

This page shows the frequency of the top 7 "L2" lineages, across recent months.

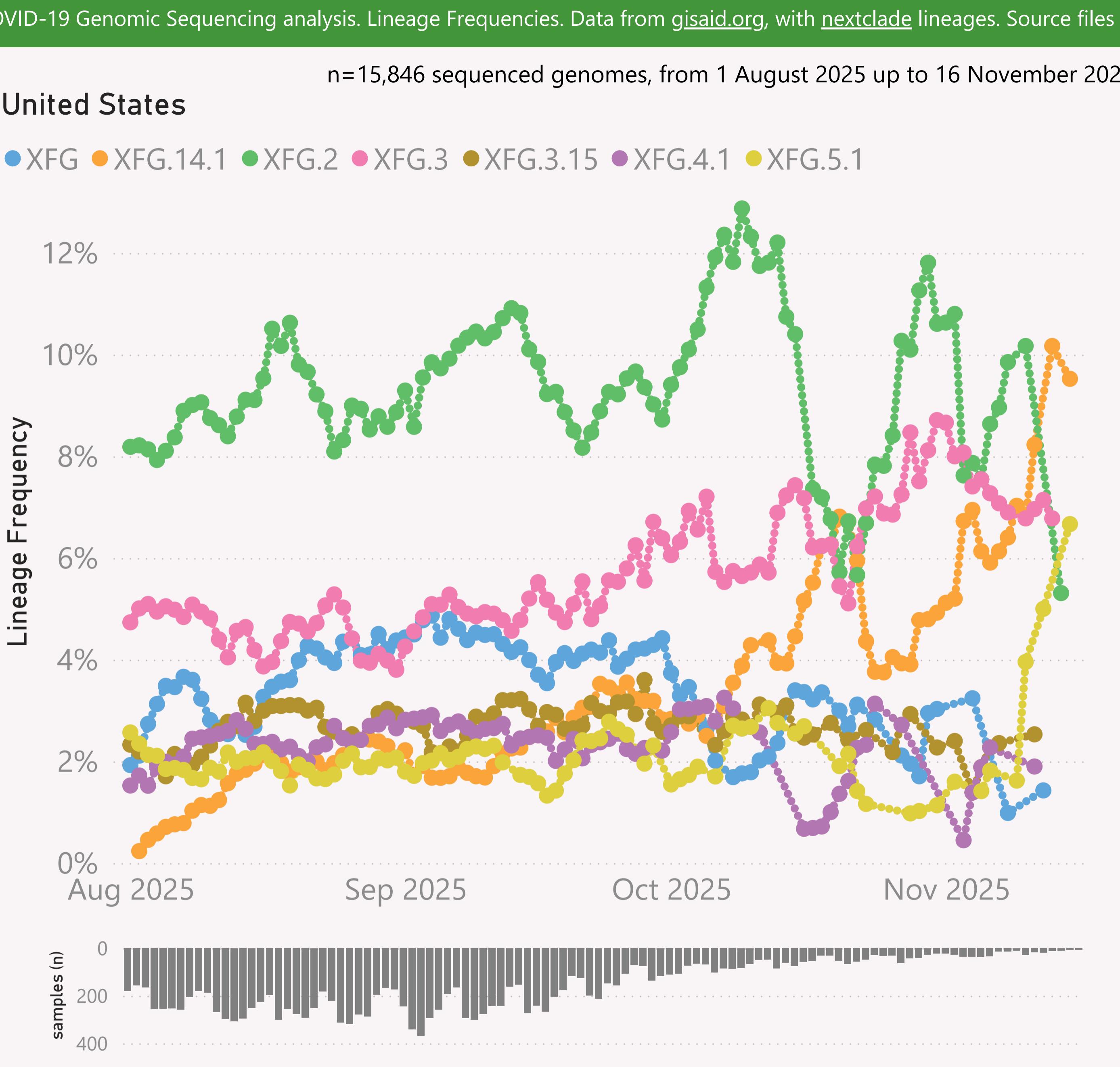
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all its descendants, e.g. the JN.* lineages.

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.



