

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.

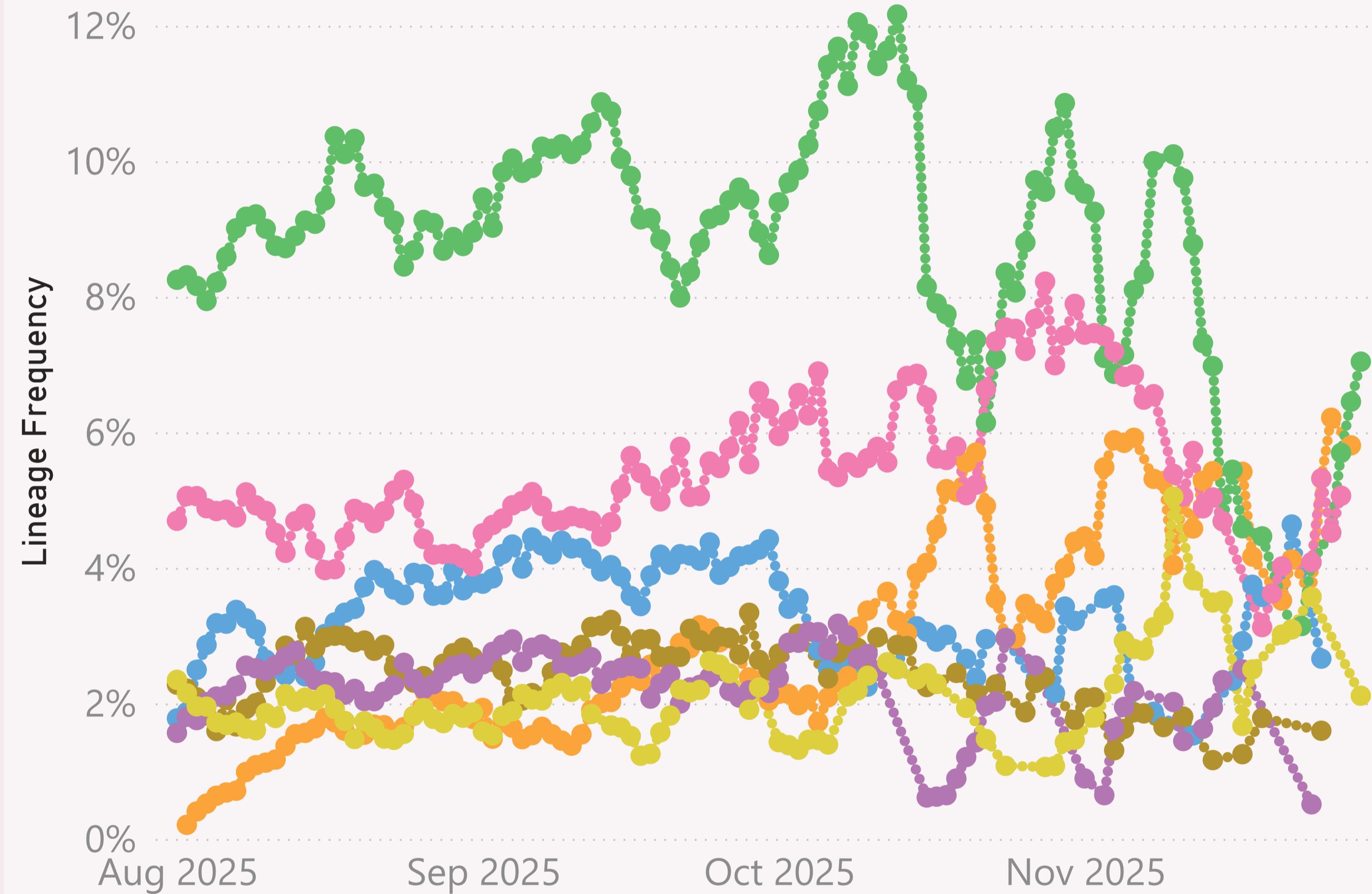
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=18,135 sequenced genomes, from 1 August 2025 up to 30 November 2025

**United States**

- XFG
- XFG.14.1
- XFG.2
- XFG.3
- XFG.3.15
- XFG.4.1
- XFG.5.1



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

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.

