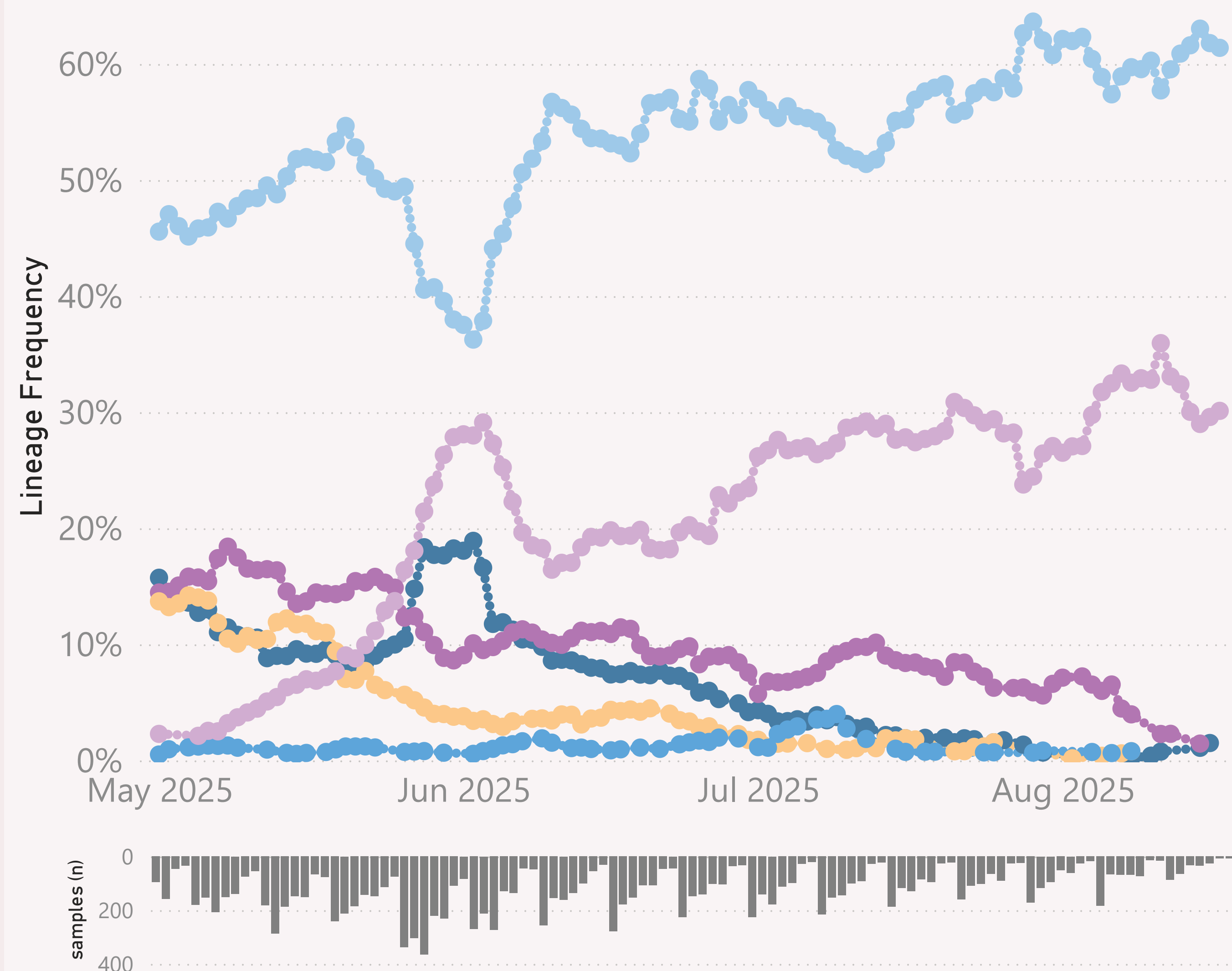


n=12,998 sequenced genomes, from 1 May 2025 up to 17 August 2025

## 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.

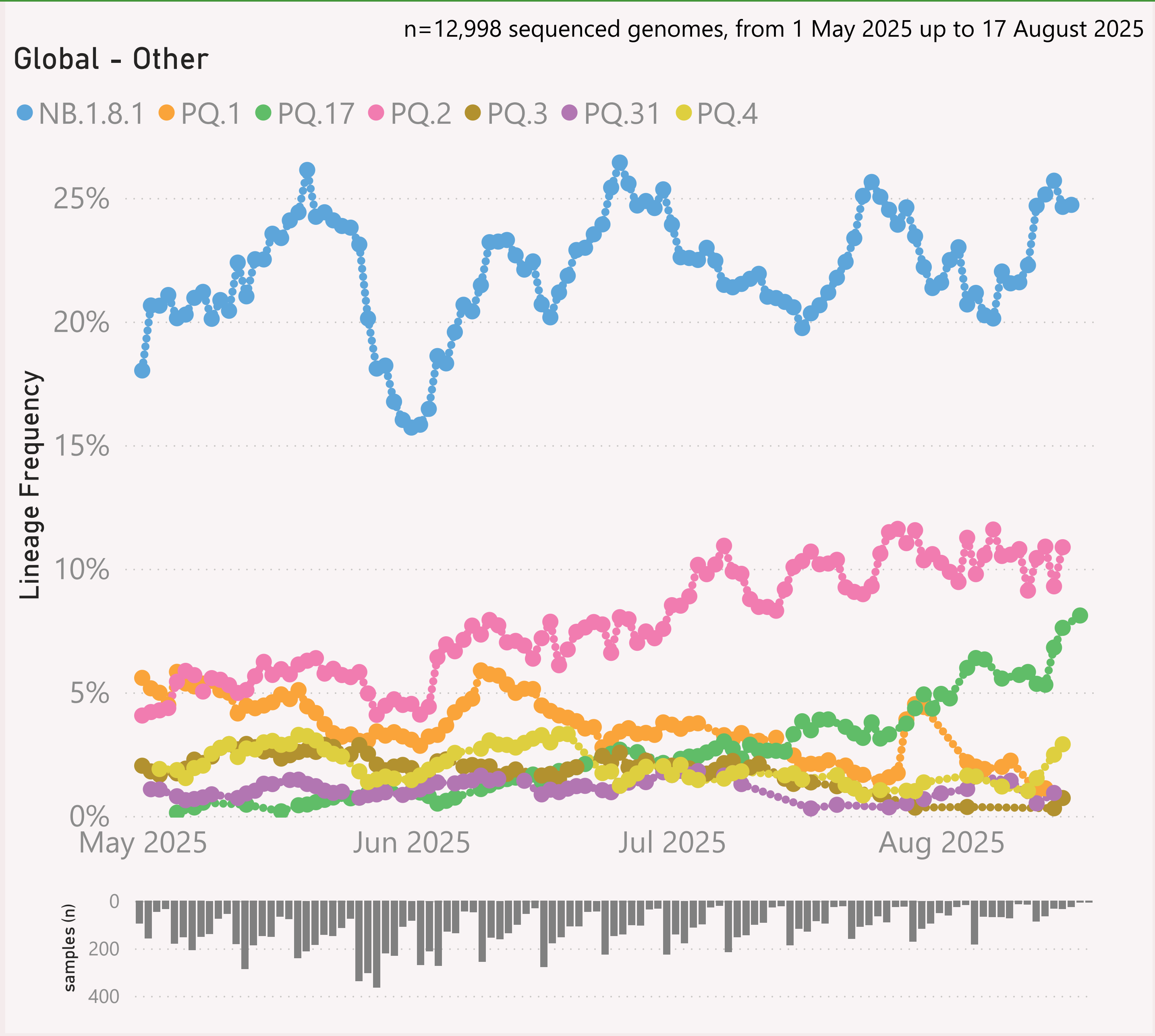
