

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

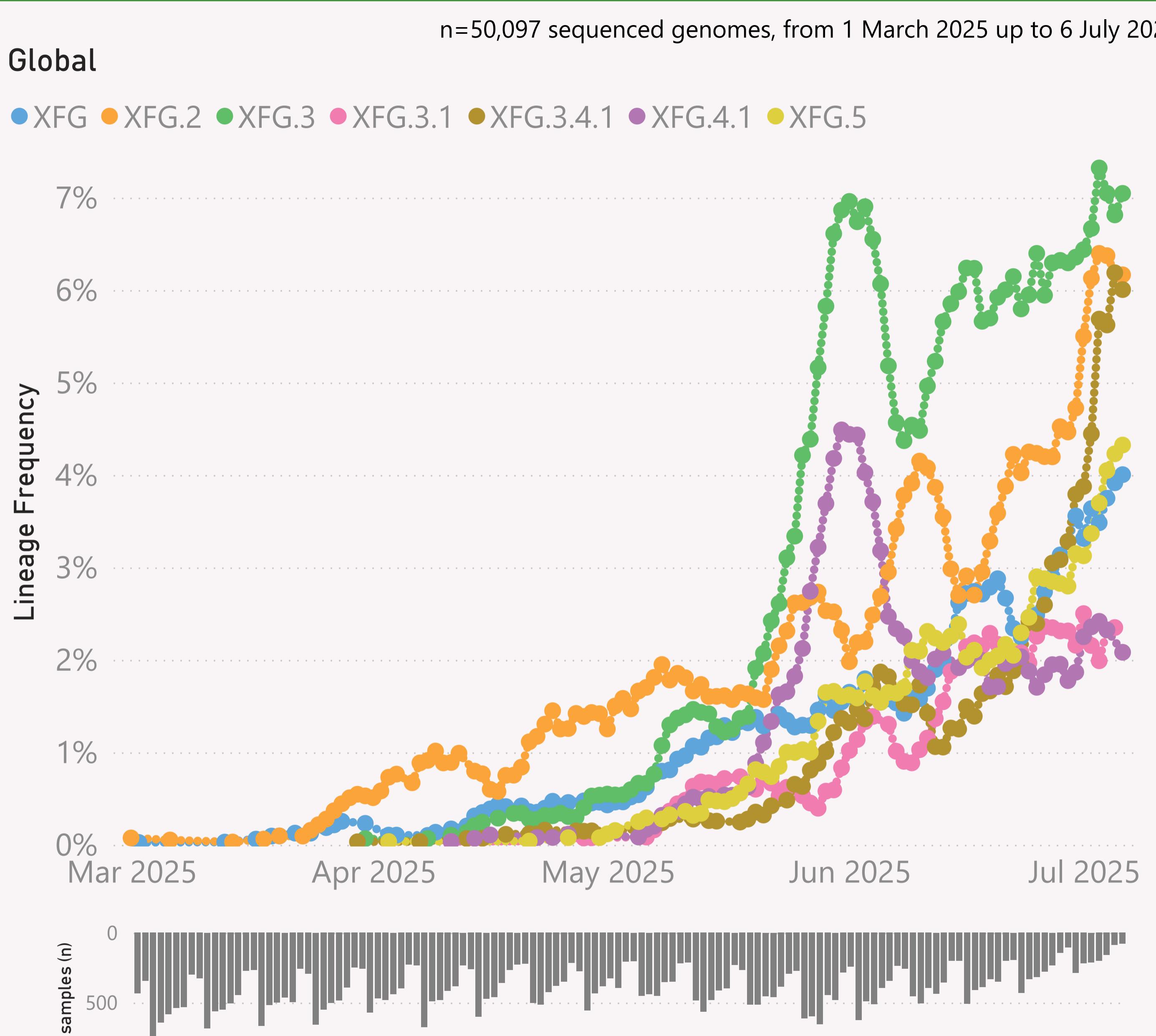
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all its descendants, e.g. the JN.* lineages.

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.



