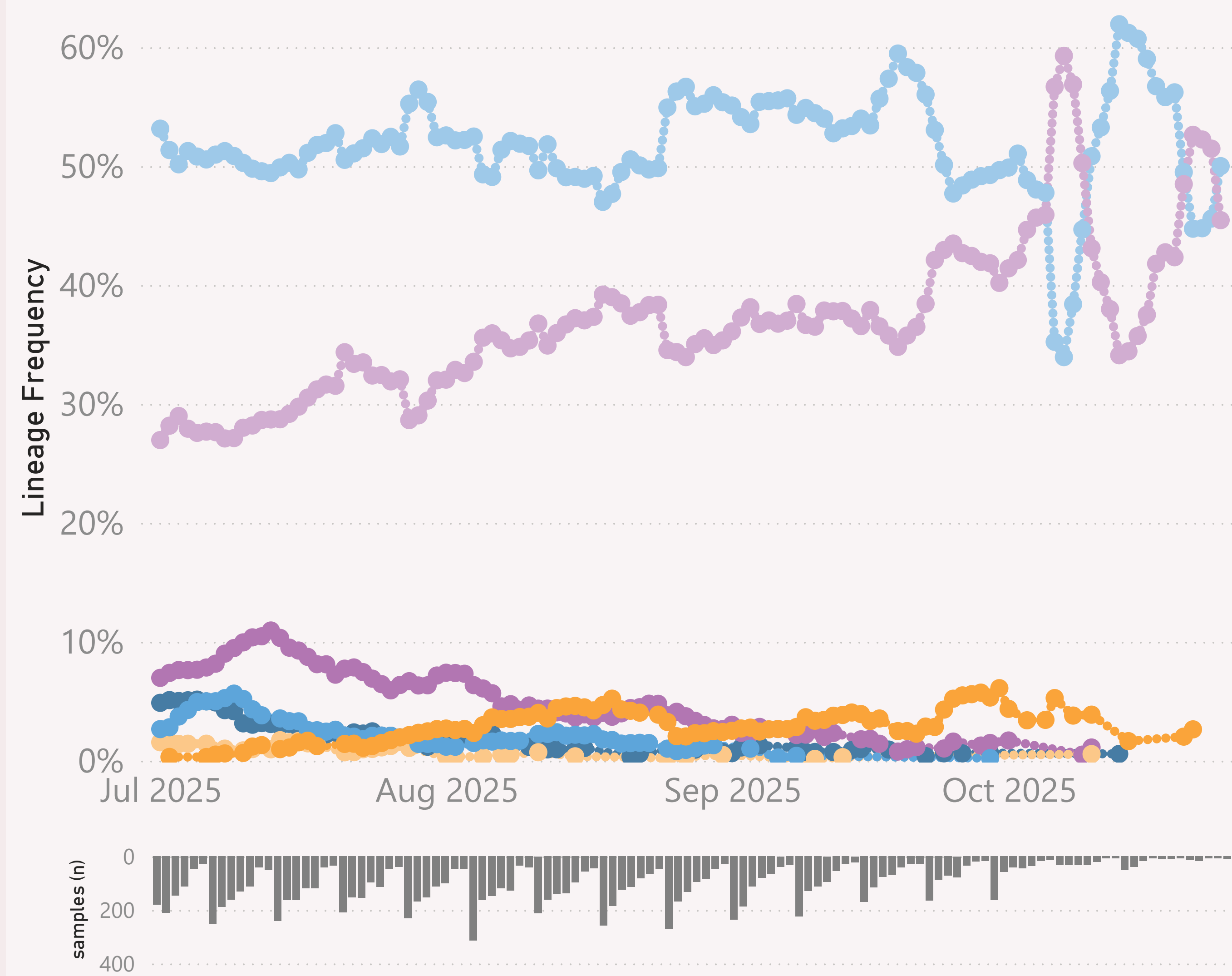n=10,891 sequenced genomes, from 1 July 2025 up to 24 October 2025

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 Europe.

