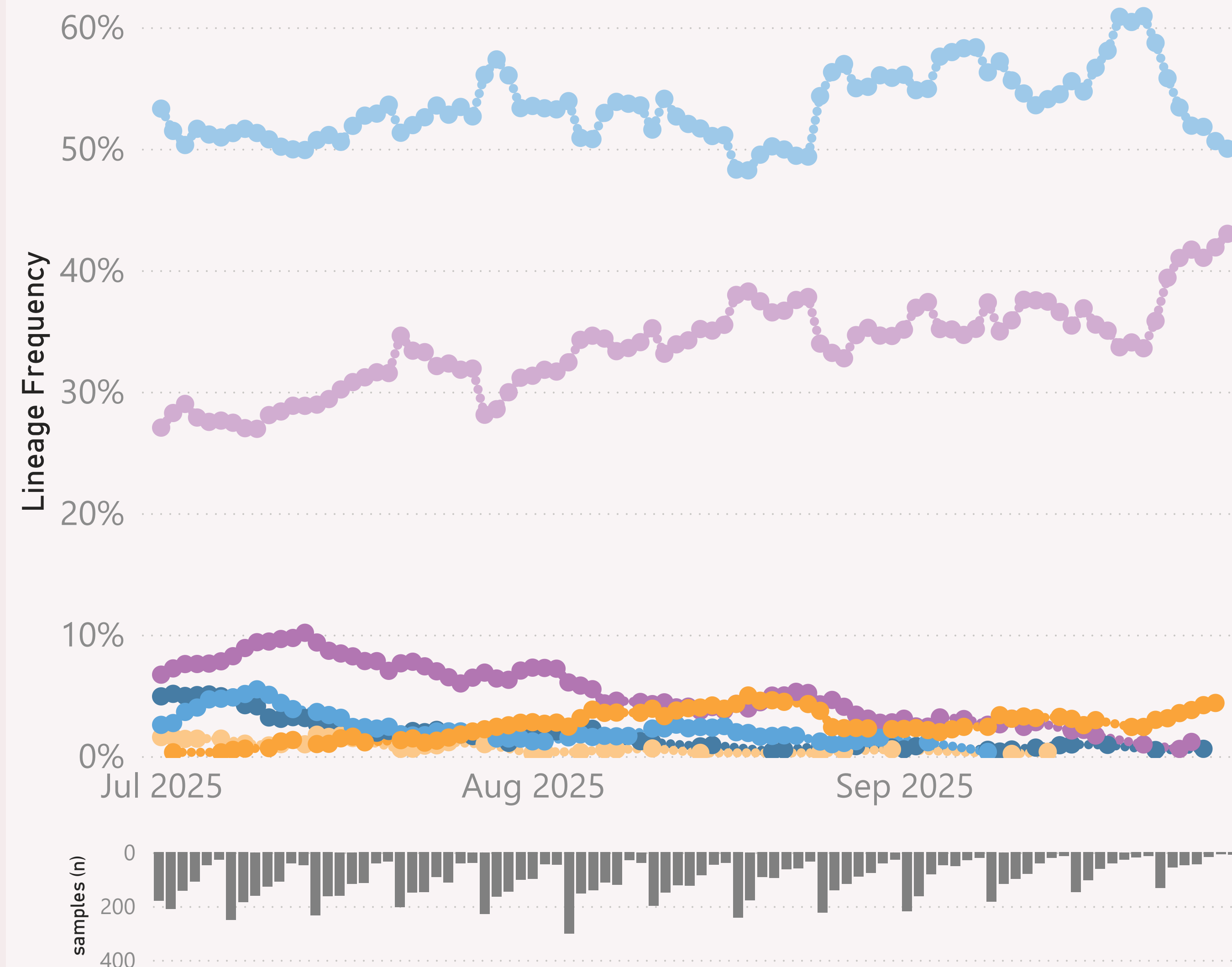


n=9,203 sequenced genomes, from 1 July 2025 up to 28 September 2025

Global - Other

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



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

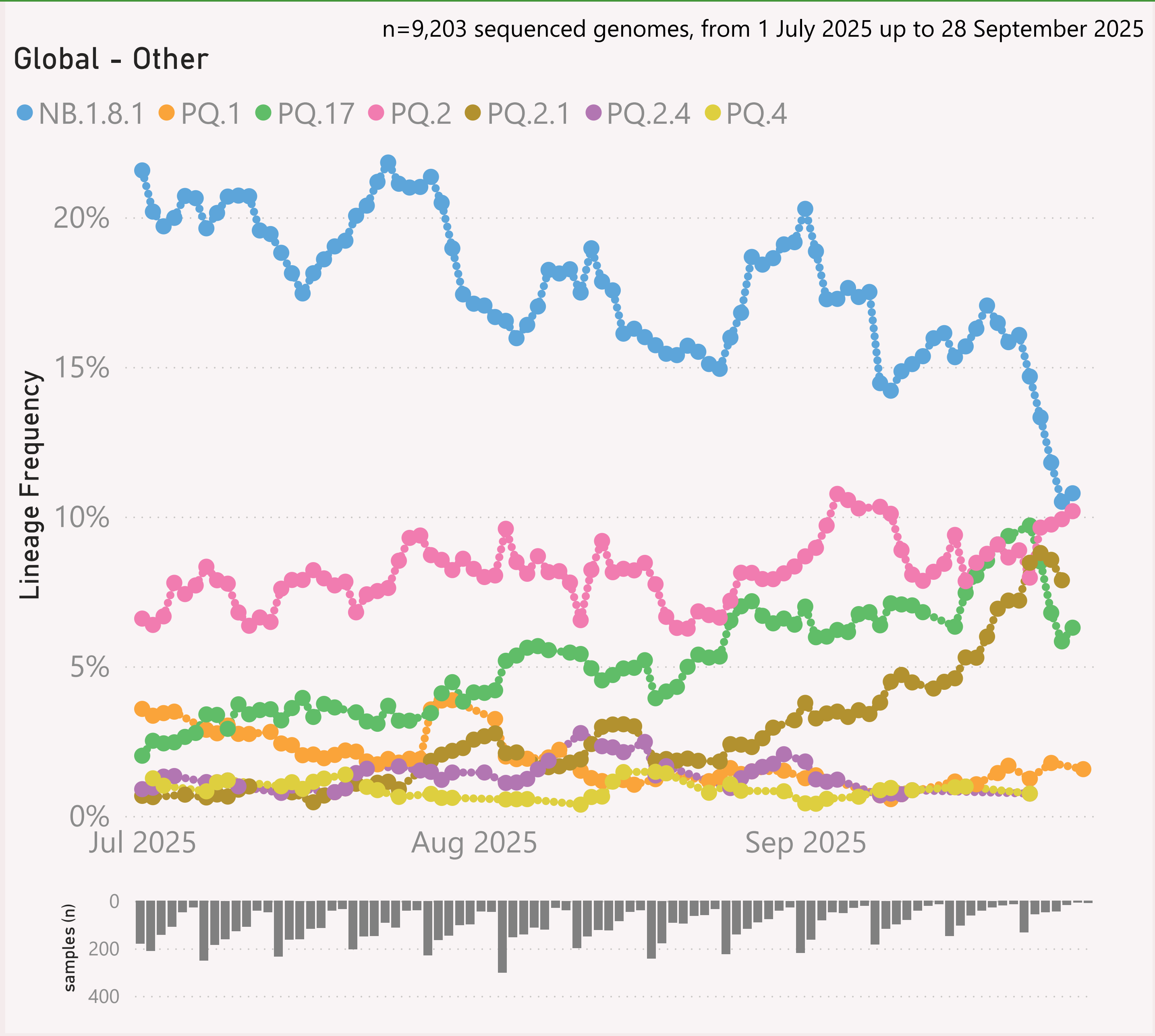
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.