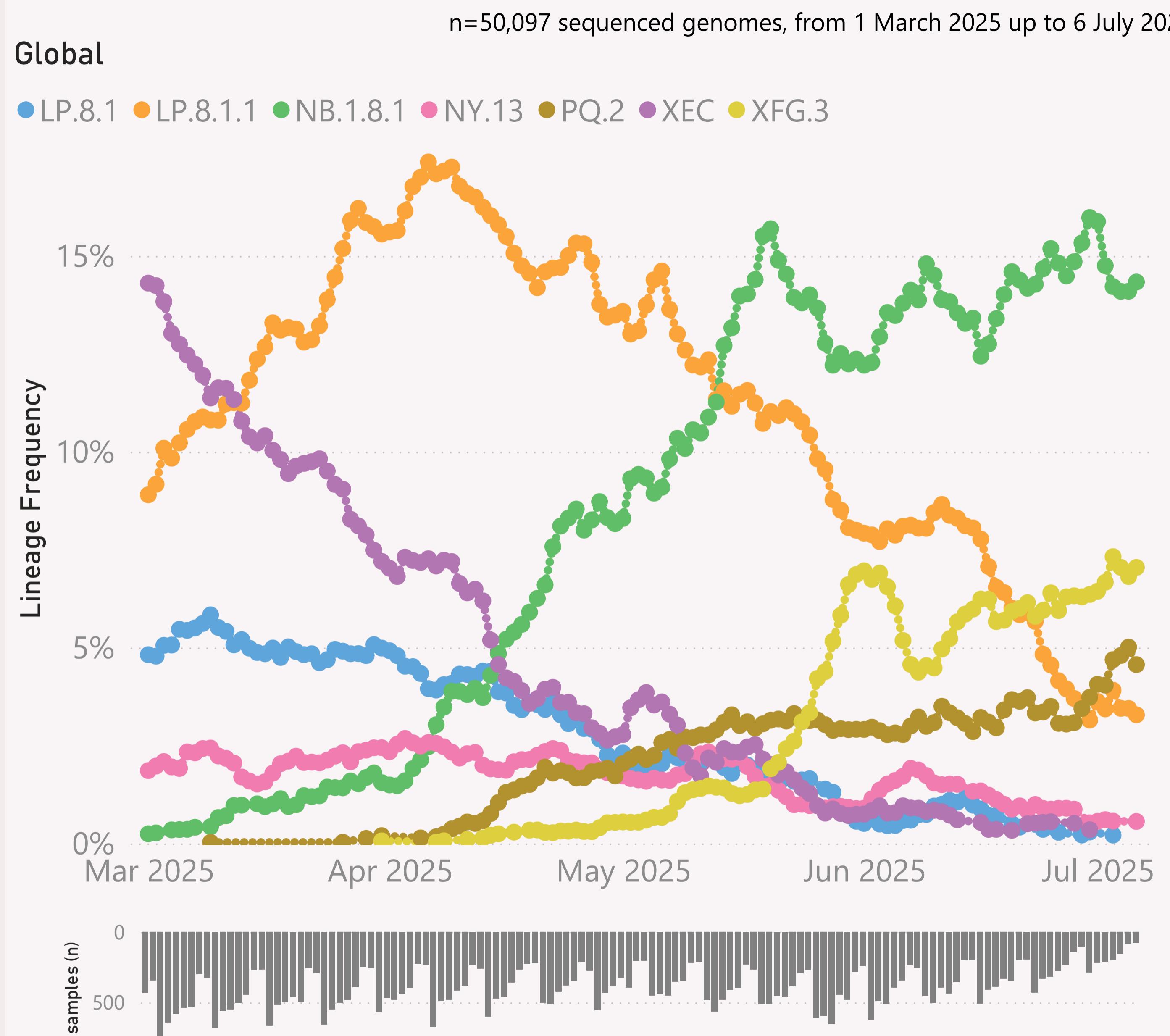
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently XFG.* Stratus.

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

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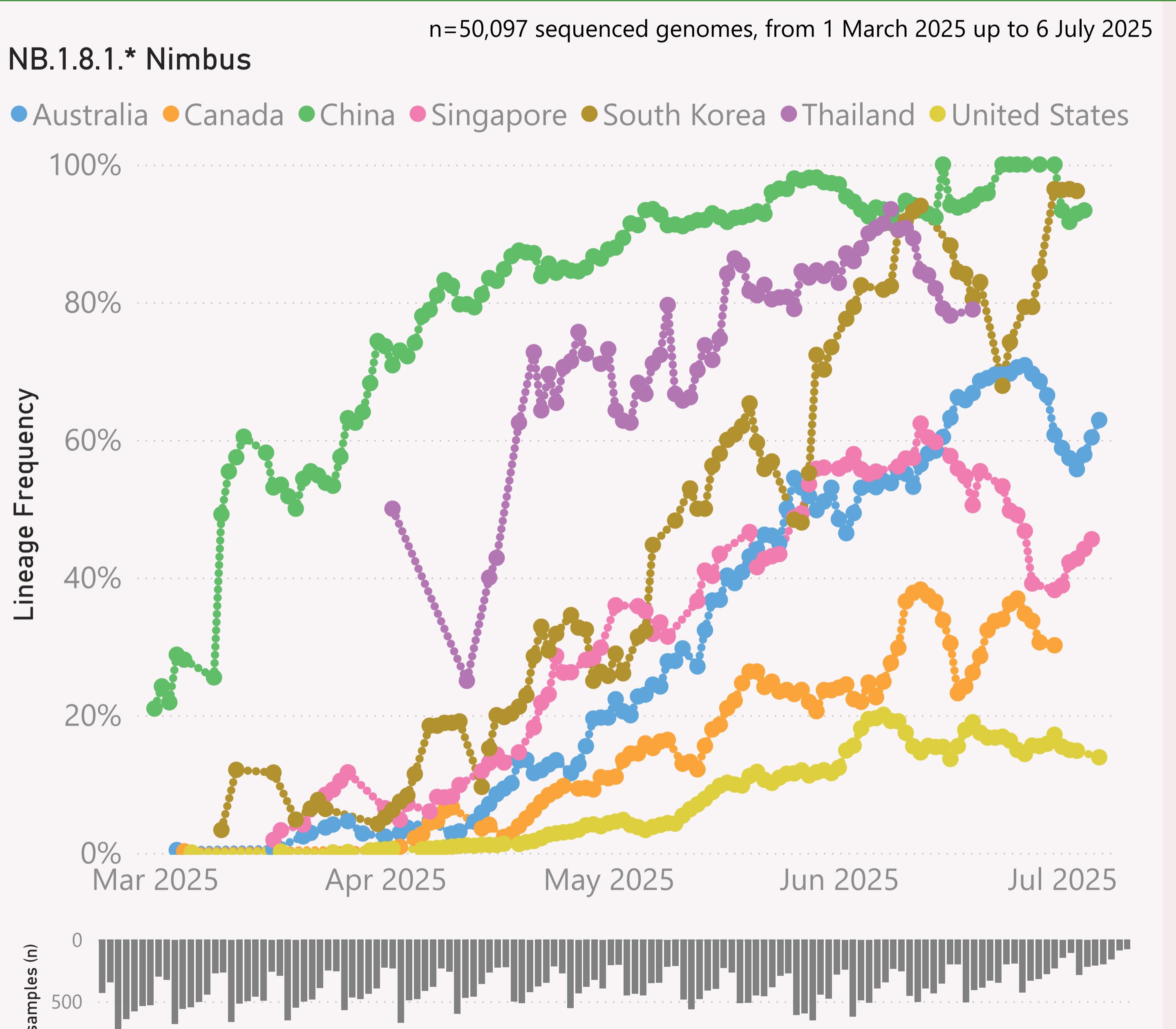
This page shows the frequency of the top 7 lineages, across recent months.

