

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.

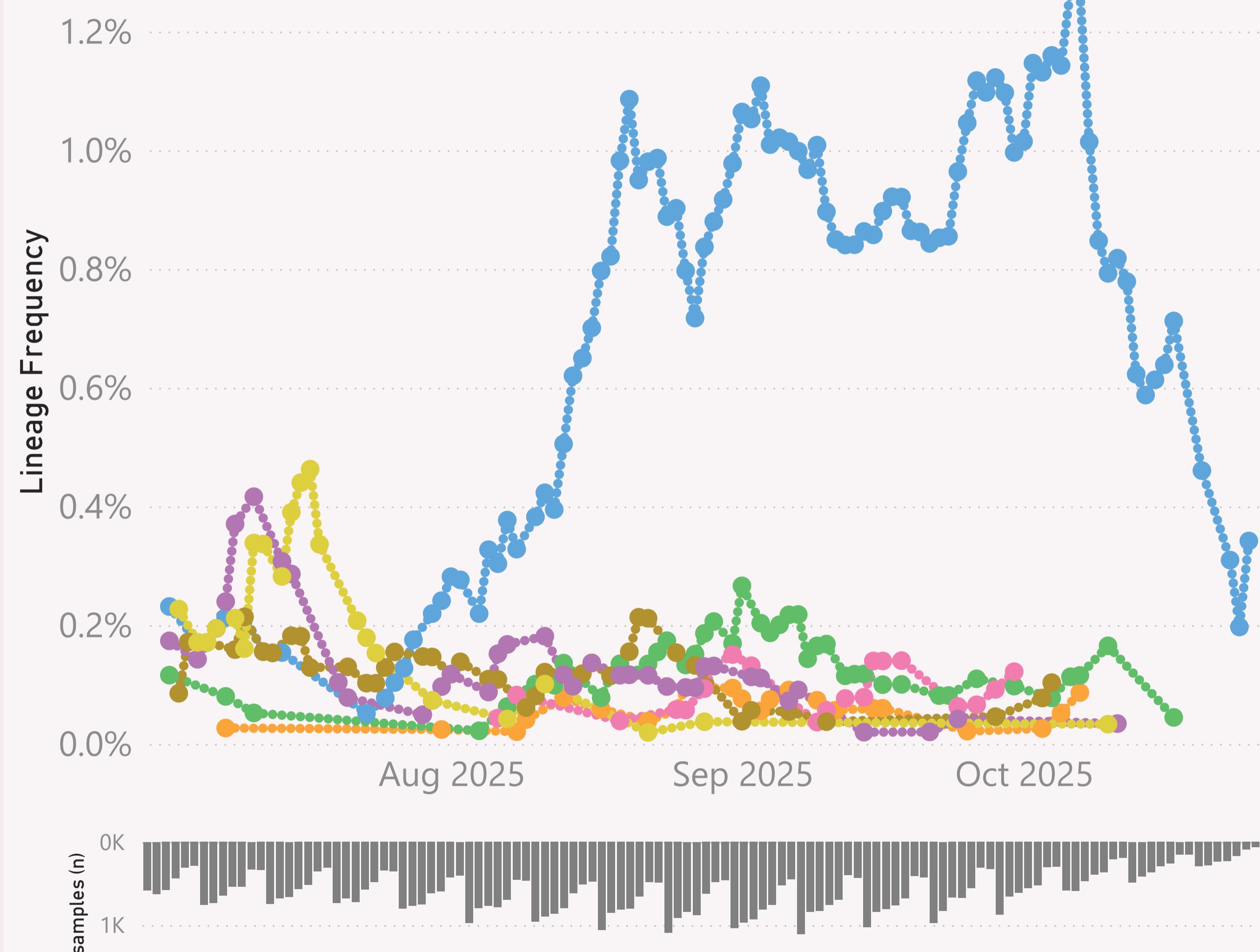
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=69,411 sequenced genomes, from 1 July 2025 up to 26 October 2025

Global

- PE.1.4 ● PE.1.4.1 ● PE.1.4.2 ● PE.1.7 ● PE.2 ● PE.3 ● PG.3.1



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.

