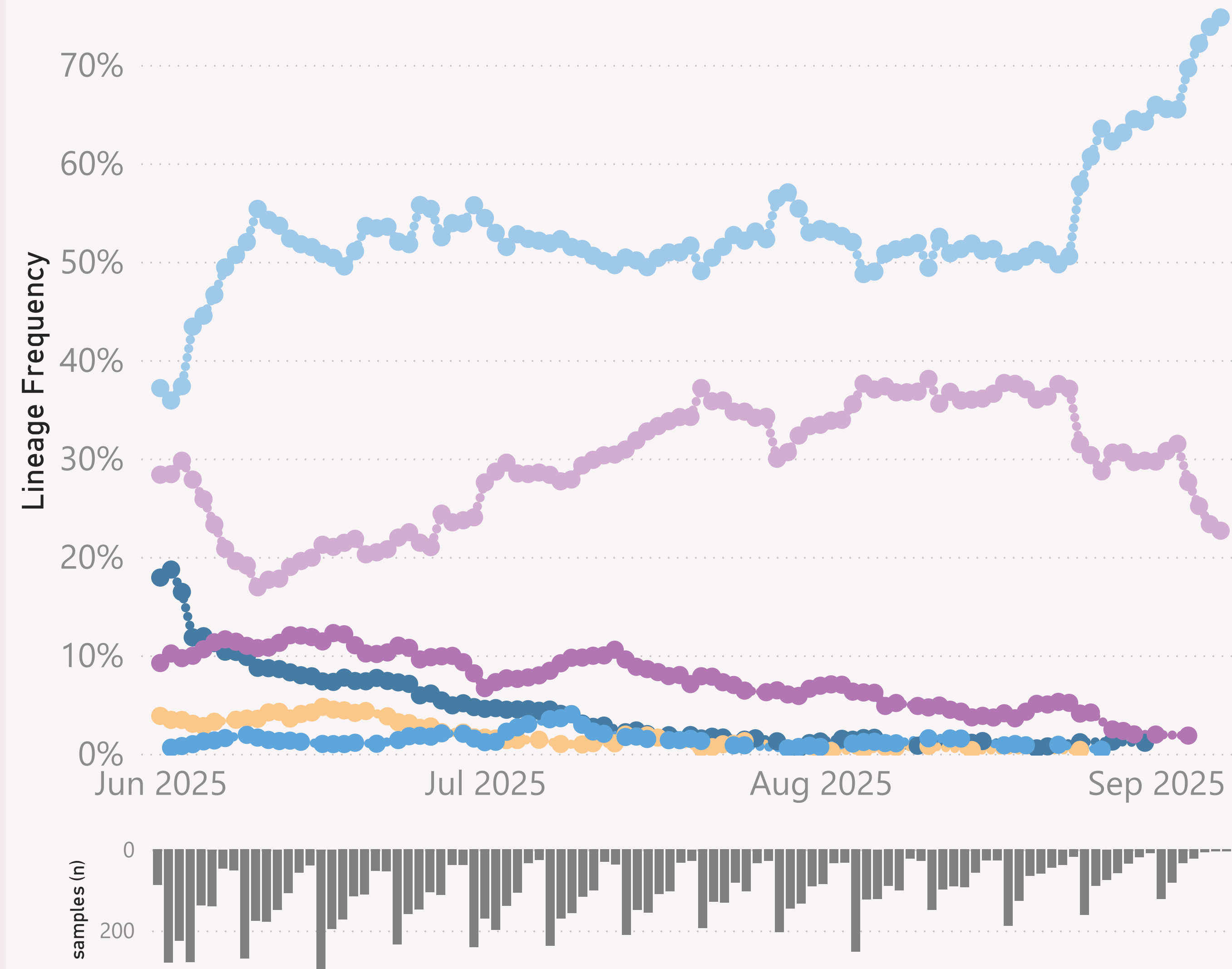


n=10,616 sequenced genomes, from 1 June 2025 up to 7 September 2025

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.

