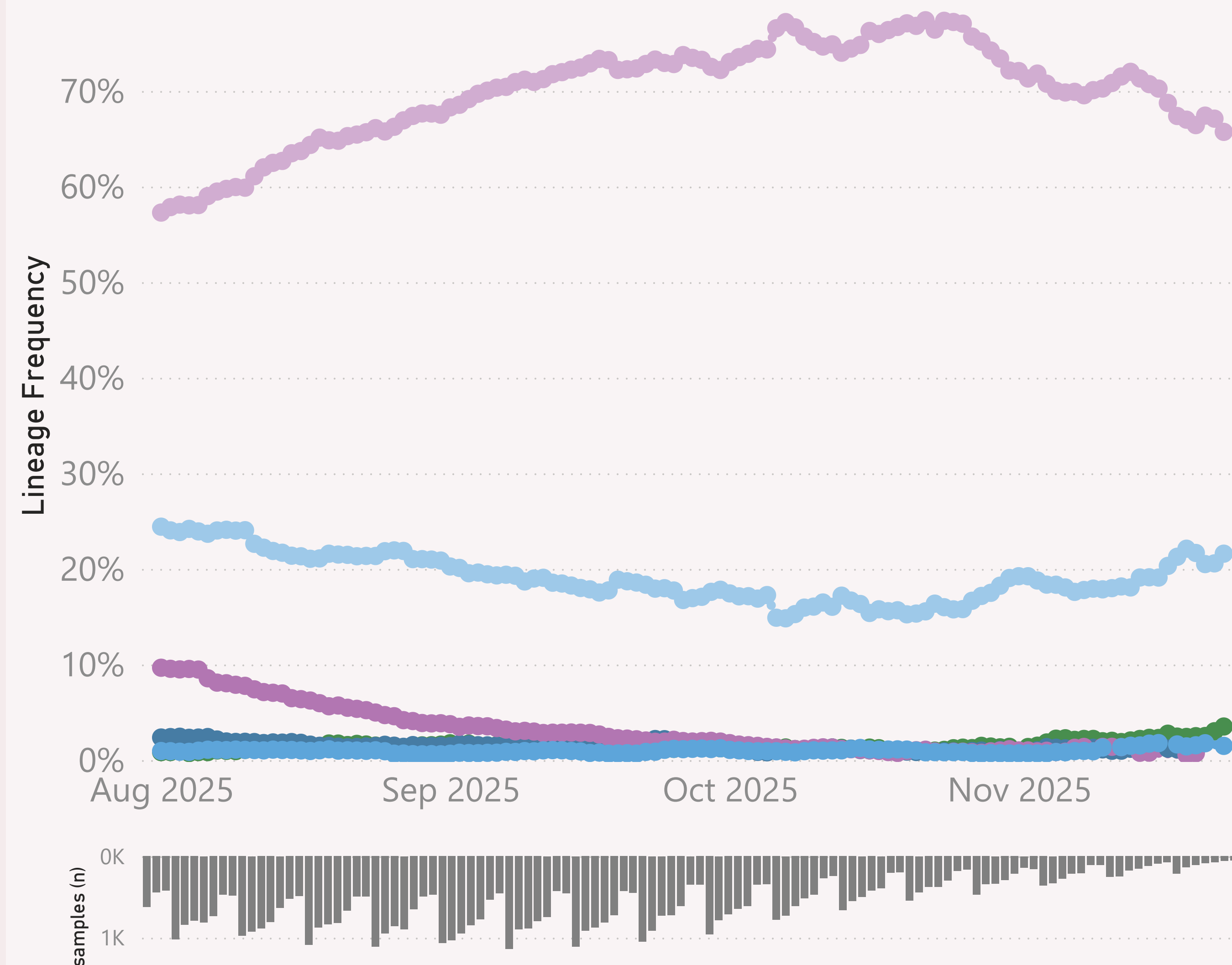


n=62,471 sequenced genomes, from 1 August 2025 up to 23 November 2025

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.