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

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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.

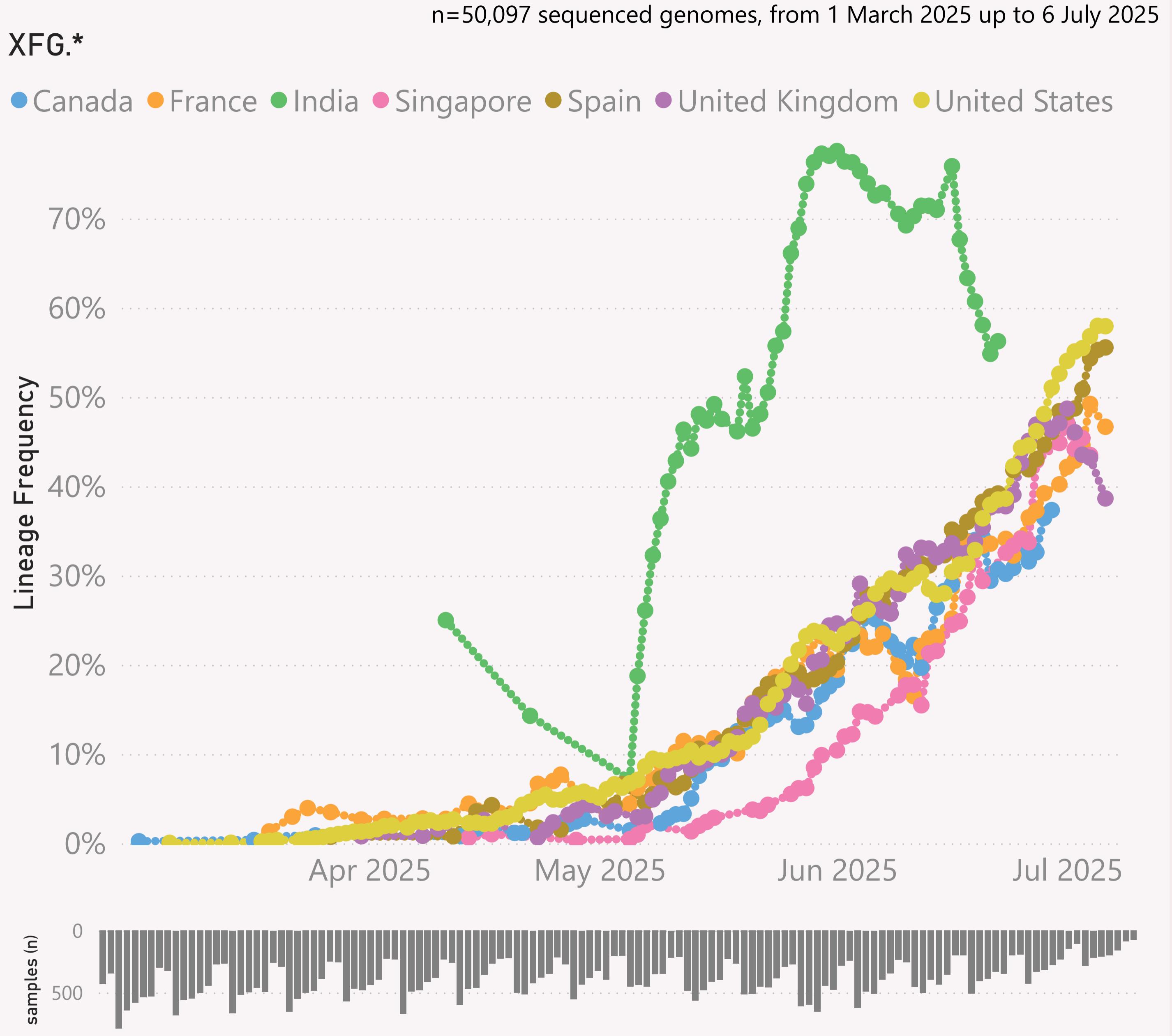
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

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.

