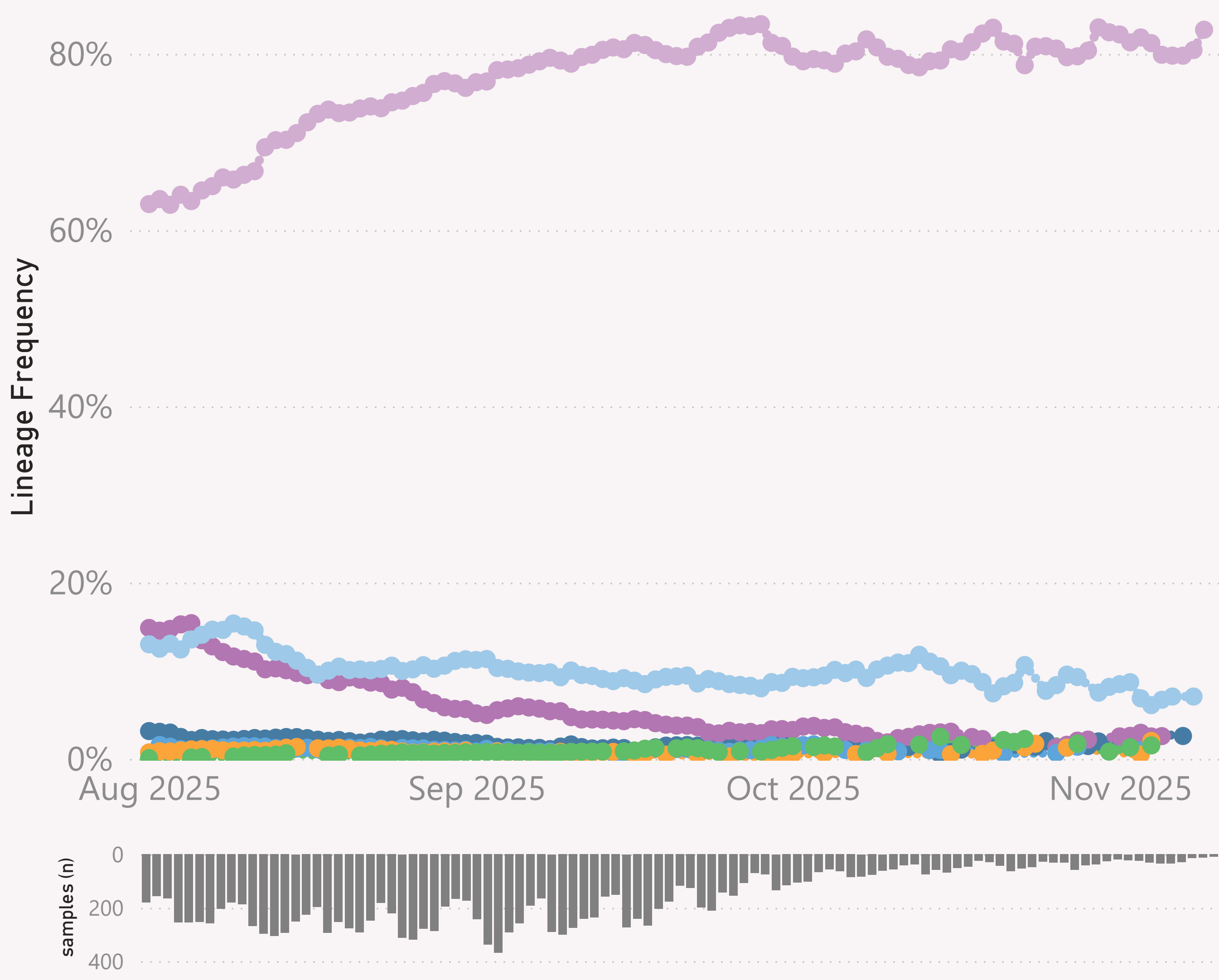


n=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

United States

● JN.1.* +FLiRT ● LP.8.1.* ● NB.1.8.1.* Nimbus ● XFC.* ● XFG.* ● XFJ.* ● XFY.*



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 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.