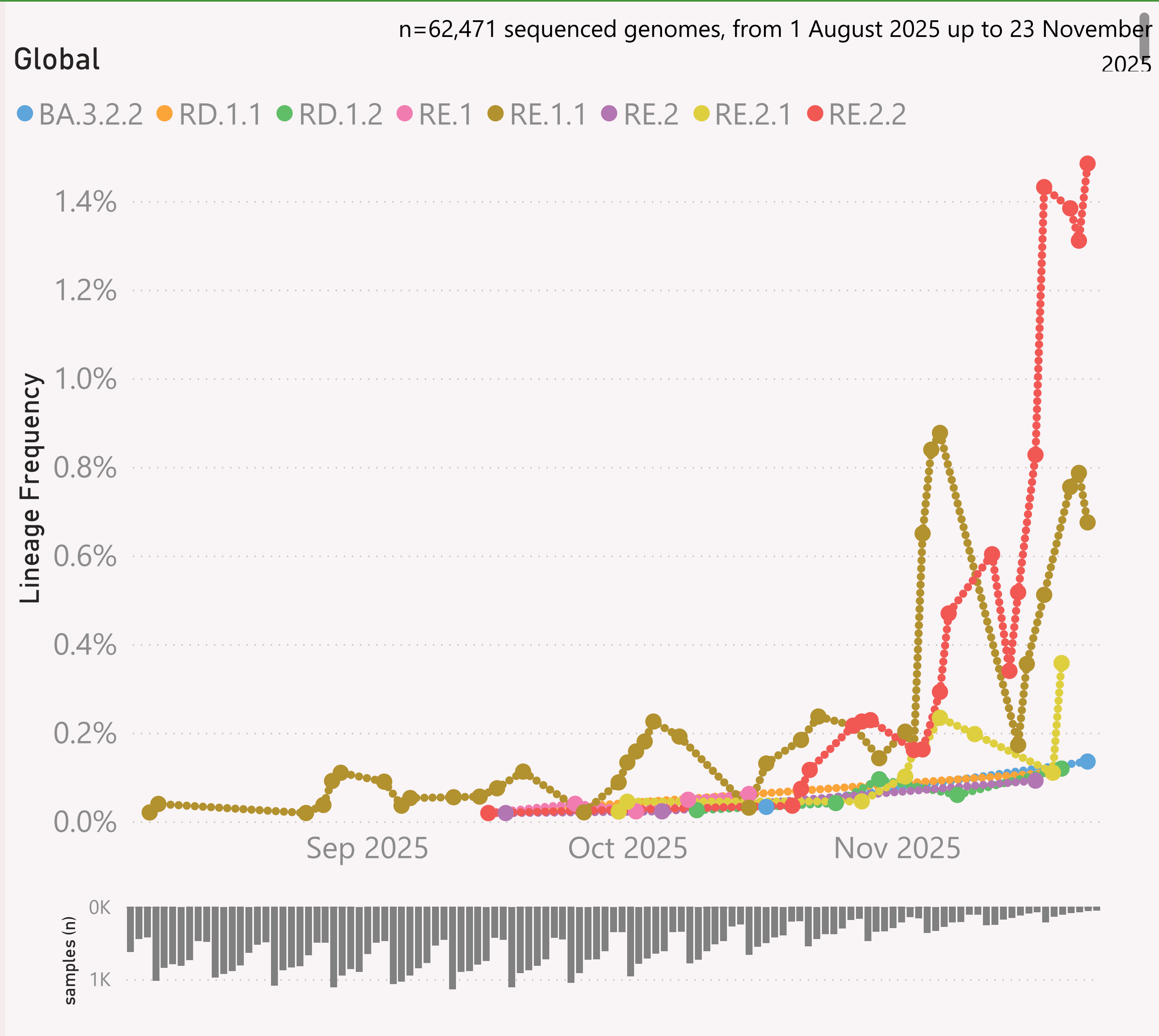
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.

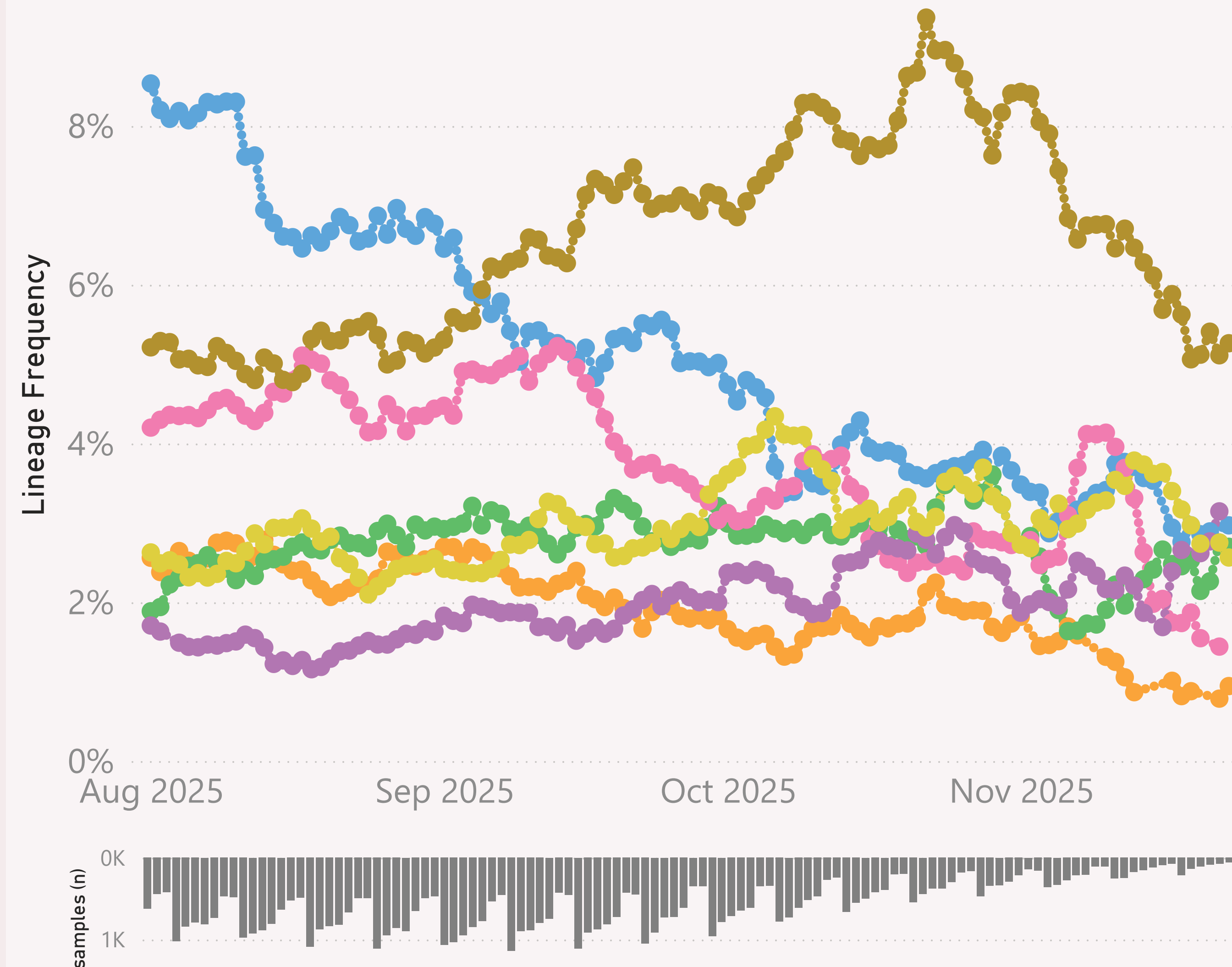
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=62,471 sequenced genomes, from 1 August 2025 up to 23 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.