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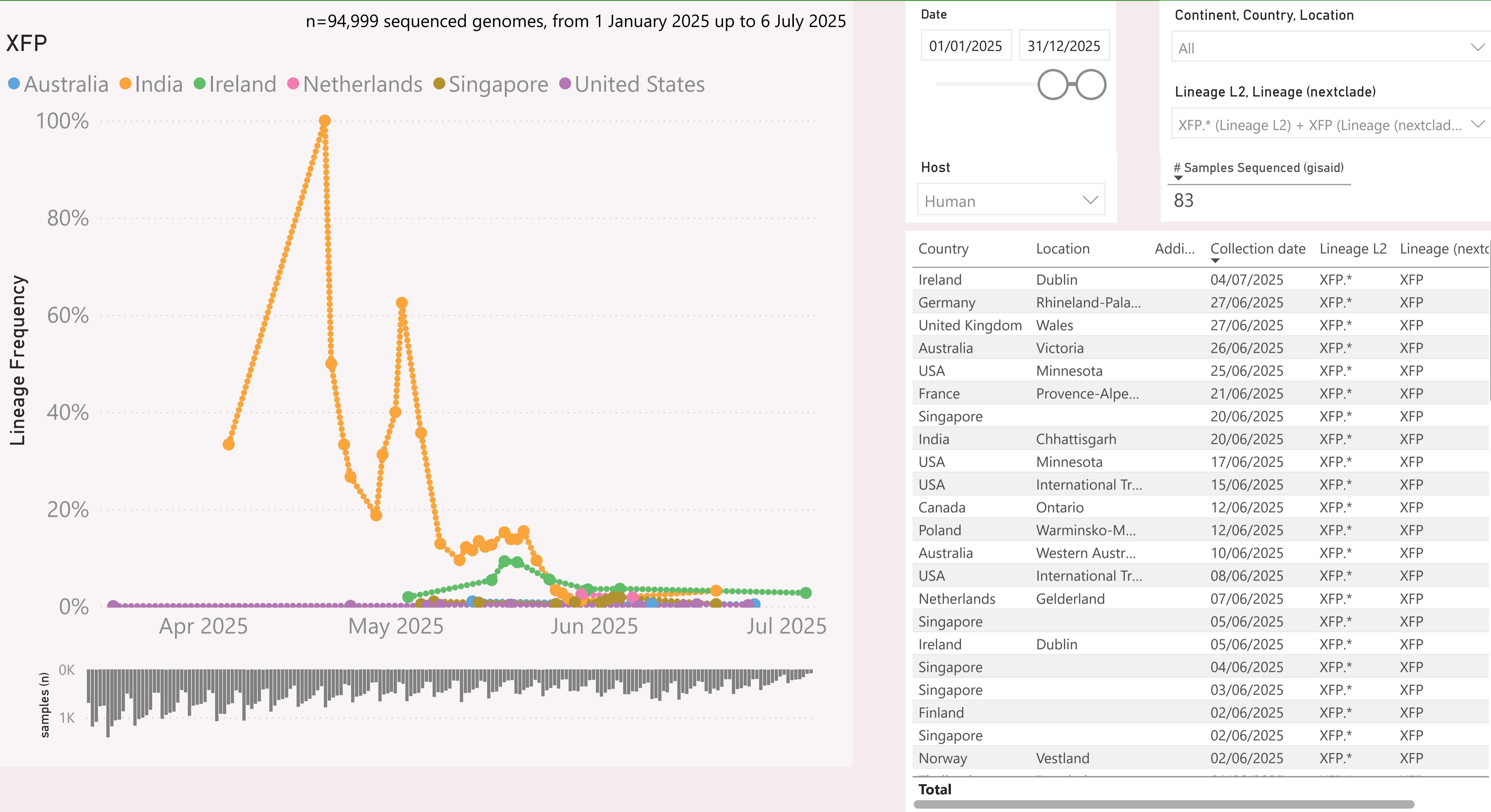
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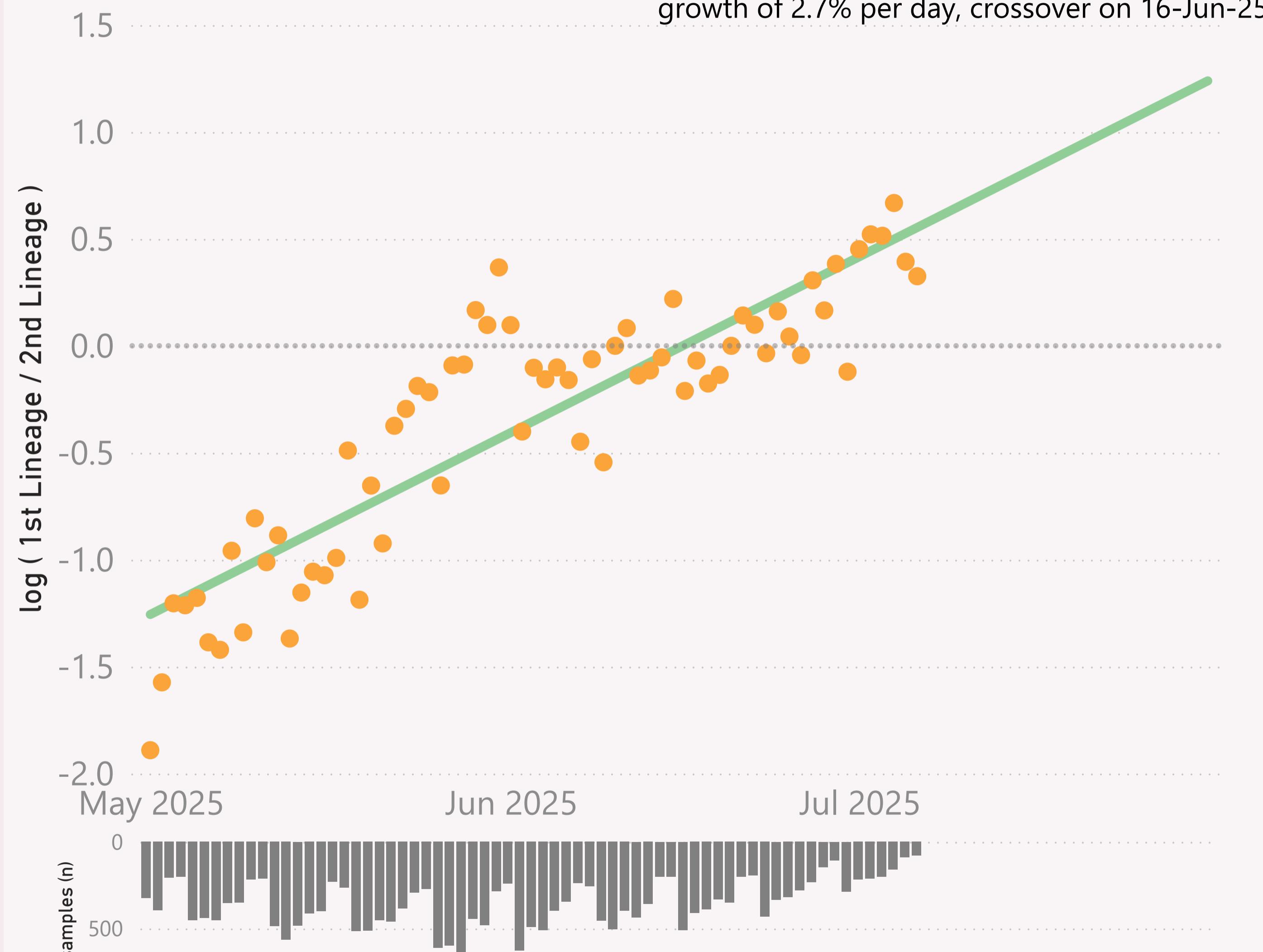


