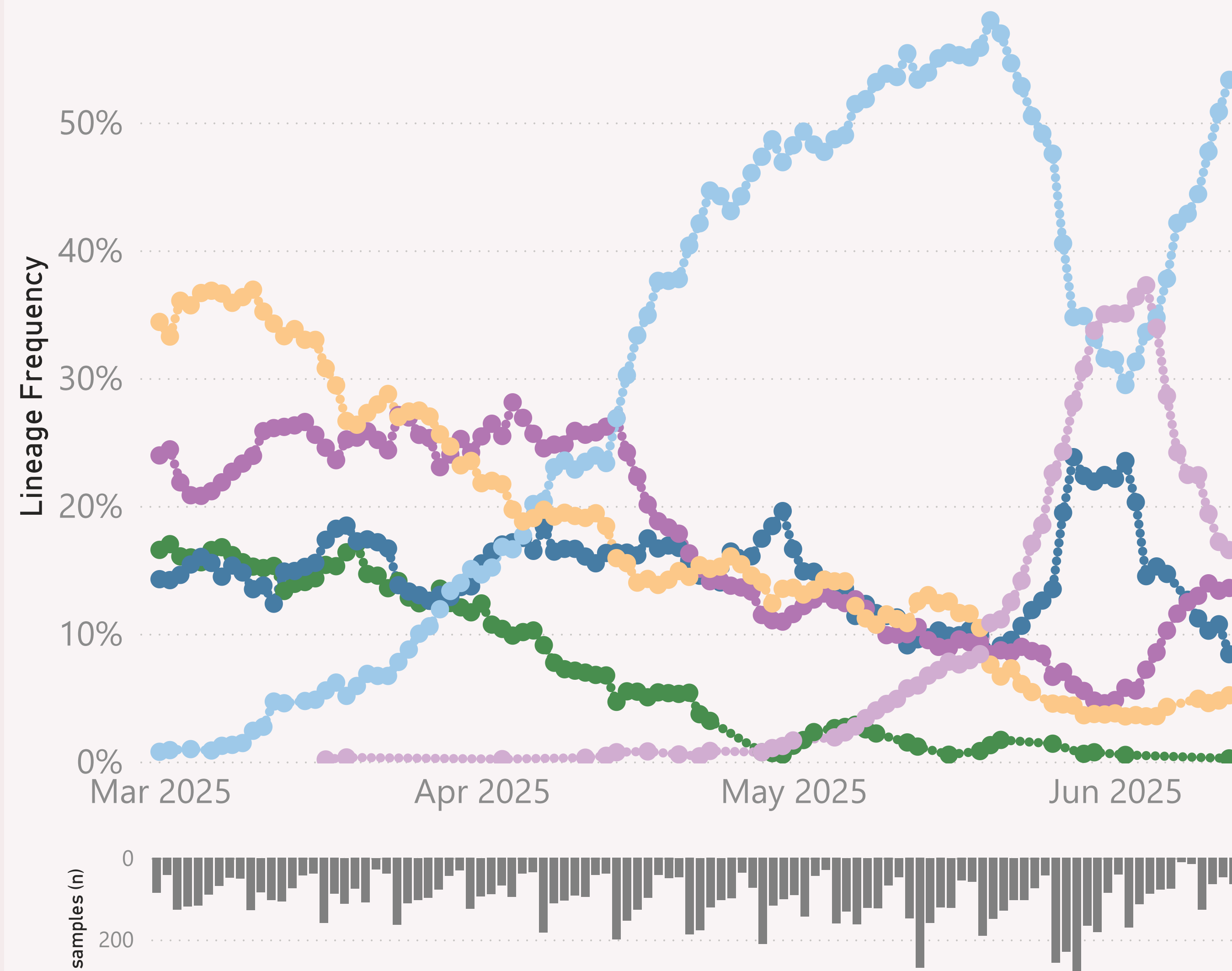


n=10,683 sequenced genomes, from 1 March 2025 up to 12 June 2025

Global - Other

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



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