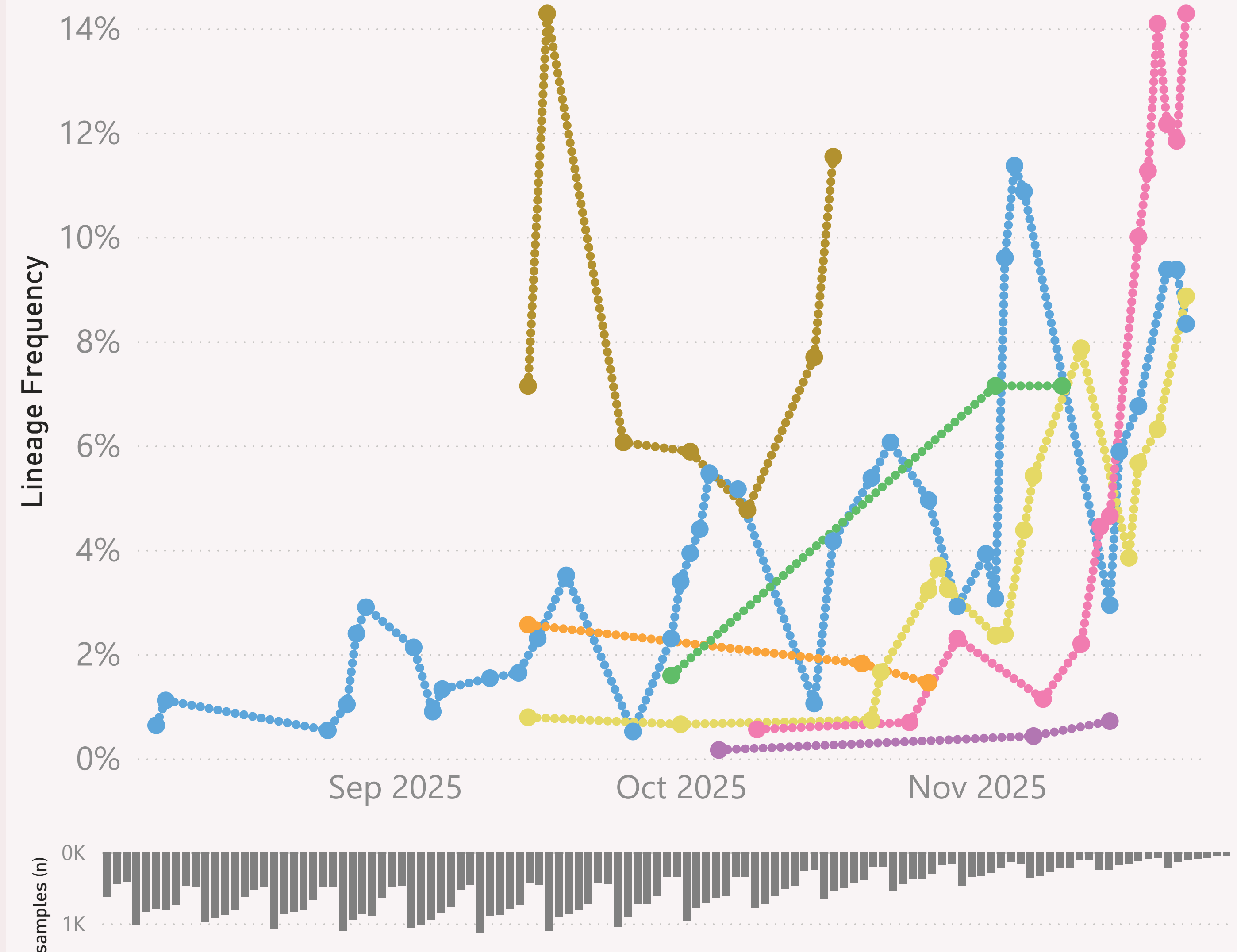
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=62,471 sequenced genomes, from 1 August 2025 up to 23 November 2025

BA.3.*

● Australia ● Denmark ● Germany ● Ireland ● Netherlands ● South A... ● United Ki...



