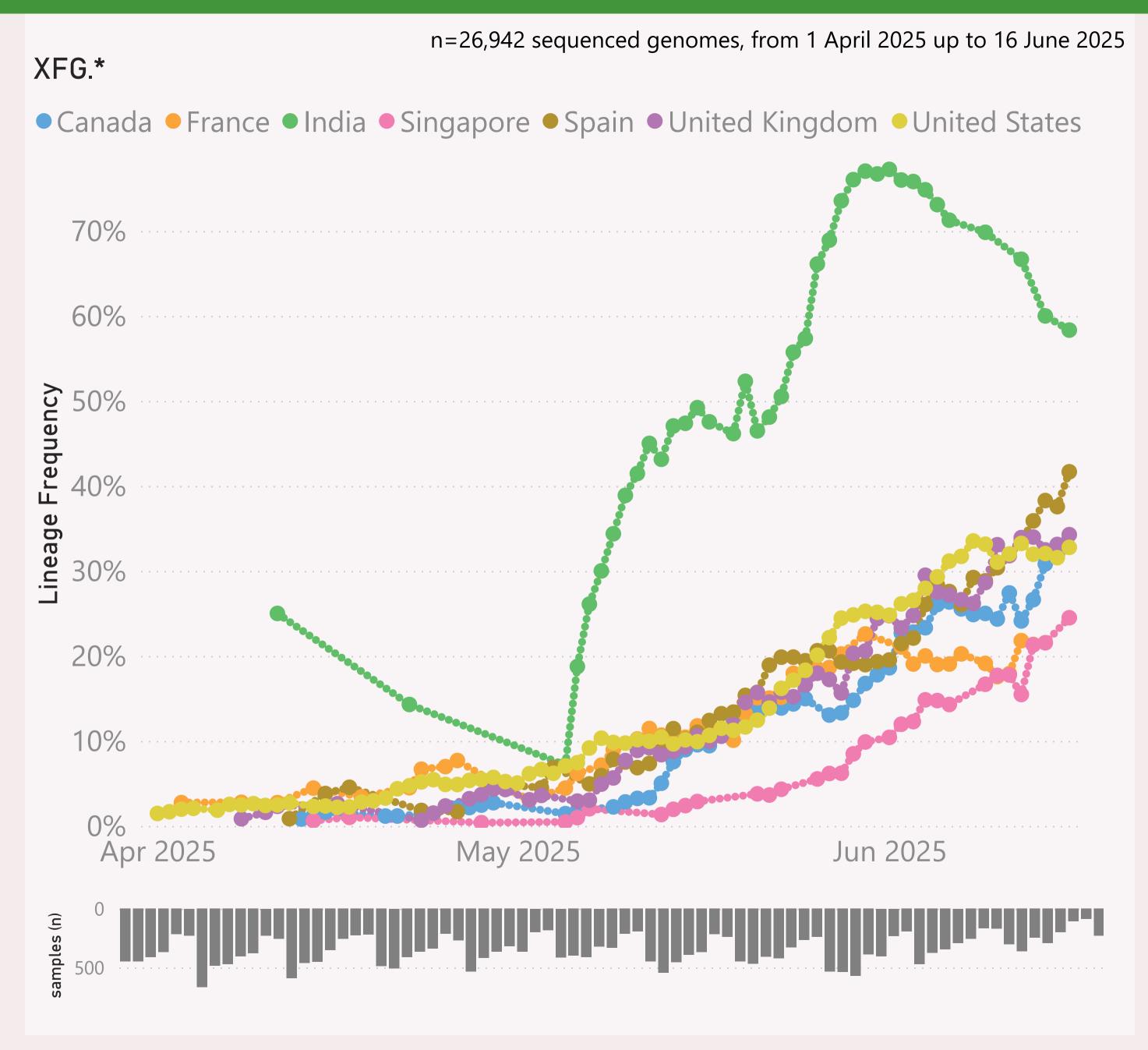
This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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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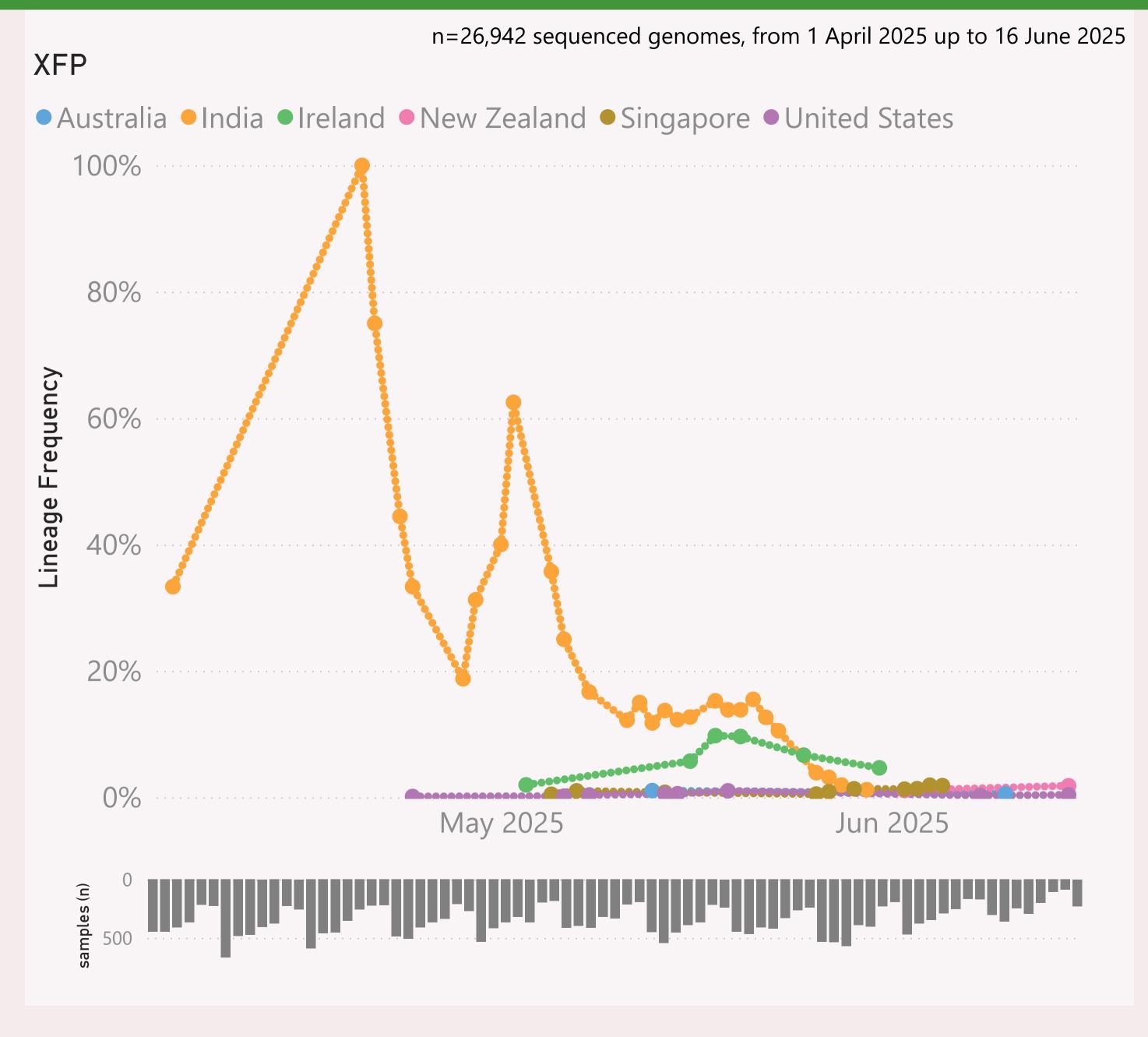
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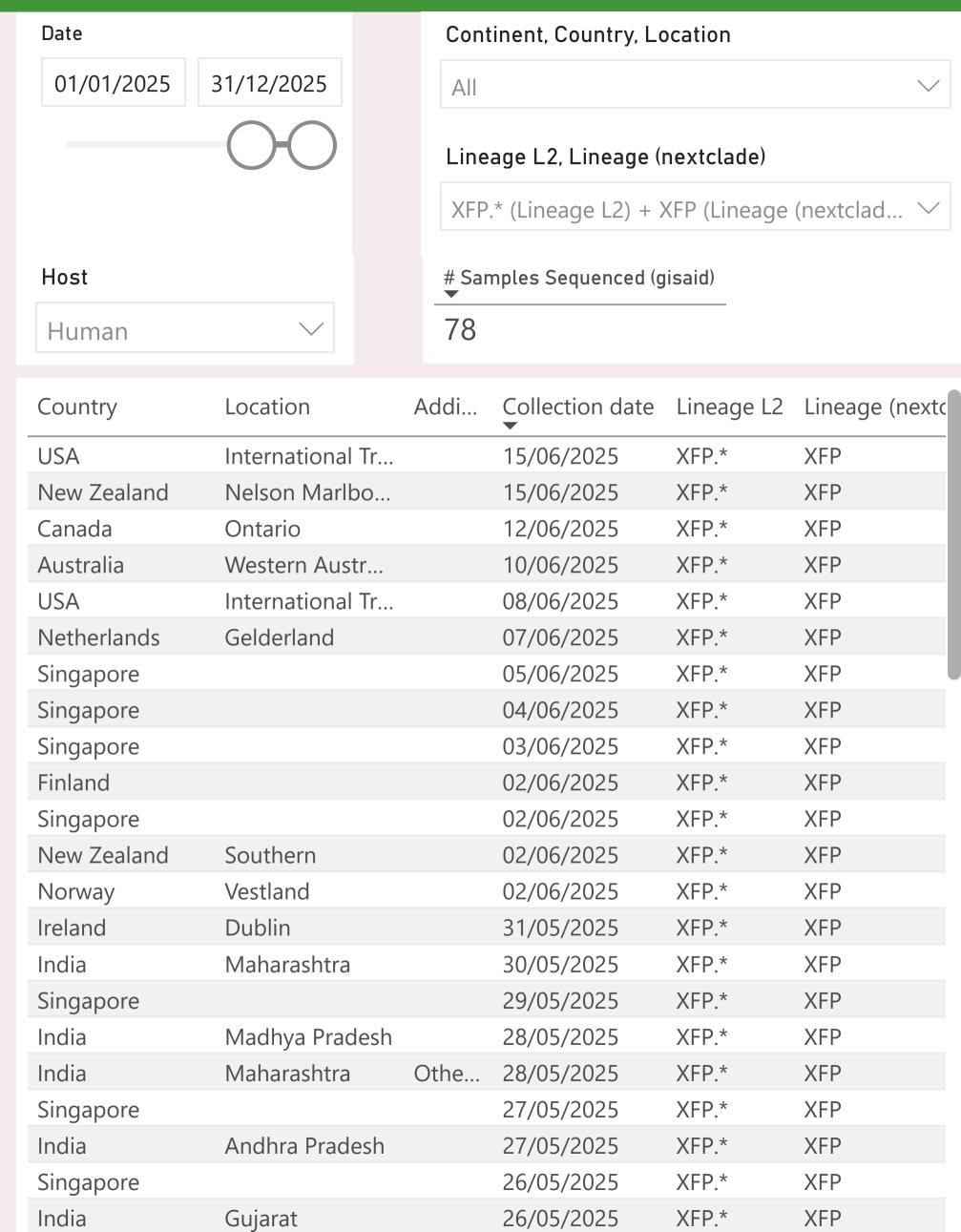
