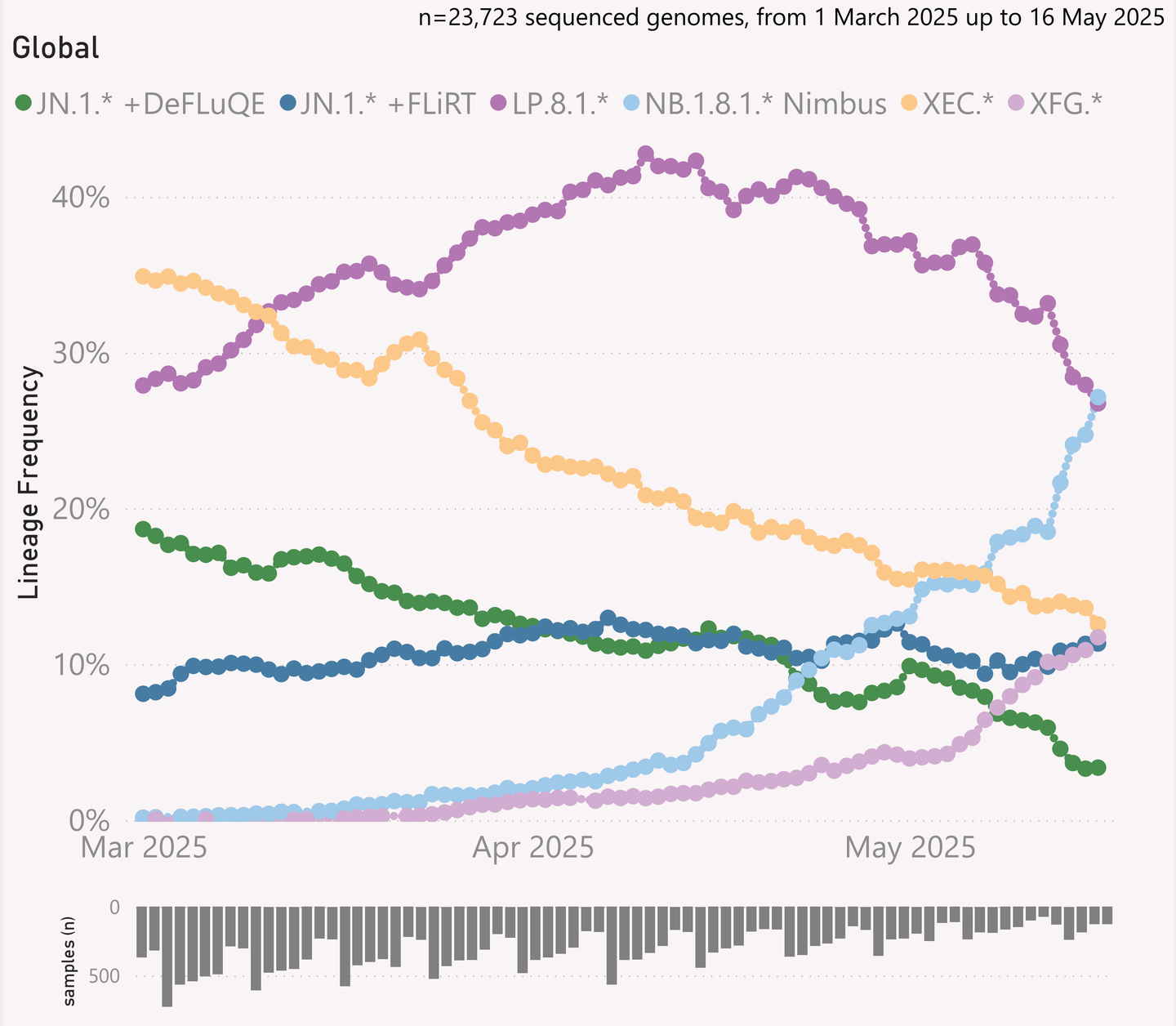
COVID-19 Genomic Sequencing analysis. Lineage Frequencies. Data from gisaid.org, with nextclade lineages. Source files and more info on github. Last Update: 2025-05-31 01:26 (UTC)