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.

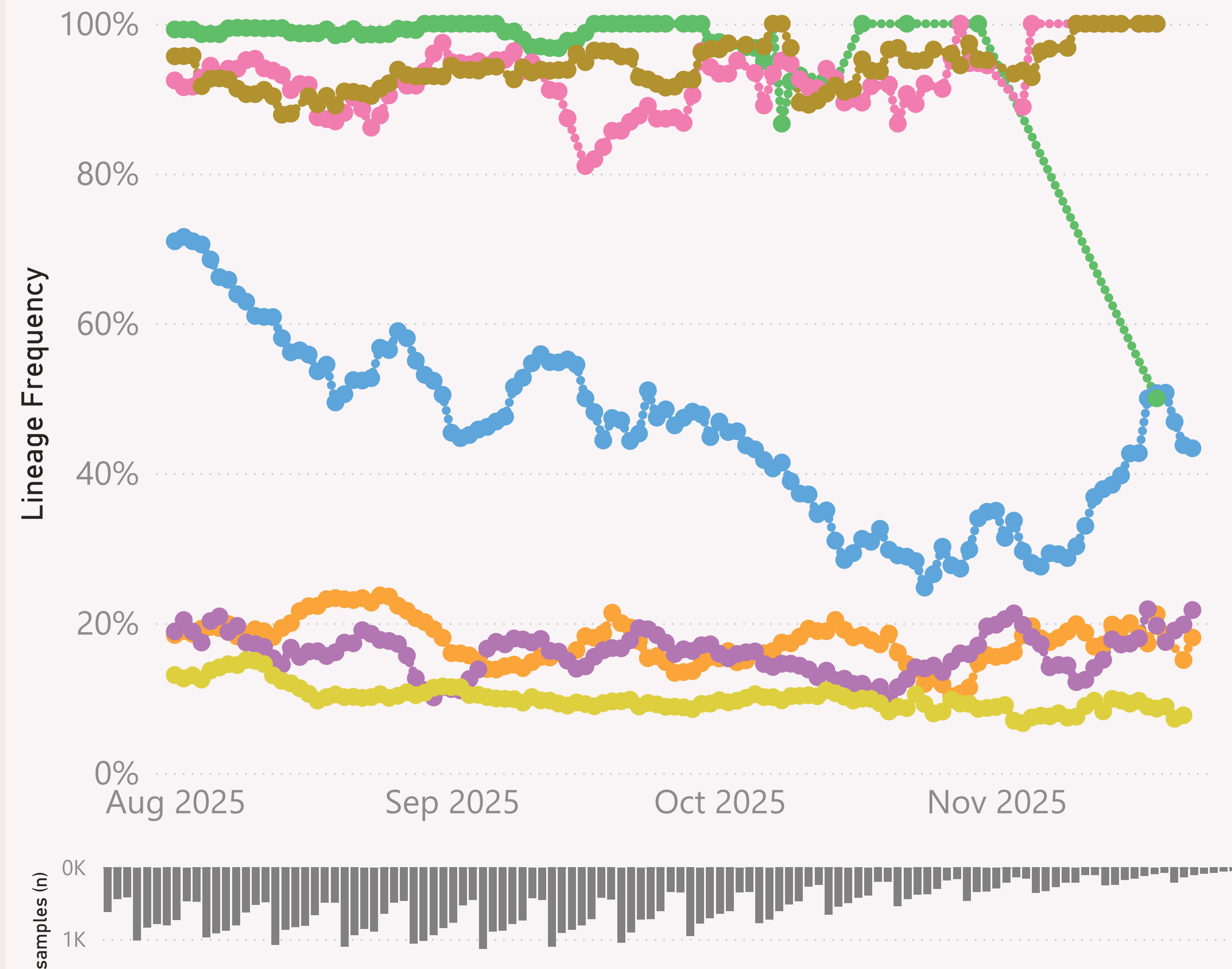
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=62,471 sequenced genomes, from 1 August 2025 up to 23 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.