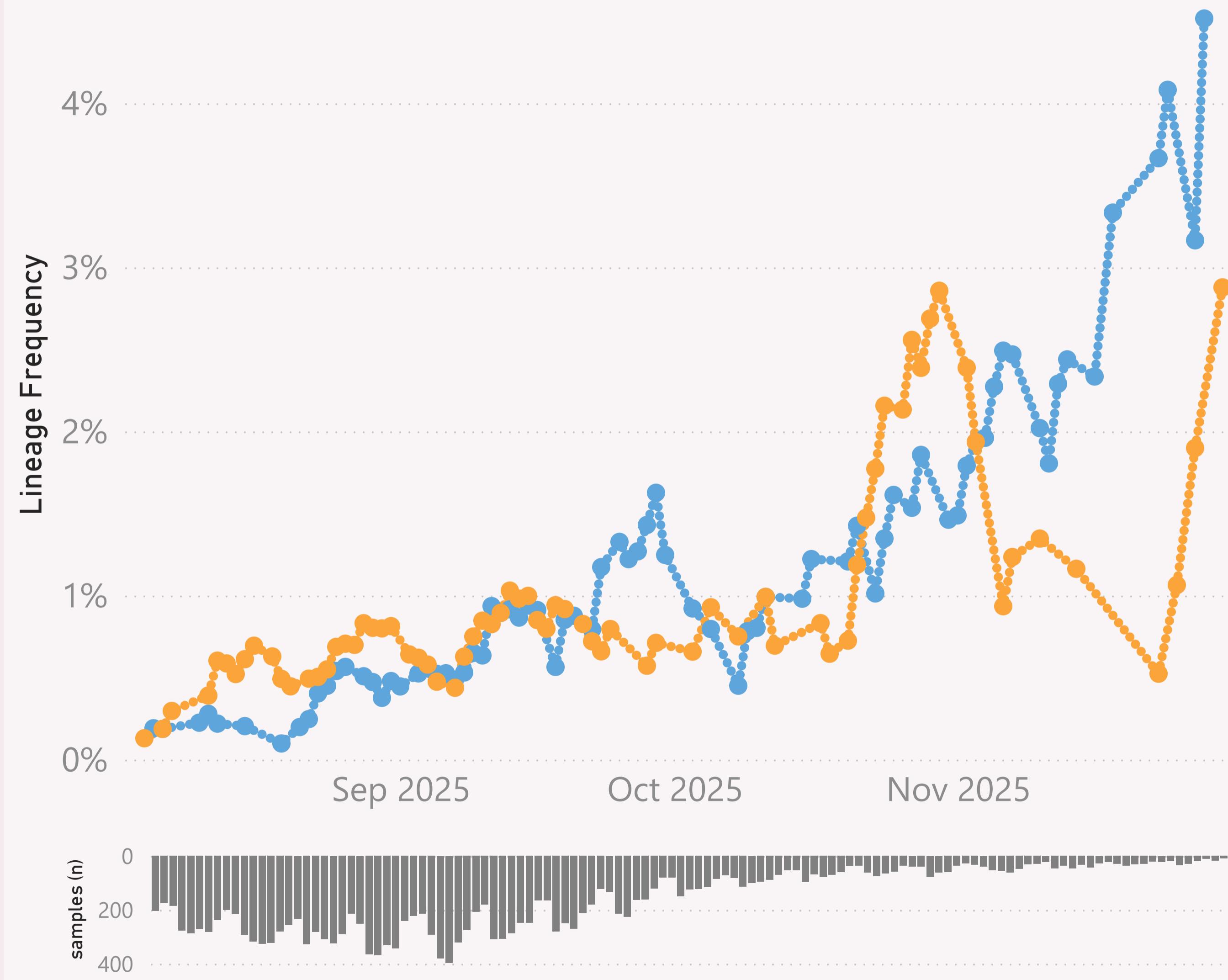
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n=18,135 sequenced genomes, from 1 August 2025 up to 30 November 2025

**United States**

● XFG.1.1 ● XFG.1.1.1



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

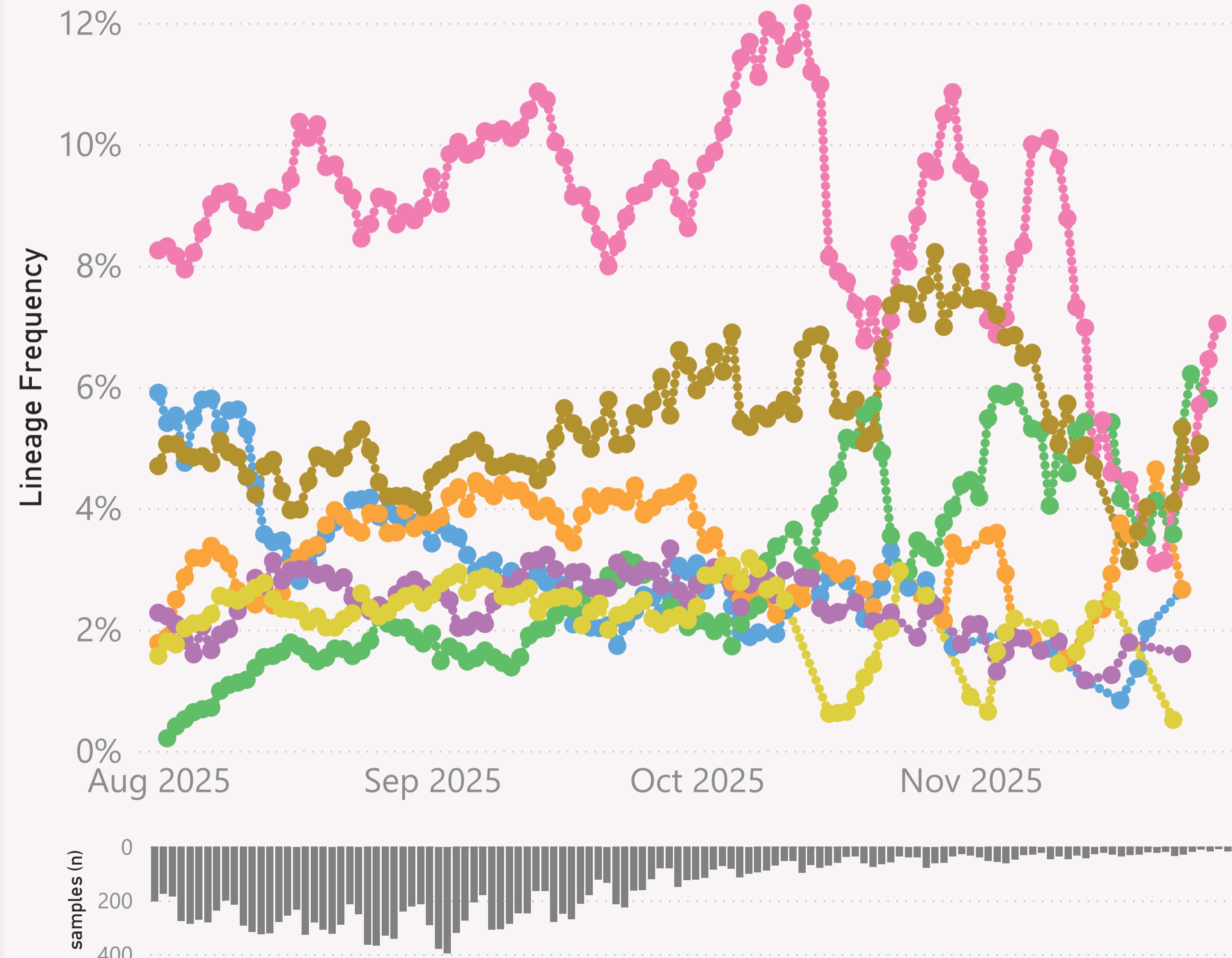
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n=18,135 sequenced genomes, from 1 August 2025 up to 30 November 2025

