n=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

Global - Other

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

This "Global - Other" report aggregates the available data from countries besides those I regularly report on: Australia, NZ, the US, Canada and Europ.
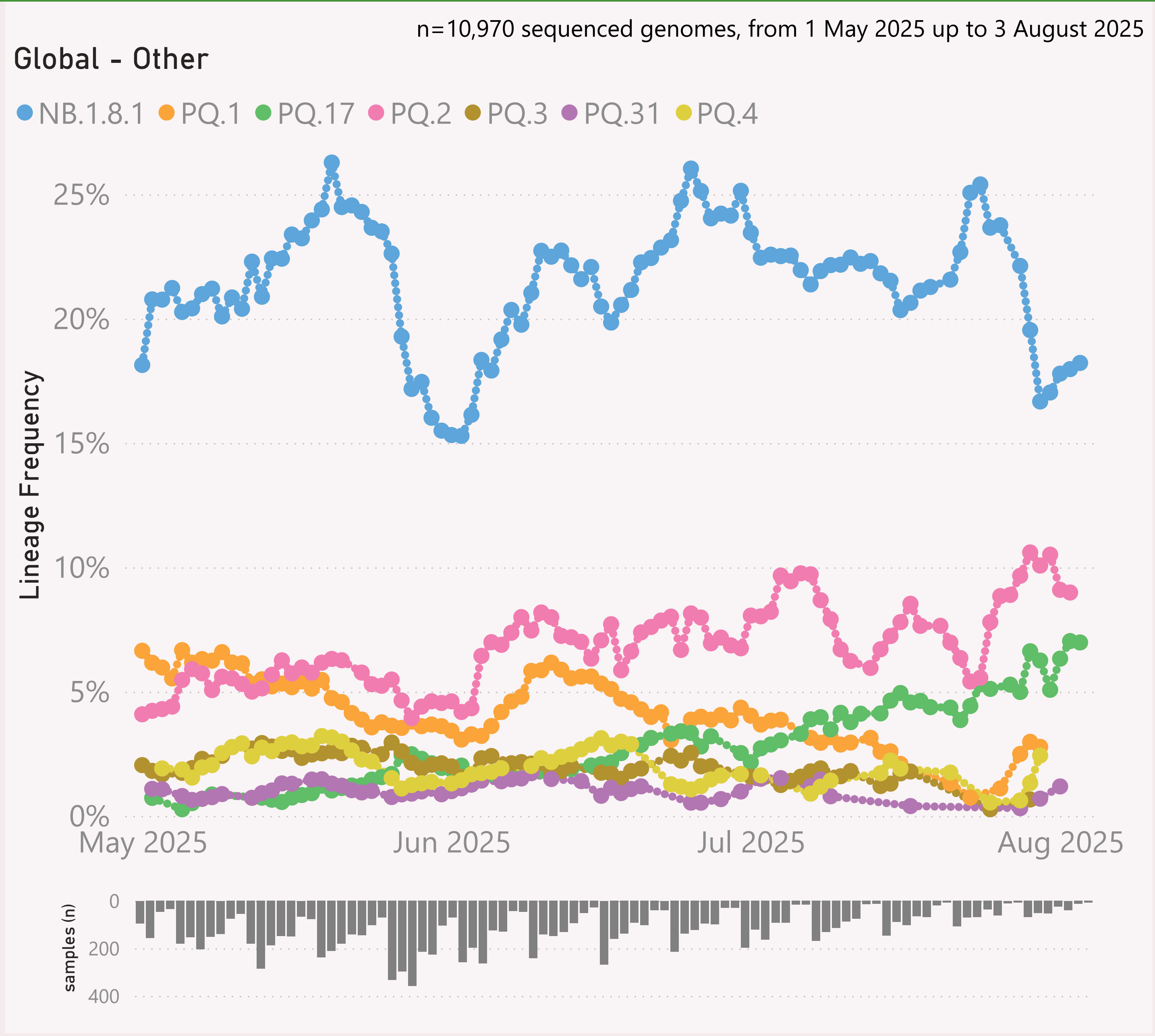
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