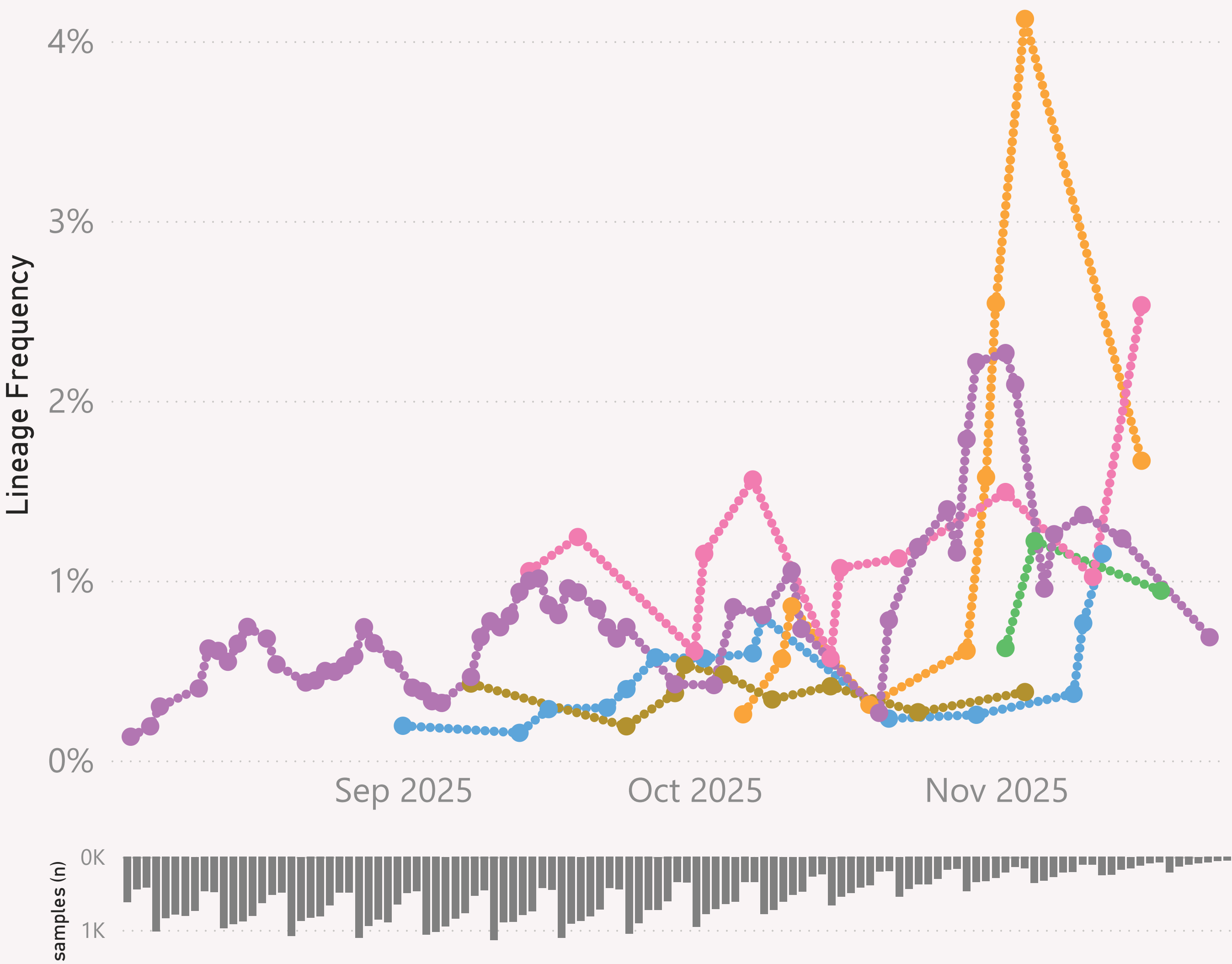
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=62,471 sequenced genomes, from 1 August 2025 up to 23 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.