n=23,723 sequenced genomes, from 1 March 2025 up to 16 May 2025



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

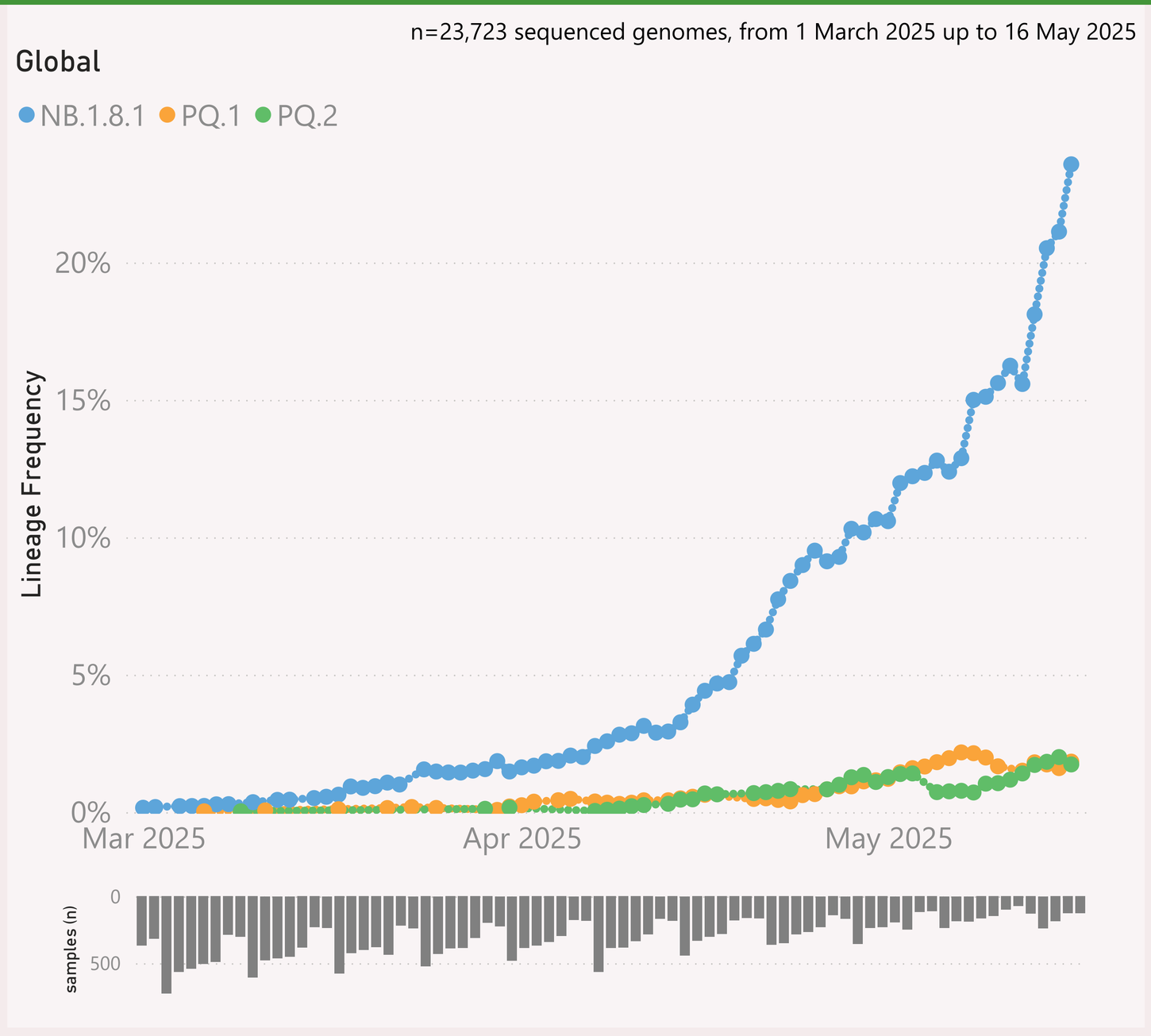
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.

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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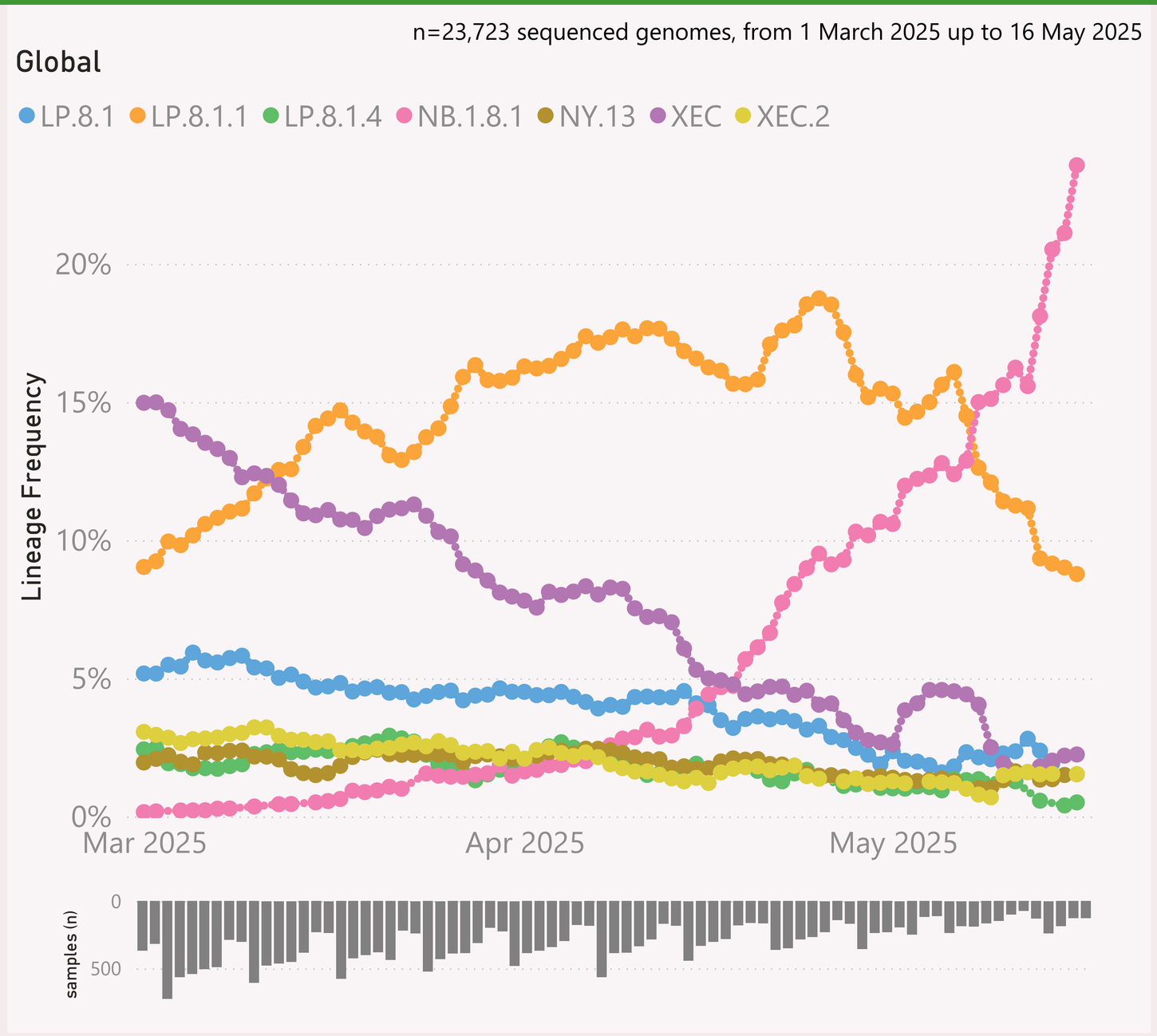

