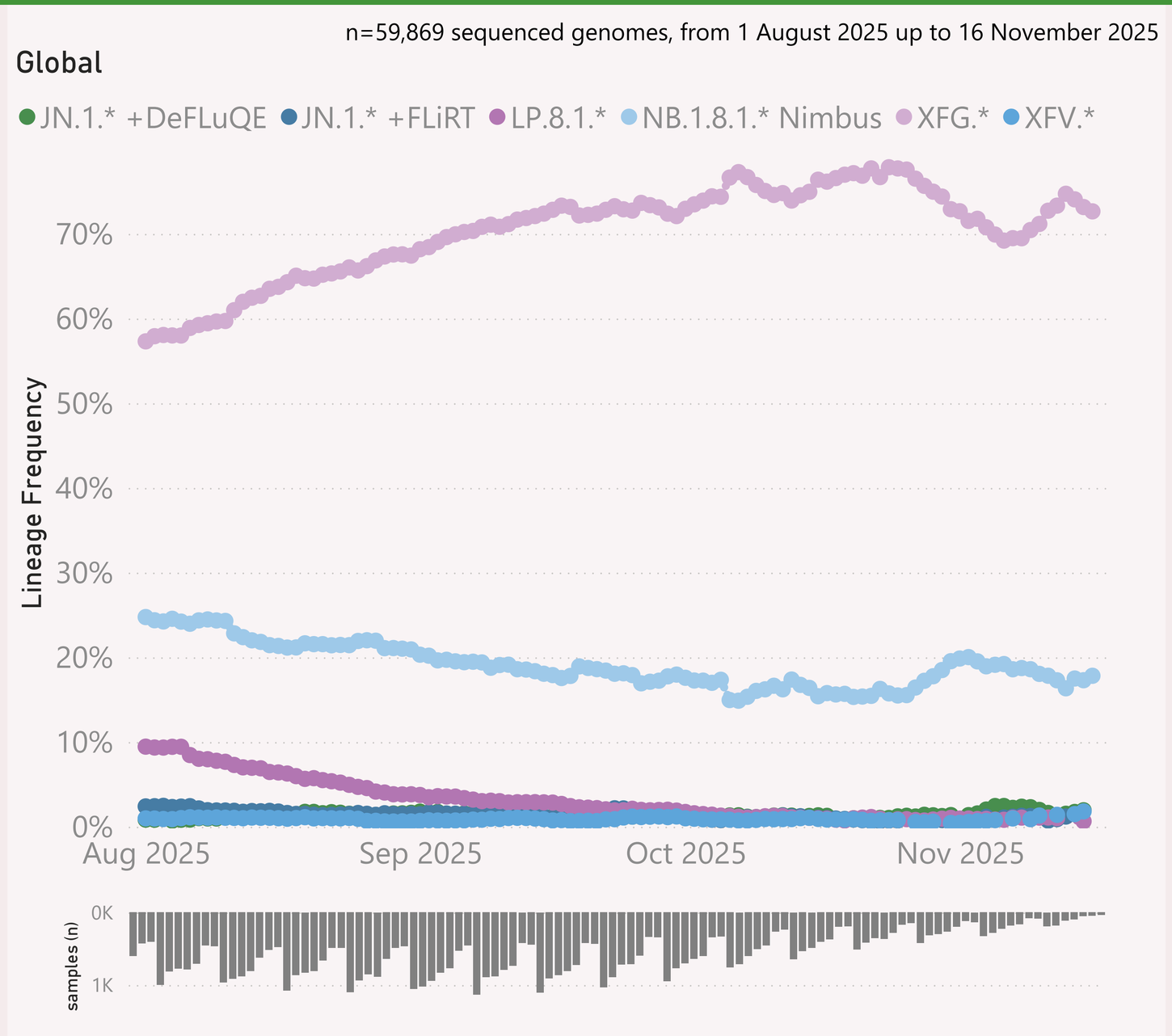


This page shows the frequency of the top 6 "L2" lineages, across recent months.