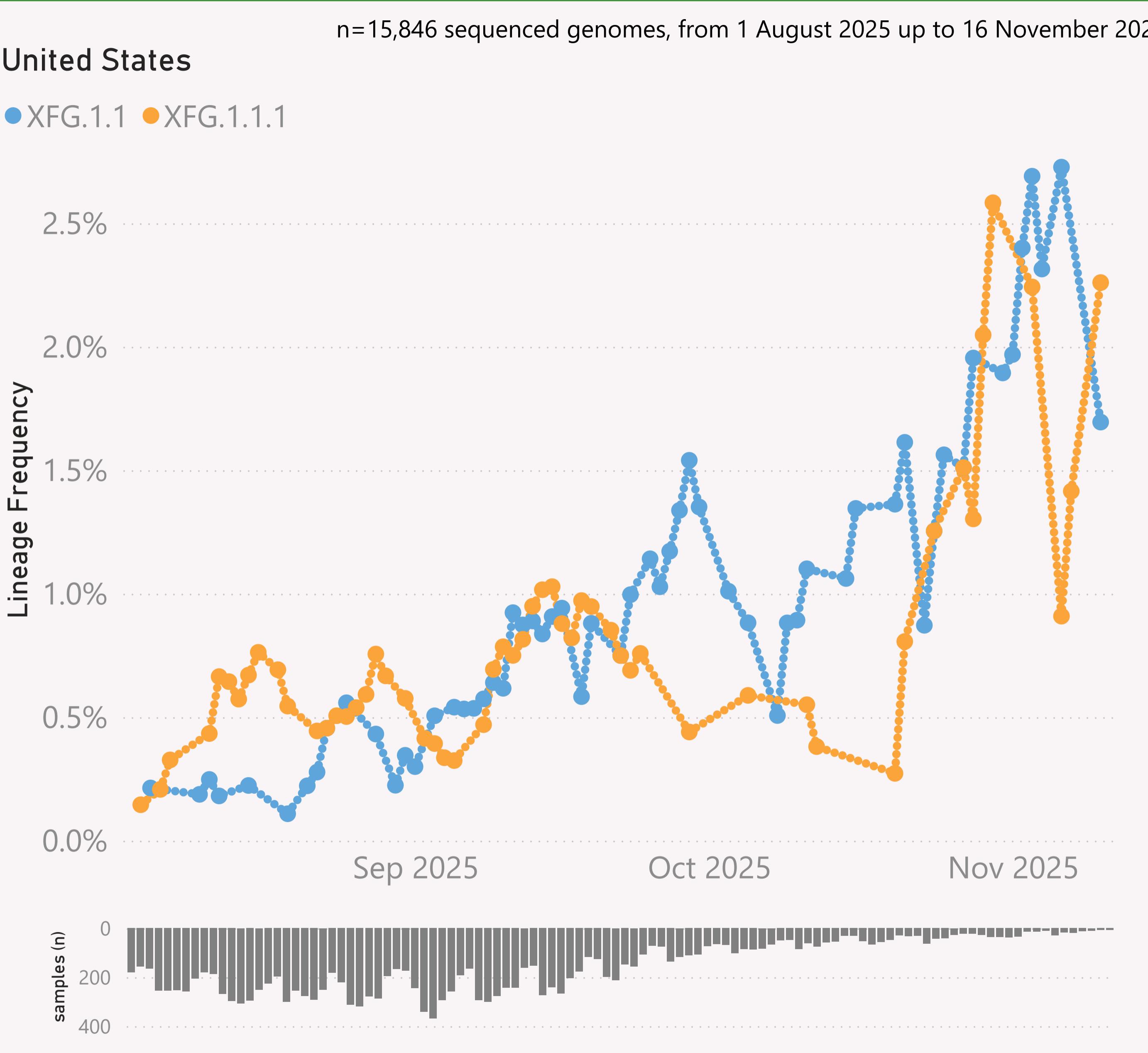
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently XFG.*.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

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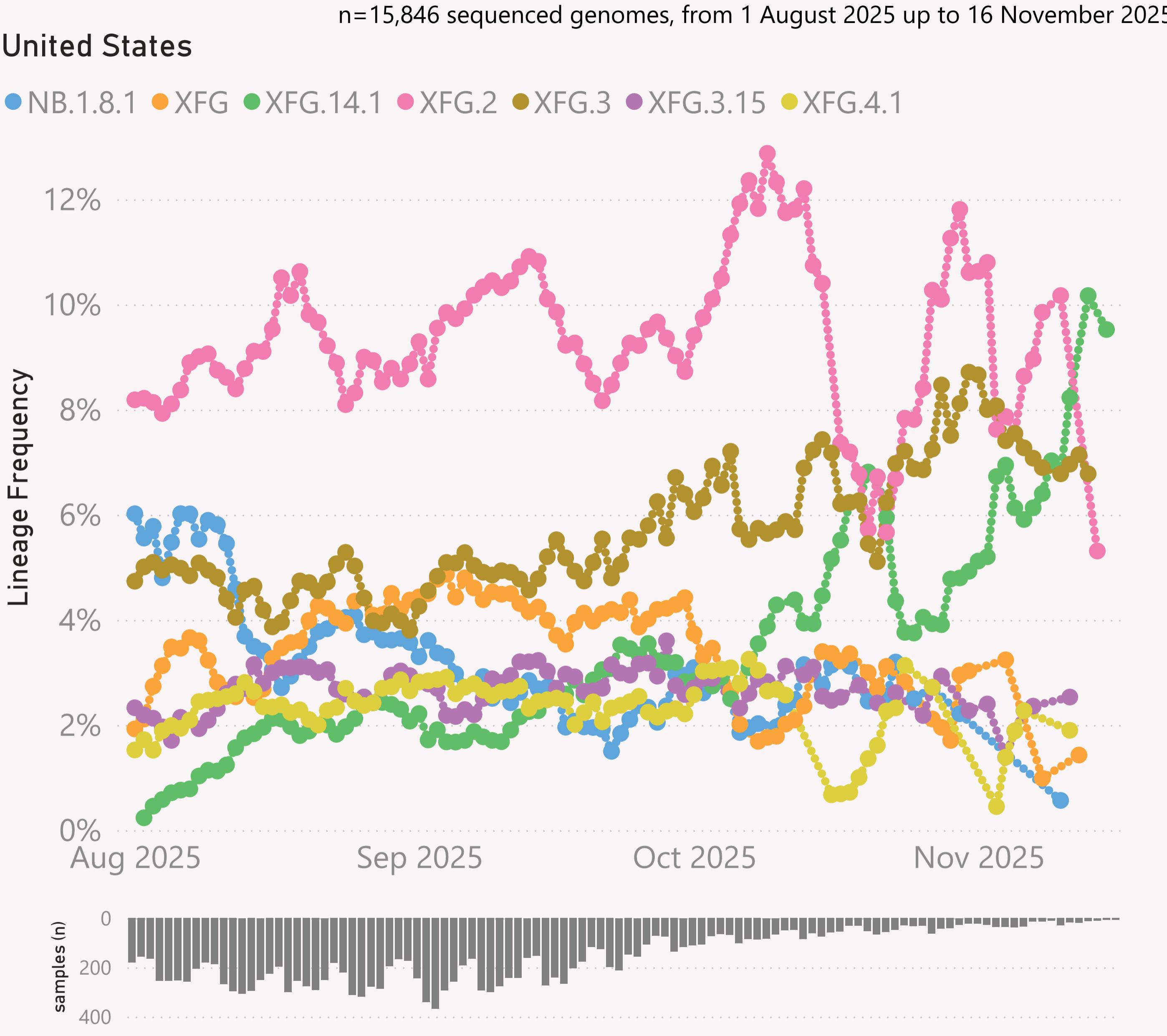
This page shows the frequency of lineages, across recent months. The lineages are filtered for a Lineage group of interest, currently XFG.1.1.* .