**United States**

- NB.1.8.1
- XFG
- XFG.14.1
- XFG.2
- XFG.3
- XFG.3.15
- XFG.4.1



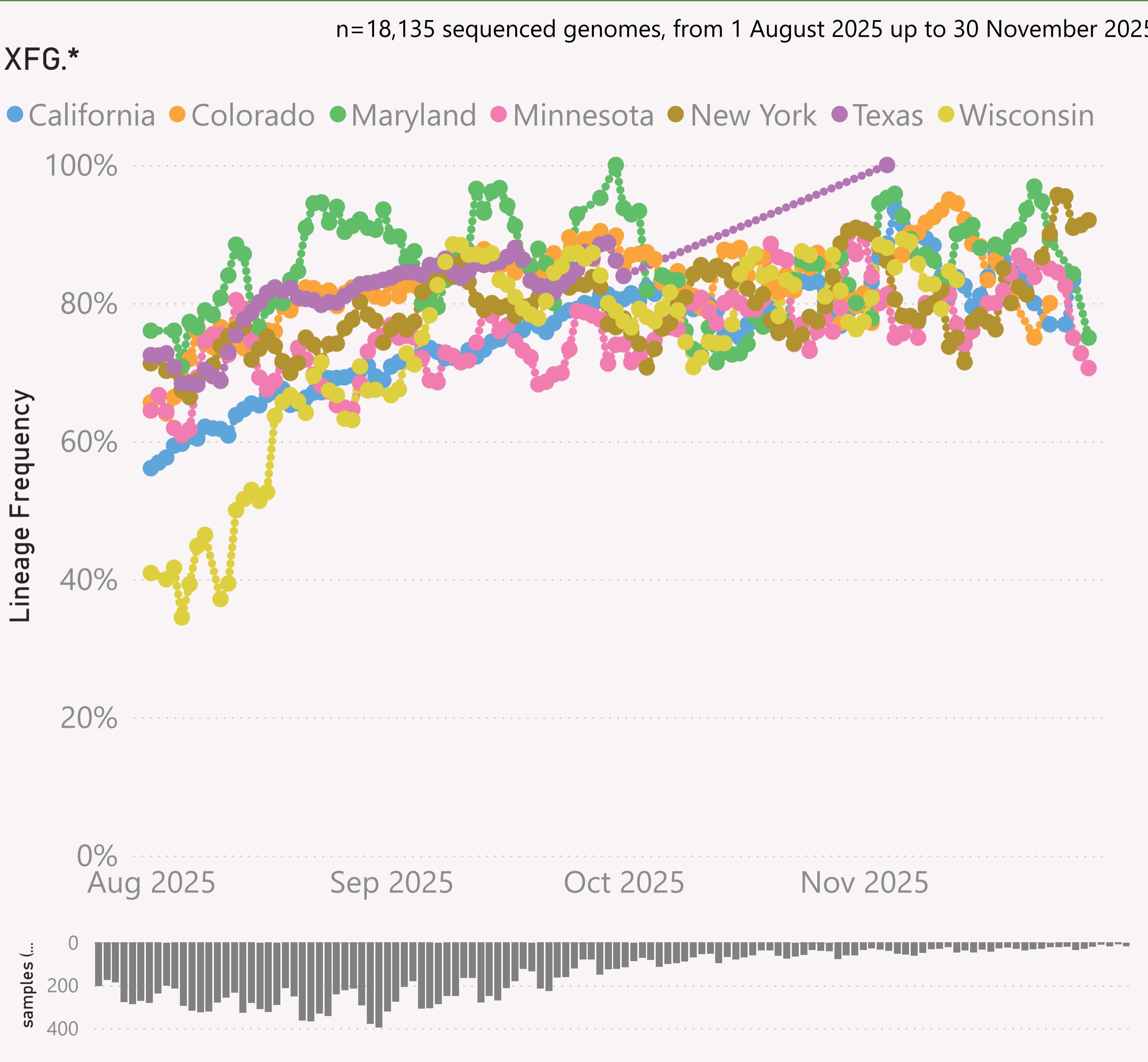
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The Lineage classifications are provided by Nextclade. The colour assignments are random.