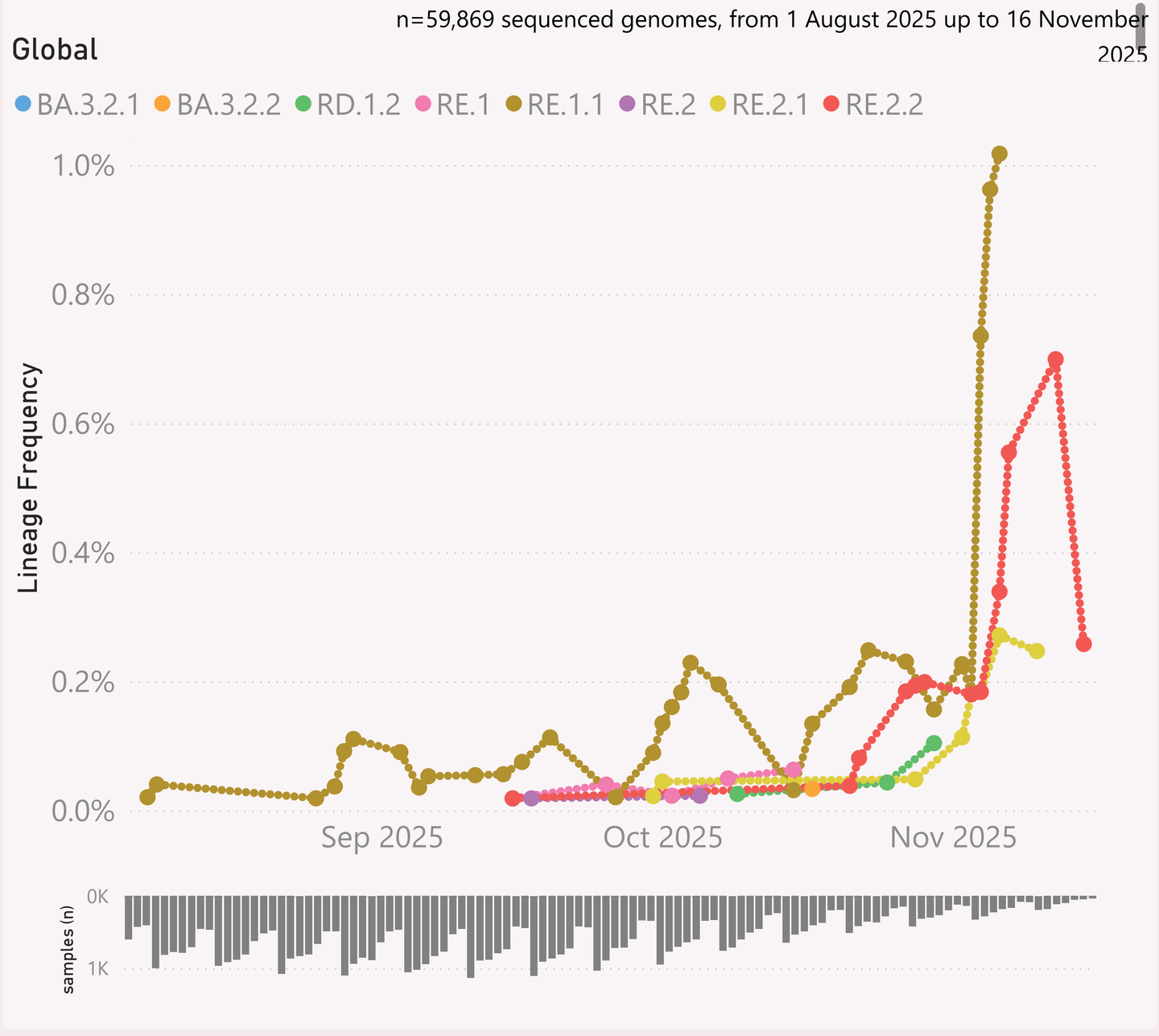
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.

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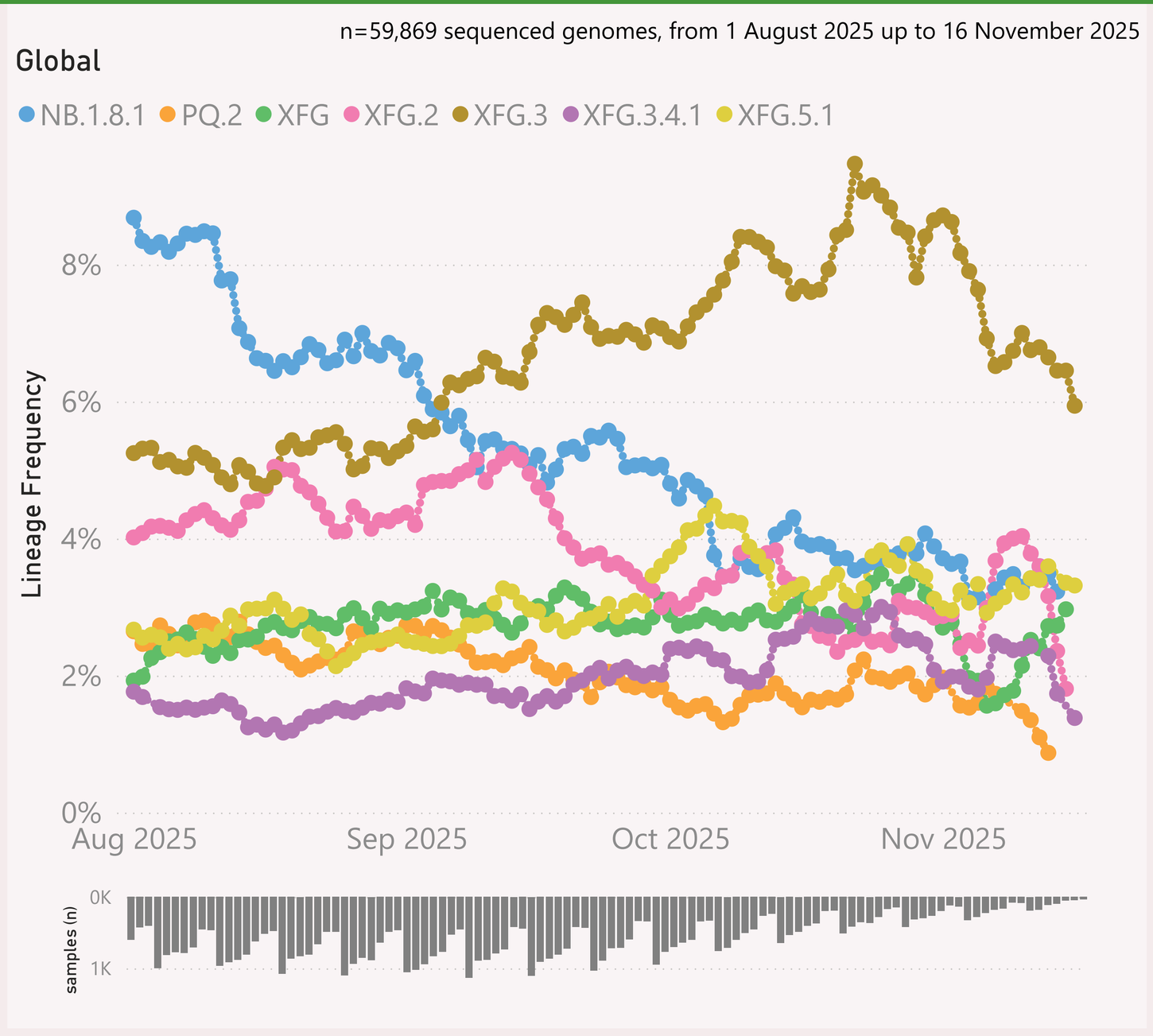
n=59,869 sequenced genomes, from 1 August 2025 up to 16 November 2025