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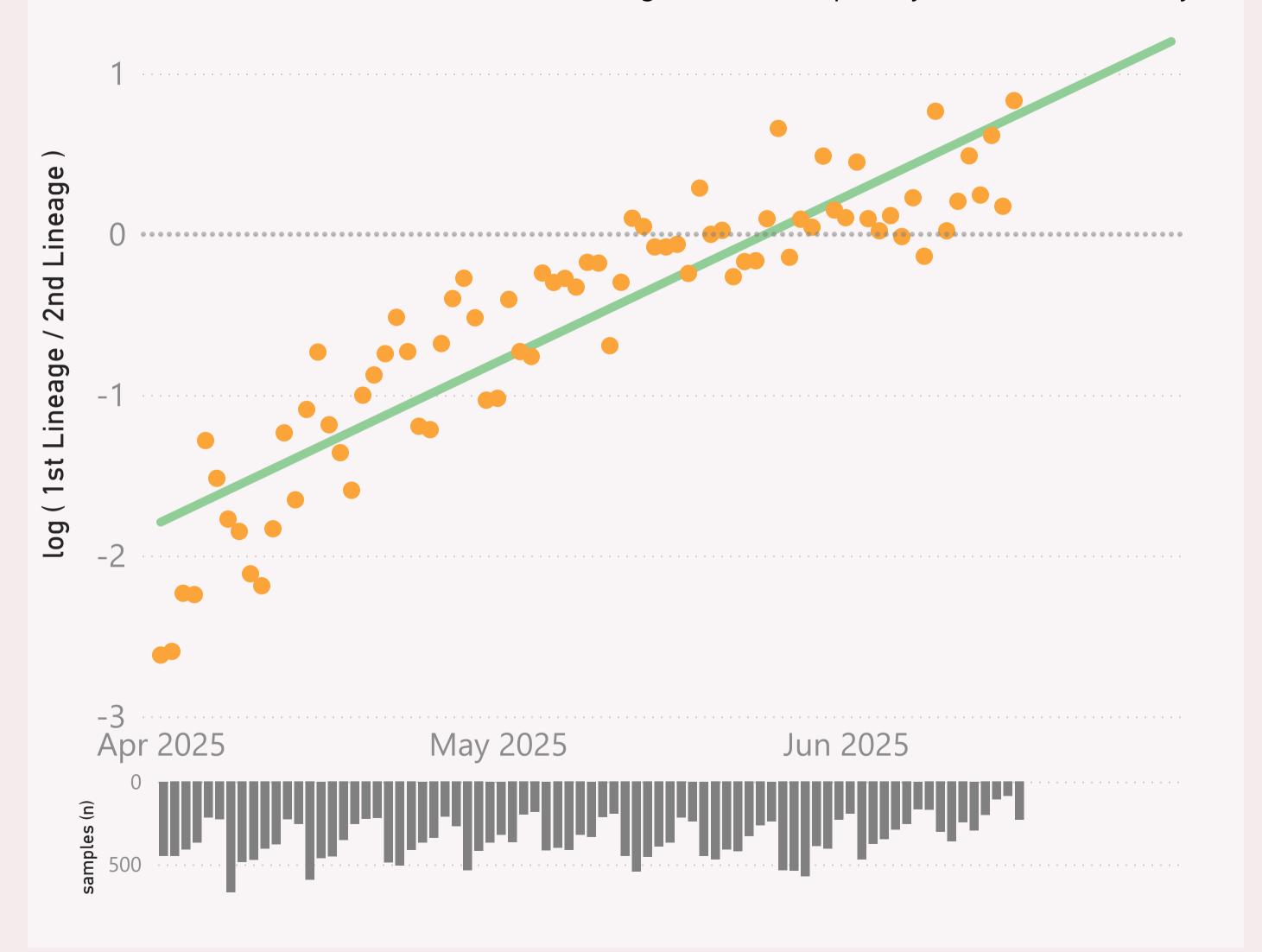
Total

n=26,942 sequenced genomes, from 1 April 2025 up to 16 June 2025

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

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

growth of 3.3% per day, crossover on 25-May-25

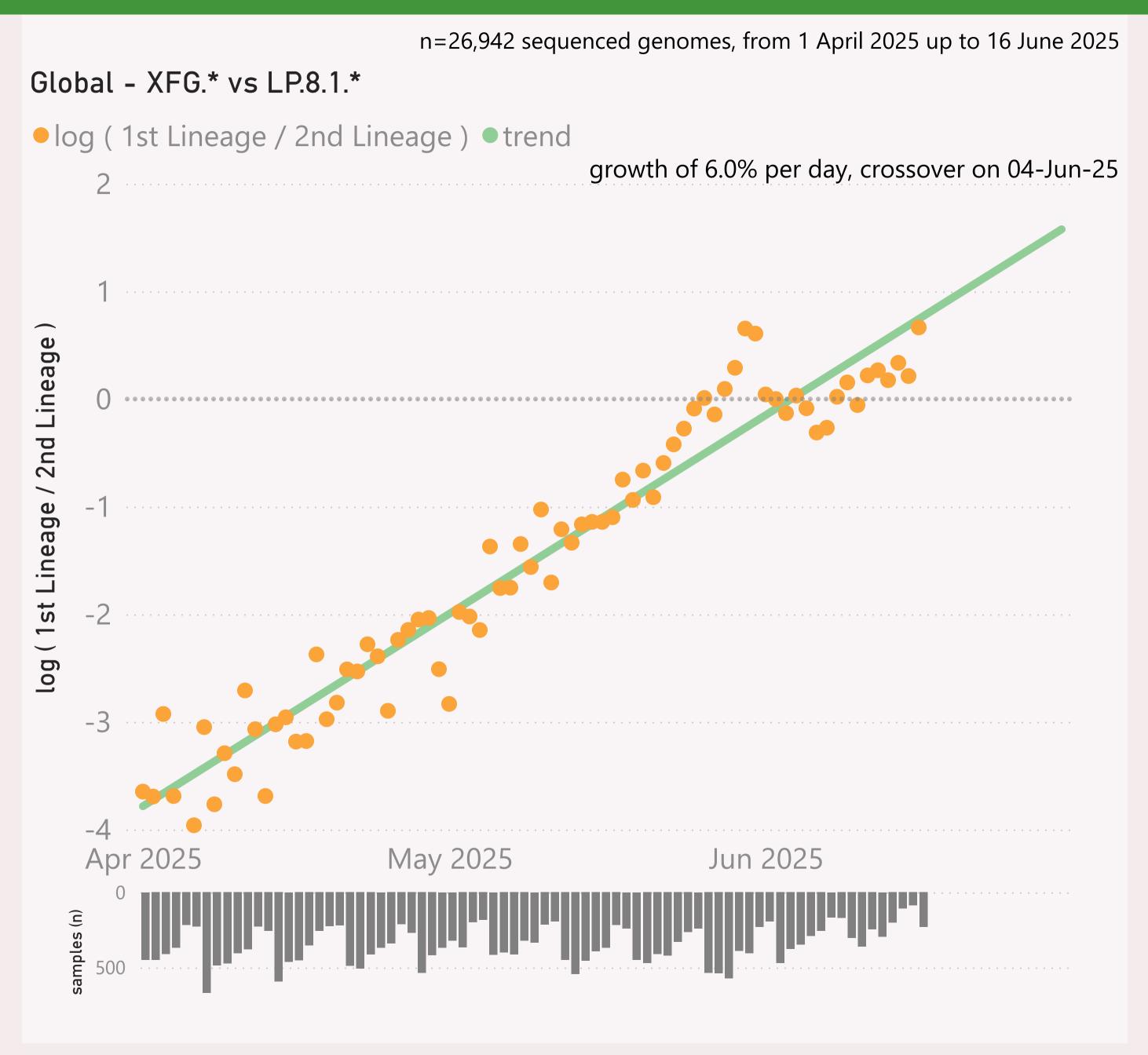


