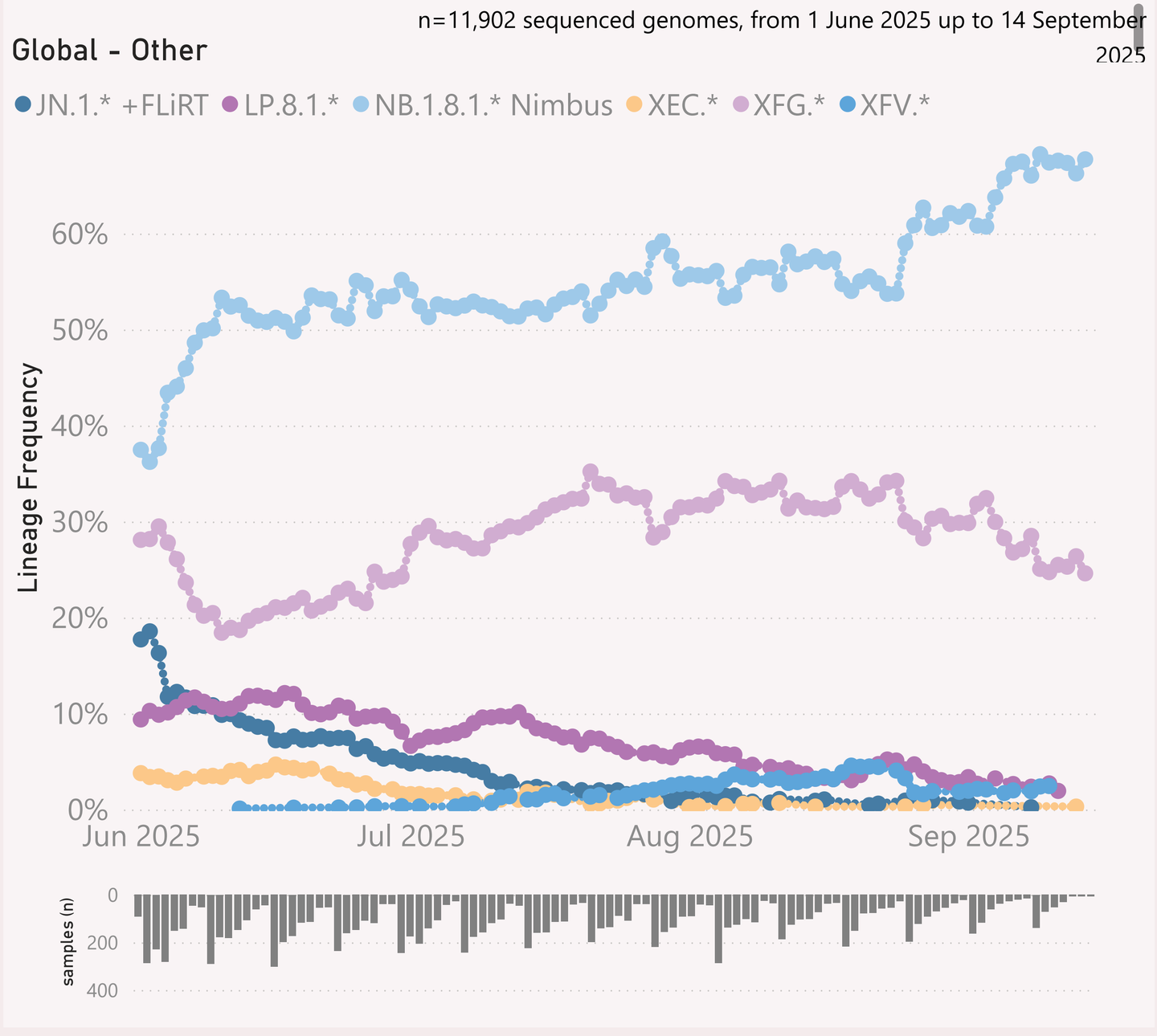


This "Global - Other" report aggregates the available data from countries besides those I regularly report on: Australia, NZ, the US, Canada and Europ.