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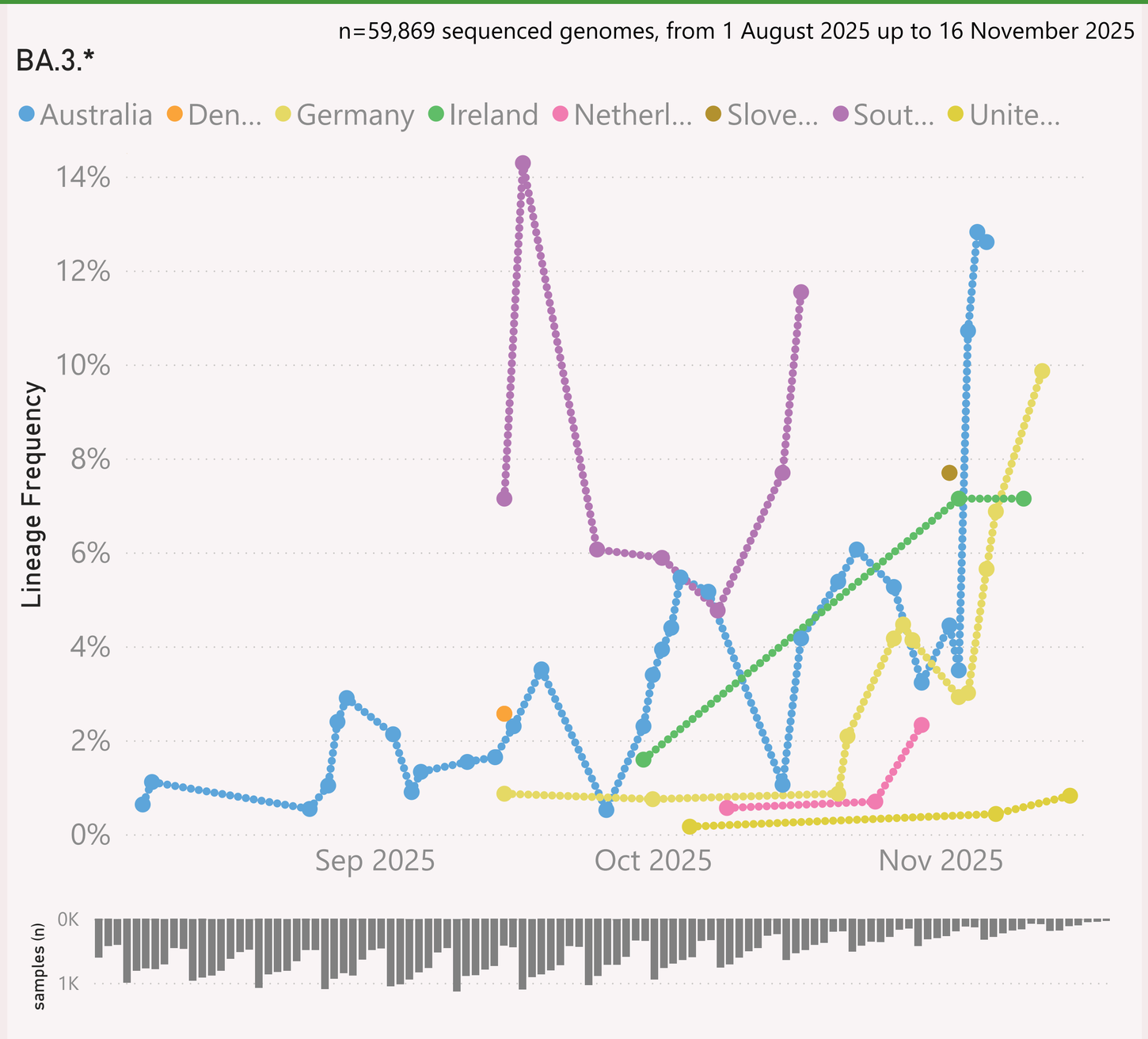

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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.