n=23,582 sequenced genomes, from 1 May 2025 up to 6 July 2025

Global - XFG.* vs NB.1.8.1.* Nimbus

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

growth of 2.7% per day, crossover on 16-Jun-25

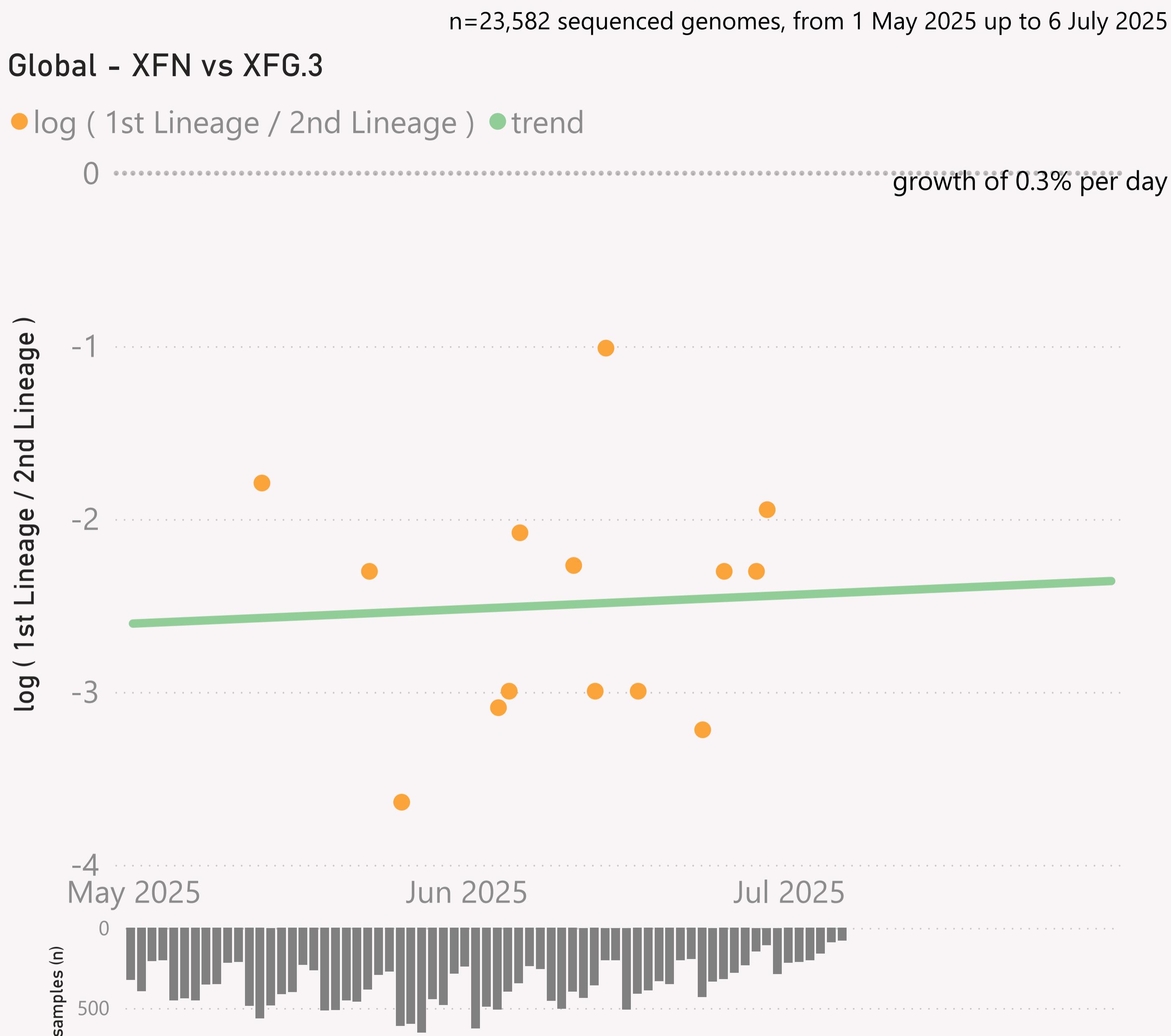


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

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.