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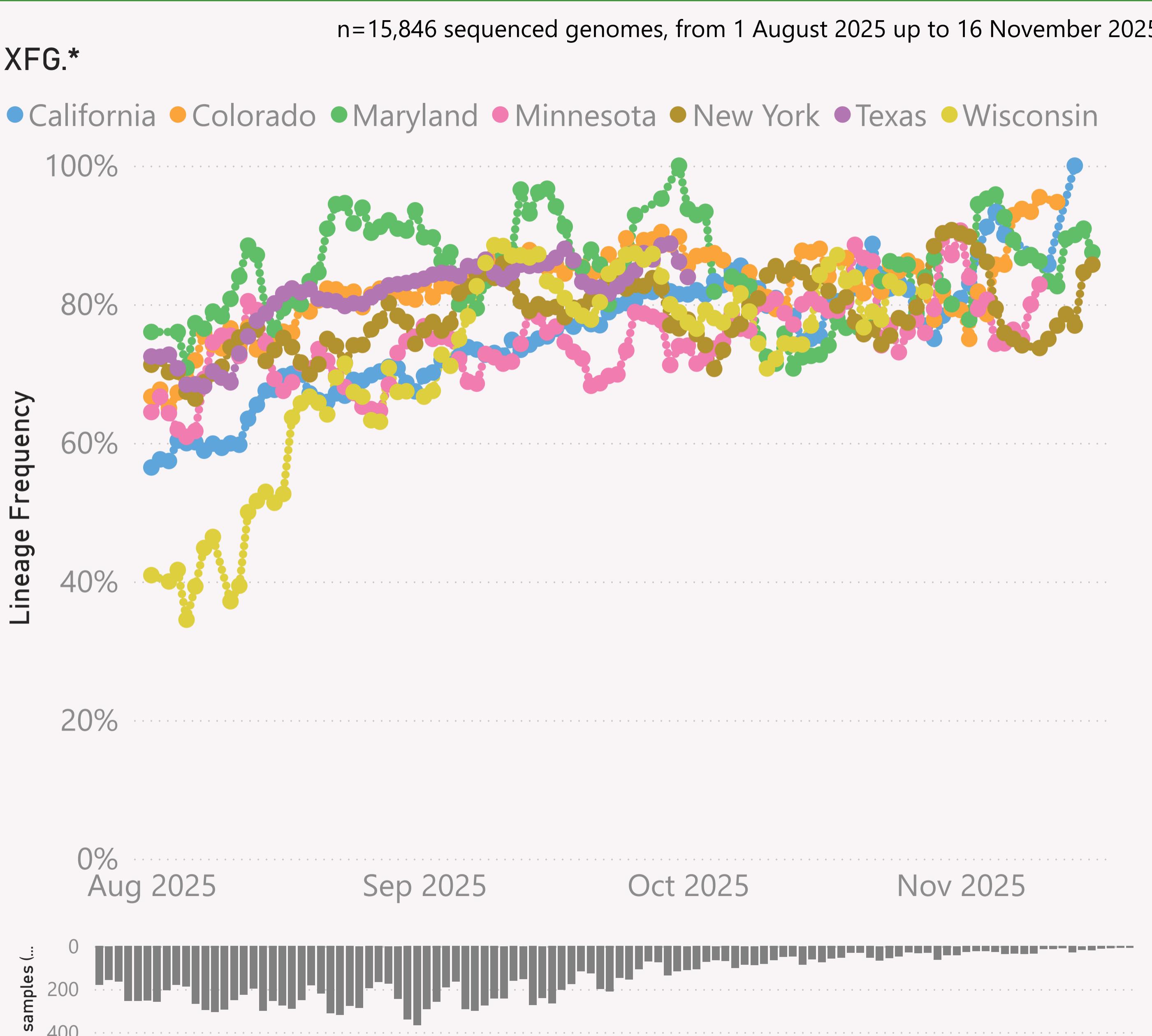
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This page shows the frequency of a selected "Lineage L2" group of interest, across the leading States, over recent months.