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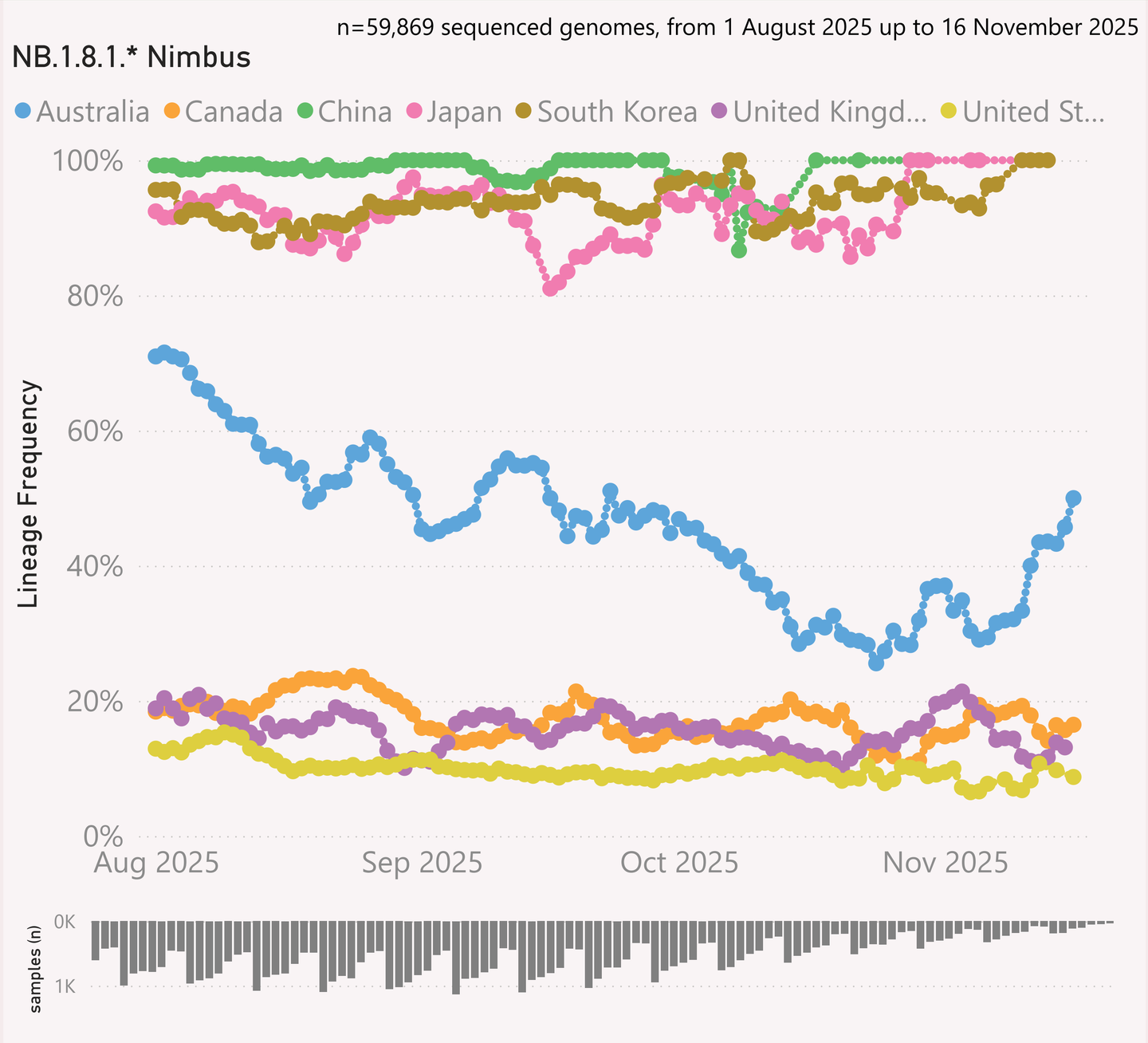

