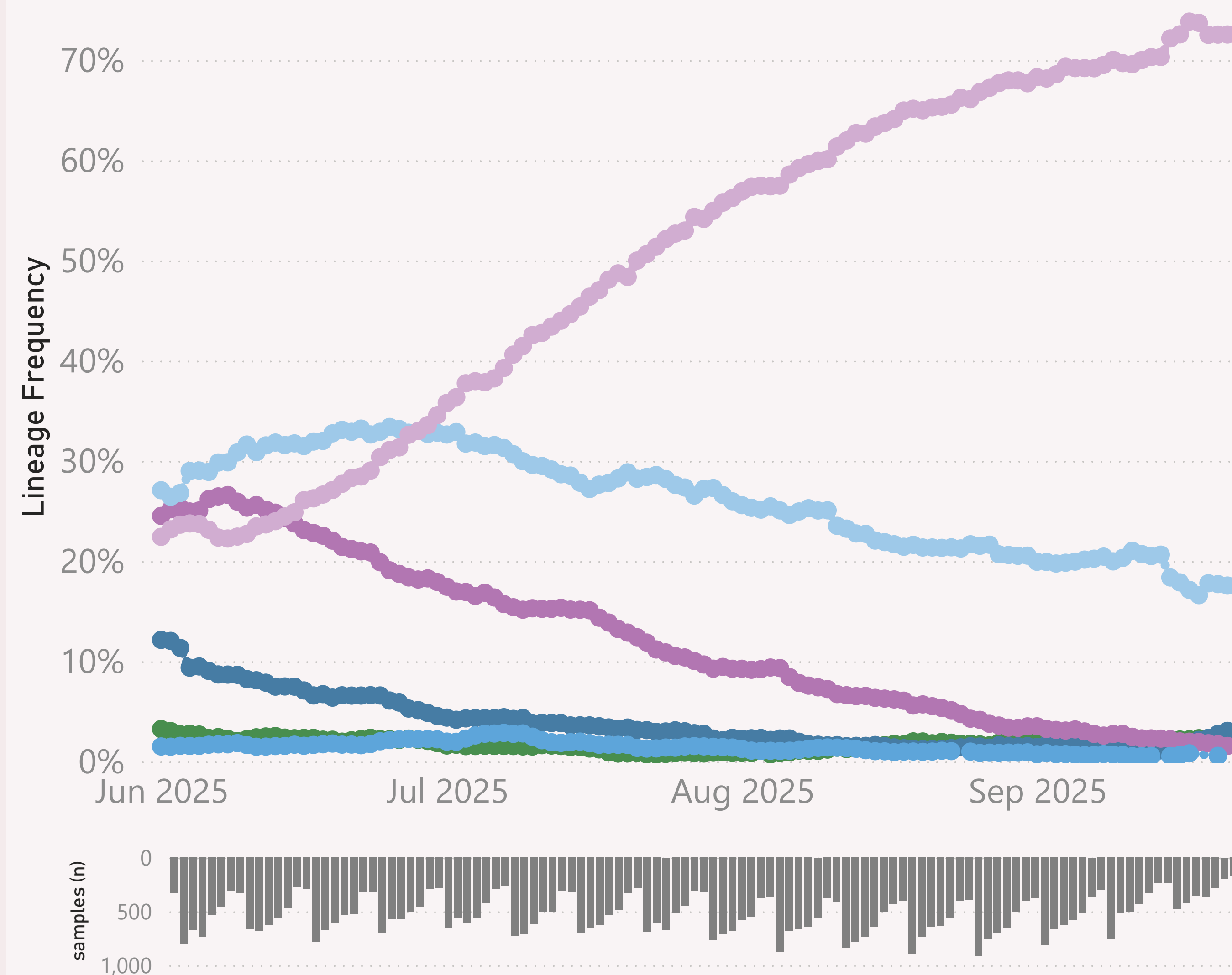n=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

Global

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

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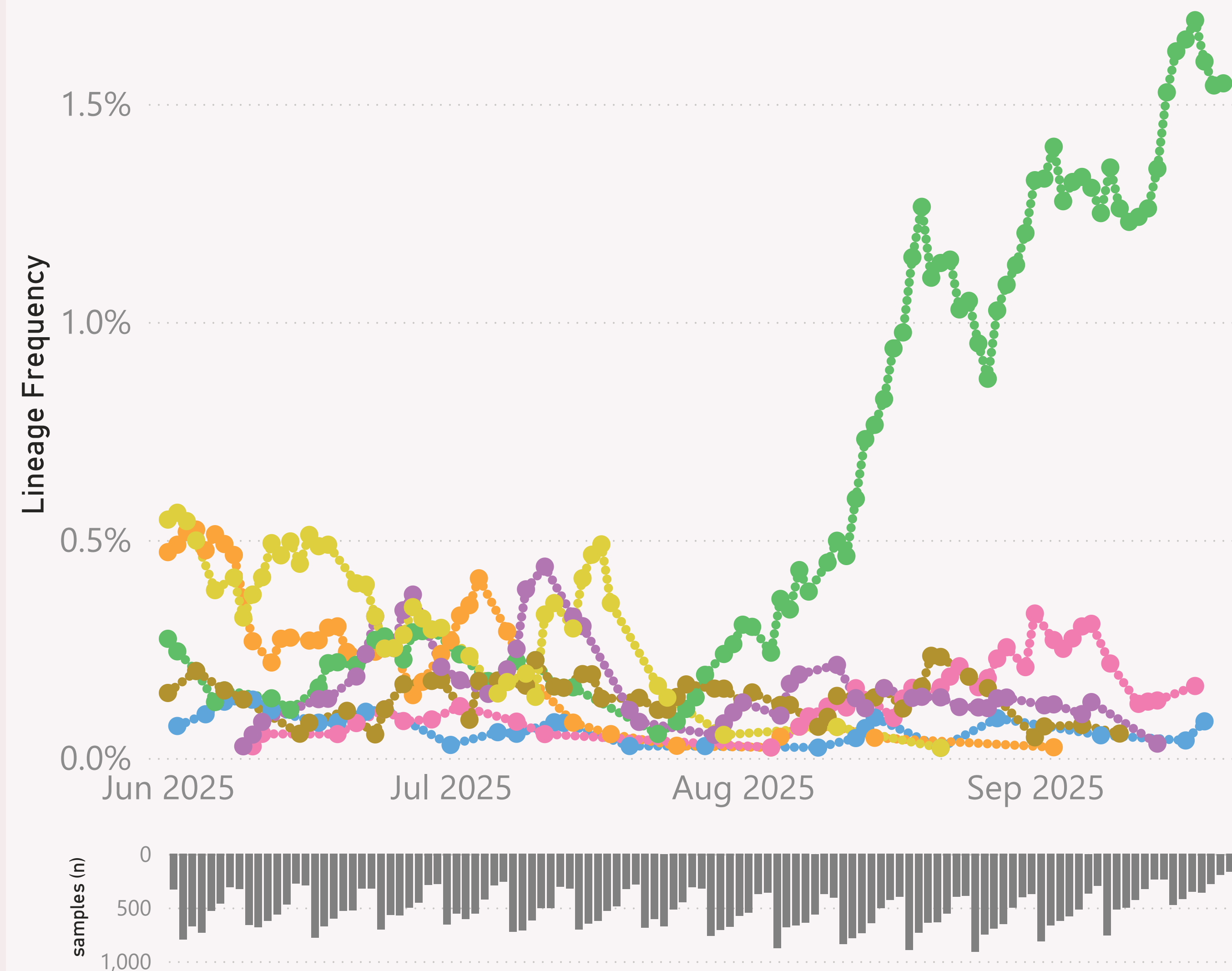
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

