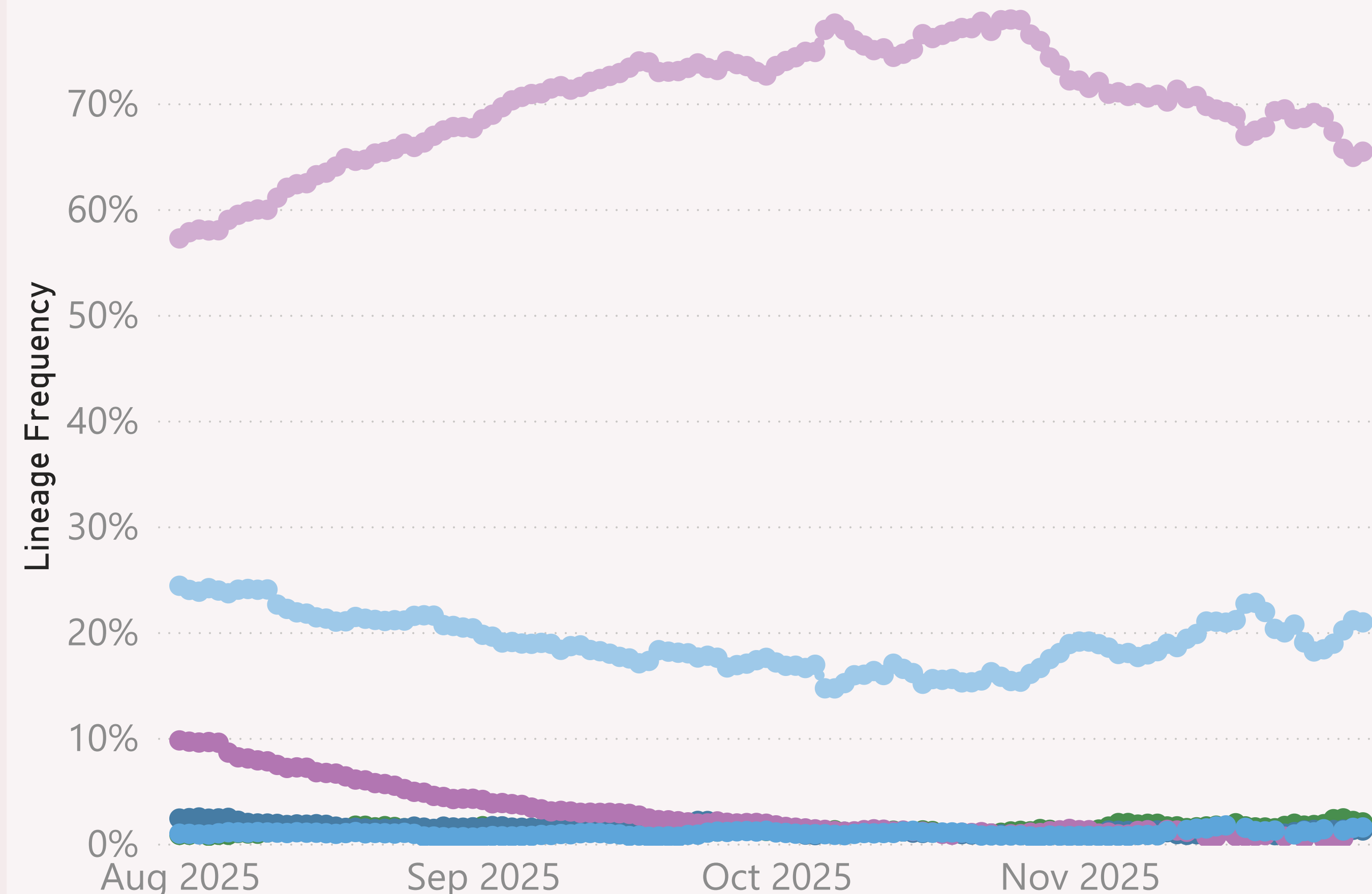


n=67,287 sequenced genomes, from 1 August 2025 up to 30 November 2025

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.

