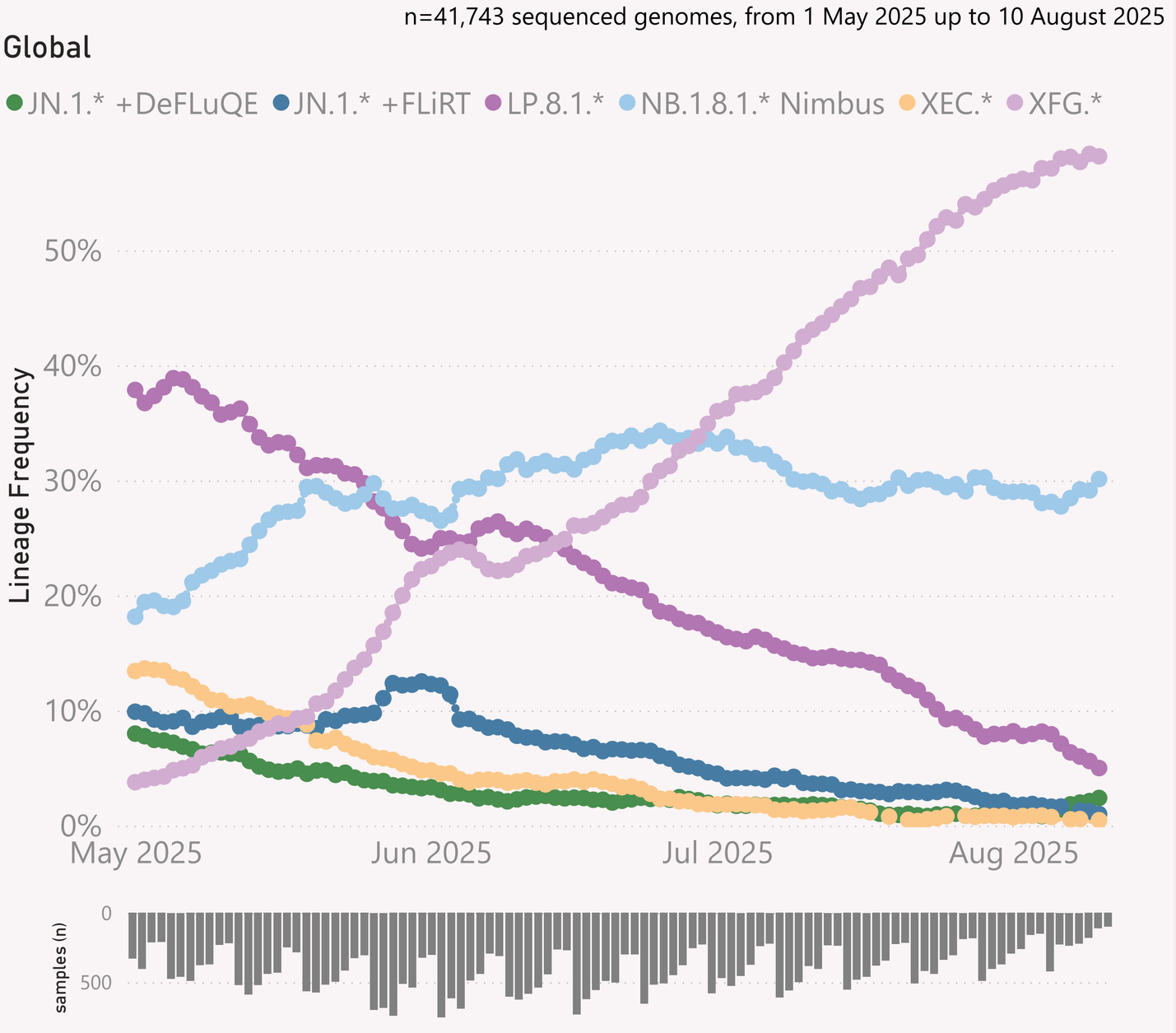
COVID-19 Genomic Sequencing analysis. Lineage Frequencies. Data from gisaid.org, with nextclade lineages. Source files and more info on github. Last Update: 2025-08-30 00:55 (UTC)