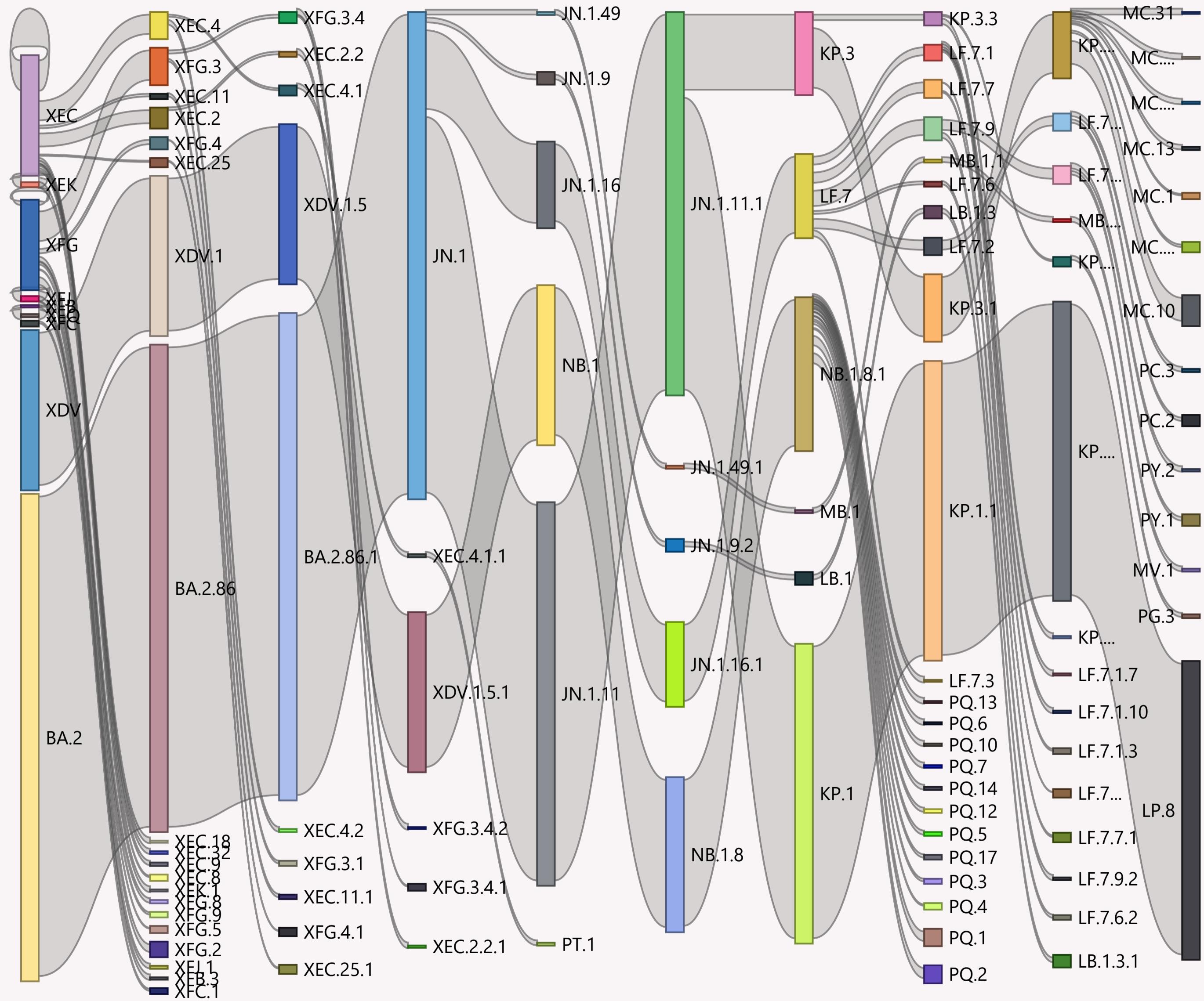
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

Global

n=50,097 sequenced genomes, from 1 March 2025 up to 6 July 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.

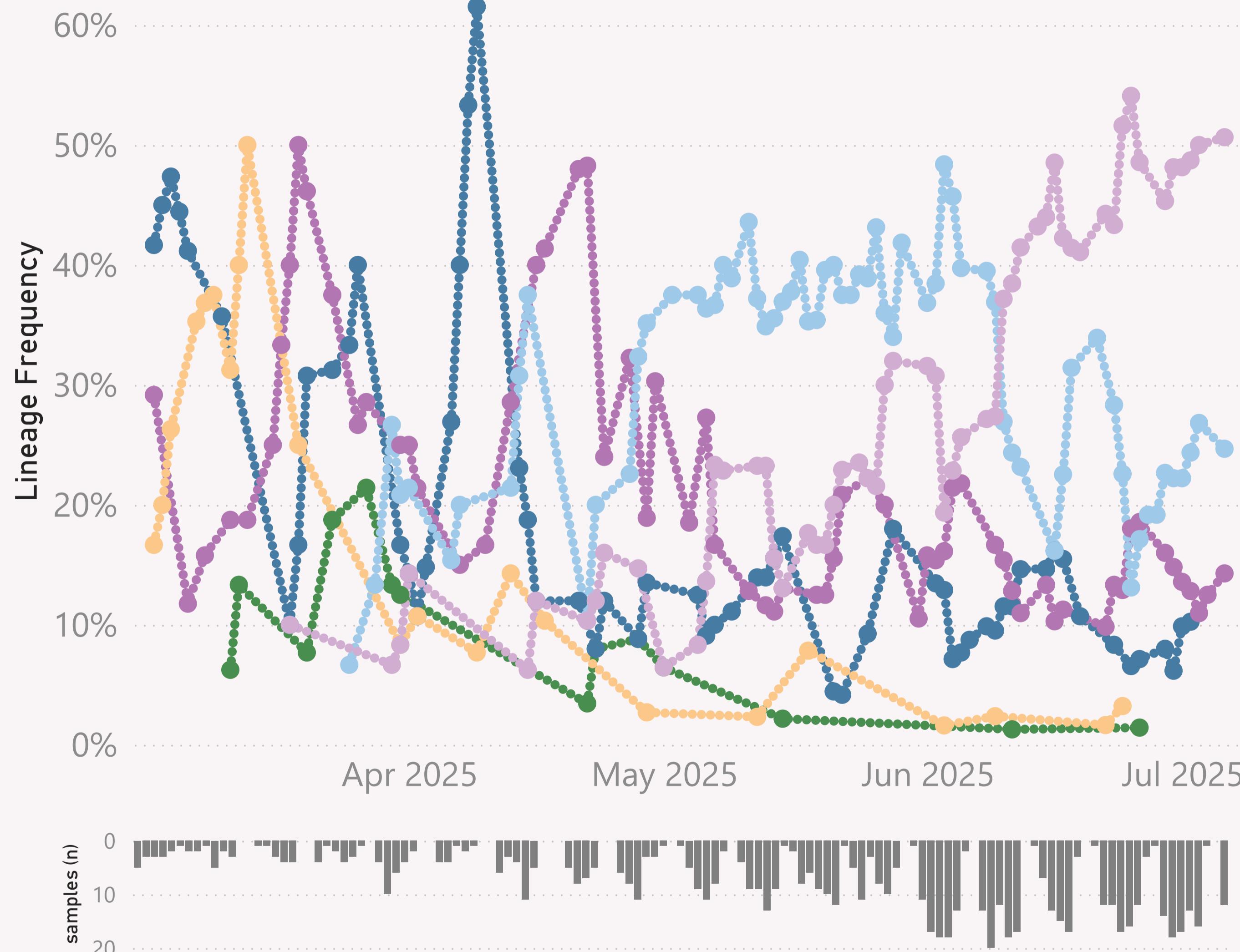
The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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.

