n=55,349 sequenced genomes, from 1 August 2025 up to 9 November 2025

Global

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

This page shows the frequency of the top 6 "L2" lineages, across recent months.
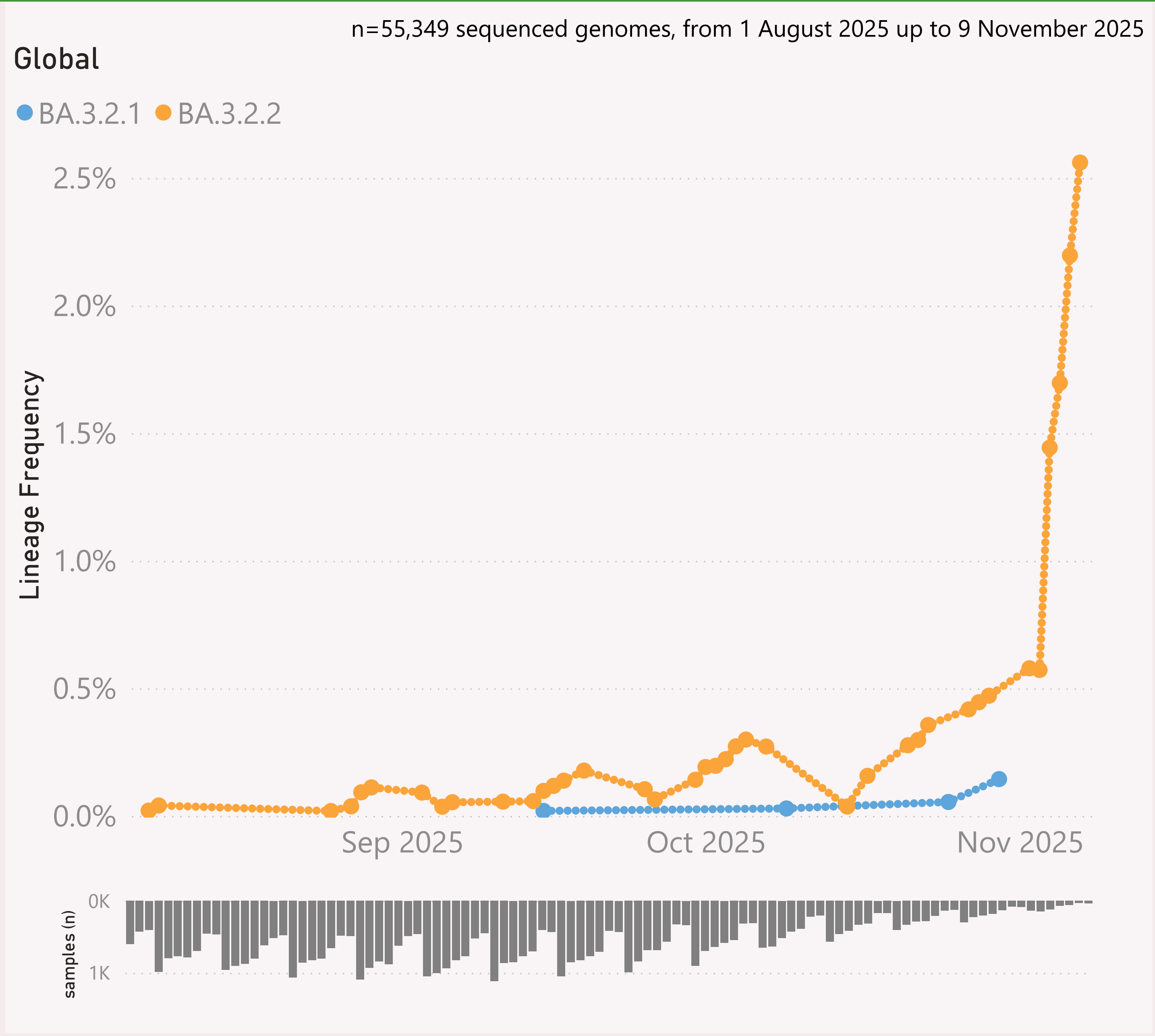
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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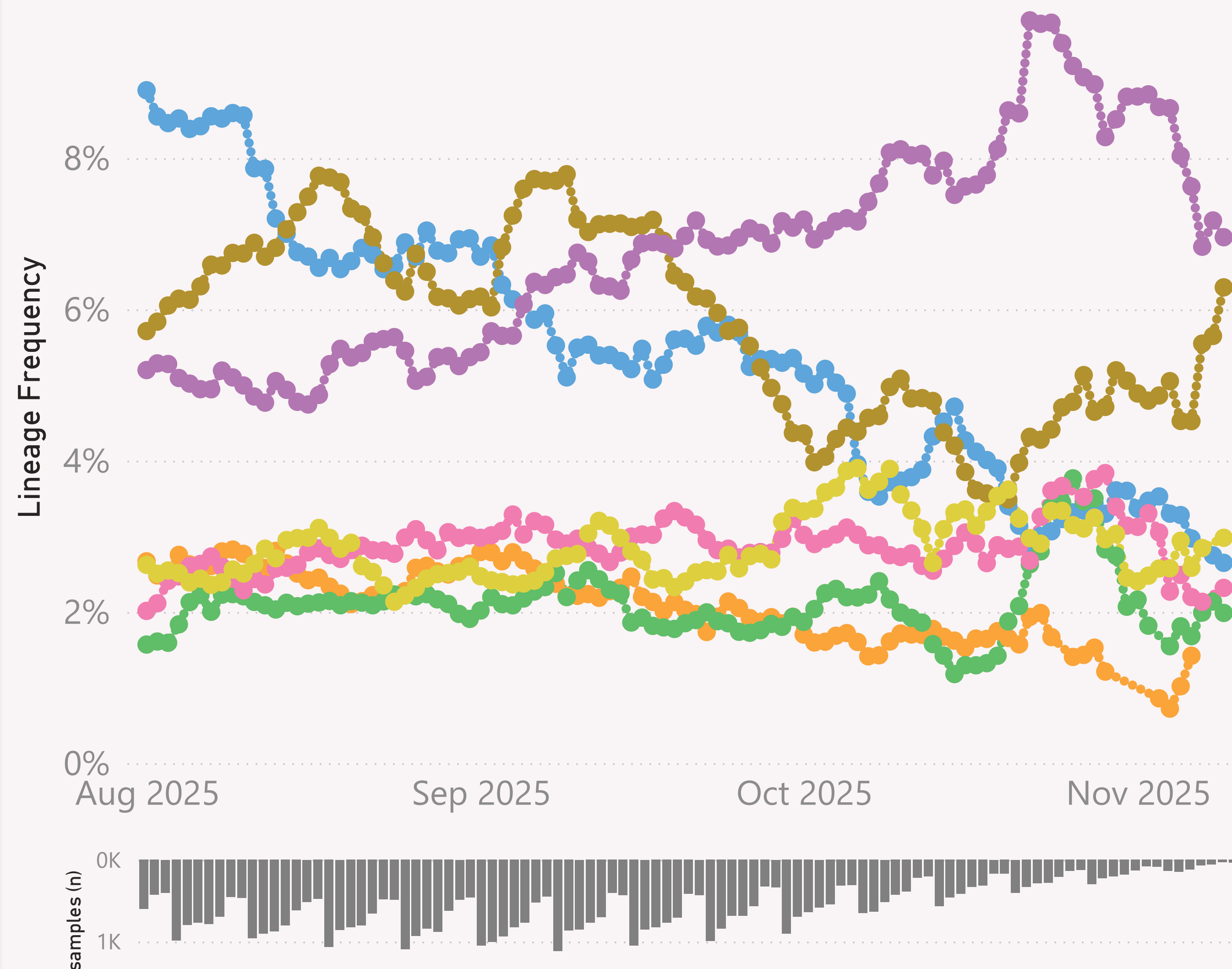
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