Global - Other

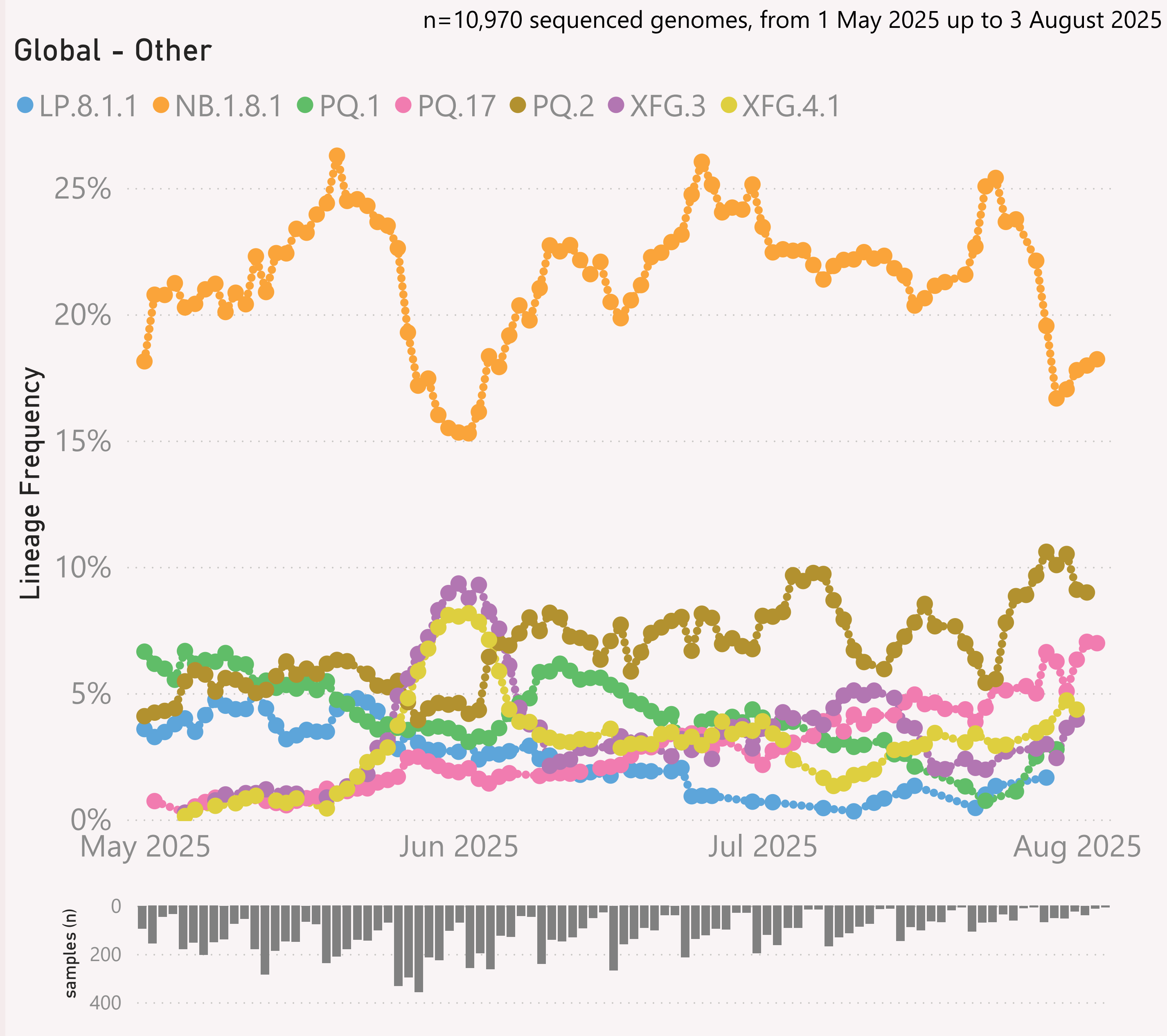- ● NB.1.8.1 ● PQ.1 ● PQ.17 ● PQ.2 ● PQ.3 ● PQ.31 ● PQ.4

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.