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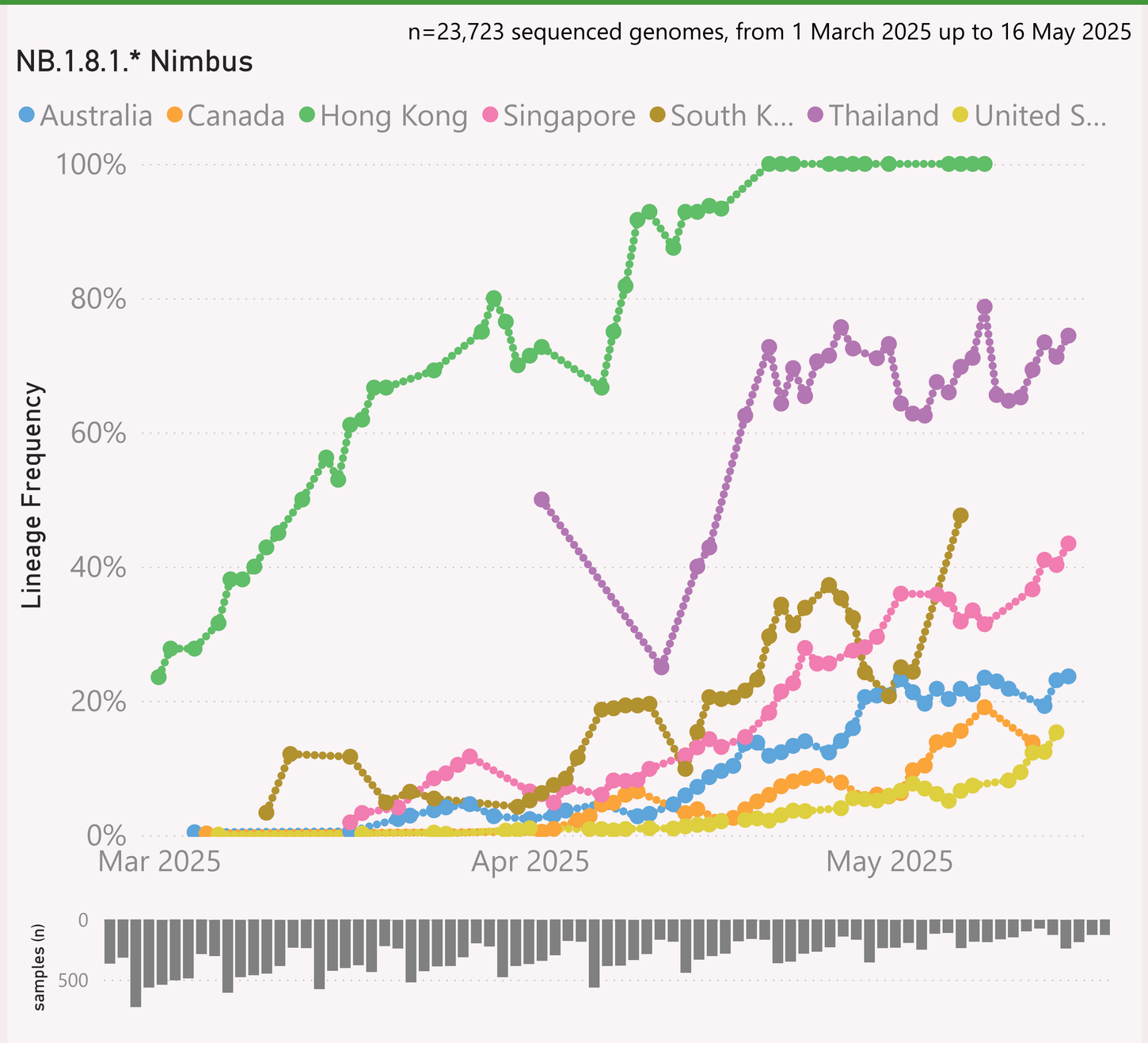