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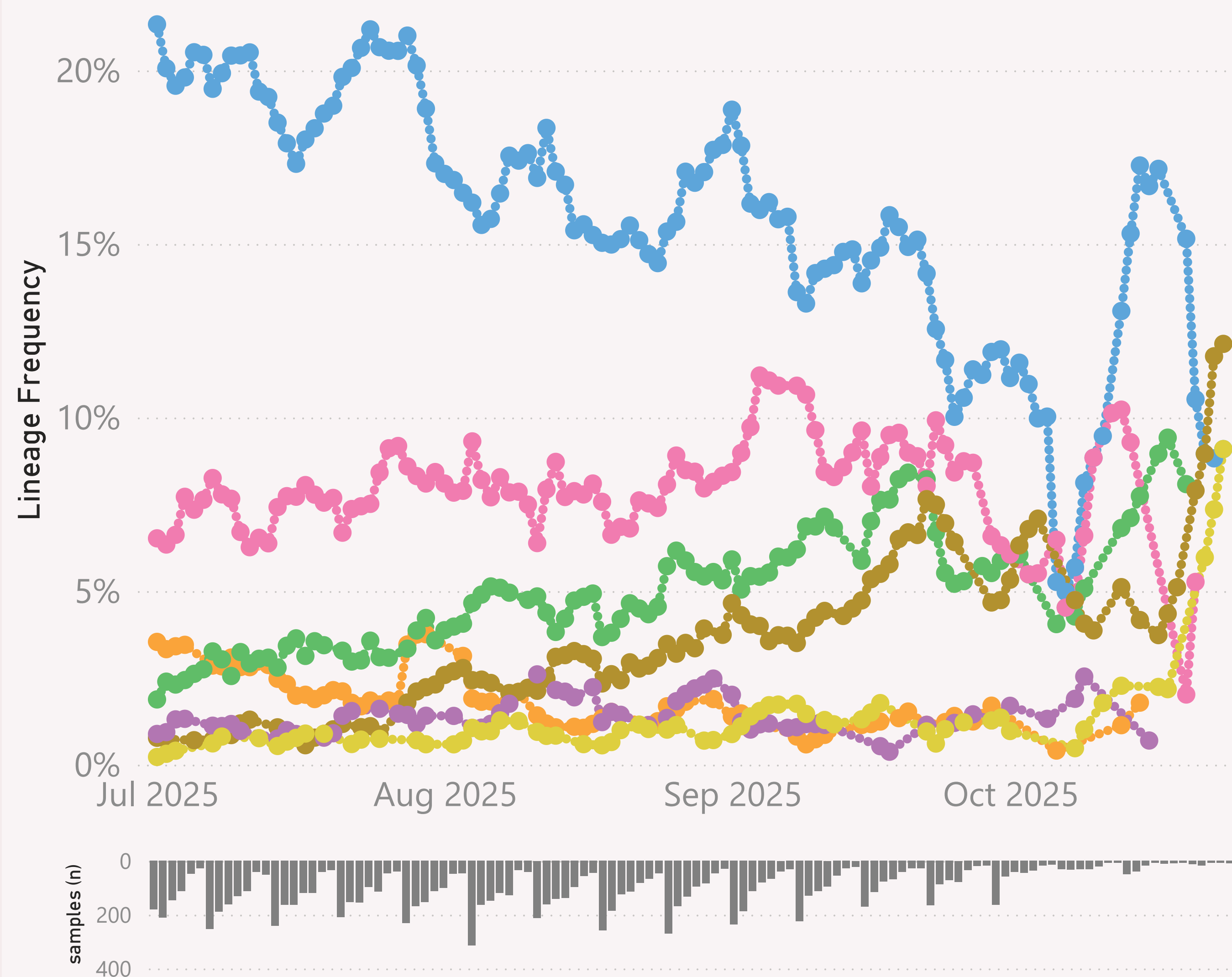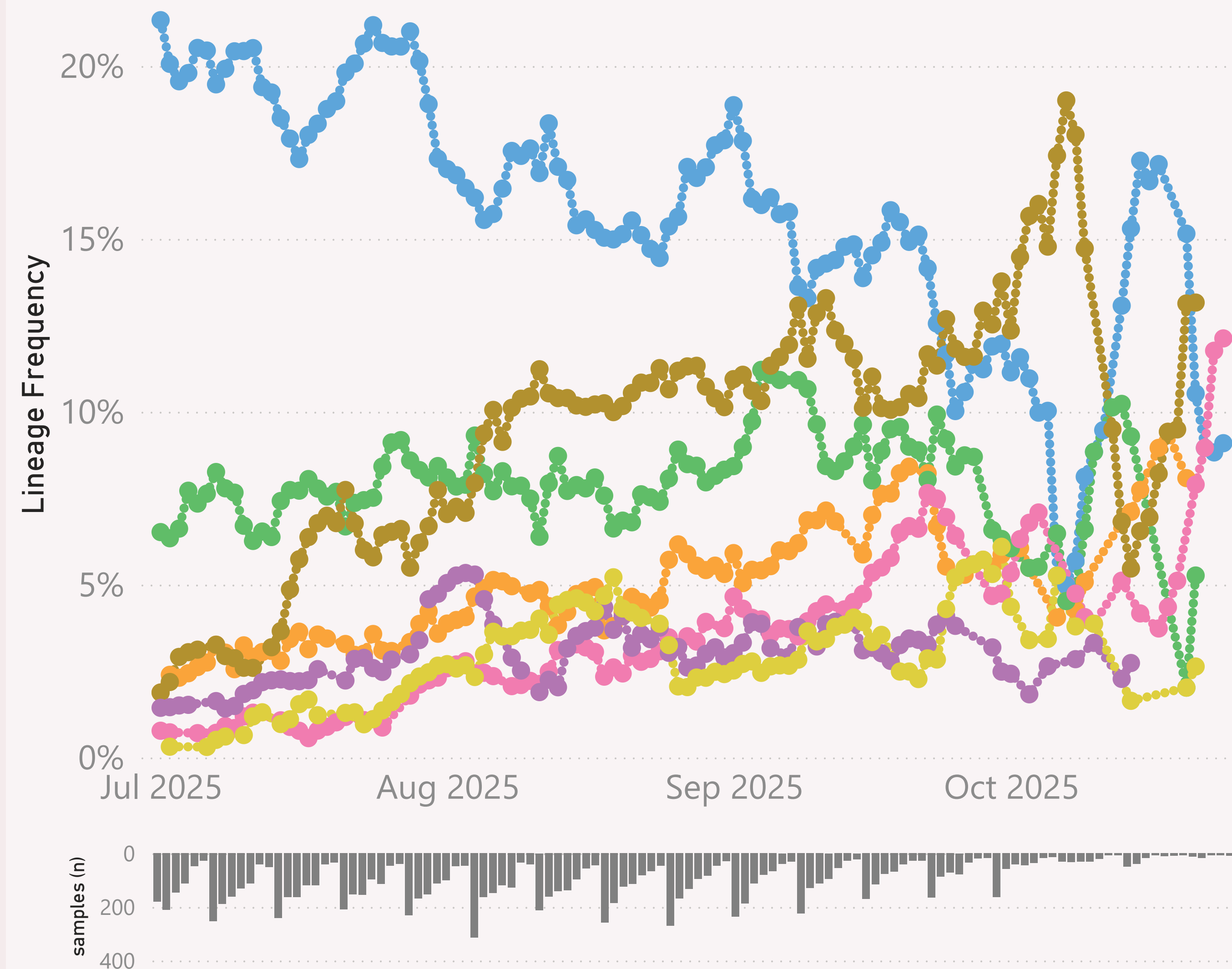
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=10,891 sequenced genomes, from 1 July 2025 up to 24 October 2025