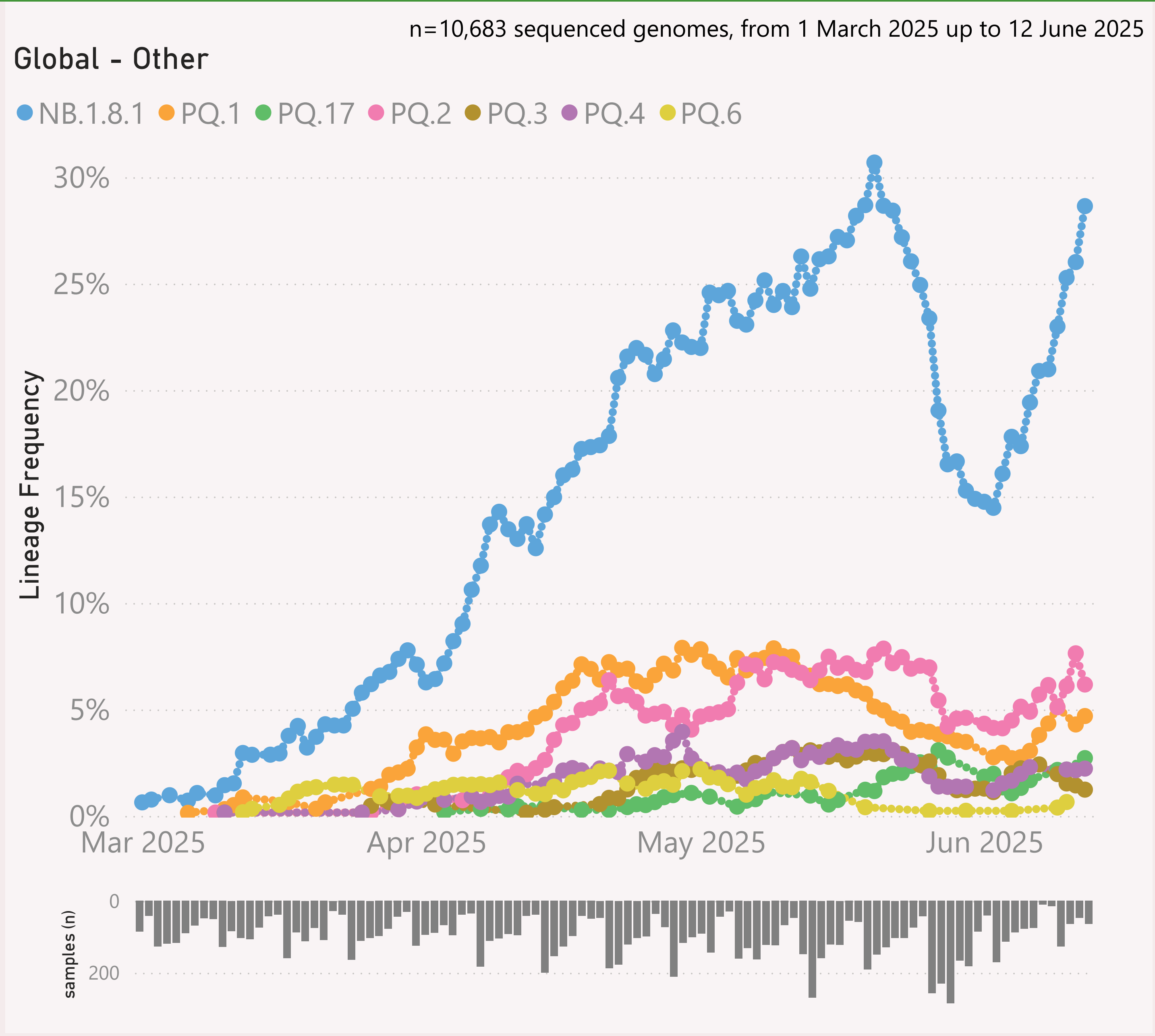
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.



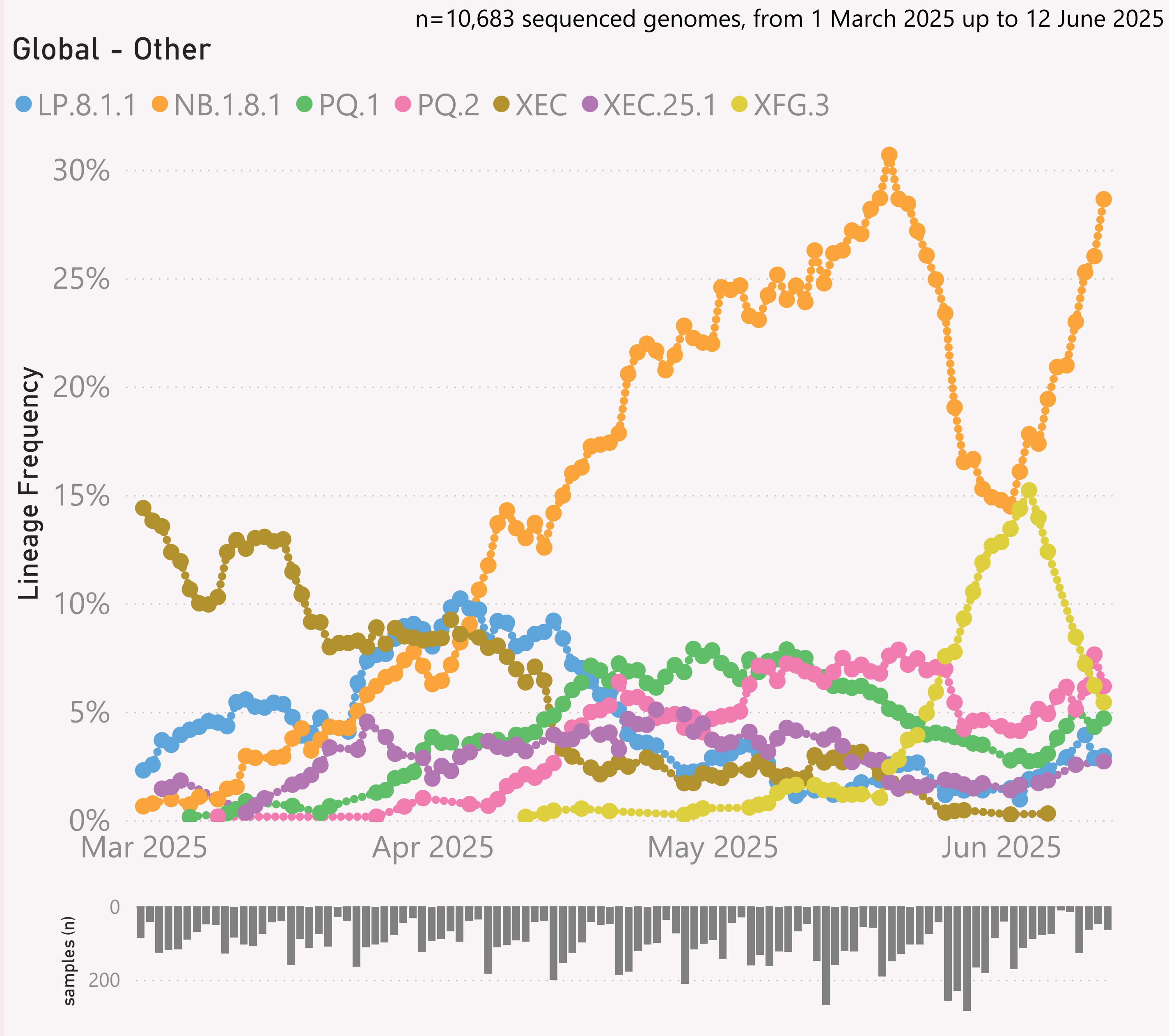
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently NB.1.8.1.* Nimbus.

