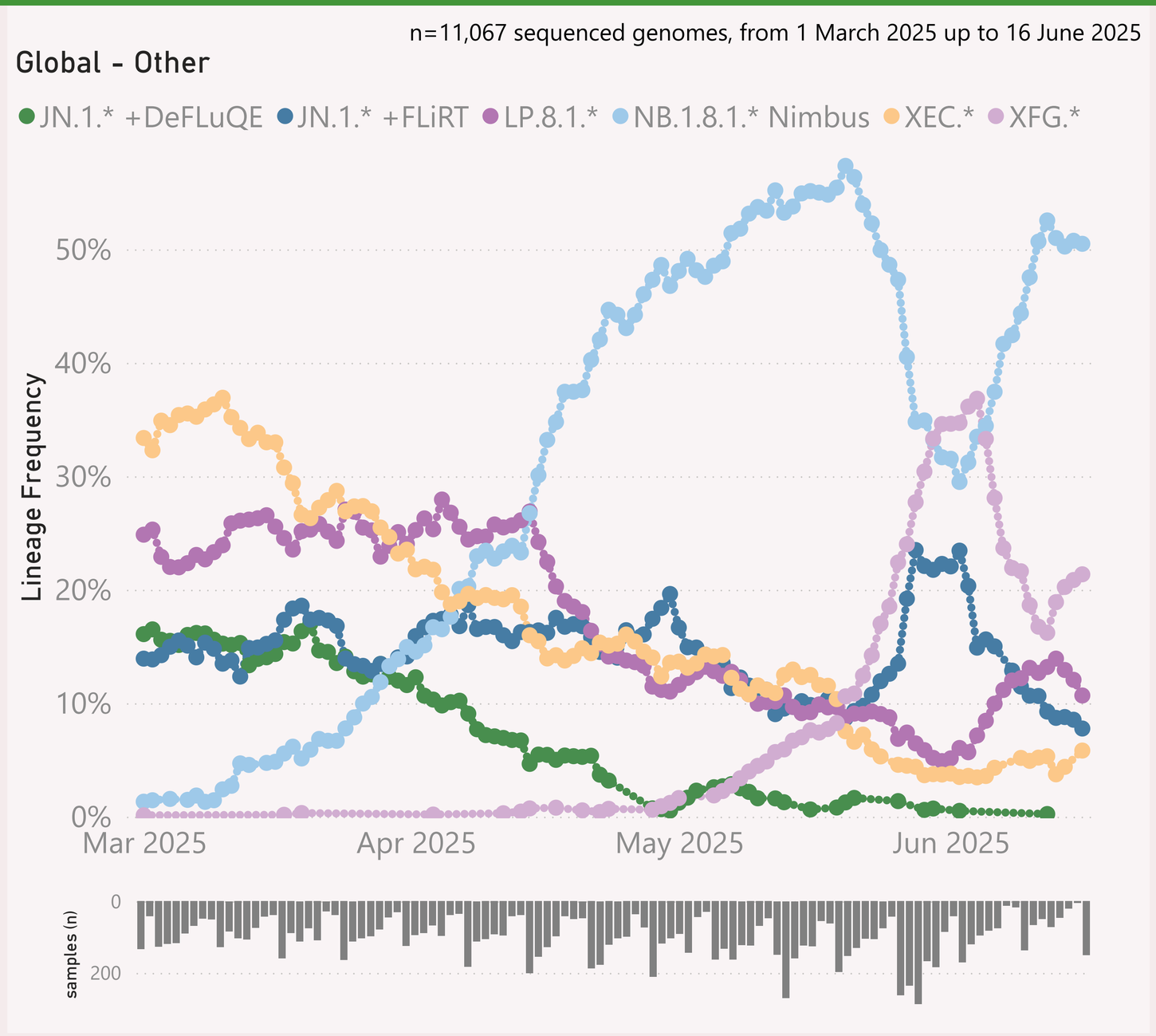
n=11,067 sequenced genomes, from 1 March 2025 up to 16 June 2025