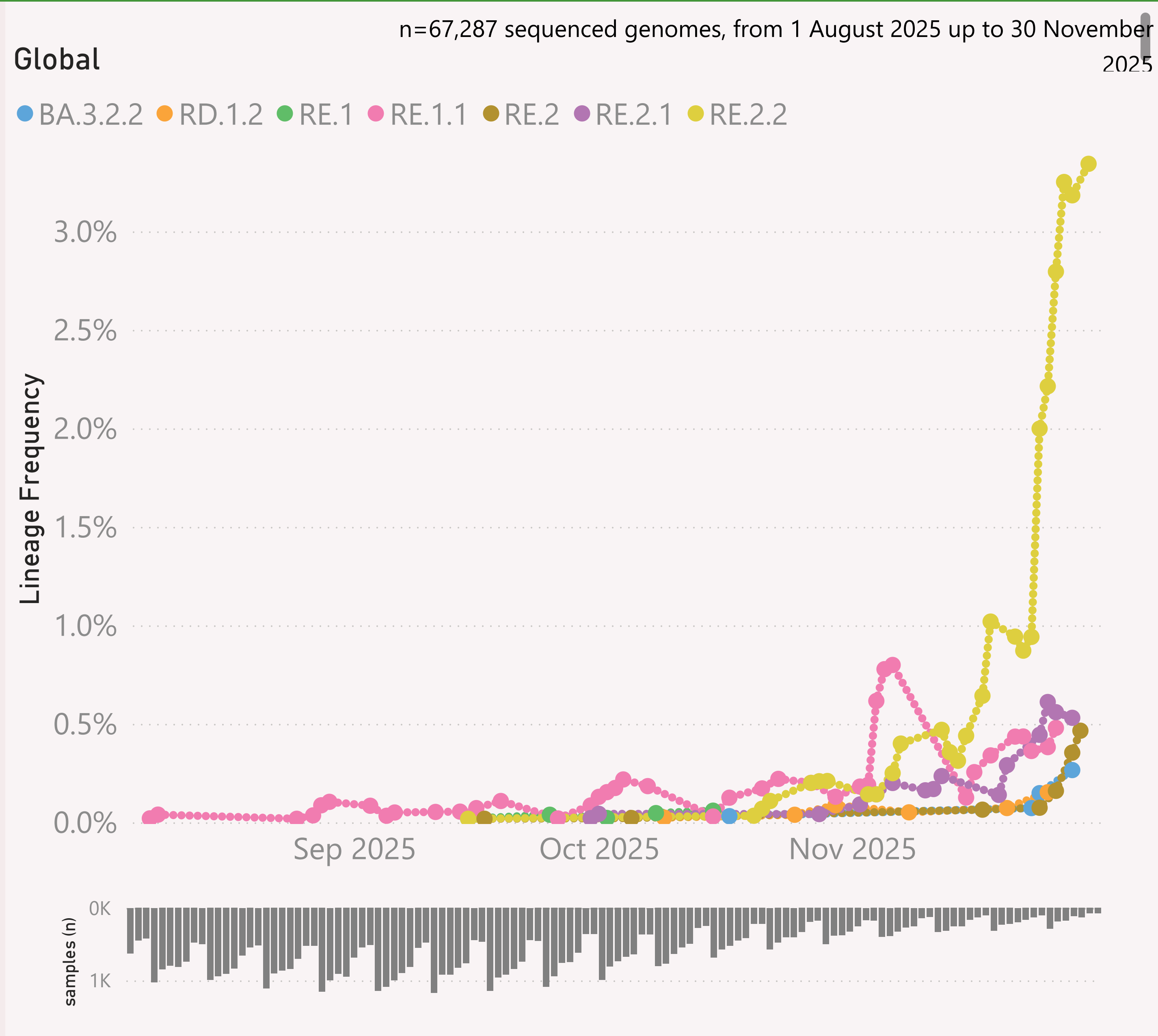
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



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.