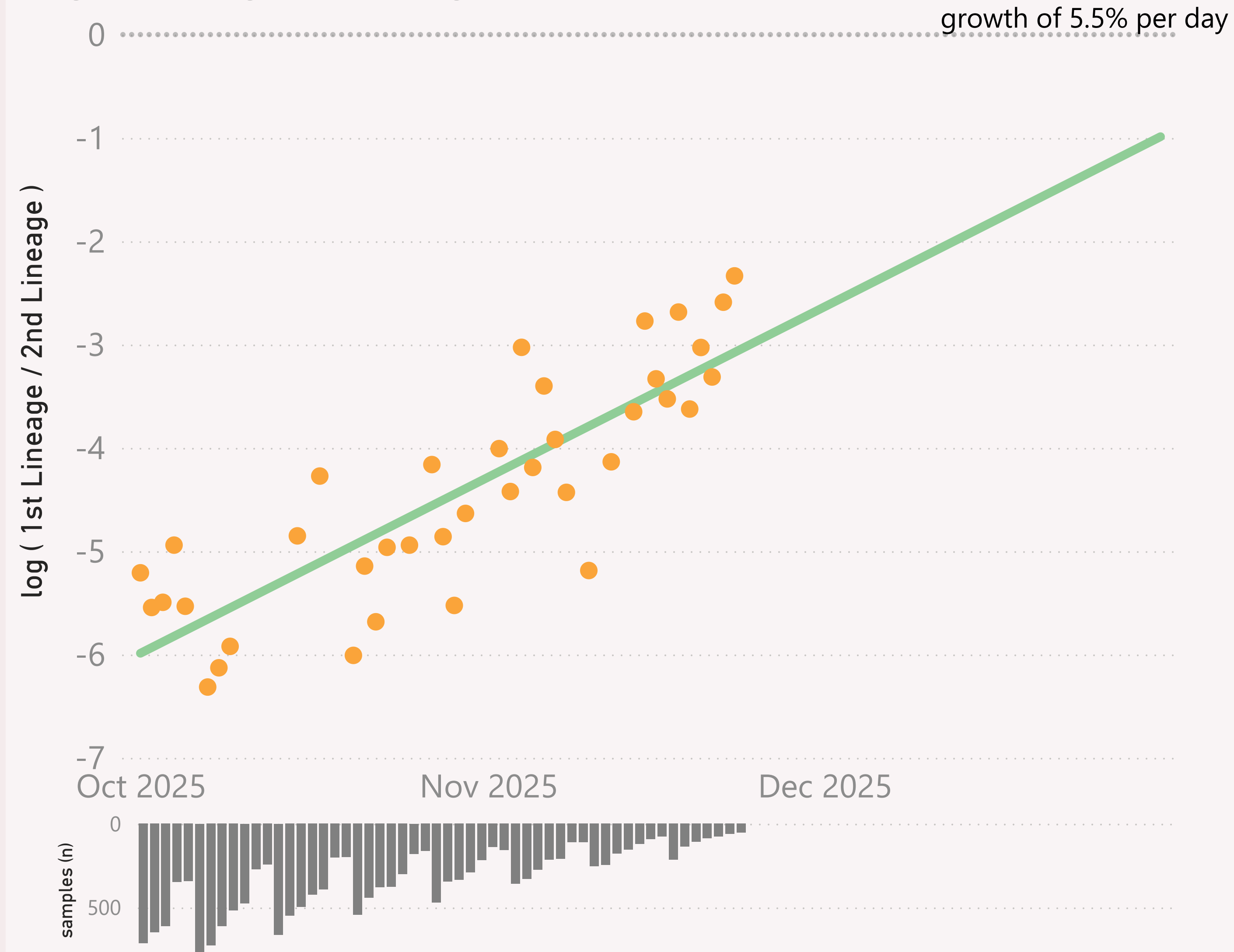
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=17,053 sequenced genomes, from 1 October 2025 up to 23 November 2025

Global - BA.3.* vs XFG.*

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

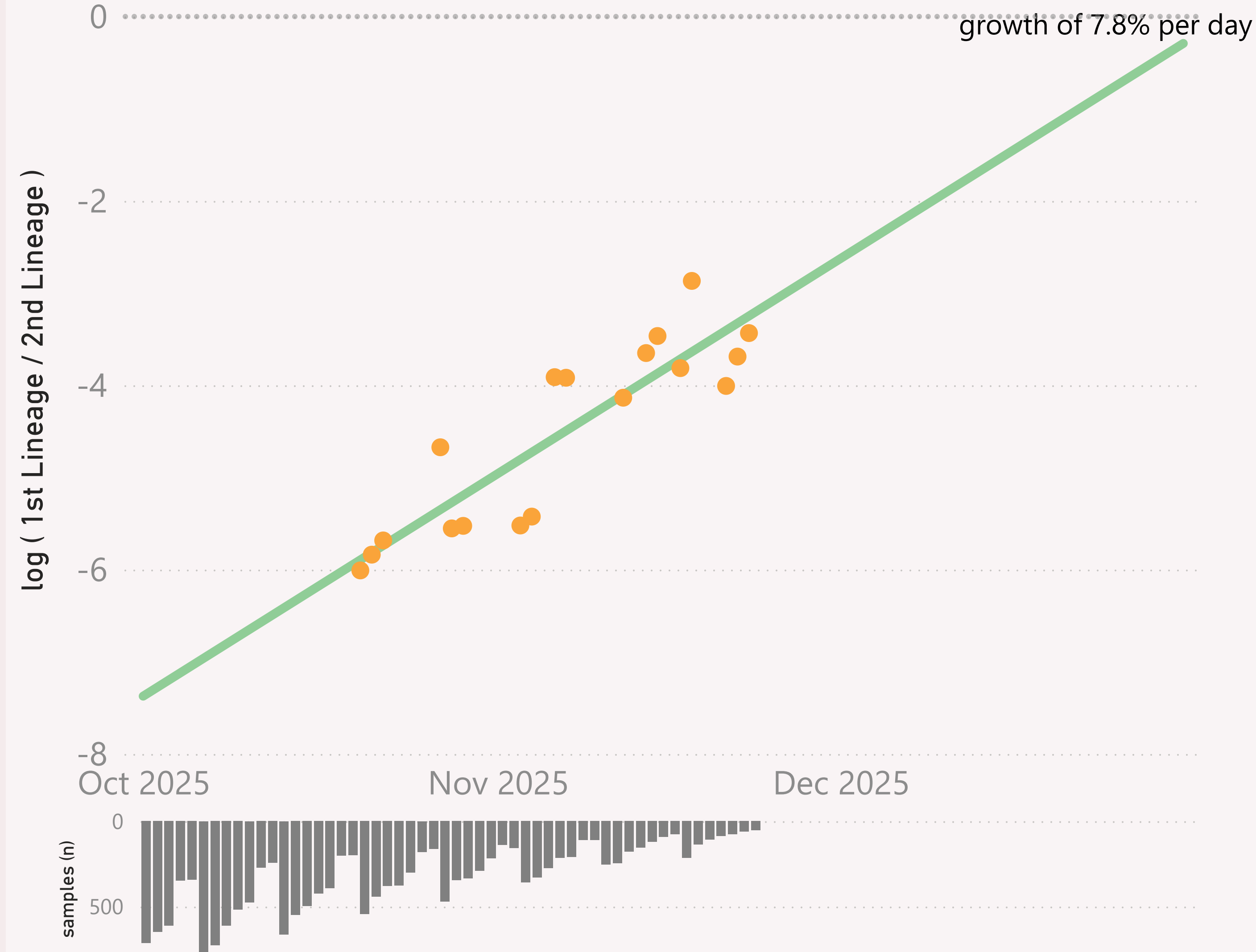
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=17,053 sequenced genomes, from 1 October 2025 up to 23 November 2025