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

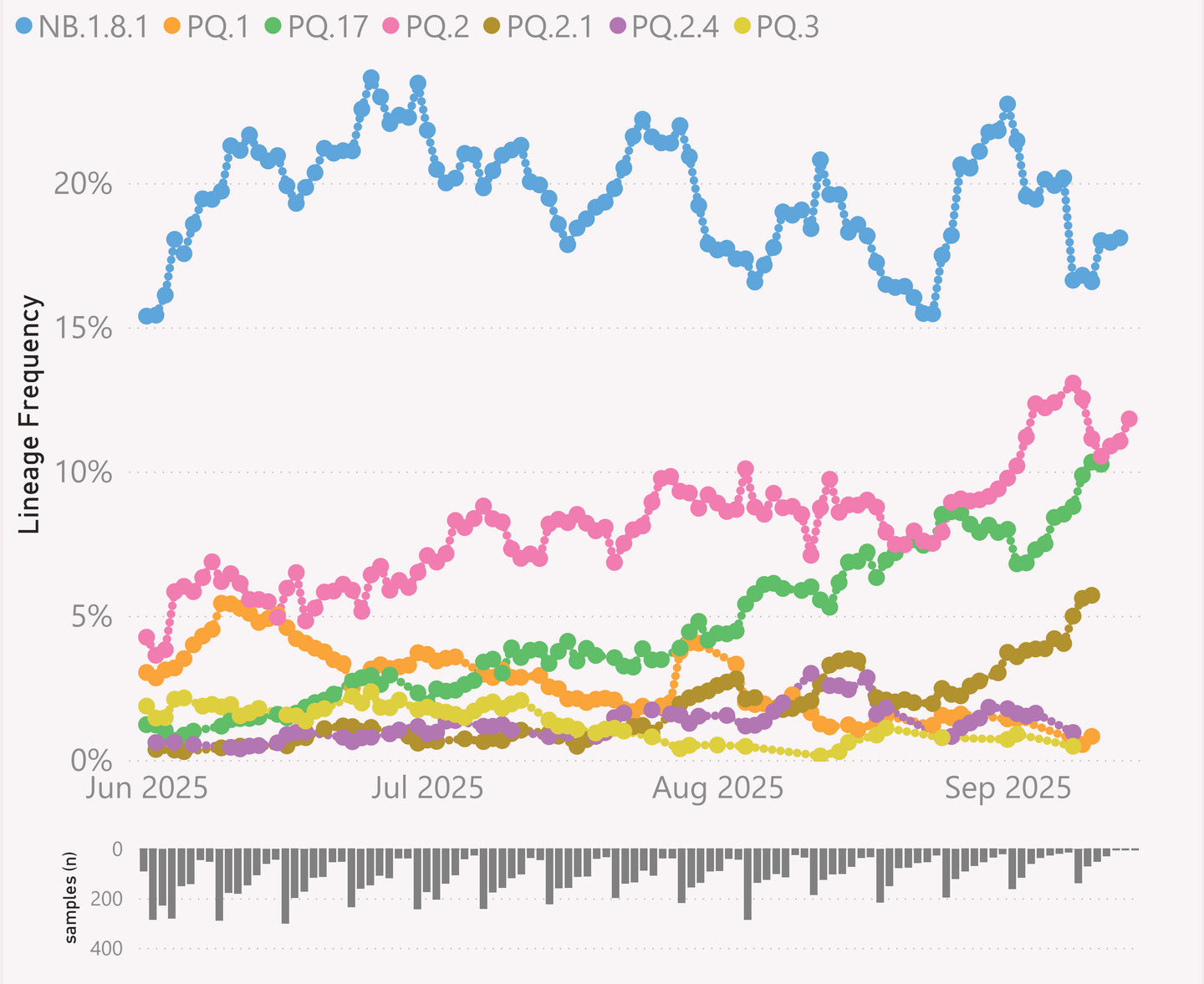
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=11,902 sequenced genomes, from 1 June 2025 up to 14 September 2025



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.

