

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 its 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.

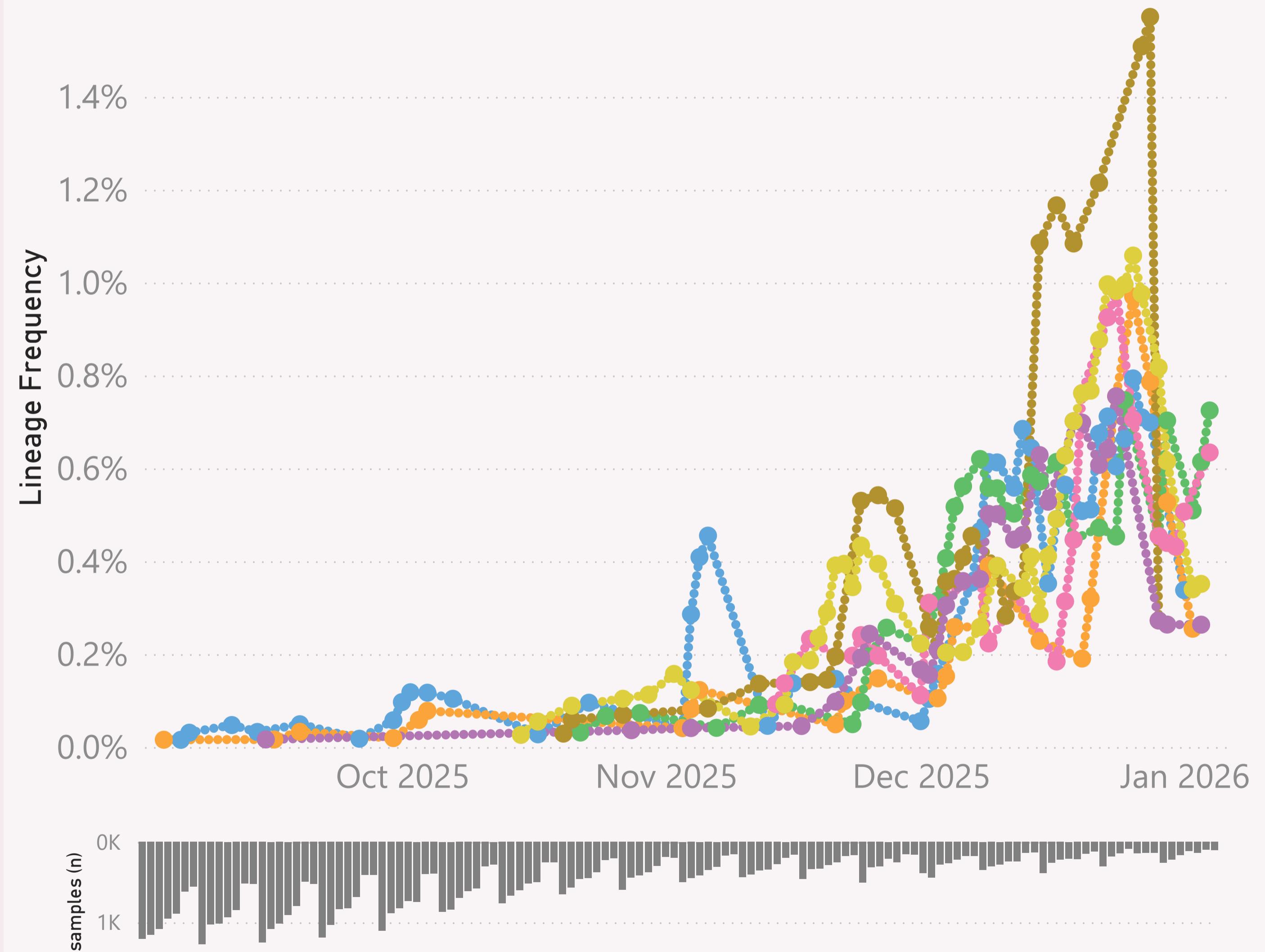
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=58,274 sequenced genomes, from 1 September 2025 up to 4 January 2026