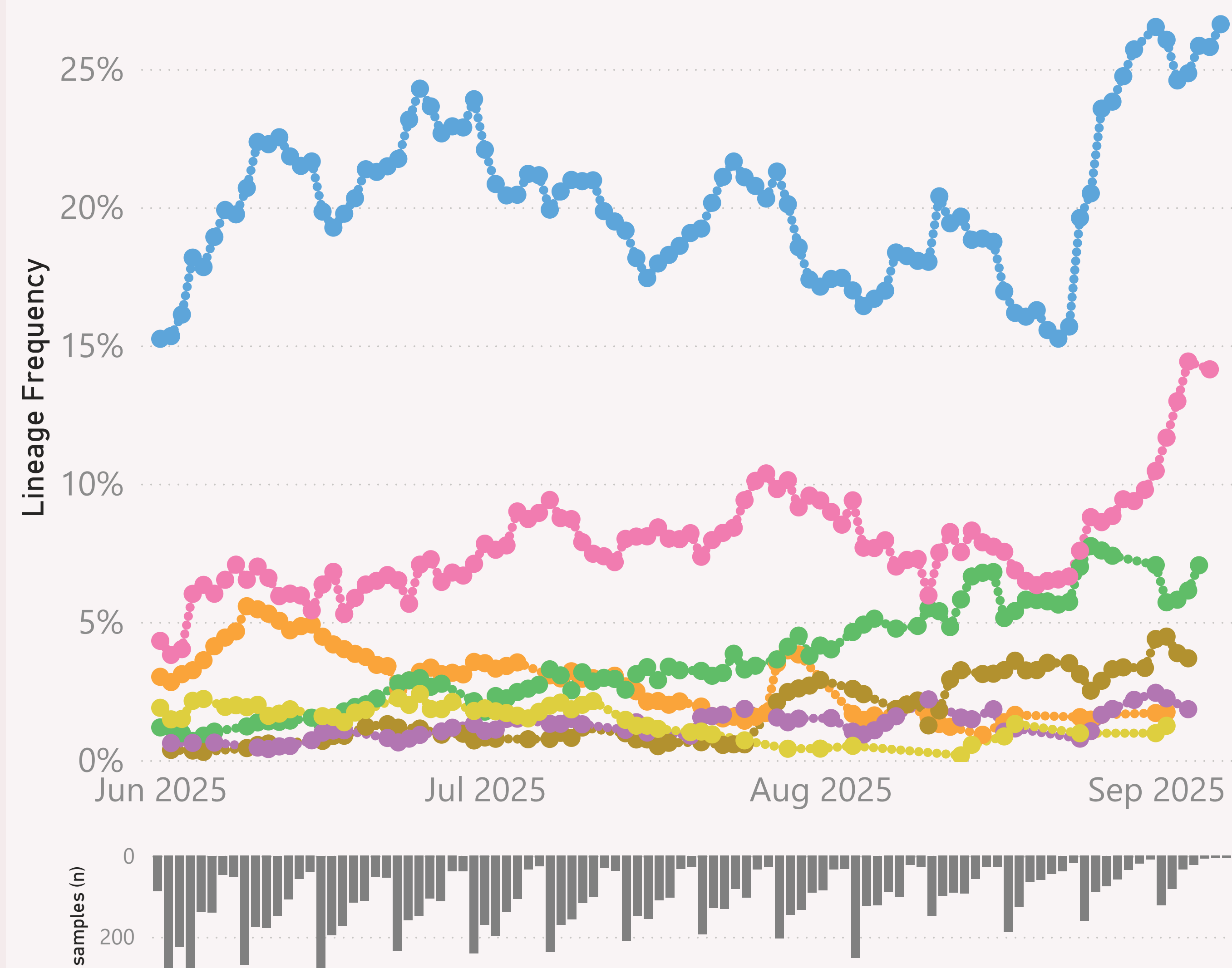
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=10,616 sequenced genomes, from 1 June 2025 up to 7 September 2025

Global - Other

● NB.1.8.1 ● PQ.1 ● PQ.17 ● PQ.2 ● PQ.2.1 ● PQ.2.4 ● PQ.3



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.