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Global

● BA.3.2.1　● BA.3.2.2

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.

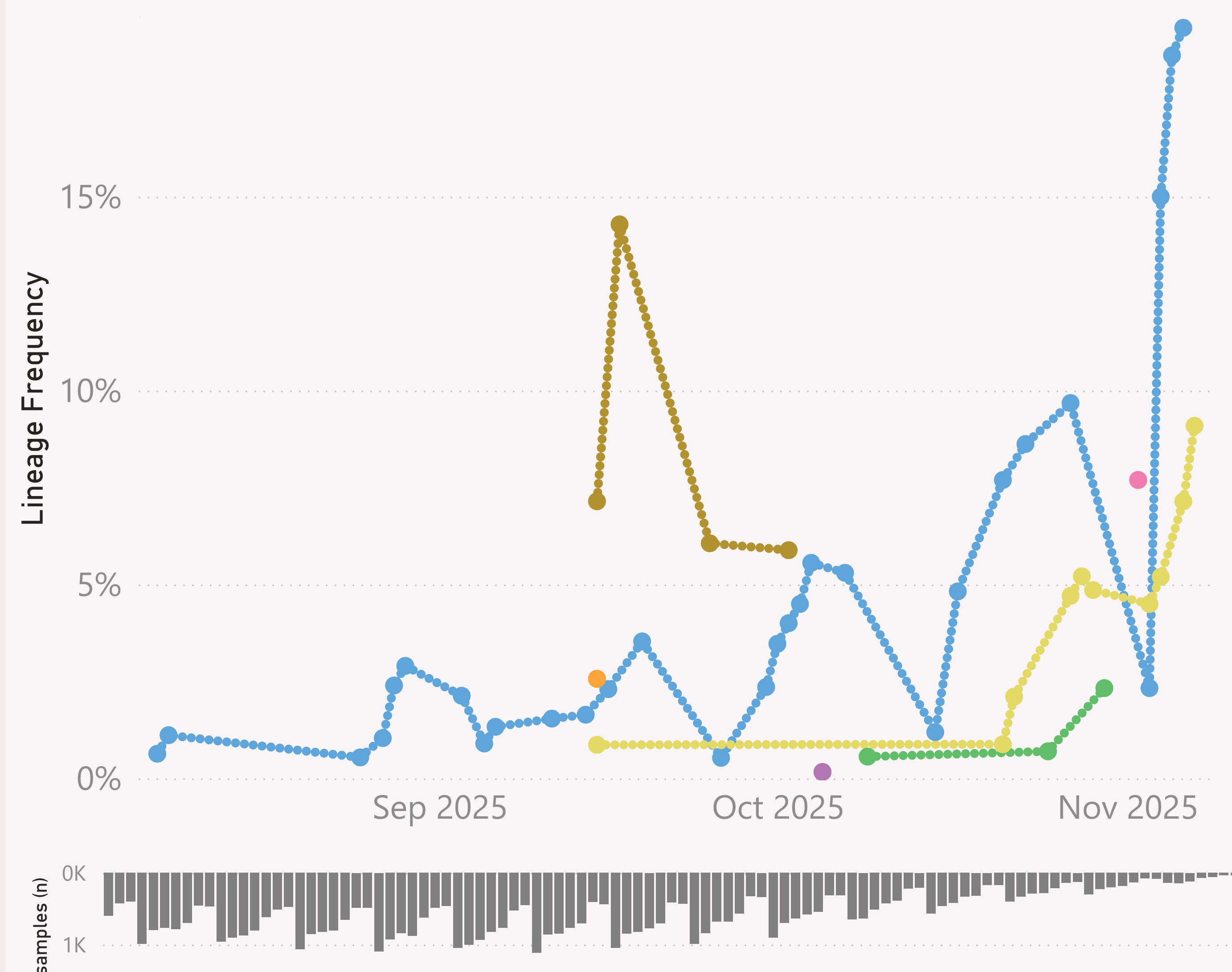The frequency shown at each point is based on the 7-day rolling average across all lineages.

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.

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Global

● NB.1.8.1 ● PQ.2 ● QF.2 ● XFG ● XFG.2 ● XFG.3 ● 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.