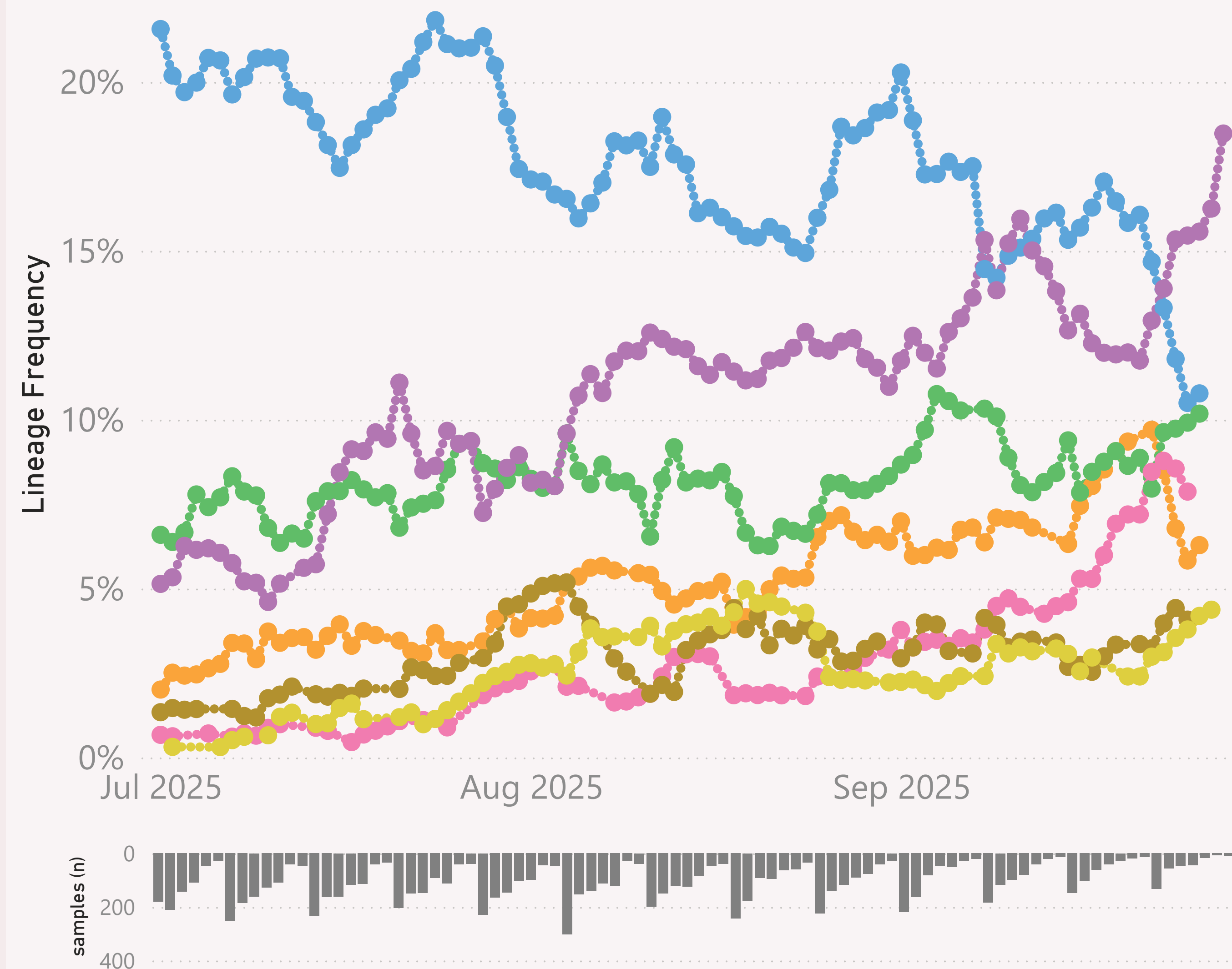
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=9,203 sequenced genomes, from 1 July 2025 up to 28 September 2025

Global - Other

● NB.1.8.1 ● PQ.17 ● PQ.2 ● PQ.2.1 ● XFG.2 ● XFG.3.4.1 ● Xfv



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.