n=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

Global - Other

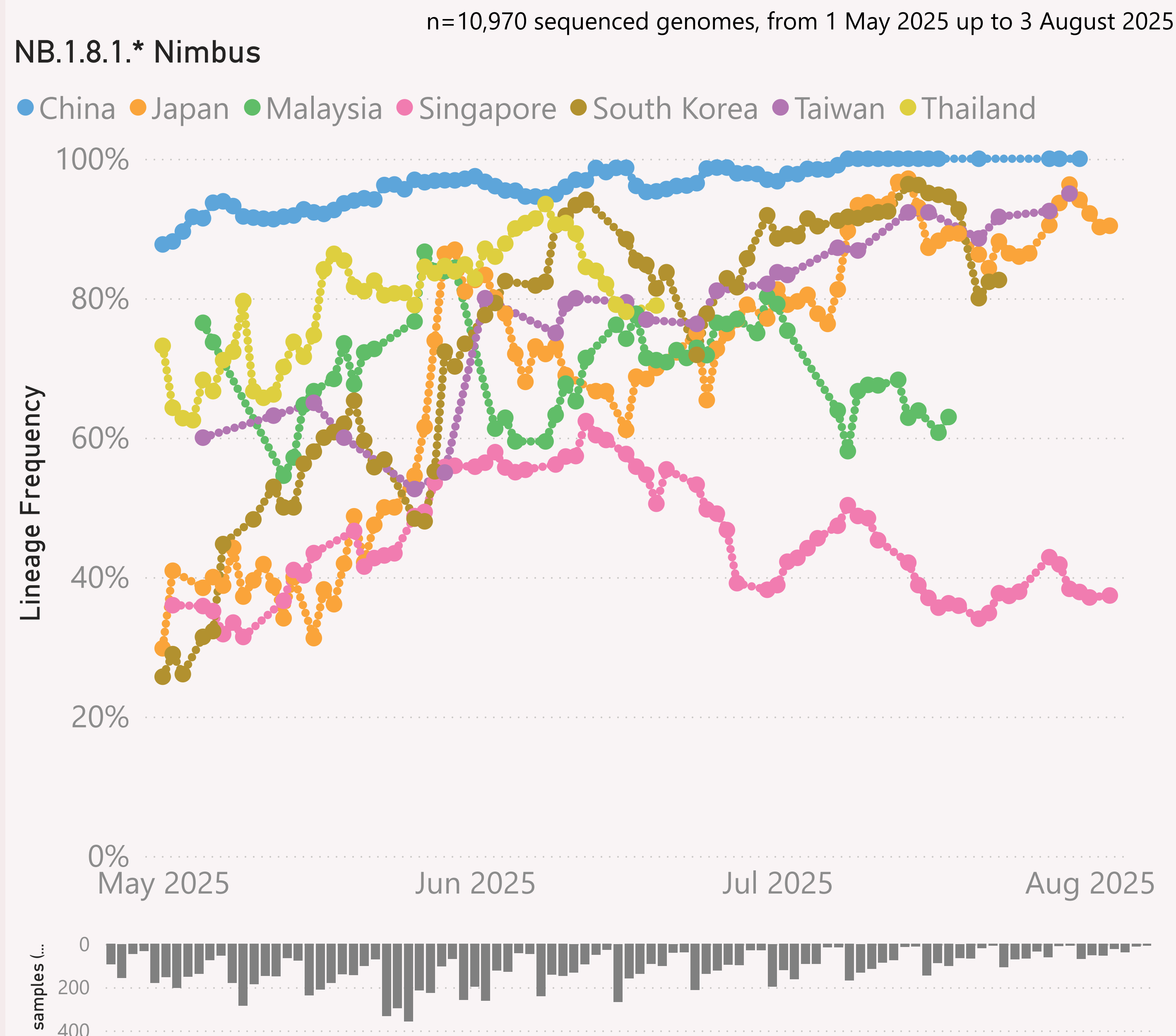● LP.8.1.1 ● NB.1.8.1 ● PQ.1 ● PQ.17 ● PQ.2 ● XFG.3 ● XFG.4.1

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.