Global - RE.2.2 vs XFG.*

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



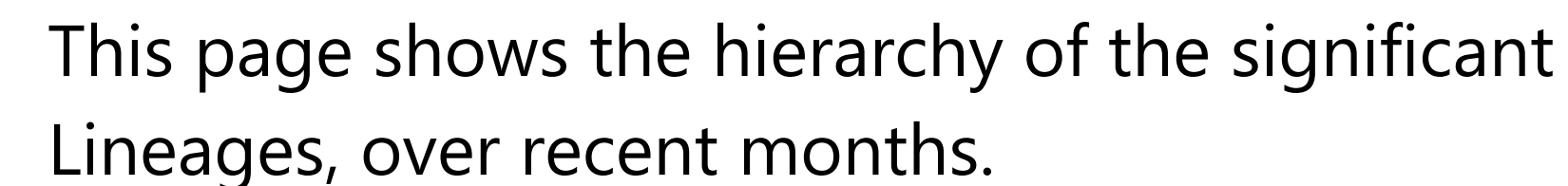
This page compares the relative frequency of a selected vs a "Lineage L2" group, over recent months. A challenging Lineage is selected first, and compared to the incumbent "Lineage L2" group.

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.

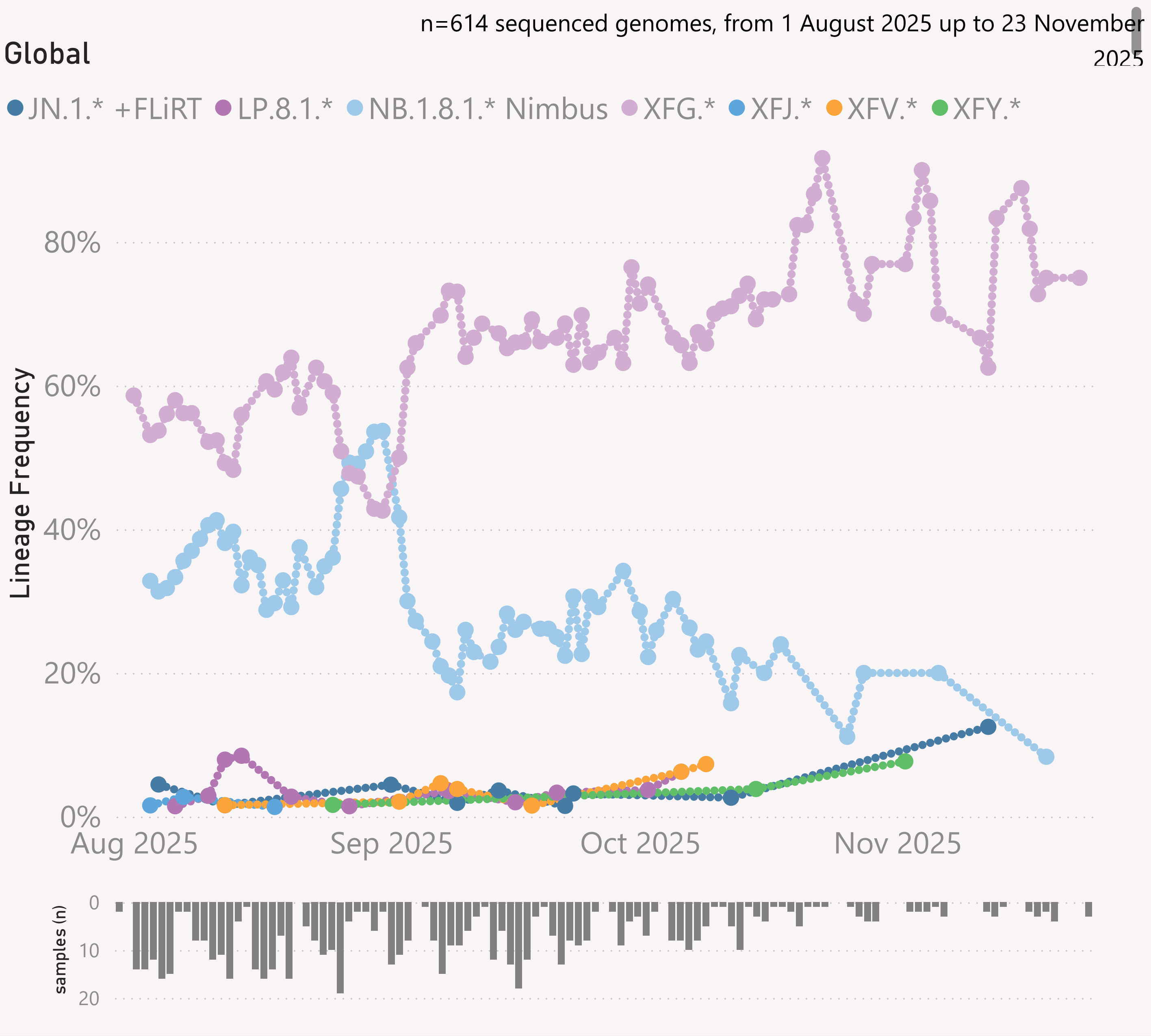
Global



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.

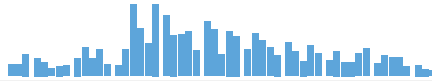




















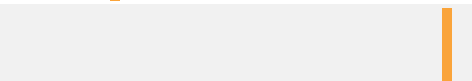



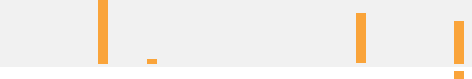



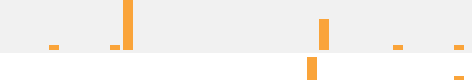





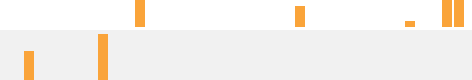



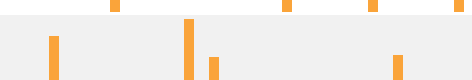


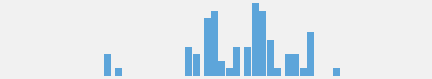
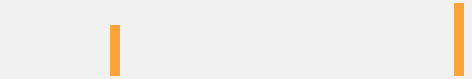



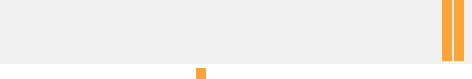


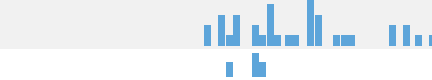



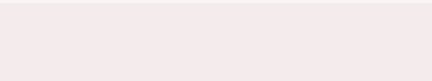
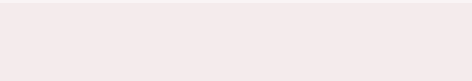
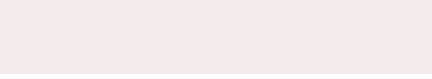
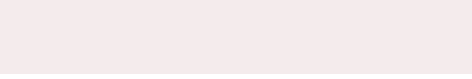


This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

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
<div>+ United States</div>	6,946	23/11/2025		25/11/2025	
<div>+ Canada</div>	2,855	23/11/2025		25/11/2025	
<div>+ United Kingdom</div>	2,771	23/11/2025		25/11/2025	