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.



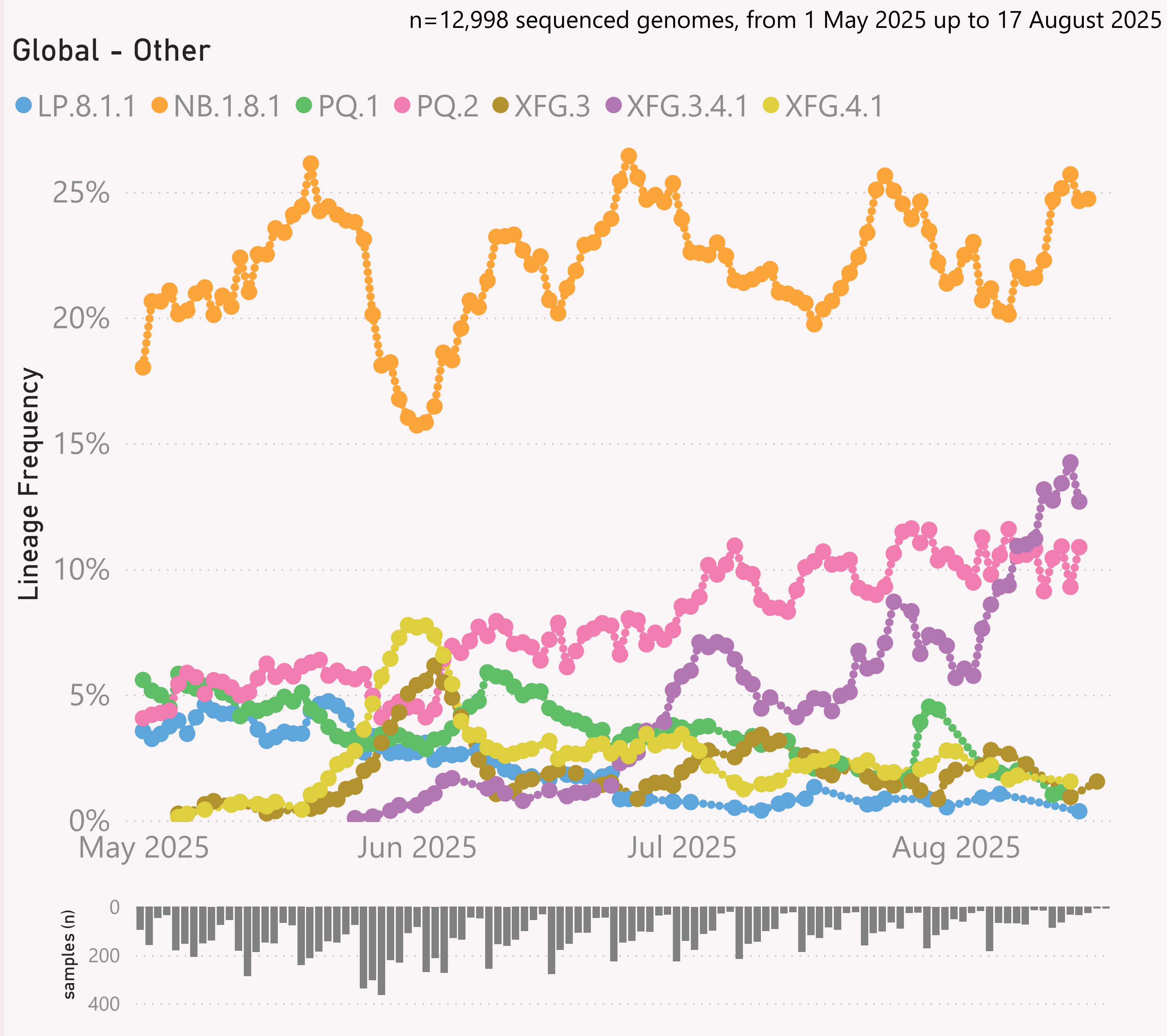
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.\* Nimbus.