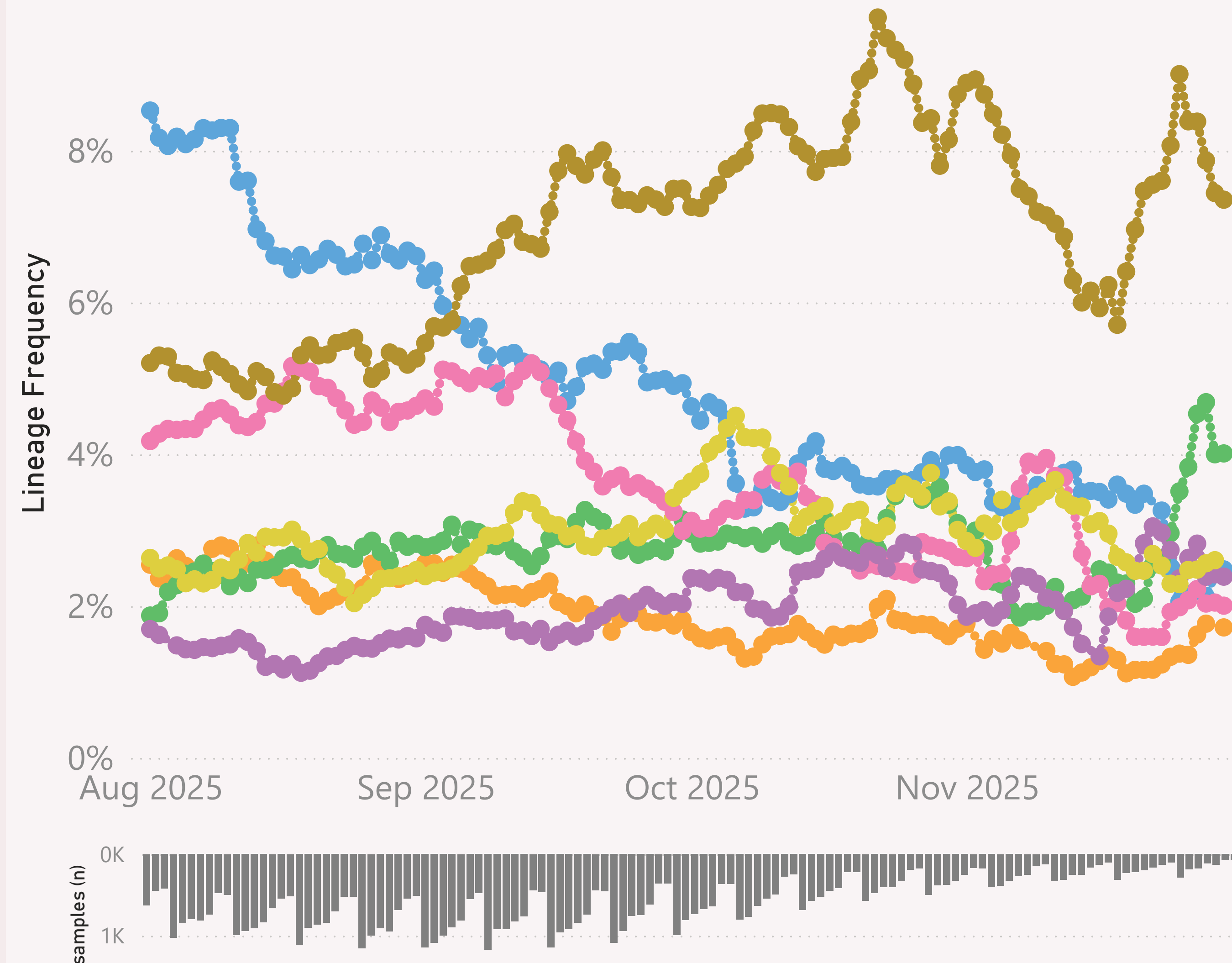
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=67,287 sequenced genomes, from 1 August 2025 up to 30 November 2025

Global

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



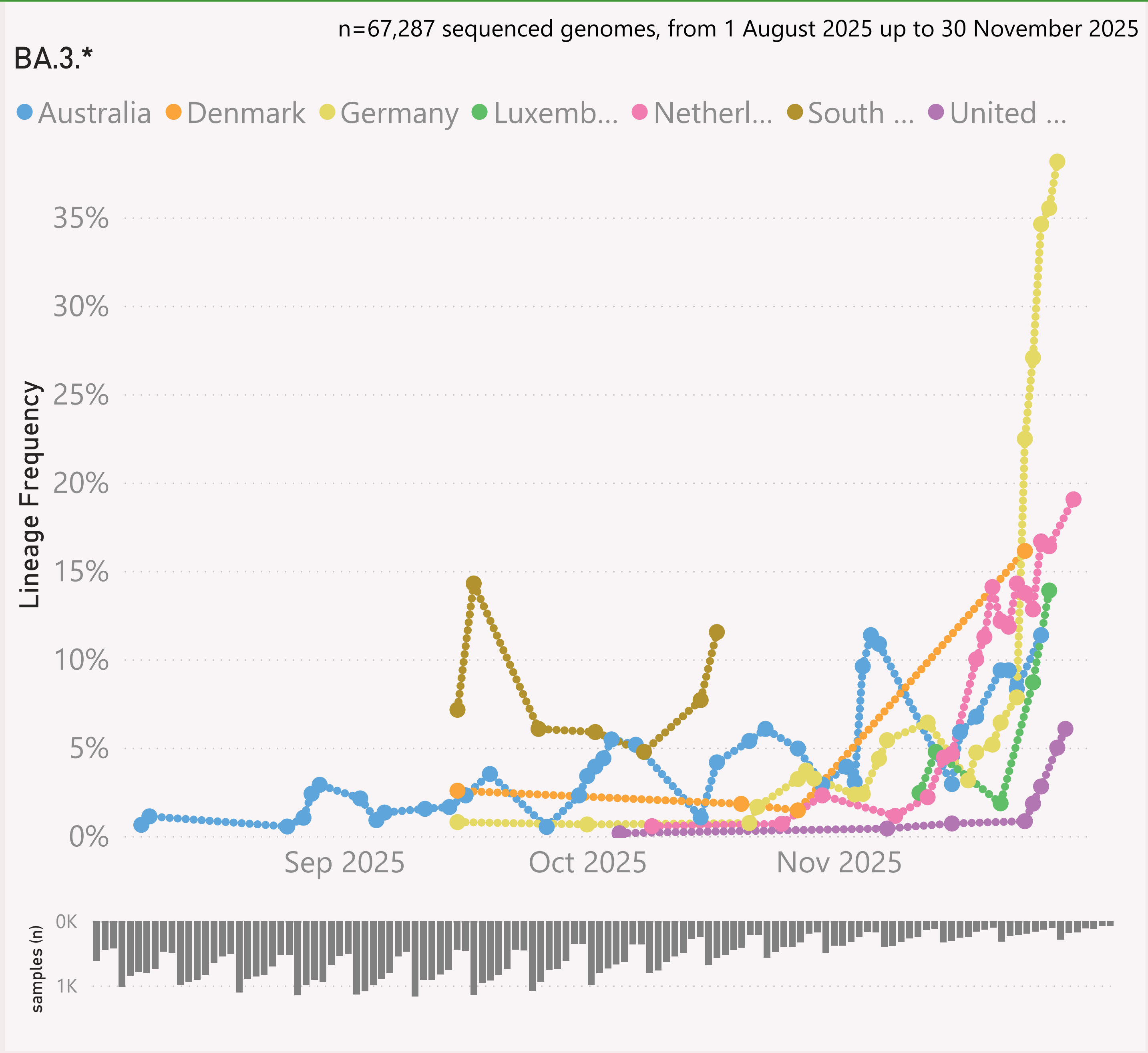
This page shows the frequency of the top 7 lineages, across recent months.