Global

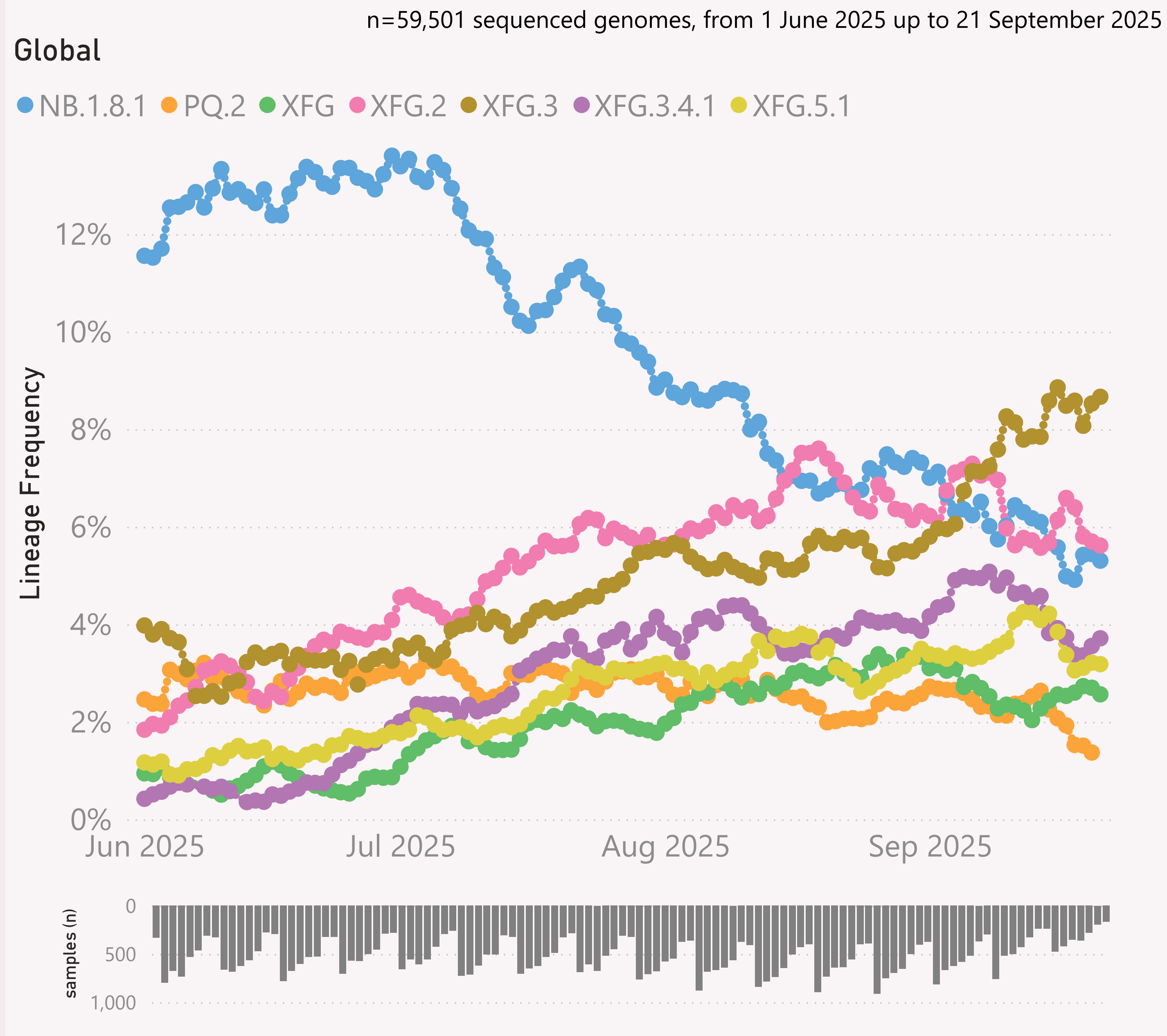●MC.10.2.1 ●MC.21.1 ●PE.1.4 ●PE.1.4.2 ●PE.2 ●PE.3 ●PG.3.1