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.

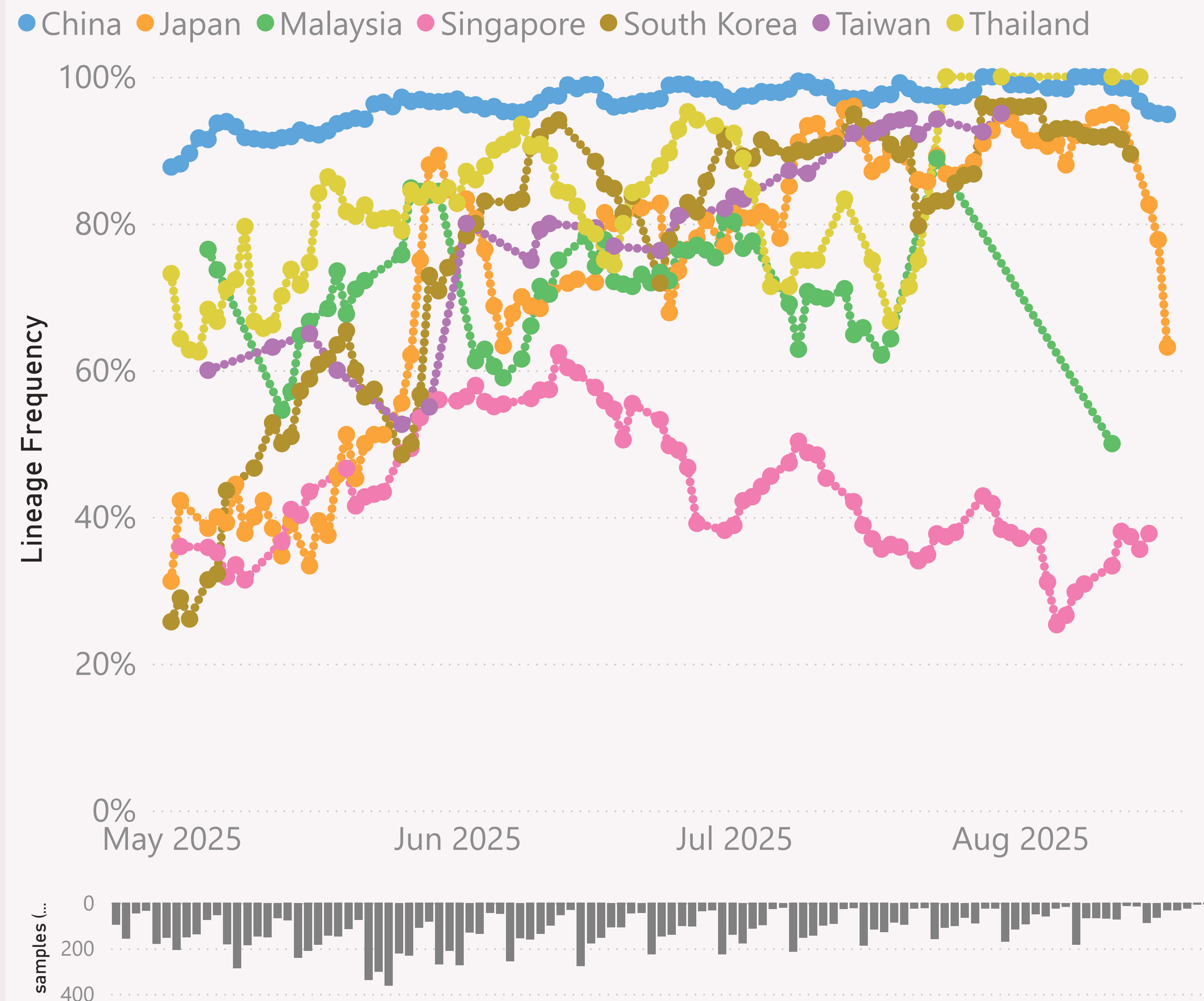
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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