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.



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.

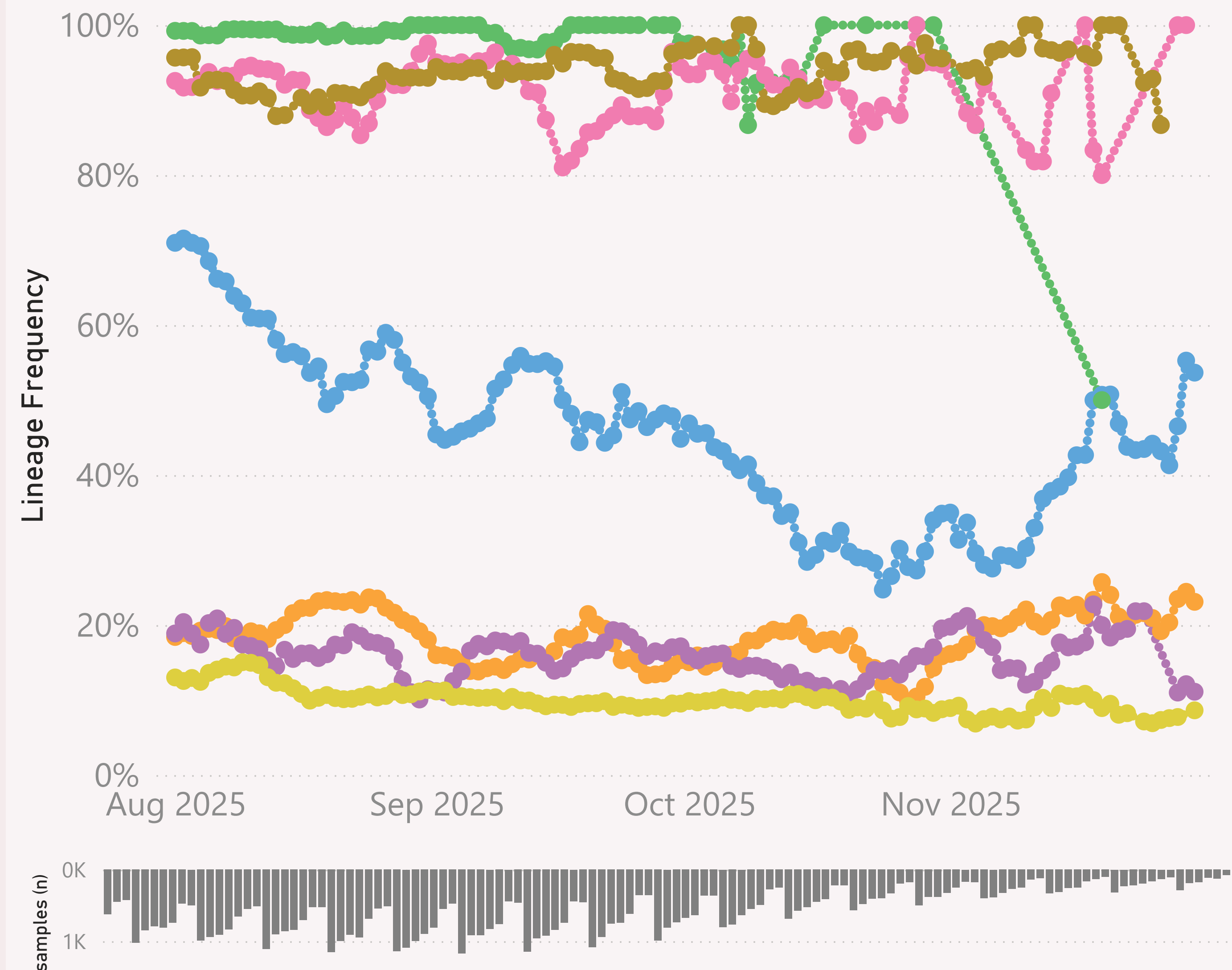
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=67,287 sequenced genomes, from 1 August 2025 up to 30 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.