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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.

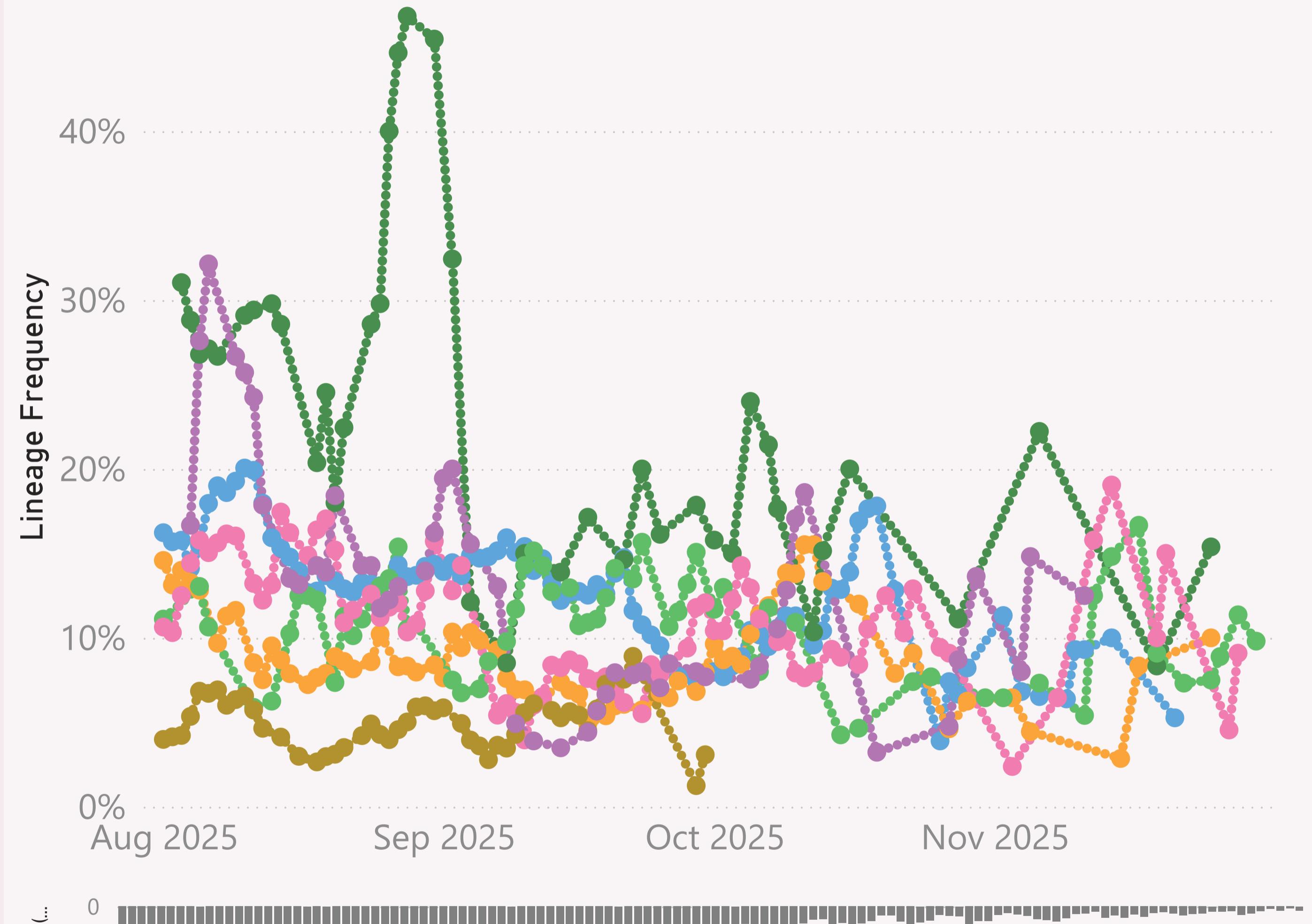
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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n=18,135 sequenced genomes, from 1 August 2025 up to 30 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.