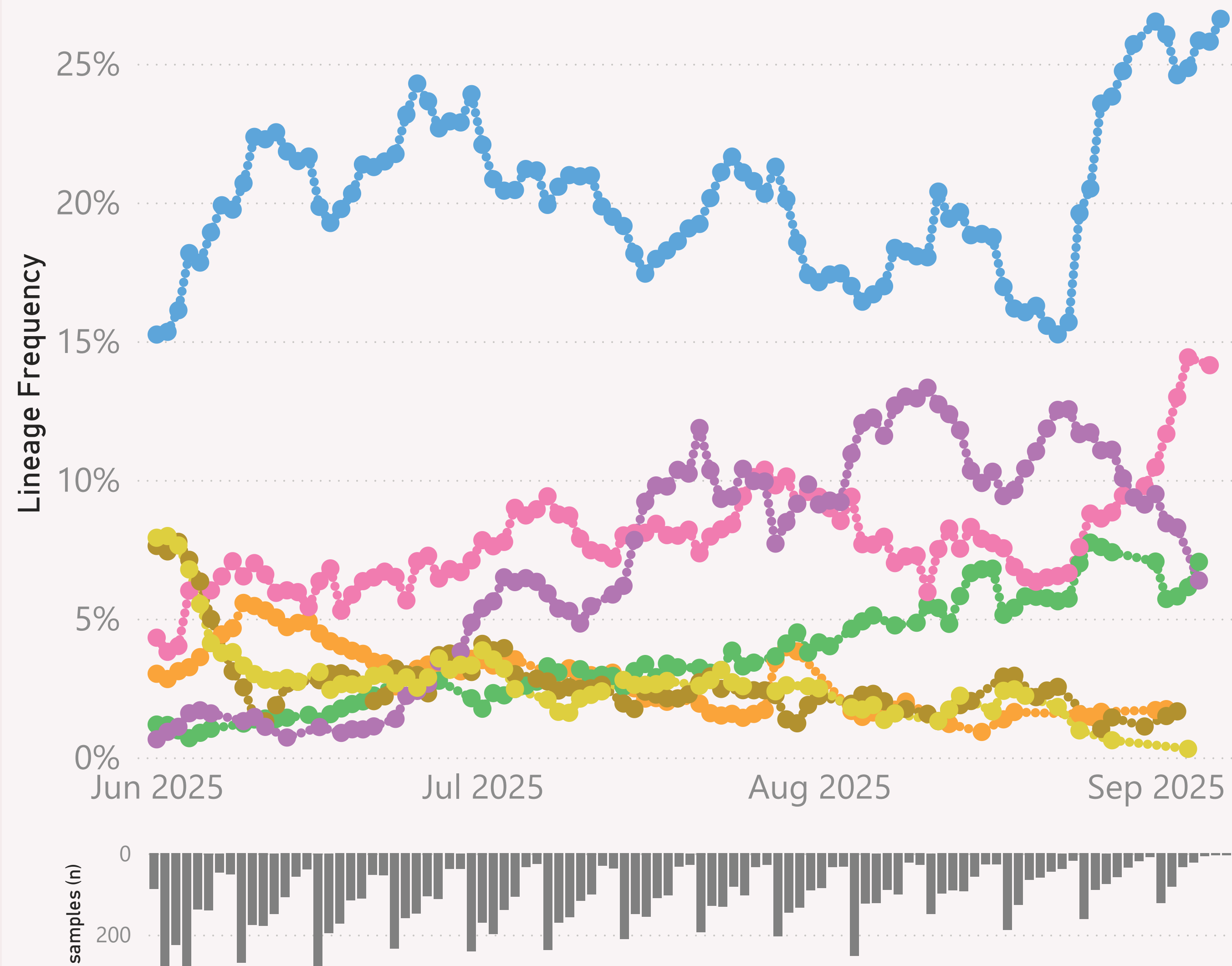
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=10,616 sequenced genomes, from 1 June 2025 up to 7 September 2025

Global - Other

● NB.1.8.1 ● PQ.1 ● PQ.17 ● PQ.2 ● XFG.3 ● XFG.3.4.1 ● 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.