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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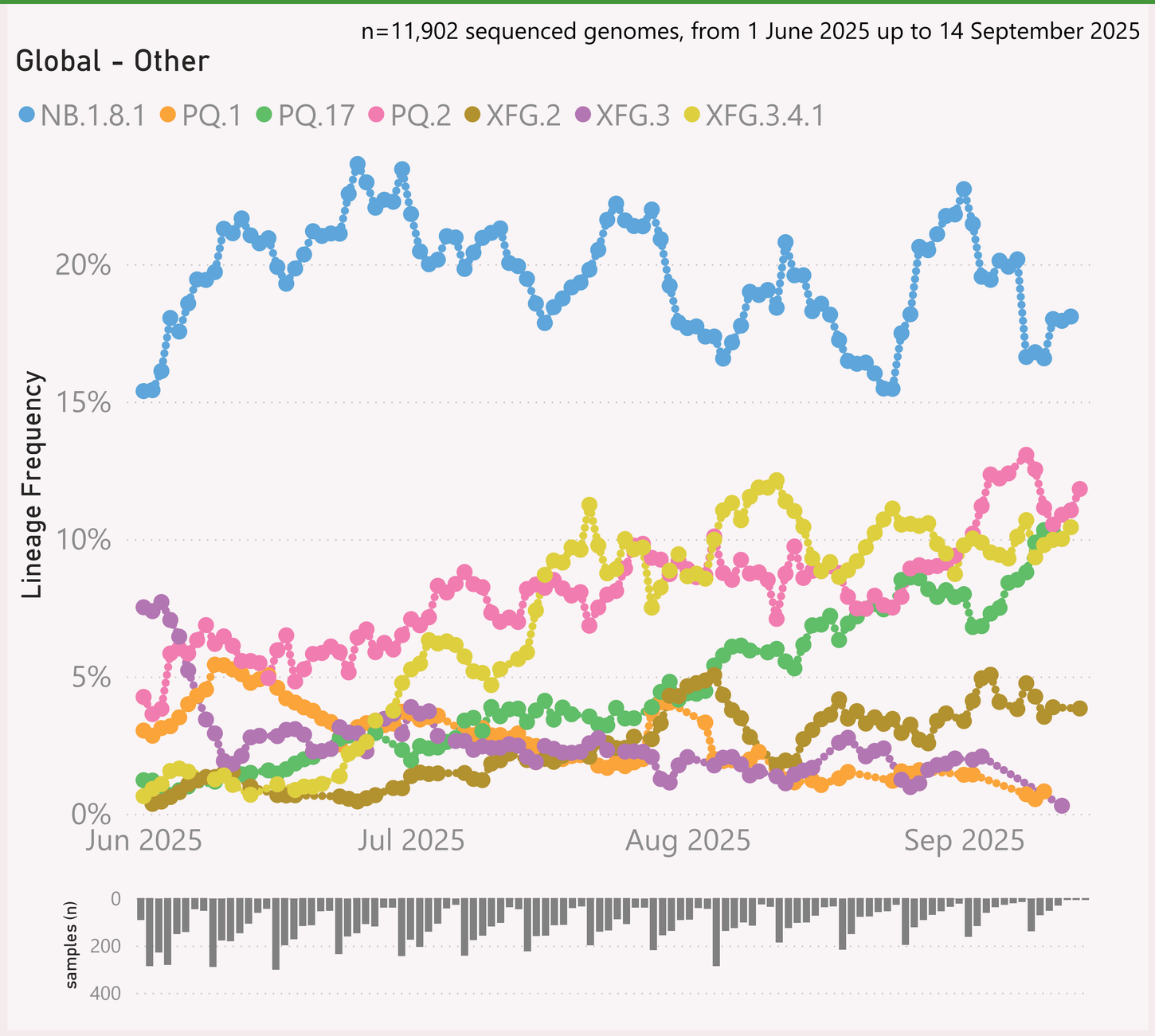

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The Lineage classifications are provided by Nextclade. The colour assignments are random.

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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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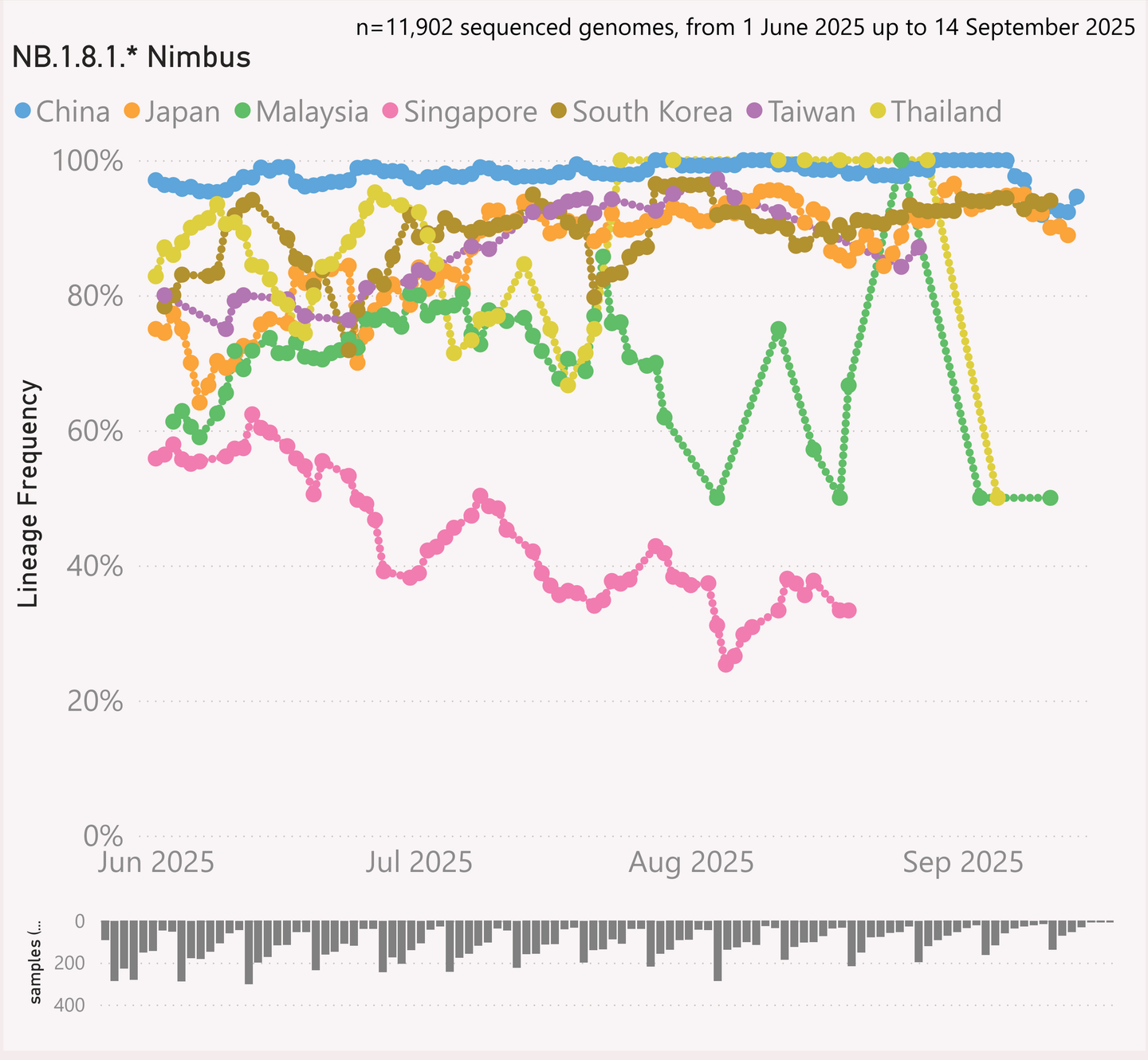
n=11,902 sequenced genomes, from 1 June 2025 up to 14 September 2025