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

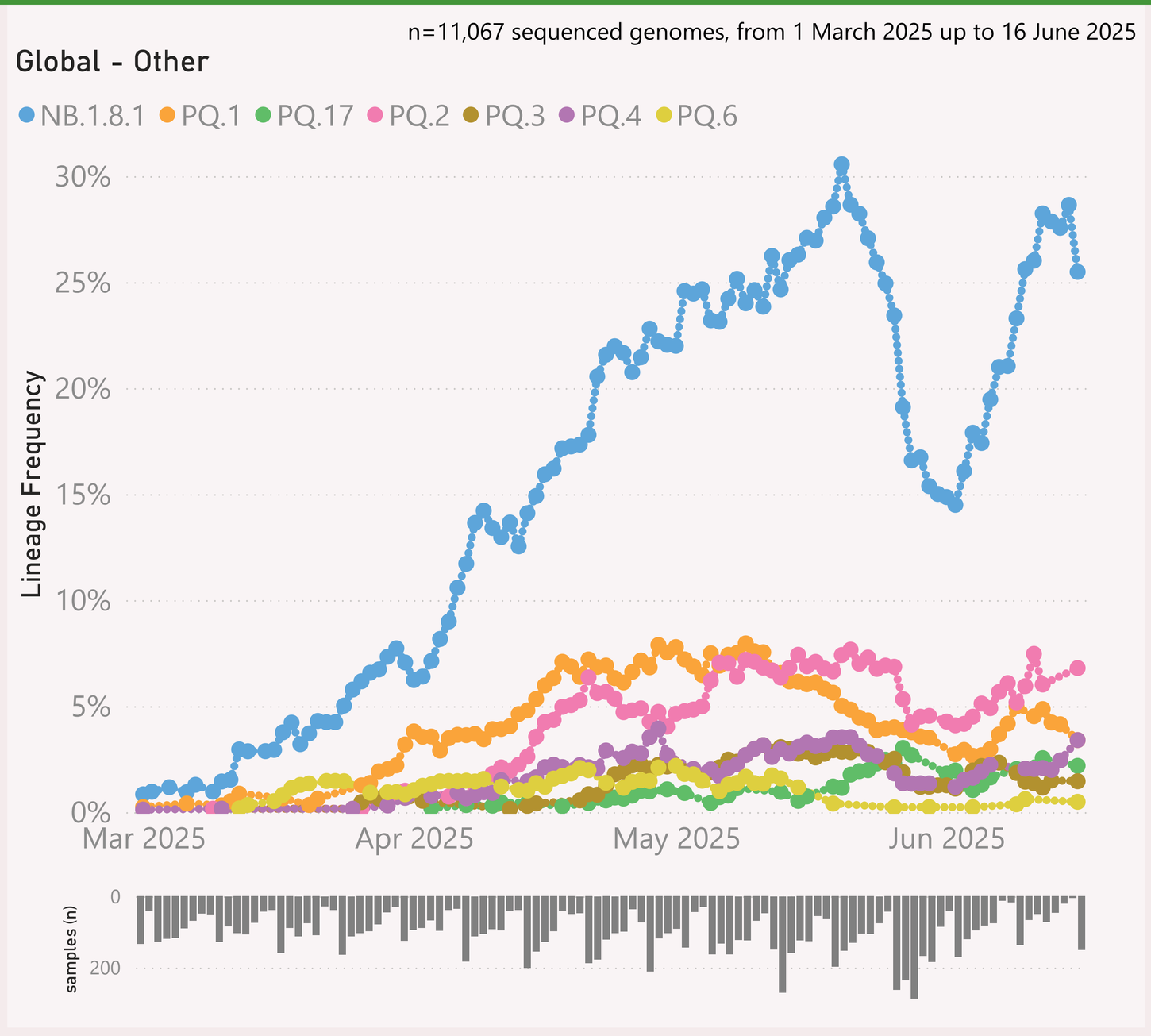
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.