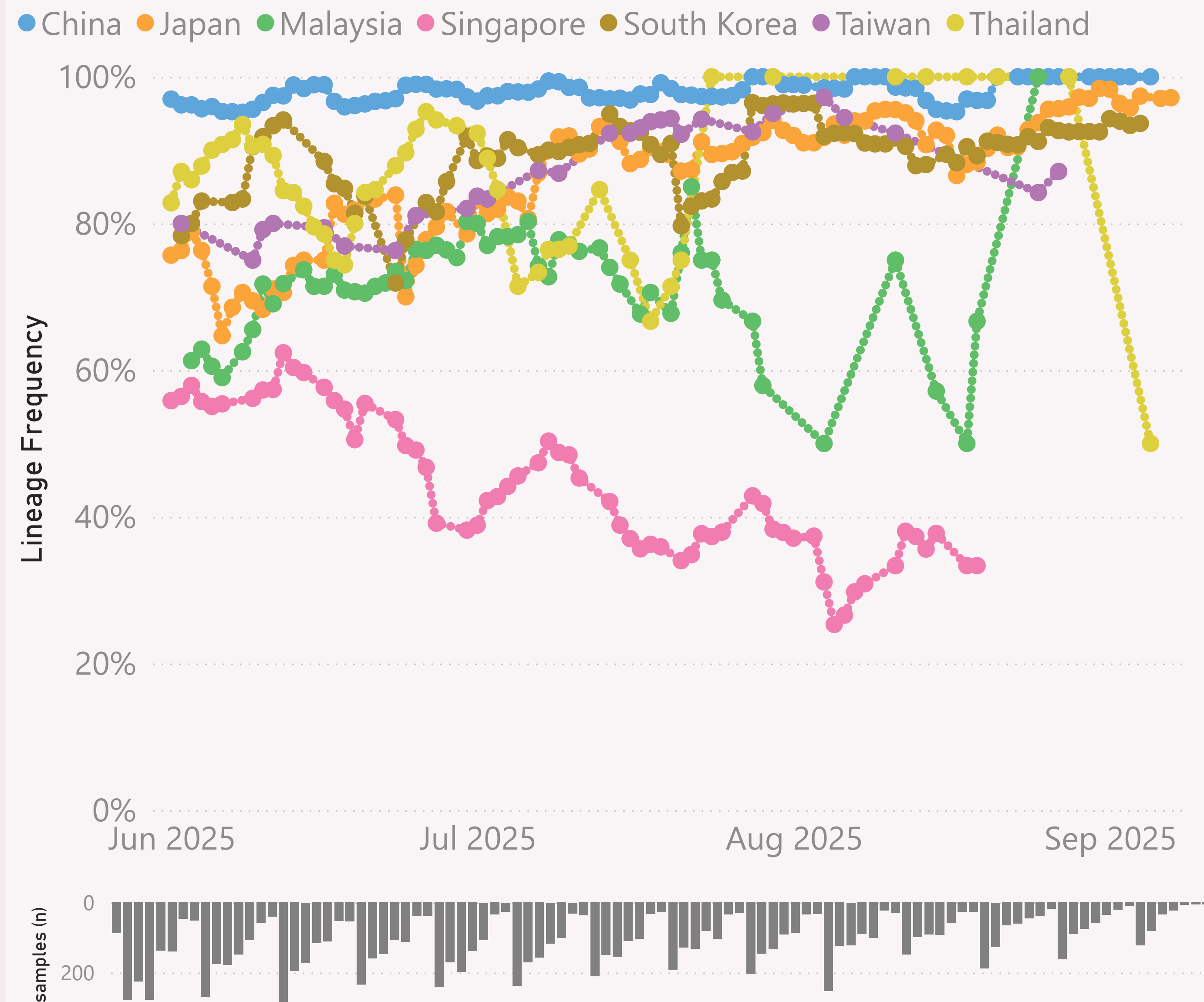
The frequency shown at each point is based on the 7-day rolling average across all lineages.

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=10,616 sequenced genomes, from 1 June 2025 up to 7 September 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.