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.



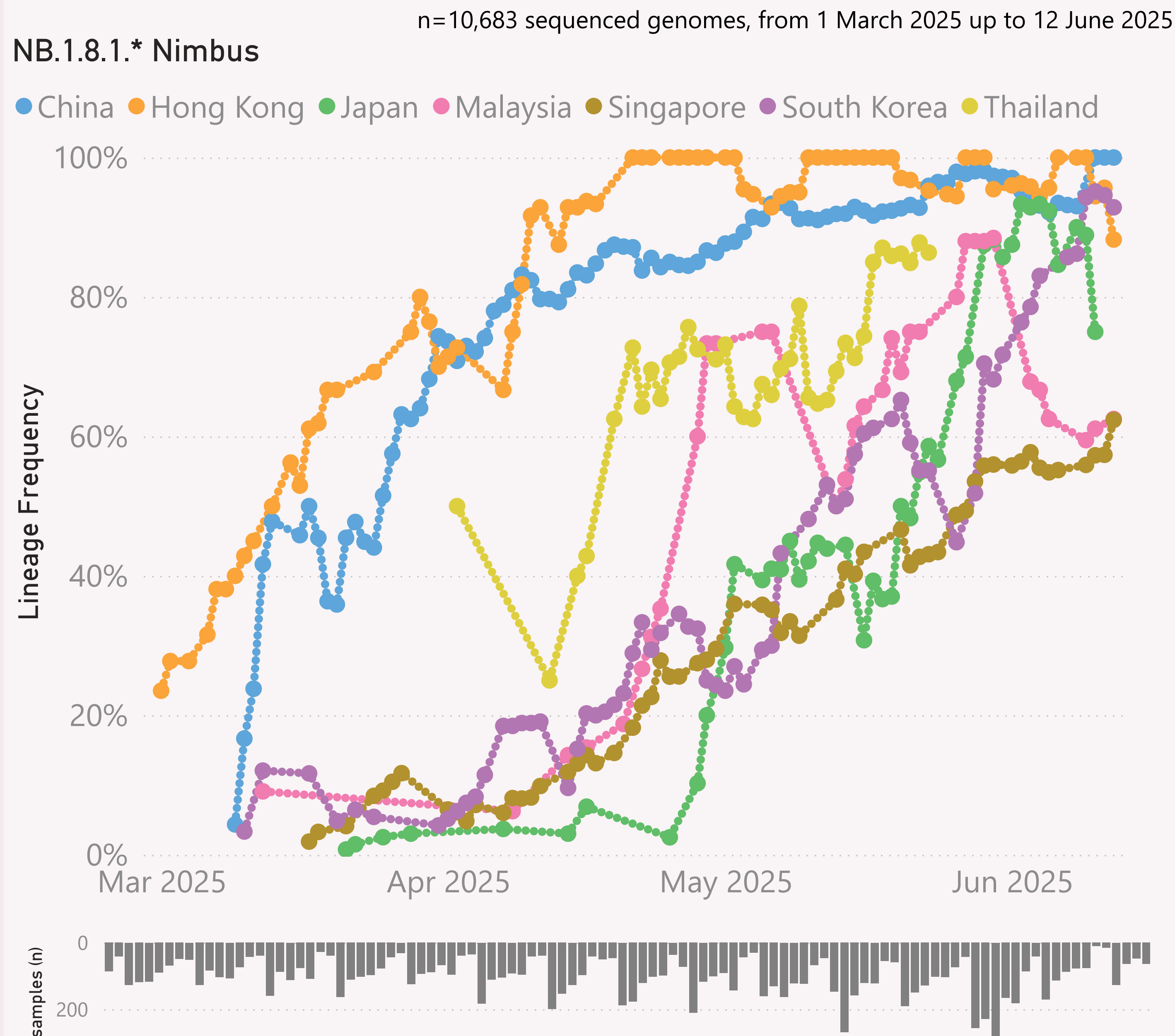
This page shows the frequency of the top 7 lineages, across recent months.