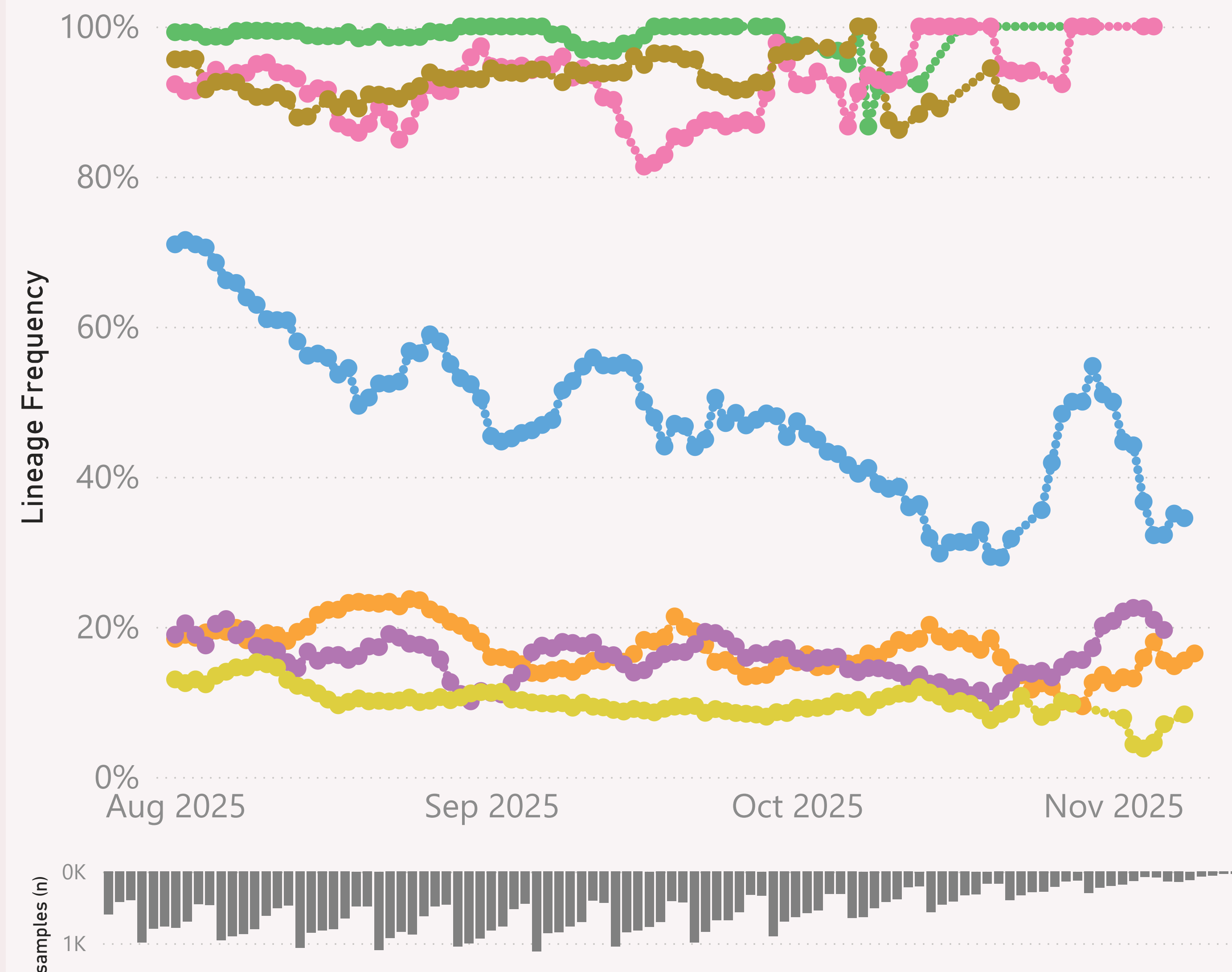The frequency shown at each point is based on the 7-day rolling average across all lineages.

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=55,349 sequenced genomes, from 1 August 2025 up to 9 November 2025

BA.3.*

- Australia
- Denmark