**Global**

- RE.1.1
- RE.1.1.1
- RE.2.2
- RE.2.2.1
- RE.2.2.3
- RE.2.2.5
- RS.1



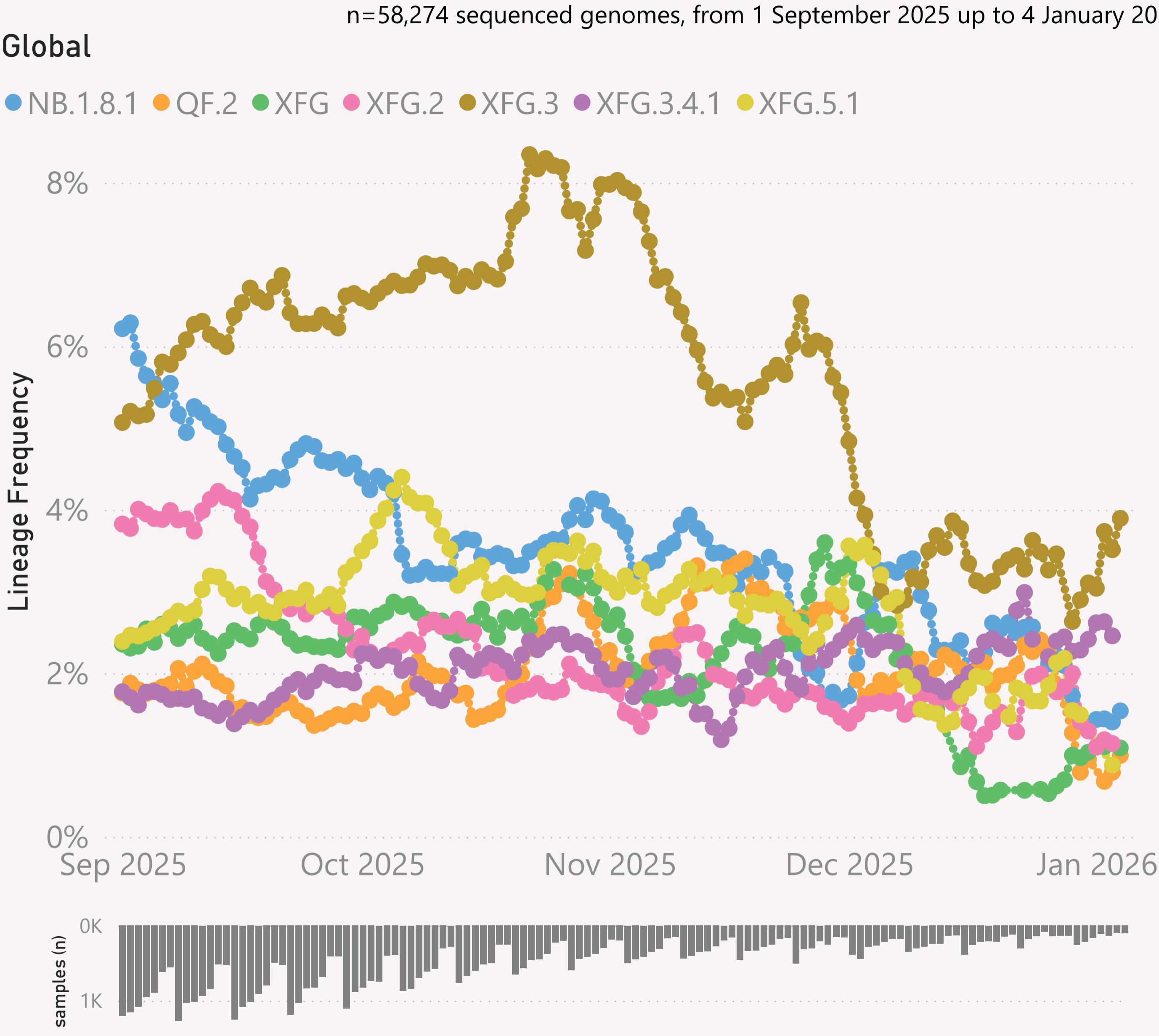
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest.

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.

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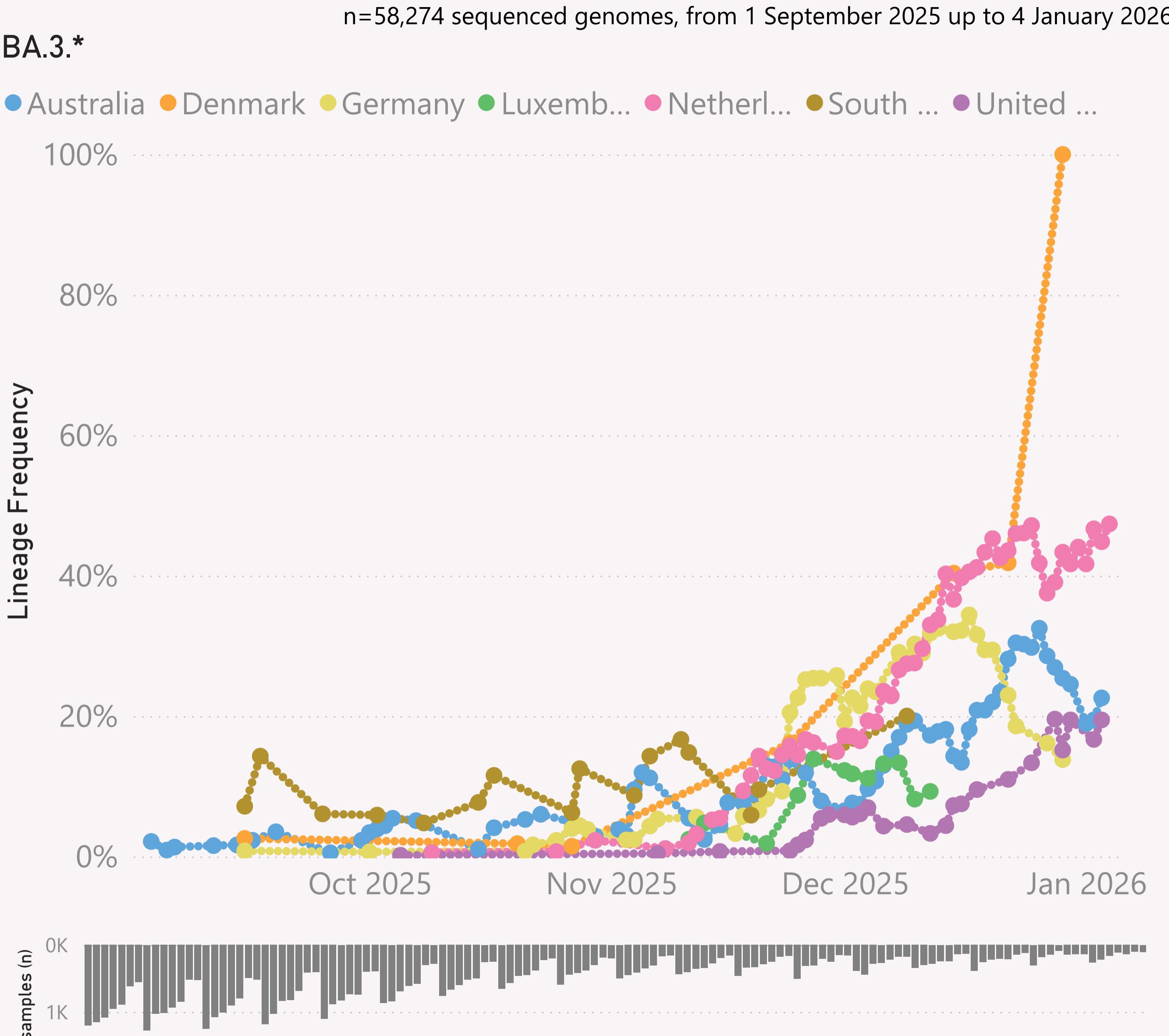
This page shows the frequency of the top 7 lineages, across recent months.