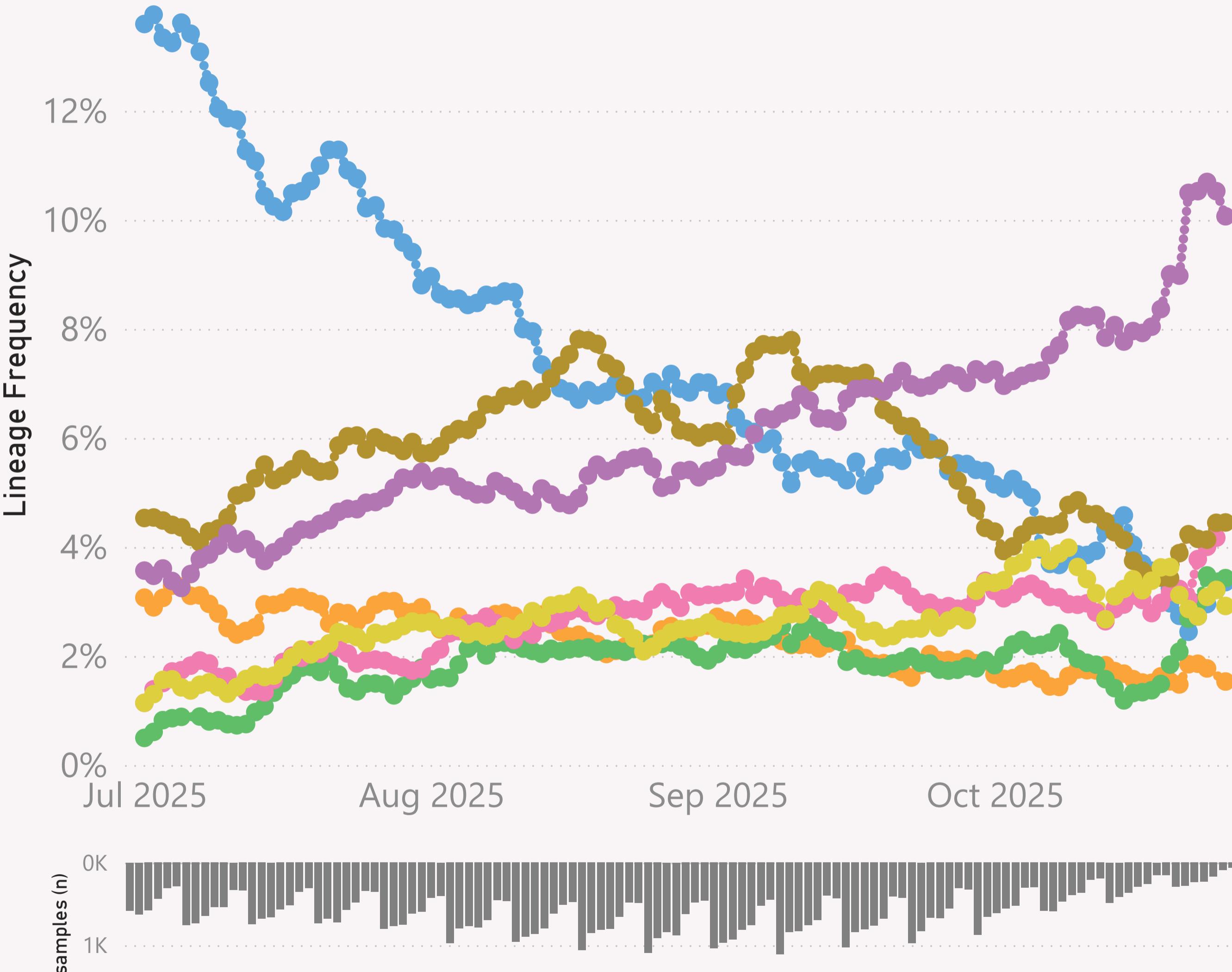
The frequency shown at each point is based on the 7-day rolling average across all lineages.