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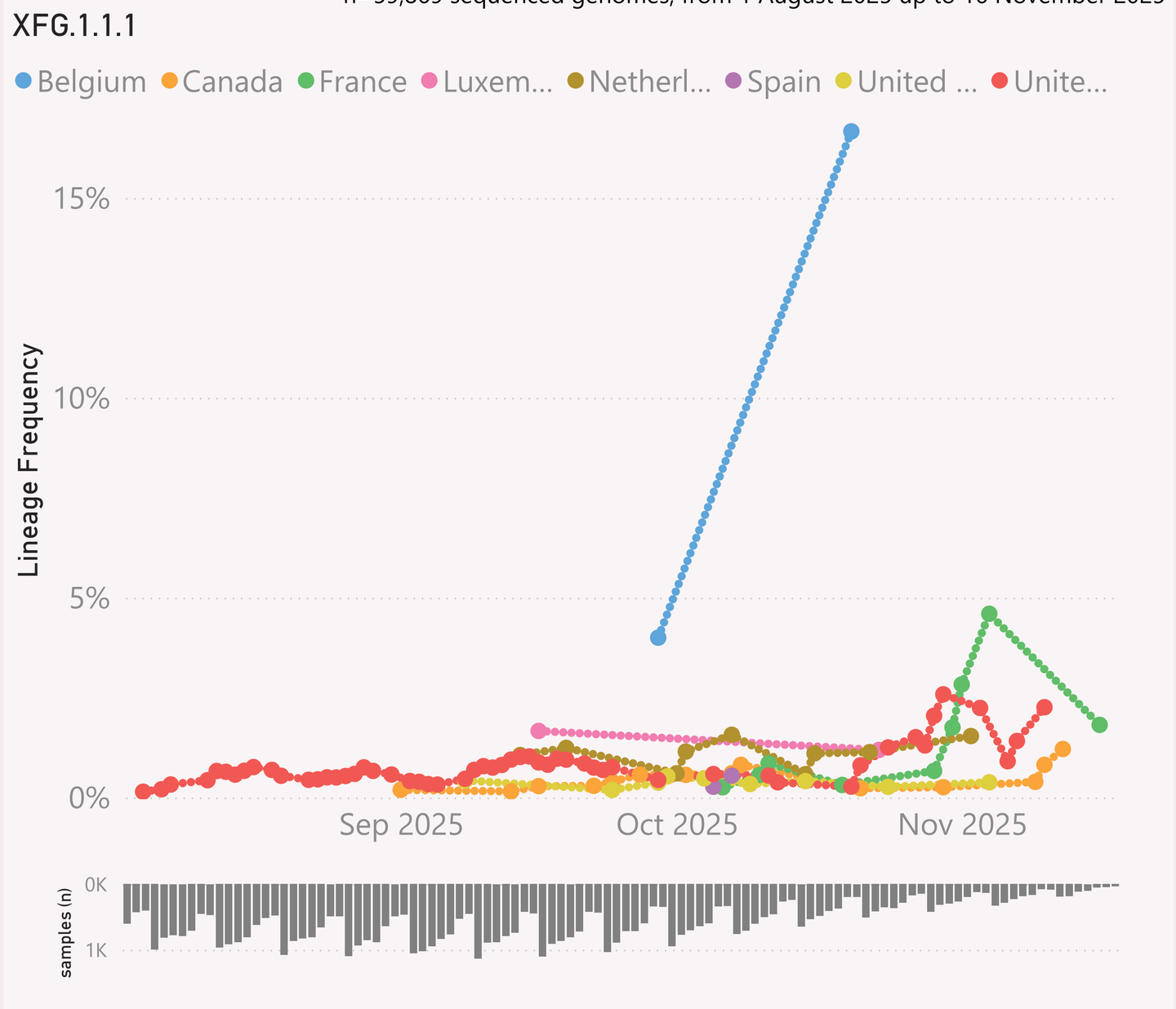


This page shows the frequency of a selected Lineage, for the 7 countries reporting the most samples over recent months.

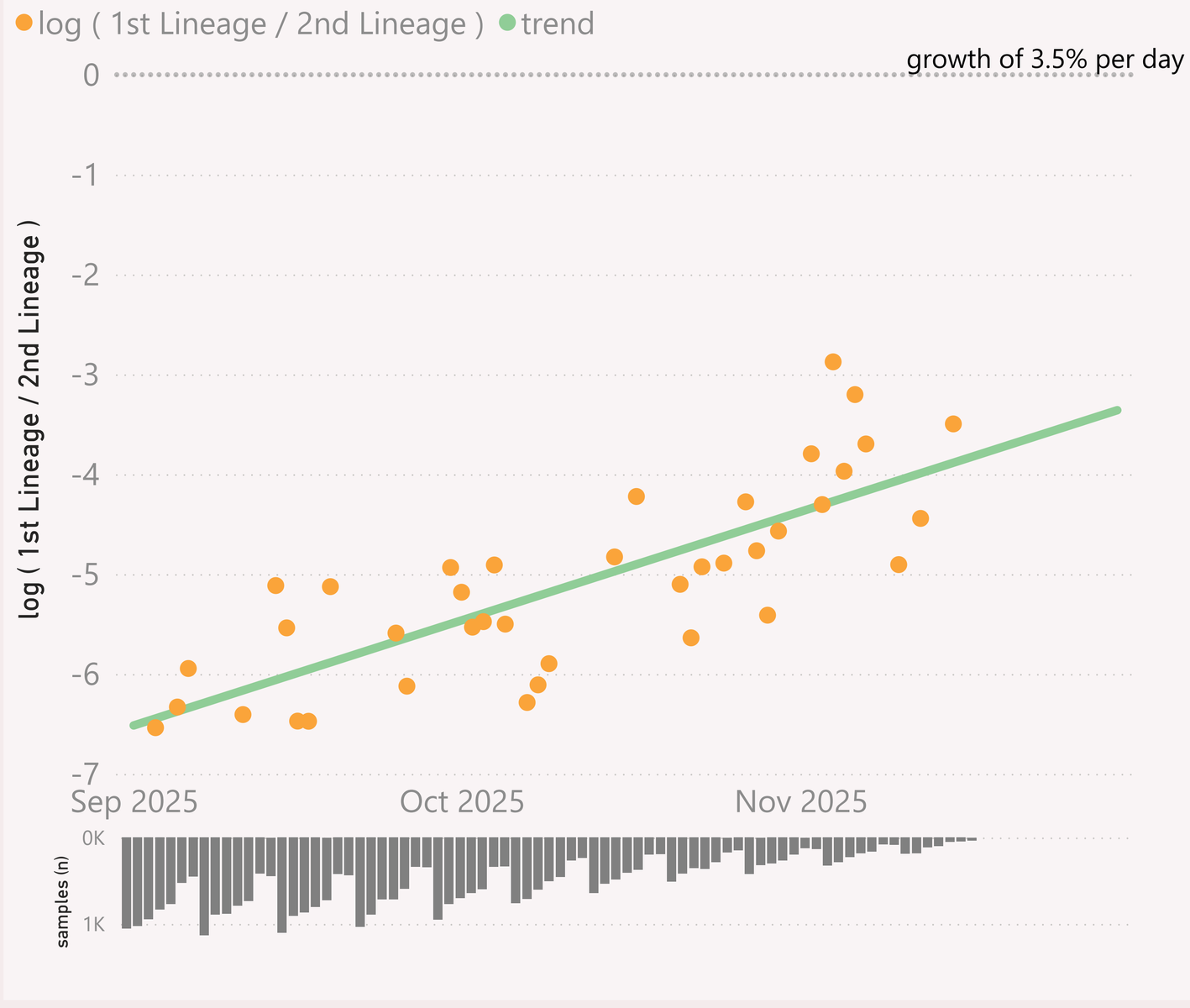
The detailed Lineage classifications are provided by Nextclade.