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.

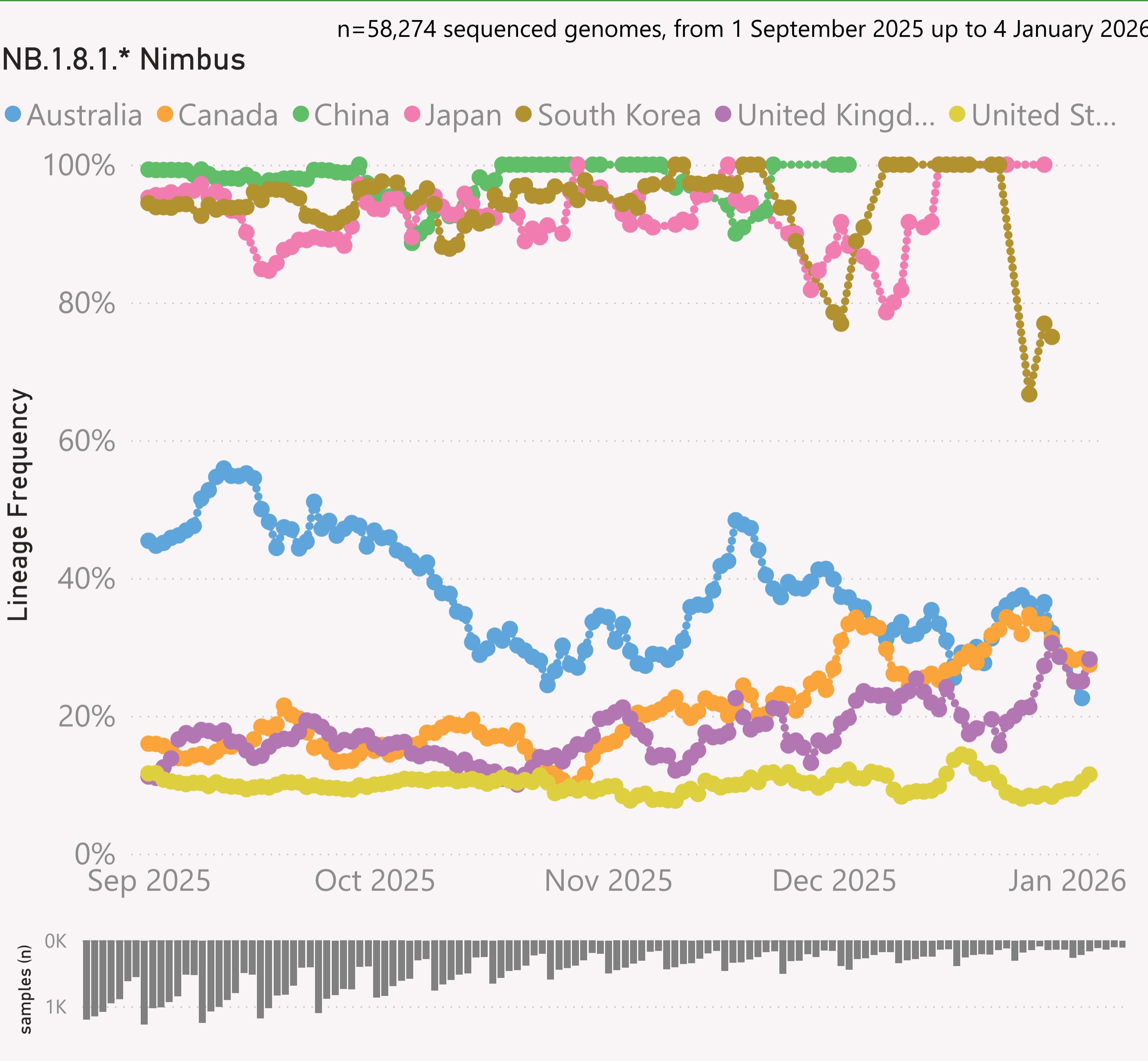
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.\* +FLiT" group includes the descendants of JN.1.\* with the mutations: F456L & R346T.