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Global

• NB.1.8.1 • PQ.2 • QF.2 • XFG • XFG.2 • XFG.3 • XFG.5.1



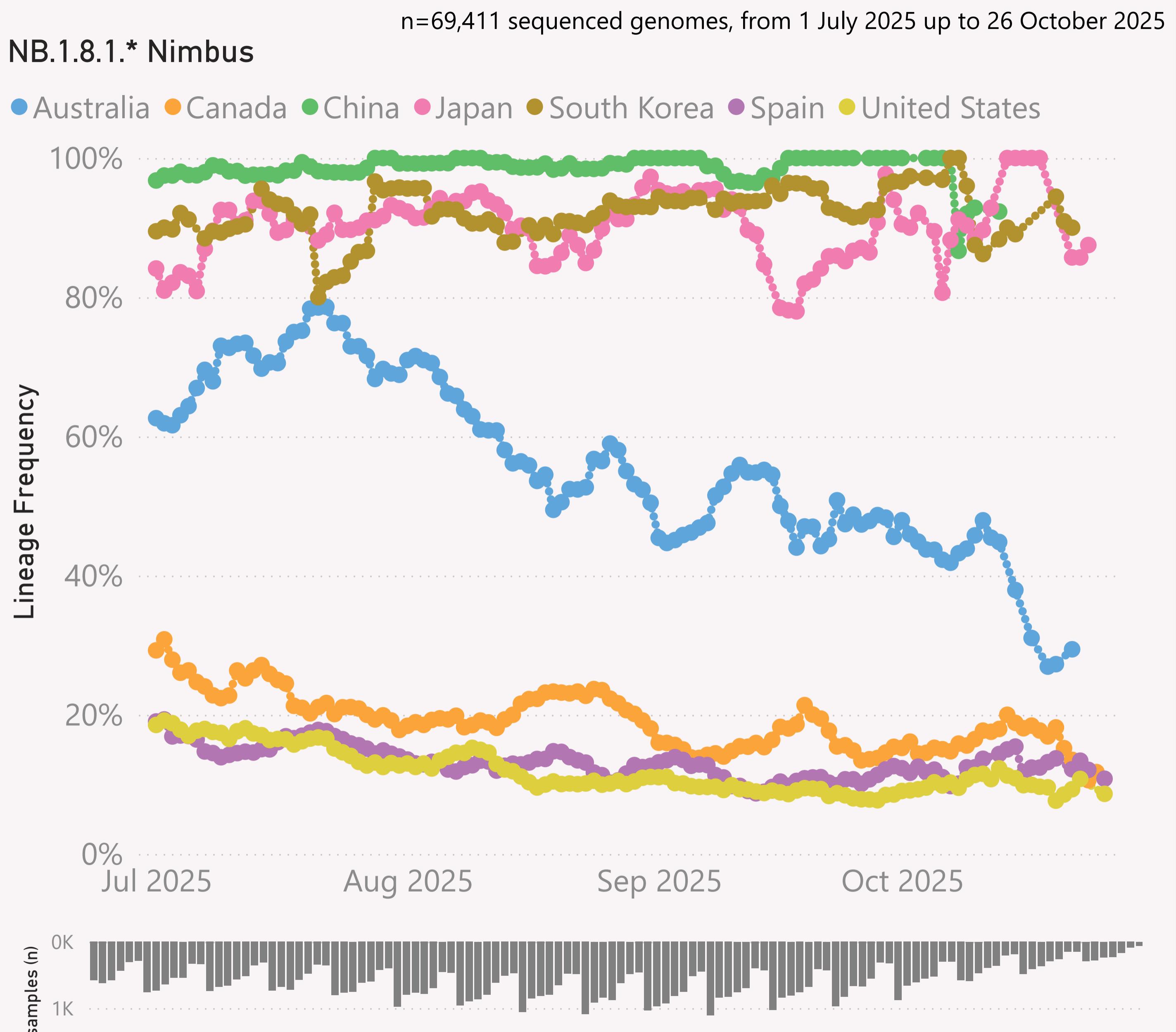
This page shows the frequency of the top 7 lineages, across recent months.

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.

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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.

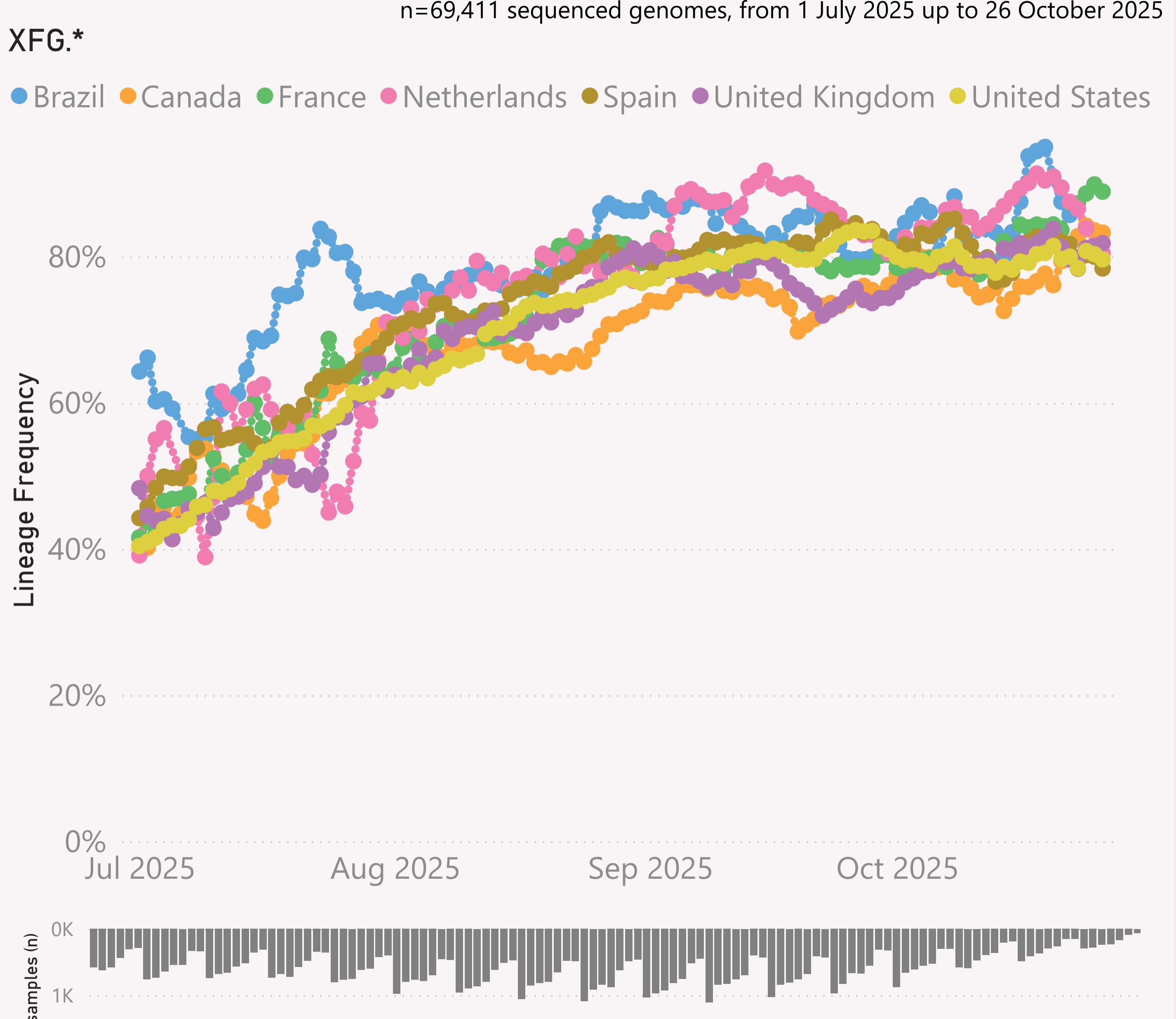
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