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.



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

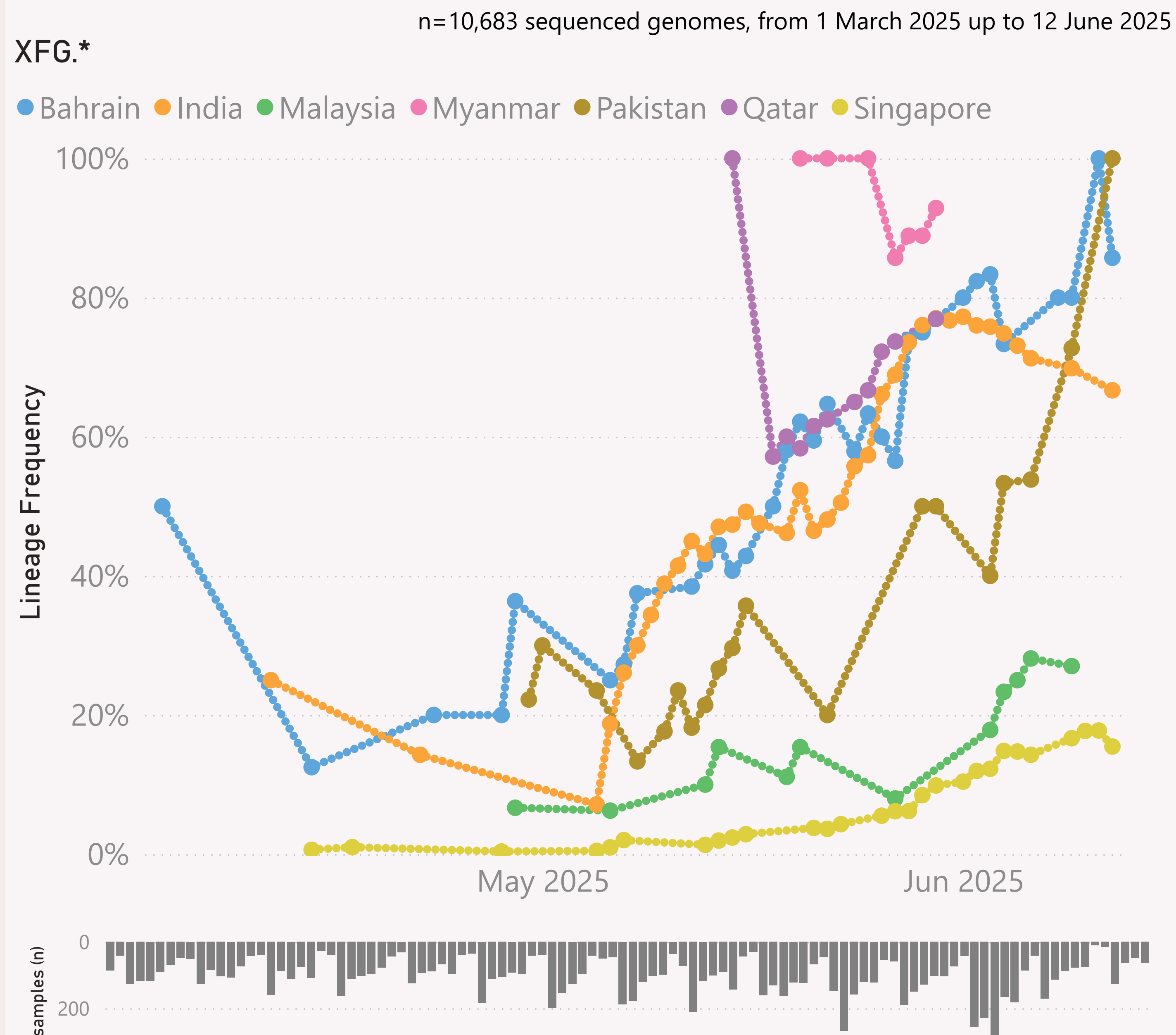
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