- Germany
- Netherla...
- Slovenia
- South Afr...
- United ...

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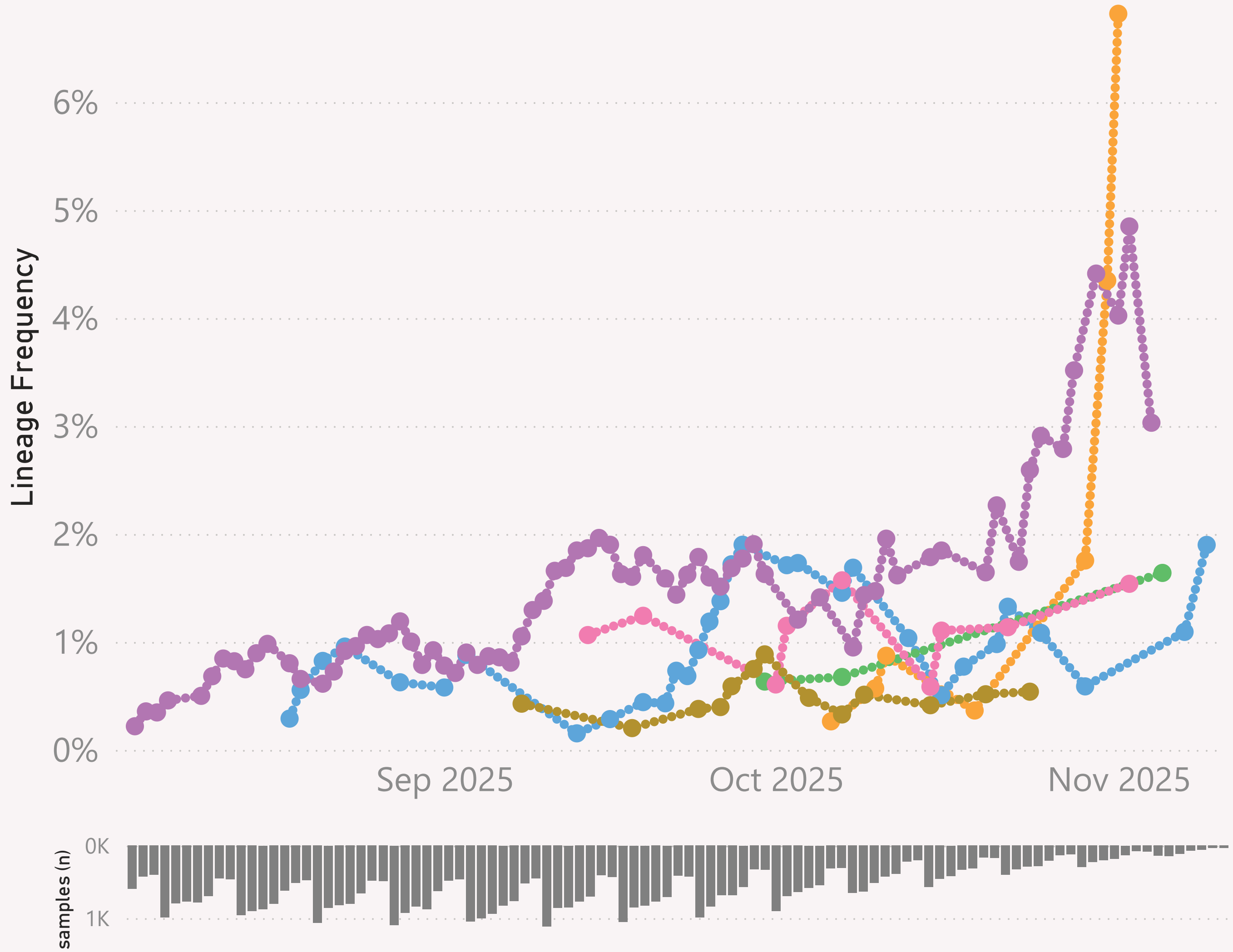
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=55,349 sequenced genomes, from 1 August 2025 up to 9 November 2025