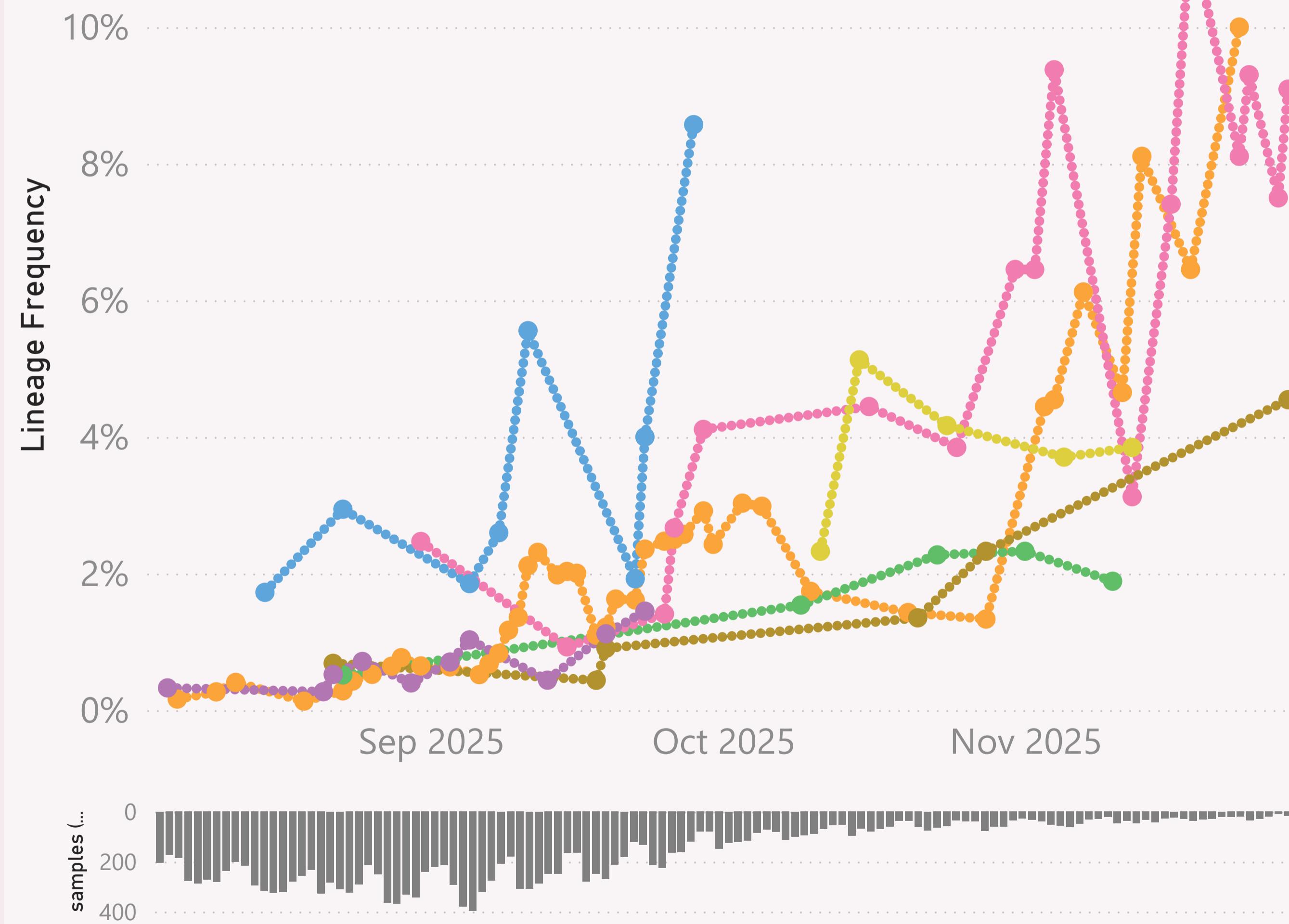
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n=18,135 sequenced genomes, from 1 August 2025 up to 30 November 2025

XFG.1.1

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



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.

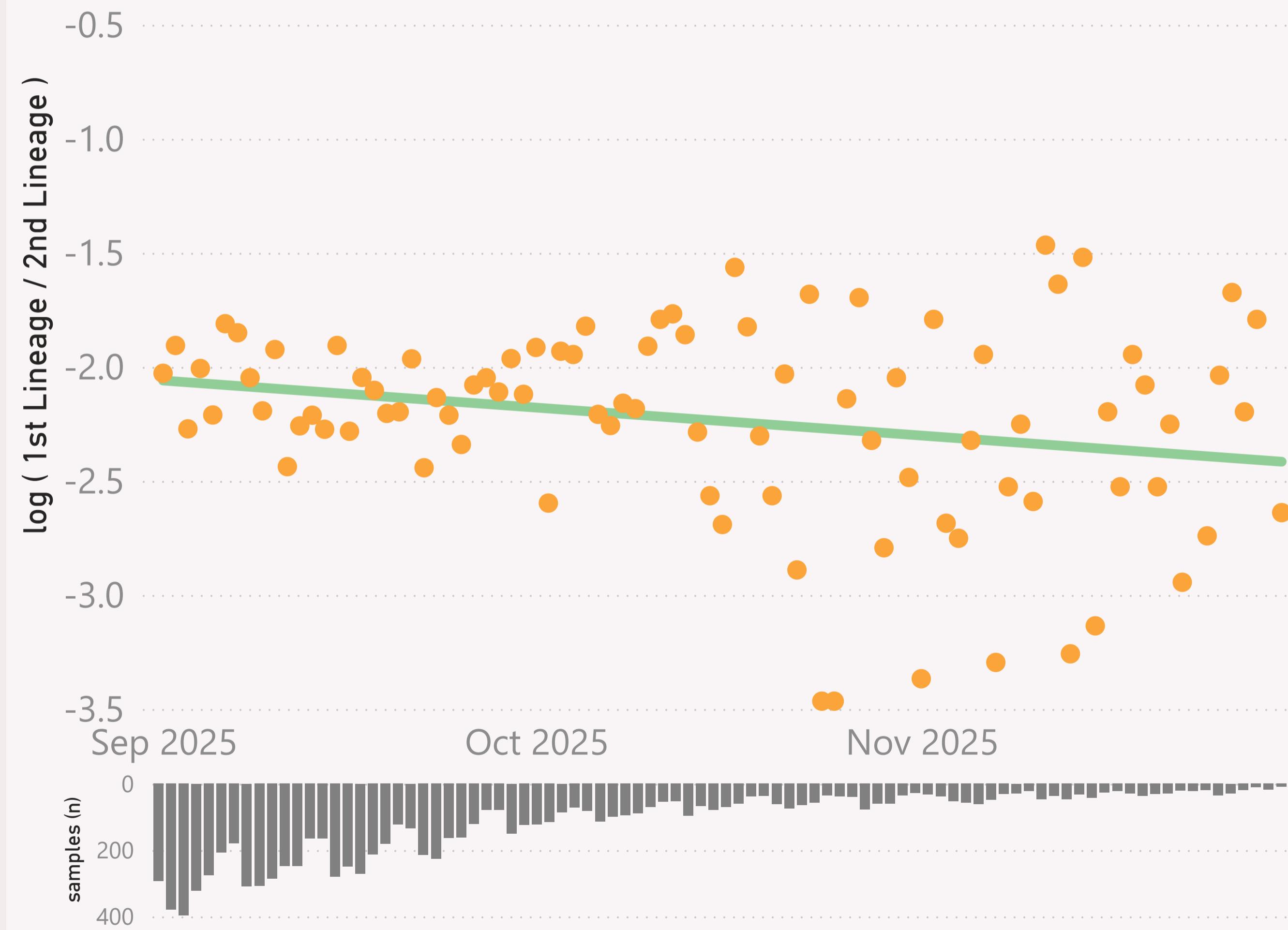
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=9,669 sequenced genomes, from 1 September 2025 up to 30 November 2025