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.



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.

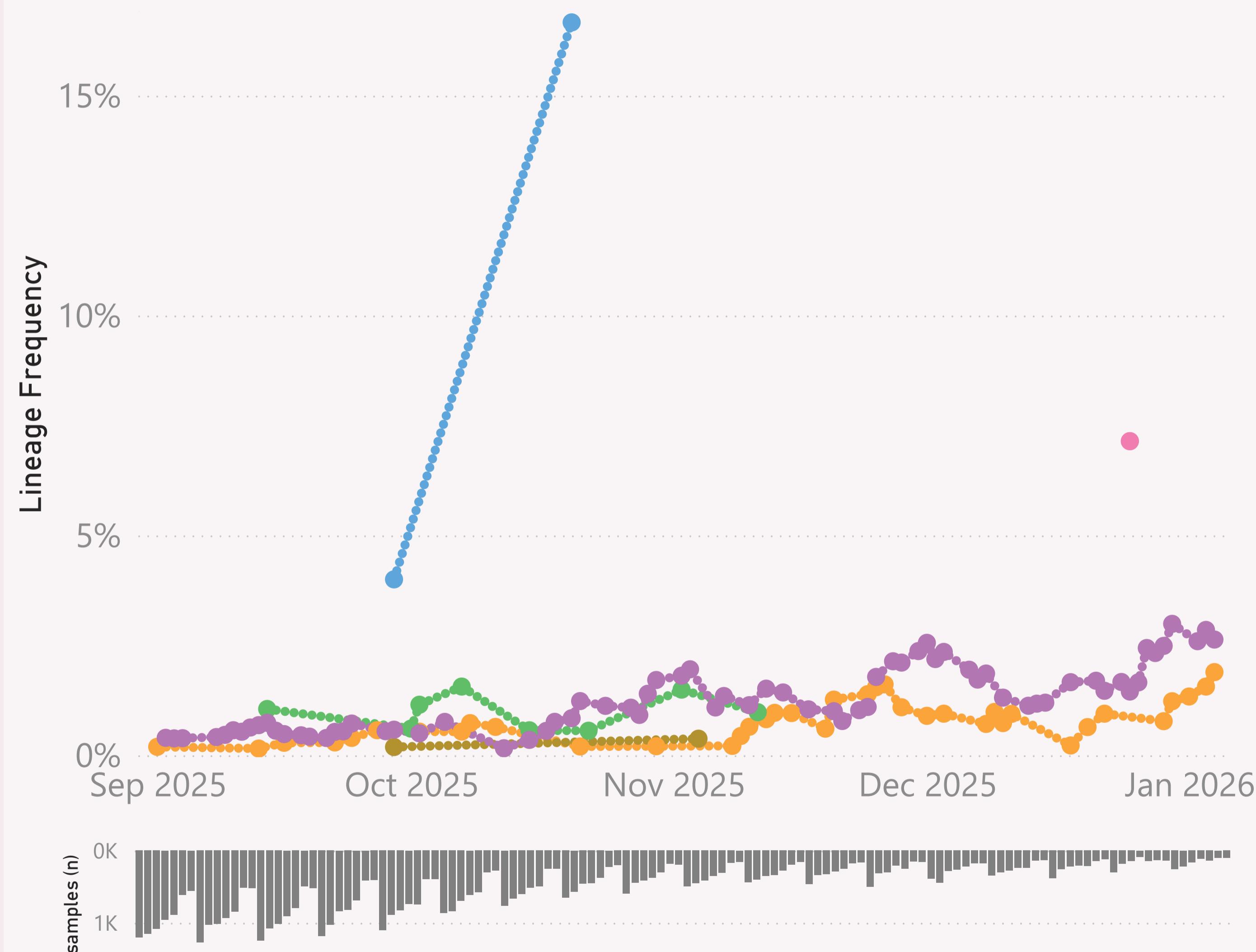
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=58,274 sequenced genomes, from 1 September 2025 up to 4 January 2026

XFG.1.1.1

- Belgium
- Canada
- Netherlands
- New Zealand
- 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.