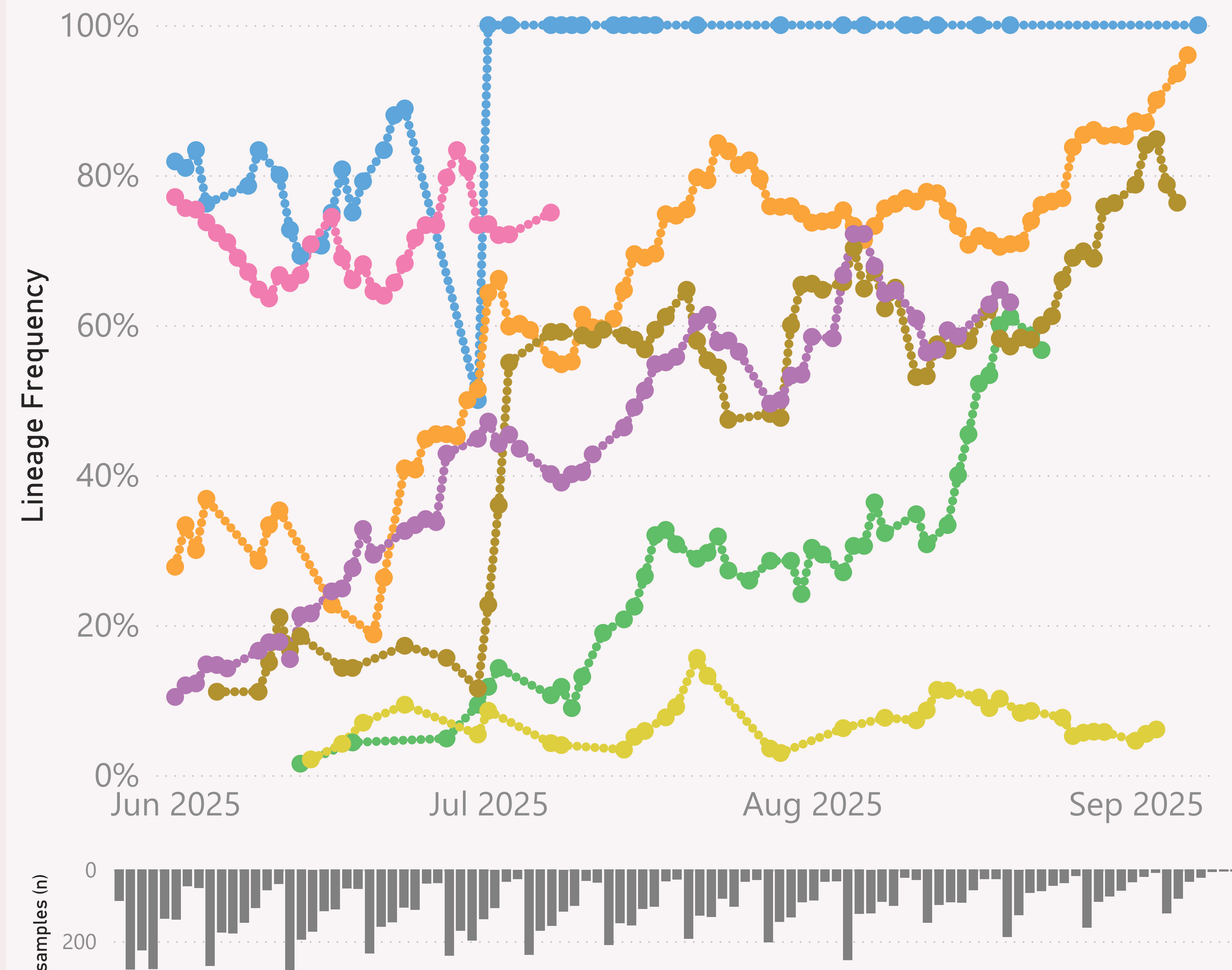
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=10,616 sequenced genomes, from 1 June 2025 up to 7 September 2025