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

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

0.0 ..... decline of -0.4% 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".

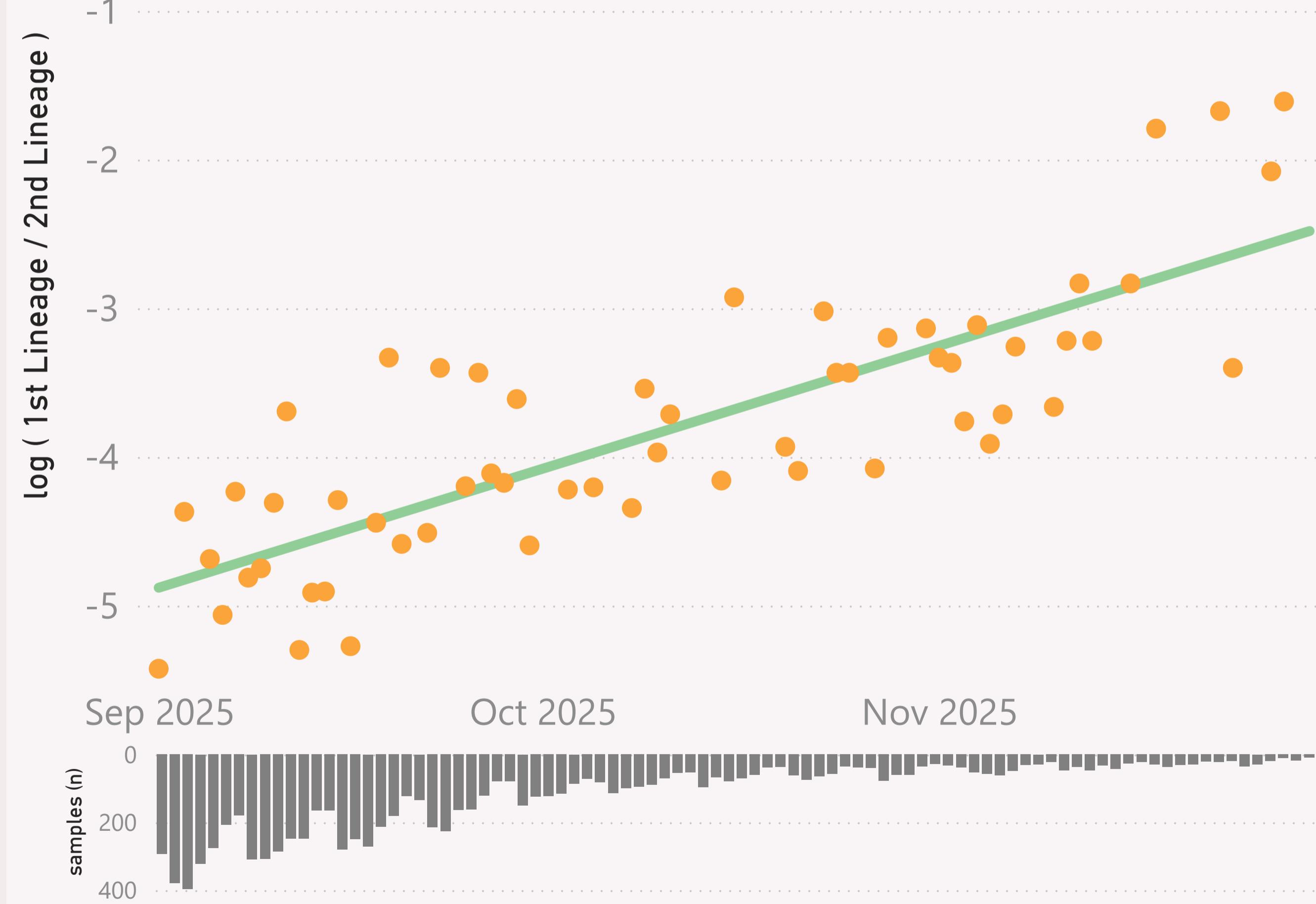
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=9,669 sequenced genomes, from 1 September 2025 up to 30 November 2025