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.

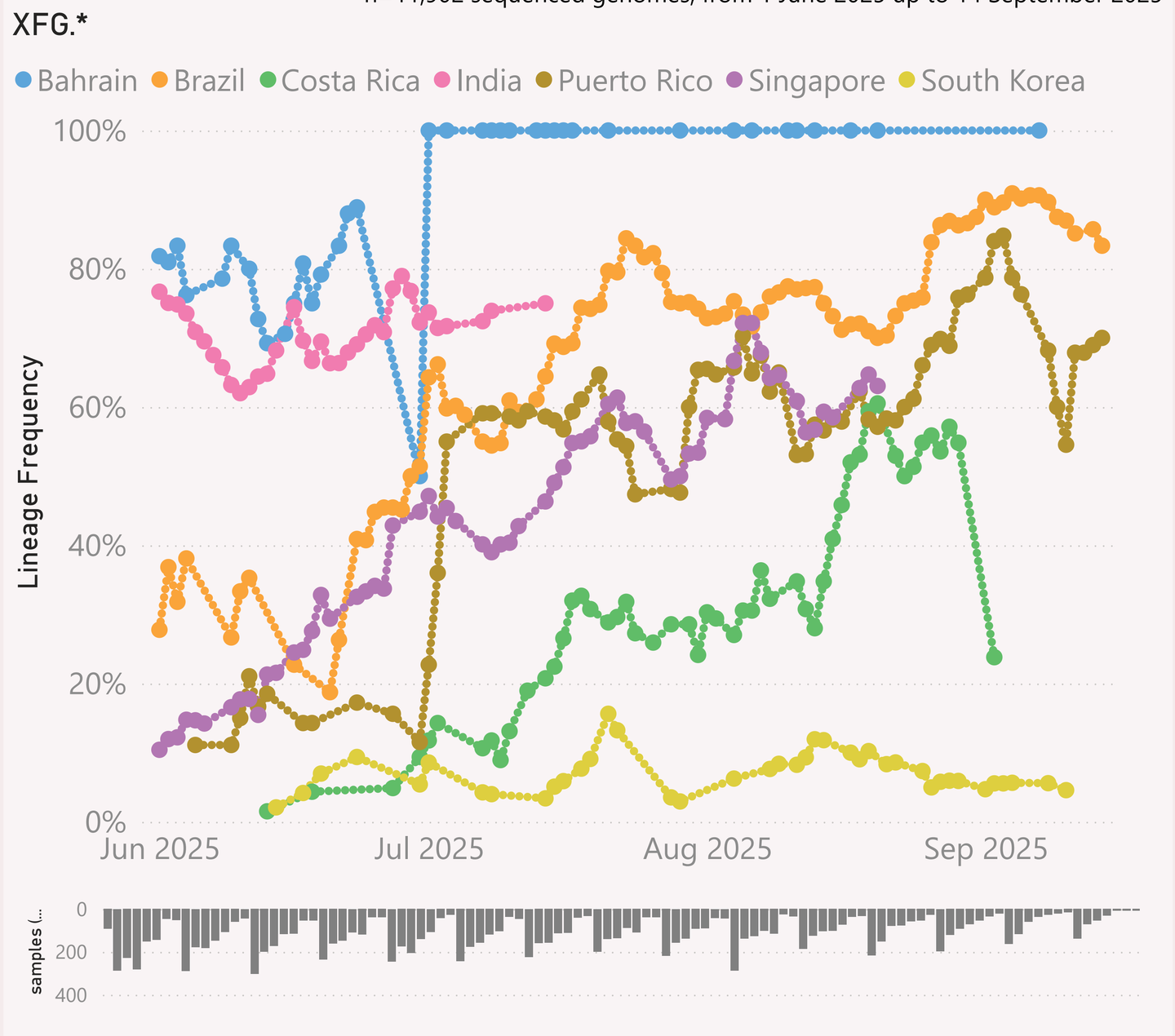
The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

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.