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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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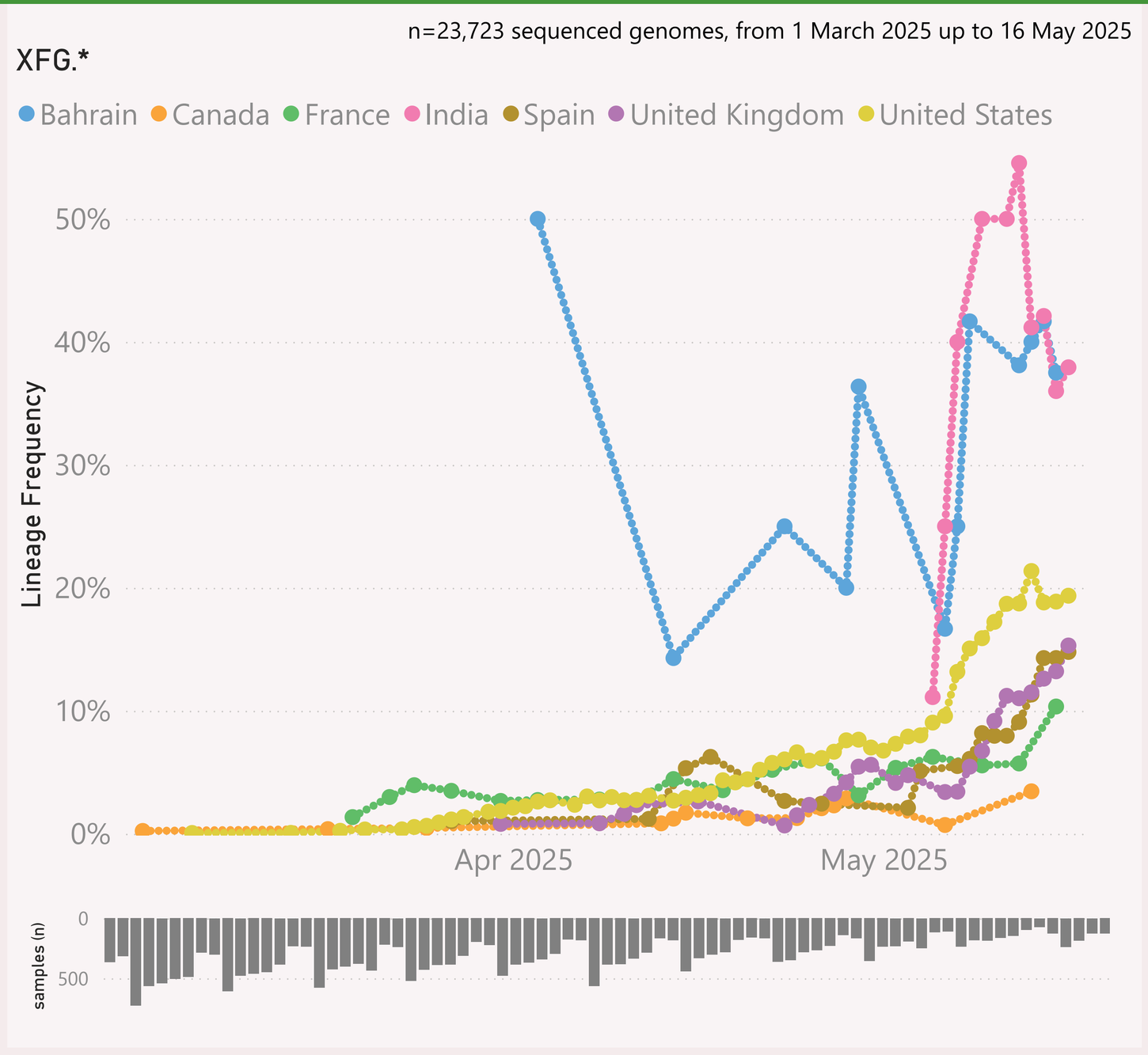