## United States - XFG.1.1 vs XFG.\*

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

0 ..... growth of 2.7% per day



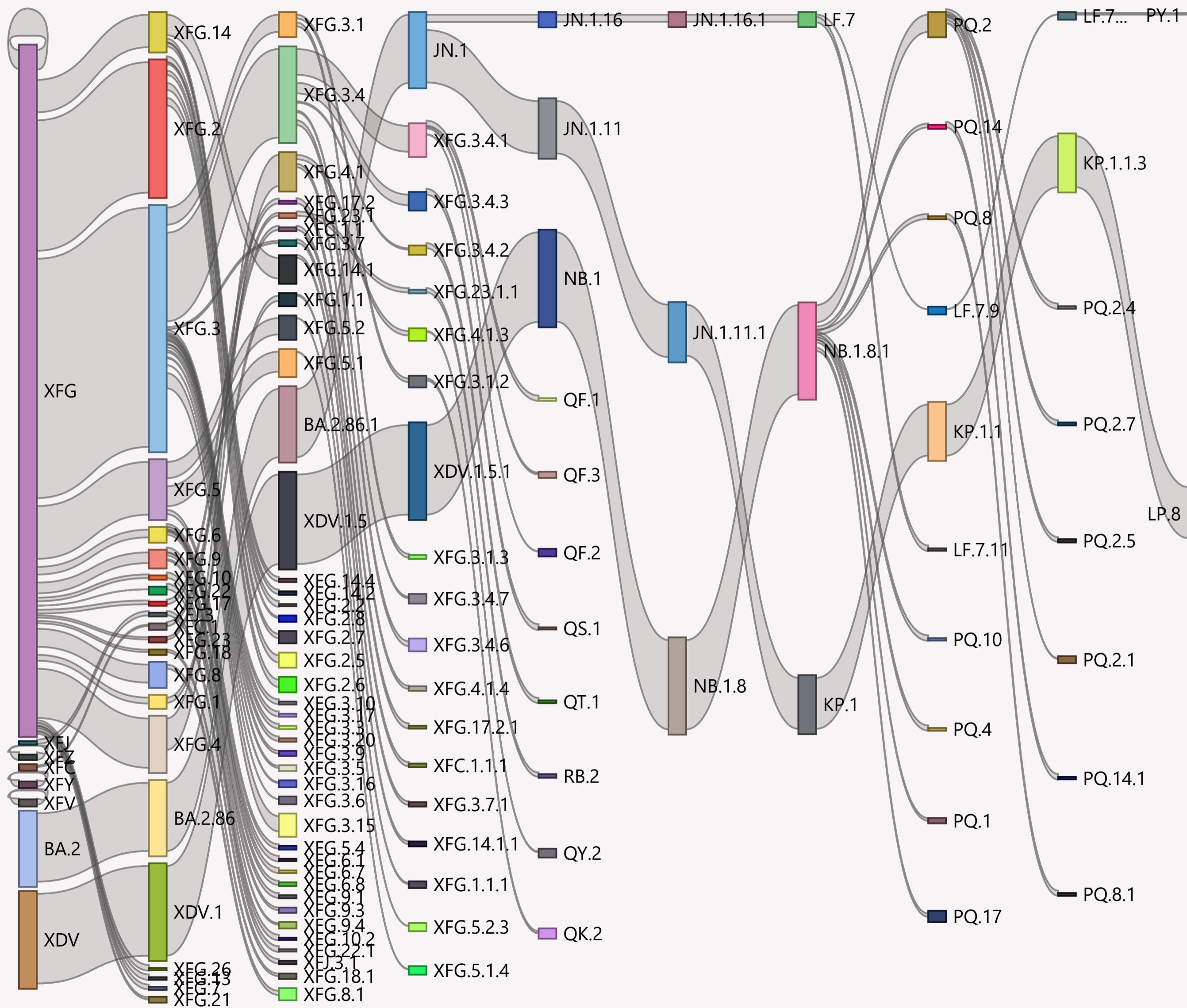
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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