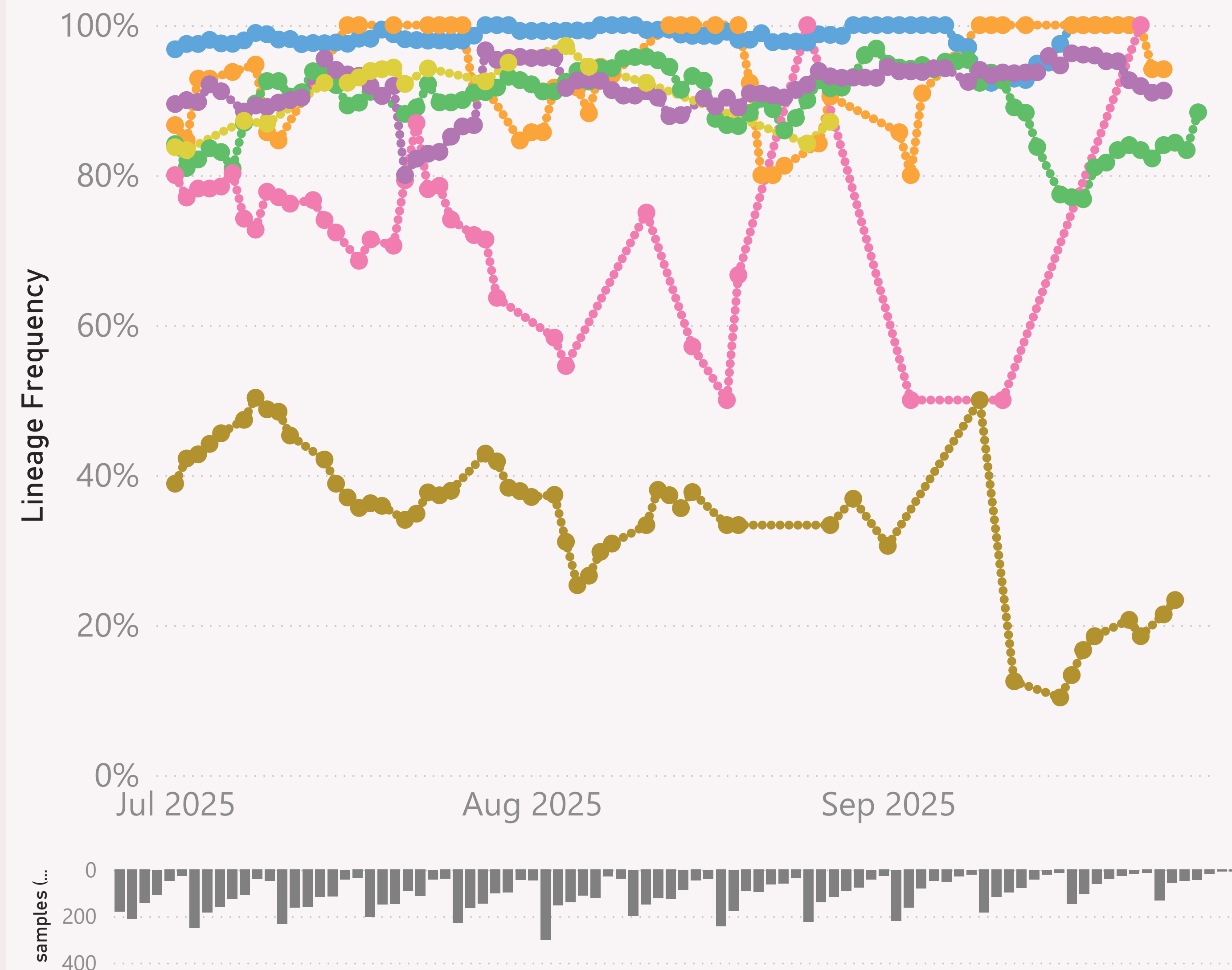
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=9,203 sequenced genomes, from 1 July 2025 up to 28 September 2025

NB.1.8.1.* Nimbus

● China ● Hong Kong ● Japan ● Malaysia ● Singapore ● South Korea ● Taiwan