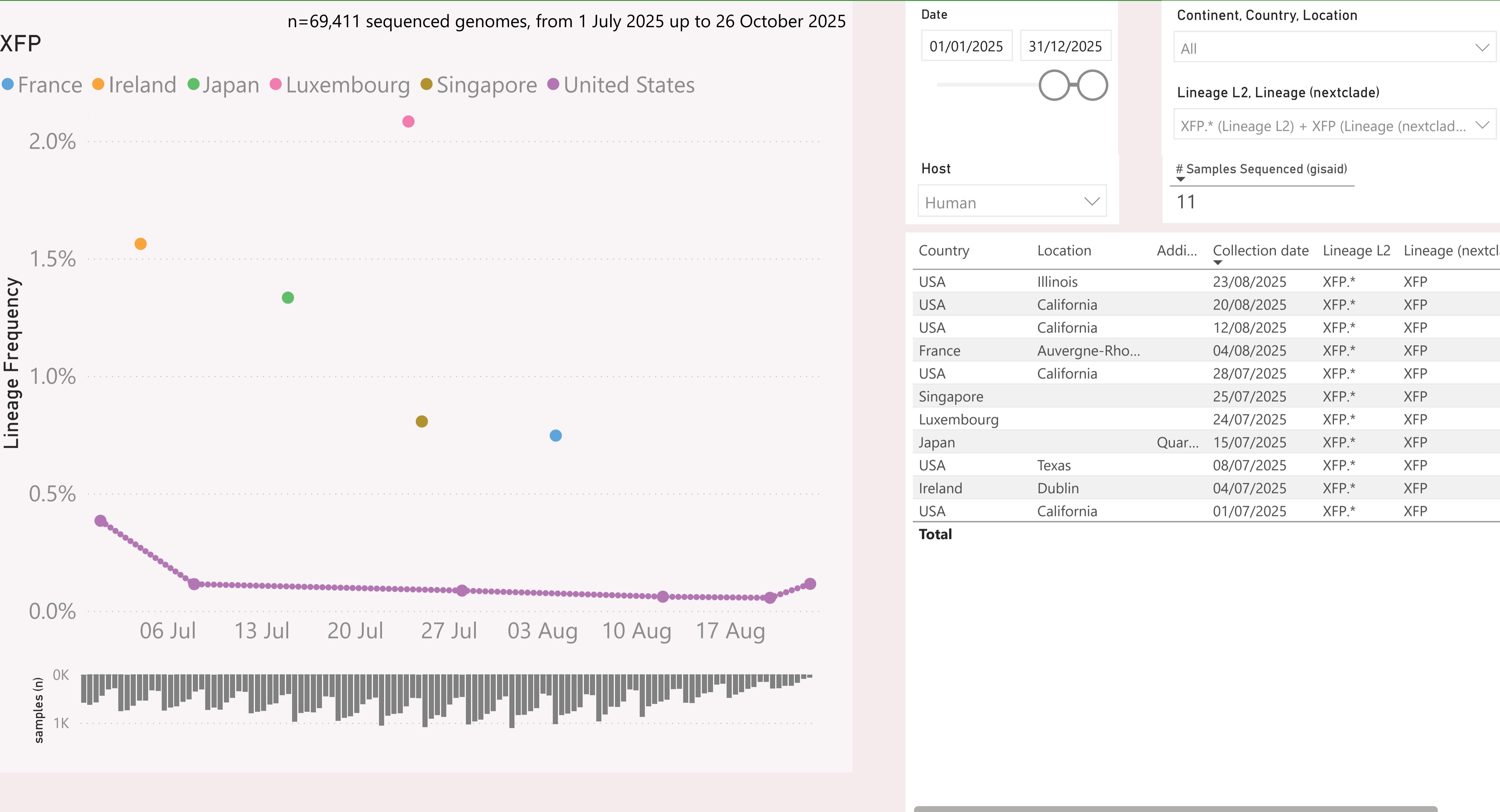
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