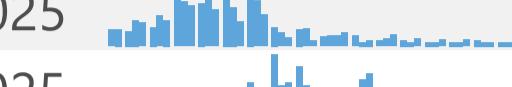
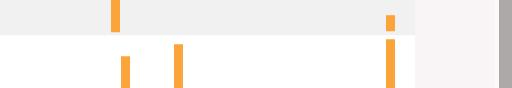
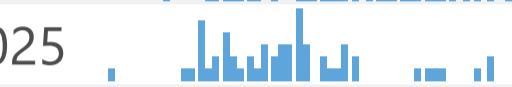
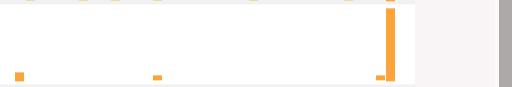
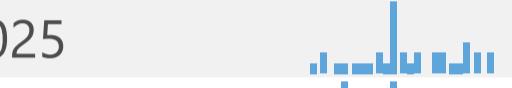
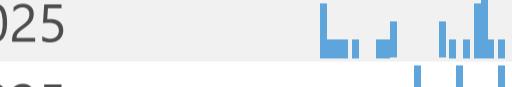
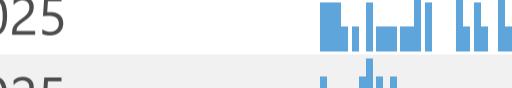
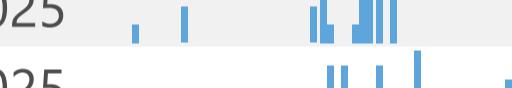
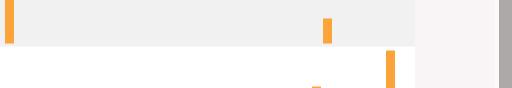
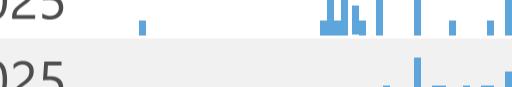
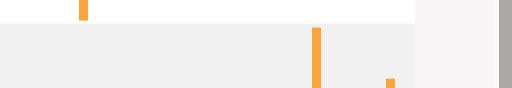
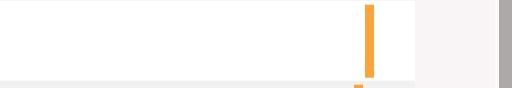
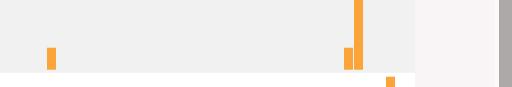
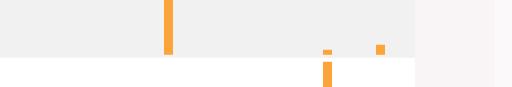
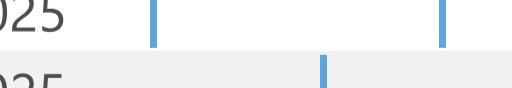
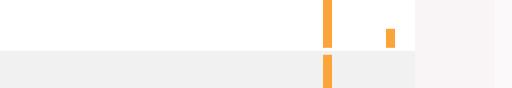
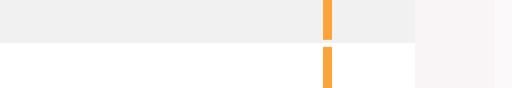
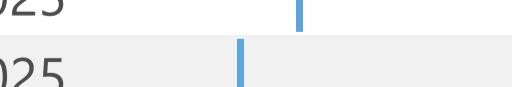
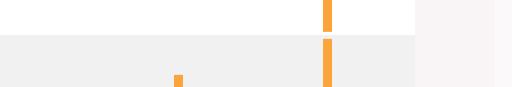
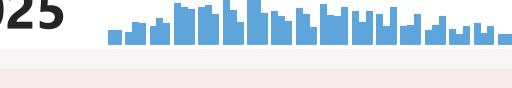
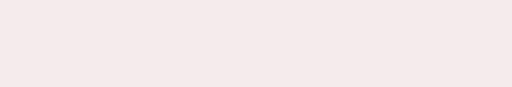
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n=18,135 sequenced genomes, from 1 August 2025 up to 30 November 2025

**United States**

## Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
United States	6,754	30/11/2025		09/12/2025	
California	3,197	28/11/2025		09/12/2025	
New York	702	30/11/2025		09/12/2025	
Wisconsin	619	13/11/2025		09/12/2025	
Colorado	345	25/11/2025		09/12/2025	
Minnesota	343	30/11/2025		09/12/2025	
Maryland	276	30/11/2025		09/12/2025	
Illinois	222	29/11/2025		09/12/2025	
Michigan	146	28/11/2025		09/12/2025	
Oregon	101	18/11/2025		26/11/2025	
Massachusetts	89	02/11/2025		09/12/2025	
Kentucky	71	26/11/2025		09/12/2025	
Connecticut	68	25/11/2025		09/12/2025	
Arizona	67	27/10/2025		03/12/2025	
New Jersey	67	28/11/2025		09/12/2025	
International Travellers	62	30/11/2025		09/12/2025	
New Mexico	62	10/09/2025		10/11/2025	
Nebraska	59	30/11/2025		09/12/2025	
New Hampshire	50	11/11/2025		20/11/2025	
Vermont	47	19/11/2025		09/12/2025	
Hawaii	46	18/11/2025		07/12/2025	
Nevada	32	18/11/2025		06/12/2025	
South Dakota	29	28/11/2025		09/12/2025	
Wyoming	28	10/11/2025		08/12/2025	
Texas	5	04/11/2025		09/12/2025	
Alaska	4	01/10/2025		03/12/2025	
South Carolina	4	02/10/2025		03/12/2025	
Florida	3	07/09/2025		03/12/2025	
Total	6,754	30/11/2025		09/12/2025	

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.