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

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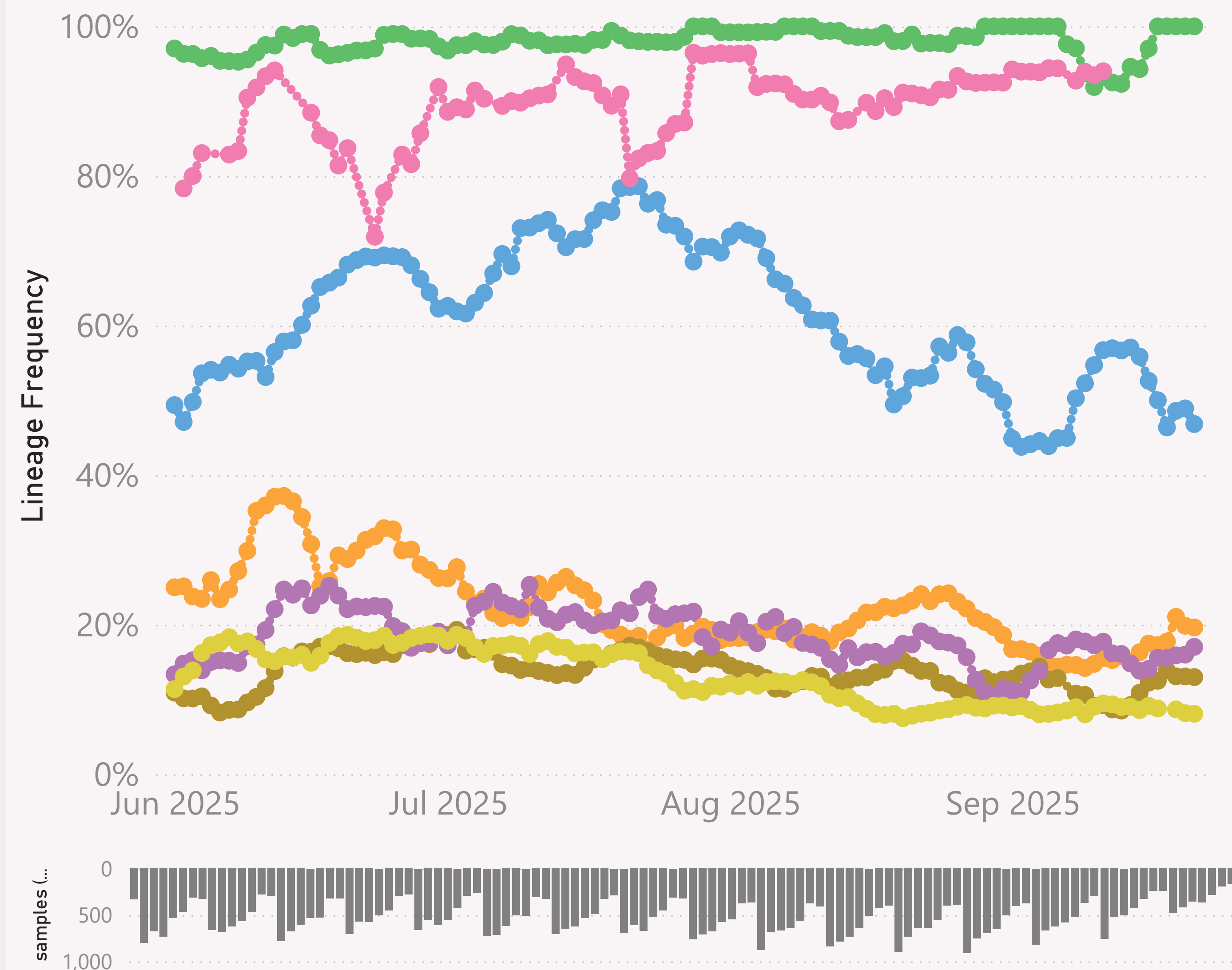
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

Global

- NB.1.8.1 ● PQ.2 ● XFG ● XFG.2 ● XFG.3 ● XFG.3.4.1 ● XFG.5.1

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.