n=12,998 sequenced genomes, from 1 May 2025 up to 17 August 2025

## NB.1.8.1.\* Nimbus



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

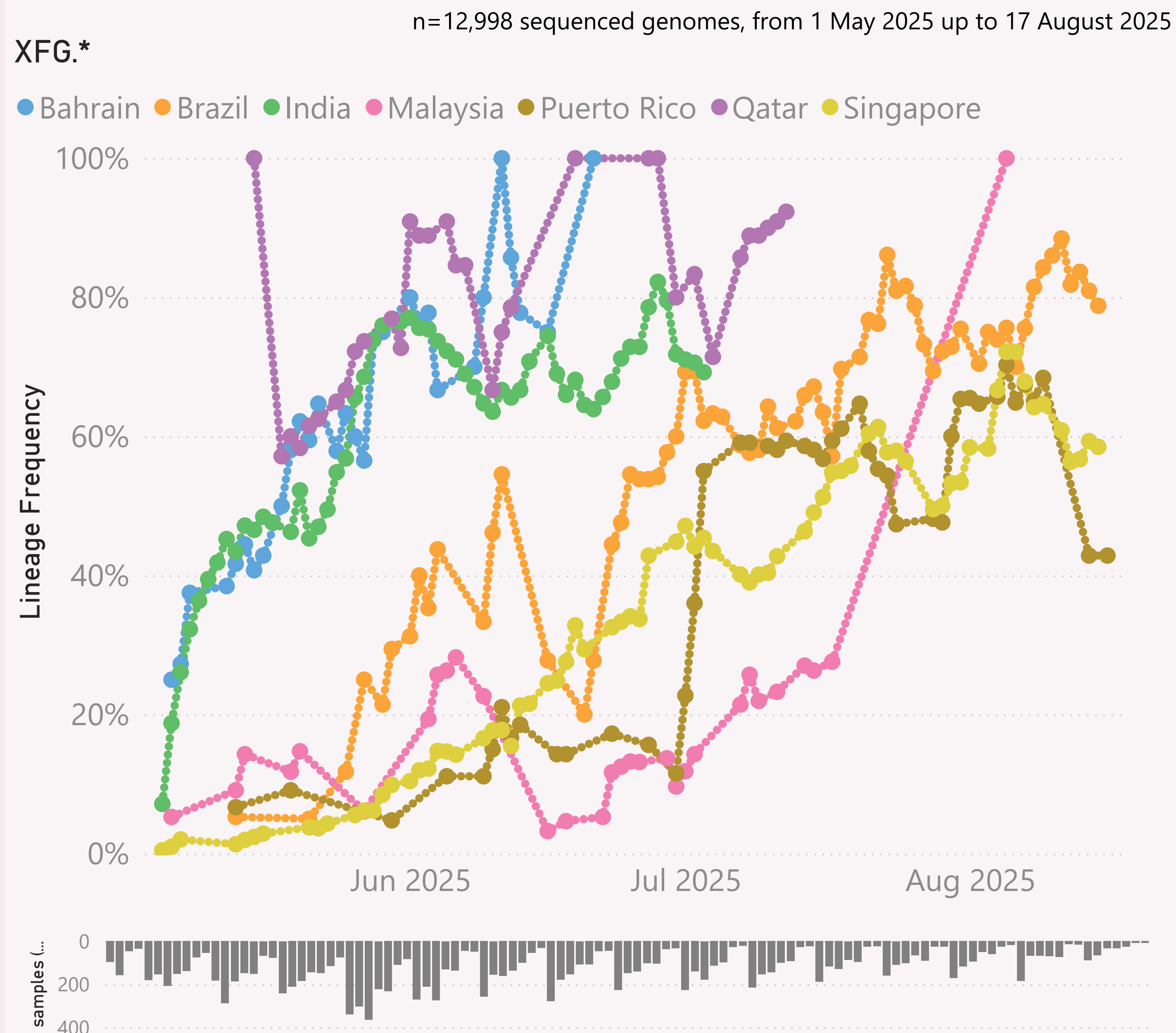
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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.