Global – Other

● NB.1.8.1 ● PQ.1 ● PQ.17 ● PQ.2 ● PQ.2.1 ● PQ.2.4 ● PQ.2.5

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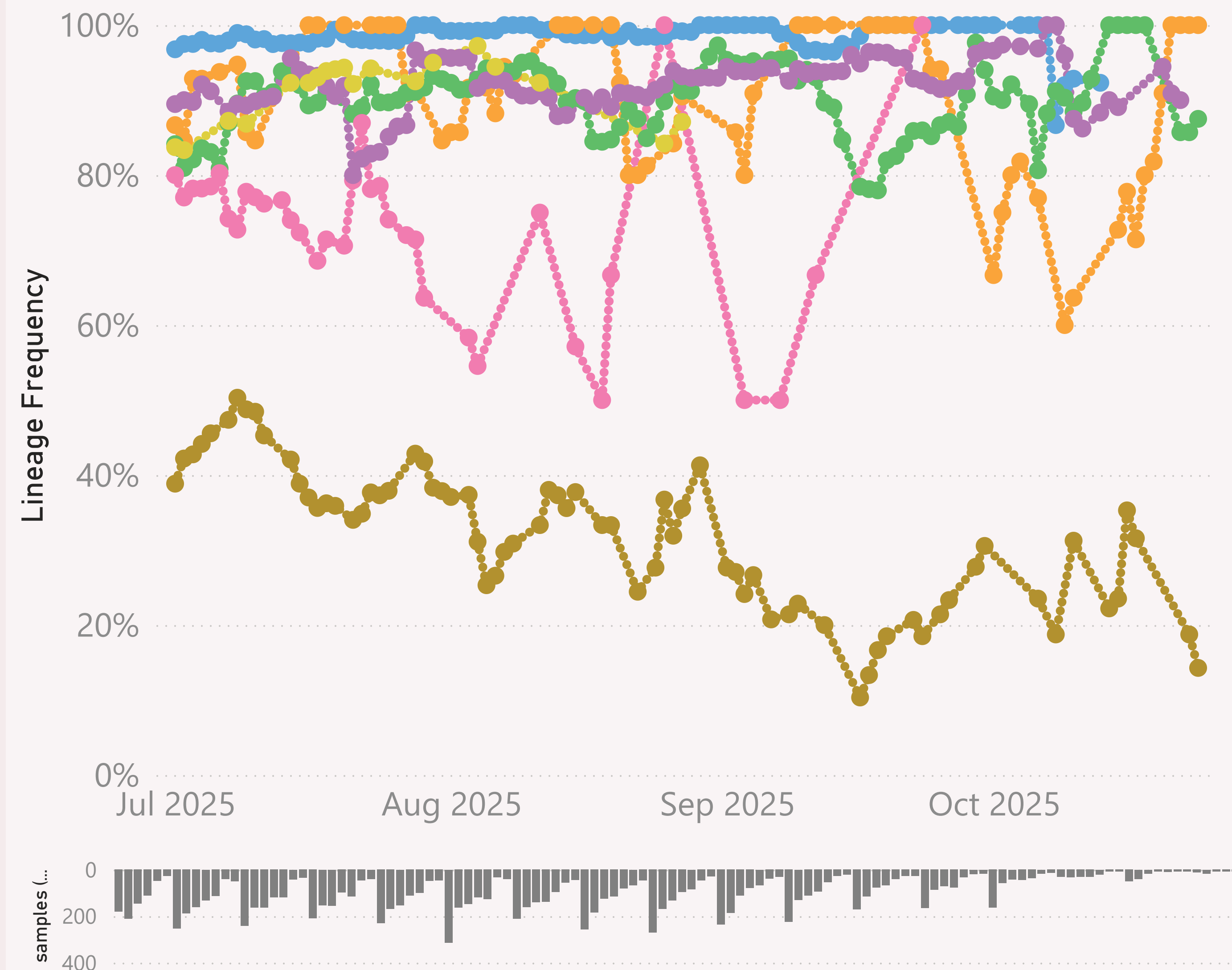
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=10,891 sequenced genomes, from 1 July 2025 up to 24 October 2025