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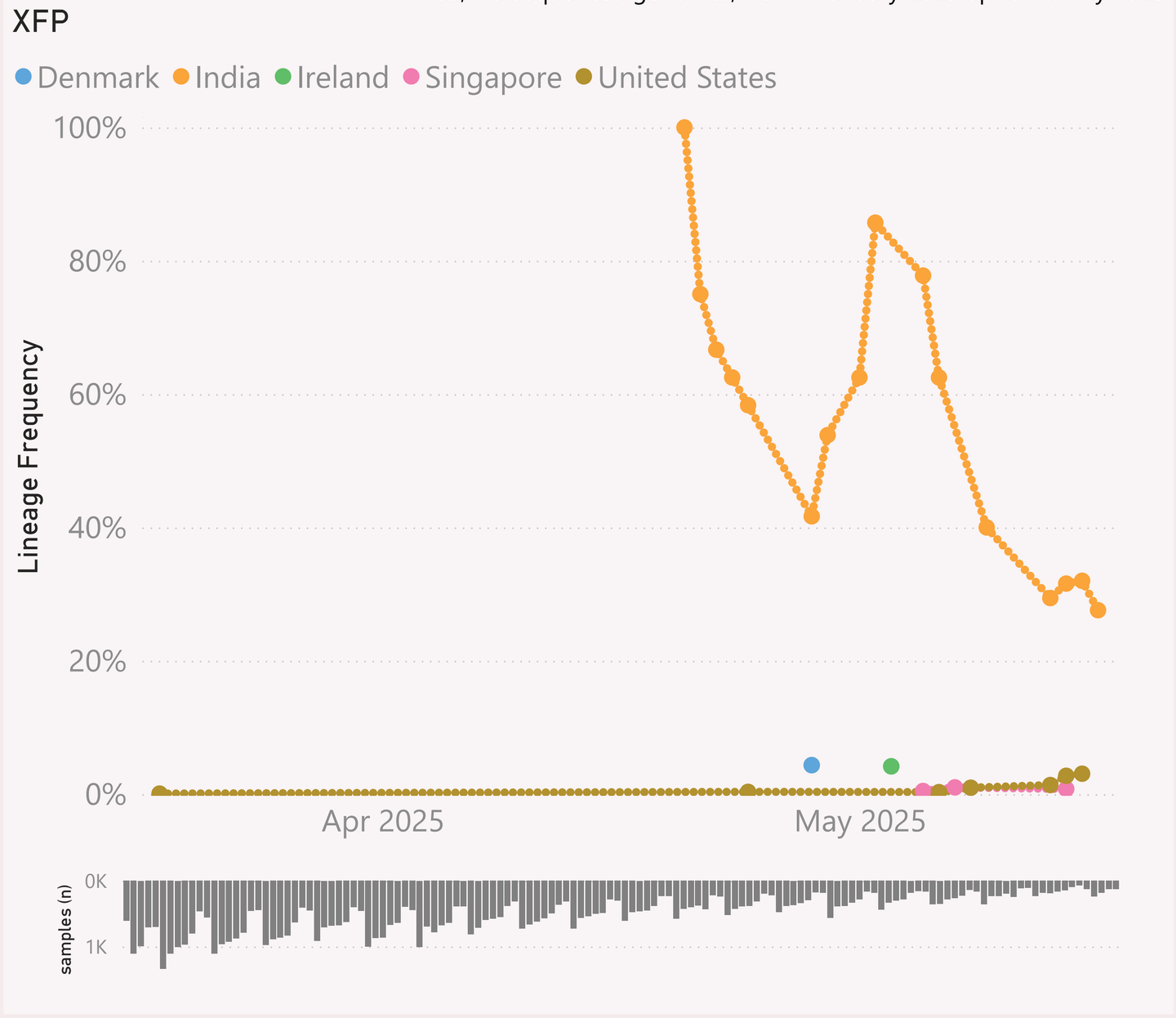
COVID-19 Genomic Sequencing analysis - selected Lineage by Country. Data from gisaid.org, with nextclade lineages Source files and info on github. Last Update: 2025-05-31 01:26 (UTC)

n=65,769 sequenced genomes, from 1 January 2025 up to 16 May 2025



Date

01/01/2025 31/12/2025

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

XFP.* (Lineage L2) + XFP (Lineage (nextclad...