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=37,639 sequenced genomes, from 1 September 2025 up to 16 November 2025

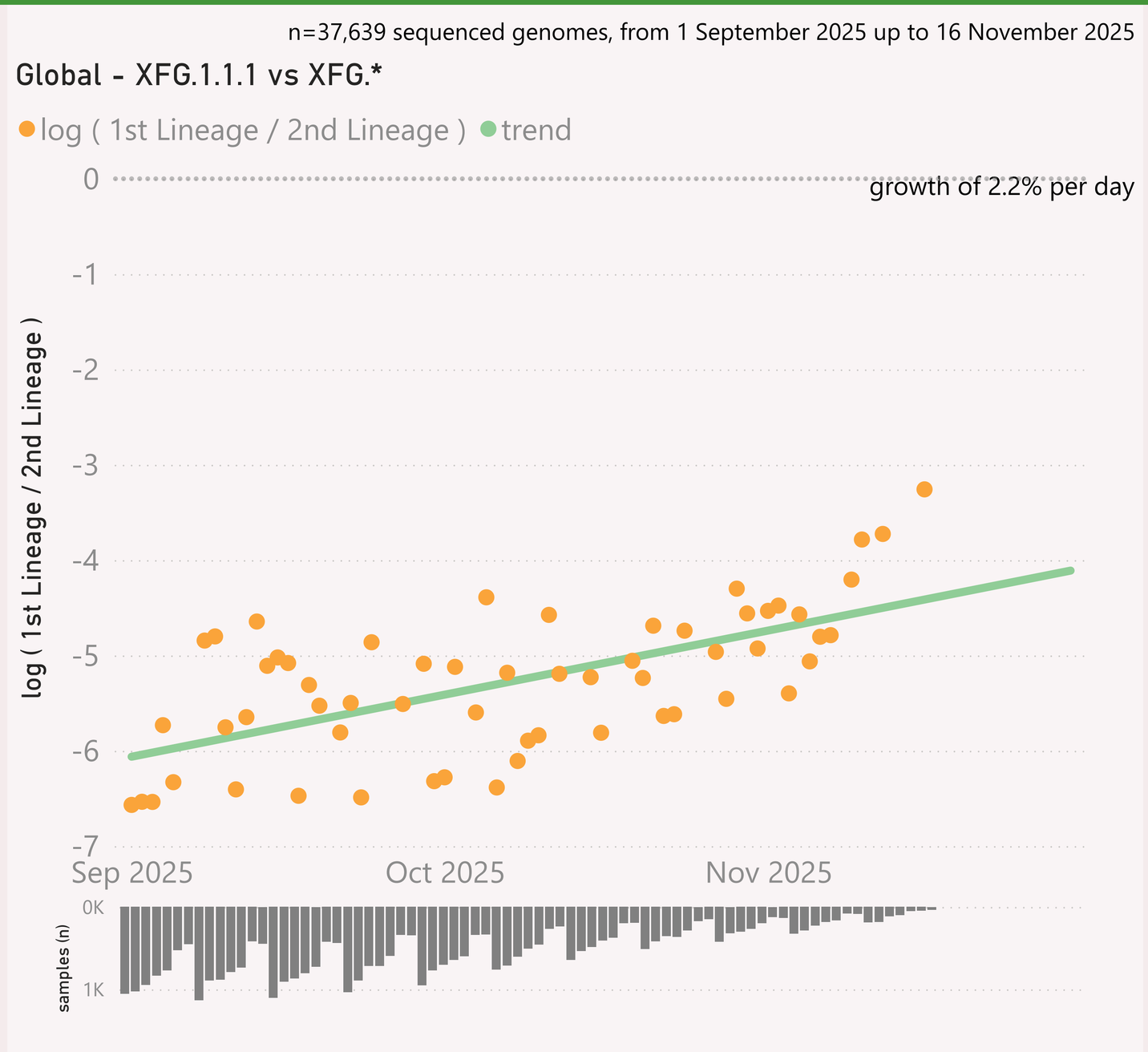


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.