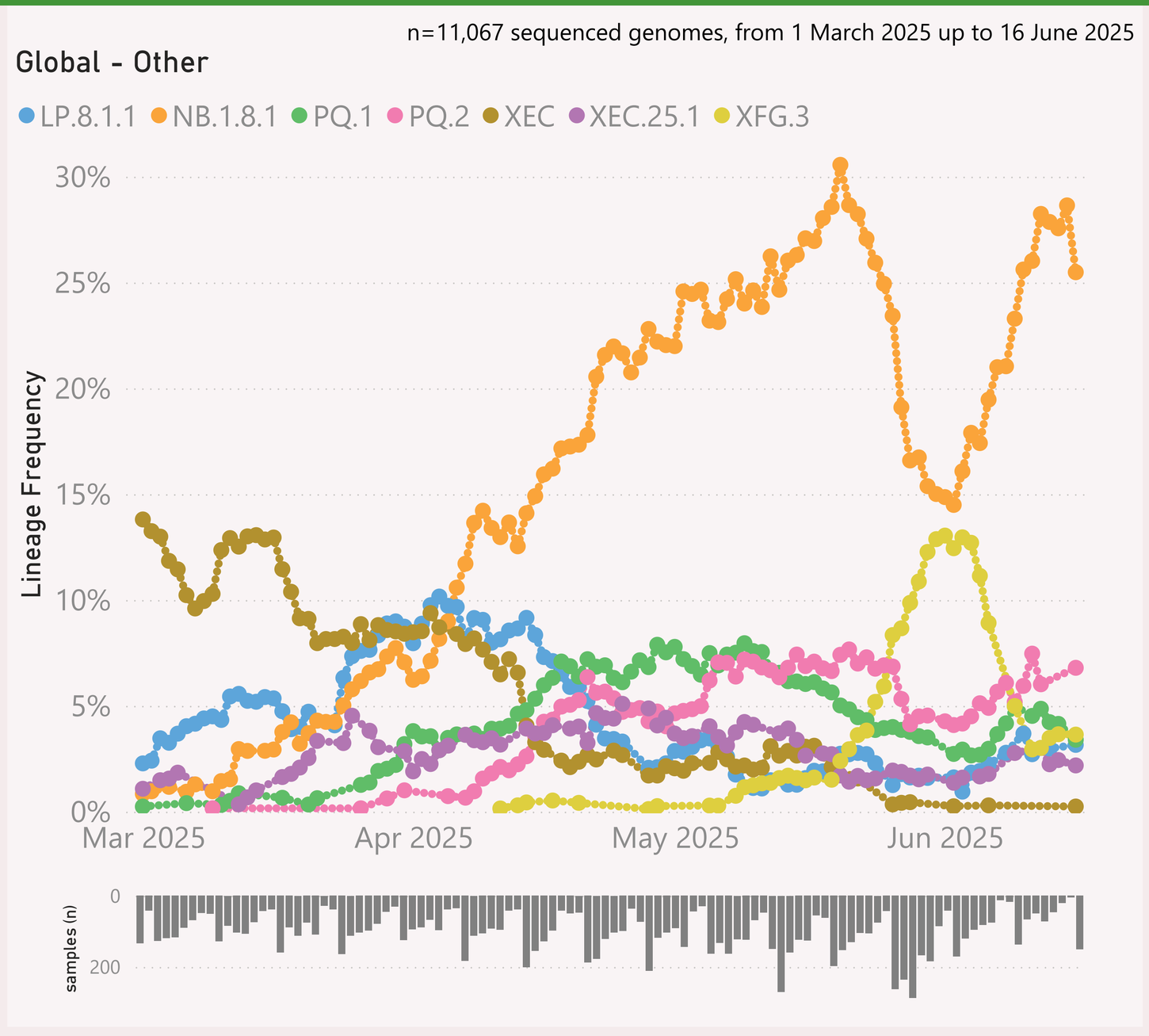
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.* Nimbus.

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.

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.

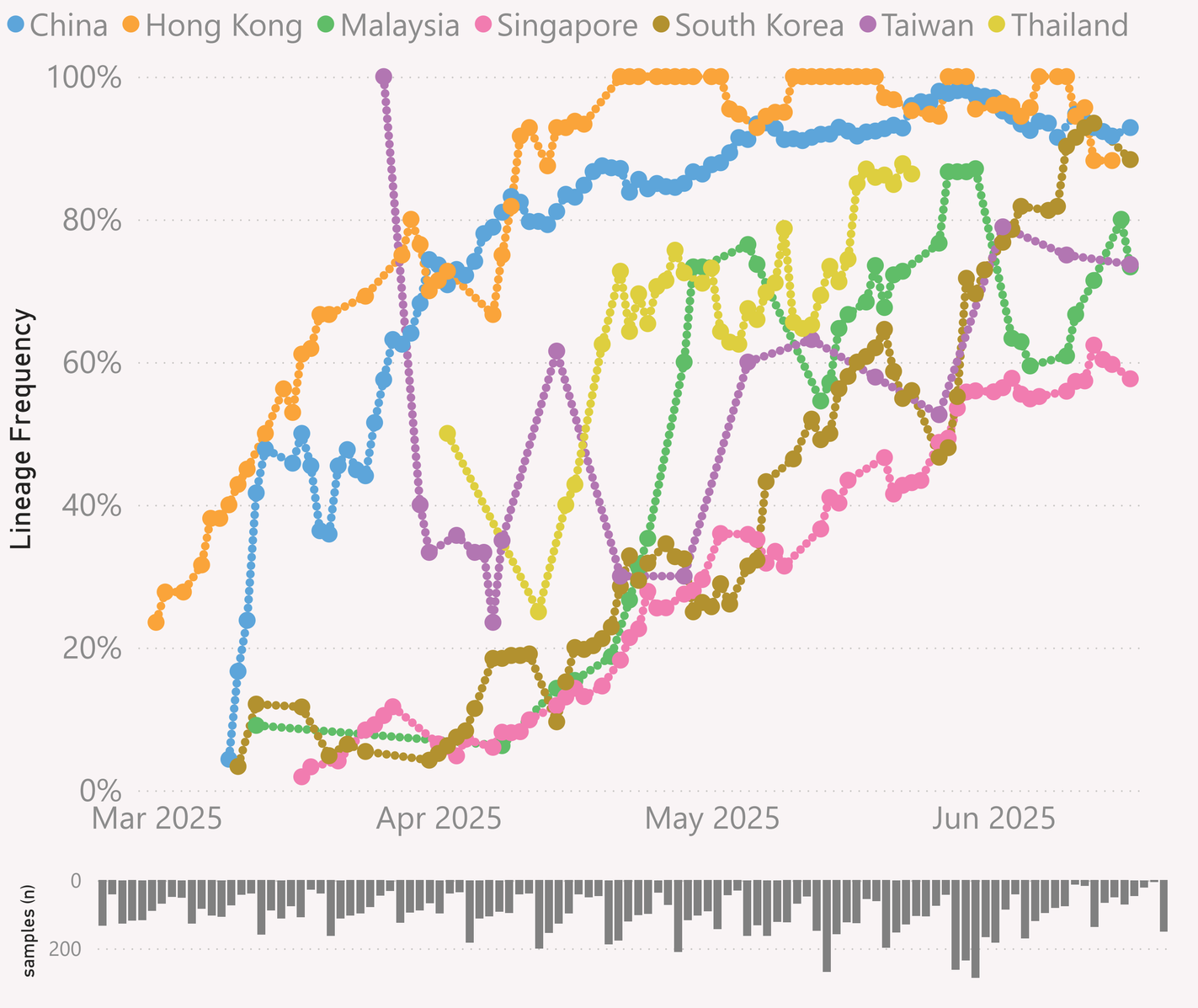
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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.