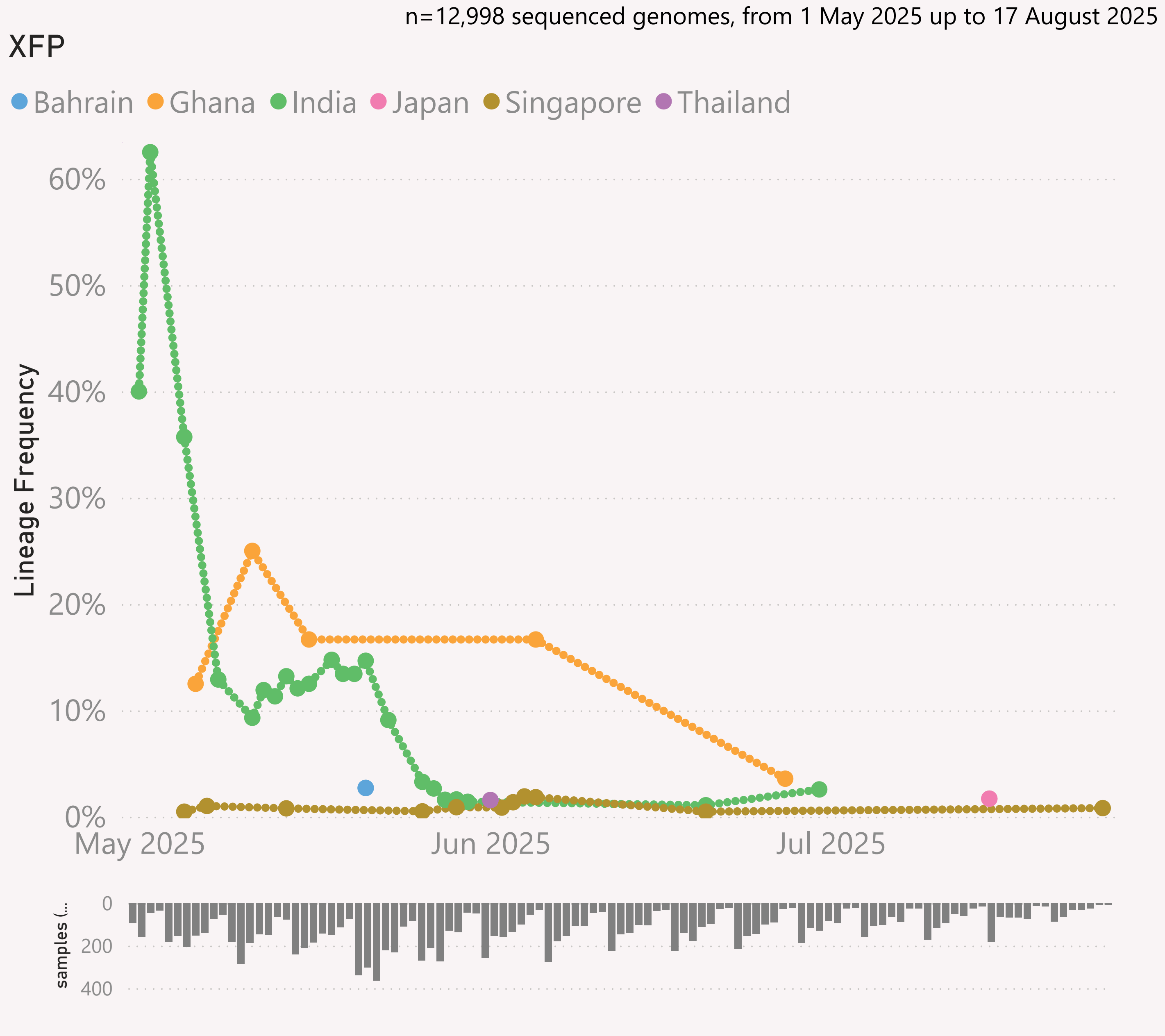
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiRT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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.



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)