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

n=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

NB.1.8.1.* Nimbus

● China ● Japan ● Malaysia ● Singapore ● South Korea ● Taiwan ● Thailand

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.
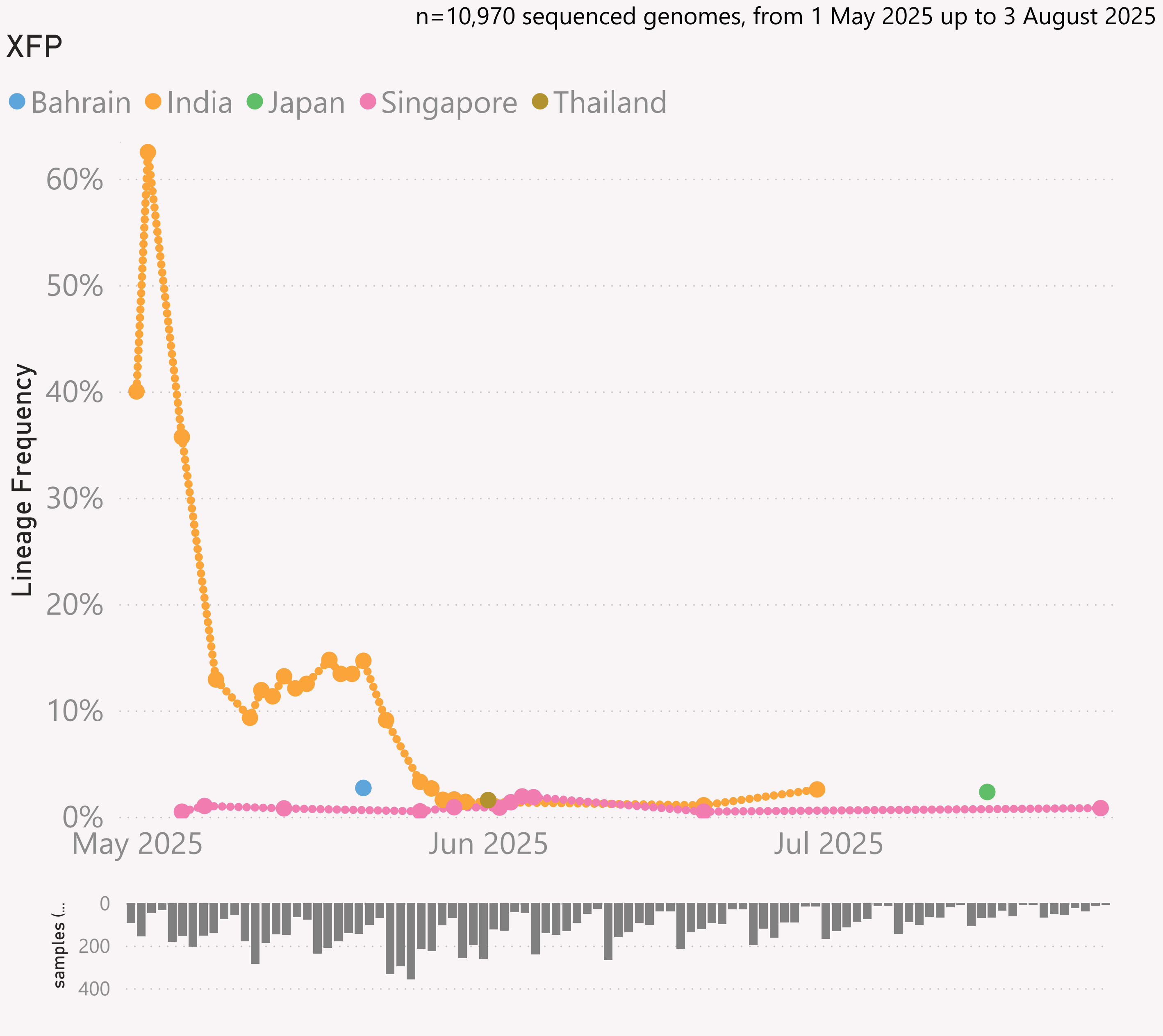
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

XFG.*

● Bahrain ● Brazil ● Costa Rica ● India ● Malaysia ● Puerto Rico ● Singapore

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.