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 "BA.2.86.*" group includes BA.2.86 and all its descendants, e.g. the JN.* lineages.

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

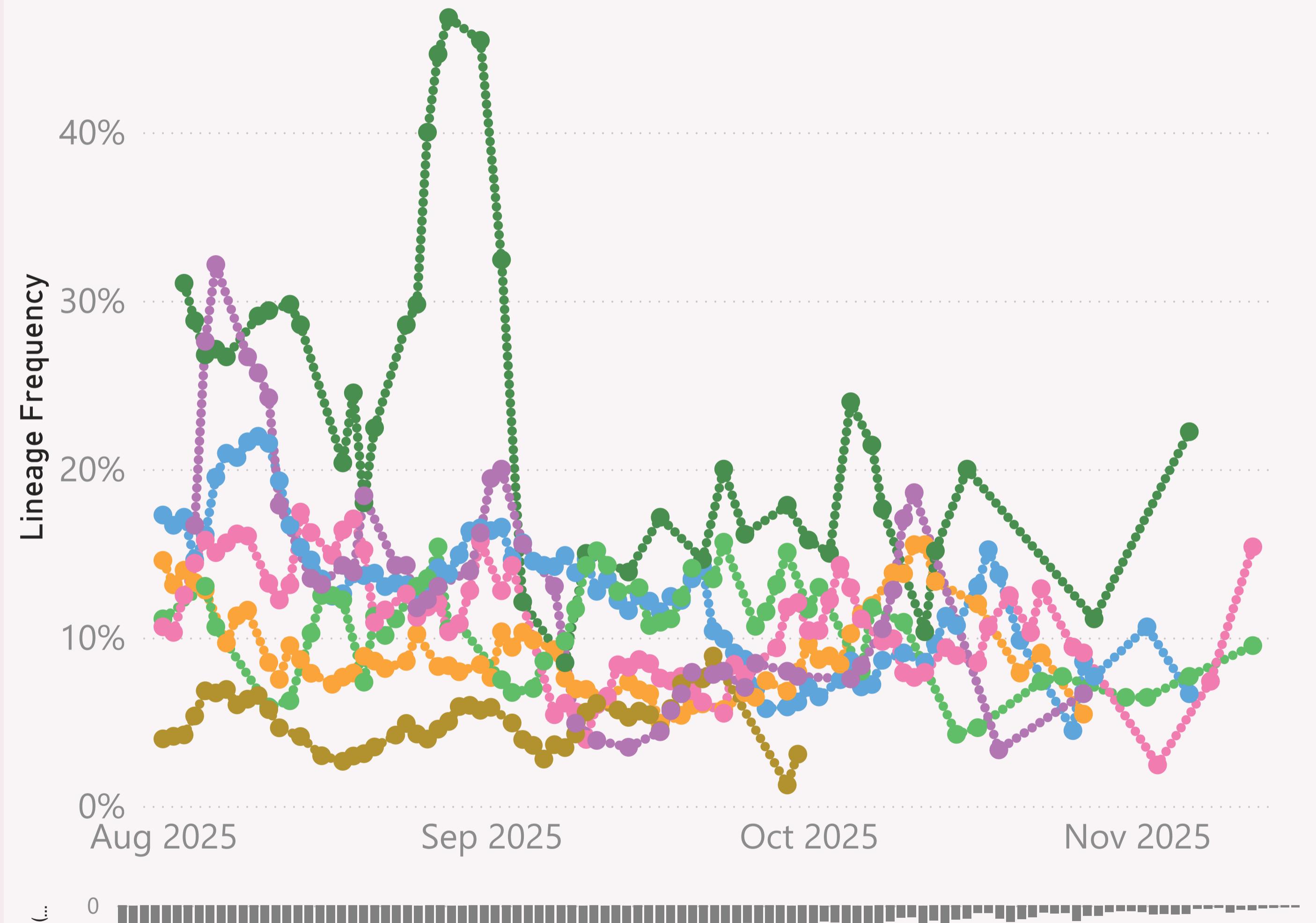
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n=15,846 sequenced genomes, from 1 August 2025 up to 16 November 2025

NB.1.8.1.* Nimbus

- California
- Colorado
- International...
- Minnesota
- New York
- Texas
- Wisconsin



This page shows the frequency of a selected "Lineage L2" group of interest, across the leading States, 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 "BA.2.86.*" group includes BA.2.86 and all its descendants, e.g. the JN.* lineages.