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.

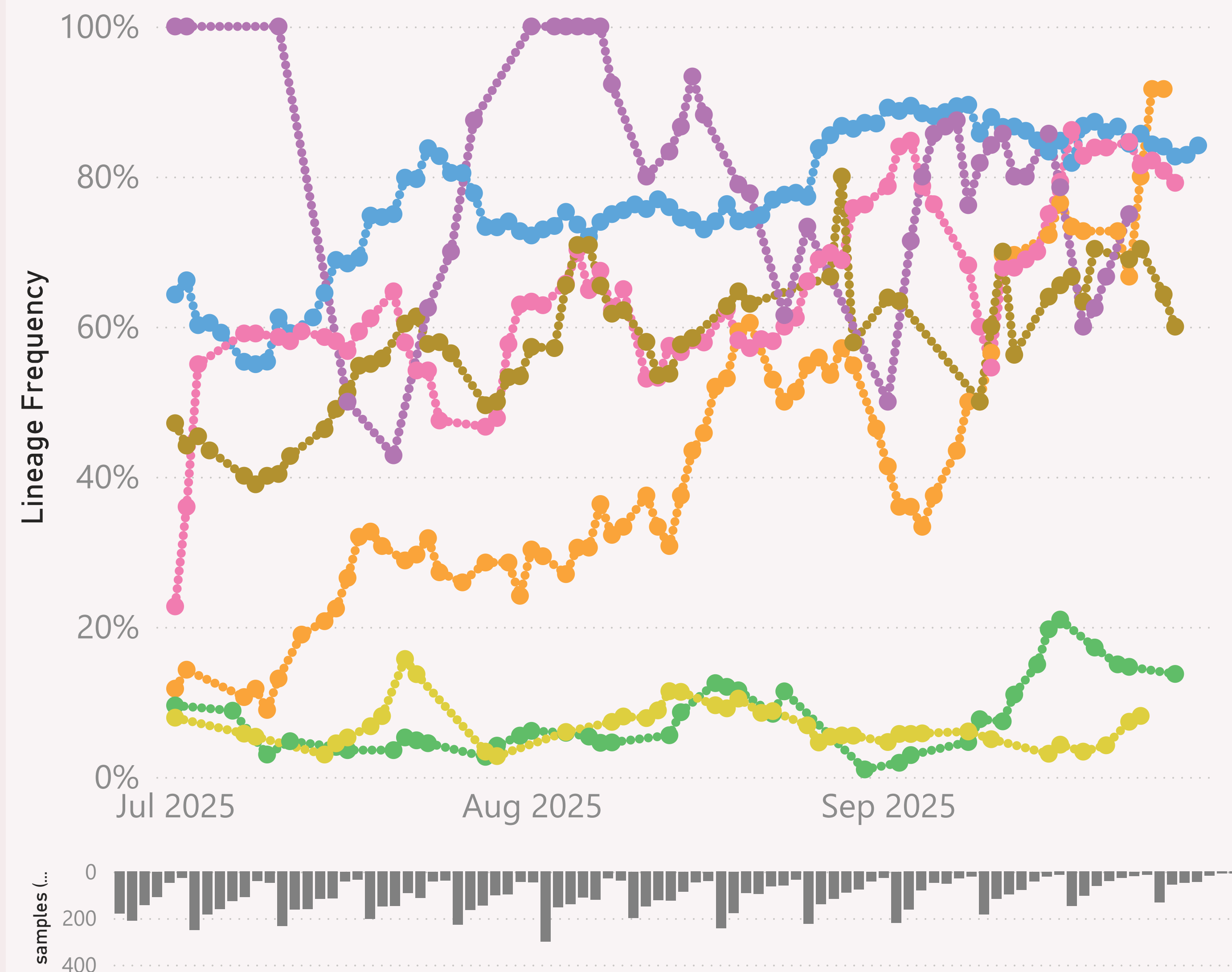
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=9,203 sequenced genomes, from 1 July 2025 up to 28 September 2025