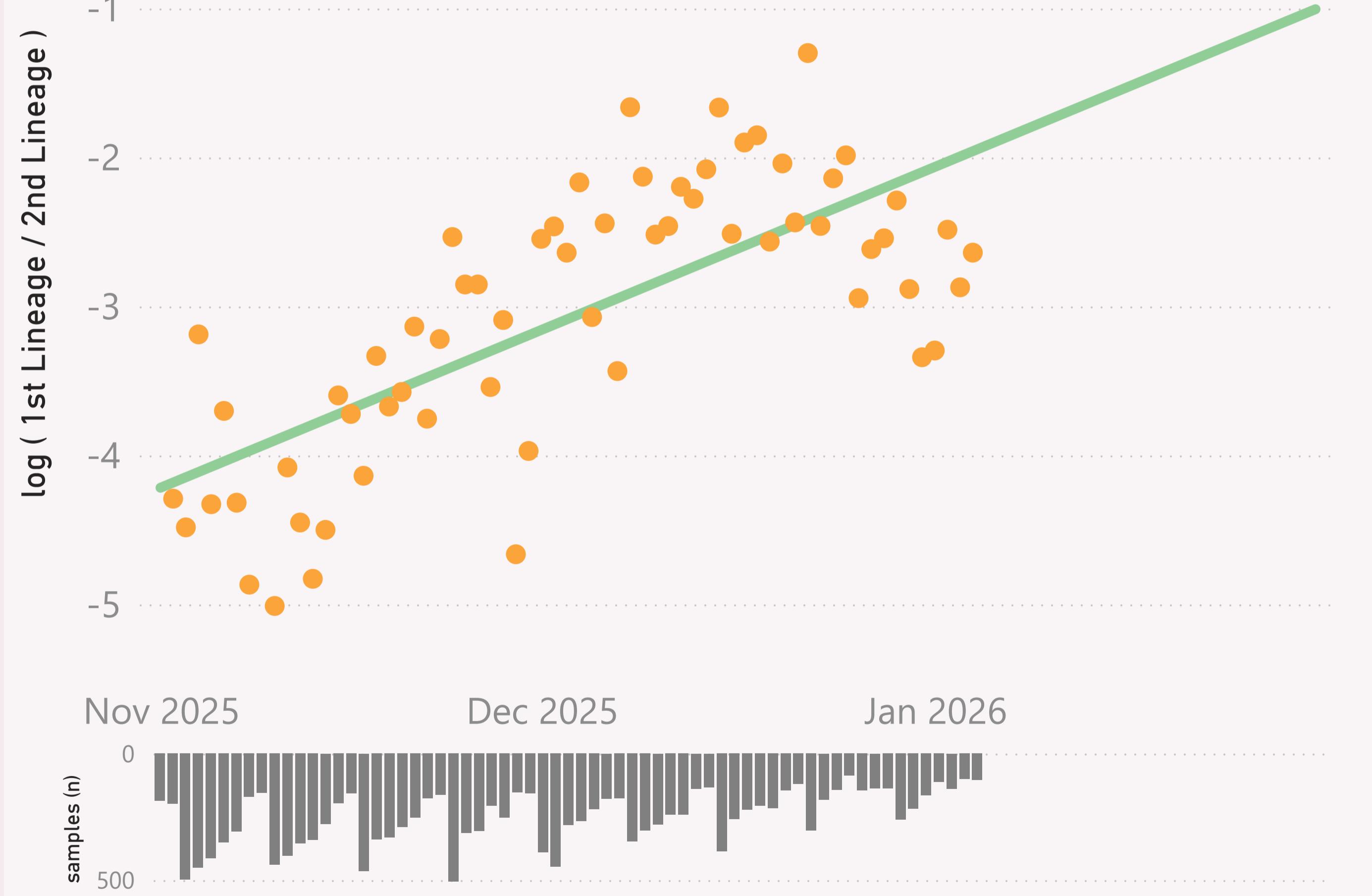
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=16,272 sequenced genomes, from 1 November 2025 up to 4 January 2026

## Global - BA.3.\* vs XFG.\*

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

0 ..... growth of 3.5% 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".

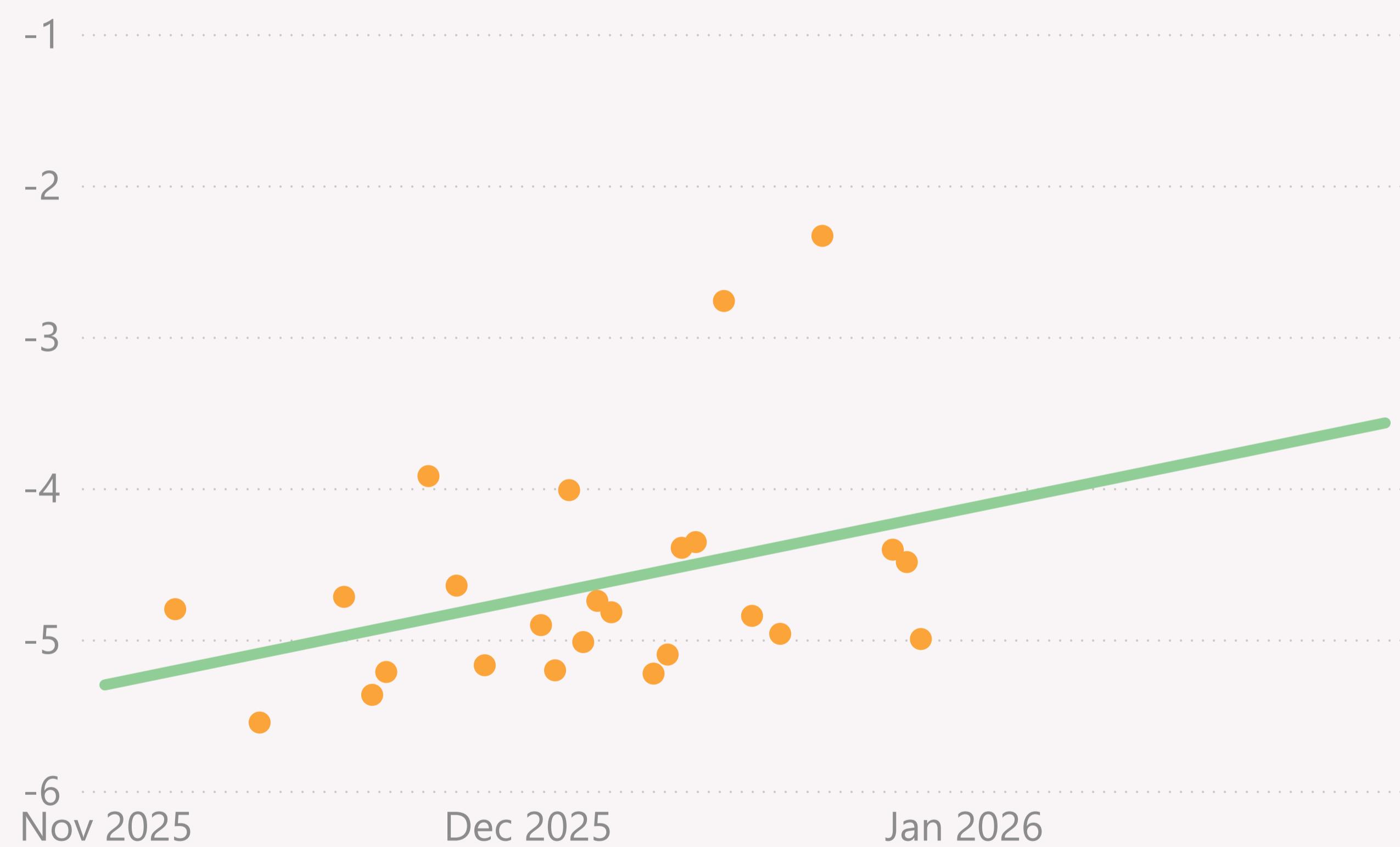
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=16,272 sequenced genomes, from 1 November 2025 up to 4 January 2026