n=41,743 sequenced genomes, from 1 May 2025 up to 10 August 2025



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

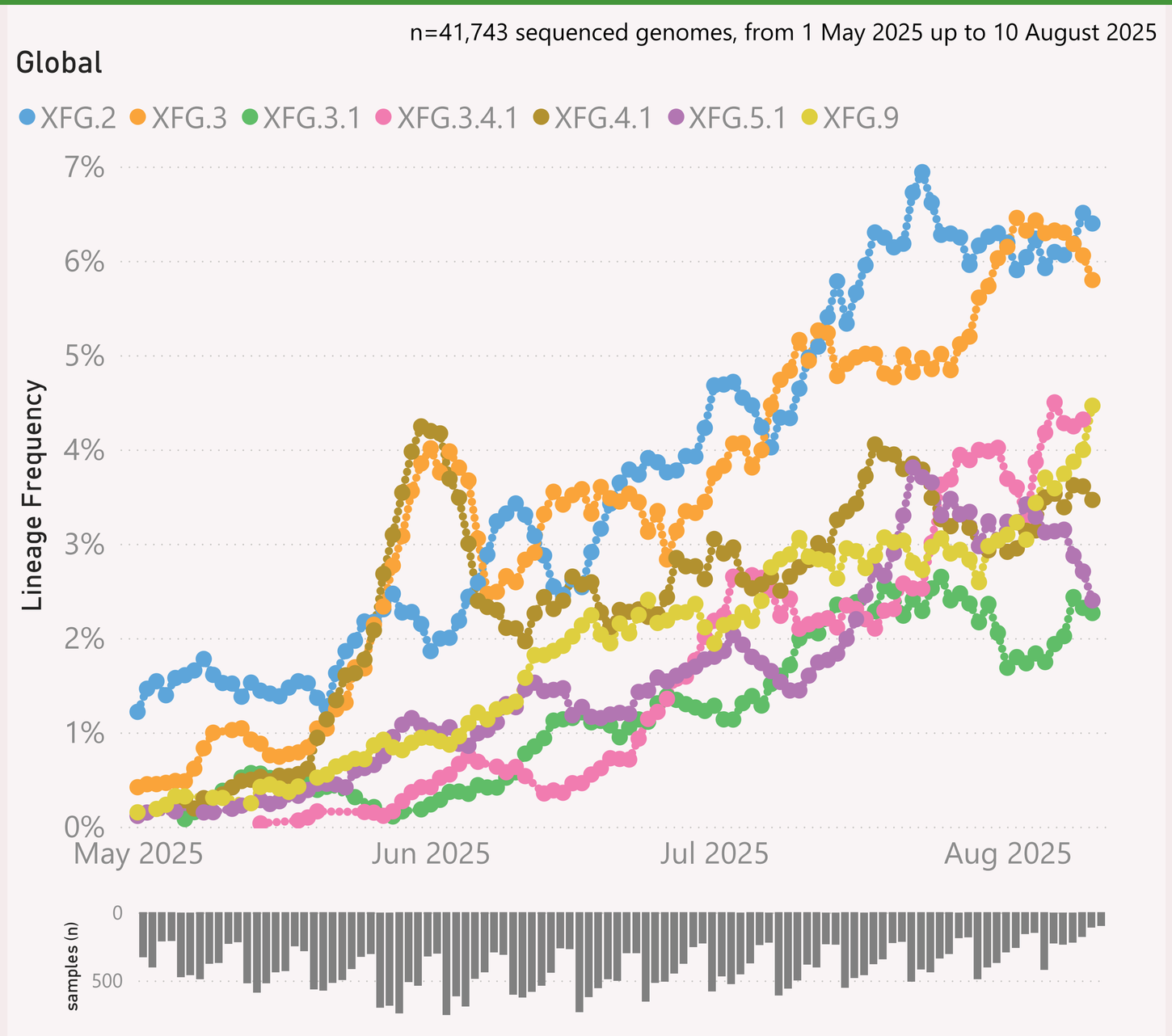
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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 XFG.* Stratus.

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

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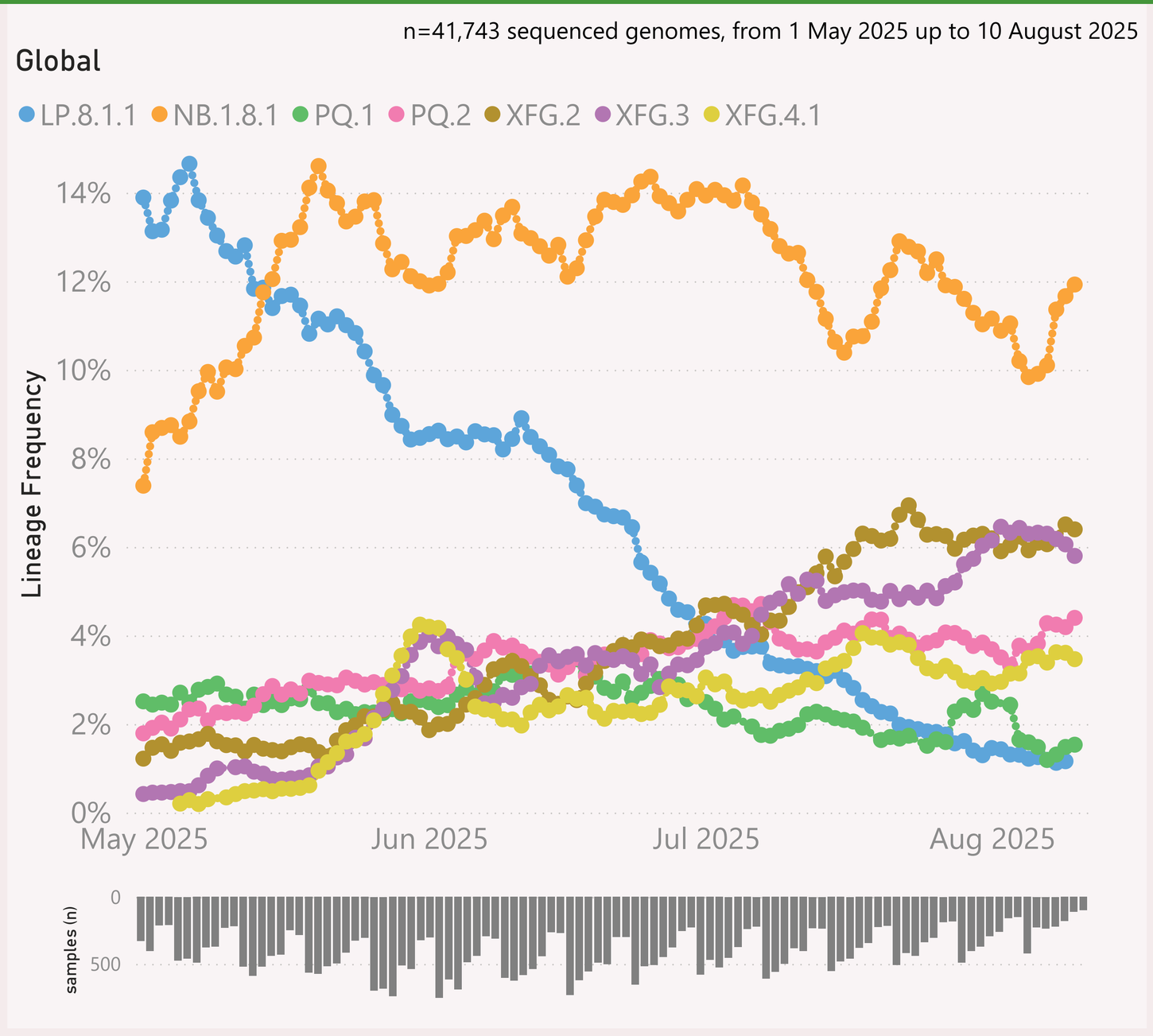