NB.1.8.1.* Nimbus

● Australia ● Canada ● China ● Japan ● South Korea ● 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.

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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=55,349 sequenced genomes, from 1 August 2025 up to 9 November 2025

XFG.1.1

● Canada　● France　● Germany　● Netherlands　● United Kingdom　● United States

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

The detailed Lineage classifications are provided by Nextclade.

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=33,277 sequenced genomes, from 1 September 2025 up to 9 November 2025

Global – BA.3.* vs XFG.*

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

growth of 3.8% per day
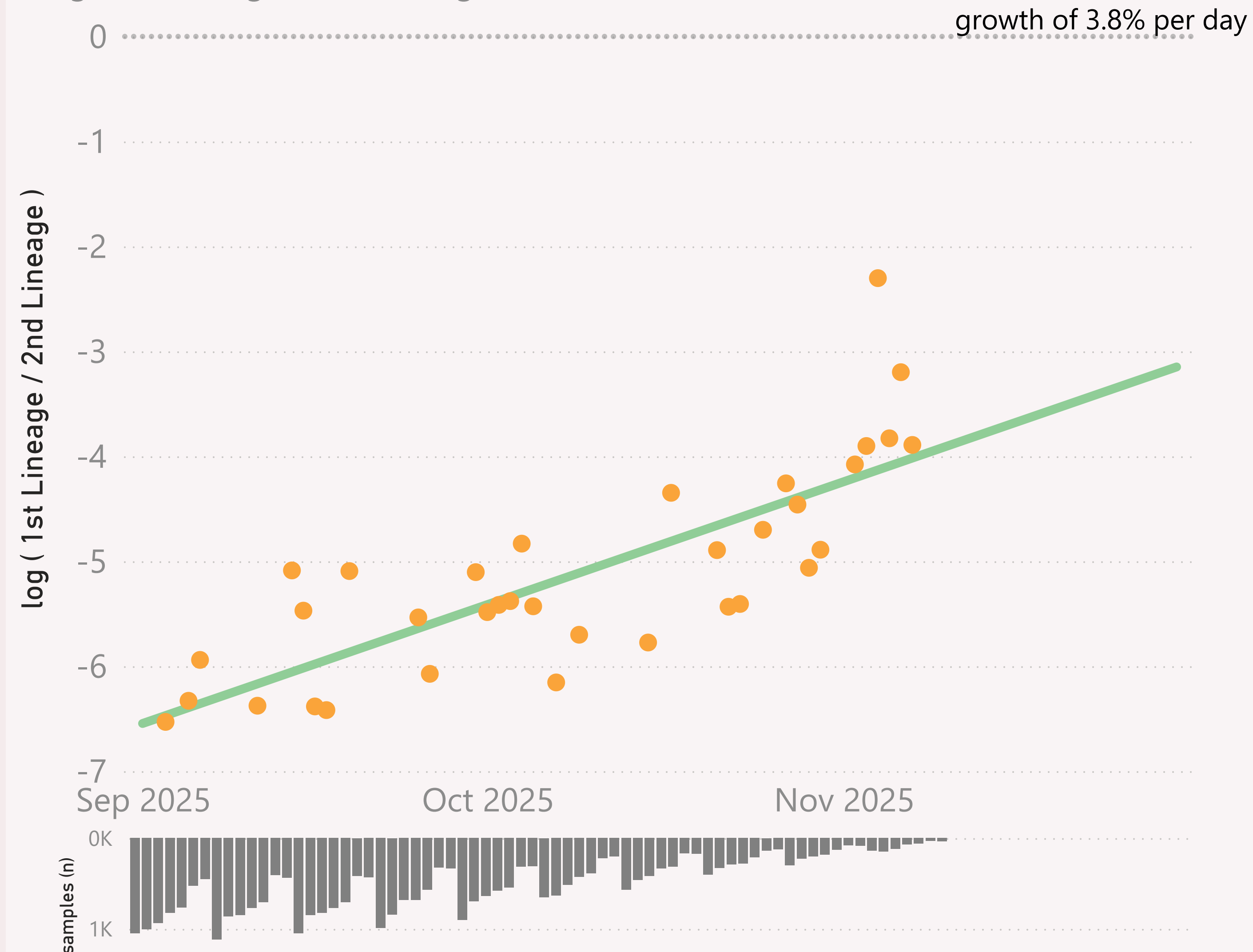
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