XFG.*

● Brazil ● Costa Rica ● Japan ● Puerto Rico ● Singapore ● South Africa ● South Kor...



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.

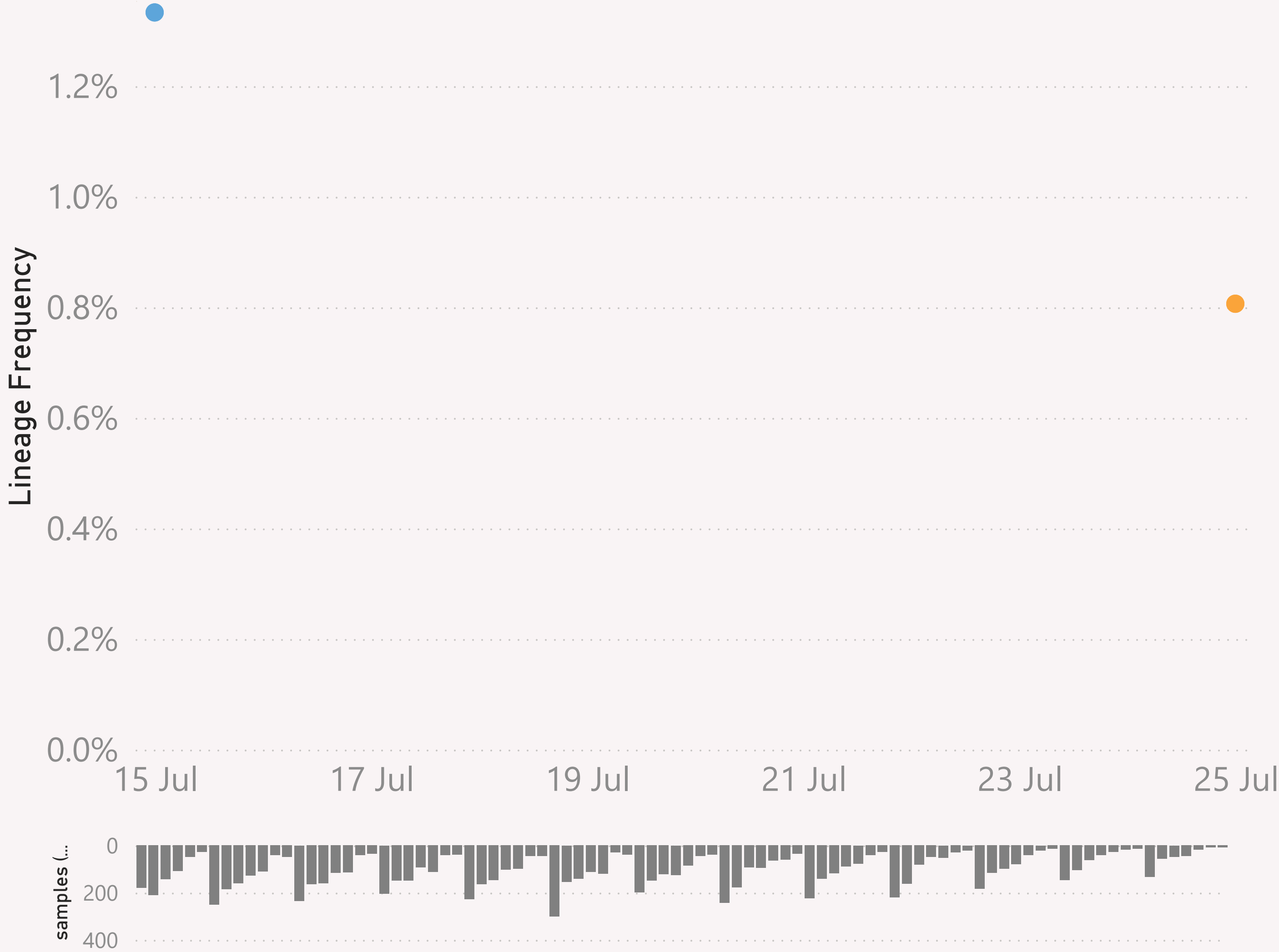
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=9,203 sequenced genomes, from 1 July 2025 up to 28 September 2025