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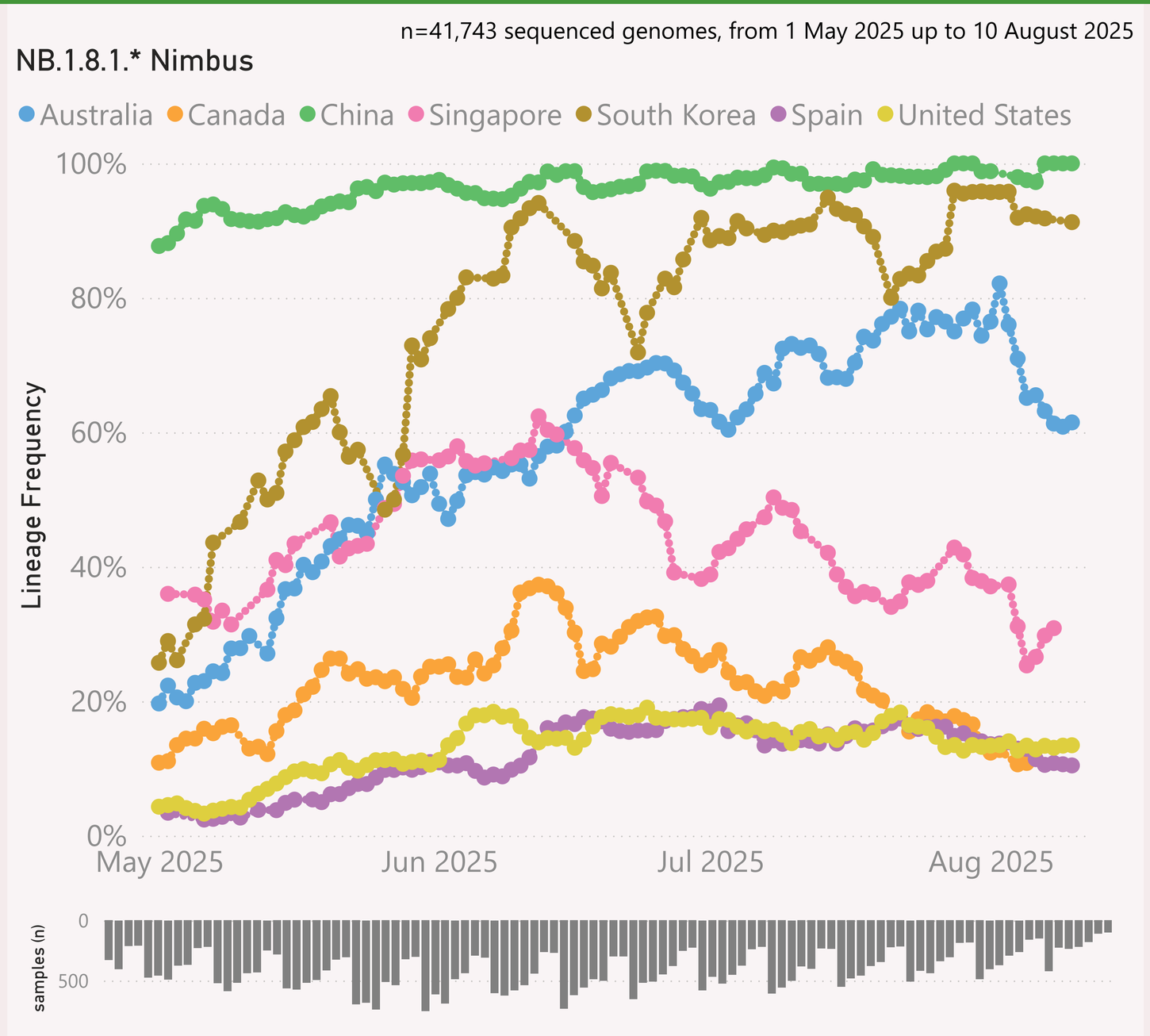