n=33,277 sequenced genomes, from 1 September 2025 up to 9 November 2025

Global – XFG.1.1 vs XFG.*

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

growth of 1.9% per day

y-axis: log (1st Lineage / 2nd Lineage), from 0 to -7

x-axis: Sep 2025, Oct 2025, Nov 2025

samples (n): 0K to 1K
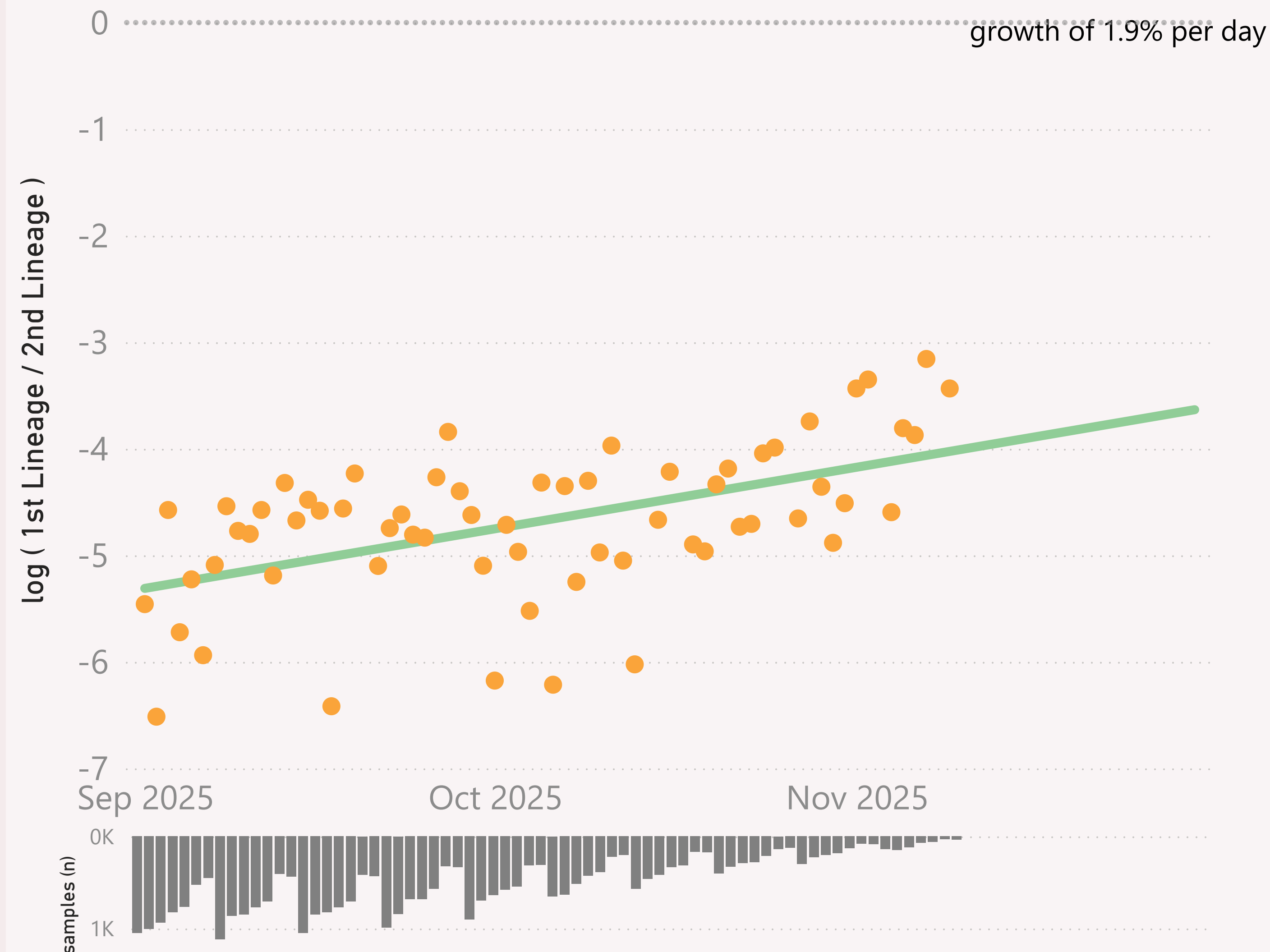
This page compares the relative frequency of a selected vs a "Lineage L2" group, over recent months. A challenging Lineage is selected first, and compared to the incumbent "Lineage L2" group.