50

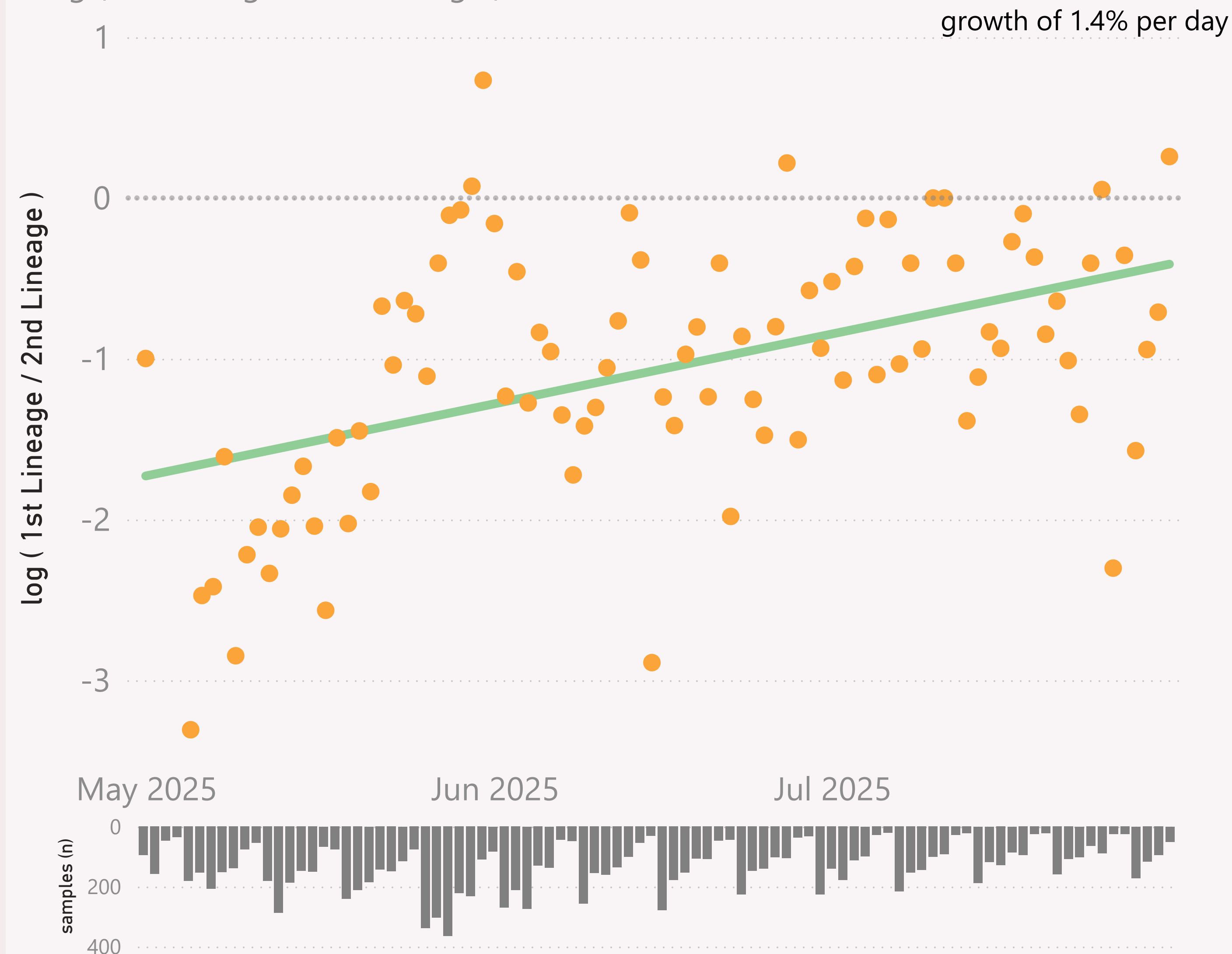
Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
Singapore			25/07/2025	XFP.*	XFP
Japan		Quar...	15/07/2025	XFP.*	XFP
India	Maharashtra		30/06/2025	XFP.*	XFP
Ghana	Ashanti		27/06/2025	XFP.*	XFP
Singapore			20/06/2025	XFP.*	XFP
India	Chhattisgarh		20/06/2025	XFP.*	XFP
Singapore			05/06/2025	XFP.*	XFP
Ghana	Greater Accra		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
Total					