XFG.*

● Bahrain ● Brazil ● Costa Rica ● India ● Puerto Rico ● Singapore ● South Korea



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

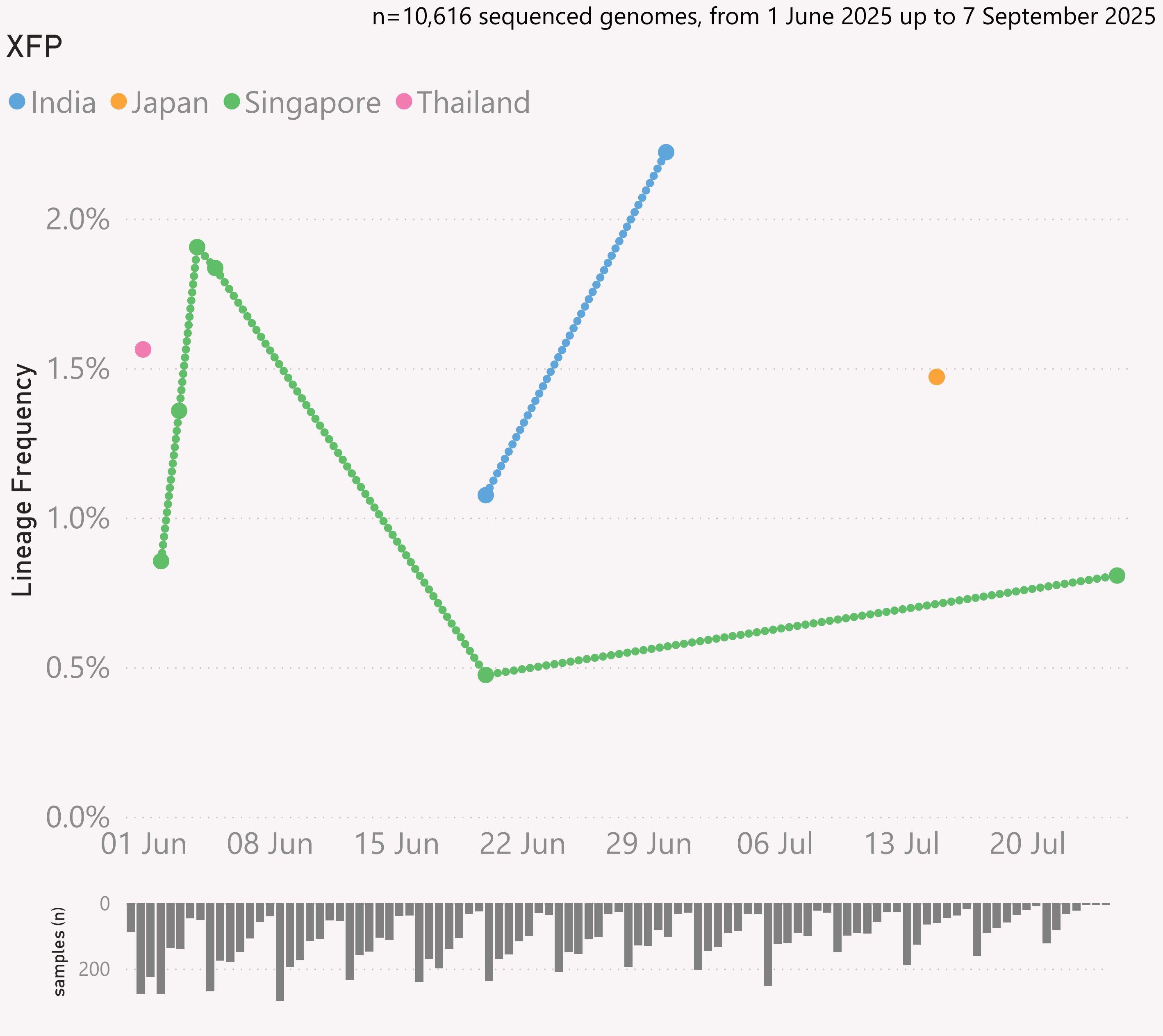
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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

01/01/202531/12/2025

Host

Human

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

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

Samples Sequenced (gisaid)