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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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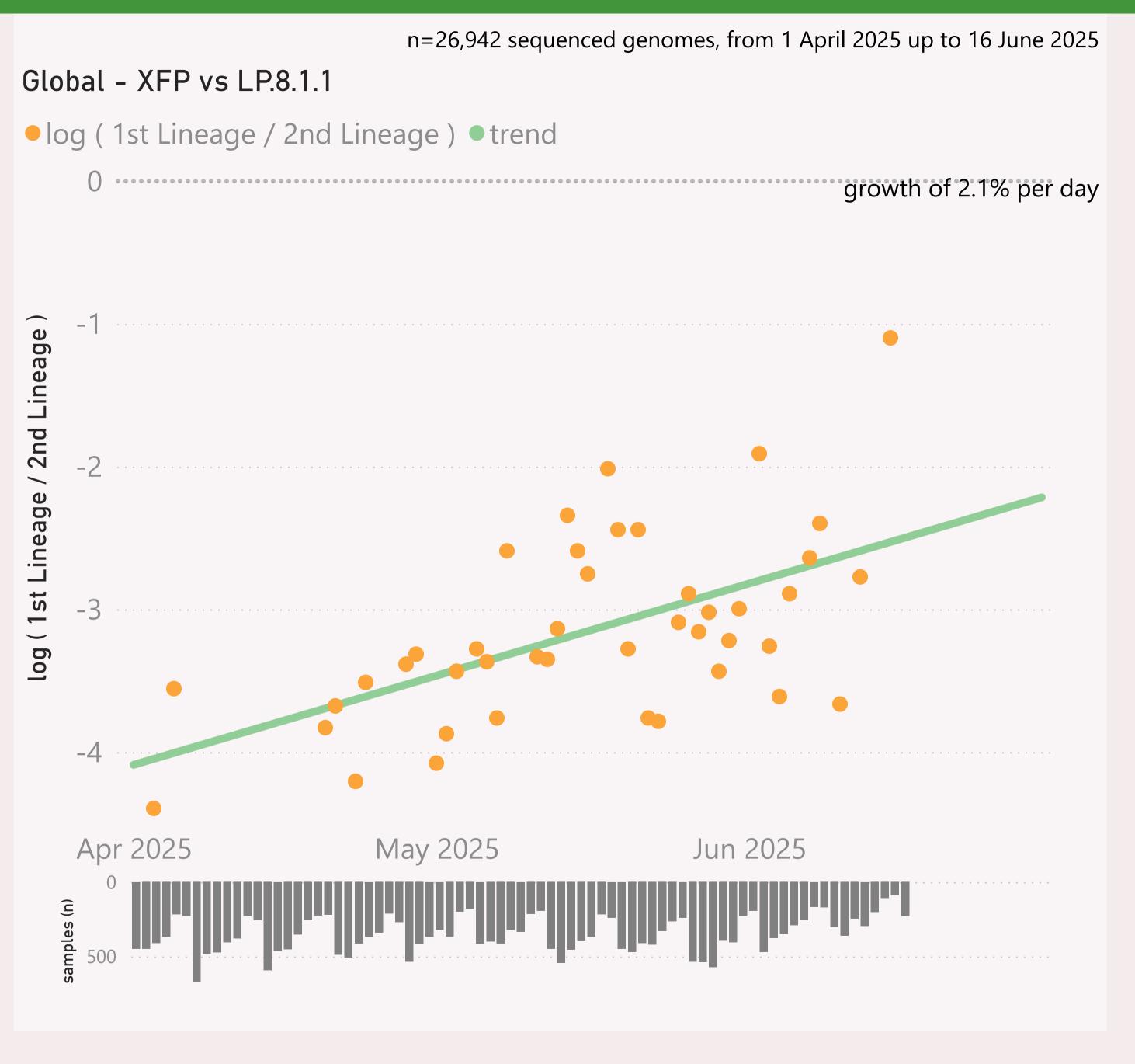


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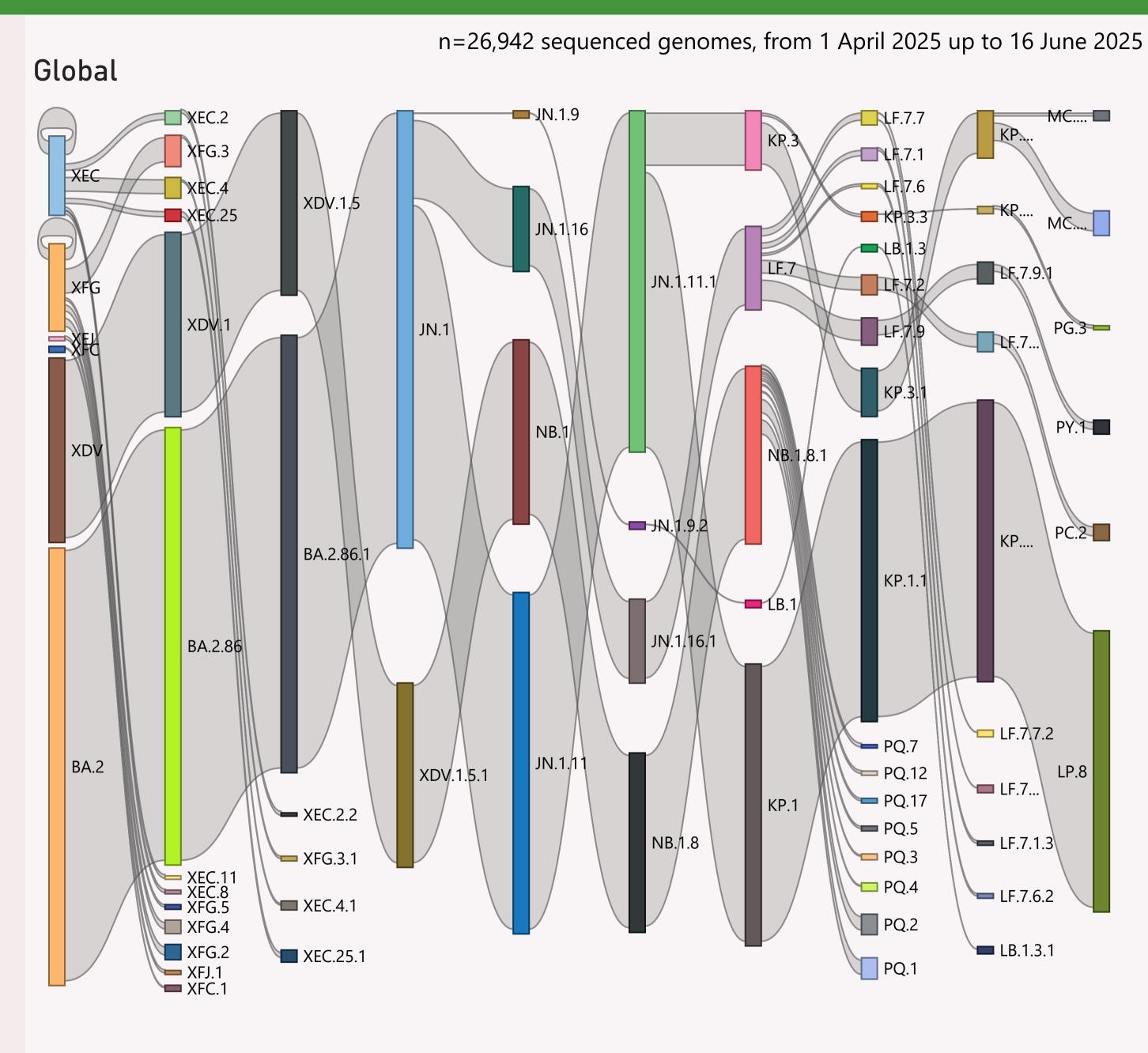


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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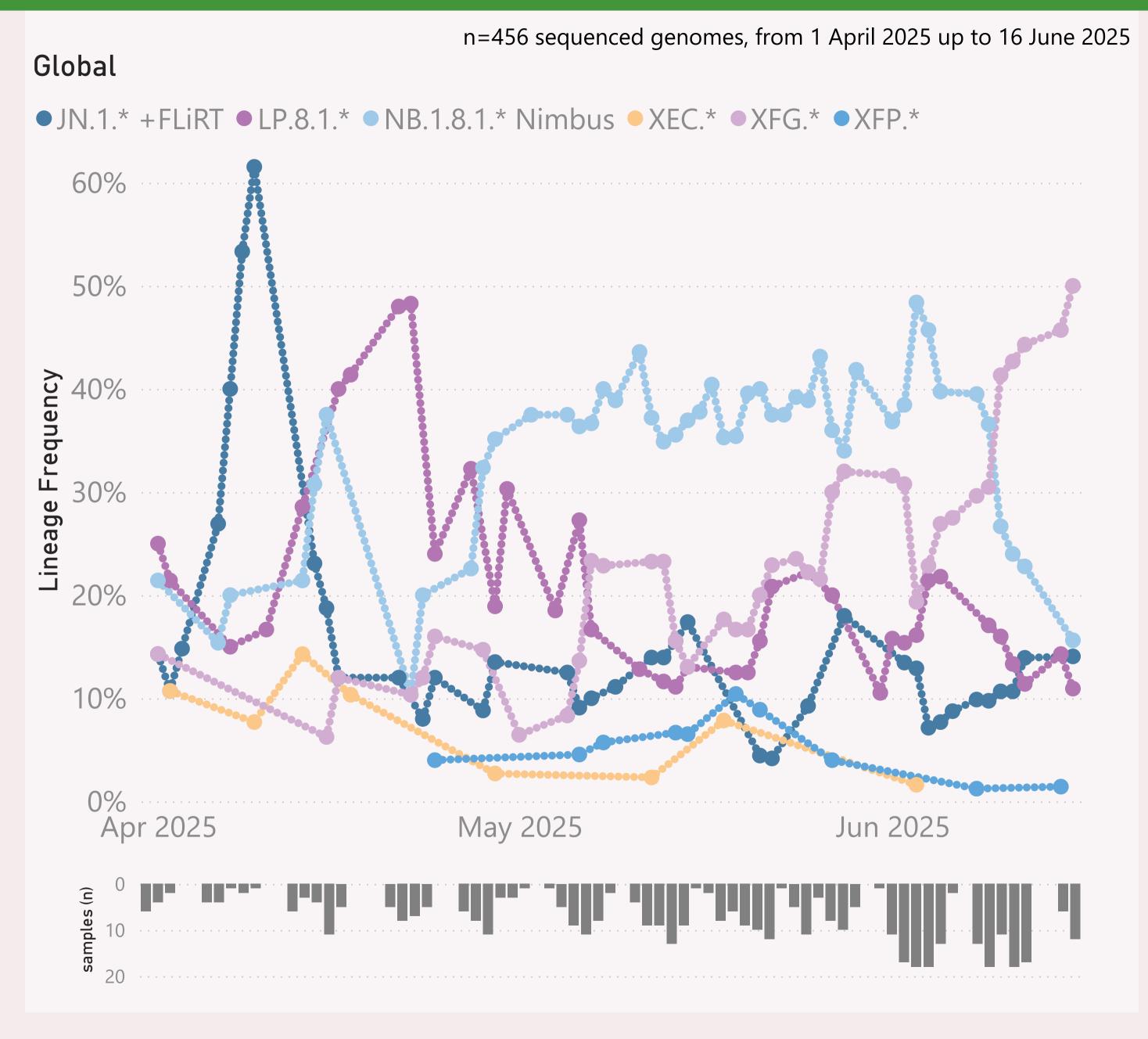