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

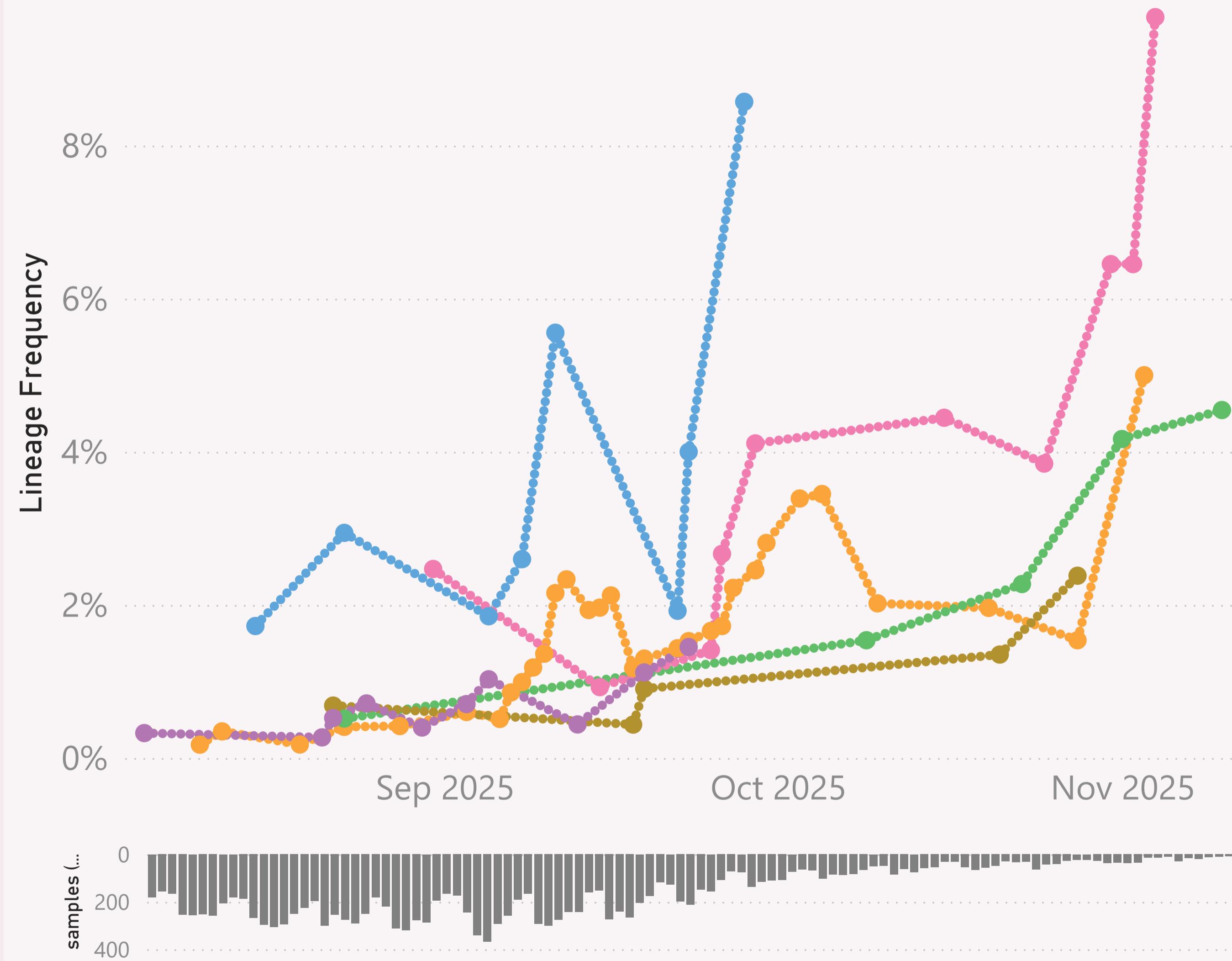
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n=15,846 sequenced genomes, from 1 August 2025 up to 16 November 2025

XFG.1.1

- Arizona
- California
- Colorado
- Minnesota
- New York
- Texas



This page shows the frequency of a selected Lineage of interest, across the leading States, over recent months.

The 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 state.

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.