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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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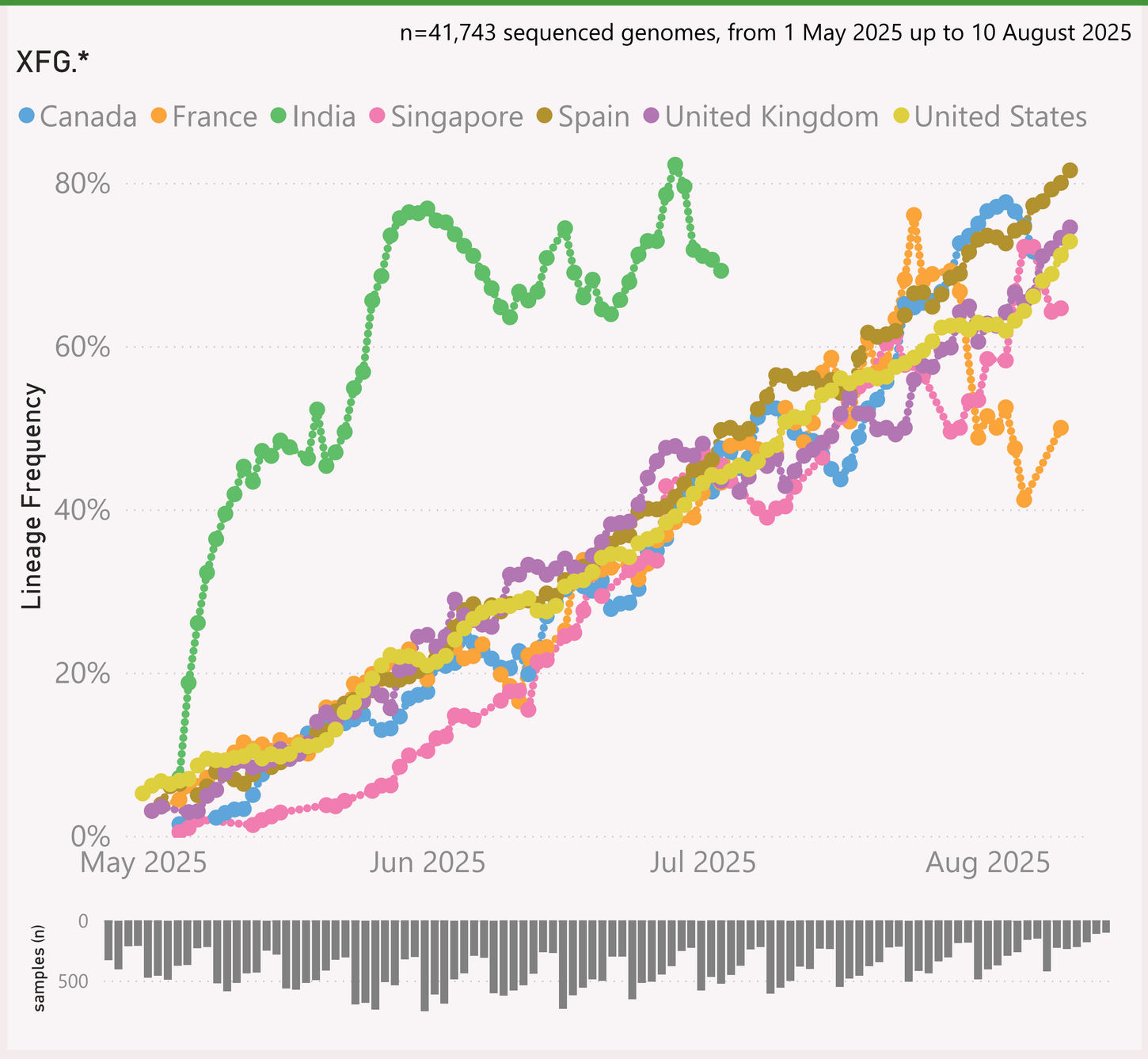