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n=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

XFP

- ● Bahrain ● India ● Japan ● Singapore ● Thailand

Date

01/01/2025   31/12/2025

Host

Human

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

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

 # Samples Sequenced (gisaid)

45

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
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
India	Maharashtra		30/05/2025	XFP.*	XFP
Singapore			29/05/2025	XFP.*	XFP
India	Karnataka		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
Total					

n=10,911 sequenced genomes, from 1 May 2025 up to 31 July 2025

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

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

growth of 2.2% per day, crossover on 28-Jul-25
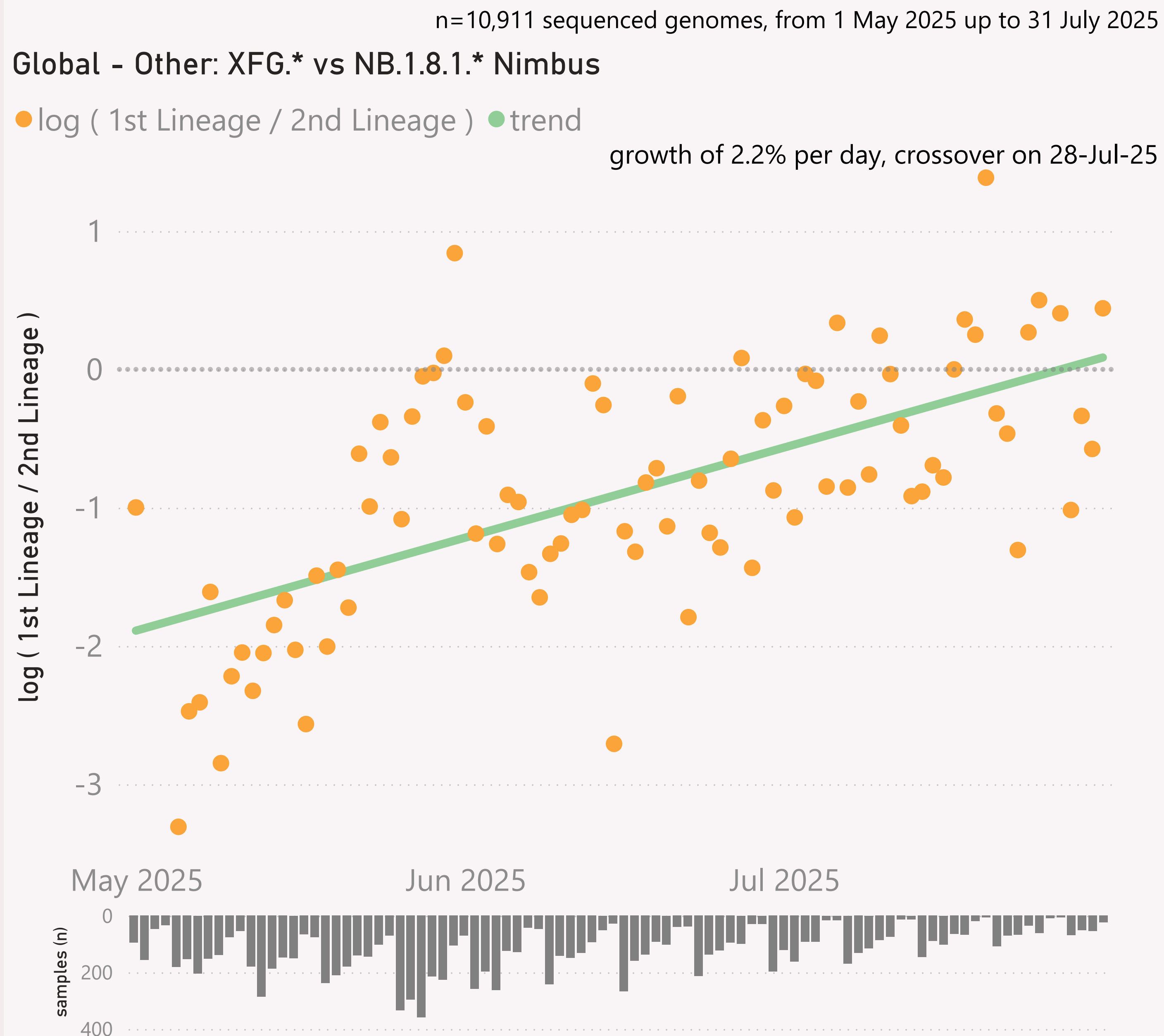
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