## Global - RE.2.2.3 vs XFG.\*

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

0 ..... growth of 1.9% per day



samples (n)

0  
500

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.

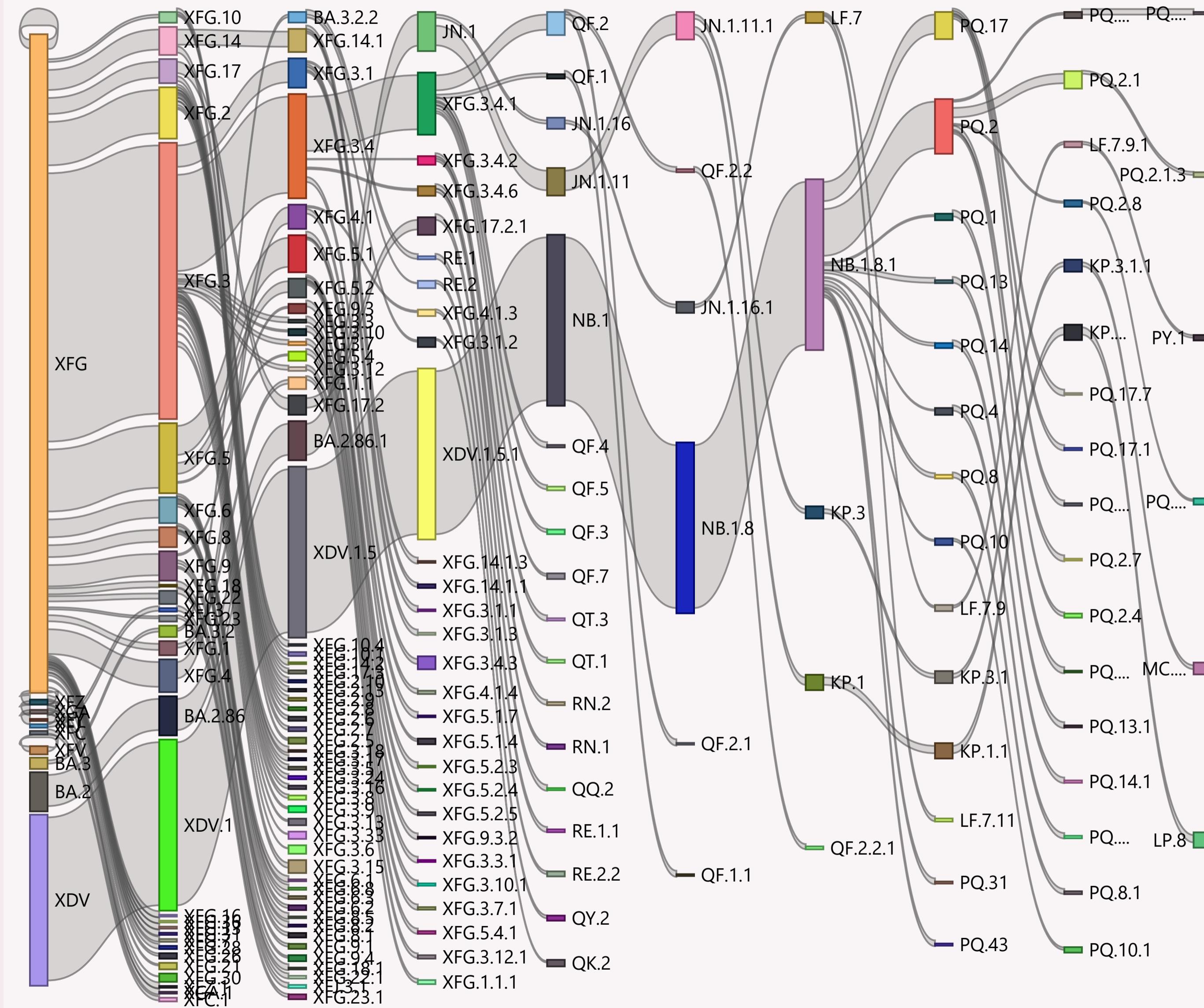
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage L2 is considered to have "crossed over" or taken over dominance from the 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=58,281 sequenced genomes, from 1 September 2025 up to 4 January 2026