Global - Other

● NB.1.8.1 ● PQ.17 ● PQ.2 ● PQ.2.1 ● QF.2 ● XFG.2 ● 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.
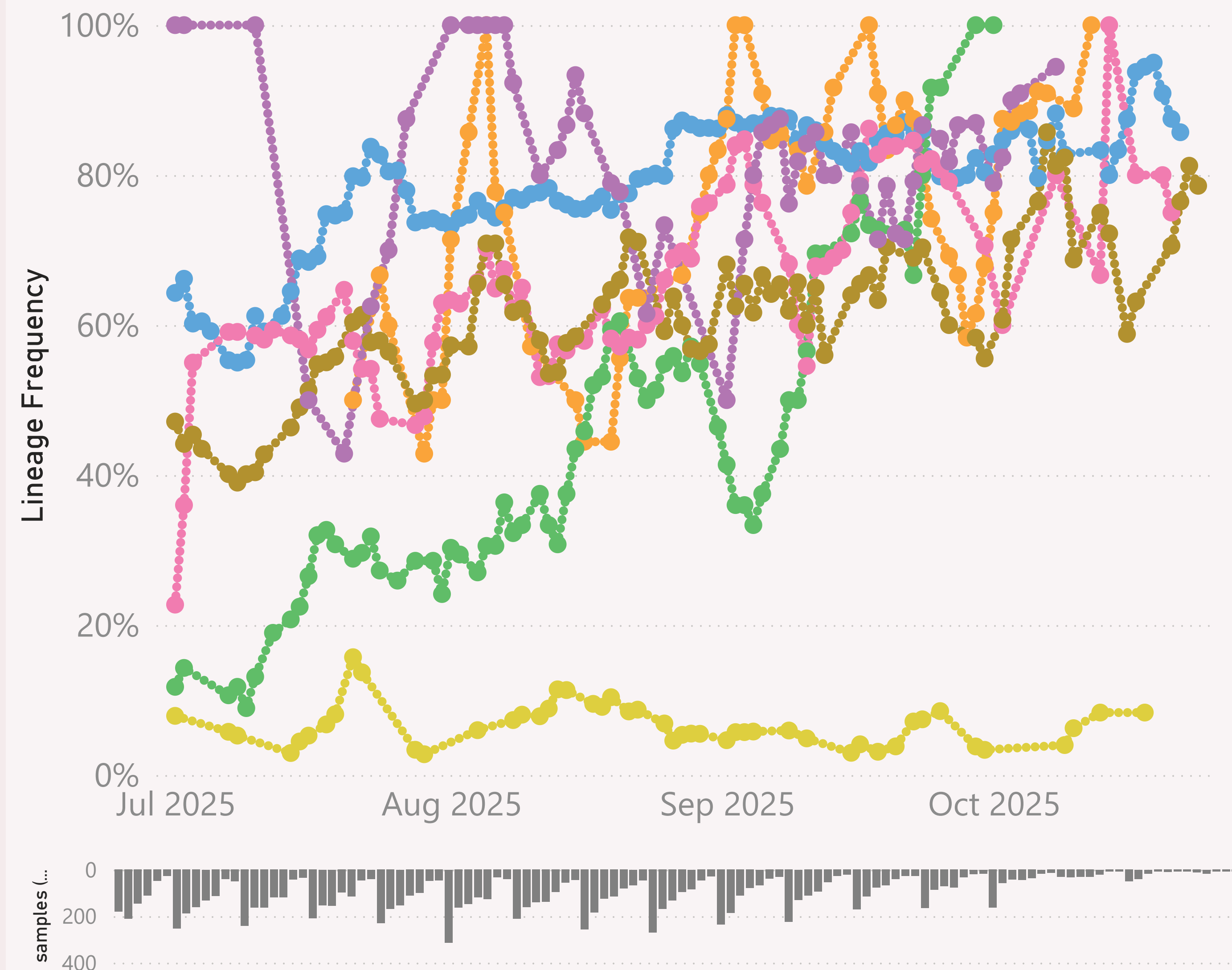
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=10,891 sequenced genomes, from 1 July 2025 up to 24 