n=12,144 sequenced genomes, from 1 May 2025 up to 31 July 2025

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

●  $\log ( 1st \text{ Lineage} / 2nd \text{ Lineage} )$  ● trend

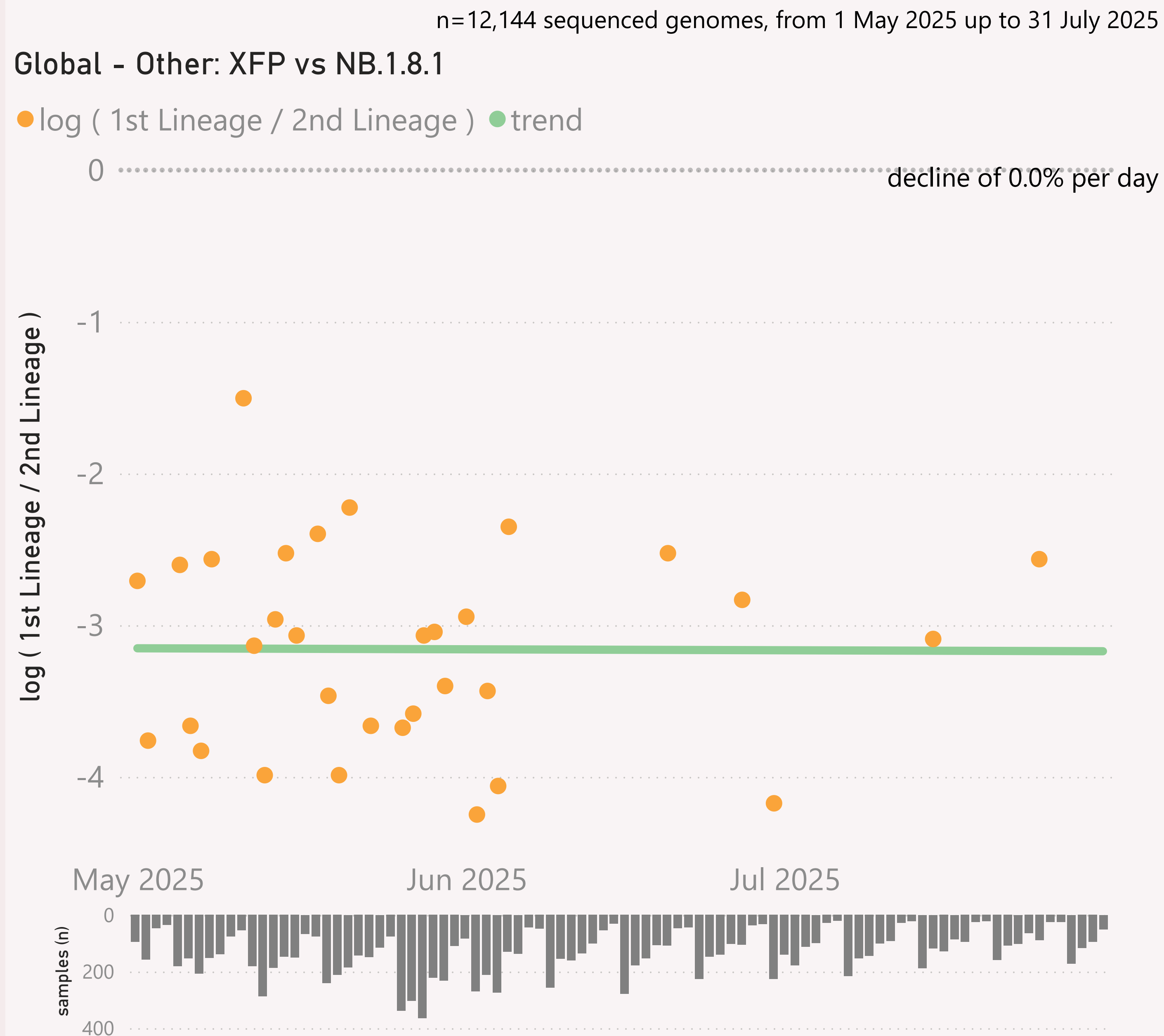


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.



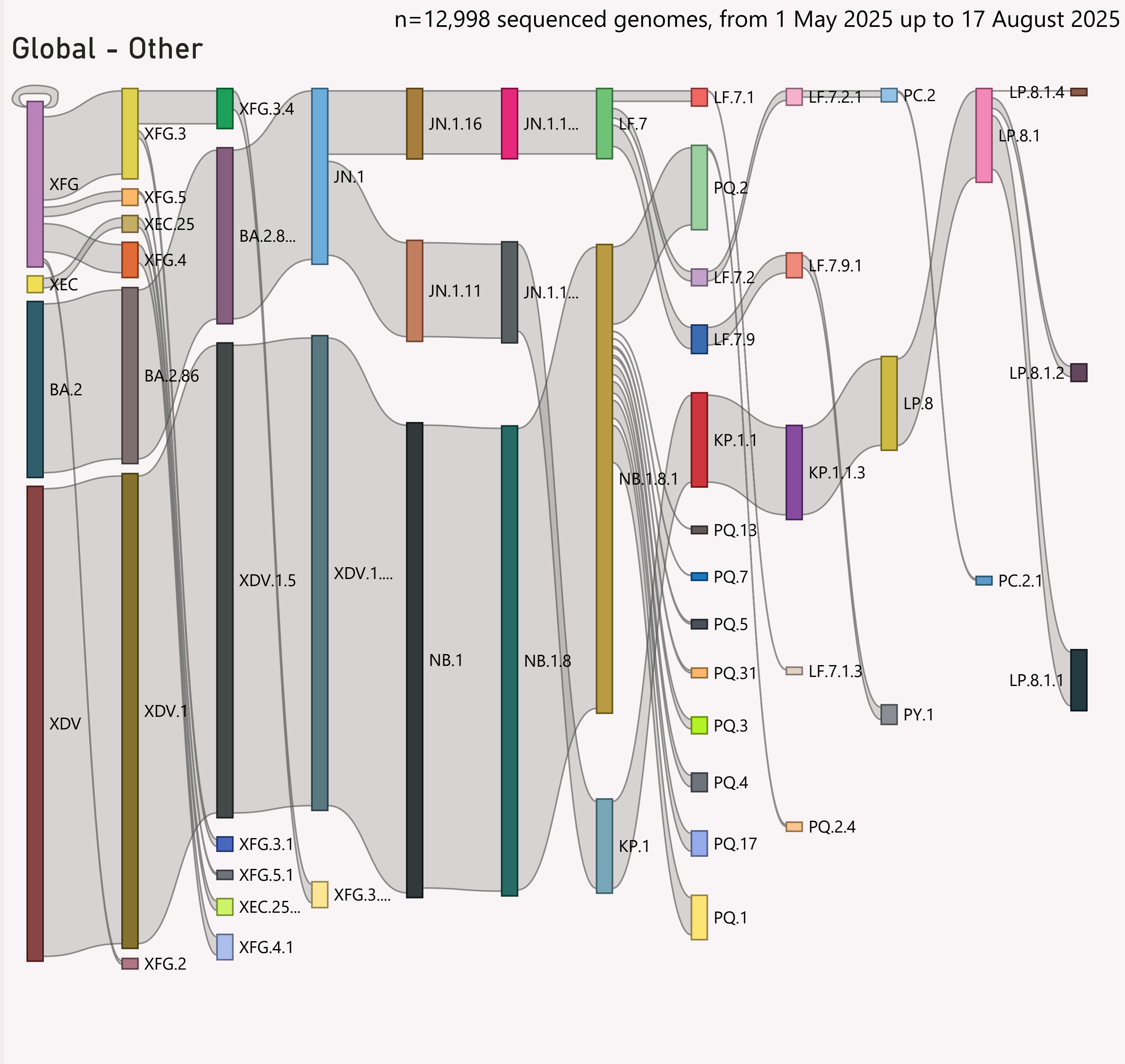
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.