n=10,911 sequenced genomes, from 1 May 2025 up to 31 July 2025

Global – Other: XFP vs NB.1.8.1

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

growth of 0.6% per day
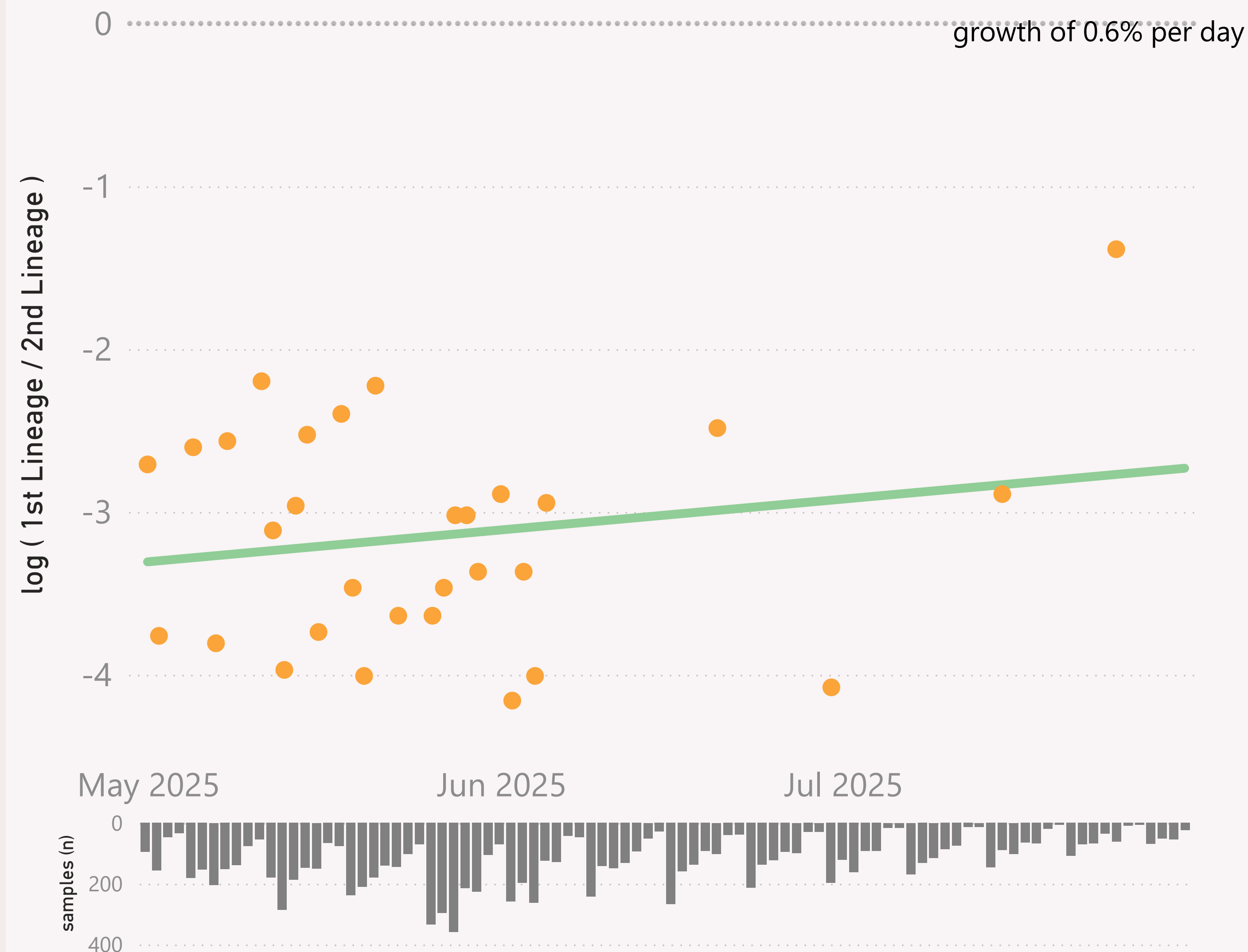
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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=10,970 sequenced genomes, from 1 May 2025 up to 3 August 2025