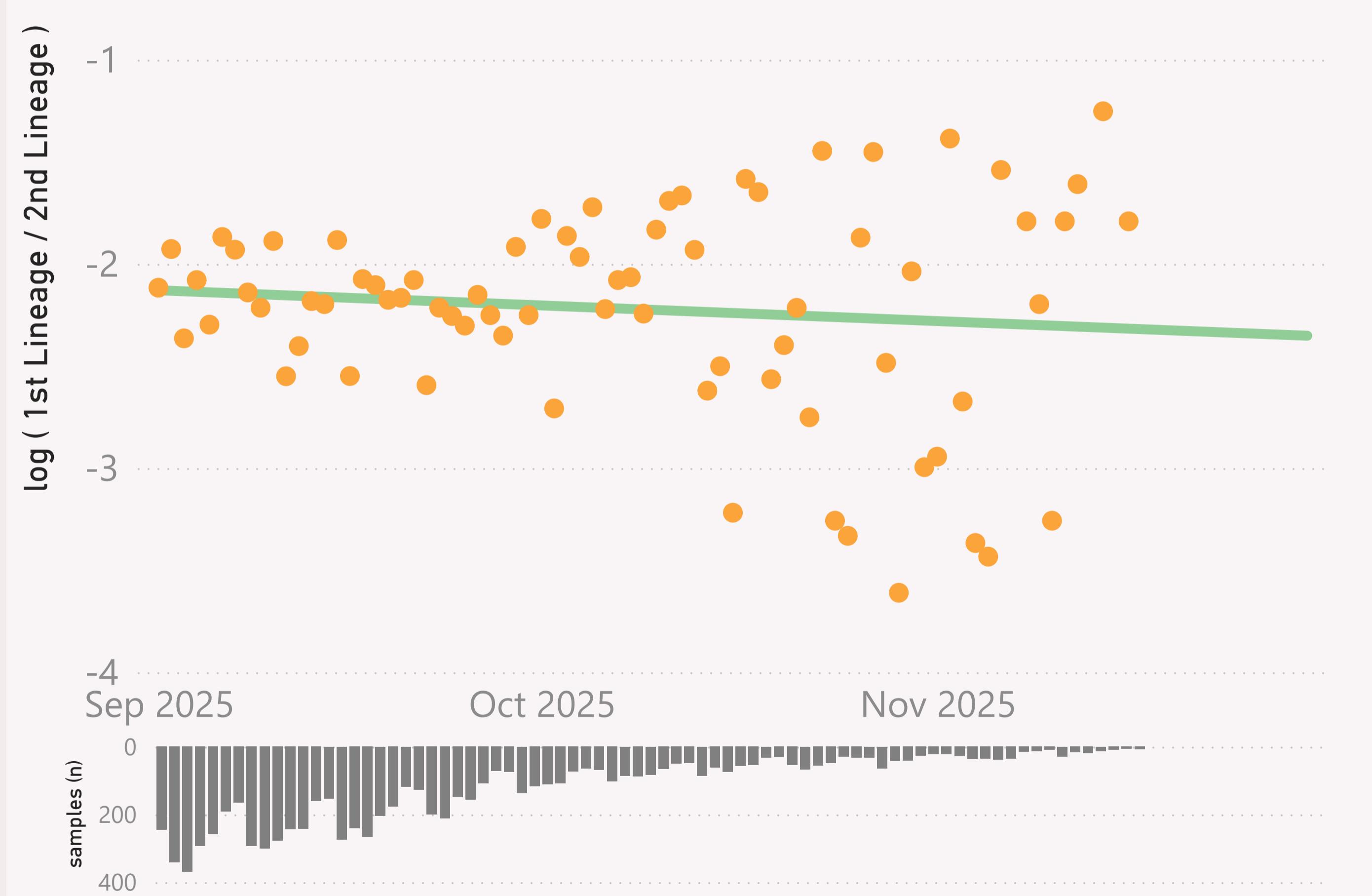
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=8,383 sequenced genomes, from 1 September 2025 up to 16 November 2025

United States - NB.1.8.1.* Nimbus vs XFG.*

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

0 decline of -0.2% 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".

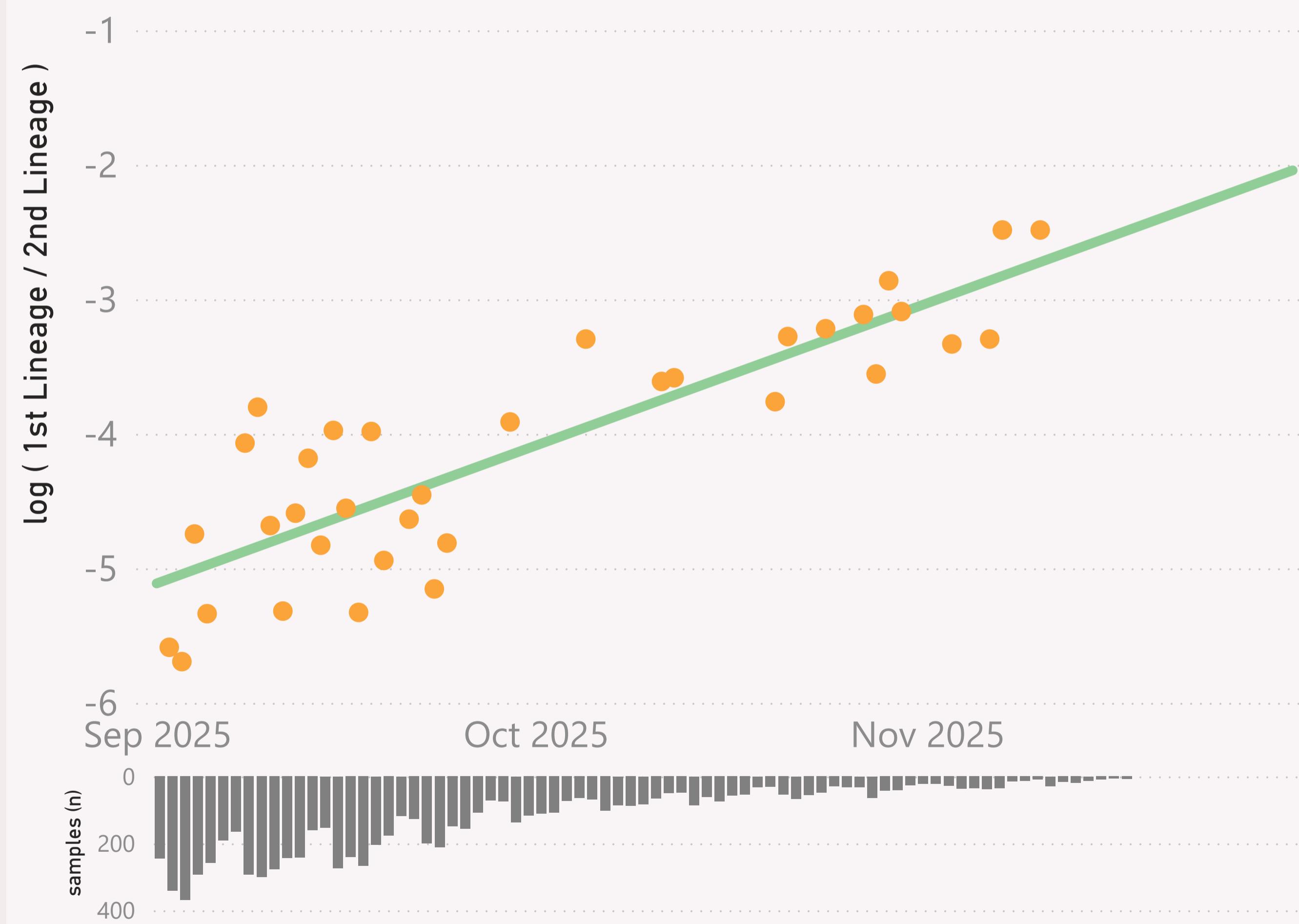
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=8,383 sequenced genomes, from 1 September 2025 up to 16 November 2025