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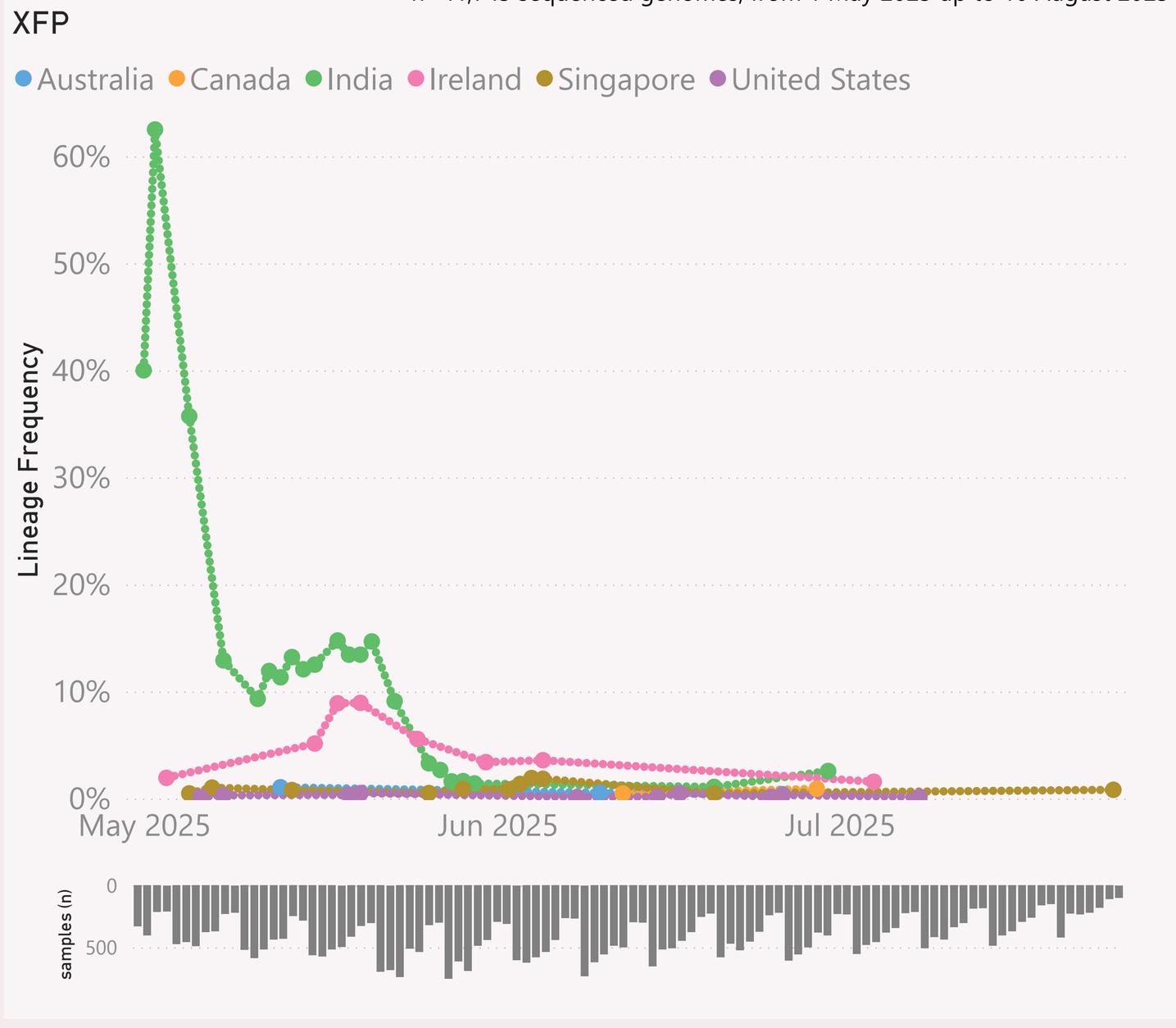
COVID-19 Genomic Sequencing analysis - selected Lineage by Country. Data from gisaid.org, with nextclade lineages Source files and info on github. Last Update: 2025-08-30 00:55 (UTC)

n=41,743 sequenced genomes, from 1 May 2025 up to 10 August 2025



Date

01/01/2025 31/12/2025

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

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

Host

Human

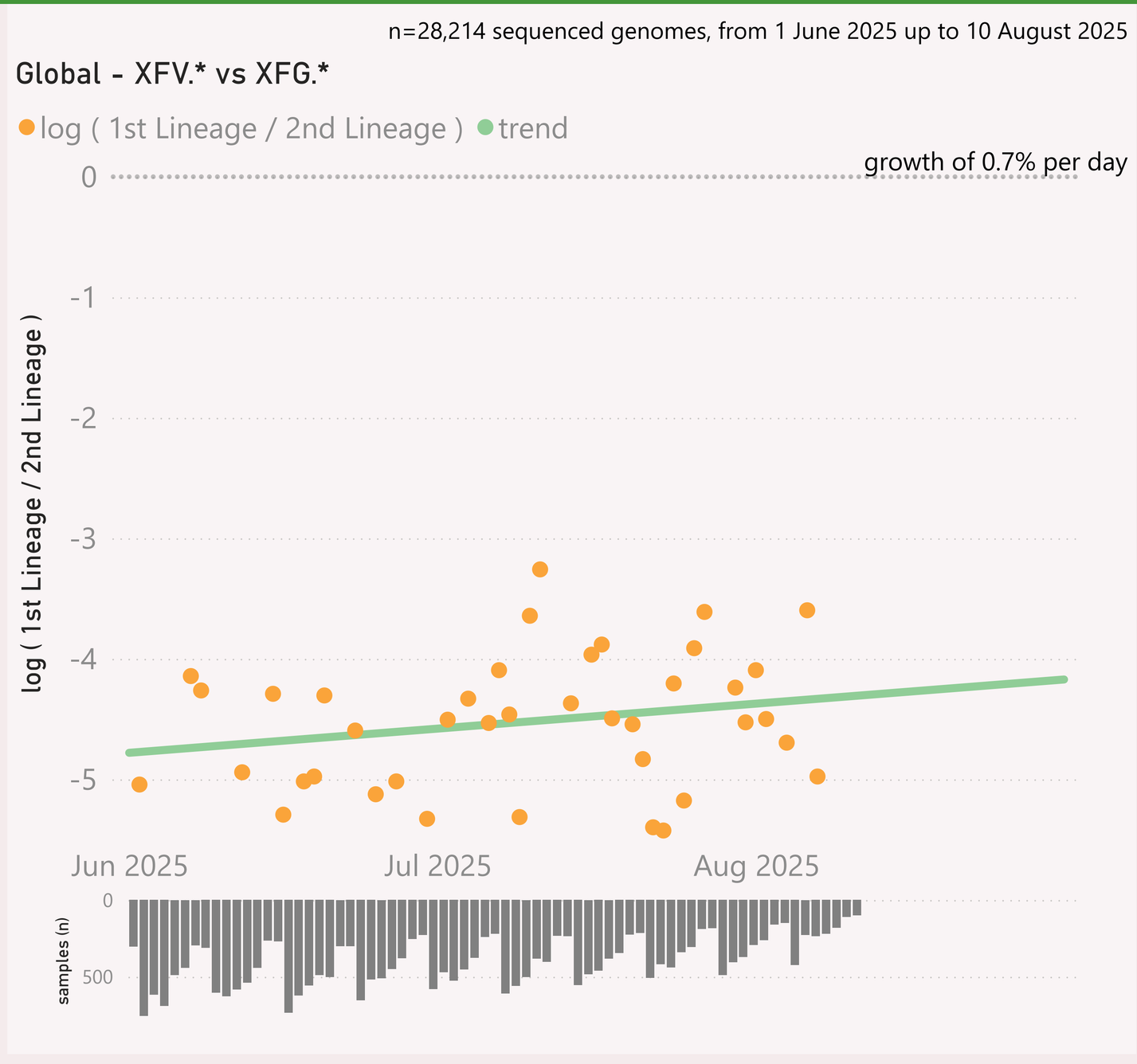
Samples Sequenced (gisaid)