October 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.
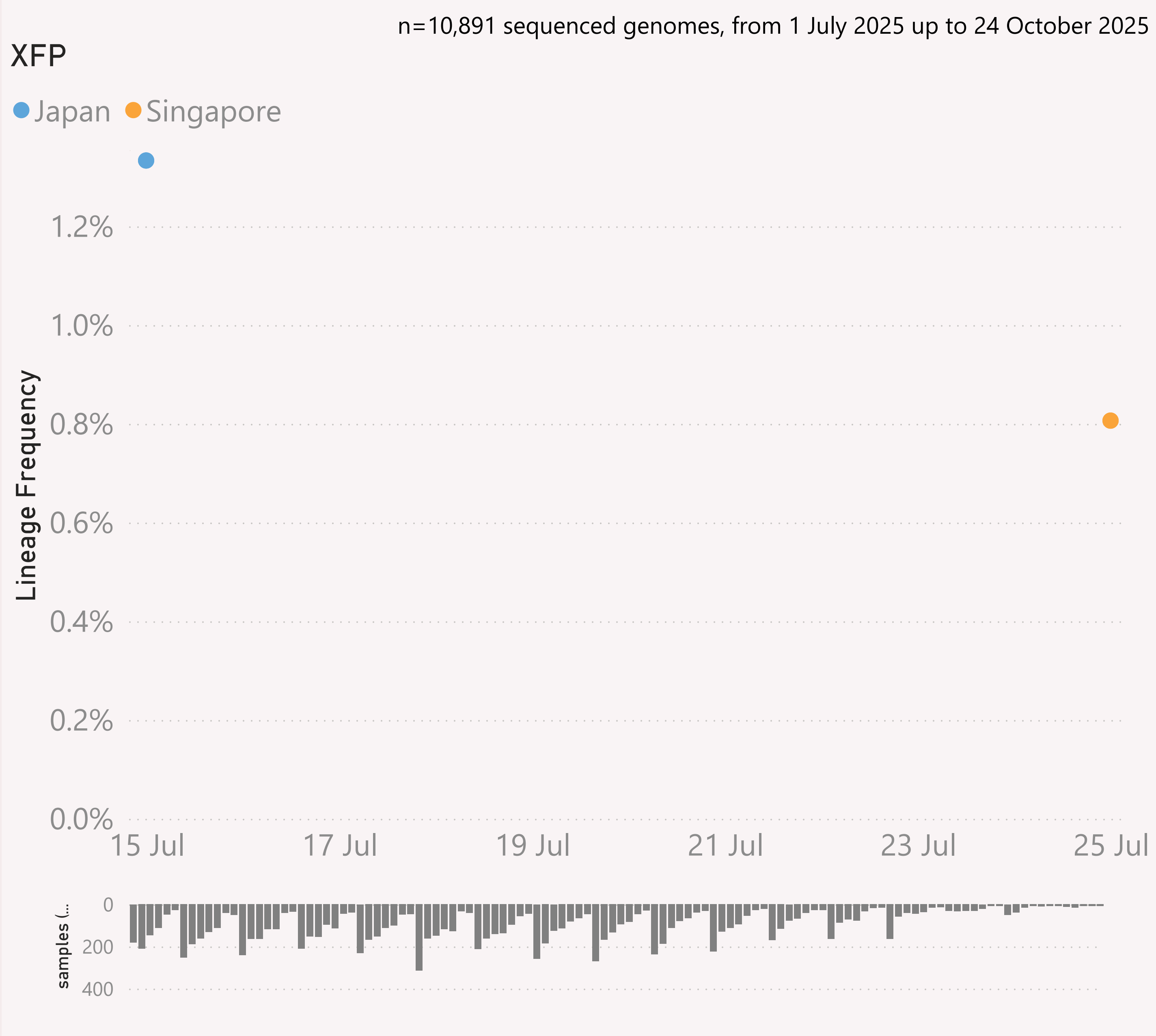
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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=10,891 sequenced genomes, from 1 July 2025 up to 24 October 2025