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

n=11,067 sequenced genomes, from 1 March 2025 up to 16 June 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.

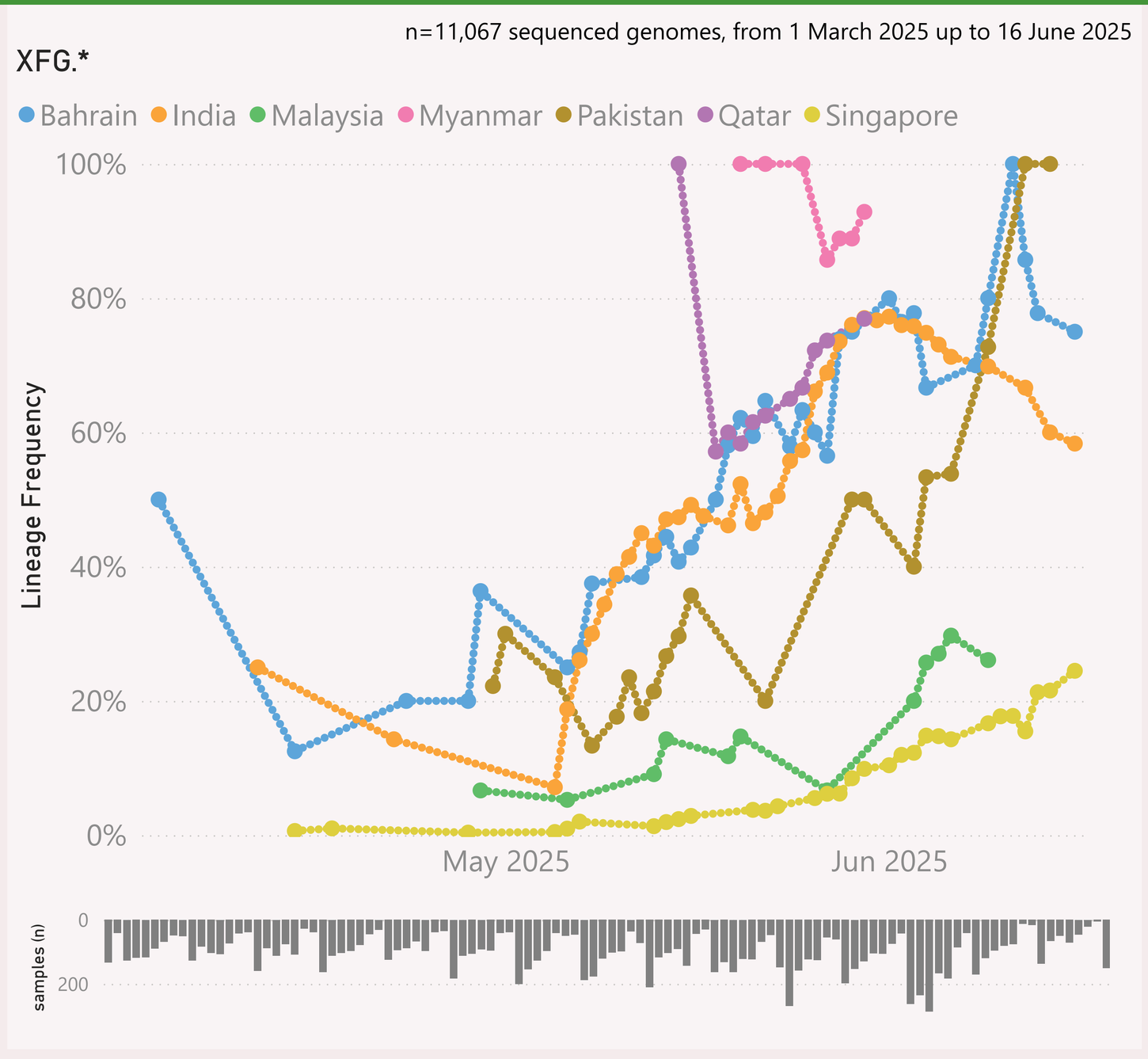
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.