Host

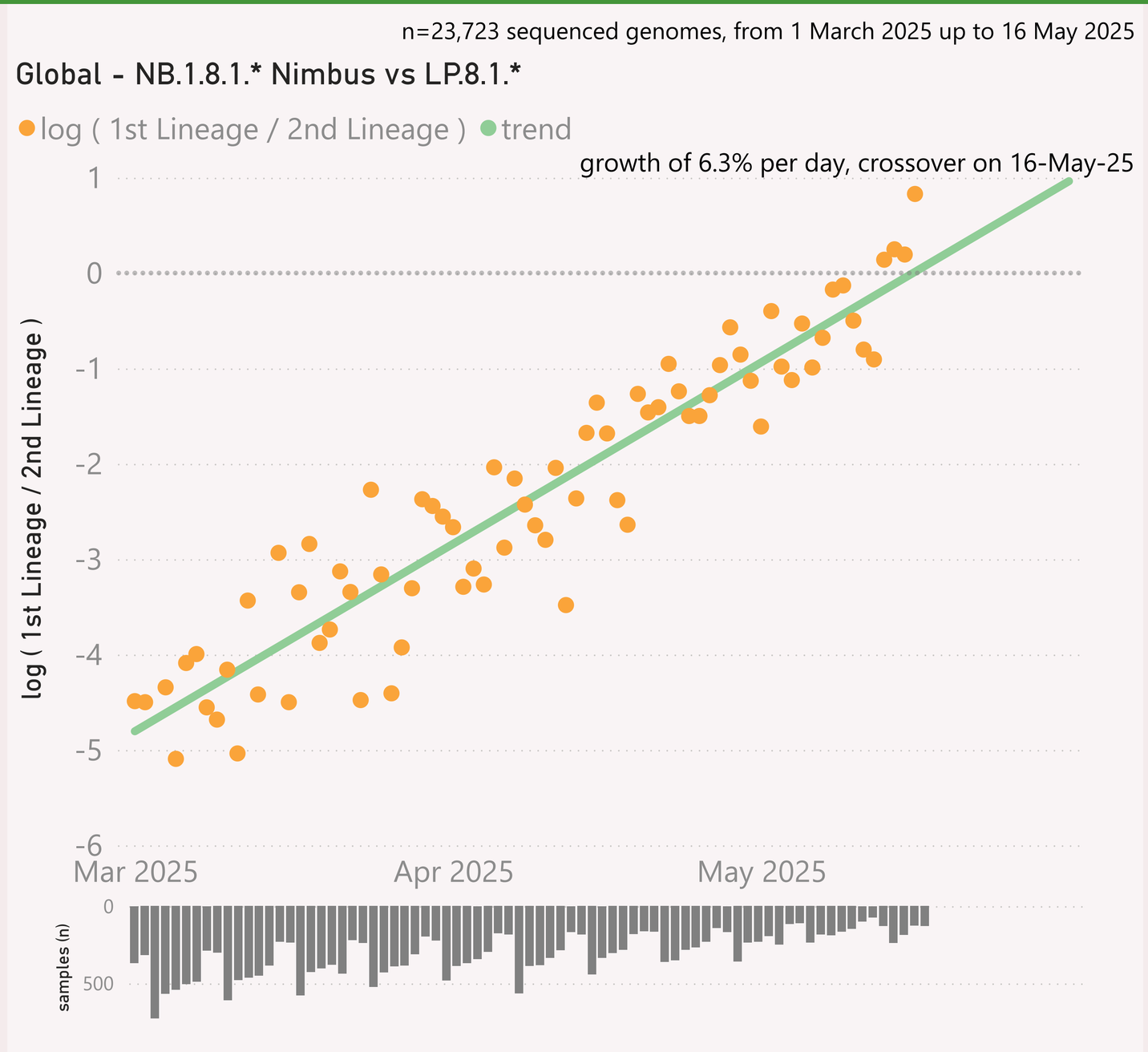
Human

Samples Sequenced (gisaid)

43

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
India	Tamil Nadu		16/05/2025	XFP.*	XFP
USA	International Tr...		15/05/2025	XFP.*	XFP
India	Kerala		15/05/2025	XFP.*	XFP
India	Tamil Nadu		15/05/2025	XFP.*	XFP
Singapore			14/05/2025	XFP.*	XFP
USA	International Tr...		14/05/2025	XFP.*	XFP
USA	International Tr...	Trave...	14/05/2025	XFP.*	XFP
India	Tamil Nadu		14/05/2025	XFP.*	XFP
USA	International Tr...		13/05/2025	XFP.*	XFP
India	Tamil Nadu		13/05/2025	XFP.*	XFP
India	Tamil Nadu		09/05/2025	XFP.*	XFP
USA	International Tr...		08/05/2025	XFP.*	XFP
Singapore			07/05/2025	XFP.*	XFP
India	Andhra Pradesh		06/05/2025	XFP.*	XFP
USA	International Tr...		06/05/2025	XFP.*	XFP
Singapore			05/05/2025	XFP.*	XFP
India	Andhra Pradesh		05/05/2025	XFP.*	XFP
India	Tamil Nadu		05/05/2025	XFP.*	XFP
Ireland	Dublin		03/05/2025	XFP.*	XFP
India	Tamil Nadu		02/05/2025	XFP.*	XFP
India	Tamil Nadu		01/05/2025	XFP.*	XFP
India	Tamil Nadu		29/04/2025	XFP.*	XFP