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=55,349 sequenced genomes, from 1 August 2025 up to 9 November 2025

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=582 sequenced genomes, from 1 August 2025 up to 6 November 2025

Global

● JN.1.* +FLiRT ● LP.8.1.* ● NB.1.8.1.* Nimbus ● XFG.* ● XFJ.* ● XFV.*
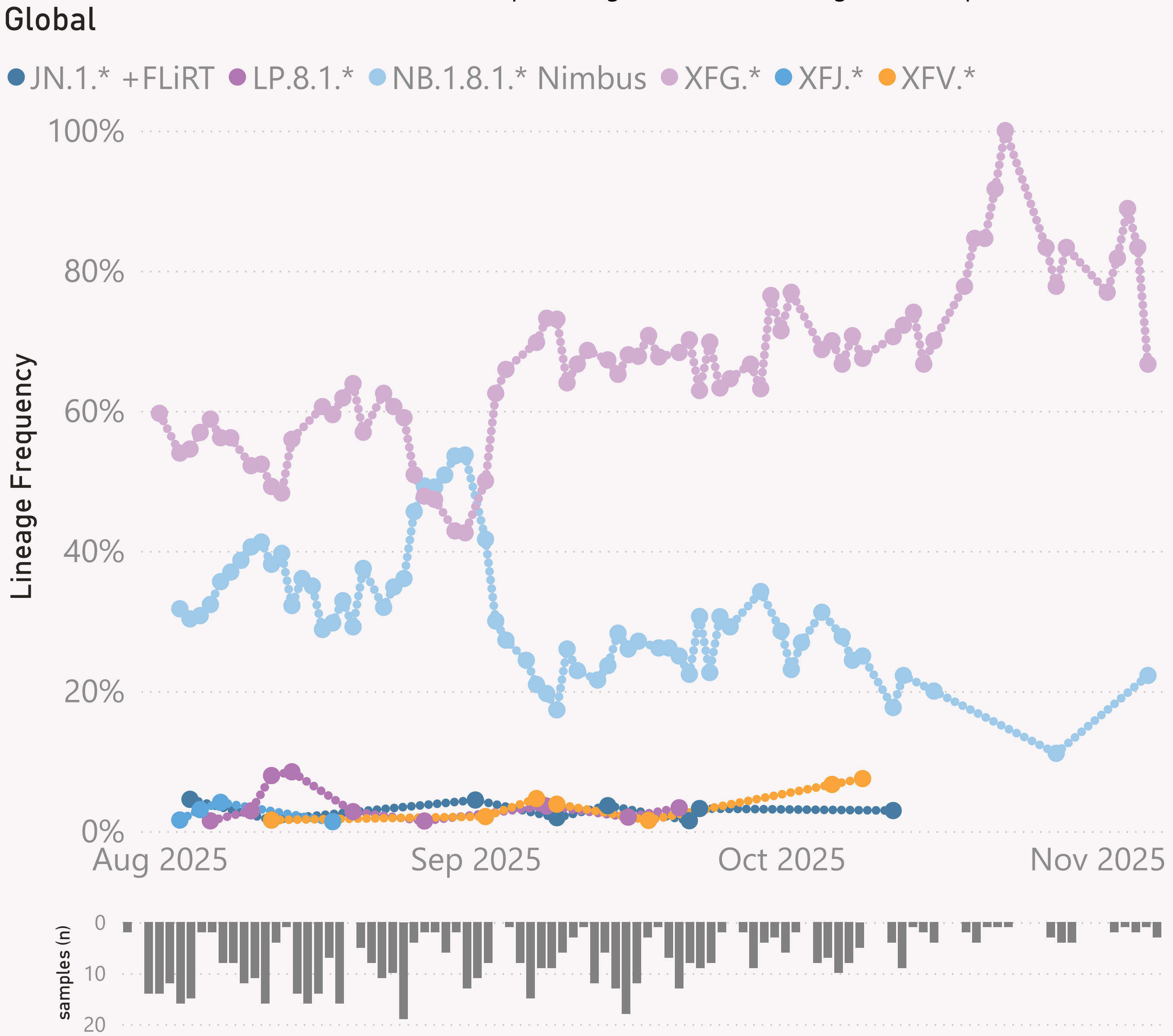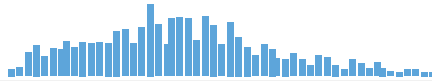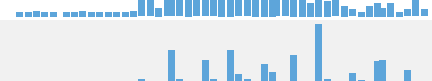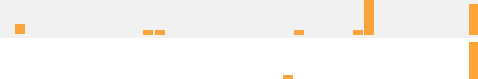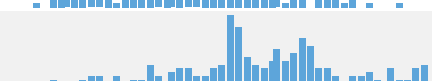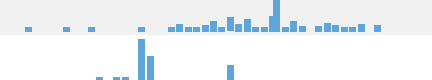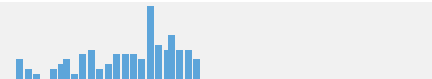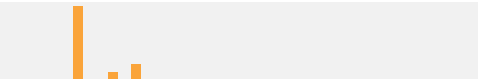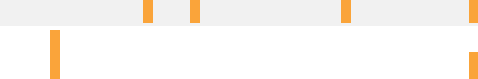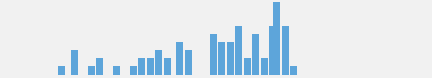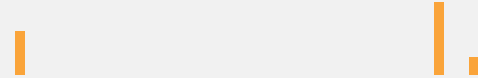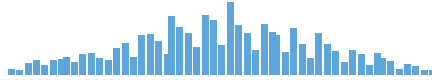
This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