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

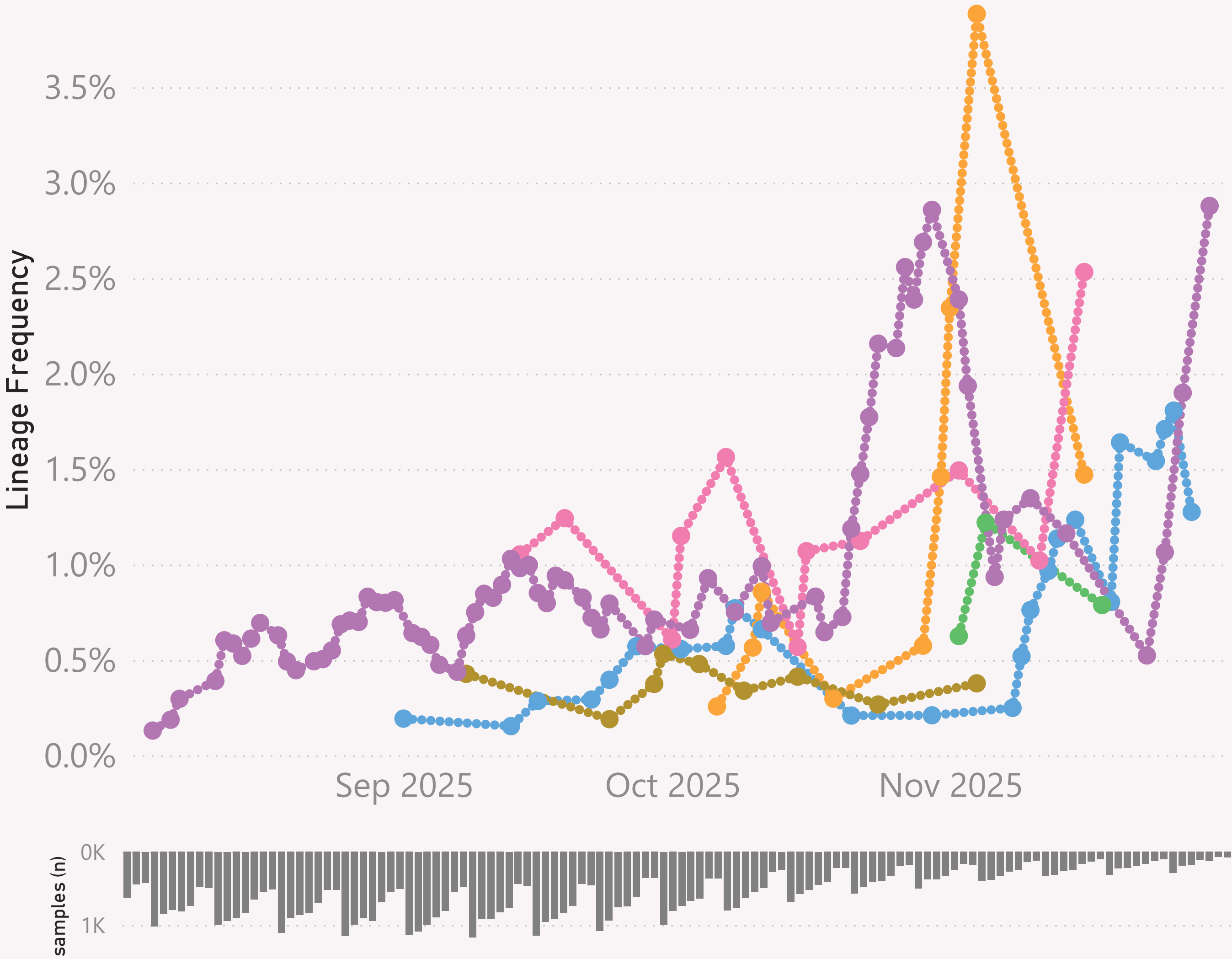
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=67,287 sequenced genomes, from 1 August 2025 up to 30 November 2025

XFG.1.1.1

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.