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

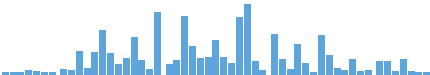




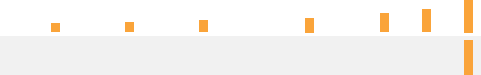



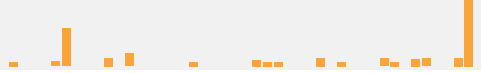





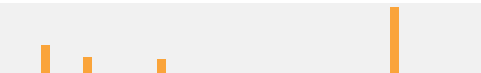



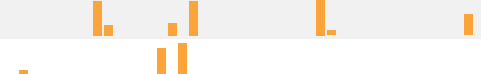




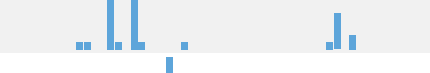

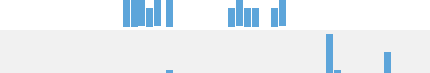






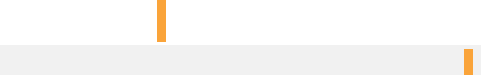



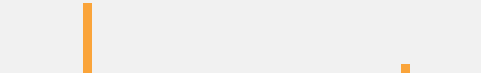



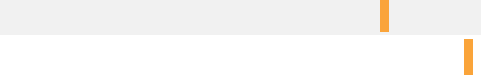
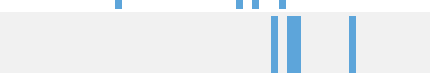
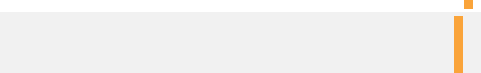


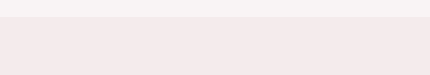
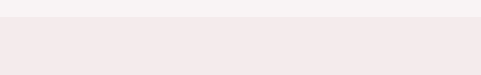
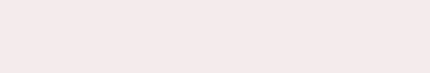
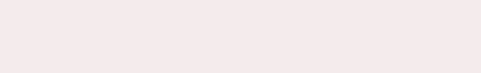
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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.

## Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
<div>+ </div> China	1,809	17/08/2025		26/08/2025	
<div>+ </div> Singapore	744	15/08/2025		25/08/2025	
<div>+ </div> South Korea	599	13/08/2025		26/08/2025	
<div>+ </div> Japan	509	17/08/2025		26/08/2025	
<div>+ </div> Mexico	485	19/06/2025		22/08/2025	
<div>+ </div> Brazil	429	15/08/2025		26/08/2025	
<div>+ </div> Costa Rica	371	12/08/2025		26/08/2025	
<div>+ </div> Thailand	317	14/08/2025		26/08/2025	
<div>+ </div> India	293	03/07/2025		17/08/2025	
<div>+ </div> Puerto Rico	232	16/08/2025		26/08/2025	
<div>+ </div> Taiwan	214	30/07/2025		26/08/2025	
<div>+ </div> Malaysia	199	11/08/2025		26/08/2025	
<div>+ </div> Cambodia	118	04/07/2025		05/08/2025	
<div>+ </div> Hong Kong	105	15/08/2025		26/08/2025	
<div>+ </div> Laos	47	29/07/2025		13/08/2025	
<div>+ </div> Dominican	46	01/08/2025		19/08/2025	
<div>+ </div> Qatar	46	12/07/2025		26/08/2025	
<div>+ </div> South Africa	40	07/08/2025		21/08/2025	
<div>+ </div> Guam	37	14/08/2025		26/08/2025	
<div>+ </div> Guatemala	36	08/08/2025		26/08/2025	
<div>+ </div> Nepal	31	22/07/2025		28/07/2025	
<div>+ </div> Chile	30	10/08/2025		26/08/2025	
<div>+ </div> Ecuador	30	17/08/2025		26/08/2025	
<div>+ </div> Kenya	29	14/07/2025		20/08/2025	
<div>+ </div> Colombia	19	31/07/2025		26/08/2025	
<div>+ </div> Kazakhstan	18	16/07/2025		18/08/2025	
<div>+ </div> Tunisia	17	11/07/2025		26/08/2025	
<div>+ </div> Pakistan	12	30/07/2025		25/08/2025	
<div>- </div> Total	6,956	17/08/2025		26/08/2025	

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.