XFG.*

Brazil ● Chile ● Costa Rica ● Puerto Rico ● Singapore ● South Africa ● 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.

n=10,891 sequenced genomes, from 1 July 2025 up to 24 October 2025

XFP

- Japan
- Singapore

Lineage Frequency

| | 15 Jul | 17 Jul | 19 Jul | 21 Jul | 23 Jul | 25 Jul |

samples (...

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)

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=6,855 sequenced genomes, from 1 August 2025 up to 24 October 2025

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

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

growth of 0.3% per day, crossover on 29-Oct-25
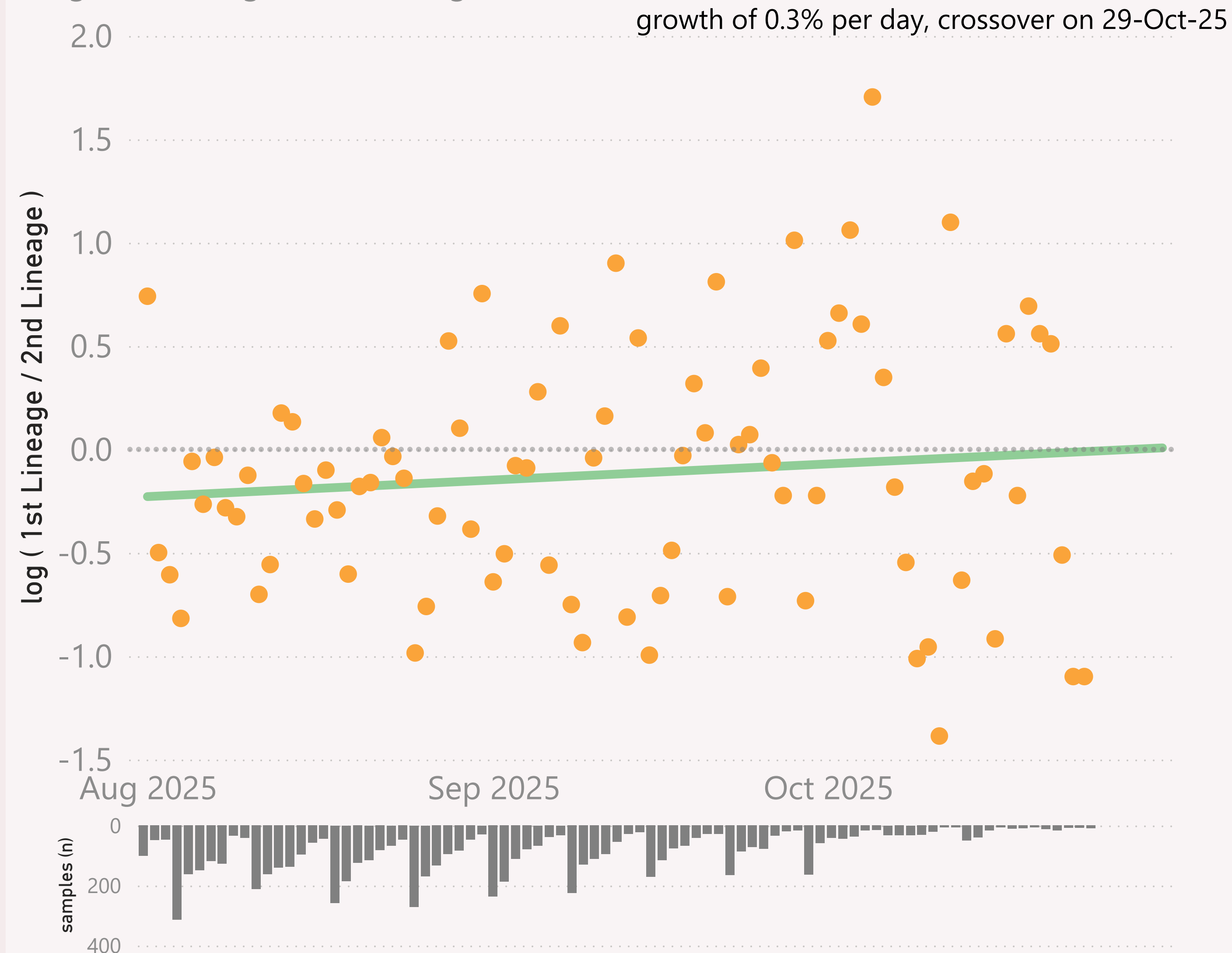
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