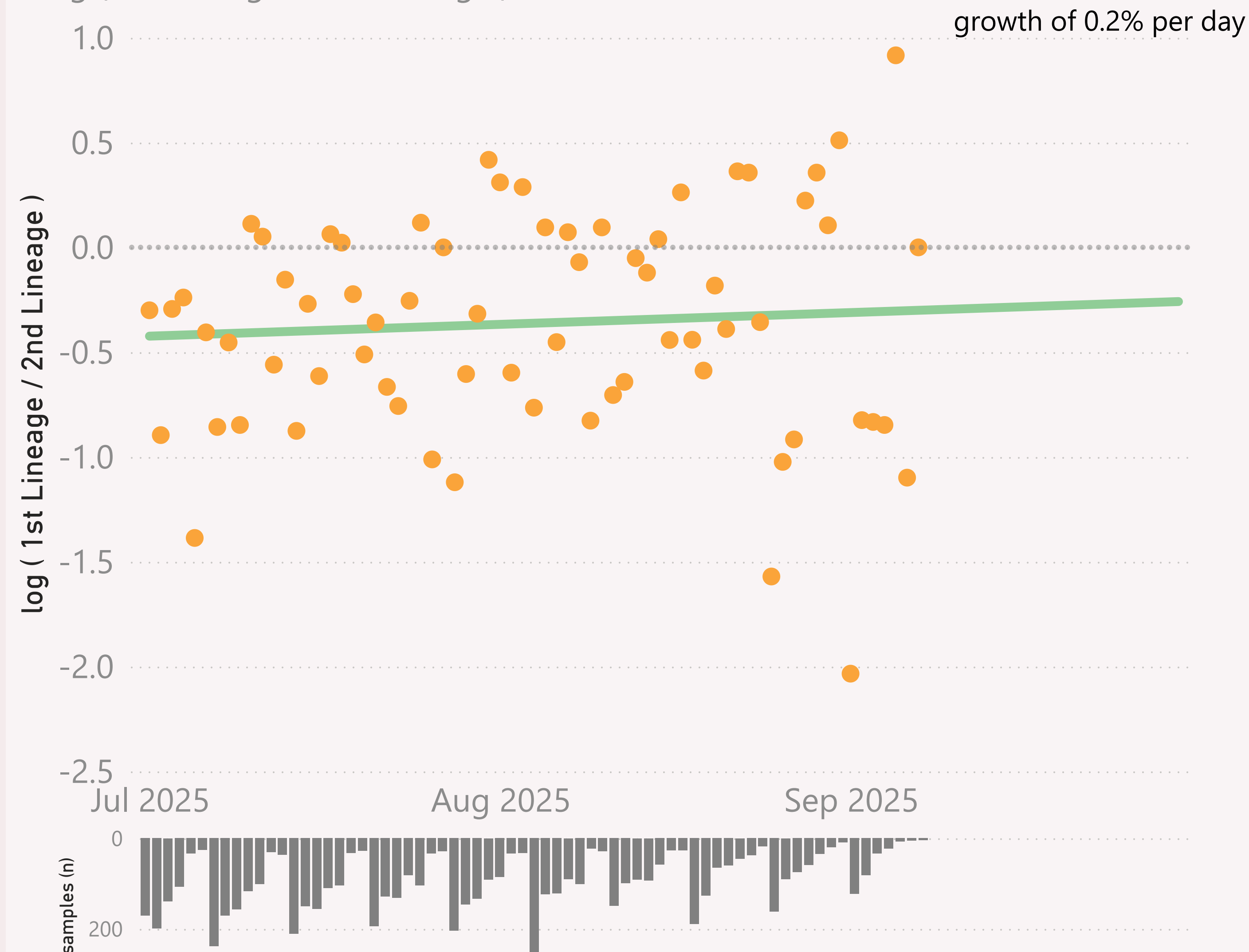
10

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=6,308 sequenced genomes, from 1 July 2025 up to 7 September 2025

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

● log (1st Lineage / 2nd 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.

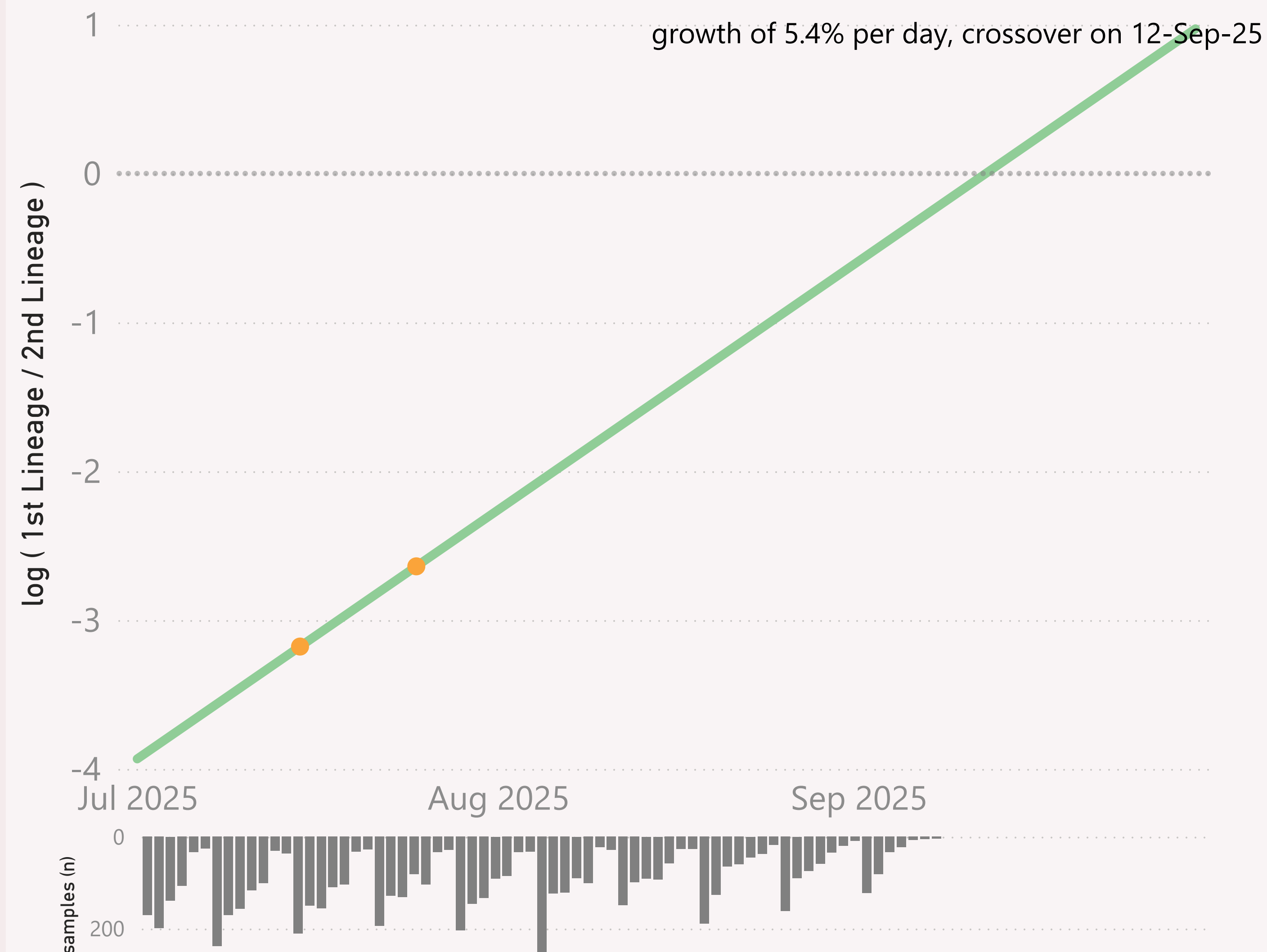
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=6,308 sequenced genomes, from 1 July 2025 up to 7 September 2025