The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=11,902 sequenced genomes, from 1 June 2025 up to 14 September 2025



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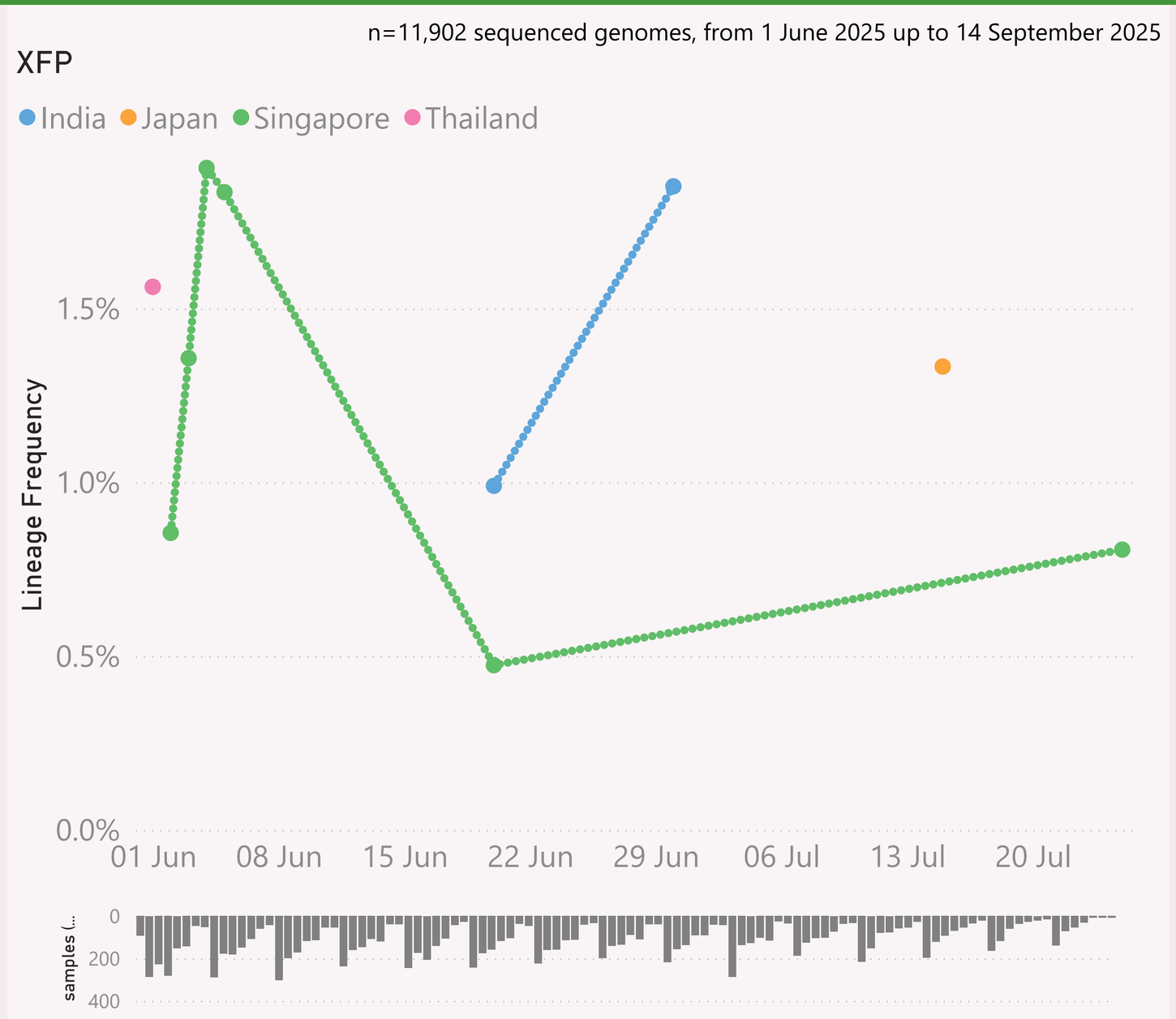
COVID-19 Genomic Sequencing analysis - selected Lineage by Country. Data from gisaid.org, with nextclade lineages Source files and info on github. Last Update: 2025-10-04 06:40 (UTC)