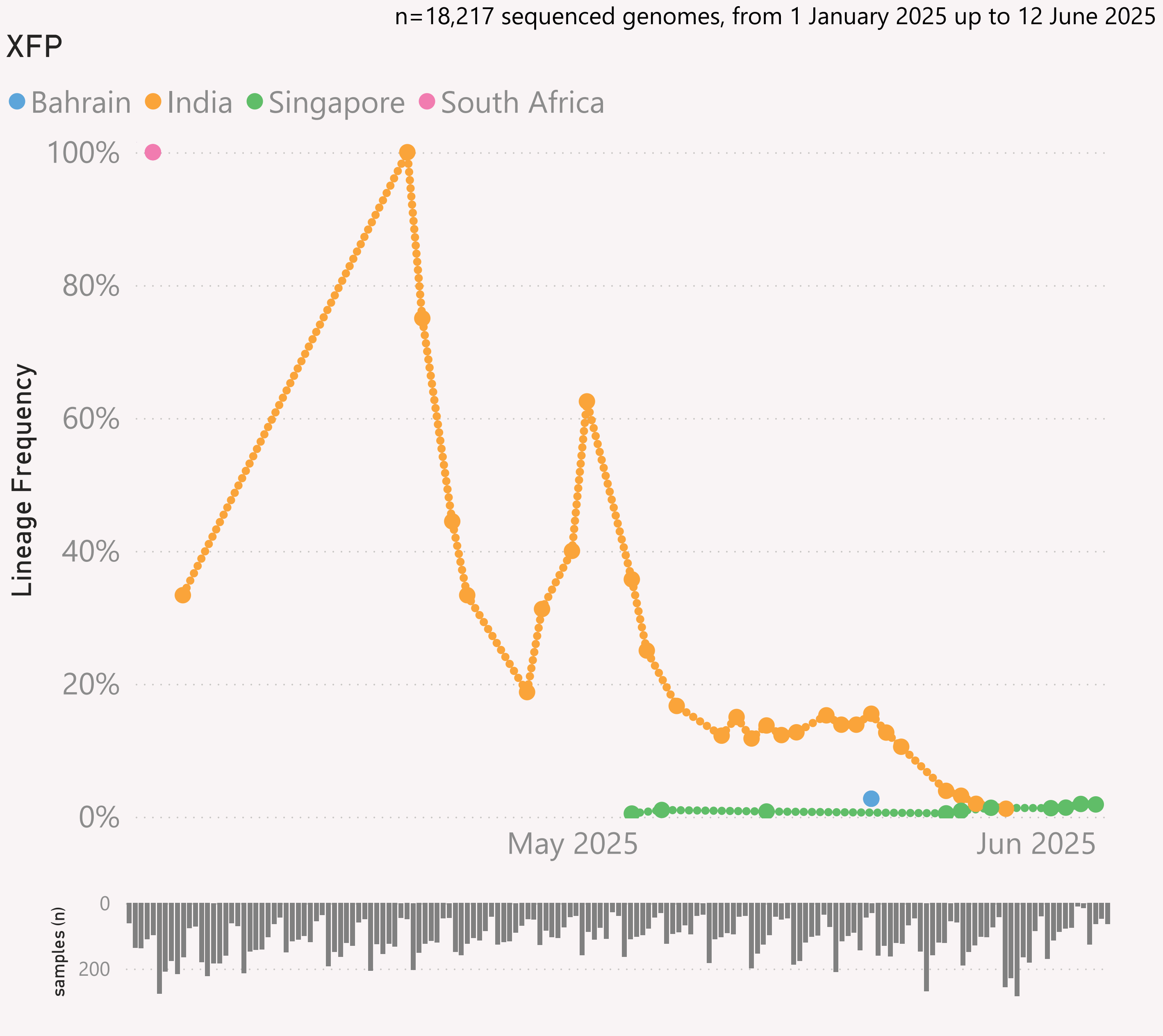
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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)