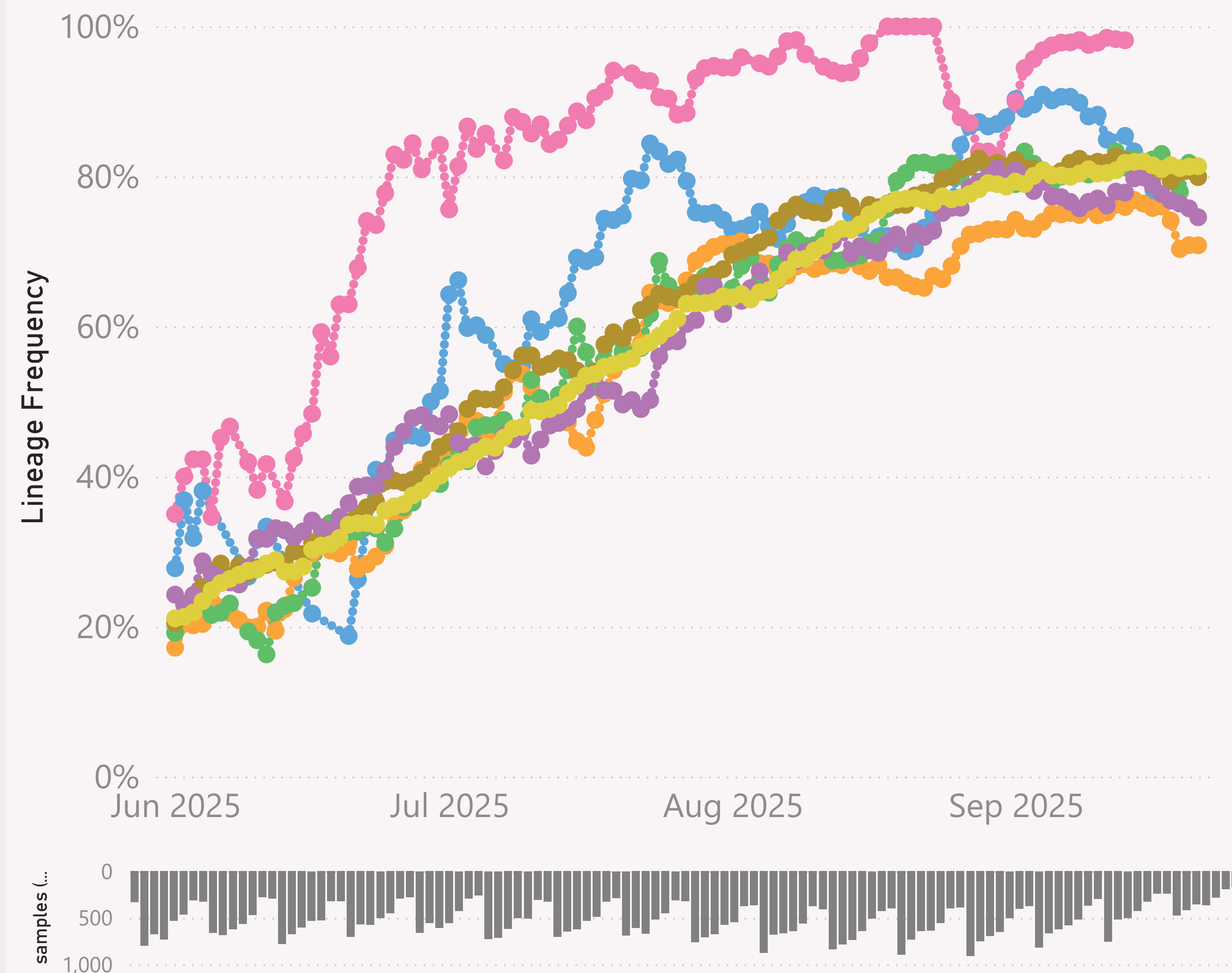The frequency shown at each point is based on the 7-day rolling average across all lineages.

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=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

NB.1.8.1.* Nimbus

- Australia
- Canada
- China
- South Korea
- Spain
- United Kingd...
- United St...

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=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

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

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n=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

XFP

- Australia
- Canada
- France
- India
- Ireland
- Singapore
- United States
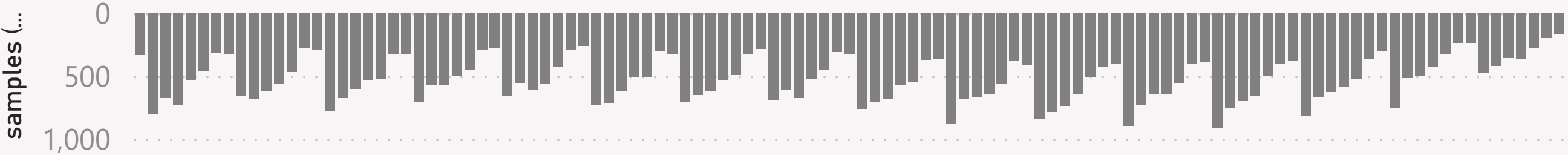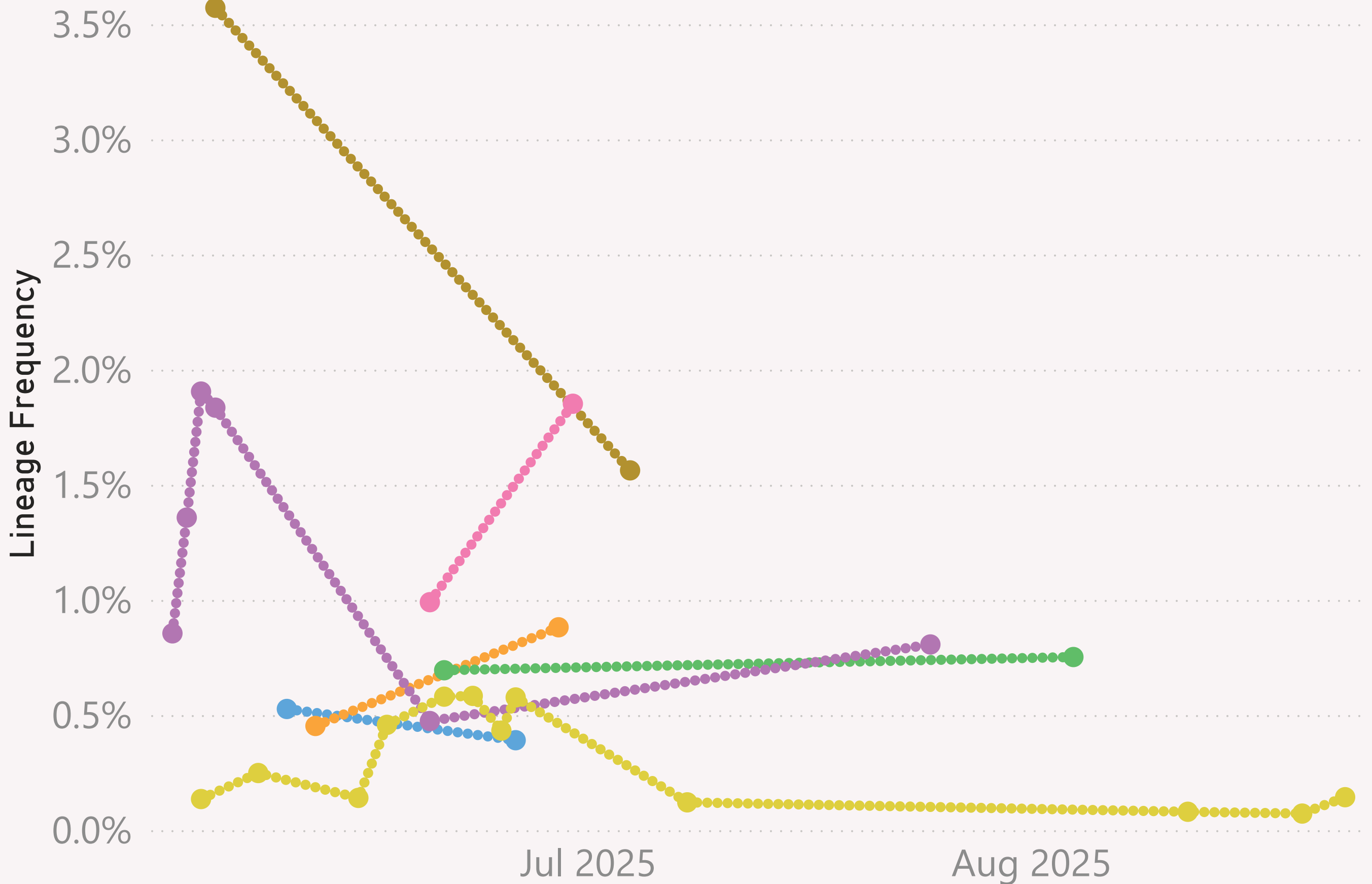
Date