82

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
Singapore			25/07/2025	XFP.*	XFP
Luxembourg			24/07/2025	XFP.*	XFP
Japan		Quar...	15/07/2025	XFP.*	XFP
USA	Texas		08/07/2025	XFP.*	XFP
Ireland	Dublin		04/07/2025	XFP.*	XFP
India	Maharashtra		30/06/2025	XFP.*	XFP
Canada	Ontario		29/06/2025	XFP.*	XFP
Germany	Rhineland-Pala...		27/06/2025	XFP.*	XFP
United Kingdom	Wales		27/06/2025	XFP.*	XFP
USA	Minnesota		26/06/2025	XFP.*	XFP
Australia	Victoria		26/06/2025	XFP.*	XFP
USA	Minnesota		25/06/2025	XFP.*	XFP
France	Provence-Alpe...		21/06/2025	XFP.*	XFP
Singapore			20/06/2025	XFP.*	XFP
India	Chhattisgarh		20/06/2025	XFP.*	XFP
USA	Massachusetts		17/06/2025	XFP.*	XFP
USA	Minnesota		17/06/2025	XFP.*	XFP
USA	International Tr...		15/06/2025	XFP.*	XFP
Canada	Ontario		12/06/2025	XFP.*	XFP
Poland	Warminsko-M...		12/06/2025	XFP.*	XFP
Australia	Western Austr...		10/06/2025	XFP.*	XFP
USA	International Tr...		08/06/2025	XFP.*	XFP

Total

n=28,214 sequenced genomes, from 1 June 2025 up to 10 August 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.

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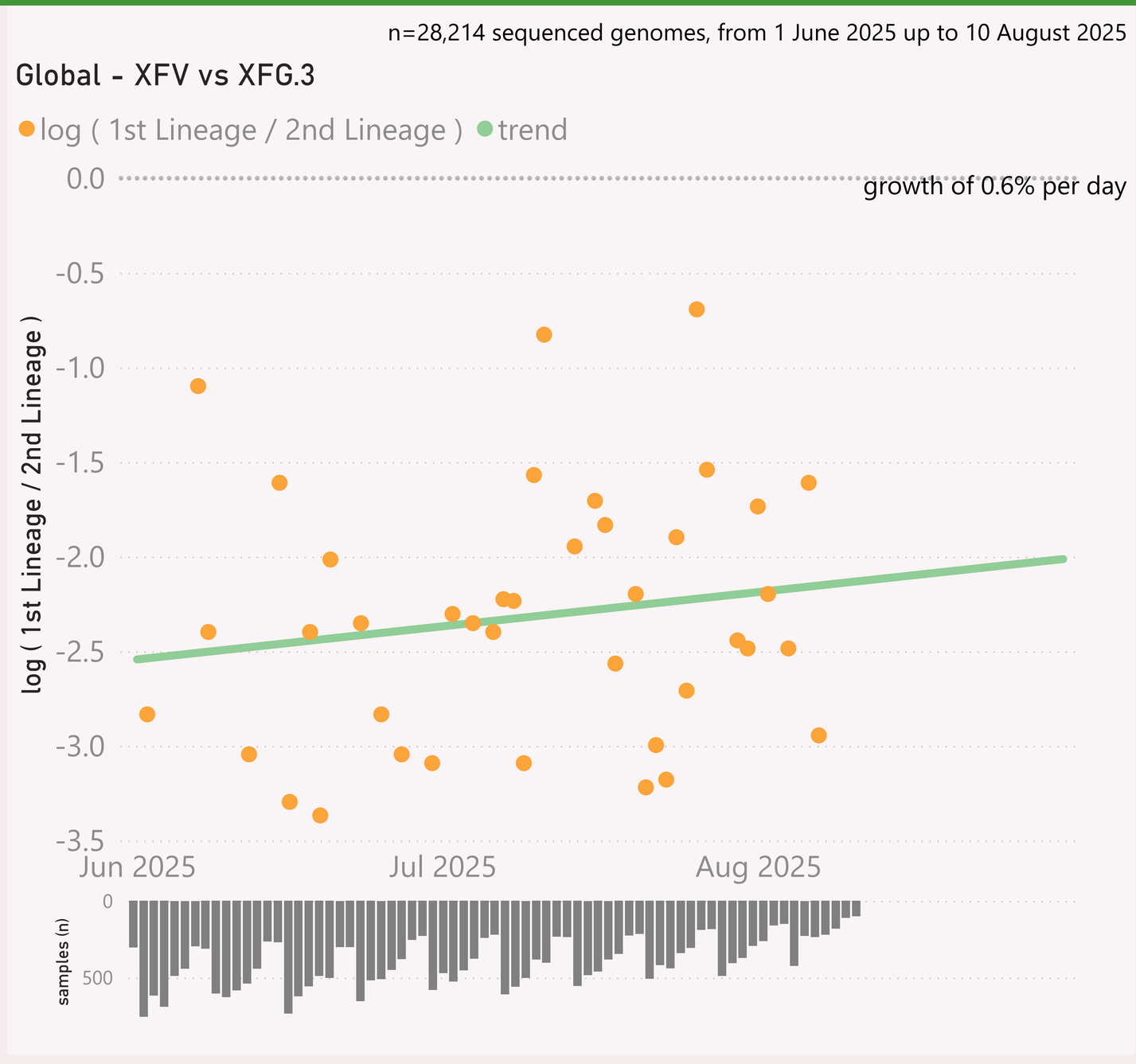