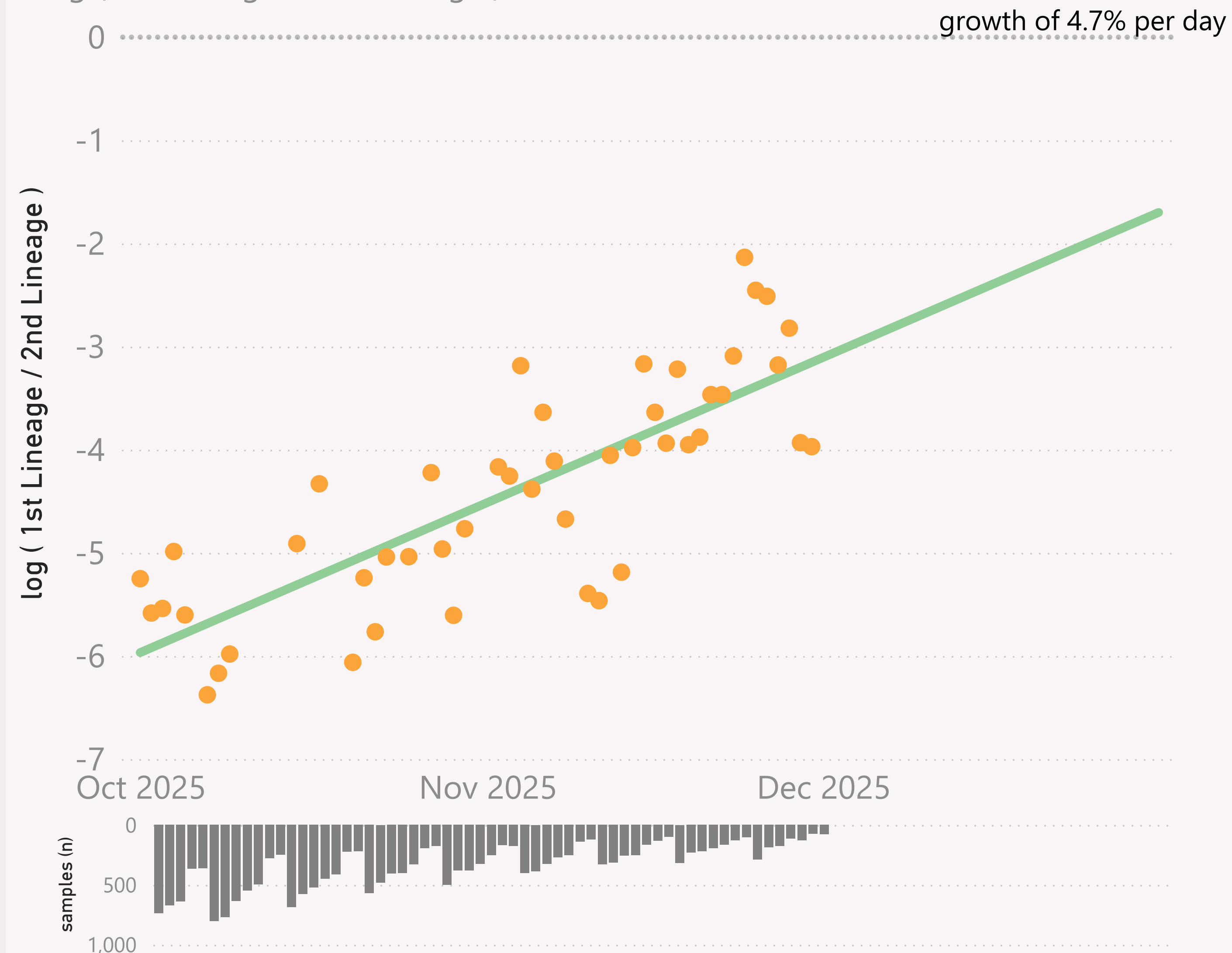
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=20,279 sequenced genomes, from 1 October 2025 up to 30 November 2025

Global - BA.3.* vs XFG.*

● 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.