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".

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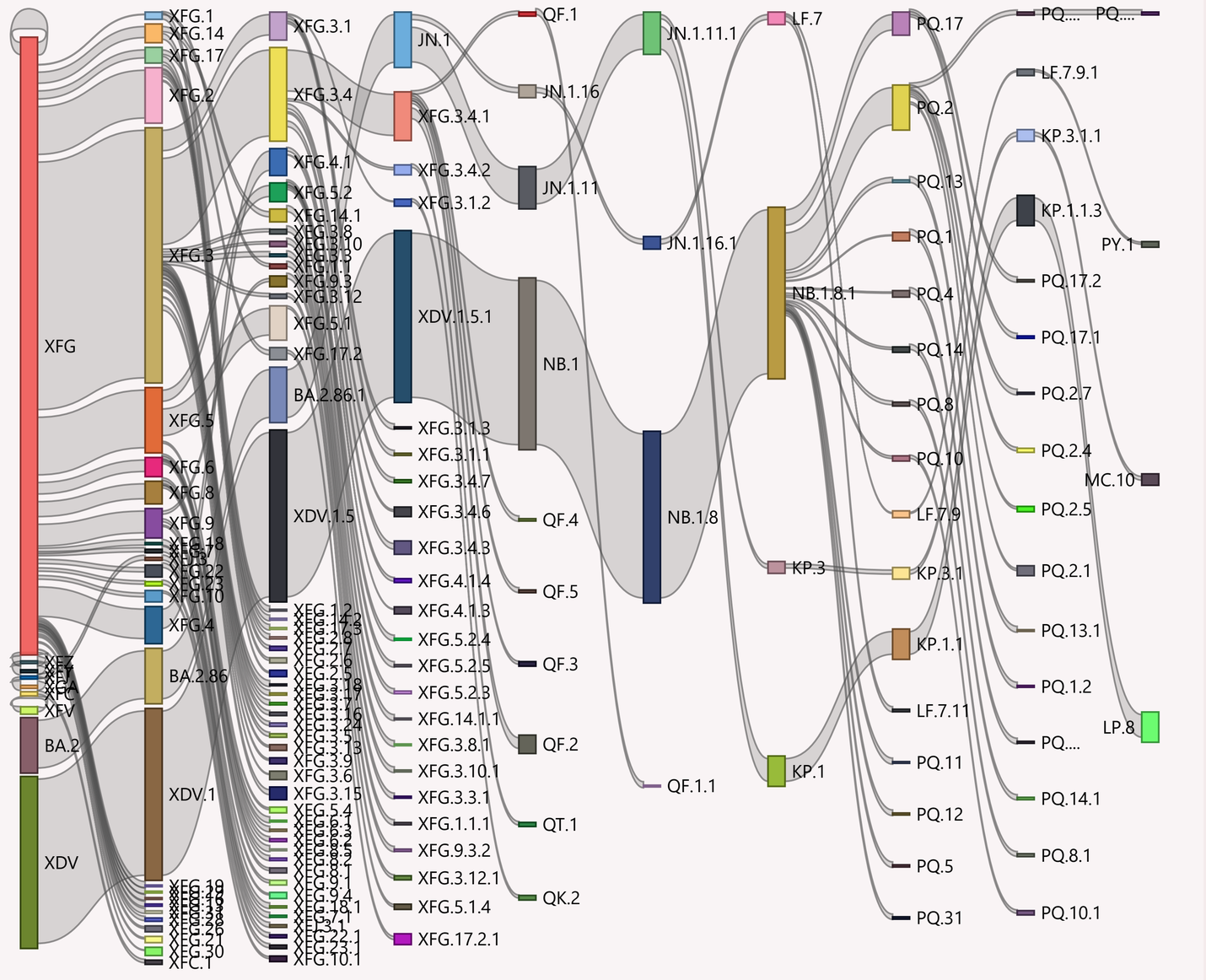


This page shows the hierarchy of the significant Lineages, over recent months.