# Global



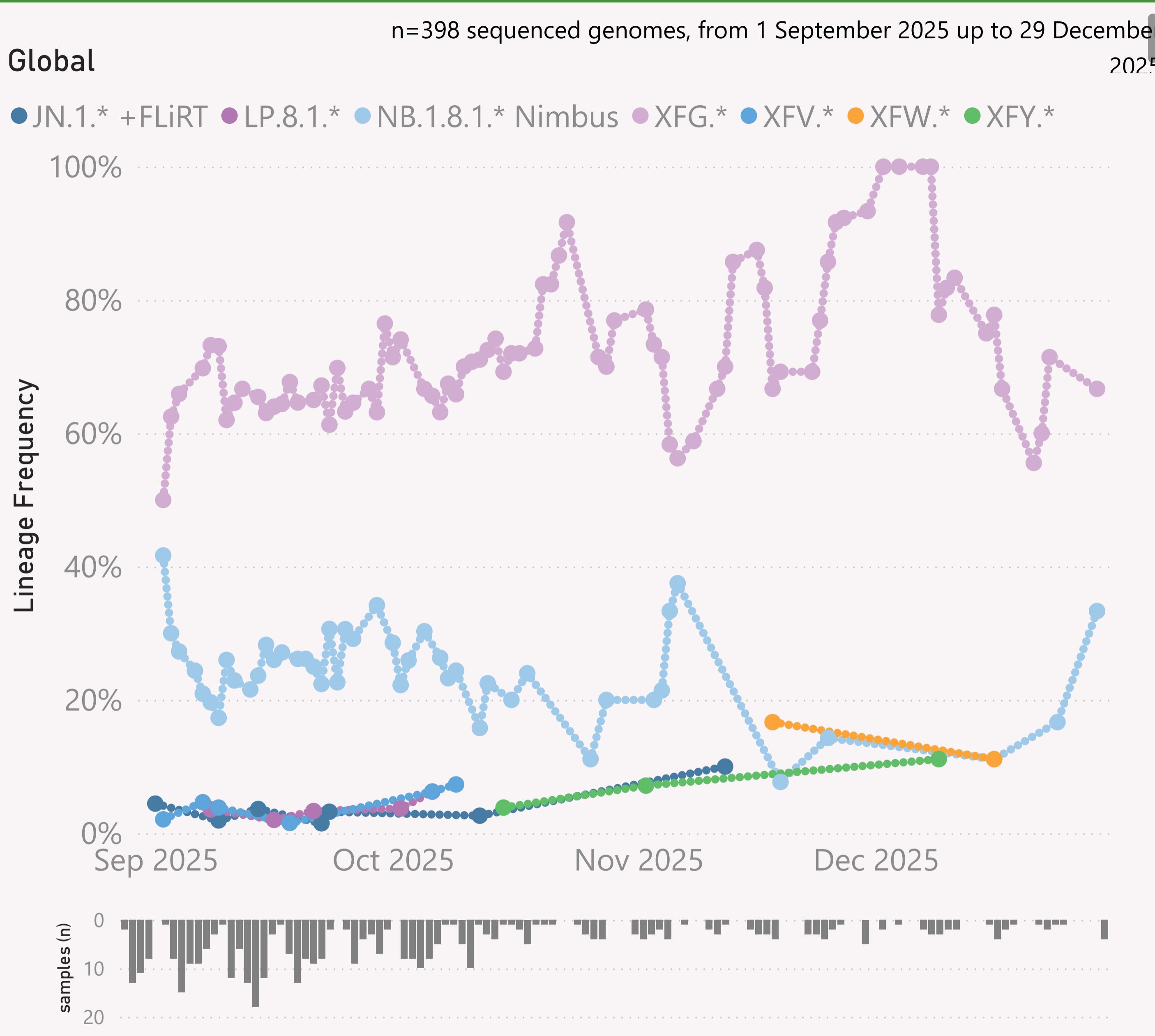
This page shows the hierarchy of the significant Lineages, over recent months.

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.