n=11,902 sequenced genomes, from 1 June 2025 up to 14 September 2025



Date

01/01/2025 31/12/2025

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

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

Host

Human

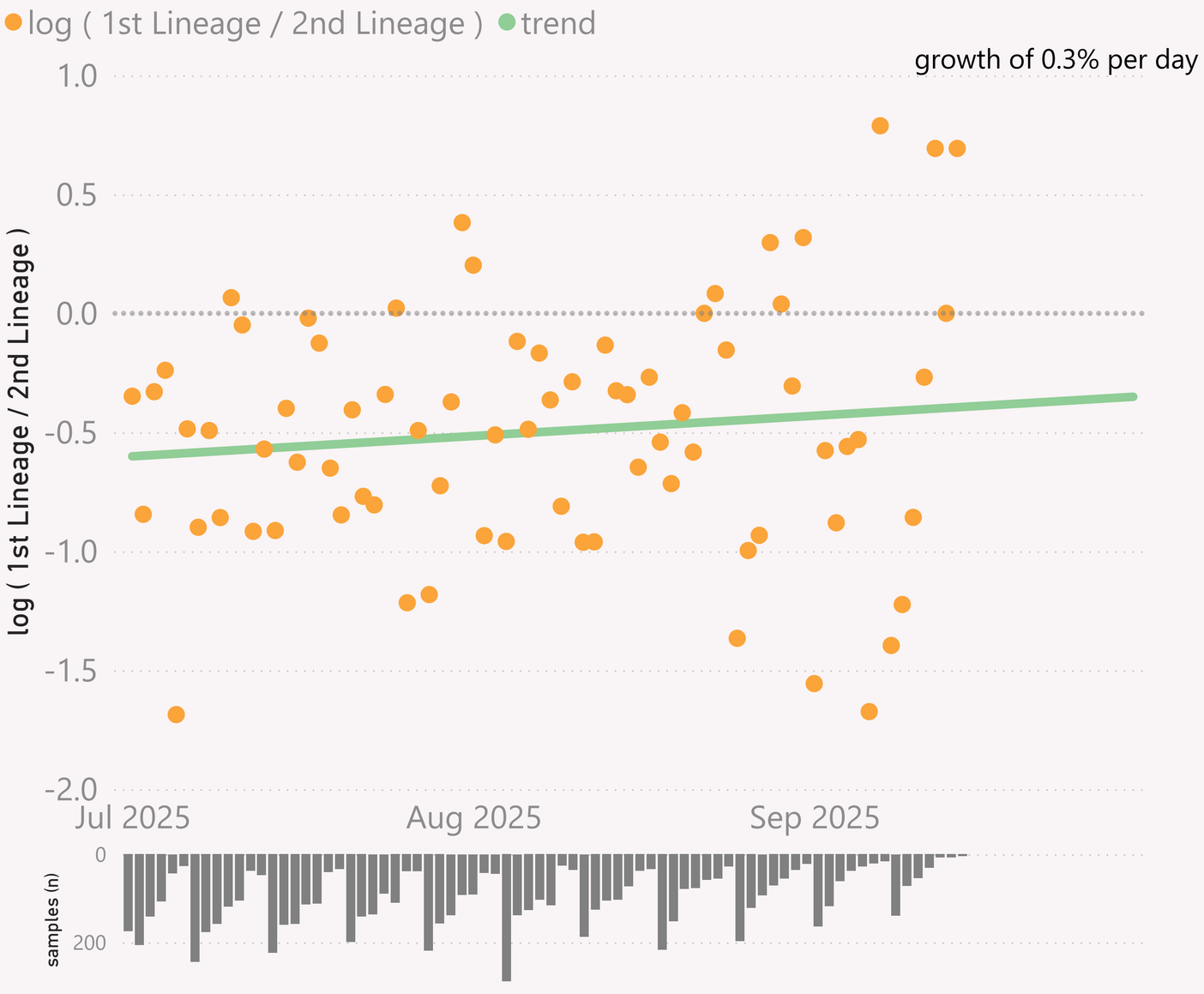
Samples Sequenced (gisaid)