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.

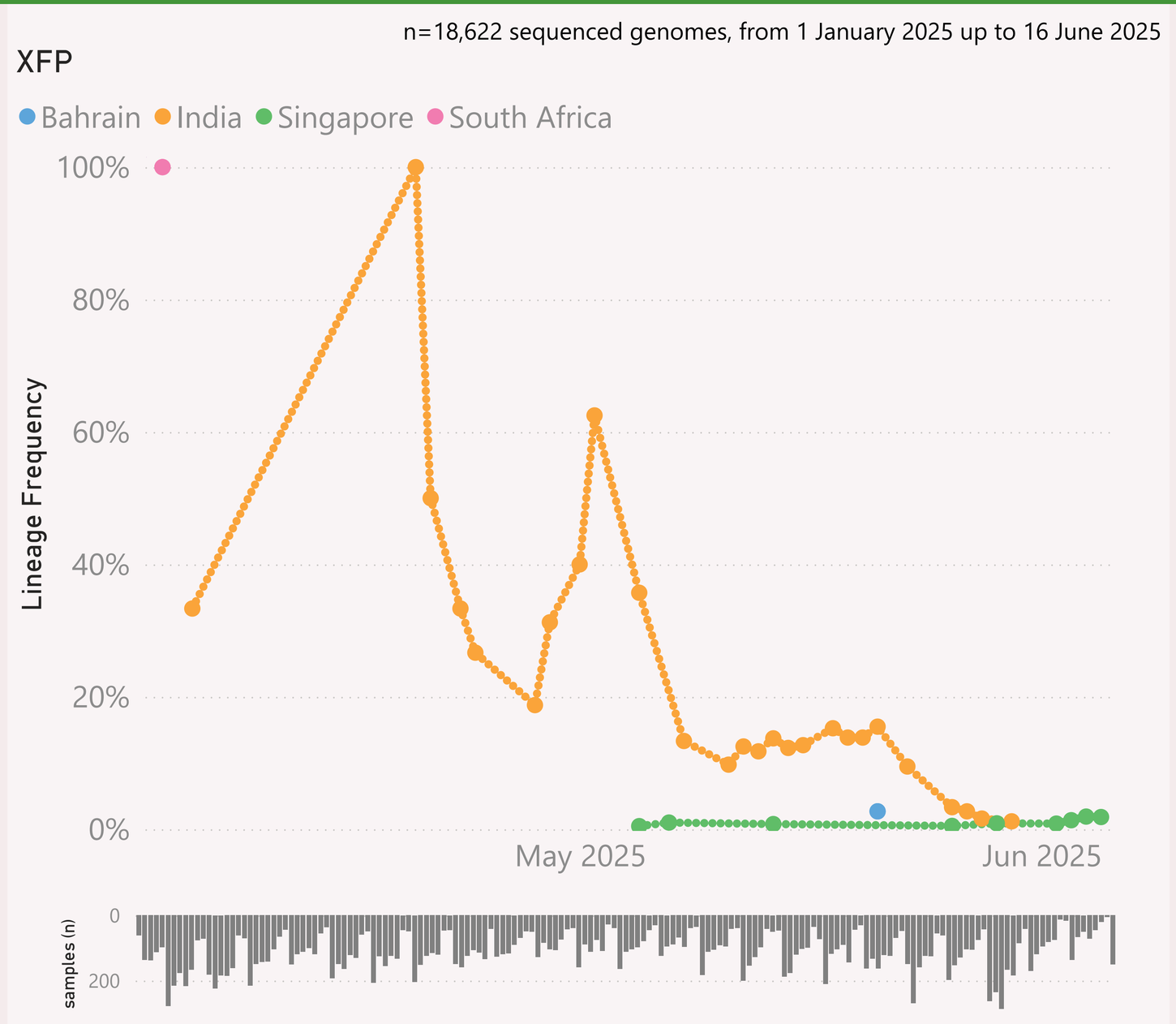
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

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.

COVID-19 Genomic Sequencing analysis - selected Lineage by Country. Data from gisaid.org, with nextclade lineages Source files and info on github. Last Update: 2025-07-12 13:59 (UTC)