Global

● JN.1.* +DeFLuQE ● JN.1.* +FLiRT ● LP.8.1.* ● NB.1.8.1.* Nimbus ● XEC.* ● XFG.*

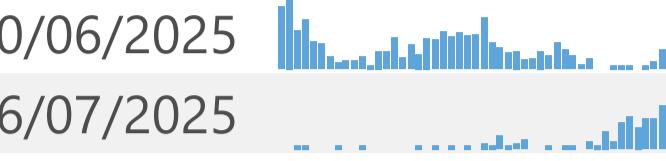
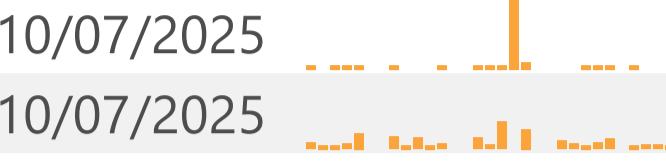
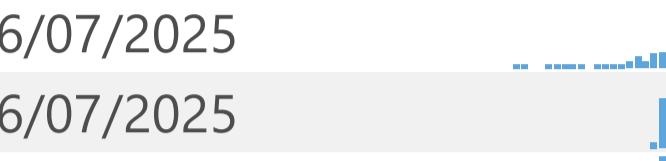
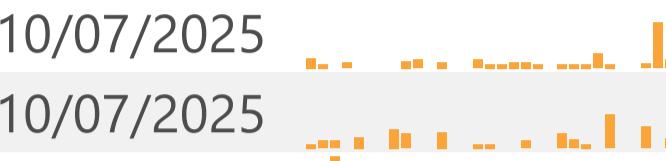
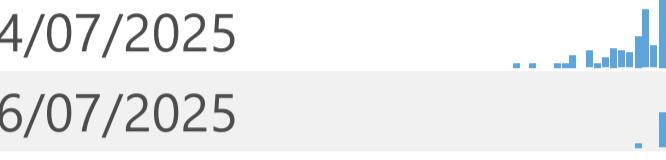
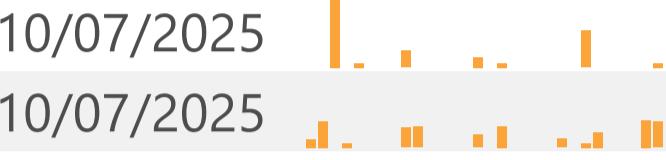
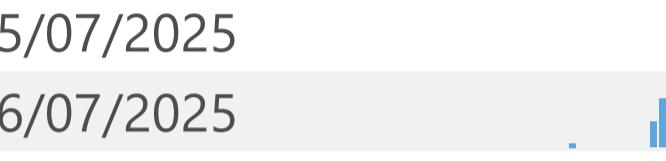
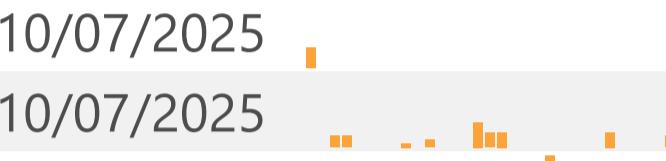
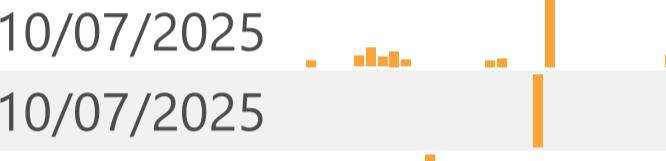
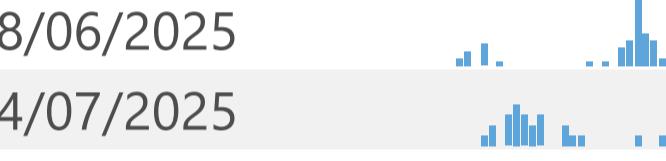
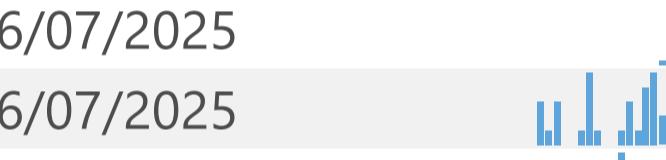
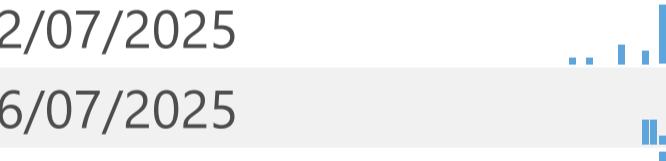
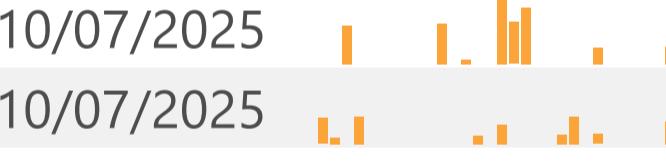
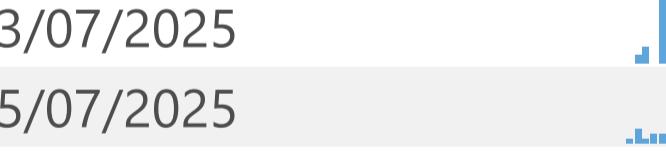
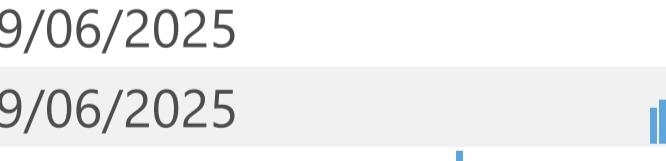
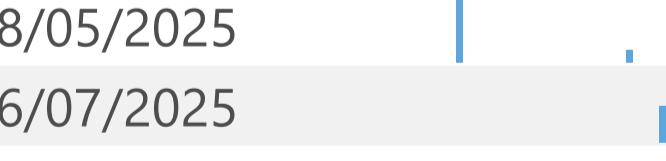
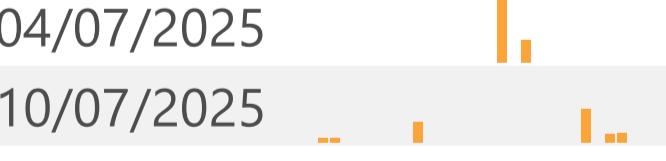
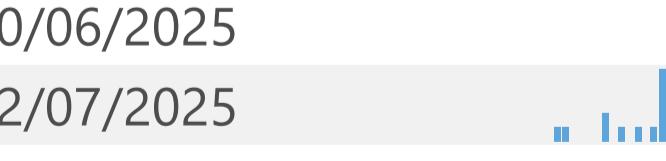
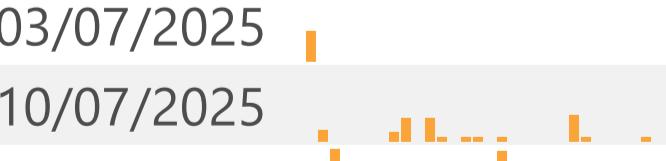
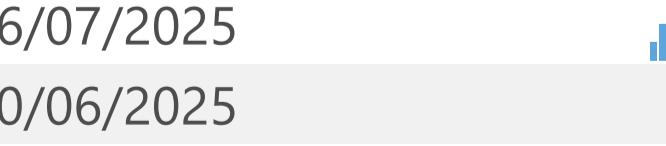
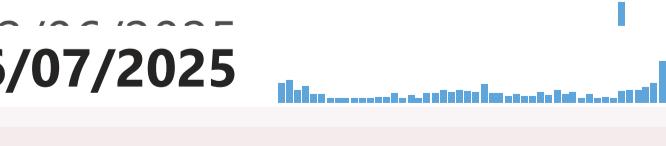
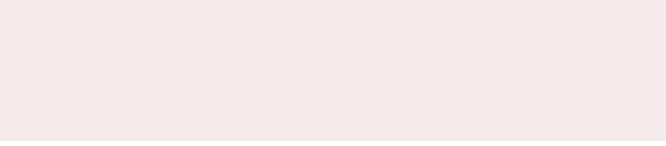
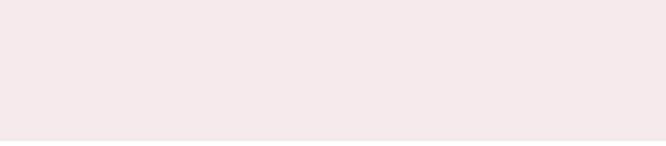