This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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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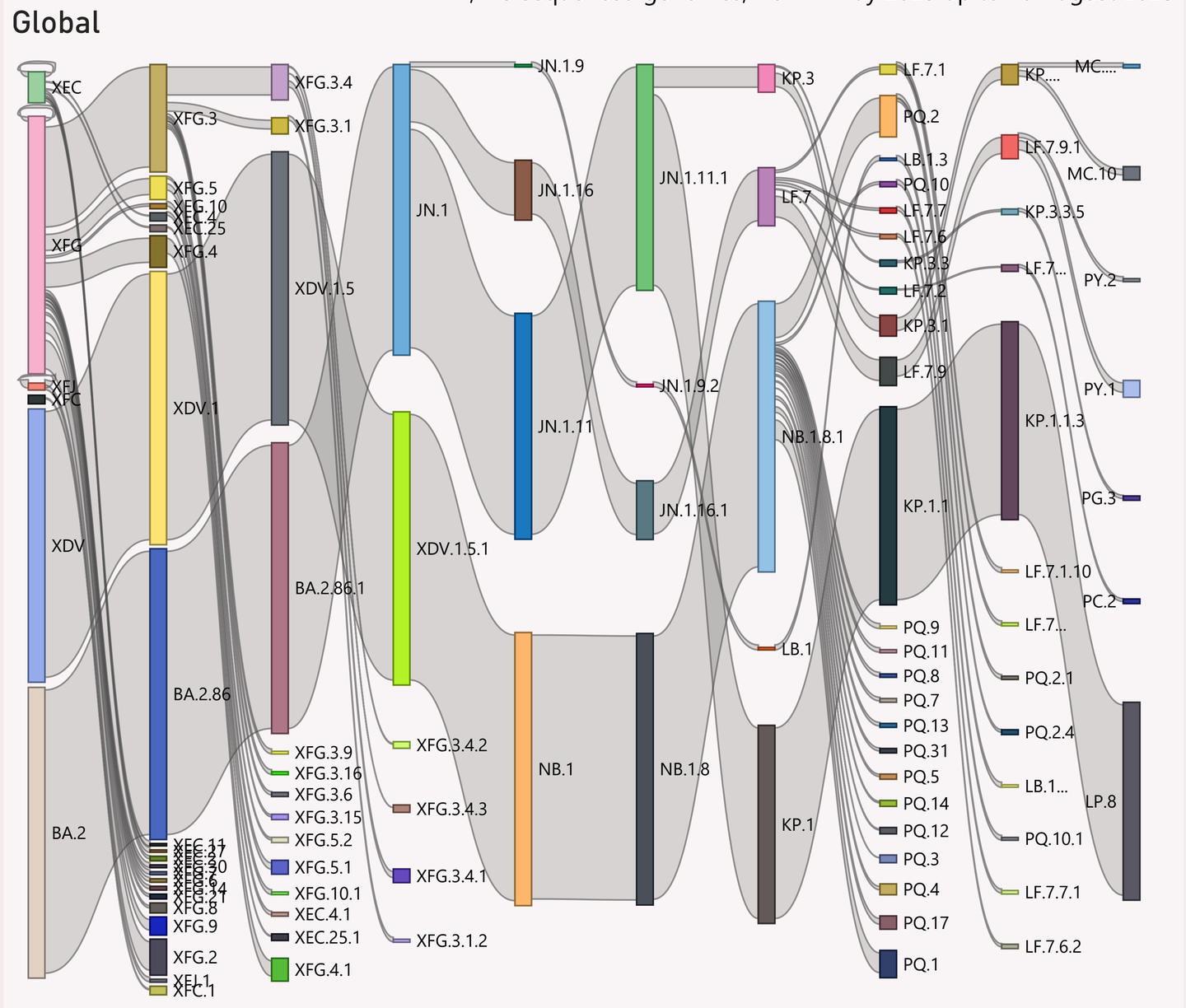