This page shows the hierarchy of the significant Lineages, over recent months.

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
	5,038	16/06/2025	addibbblack	22/06/2025	taraaa taraa ah ah ah
	1,901	16/06/2025	alitikbiditas.	22/06/2025	and a march
⊞ Spain	1,868	16/06/2025	amadalada (22/06/2025	
⊕ China	1,826	16/06/2025	and dublishing	22/06/2025	
	1,623	16/06/2025	diablidable	22/06/2025	a a caractera.
	1,615	16/06/2025	adia constal	22/06/2025	- 1 i i i i i i i i i i
Australia	1,407	16/06/2025	e consistenti filitati e	22/06/2025	ate and account of
⊕ France	867	16/06/2025	man ldullitaald.	22/06/2025	The community of the Land
⊞ India	828	16/06/2025		22/06/2025	. Condition of
	401	15/06/2025	a.matriffffifid.	22/06/2025	5 () () () () ()
⊞ South Korea	389	12/06/2025	and the state of t	22/06/2025	and a stand
⊕ Ireland	325	16/06/2025	an industrabile	22/06/2025	and the second
H Mexico	277	16/06/2025	adla	22/06/2025	
	275	23/05/2025	saladdh	30/05/2025	
⊞ Japan	266	12/06/2025	a lann deldamaa t	22/06/2025	أمر علاء من بالنسا
Malaysia	187	16/06/2025	and a control of the con-	22/06/2025	
⊕ Costa Rica	182	14/06/2025	taratahdb.	22/06/2025	
H Germany	178	12/06/2025	al adaption base	22/06/2025	
	174	09/06/2025	artitle beheld be	22/06/2025	
	170	02/06/2025	alphana a alda	19/06/2025	
⊕ Brazil	158	04/06/2025	Militaria	22/06/2025	and the rest
	154	14/06/2025	attatialah disam	22/06/2025	and the late
⊕ Bahrain	152	16/06/2025	and a distribution of	22/06/2025	
	146	28/05/2025		22/06/2025	lı.
⊕ Puerto Rico	138	16/06/2025	contrada li dalla	22/06/2025	a a 1 H.
	137	03/06/2025	ana lihita	22/06/2025	
⊞ Taiwan	115	16/06/2025		22/06/2025	
⊞ Italy	102	07/06/2025	hill tederled act.	22/06/2025	alteria de albacer
Total	21,909	16/06/2025	aanaantihihhiin	22/06/2025	

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.