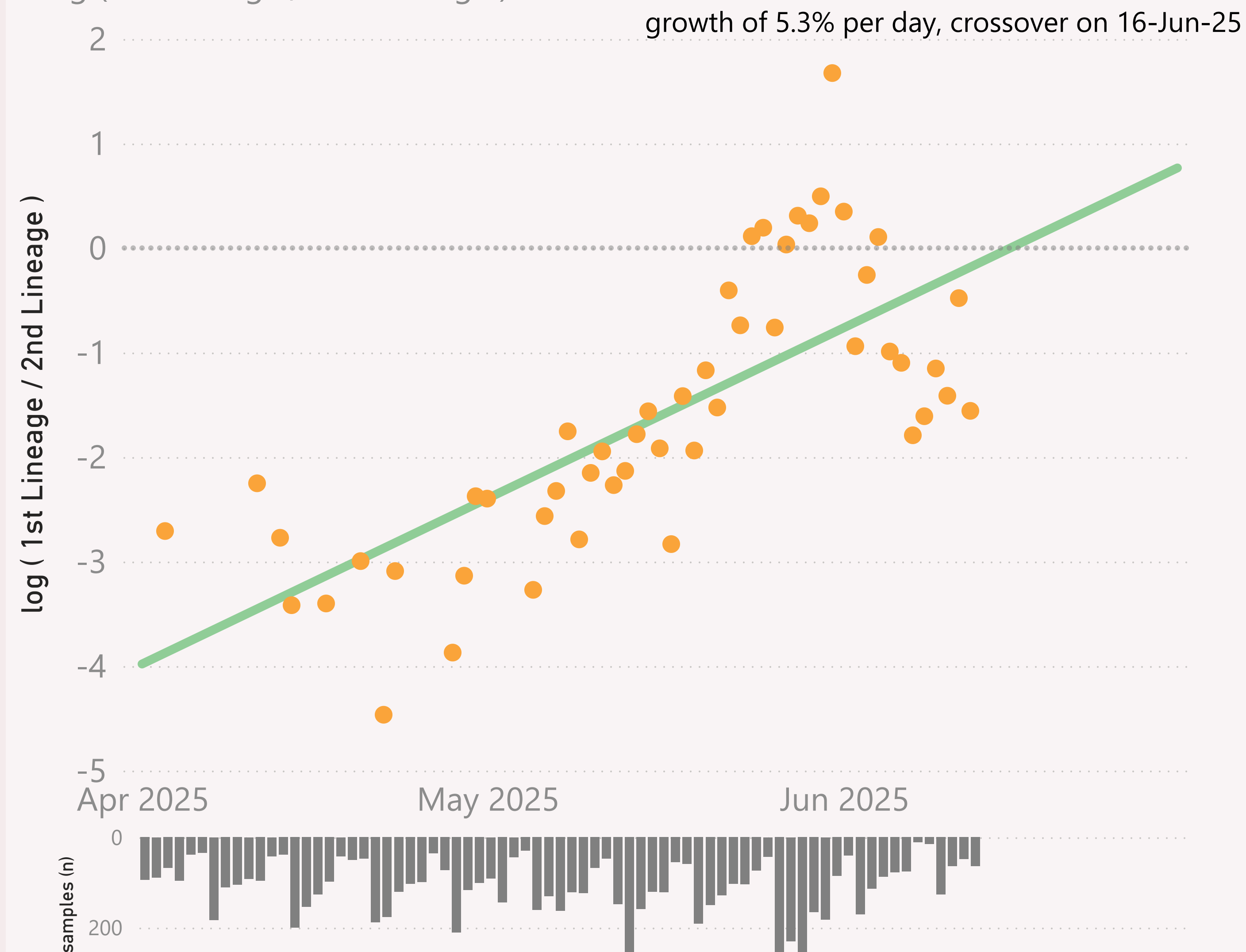
51

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
Singapore			27/05/2025	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
India	Gujarat		22/05/2025	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
Total					

n=7,988 sequenced genomes, from 1 April 2025 up to 12 June 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.

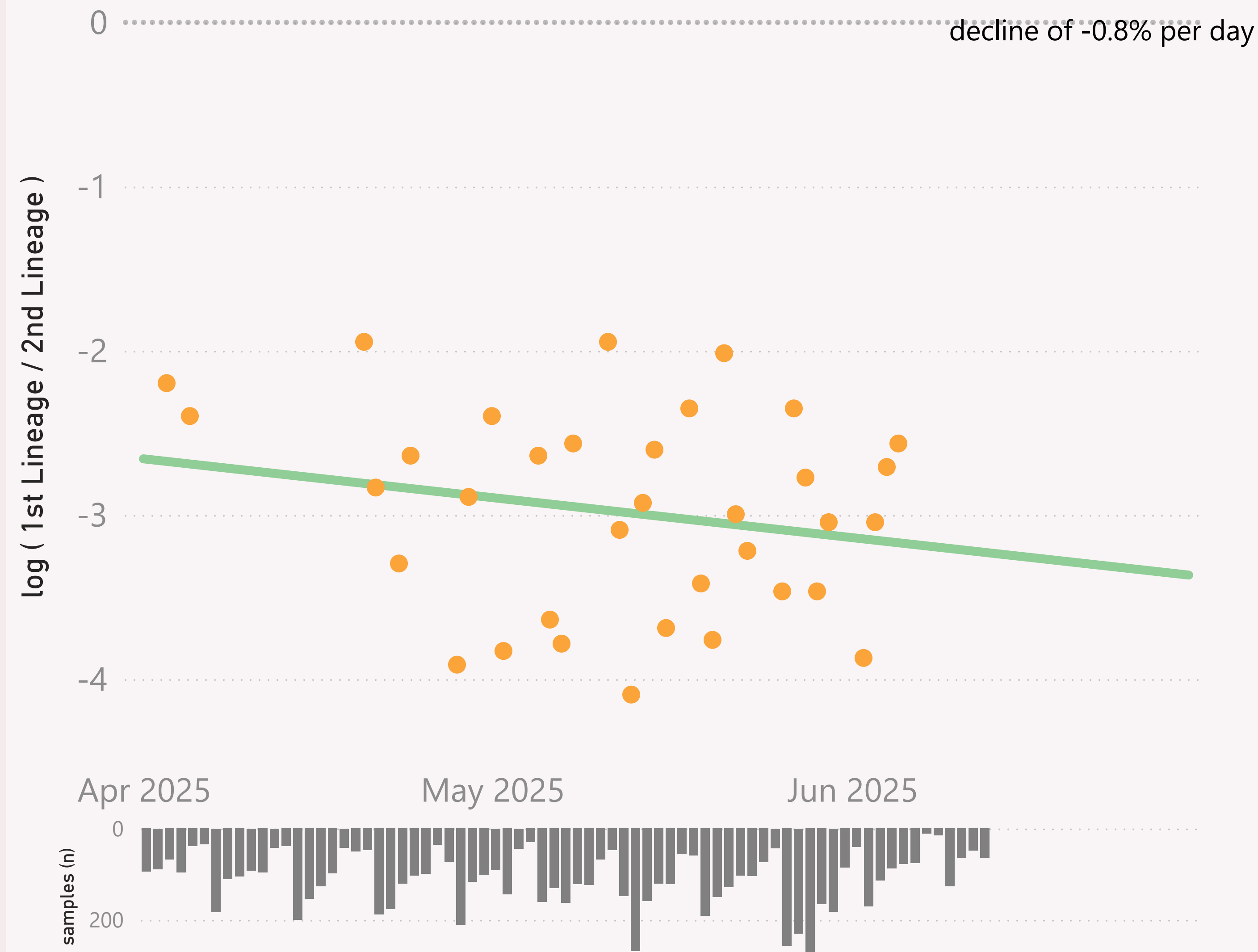
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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.