United States - XFG.1.1.1 vs XFG.*

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

0 growth of 3.4% 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.

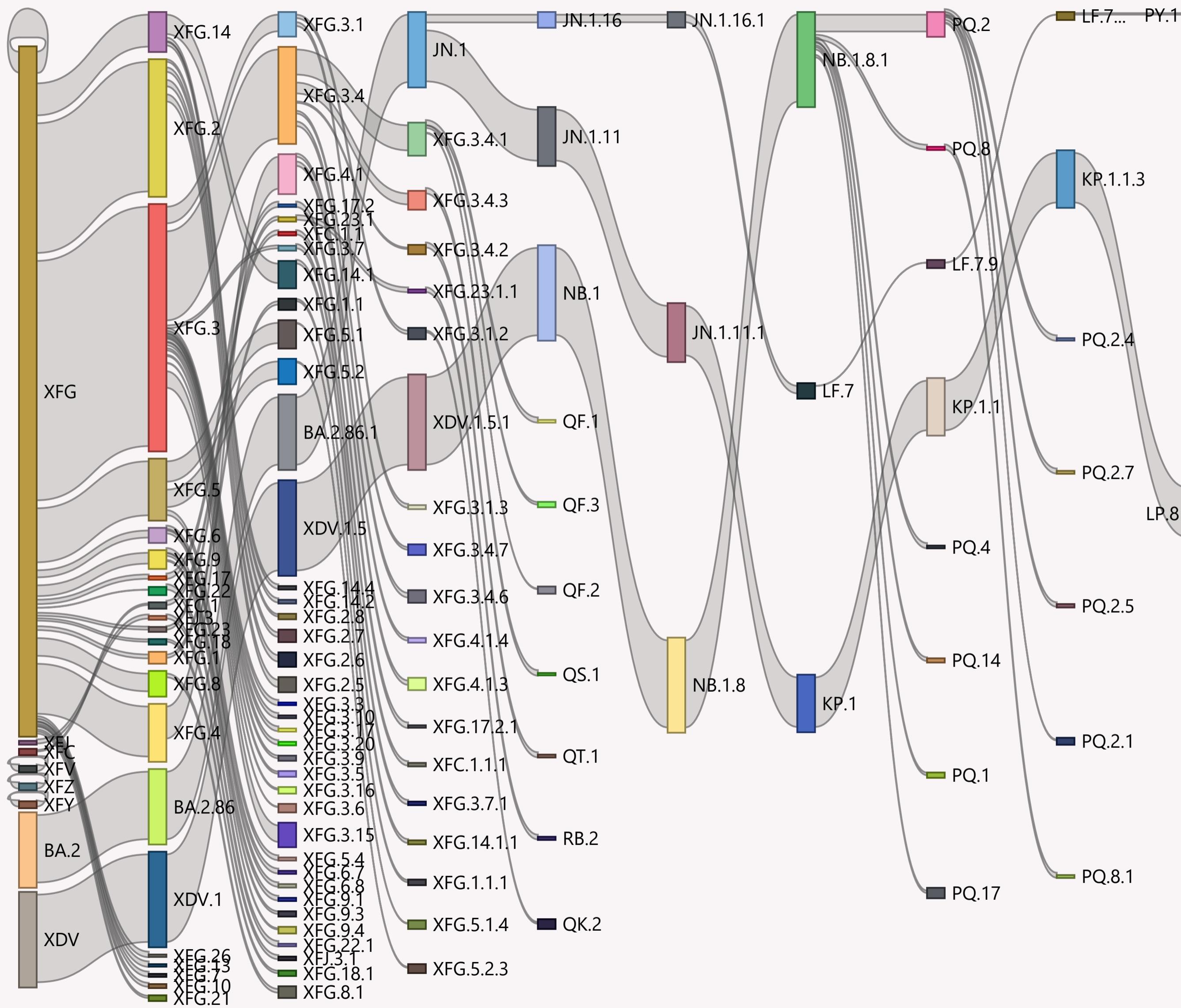
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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.