Global - Other: XFP vs NB.1.8.1

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



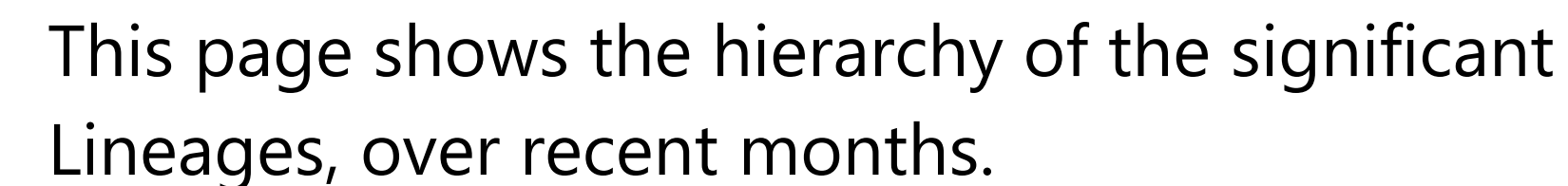
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

Global - Other



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
⊕ South Korea	1,047	04/09/2025		17/09/2025	
⊕ Brazil	993	06/09/2025		17/09/2025	
⊕ China	743	07/09/2025		17/09/2025	
⊕ Japan	708	07/09/2025		17/09/2025	
⊕ Puerto Rico	328	06/09/2025		17/09/2025	
⊕ Singapore	312	20/08/2025		25/08/2025	
⊕ Costa Rica	307	26/08/2025		17/09/2025	
⊕ Malaysia	210	25/08/2025		17/09/2025	
⊕ India	204	07/07/2025		17/09/2025	
⊕ Mexico	158	10/07/2025		17/09/2025	
⊕ Taiwan	102	27/08/2025		11/09/2025	
⊕ Thailand	90	05/09/2025		17/09/2025	
⊕ Hong Kong	85	04/09/2025		17/09/2025	
⊕ Bahrain	73	07/09/2025		17/09/2025	
⊕ Oman	55	03/07/2025		17/09/2025	
⊕ Kazakhstan	51	29/07/2025		11/09/2025	
⊕ South Africa	50	25/08/2025		17/09/2025	
⊕ Qatar	45	12/07/2025		28/08/2025	
⊕ Ecuador	44	27/08/2025		09/09/2025	
⊕ Egypt	42	03/09/2025		17/09/2025	
⊕ Guam	34	18/08/2025		26/08/2025	
⊕ Guatemala	33	08/08/2025		29/08/2025	
⊕ Cambodia	32	04/09/2025		17/09/2025	
⊕ Brunei	30	08/07/2025		09/09/2025	
⊕ Chile	29	10/08/2025		05/09/2025	
⊕ Laos	29	21/08/2025		17/09/2025	
⊕ Dominican	27	01/08/2025		19/08/2025	
⊕ Lebanon	21	20/08/2025		17/09/2025	
— Total	6,043	07/09/2025		17/09/2025	

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.