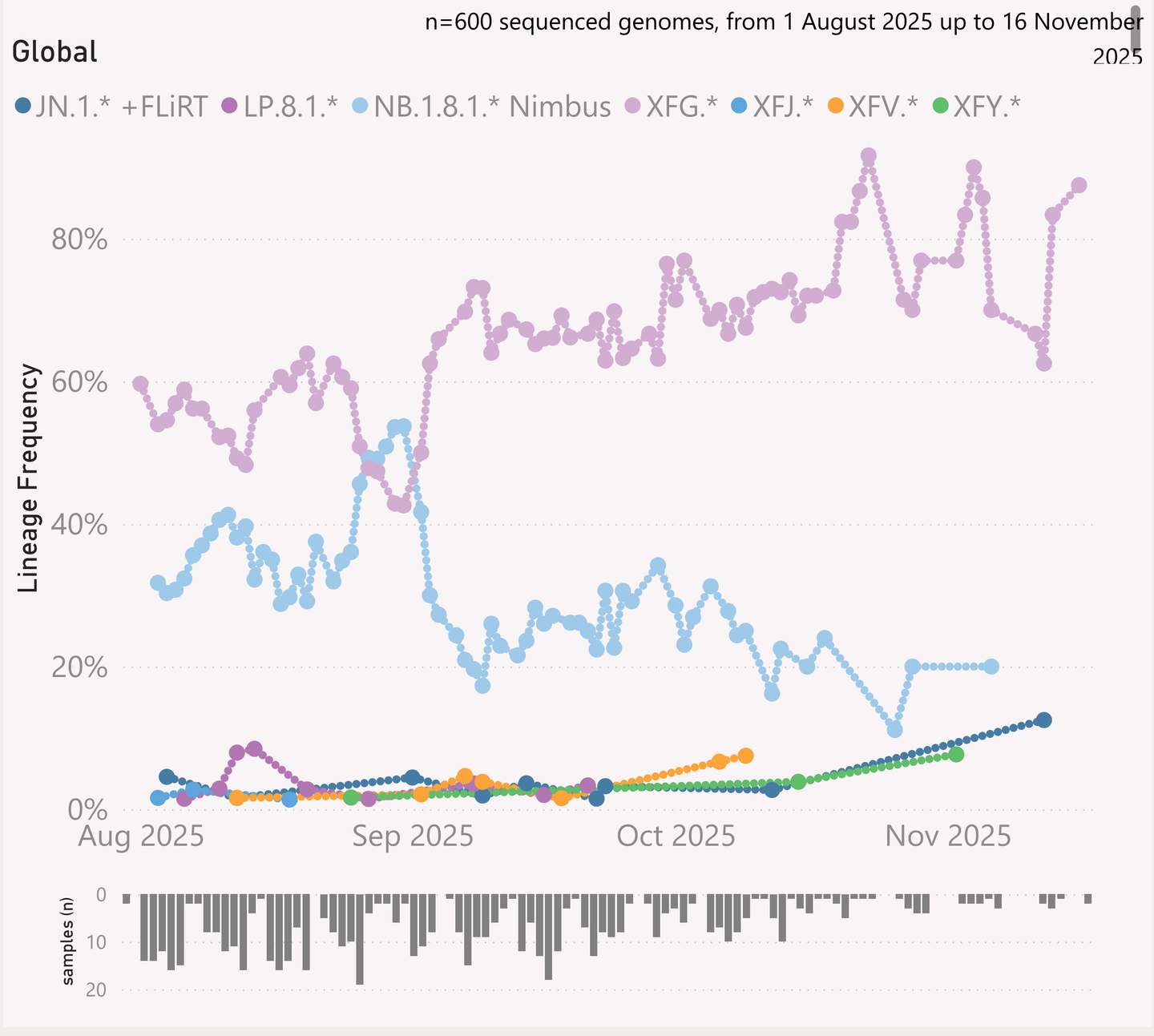
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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 - International Travellers only. Data from gisaid.org, with nextclade lineages. Source files and more info on github. Last Update: 2025-12-05 23:38 (UTC)



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: 2025-12-05 23:38 (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	6,936	16/11/2025		15/11/2025	
Canada	3,256	16/11/2025		15/11/2025	
United Kingdom	3,143	16/11/2025		15/11/2025	
Spain	2,918	16/11/2025		15/11/2025	
France	1,895	16/11/2025		15/11/2025	
Netherlands	1,132	10/11/2025		15/11/2025	
Germany	963	16/11/2025		15/11/2025	
Australia	932	16/11/2025		15/11/2025	
Brazil	832	07/11/2025		15/11/2025	
Italy	813	16/11/2025		15/11/2025	
South Korea	798	13/11/2025		15/11/2025	
Luxembourg	638	31/10/2025		15/11/2025	
Russia	602	15/11/2025		15/11/2025	
Japan	505	11/11/2025		15/11/2025	
Denmark	472	10/11/2025		15/11/2025	
China	377	30/10/2025		15/11/2025	
Slovenia	375	15/11/2025		15/11/2025	
Poland	346	15/11/2025		15/11/2025	
Ireland	337	12/11/2025		15/11/2025	
Sweden	276	10/11/2025		15/11/2025	
Ukraine	273	02/11/2025		15/11/2025	
Singapore	252	13/11/2025		15/11/2025	
New Zealand	204	16/11/2025		15/11/2025	
South Africa	170	28/10/2025		15/11/2025	
Lithuania	158	29/09/2025		19/10/2025	
Slovakia	121	14/11/2025		15/11/2025	
Belgium	104	01/11/2025		15/11/2025	
Costa Rica	91	26/10/2025		15/11/2025	
Total	**29,814**	**16/11/2025**		**15/11/2025**	

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.