n=18,622 sequenced genomes, from 1 January 2025 up to 16 June 2025



Date

01/01/2025 31/12/2025

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

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

Host

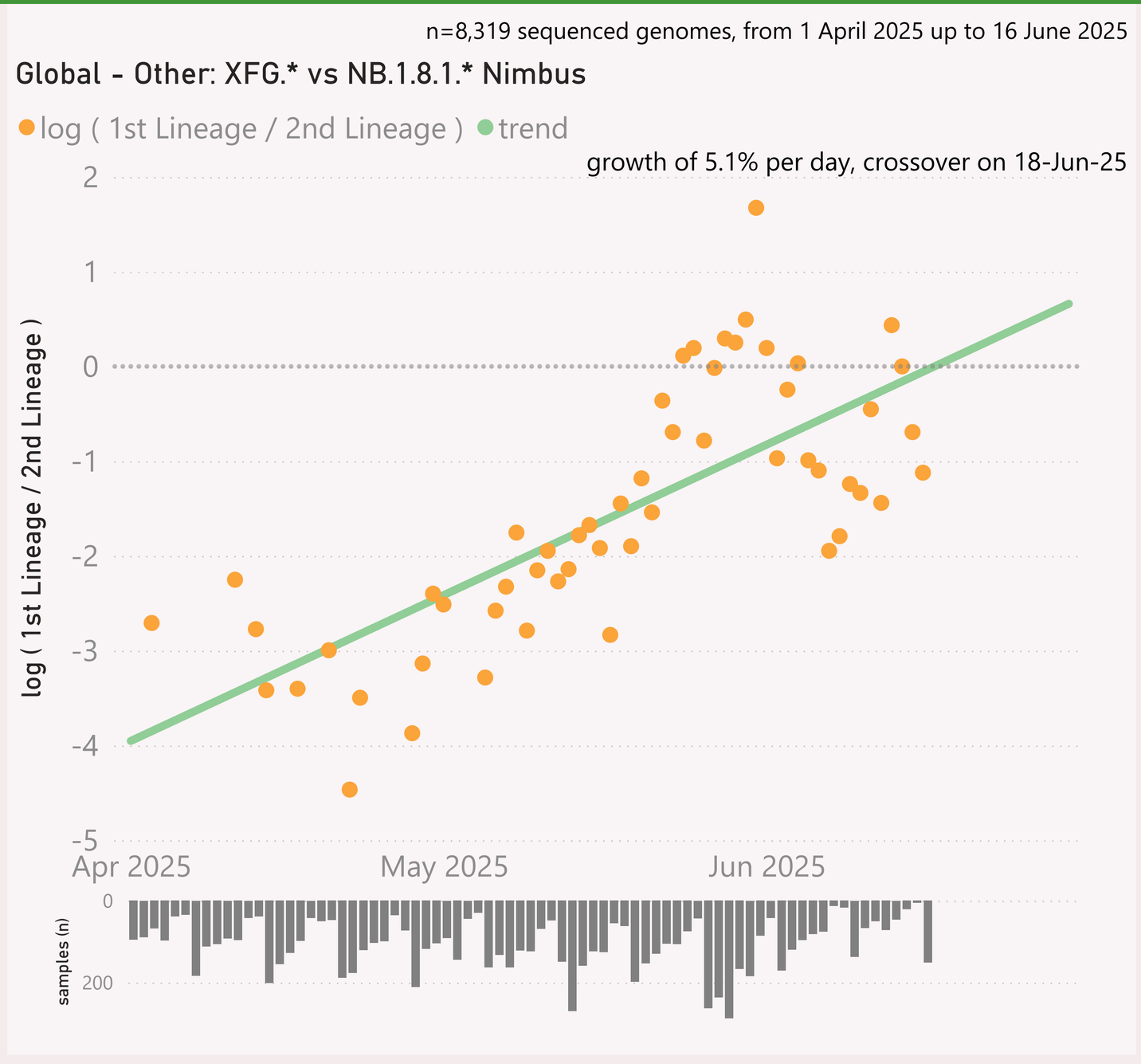
Human

Samples Sequenced (gisaid)

47

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
Singapore			05/06/2025	XFP.*	XFP
Singapore			04/06/2025	XFP.*	XFP
Singapore			03/06/2025	XFP.*	XFP
Singapore			02/06/2025	XFP.*	XFP
India	Maharashtra		30/05/2025	XFP.*	XFP
Singapore			29/05/2025	XFP.*	XFP
India	Madhya Pradesh		28/05/2025	XFP.*	XFP
India	Maharashtra	Othe...	28/05/2025	XFP.*	XFP
India	Andhra Pradesh		27/05/2025	XFP.*	XFP
Singapore			26/05/2025	XFP.*	XFP
India	Gujarat		26/05/2025	XFP.*	XFP
India	Karnataka		23/05/2025	XFP.*	XFP
Bahrain			21/05/2025	XFP.*	XFP
India	Maharashtra	Othe...	21/05/2025	XFP.*	XFP
India	Tamil Nadu		21/05/2025	XFP.*	XFP
India	Tamil Nadu		20/05/2025	XFP.*	XFP
India	Maharashtra		19/05/2025	XFP.*	XFP
India	Tamil Nadu		19/05/2025	XFP.*	XFP
India	Tamil Nadu		18/05/2025	XFP.*	XFP
India	Tamil Nadu		16/05/2025	XFP.*	XFP
India	Kerala		15/05/2025	XFP.*	XFP
India	Tamil Nadu		15/05/2025	XFP.*	XFP