XFP

Japan Singapore



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)

2

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextcla
Singapore			25/07/2025	XFP.*	XFP
Japan		Quar...	15/07/2025	XFP.*	XFP

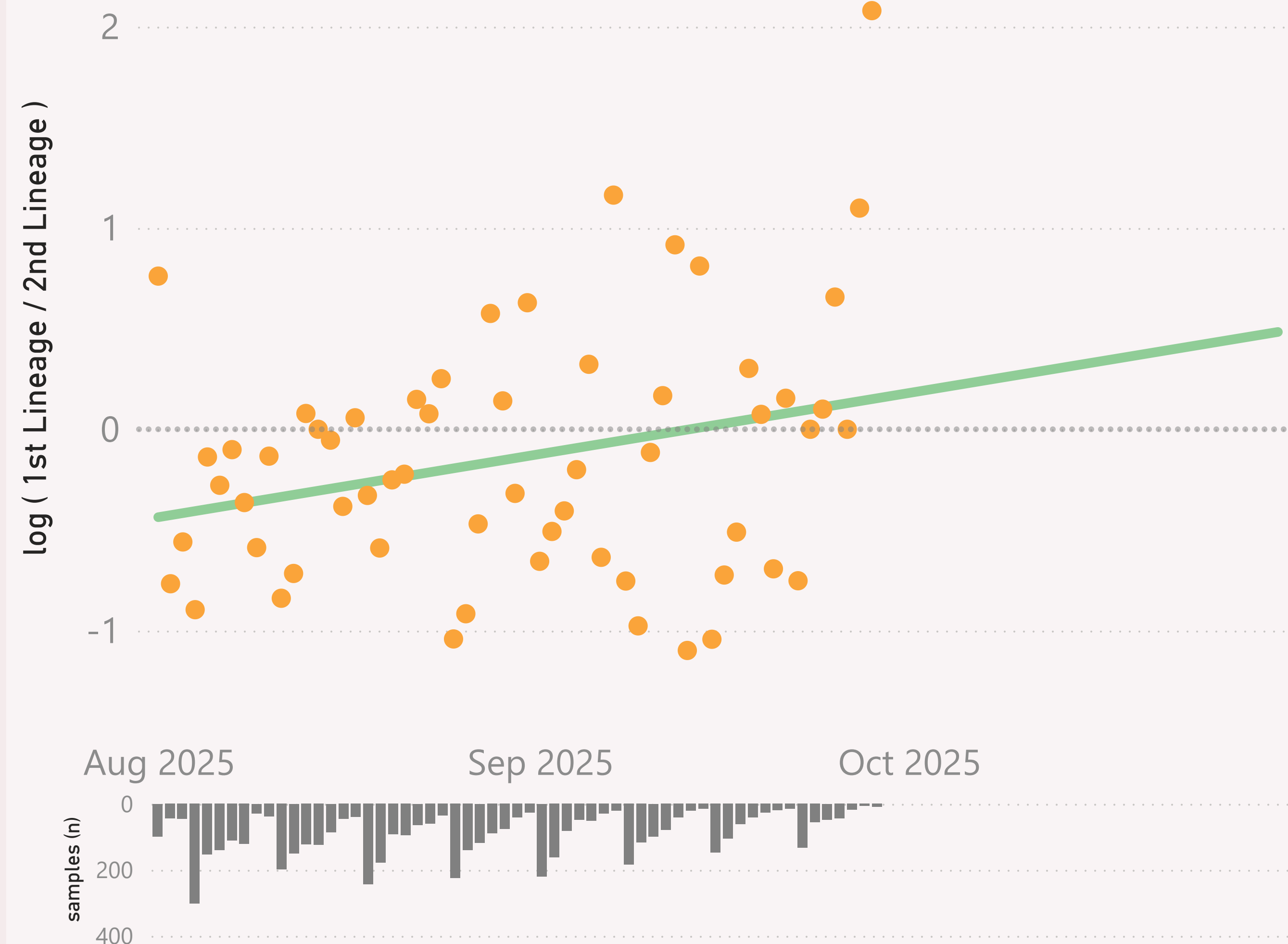
Total