| 01/01/2025 | 31/12/2025 |

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

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

Host

Human

Samples Sequenced (gisaid)

39

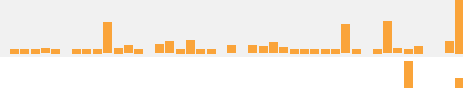| Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
USA	Illinois		23/08/2025	XFP.*	XFP
USA	California		20/08/2025	XFP.*	XFP
USA	California		12/08/2025	XFP.*	XFP
France	Auvergne-Rho...		04/08/2025	XFP.*	XFP
Singapore			25/07/2025	XFP.*	XFP
Luxembourg			24/07/2025	XFP.*	XFP
Japan		Quar...	15/07/2025	XFP.*	XFP
USA	Texas		08/07/2025	XFP.*	XFP
Ireland	Dublin		04/07/2025	XFP.*	XFP
India	Maharashtra		30/06/2025	XFP.*	XFP
Canada	Ontario		29/06/2025	XFP.*	XFP
Germany	Rhineland-Pala...		27/06/2025	XFP.*	XFP
United Kingdom	Wales		27/06/2025	XFP.*	XFP
USA	Minnesota		26/06/2025	XFP.*	XFP
Australia	Victoria		26/06/2025	XFP.*	XFP
USA	Minnesota		25/06/2025	XFP.*	XFP
USA	California		23/06/2025	XFP.*	XFP
USA	Oregon		21/06/2025	XFP.*	XFP
France	Provence-Alpe...		21/06/2025	XFP.*	XFP
Singapore			20/06/2025	XFP.*	XFP
India	Chhattisgarh		20/06/2025	XFP.*	XFP
USA	Massachusetts		17/06/2025	XFP.*	XFP

Total

n=43,928 sequenced genomes, from 1 July 2025 up to 21 September 2025

Global – XGA vs XFG.*

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

growth of 0.6% per day
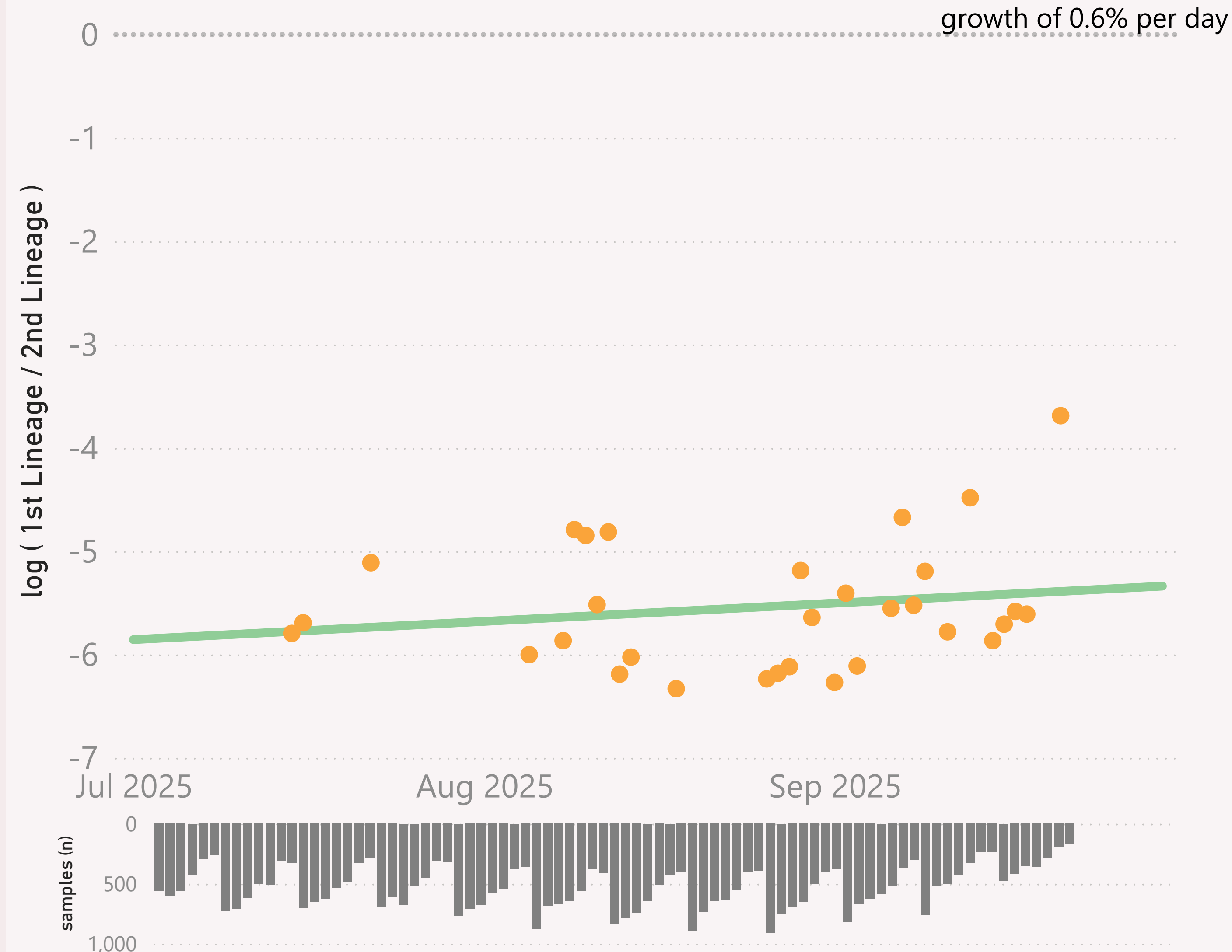
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