Total

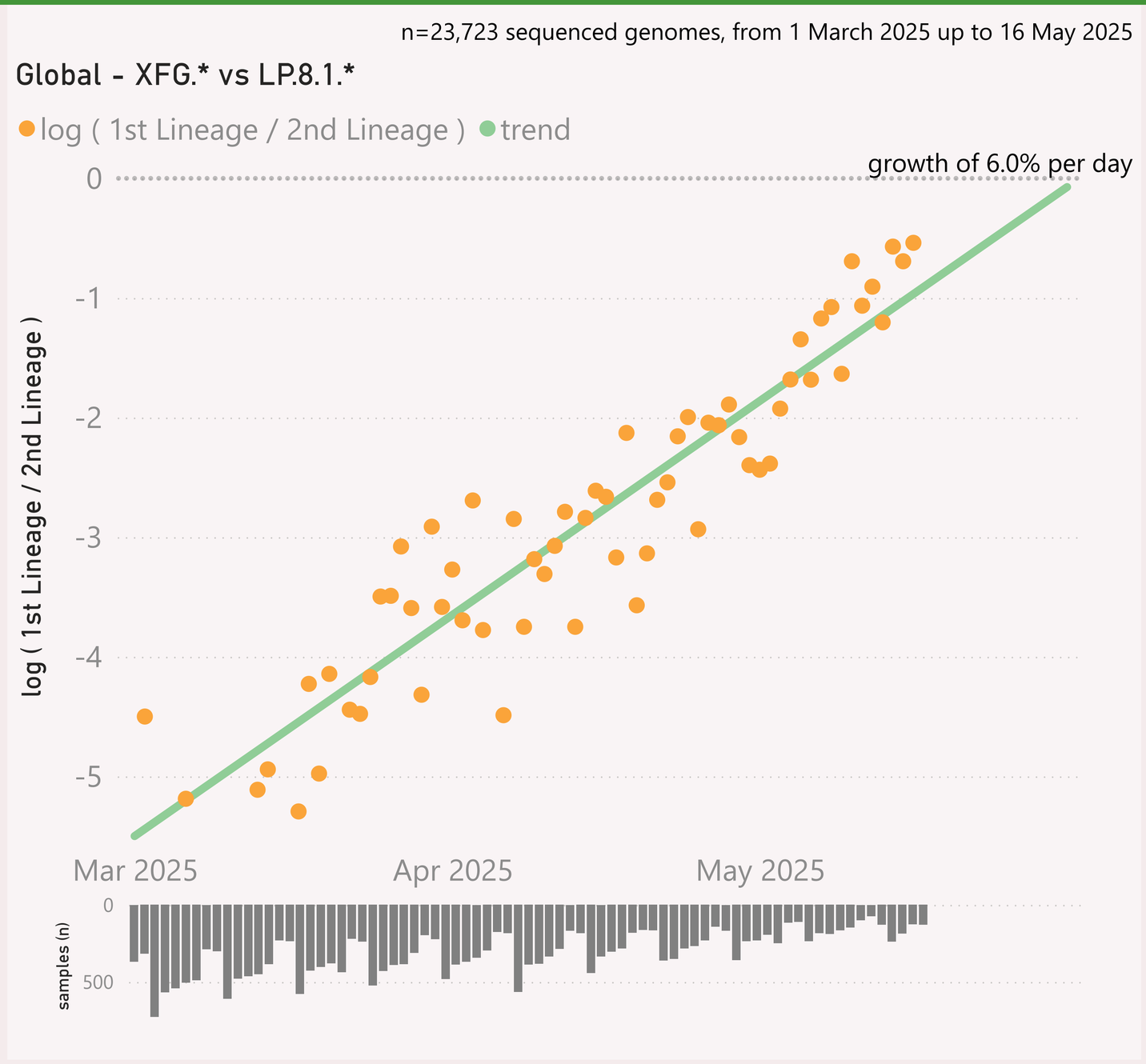


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.



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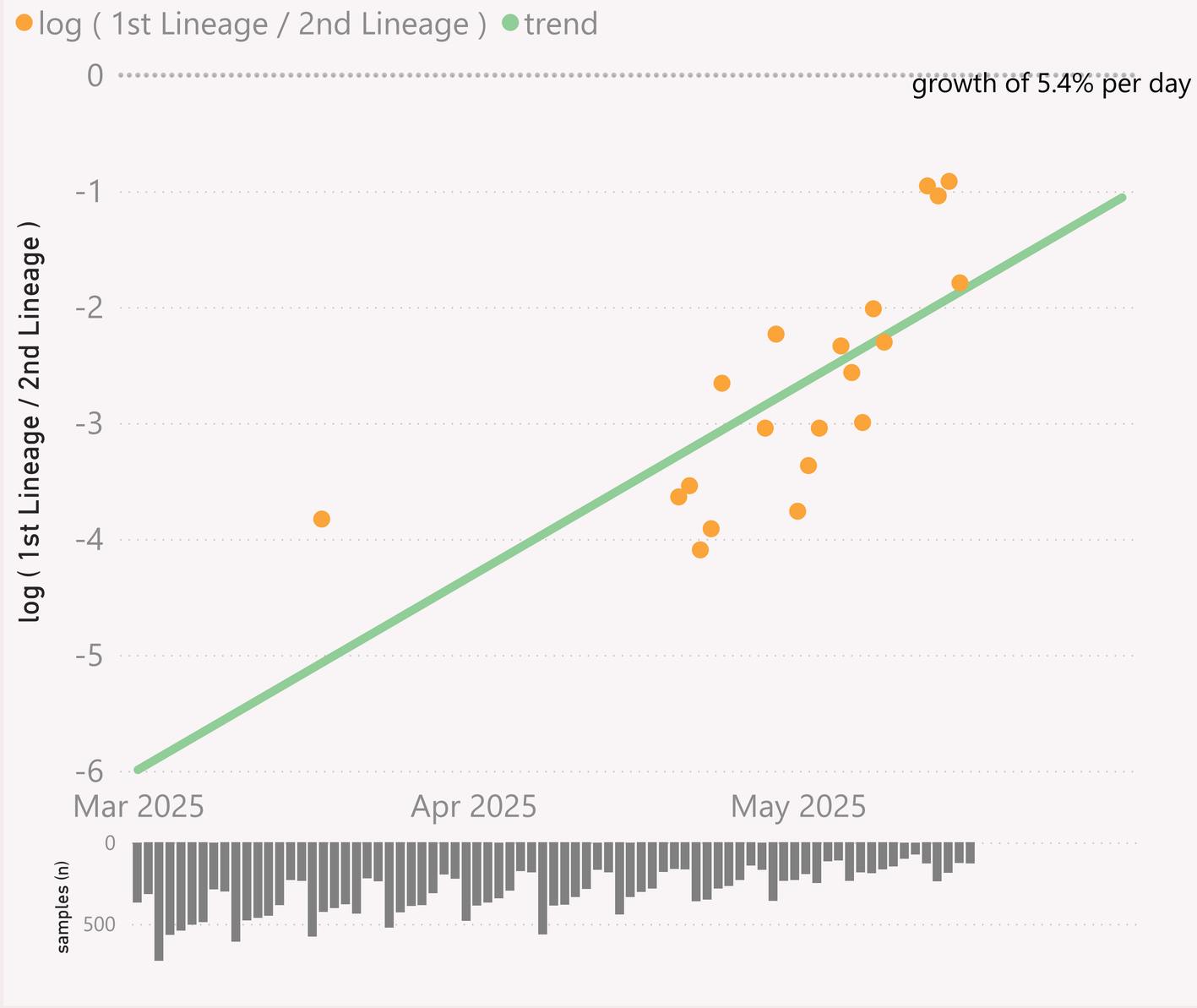

This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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

The Lineage classifications are provided by Nextclade.