n=5,253 sequenced genomes, from 1 August 2025 up to 28 September 2025

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

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

growth of 1.0% per day, crossover on 14-Sep-25

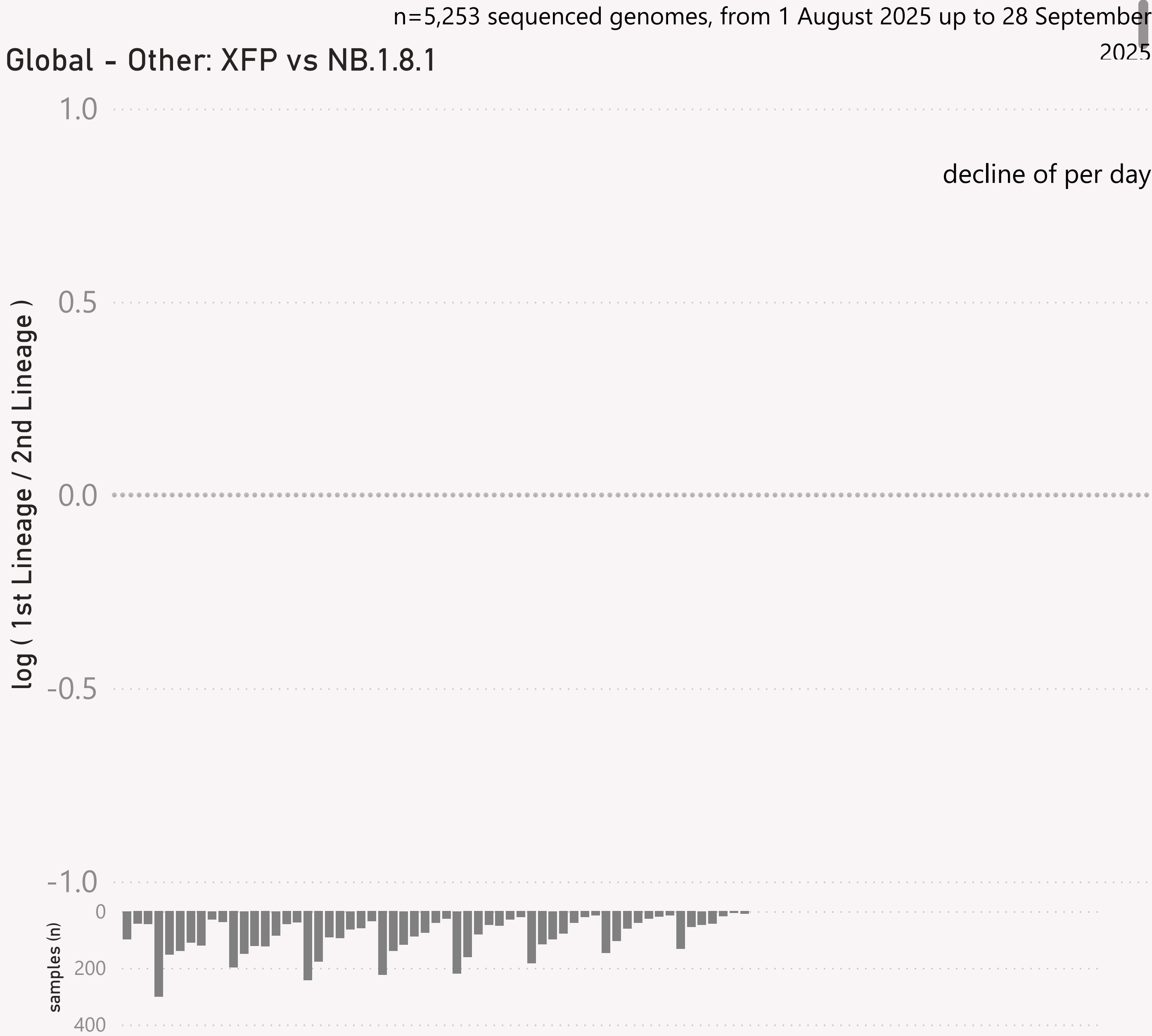


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.