COVID-19 Genomic Sequencing analysis. Data from gisaid.org, with nextclade lineages Source files and more info on github.

Last Update: 2025-10-11 02:51 (UTC)

n=43,928 sequenced genomes, from 1 July 2025 up to 21 September 2025

Global - PY.1.1.1 vs XFG.3

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

growth of 0.0% per day
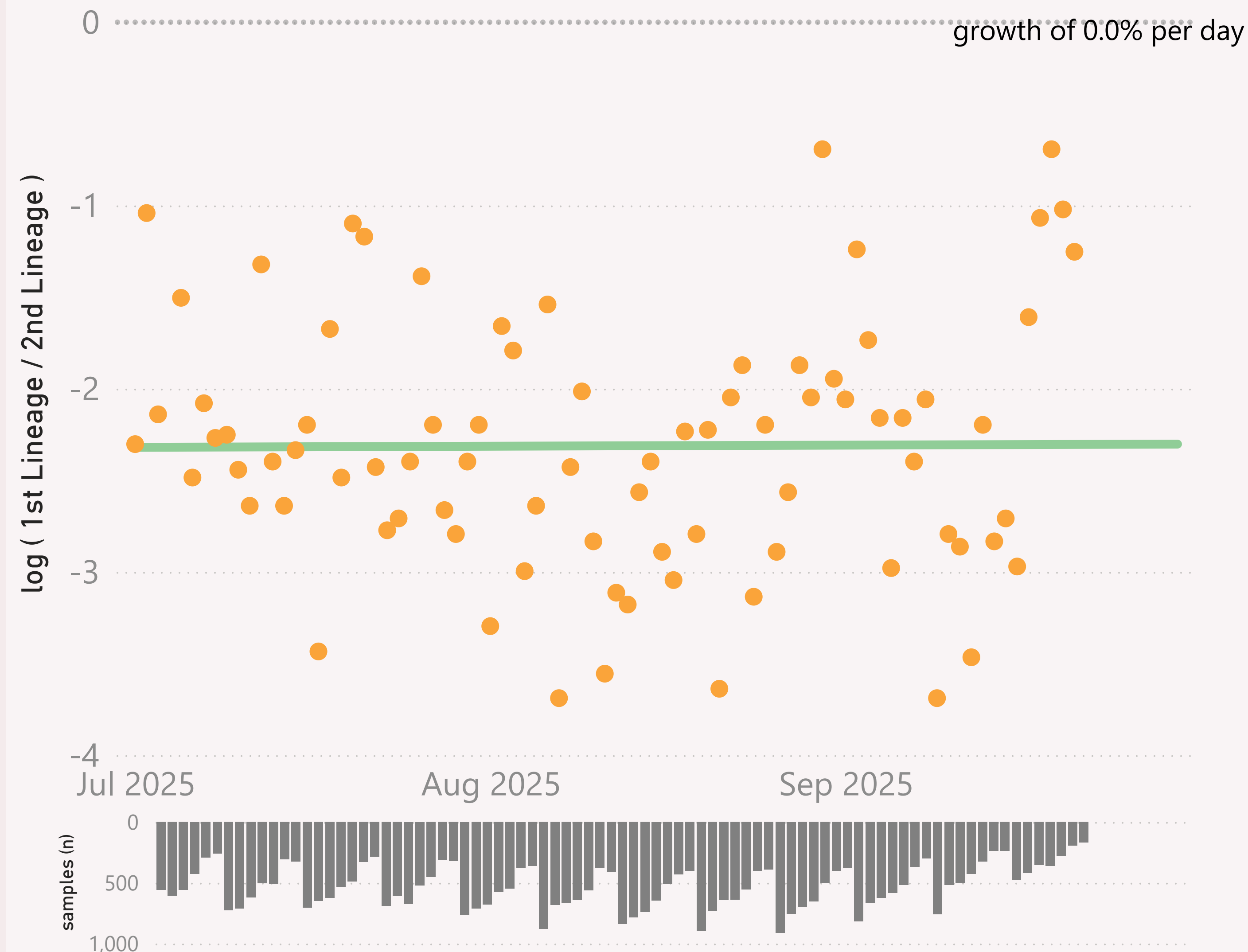
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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=59,501 sequenced genomes, from 1 June 2025 up to 21 September 2025