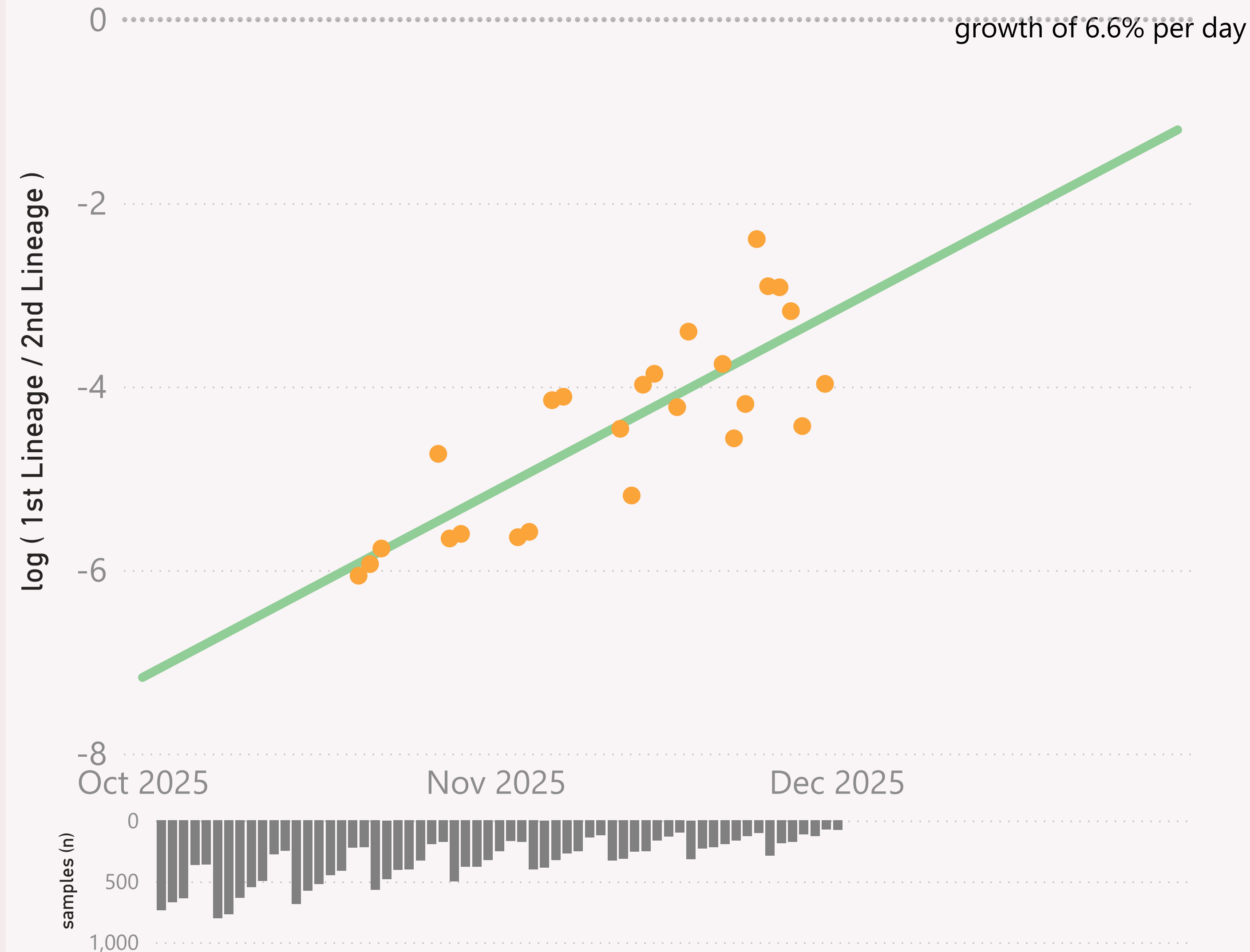
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=20,279 sequenced genomes, from 1 October 2025 up to 30 November 2025