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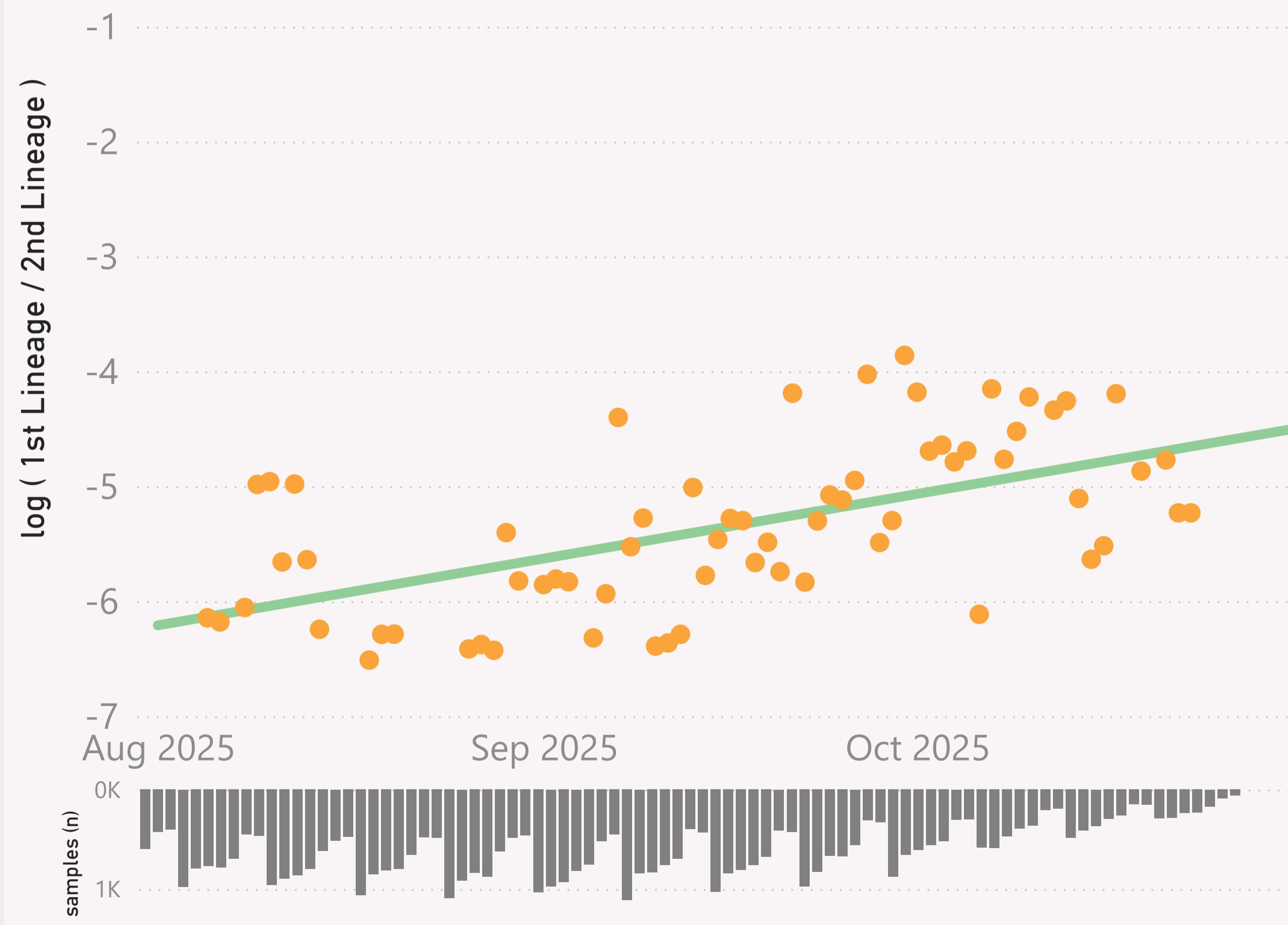


n=51,988 sequenced genomes, from 1 August 2025 up to 26 October 2025

Global - XGA vs XFG.*

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

0 growth of 1.9% 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".