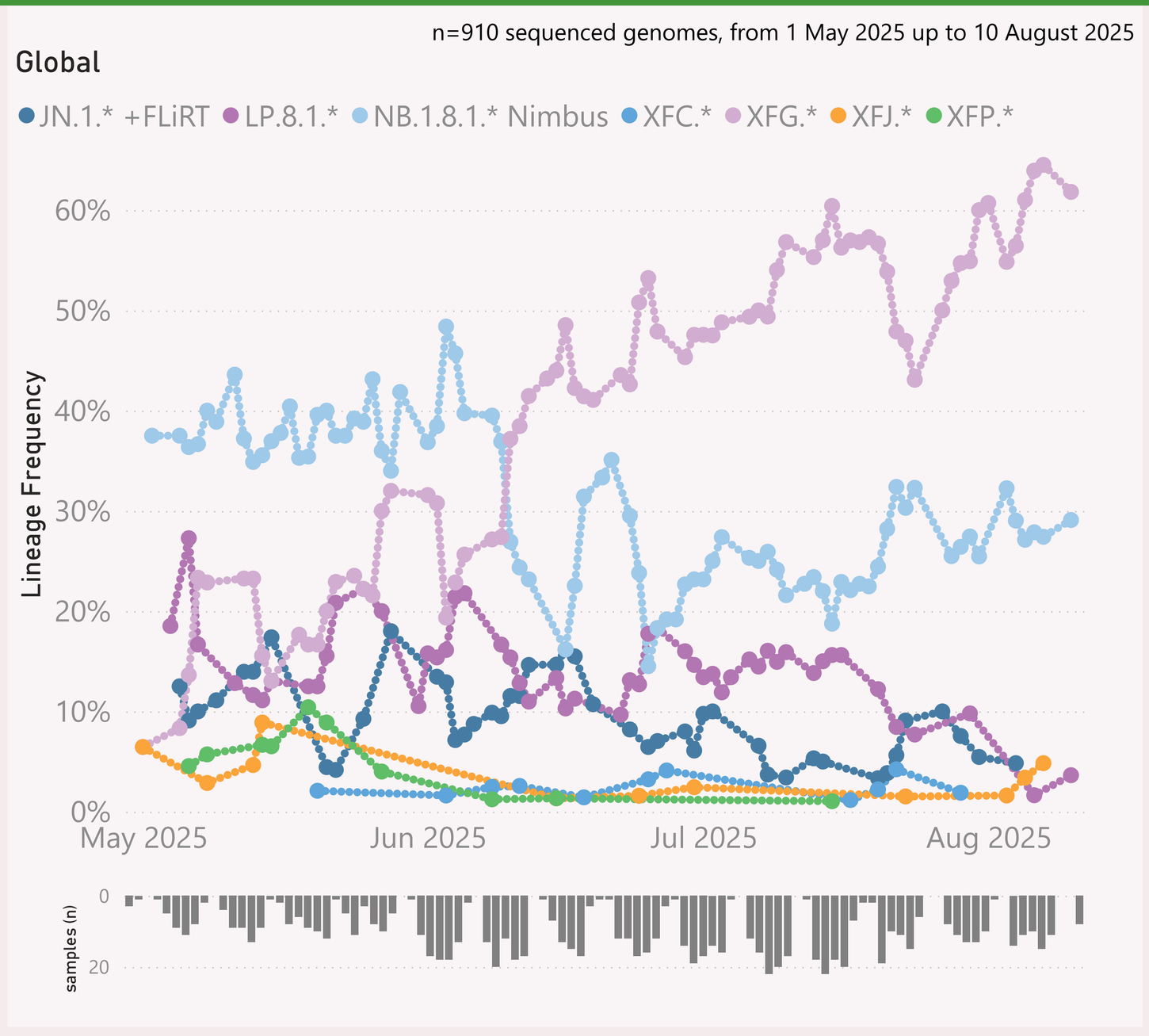
This page shows the hierarchy of the significant Lineages, over recent months.

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.

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

Last Update: 2025-08-30 00:55 (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	6,089	10/08/2025		18/08/2025	
Spain	3,526	10/08/2025		18/08/2025	
United Kingdom	1,993	10/08/2025		18/08/2025	
China	1,642	10/08/2025		18/08/2025	
Canada	1,392	06/08/2025		18/08/2025	
Australia	1,186	10/08/2025		18/08/2025	
Singapore	842	09/08/2025		18/08/2025	
France	674	09/08/2025		18/08/2025	
New Zealand	566	10/08/2025		18/08/2025	
Ireland	528	10/08/2025		18/08/2025	
South Korea	526	10/08/2025		18/08/2025	
Mexico	485	19/06/2025		18/08/2025	
Portugal	434	03/08/2025		18/08/2025	
Brazil	422	07/08/2025		18/08/2025	
Japan	408	10/08/2025		18/08/2025	
Russia	376	05/08/2025		18/08/2025	
Luxembourg	361	04/08/2025		18/08/2025	
Thailand	315	30/07/2025		18/08/2025	
Costa Rica	312	25/07/2025		18/08/2025	
India	293	03/07/2025		17/08/2025	
Malaysia	288	05/08/2025		18/08/2025	
Germany	284	10/08/2025		18/08/2025	
Puerto Rico	225	09/08/2025		18/08/2025	
Netherlands	219	20/07/2025		11/08/2025	
Taiwan	198	30/07/2025		01/08/2025	
Denmark	197	04/08/2025		18/08/2025	
Italy	194	09/08/2025		18/08/2025	
Sweden	173	03/08/2025		18/08/2025	
Total	**25,252**	**10/08/2025**		**18/08/2025**	

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.