Total



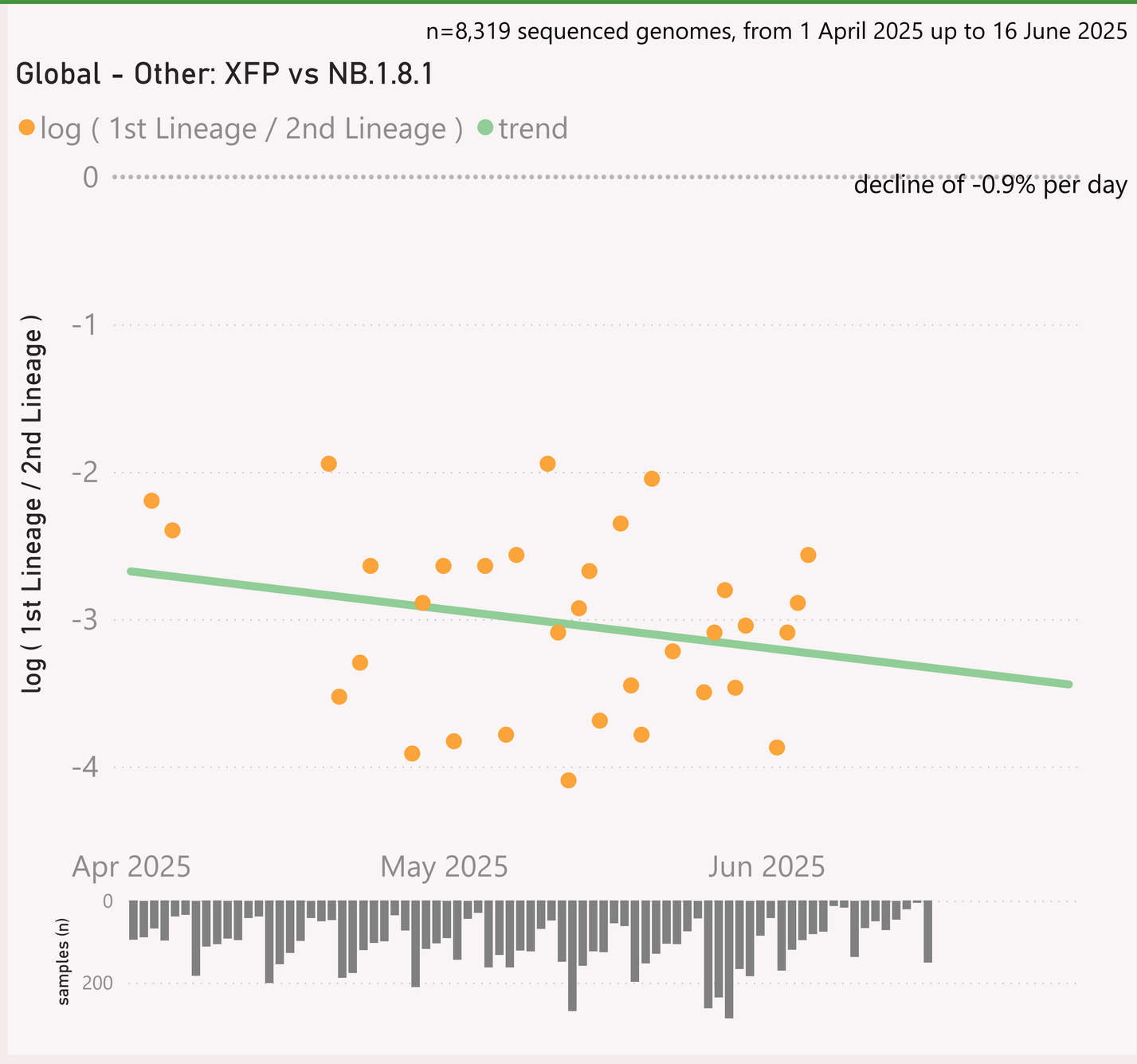
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