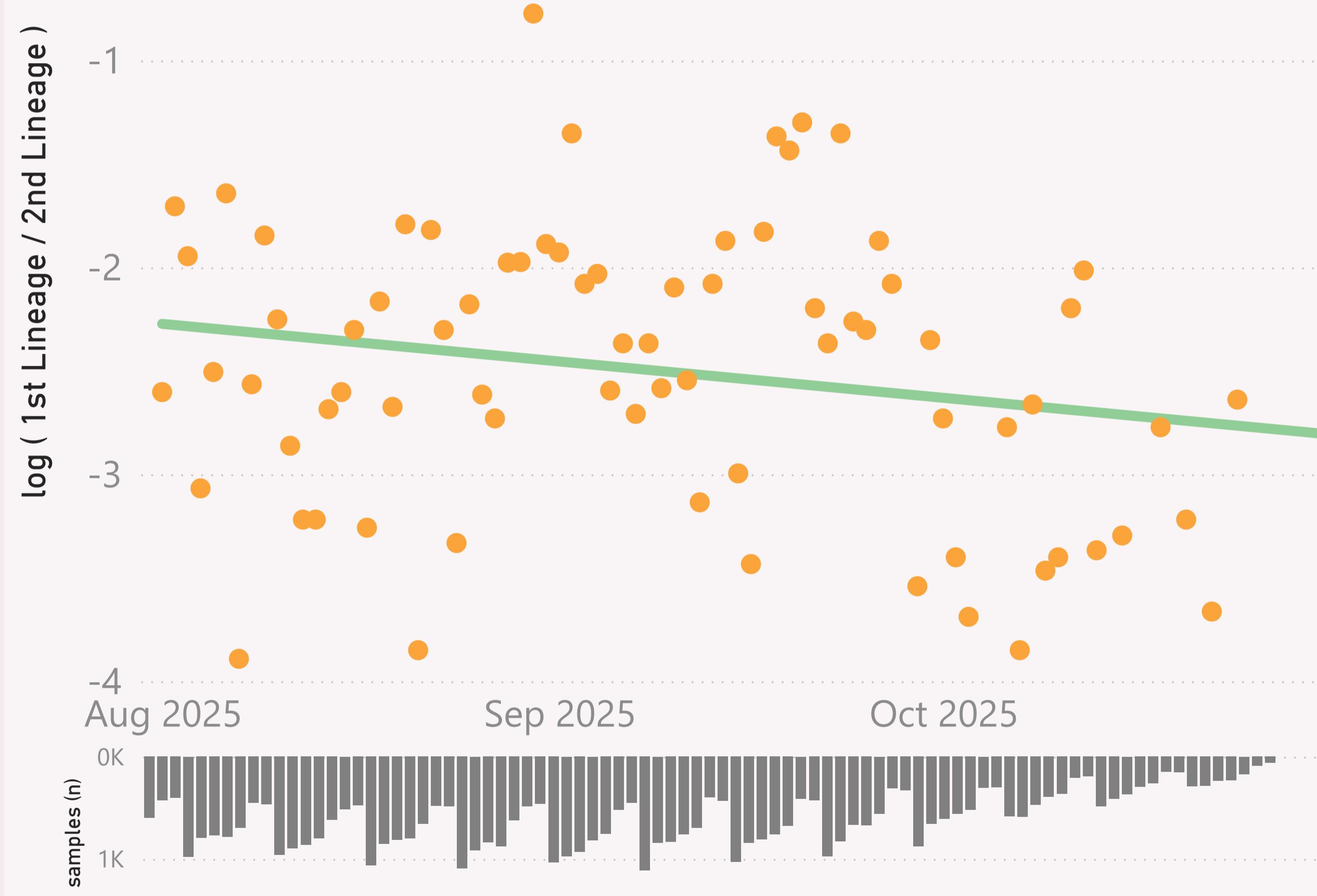
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=51,988 sequenced genomes, from 1 August 2025 up to 26 October 2025