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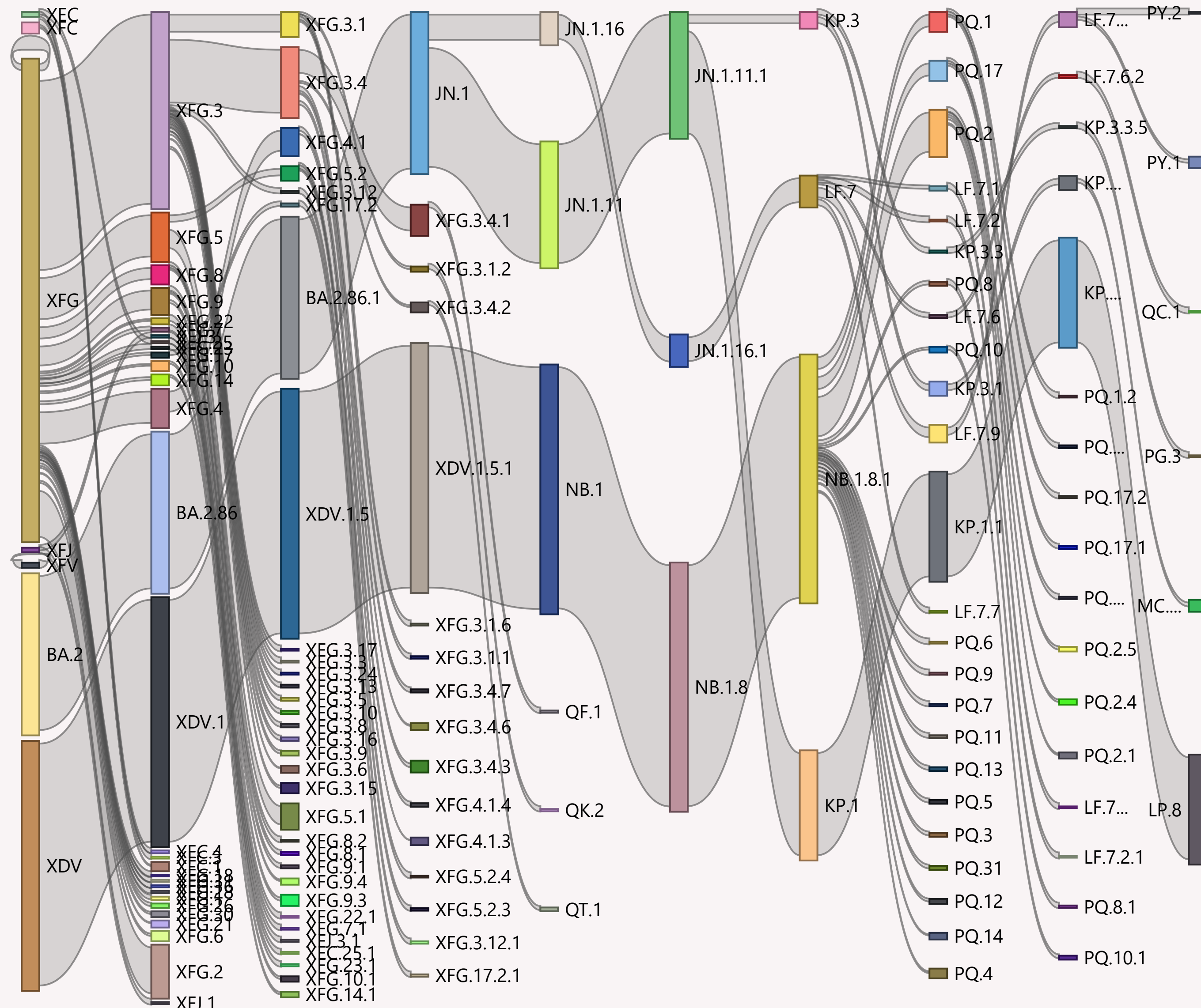
This page shows the hierarchy of the significant Lineages, over recent months.

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.