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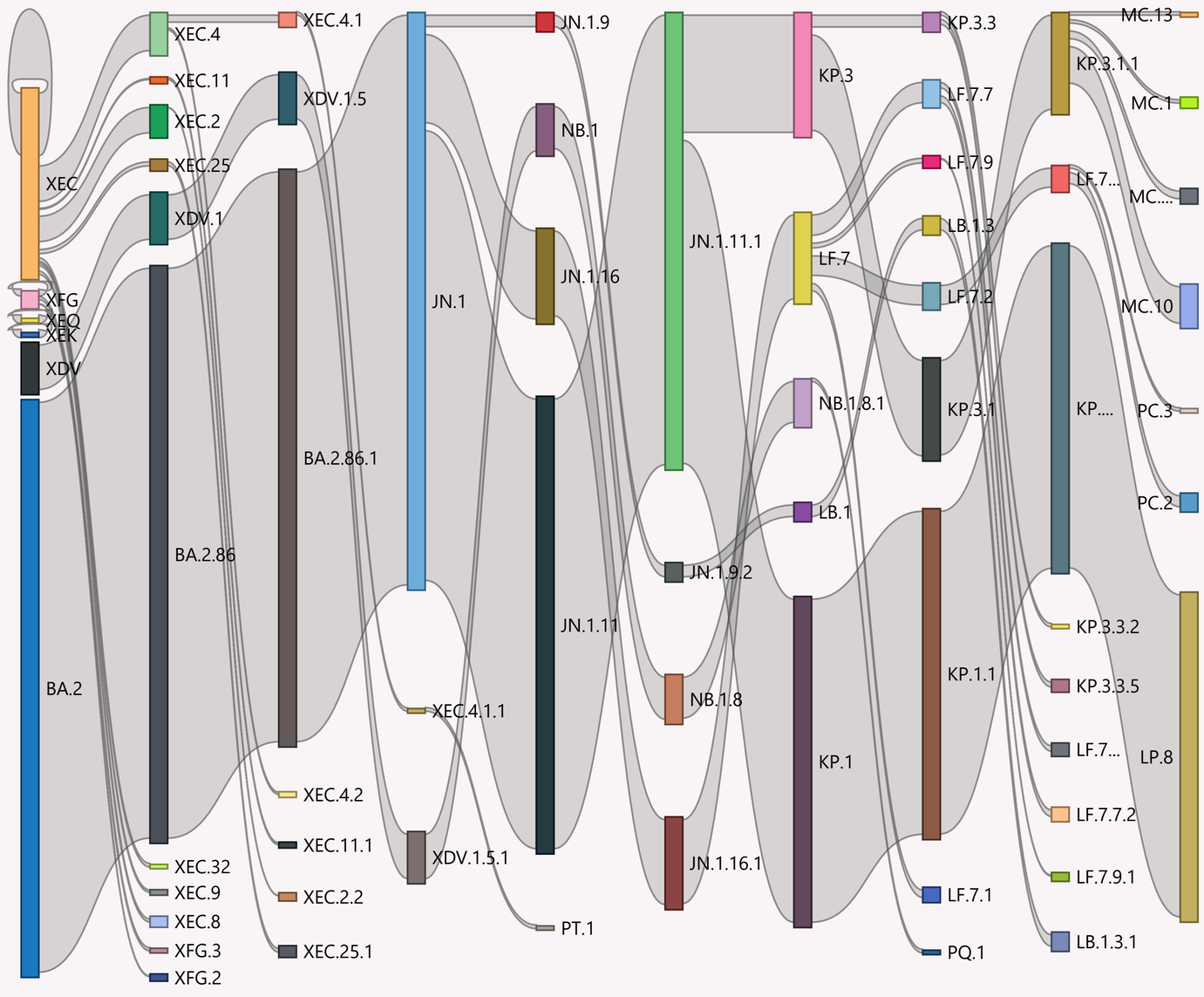
n=23,723 sequenced genomes, from 1 March 2025 up to 16 May 2025

Global



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.

COVID-19 Genomic Sequencing analysis - Data Currency. Data from gisaid.org. Source files and info on github.

Last Update: 2025-05-31 01:26 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
United States	11,304	16/05/2025		10/05/2025	
Canada	1,806	14/05/2025		10/05/2025	
Australia	1,455	16/05/2025		10/05/2025	
Singapore	1,382	16/05/2025		10/05/2025	
France	1,375	16/05/2025		10/05/2025	
United Kingdom	1,070	16/05/2025		10/05/2025	
Japan	1,048	15/05/2025		10/05/2025	
Brazil	942	13/05/2025		10/05/2025	
Spain	935	16/05/2025		10/05/2025	
South Korea	560	07/05/2025		10/05/2025	
New Zealand	322	16/05/2025		10/05/2025	
Thailand	291	16/05/2025		10/05/2025	
Chile	246	22/04/2025		05/05/2025	
Ireland	207	16/05/2025		10/05/2025	
Denmark	198	05/05/2025		10/05/2025	
Peru	198	01/04/2025		10/05/2025	
Germany	194	15/05/2025		10/05/2025	
Italy	189	09/05/2025		10/05/2025	
Mexico	187	13/05/2025		10/05/2025	
Netherlands	172	09/05/2025		10/05/2025	
Argentina	171	31/03/2025		10/05/2025	
Luxembourg	138	01/04/2025		16/04/2025	
Costa Rica	124	27/04/2025		10/05/2025	
Puerto Rico	113	16/05/2025		10/05/2025	
Hong Kong	99	09/05/2025		10/05/2025	
Kazakhstan	95	07/02/2024		08/05/2025	
Finland	88	05/05/2025		10/05/2025	
Sweden	88	15/05/2025		10/05/2025	
Total	**26,116**	**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.