Global - PY.1.1.1 vs XFG.3

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

0 decline of -0.6% per day

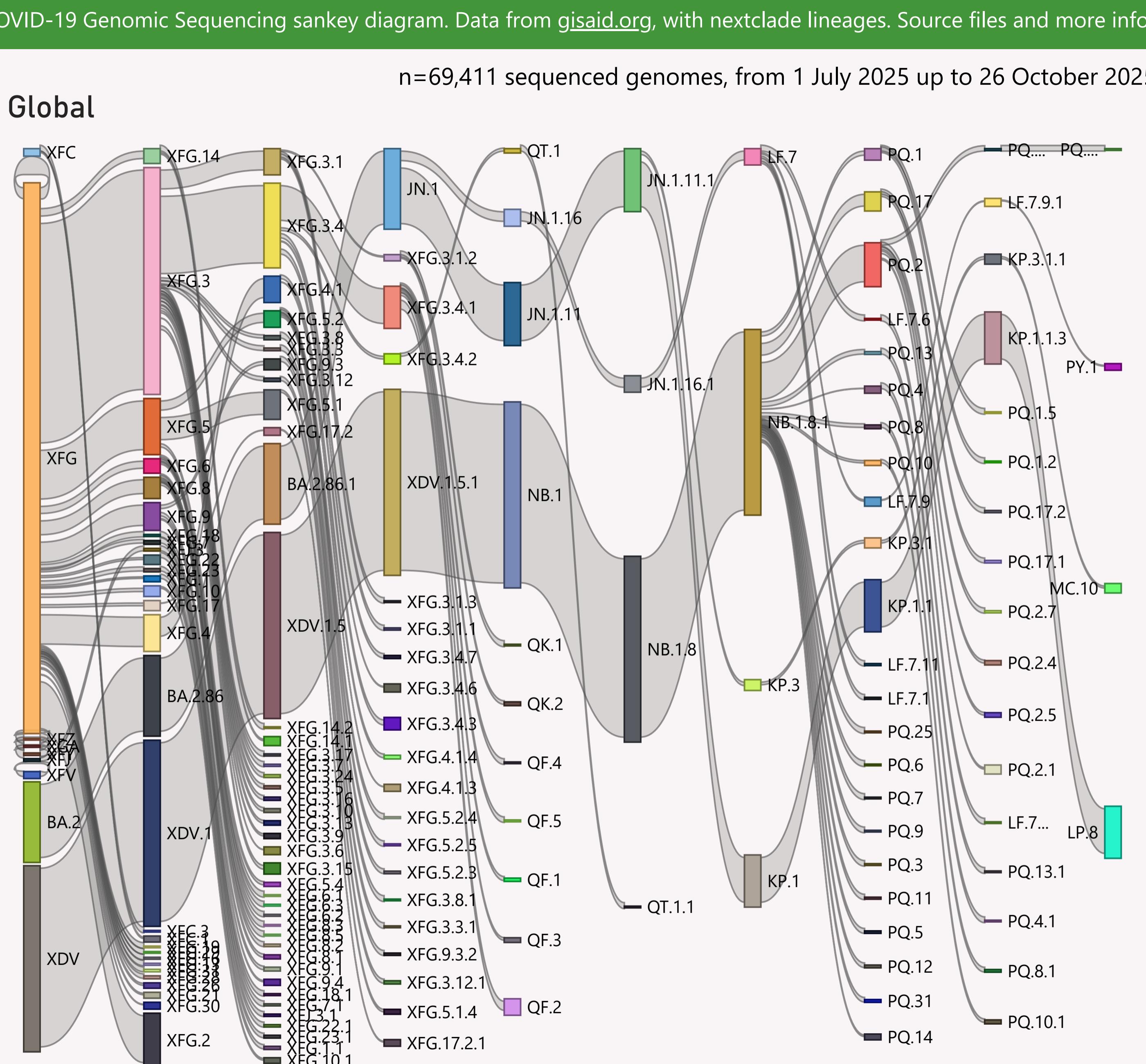


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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 is considered to have "crossed over" or taken over dominance from the incumbent Lineage

The Lineage classifications are provided by Nextclade.

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.