n=6,855 sequenced genomes, from 1 August 2025 up to 24 October 2025

Global – Other: XFP vs NB.1.8.1

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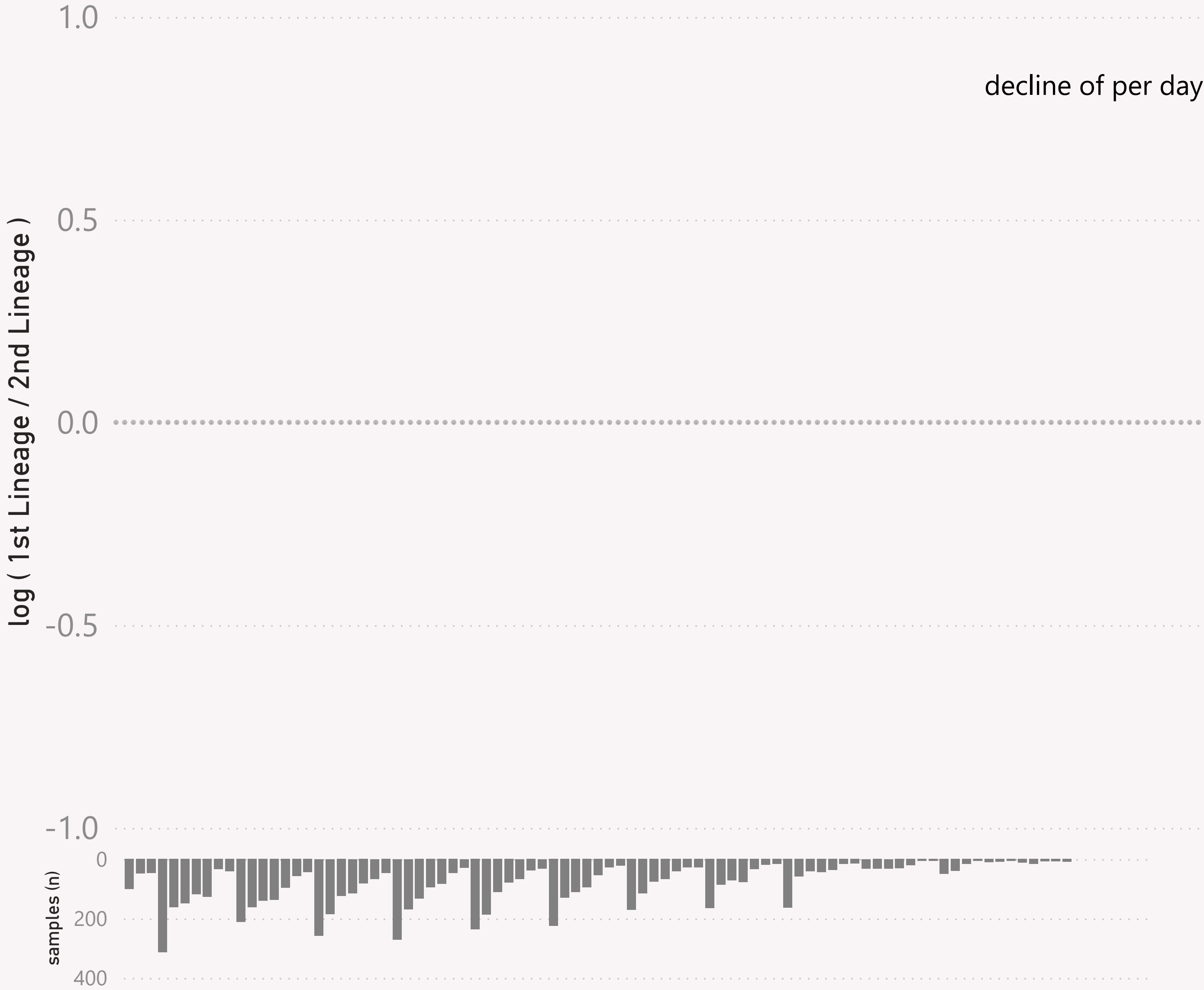
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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=10,891 sequenced genomes, from 1 July 2025 up to 24 October 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.
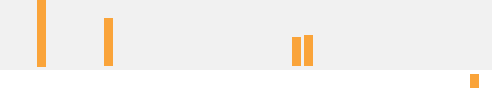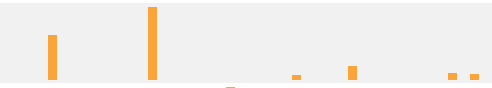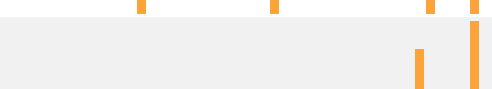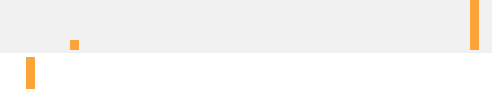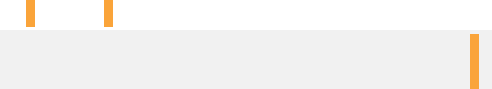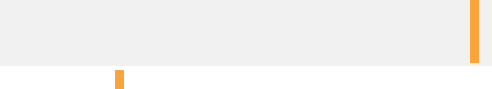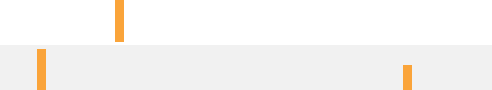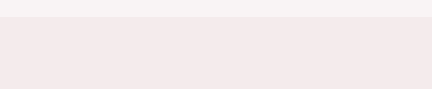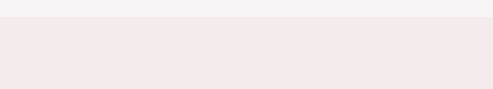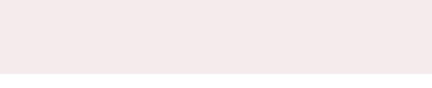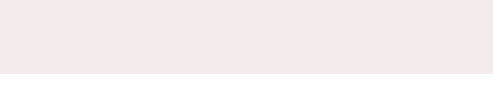
The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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.