n=8,319 sequenced genomes, from 1 April 2025 up to 16 June 2025



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

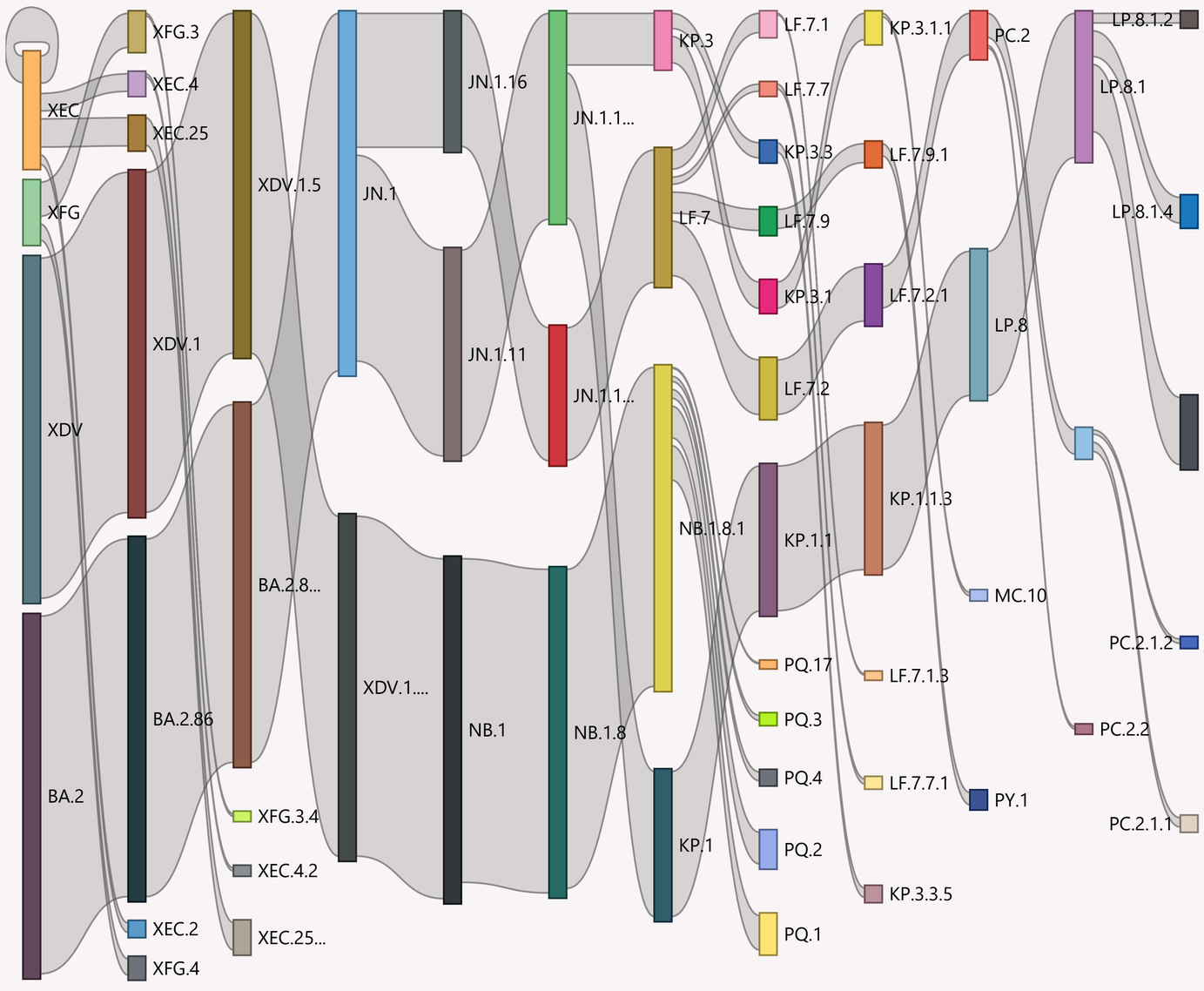
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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=11,067 sequenced genomes, from 1 March 2025 up to 16 June 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: 2025-07-12 13:59 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
China	2,041	16/06/2025		27/06/2025	
Singapore	1,620	16/06/2025		27/06/2025	
India	843	16/06/2025		27/06/2025	
Japan	687	16/06/2025		27/06/2025	
Brazil	684	16/06/2025		27/06/2025	
Mexico	623	16/06/2025		27/06/2025	
Kenya	375	28/01/2025		27/06/2025	
Malaysia	371	16/06/2025		27/06/2025	
South Korea	371	16/06/2025		27/06/2025	
Thailand	281	23/05/2025		30/05/2025	
Kazakhstan	218	28/05/2025		27/06/2025	
Costa Rica	182	14/06/2025		27/06/2025	
Bahrain	162	16/06/2025		27/06/2025	
Hong Kong	154	14/06/2025		27/06/2025	
Puerto Rico	127	16/06/2025		26/06/2025	
Taiwan	115	16/06/2025		27/06/2025	
Pakistan	90	14/06/2025		27/06/2025	
Israel	88	01/05/2025		27/06/2025	
South Africa	84	05/06/2025		27/06/2025	
Argentina	81	31/03/2025		22/05/2025	
Ghana	60	13/06/2025		27/06/2025	
Vietnam	51	30/05/2025		18/06/2025	
Qatar	40	30/05/2025		16/06/2025	
Guatemala	38	27/05/2025		27/06/2025	
Paraguay	36	13/01/2025		26/06/2025	
French Guiana	34	11/06/2025		23/06/2025	
Egypt	31	27/04/2025		19/06/2025	
Senegal	24	28/04/2025		27/06/2025	
Total	**9,747**	**16/06/2025**		**27/06/2025**	

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.