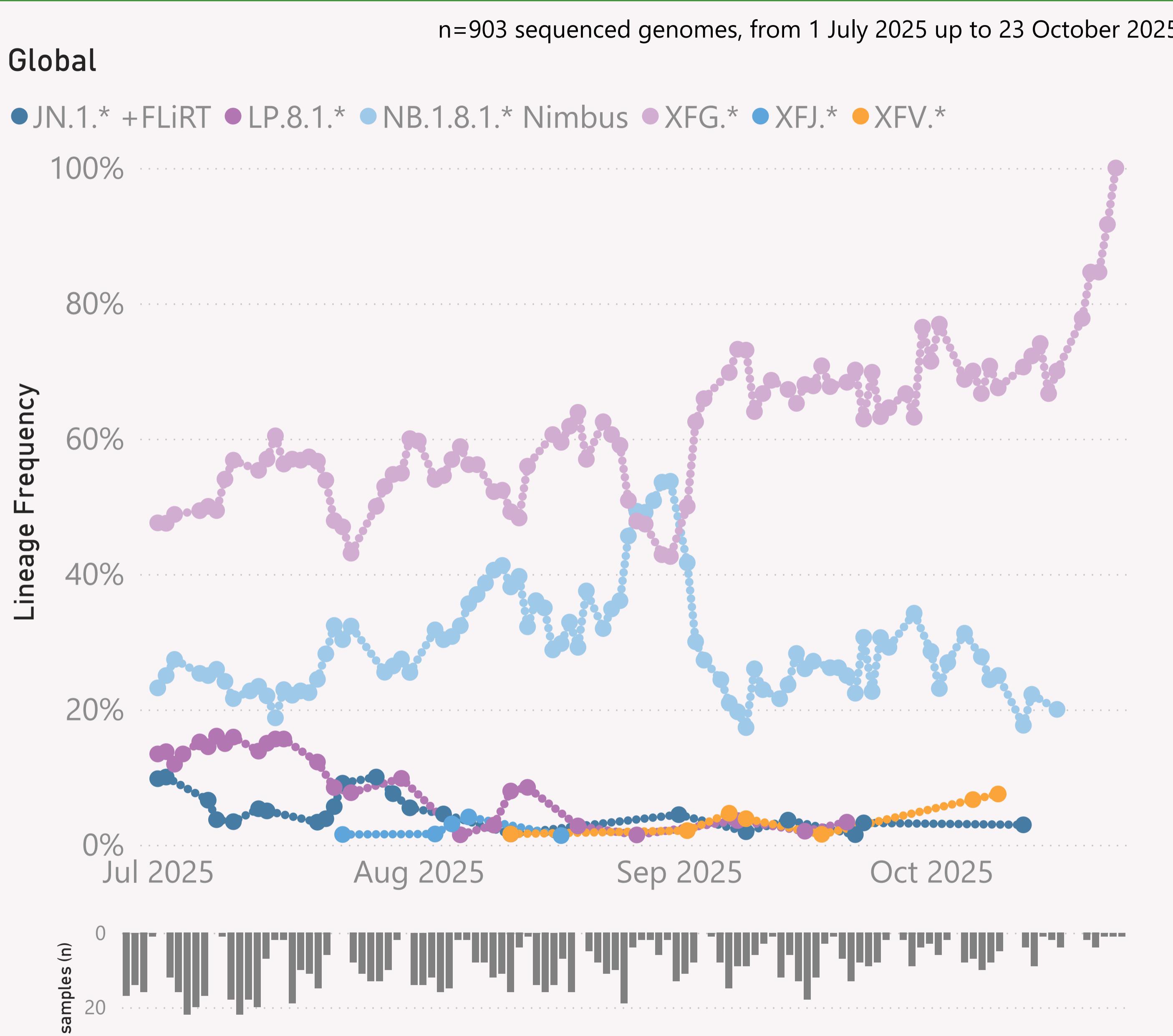
This page shows the hierarchy of the significant Lineages, over recent months.

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	11,519	26/10/2025		01/11/2025	
Canada	4,915	26/10/2025		01/11/2025	
Spain	4,696	26/10/2025		01/11/2025	
United Kingdom	3,829	26/10/2025		01/11/2025	
France	2,301	26/10/2025		01/11/2025	
Netherlands	1,327	26/10/2025		01/11/2025	
Australia	1,183	23/10/2025		01/11/2025	
Brazil	1,115	22/10/2025		01/11/2025	
South Korea	1,096	22/10/2025		01/11/2025	
Italy	910	26/10/2025		01/11/2025	
Germany	840	25/10/2025		01/11/2025	
China	812	13/10/2025		29/10/2025	
Japan	539	24/10/2025		01/11/2025	
Luxembourg	538	10/10/2025		28/10/2025	
Denmark	465	06/10/2025		31/10/2025	
Russia	398	30/09/2025		06/10/2025	
Slovenia	393	25/10/2025		01/11/2025	
Ukraine	385	26/10/2025		01/11/2025	
Ireland	365	21/10/2025		01/11/2025	
Poland	328	26/10/2025		01/11/2025	
Singapore	277	24/10/2025		01/11/2025	
New Zealand	255	25/10/2025		01/11/2025	
Sweden	248	26/10/2025		01/11/2025	
Switzerland	209	15/09/2025		09/10/2025	
Finland	194	19/10/2025		01/11/2025	
Lithuania	180	29/09/2025		19/10/2025	
Costa Rica	176	01/10/2025		17/10/2025	
Belgium	170	23/10/2025		01/11/2025	
Total	41,233	26/10/2025		01/11/2025	

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.