This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

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
Canada	24,970	30/06/2025		10/07/2025	
United States	7,602	06/07/2025		10/07/2025	
Spain	2,820	06/07/2025		10/07/2025	
United Kingdom	1,858	06/07/2025		10/07/2025	
China	1,763	04/07/2025		10/07/2025	
Australia	1,572	06/07/2025		10/07/2025	
Singapore	1,264	05/07/2025		10/07/2025	
France	968	06/07/2025		10/07/2025	
India	827	22/06/2025		10/07/2025	
Russia	772	01/07/2025		10/07/2025	
Mexico	712	18/06/2025		10/07/2025	
Netherlands	594	04/07/2025		10/07/2025	
New Zealand	541	06/07/2025		10/07/2025	
Japan	476	06/07/2025		10/07/2025	
Brazil	463	05/07/2025		10/07/2025	
Kenya	453	27/06/2025		10/07/2025	
Malaysia	424	02/07/2025		10/07/2025	
Ireland	422	06/07/2025		10/07/2025	
South Korea	363	03/07/2025		10/07/2025	
Luxembourg	351	05/07/2025		10/07/2025	
Thailand	235	19/06/2025		10/07/2025	
Costa Rica	230	19/06/2025		10/07/2025	
Kazakhstan	218	28/05/2025		04/07/2025	
Germany	208	06/07/2025		10/07/2025	
Taiwan	192	30/06/2025		03/07/2025	
Italy	170	02/07/2025		10/07/2025	
Hong Kong	166	06/07/2025		10/07/2025	
Denmark	164	30/06/2025		10/07/2025	
Total	52,838	06/07/2025		10/07/2025	

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.