Global - Other
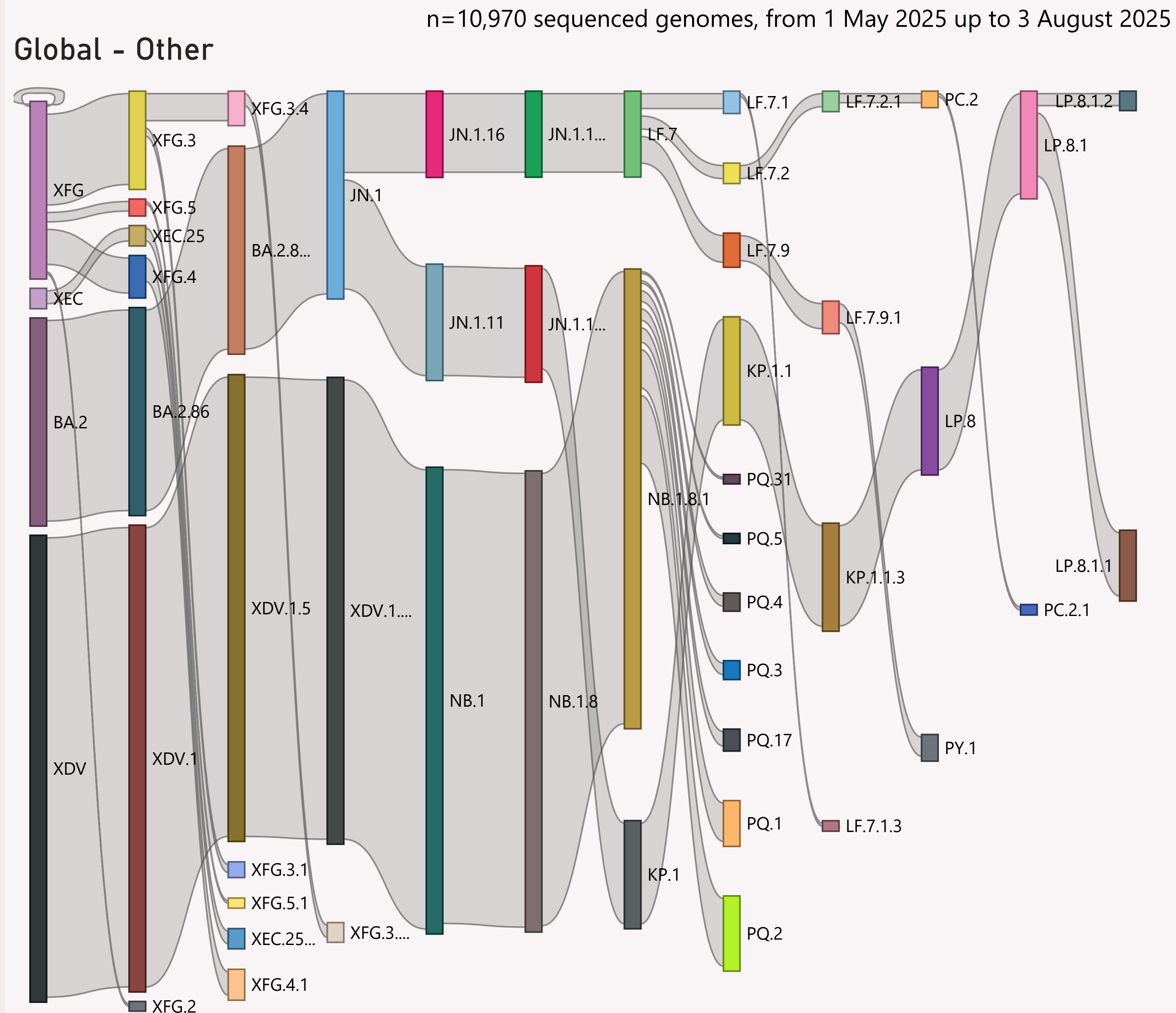
This page shows the hierarchy of the significant Lineages, over recent months.
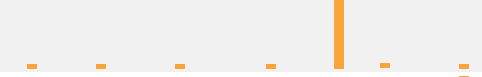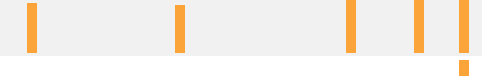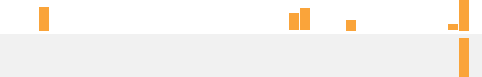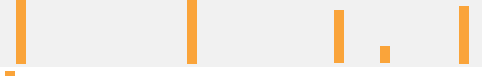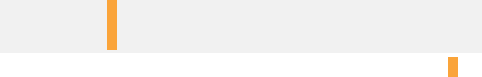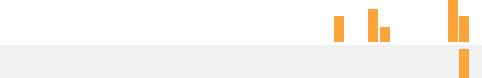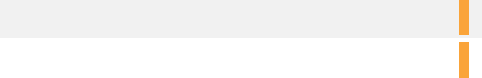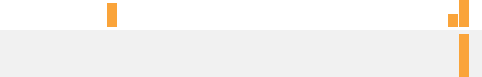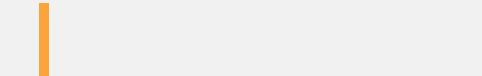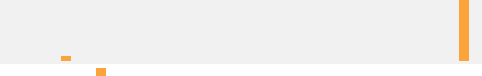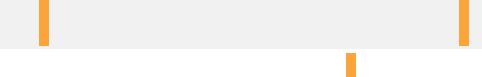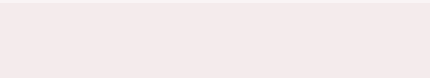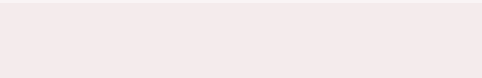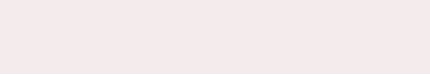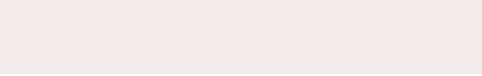
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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: 2025-08-23 01:55 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ Singapore	1,556	03/08/2025		08/08/2025	
⊞ China	1,141	31/07/2025		08/08/2025	
⊞ Mexico	529	19/06/2025		08/08/2025	