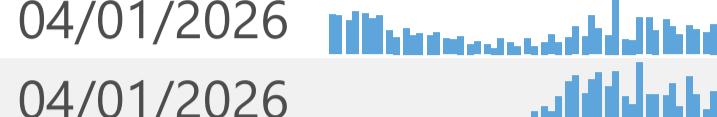
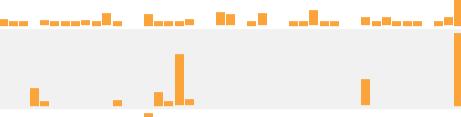
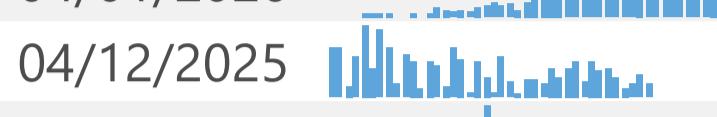
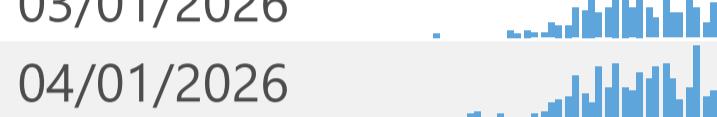
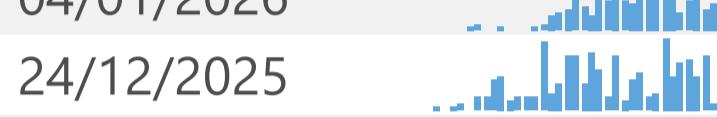
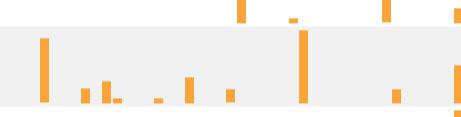
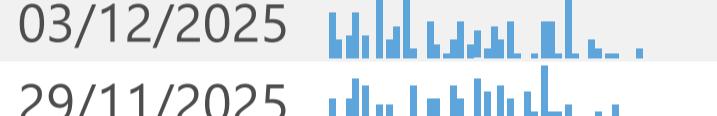
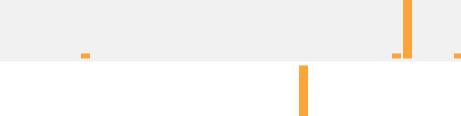
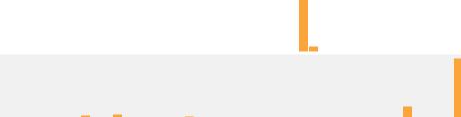
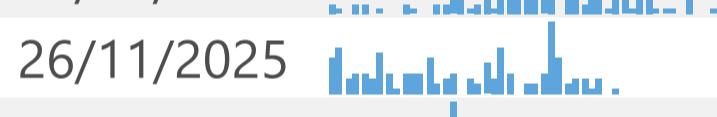
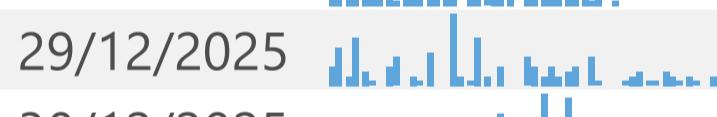
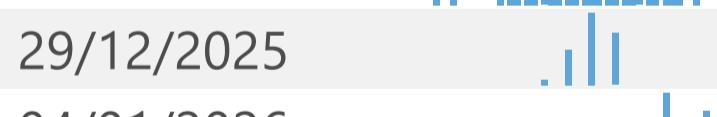
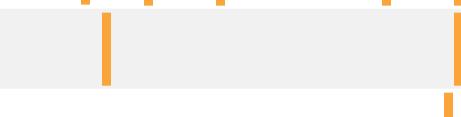
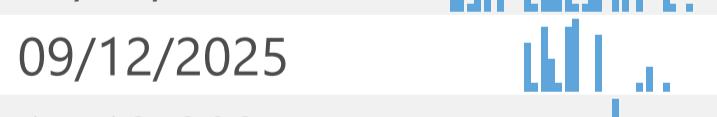
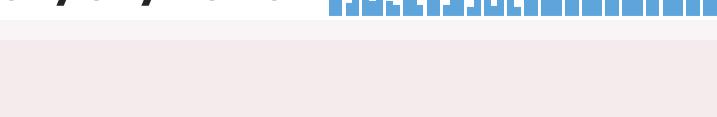


This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

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	6,005	04/01/2026		14/01/2026	
Canada	4,259	04/01/2026		14/01/2026	
Russia	1,078	04/12/2025		23/12/2025	
Spain	1,064	03/01/2026		14/01/2026	
Germany	953	02/01/2026		14/01/2026	
United Kingdom	916	04/01/2026		14/01/2026	
Australia	762	03/01/2026		14/01/2026	
Netherlands	674	04/01/2026		14/01/2026	
Chile	667	24/12/2025		14/01/2026	
France	657	04/01/2026		14/01/2026	
Italy	636	03/01/2026		14/01/2026	
China	448	03/12/2025		14/01/2026	
Lithuania	426	29/11/2025		31/12/2025	
Brazil	374	25/12/2025		14/01/2026	
Argentina	323	26/11/2025		14/01/2026	
Japan	319	29/12/2025		14/01/2026	
South Korea	312	30/12/2025		14/01/2026	
Luxembourg	295	15/12/2025		14/01/2026	
Sweden	234	30/12/2025		14/01/2026	
Denmark	226	29/12/2025		14/01/2026	
New Zealand	200	04/01/2026		14/01/2026	
Ukraine	175	16/12/2025		12/01/2026	
South Africa	102	09/12/2025		14/01/2026	
Poland	94	15/12/2025		14/01/2026	
Ireland	93	04/01/2026		14/01/2026	
Singapore	88	02/01/2026		13/01/2026	
Finland	84	11/12/2025		19/12/2025	
Slovenia	78	29/12/2025		05/01/2026	
<b>Total</b>	<b>22,138</b>	<b>04/01/2026</b>		<b>14/01/2026</b>	

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.