n=7,988 sequenced genomes, from 1 April 2025 up to 12 June 2025

Global - Other: XFP vs NB.1.8.1

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



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

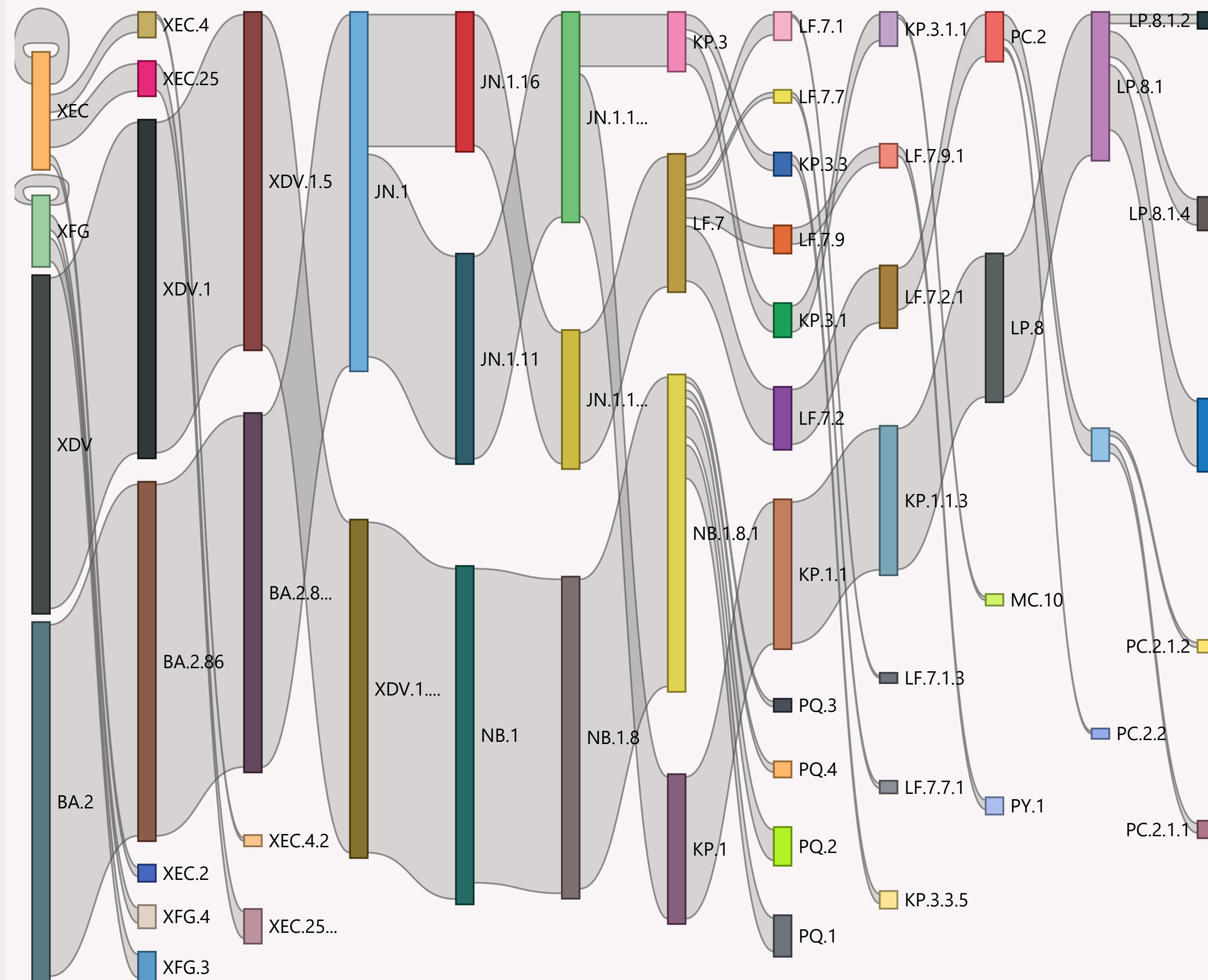
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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=10,683 sequenced genomes, from 1 March 2025 up to 12 June 2025