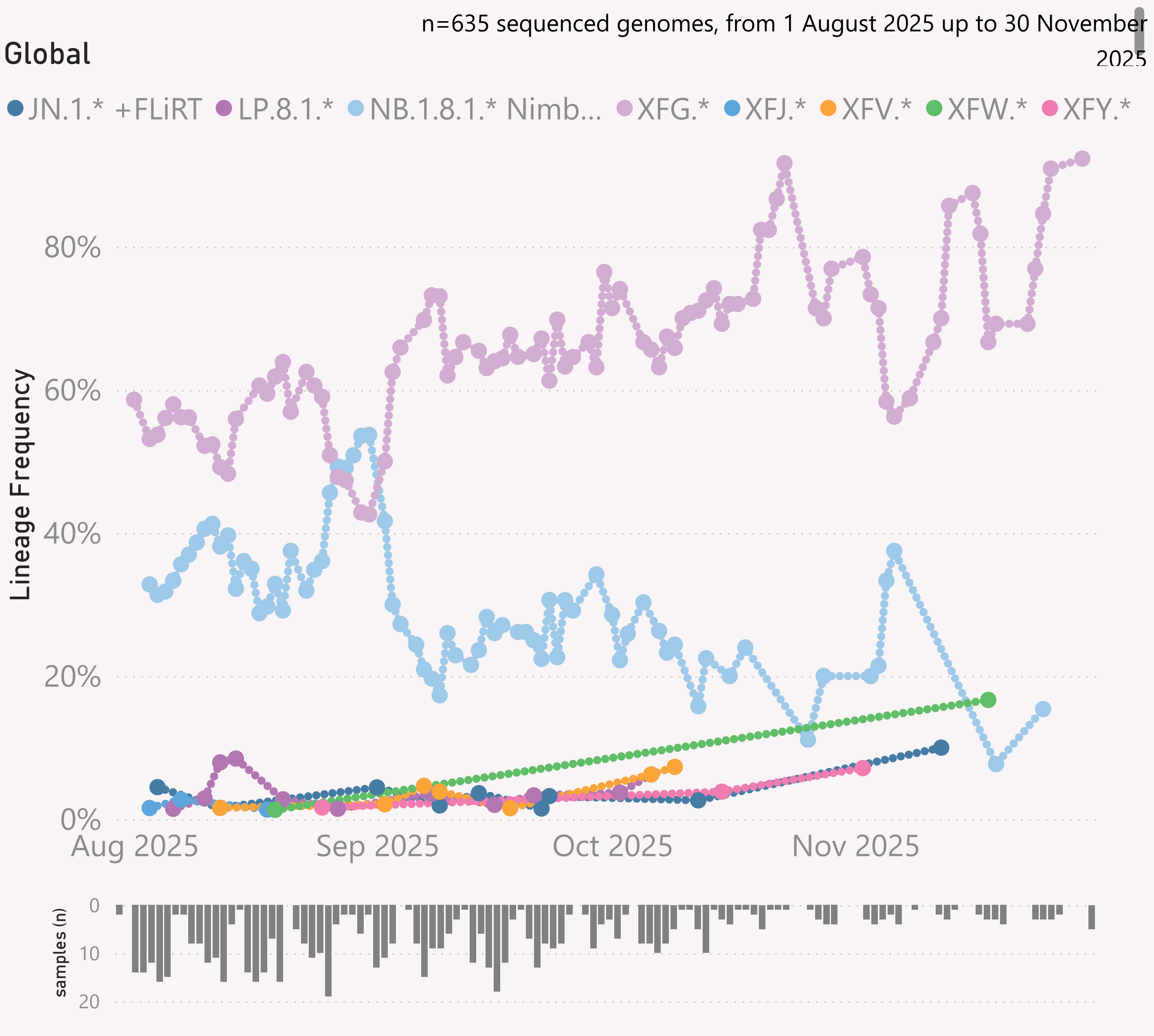
Global - RE.2.2 vs XFG.*

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



Global








































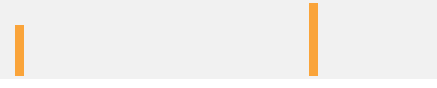





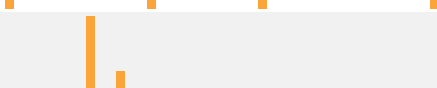


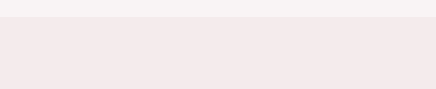
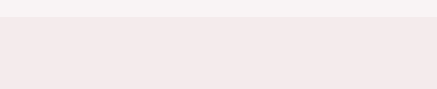
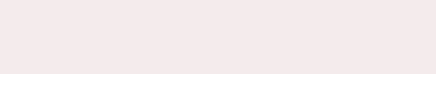
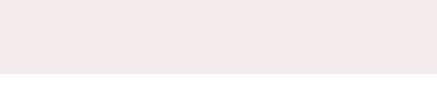
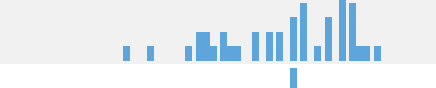
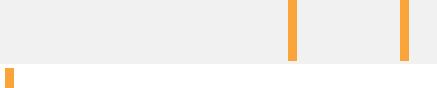








This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

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.

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
United States	6,754	30/11/2025		09/12/2025	
Canada	3,939	30/11/2025		09/12/2025	
United Kingdom	2,071	30/11/2025		09/12/2025	
Spain	2,002	30/11/2025		09/12/2025	
Russia	1,387	25/11/2025		09/12/2025	
France	1,218	30/11/2025		09/12/2025	
Germany	1,080	30/11/2025		09/12/2025	
Netherlands	870	30/11/2025		09/12/2025	
Italy	868	30/11/2025		09/12/2025	
Luxembourg	821	30/11/2025		09/12/2025	
Australia	742	30/11/2025		09/12/2025	
Denmark	585	24/11/2025		09/12/2025	
Brazil	506	25/11/2025		09/12/2025	
South Korea	462	27/11/2025		09/12/2025	
Japan	417	29/11/2025		09/12/2025	
Poland	381	26/11/2025		09/12/2025	
China	375	24/11/2025		09/12/2025	
Sweden	305	30/11/2025		09/12/2025	
Ireland	297	30/11/2025		09/12/2025	
Ukraine	271	28/11/2025		09/12/2025	
Slovenia	197	30/11/2025		08/12/2025	
Singapore	180	28/11/2025		09/12/2025	
New Zealand	152	30/11/2025		09/12/2025	
South Africa	148	28/10/2025		26/11/2025	
Finland	138	30/11/2025		09/12/2025	
Slovakia	113	14/11/2025		05/12/2025	
Belgium	90	30/11/2025		09/12/2025	
Chile	88	12/10/2025		07/11/2025	
Total	27,288	30/11/2025		09/12/2025	

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.