<div>+ Spain</div>	2,705	23/11/2025		25/11/2025	
<div>+ France</div>	1,489	22/11/2025		25/11/2025	
<div>+ Germany</div>	1,155	23/11/2025		25/11/2025	
<div>+ Netherlands</div>	930	23/11/2025		25/11/2025	
<div>+ Australia</div>	864	23/11/2025		25/11/2025	
<div>+ Italy</div>	787	23/11/2025		25/11/2025	
<div>+ Brazil</div>	772	12/11/2025		25/11/2025	
<div>+ Luxembourg</div>	638	31/10/2025		21/11/2025	
<div>+ Russia</div>	602	15/11/2025		24/11/2025	
<div>+ South Korea</div>	586	19/11/2025		25/11/2025	
<div>+ Denmark</div>	554	17/11/2025		25/11/2025	
<div>+ Japan</div>	481	19/11/2025		25/11/2025	
<div>+ China</div>	389	19/11/2025		25/11/2025	
<div>+ Poland</div>	350	22/11/2025		25/11/2025	
<div>+ Ireland</div>	276	12/11/2025		25/11/2025	
<div>+ Ukraine</div>	270	21/11/2025		25/11/2025	
<div>+ Singapore</div>	263	21/11/2025		25/11/2025	
<div>+ Sweden</div>	256	22/11/2025		25/11/2025	
<div>+ Slovenia</div>	247	22/11/2025		25/11/2025	
<div>+ Lithuania</div>	158	29/09/2025		19/10/2025	
<div>+ South Africa</div>	148	28/10/2025		25/11/2025	
<div>+ New Zealand</div>	147	23/11/2025		25/11/2025	
<div>+ Slovakia</div>	113	14/11/2025		25/11/2025	
<div>+ Chile</div>	88	12/10/2025		07/11/2025	
<div>+ Belgium</div>	87	23/11/2025		25/11/2025	
<div>+ Total</div>	27,729	23/11/2025		25/11/2025	

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.