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

Last Update: 2025-11-15 00:28 (UTC)

Data Submitted in the last 8 weeks

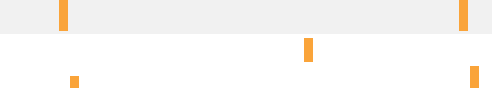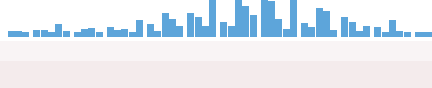| Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ Brazil	1,115	22/10/2025		01/11/2025	
⊞ South Korea	1,096	22/10/2025		01/11/2025	
⊞ China	812	13/10/2025		29/10/2025	
⊞ Japan	539	24/10/2025		01/11/2025	
⊞ Singapore	277	24/10/2025		01/11/2025	
⊞ Costa Rica	176	01/10/2025		17/10/2025	
⊞ Chile	131	12/10/2025		01/11/2025	
⊞ Argentina	128	30/08/2025		08/10/2025	
⊞ South Africa	127	08/10/2025		28/10/2025	
⊞ Puerto Rico	111	21/10/2025		01/11/2025	
⊞ Guatemala	105	17/10/2025		01/11/2025	
⊞ Ecuador	88	23/10/2025		01/11/2025	
⊞ Hong Kong	77	24/10/2025		01/11/2025	
⊞ Mexico	66	12/09/2025		01/11/2025	
⊞ Bahrain	44	08/10/2025		27/10/2025	
⊞ Thailand	44	08/10/2025		01/11/2025	
⊞ India	28	16/07/2025		29/09/2025	
⊞ Zambia	25	22/10/2025		01/11/2025	
⊞ Malaysia	22	23/09/2025		28/10/2025	
⊞ Cote d'Ivoire	19	19/09/2025		01/11/2025	
⊞ French Guiana	17	08/09/2025		30/09/2025	
⊞ Ghana	16	26/09/2025		26/10/2025	
⊞ Indonesia	14	19/08/2025		04/10/2025	
⊞ Dominican	11	16/09/2025		15/10/2025	
⊞ Oman	11	03/07/2025		24/09/2025	
⊞ Senegal	11	28/08/2025		16/10/2025	
⊞ Barbados	10	24/09/2025		10/10/2025	
⊞ Laos	8	21/08/2025		31/10/2025	
Total	**5,163**	**24/10/2025**		**01/11/2025**	

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.