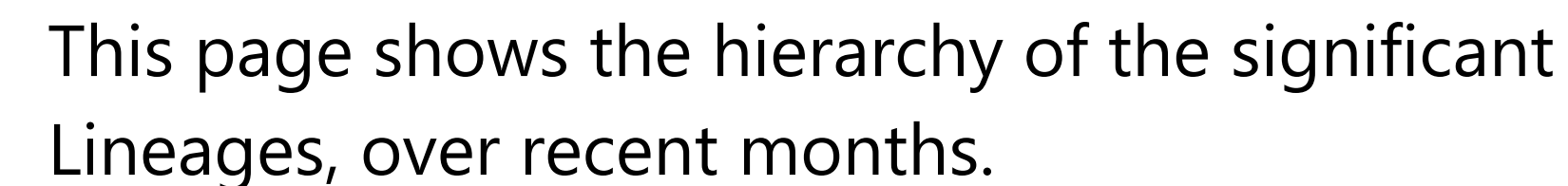
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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

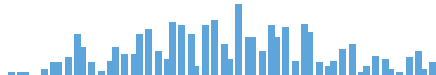














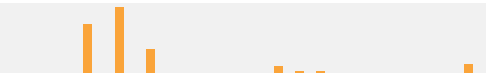



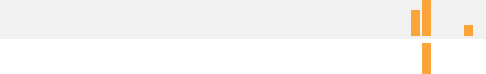




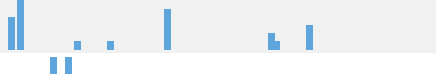






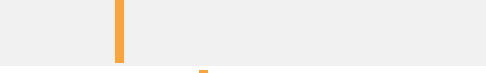





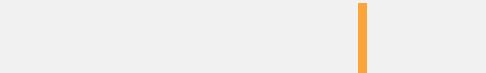








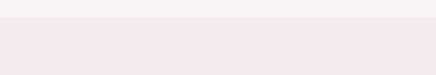
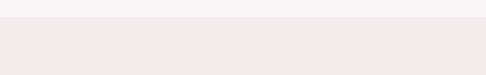
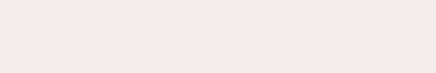
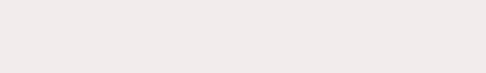


The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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
<div>+ </div> Brazil	1,396	28/09/2025		14/10/2025	
<div>+ </div> South Korea	1,295	25/09/2025		14/10/2025	
<div>+ </div> Japan	763	28/09/2025		14/10/2025	
<div>+ </div> China	581	22/09/2025		11/10/2025	
<div>+ </div> Puerto Rico	304	26/09/2025		14/10/2025	
<div>+ </div> Costa Rica	233	25/09/2025		14/10/2025	
<div>+ </div> Argentina	128	30/08/2025		08/10/2025	
<div>+ </div> Singapore	114	26/09/2025		14/10/2025	
<div>+ </div> Taiwan	102	27/08/2025		11/09/2025	
<div>+ </div> Malaysia	95	23/09/2025		14/10/2025	
<div>+ </div> Ecuador	94	27/09/2025		14/10/2025	
<div>+ </div> Guatemala	85	25/09/2025		14/10/2025	
<div>+ </div> South Africa	82	22/09/2025		13/10/2025	
<div>+ </div> Chile	72	13/09/2025		29/09/2025	
<div>+ </div> Hong Kong	71	25/09/2025		14/10/2025	
<div>+ </div> Egypt	42	03/09/2025		18/09/2025	
<div>+ </div> Bahrain	33	07/09/2025		21/09/2025	
<div>+ </div> Barbados	29	24/09/2025		10/10/2025	
<div>+ </div> India	28	16/07/2025		29/09/2025	
<div>+ </div> Kazakhstan	20	29/07/2025		11/09/2025	
<div>+ </div> Lebanon	18	20/08/2025		19/09/2025	
<div>+ </div> French Guiana	17	08/09/2025		30/09/2025	
<div>+ </div> Cambodia	15	04/09/2025		19/09/2025	
<div>+ </div> Indonesia	14	19/08/2025		04/10/2025	
<div>+ </div> Mexico	12	10/07/2025		19/09/2025	
<div>+ </div> Dominican	11	16/09/2025		14/10/2025	
<div>+ </div> Oman	11	03/07/2025		24/09/2025	
<div>+ </div> Senegal	11	28/08/2025		14/10/2025	
<div>+ </div> Total	5,734	28/09/2025		14/10/2025	

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.