10

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextcla
Singapore			25/07/2025	XFP.*	XFP
Japan		Quar...	15/07/2025	XFP.*	XFP
India	Maharashtra		30/06/2025	XFP.*	XFP
Singapore			20/06/2025	XFP.*	XFP
India	Chhattisgarh		20/06/2025	XFP.*	XFP
Singapore			05/06/2025	XFP.*	XFP
Singapore			04/06/2025	XFP.*	XFP
Singapore			03/06/2025	XFP.*	XFP
Singapore			02/06/2025	XFP.*	XFP
Thailand	Bangkok		01/06/2025	XFP.*	XFP
Total					

n=7,487 sequenced genomes, from 1 July 2025 up to 14 September 2025

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

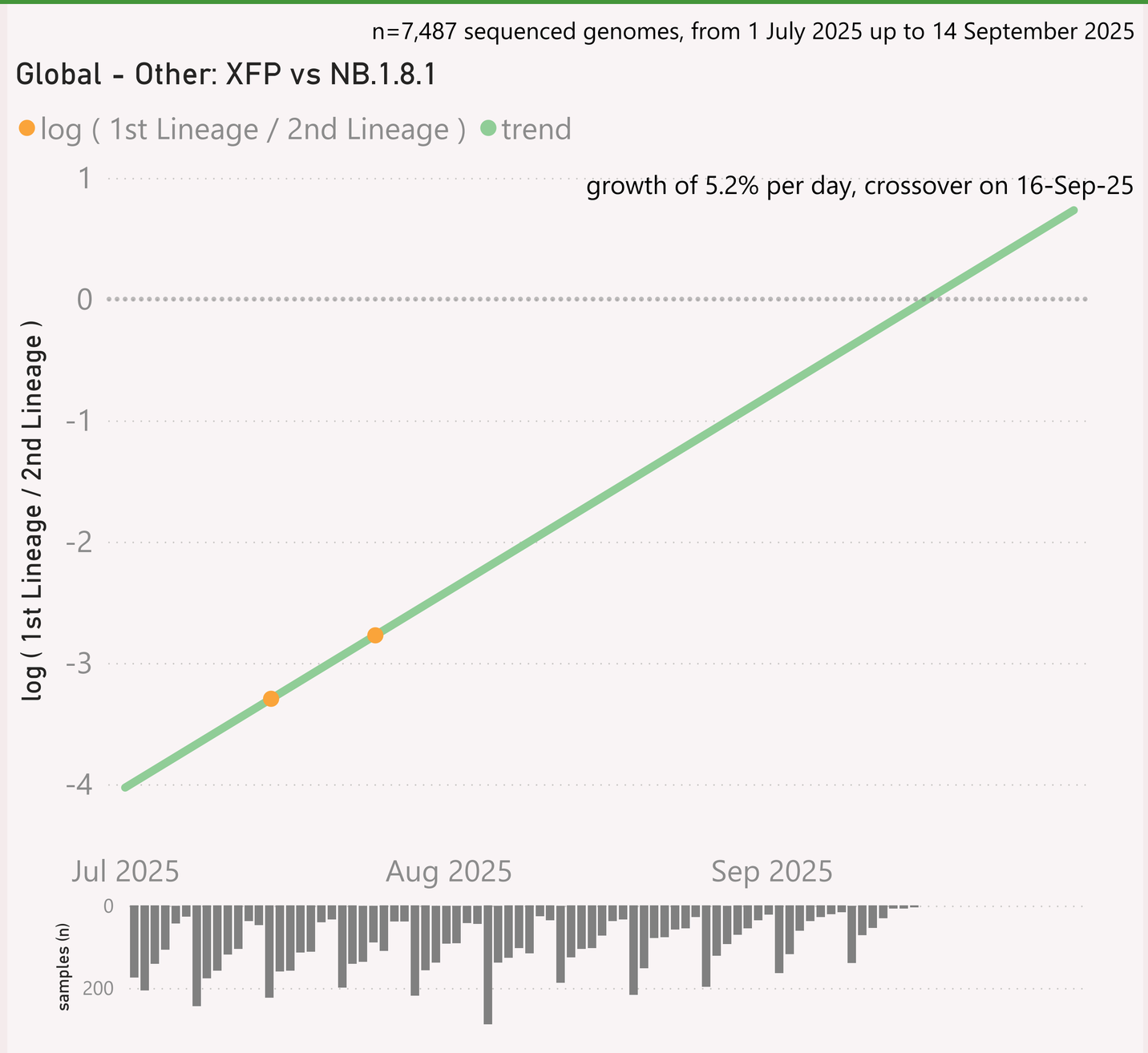


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

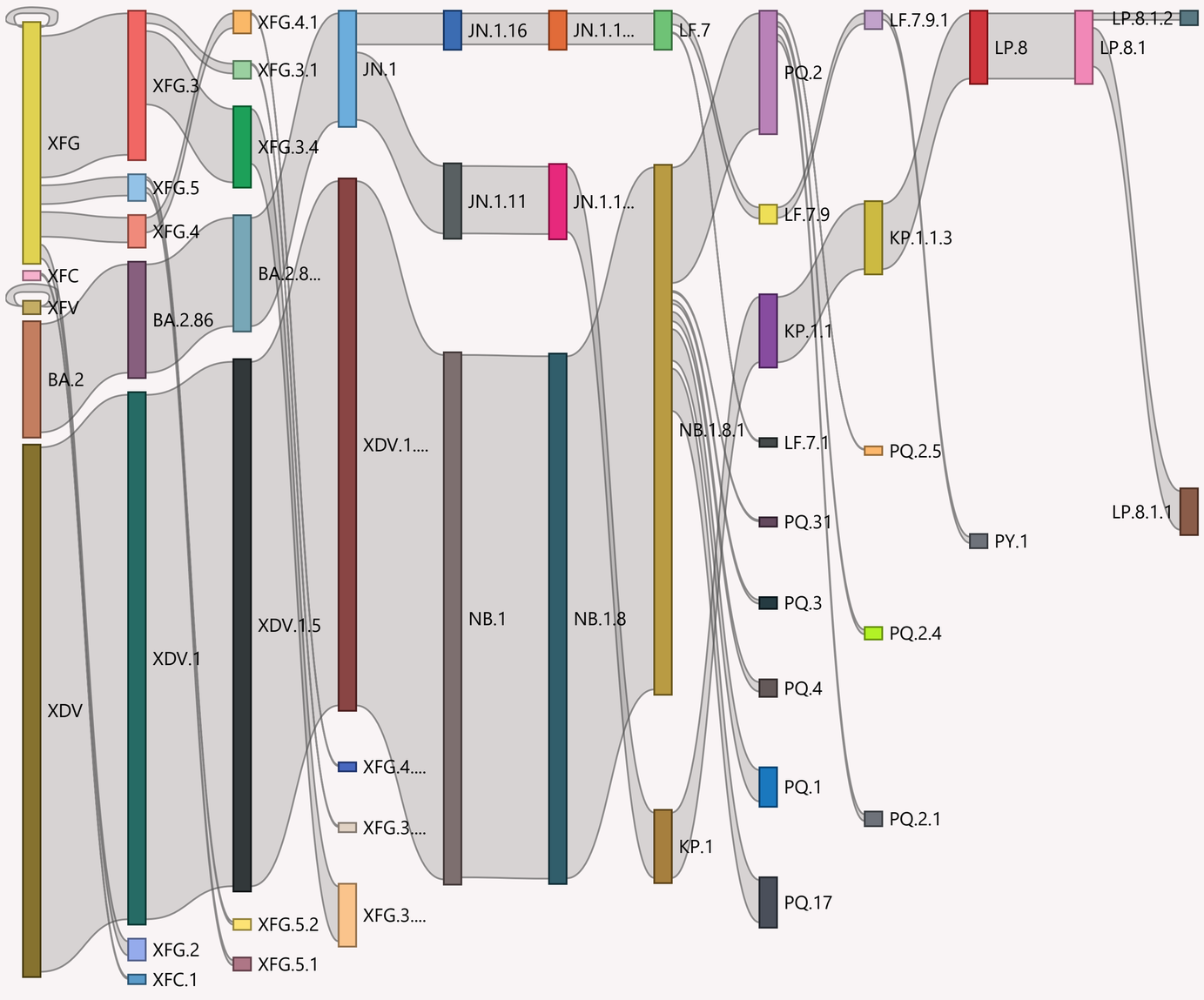
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

n=11,902 sequenced genomes, from 1 June 2025 up to 14 September 2025

Global - Other



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: 2025-10-04 06:40 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
China	1,279	14/09/2025		24/09/2025	
South Korea	1,244	11/09/2025		24/09/2025	