Global - Other



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



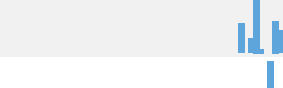





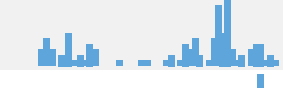





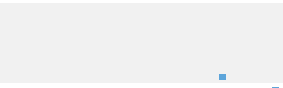
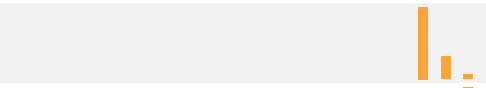




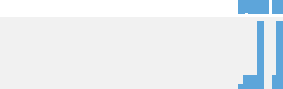
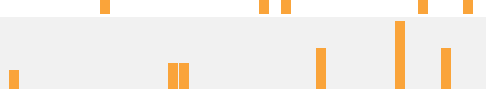








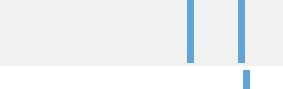

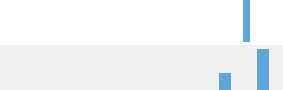
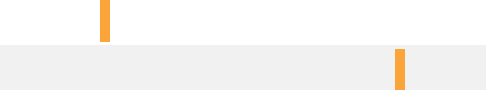
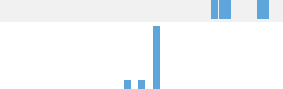

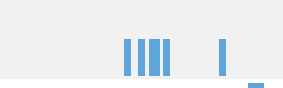
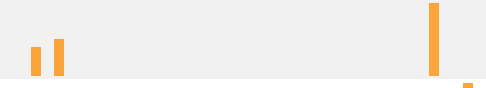


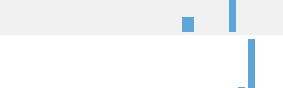

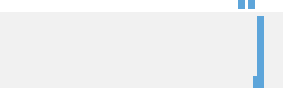



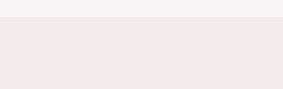
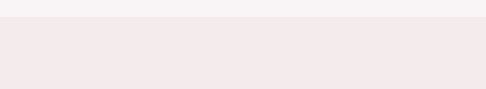
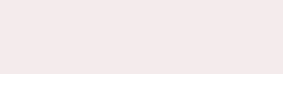
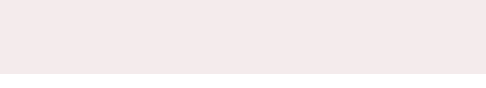
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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.

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	2,057	12/06/2025		22/06/2025	
<div>+ </div> Singapore	1,508	12/06/2025		22/06/2025	
<div>+ </div> India	835	12/06/2025		22/06/2025	
<div>+ </div> Brazil	713	04/06/2025		22/06/2025	
<div>+ </div> Japan	712	12/06/2025		22/06/2025	
<div>+ </div> Mexico	620	10/06/2025		22/06/2025	
<div>+ </div> South Korea	391	12/06/2025		22/06/2025	
<div>+ </div> Malaysia	331	12/06/2025		22/06/2025	
<div>+ </div> Thailand	281	23/05/2025		30/05/2025	
<div>+ </div> Kazakhstan	218	28/05/2025		22/06/2025	
<div>+ </div> Costa Rica	181	12/06/2025		22/06/2025	
<div>+ </div> Bahrain	158	12/06/2025		22/06/2025	
<div>+ </div> Hong Kong	153	12/06/2025		22/06/2025	
<div>+ </div> Puerto Rico	130	12/06/2025		20/06/2025	
<div>+ </div> Taiwan	96	09/06/2025		22/06/2025	
<div>+ </div> Pakistan	89	12/06/2025		22/06/2025	
<div>+ </div> South Africa	84	05/06/2025		22/06/2025	
<div>+ </div> Argentina	81	31/03/2025		22/05/2025	
<div>+ </div> Vietnam	51	30/05/2025		18/06/2025	
<div>+ </div> Ghana	44	28/05/2025		22/06/2025	
<div>+ </div> Israel	40	01/05/2025		21/05/2025	
<div>+ </div> Qatar	40	30/05/2025		16/06/2025	
<div>+ </div> Paraguay	36	13/01/2025		22/06/2025	
<div>+ </div> Peru	34	01/04/2025		19/06/2025	
<div>+ </div> French Guiana	33	11/06/2025		22/06/2025	
<div>+ </div> Egypt	31	27/04/2025		19/06/2025	
<div>+ </div> Guatemala	28	15/05/2025		05/06/2025	
<div>+ </div> Cambodia	27	19/05/2025		25/05/2025	
<div>+ </div> Total	9,190	12/06/2025		22/06/2025	

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.