n=15,846 sequenced genomes, from 1 August 2025 up to 16 November 2025

United States



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

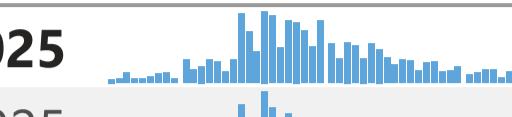
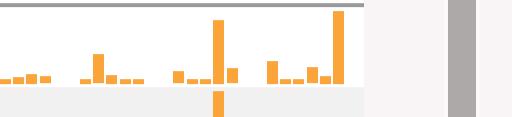
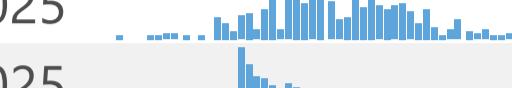
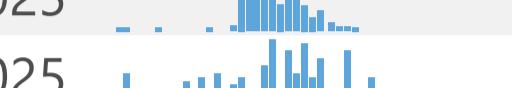
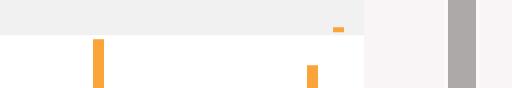
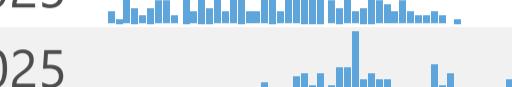
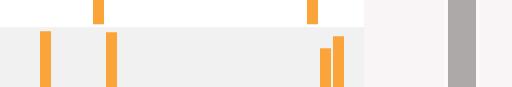
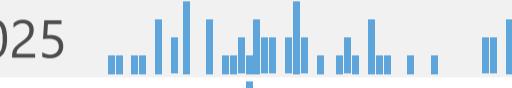
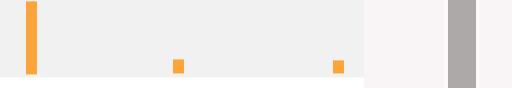
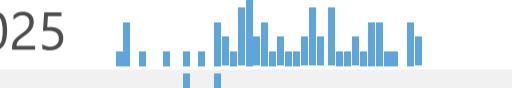
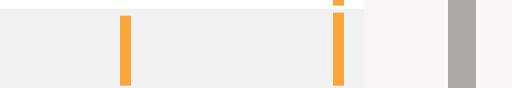
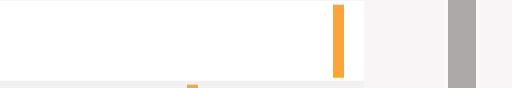
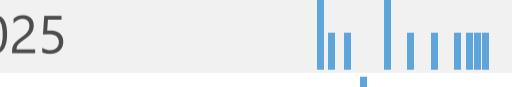
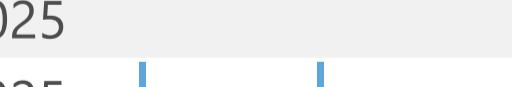
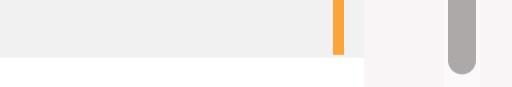
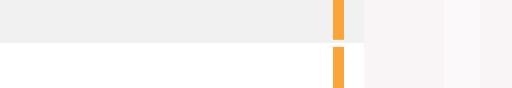
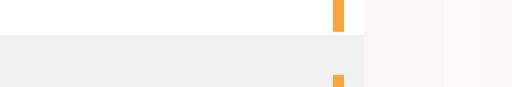
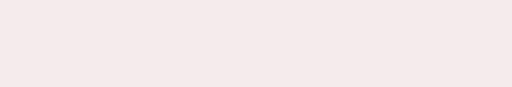
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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.

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	
California	2,218	14/11/2025		15/11/2025	
New York	1,066	16/11/2025		15/11/2025	
Texas	777	02/10/2025		15/11/2025	
Wisconsin	547	29/10/2025		13/11/2025	
Colorado	439	12/11/2025		15/11/2025	
Minnesota	379	12/11/2025		15/11/2025	
Maryland	230	16/11/2025		15/11/2025	
Illinois	189	12/11/2025		15/11/2025	
Kentucky	164	12/11/2025		15/11/2025	
New Jersey	114	18/10/2025		15/11/2025	
New Mexico	108	10/09/2025		10/11/2025	
Oregon	107	14/11/2025		15/11/2025	
Connecticut	100	14/11/2025		15/11/2025	
Massachusetts	96	06/10/2025		15/11/2025	
International Travellers	89	16/11/2025		15/11/2025	
Arizona	67	27/10/2025		15/11/2025	
Vermont	58	10/11/2025		15/11/2025	
New Hampshire	50	11/11/2025		15/11/2025	
Nebraska	49	16/11/2025		15/11/2025	
Wyoming	25	06/11/2025		15/11/2025	
Michigan	21	04/11/2025		15/11/2025	
Nevada	11	01/11/2025		07/11/2025	
Alaska	8	01/10/2025		15/11/2025	
Missouri	4	29/09/2025		12/11/2025	
South Carolina	4	02/10/2025		15/11/2025	
Florida	3	07/09/2025		15/11/2025	
Louisiana	3	01/10/2025		15/11/2025	
Total	6,936	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. A breakdown of the leading states (by volume) is shown.

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.