n=1,067 sequenced genomes, from 1 June 2025 up to 21 September 2025
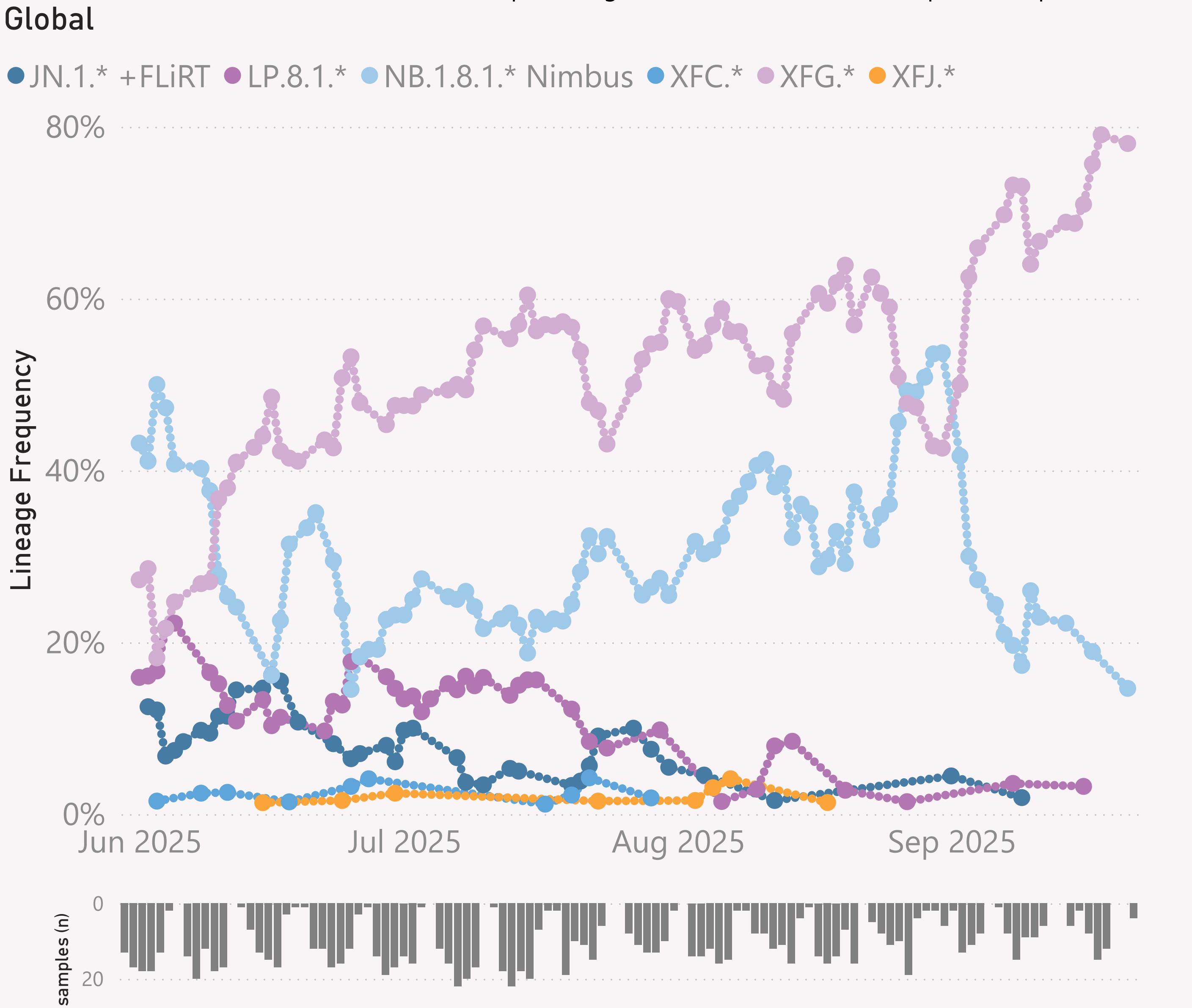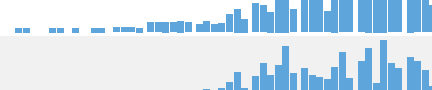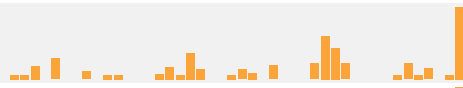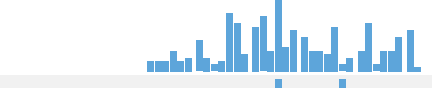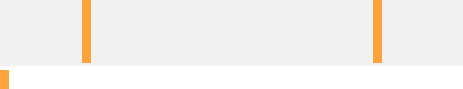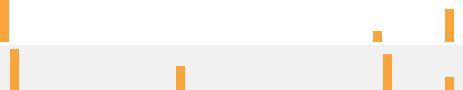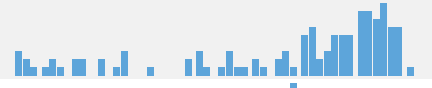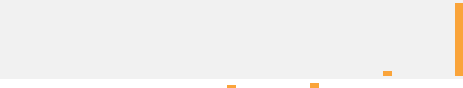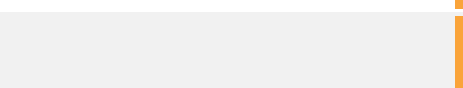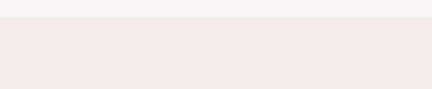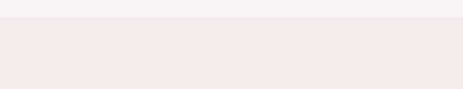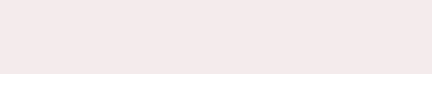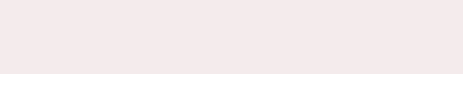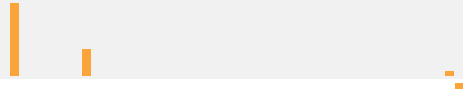
This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

This is probably a more randomised sample than the "Global" aggregate of all samples submitted to GISAID, as those are dominated by the US and Canada

These samples are mainly collected from arrivals into the US and Japan.

COVID-19 Genomic Sequencing analysis - Data Currency. Data from gisaid.org. Source files and info on github.

Last Update: 2025-10-11 02:51 (UTC)

Data Submitted in the last 8 weeks

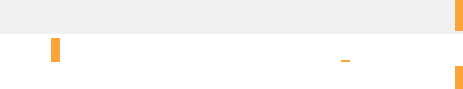| Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ United States	10,975	21/09/2025		30/09/2025	
⊞ Spain	4,435	21/09/2025		30/09/2025	
⊞ Canada	3,707	21/09/2025		30/09/2025	
⊞ United Kingdom	3,543	21/09/2025		30/09/2025	
⊞ Australia	1,529	21/09/2025		30/09/2025	
⊞ France	1,393	21/09/2025		30/09/2025	
⊞ China	1,284	21/09/2025		29/09/2025	
⊞ South Korea	1,190	11/09/2025		30/09/2025	
⊞ Brazil	1,104	17/09/2025		30/09/2025	
⊞ Japan	776	17/09/2025		30/09/2025	
⊞ Russia	676	13/09/2025		30/09/2025	
⊞ Netherlands	627	21/09/2025		29/09/2025	
⊞ Germany	538	21/09/2025		30/09/2025	
⊞ Italy	503	21/09/2025		30/09/2025	
⊞ Ireland	497	20/09/2025		30/09/2025	
⊞ New Zealand	474	21/09/2025		29/09/2025	
⊞ Ukraine	417	19/09/2025		30/09/2025	
⊞ Puerto Rico	389	20/09/2025		30/09/2025	
⊞ Denmark	372	15/09/2025		30/09/2025	
⊞ Luxembourg	363	31/08/2025		22/09/2025	
⊞ India	266	16/07/2025		29/09/2025	
⊞ Costa Rica	253	04/09/2025		29/09/2025	
⊞ Portugal	243	03/08/2025		29/08/2025	
⊞ Switzerland	234	15/09/2025		30/09/2025	
⊞ Sweden	212	20/09/2025		30/09/2025	
⊞ Singapore	211	19/09/2025		29/09/2025	
⊞ Finland	180	11/09/2025		30/09/2025	
⊞ Argentina	167	30/08/2025		30/09/2025	
Total	**38,555**	**21/09/2025**		**30/09/2025**	

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.