⊞ Costa Rica	379	25/07/2025		08/08/2025	
⊞ Japan	367	03/08/2025		08/08/2025	
⊞ Brazil	349	03/08/2025		08/08/2025	
⊞ India	347	03/07/2025		08/08/2025	
⊞ South Korea	339	23/07/2025		08/08/2025	
⊞ Taiwan	333	30/07/2025		01/08/2025	
⊞ Malaysia	276	18/07/2025		08/08/2025	
⊞ Thailand	235	19/06/2025		14/07/2025	
⊞ Puerto Rico	187	02/08/2025		08/08/2025	
⊞ Cambodia	118	04/07/2025		05/08/2025	
⊞ Hong Kong	111	03/08/2025		08/08/2025	
⊞ Bahrain	89	21/06/2025		29/06/2025	
⊞ Ghana	55	27/06/2025		08/07/2025	
⊞ Laos	47	29/07/2025		08/08/2025	
⊞ Dominican	46	01/08/2025		08/08/2025	
⊞ Guatemala	42	18/07/2025		08/08/2025	
⊞ South Africa	37	03/08/2025		08/08/2025	
⊞ Nepal	31	22/07/2025		28/07/2025	
⊞ Kenya	29	14/07/2025		08/08/2025	
⊞ Vietnam	28	27/06/2025		13/07/2025	
⊞ Venezuela	21	18/06/2025		02/07/2025	
⊞ Guam	20	30/07/2025		08/08/2025	
⊞ Kazakhstan	19	16/07/2025		08/08/2025	
⊞ Indonesia	17	23/07/2025		08/08/2025	
⊞ New Caledonia	14	28/07/2025		08/08/2025	
Total	**6,838**	**03/08/2025**		**08/08/2025**	

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.