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: 2025-11-22 07:40 (UTC)

Data Submitted in the last 8 weeks

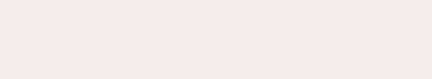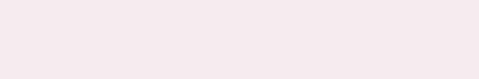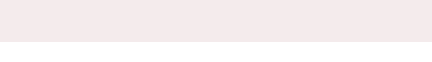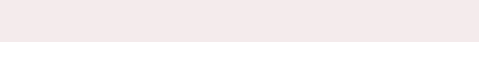| Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ United States	10,277	09/11/2025		07/11/2025	
⊞ Canada	4,456	09/11/2025		07/11/2025	
⊞ Spain	3,714	09/11/2025		07/11/2025	
⊞ United Kingdom	3,712	08/11/2025		07/11/2025	
⊞ France	2,039	04/11/2025		07/11/2025	
⊞ Netherlands	1,287	09/11/2025		07/11/2025	
⊞ Australia	1,066	08/11/2025		07/11/2025	
⊞ Germany	1,020	07/11/2025		07/11/2025	
⊞ Italy	951	08/11/2025		07/11/2025	
⊞ Brazil	946	30/10/2025		07/11/2025	
⊞ South Korea	833	22/10/2025		07/11/2025	
⊞ Japan	535	05/11/2025		07/11/2025	
⊞ Denmark	498	03/11/2025		07/11/2025	
⊞ China	420	30/10/2025		07/11/2025	
⊞ Ireland	409	02/11/2025		07/11/2025	
⊞ Slovenia	408	09/11/2025		07/11/2025	
⊞ Luxembourg	360	10/10/2025		28/10/2025	
⊞ Poland	331	29/10/2025		07/11/2025	
⊞ Singapore	303	07/11/2025		07/11/2025	
⊞ Sweden	294	02/11/2025		07/11/2025	
⊞ Russia	252	30/09/2025		06/10/2025	
⊞ Ukraine	224	28/10/2025		07/11/2025	
⊞ New Zealand	182	25/10/2025		02/11/2025	
⊞ Switzerland	181	15/09/2025		09/10/2025	
⊞ Lithuania	158	29/09/2025		19/10/2025	
⊞ Belgium	144	01/11/2025		07/11/2025	
⊞ Finland	141	19/10/2025		07/11/2025	
⊞ Chile	131	12/10/2025		07/11/2025	
Total	**36,495**	**09/11/2025**		**07/11/2025**	

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.