Brazil	1,109	14/09/2025		24/09/2025	
Japan	848	13/09/2025		24/09/2025	
Puerto Rico	358	14/09/2025		24/09/2025	
Costa Rica	275	04/09/2025		24/09/2025	
India	266	16/07/2025		24/09/2025	
Malaysia	218	11/09/2025		24/09/2025	
Singapore	203	20/08/2025		25/08/2025	
Mexico	158	10/07/2025		19/09/2025	
Taiwan	102	27/08/2025		11/09/2025	
Hong Kong	97	13/09/2025		24/09/2025	
Thailand	90	05/09/2025		24/09/2025	
Bahrain	73	07/09/2025		21/09/2025	
Chile	72	13/09/2025		24/09/2025	
Ecuador	71	12/09/2025		24/09/2025	
Oman	55	03/07/2025		24/09/2025	
Kazakhstan	51	29/07/2025		11/09/2025	
South Africa	50	25/08/2025		24/09/2025	
Qatar	45	12/07/2025		28/08/2025	
Egypt	42	03/09/2025		18/09/2025	
Brunei	30	08/07/2025		09/09/2025	
Guatemala	30	08/08/2025		29/08/2025	
Lebanon	21	20/08/2025		19/09/2025	
French Guiana	20	08/09/2025		24/09/2025	
Guam	20	18/08/2025		26/08/2025	
Barbados	19	28/08/2025		08/09/2025	
Myanmar	17	12/09/2025		24/09/2025	
Total	**7,027**	**14/09/2025**		**24/09/2025**	

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.