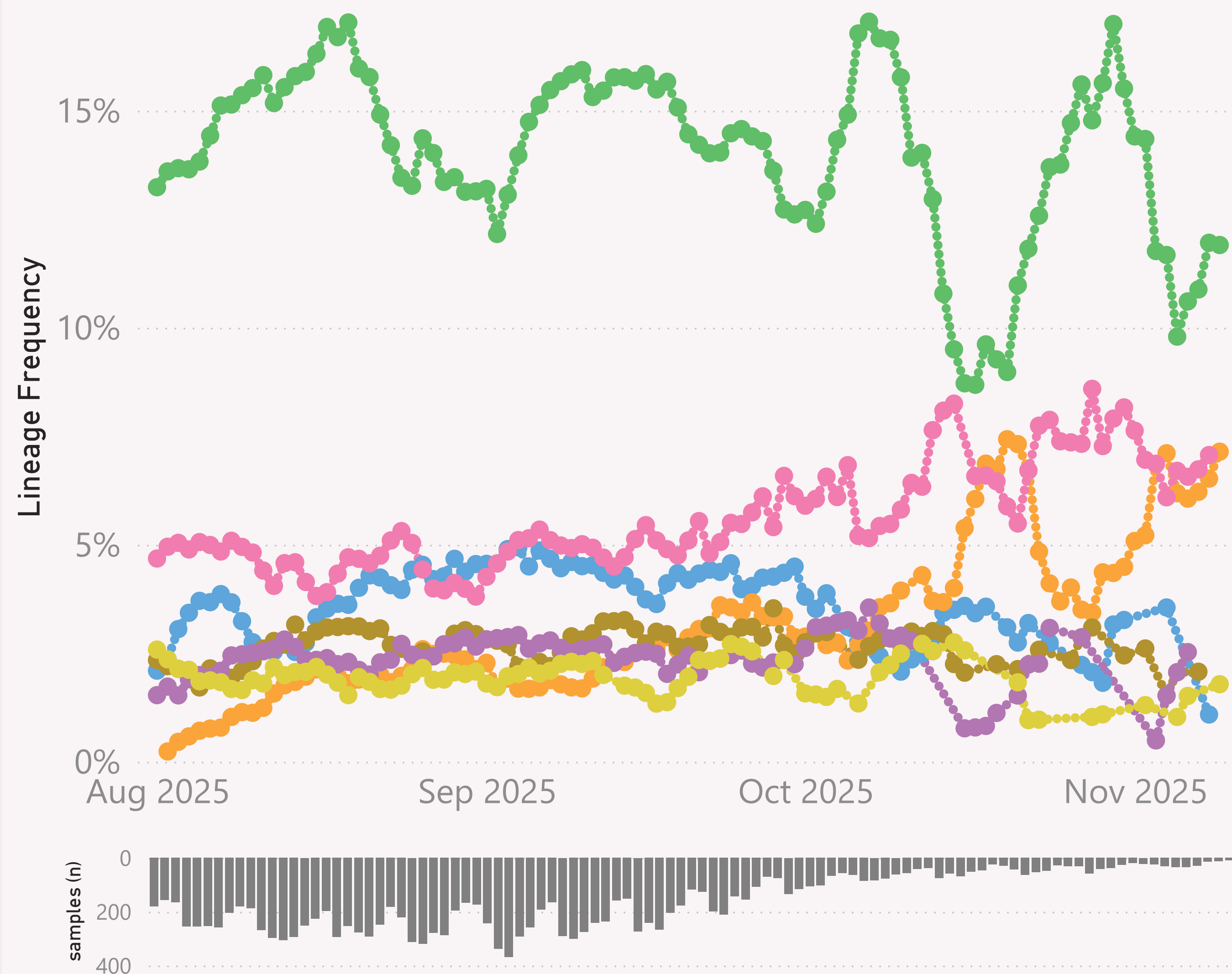
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=15,471 sequenced genomes, from 1 August 2025 up to 9 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.

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=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

United States

● XFG.1.1



This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a Lineage group of interest, currently XFG.1.1.* .

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.

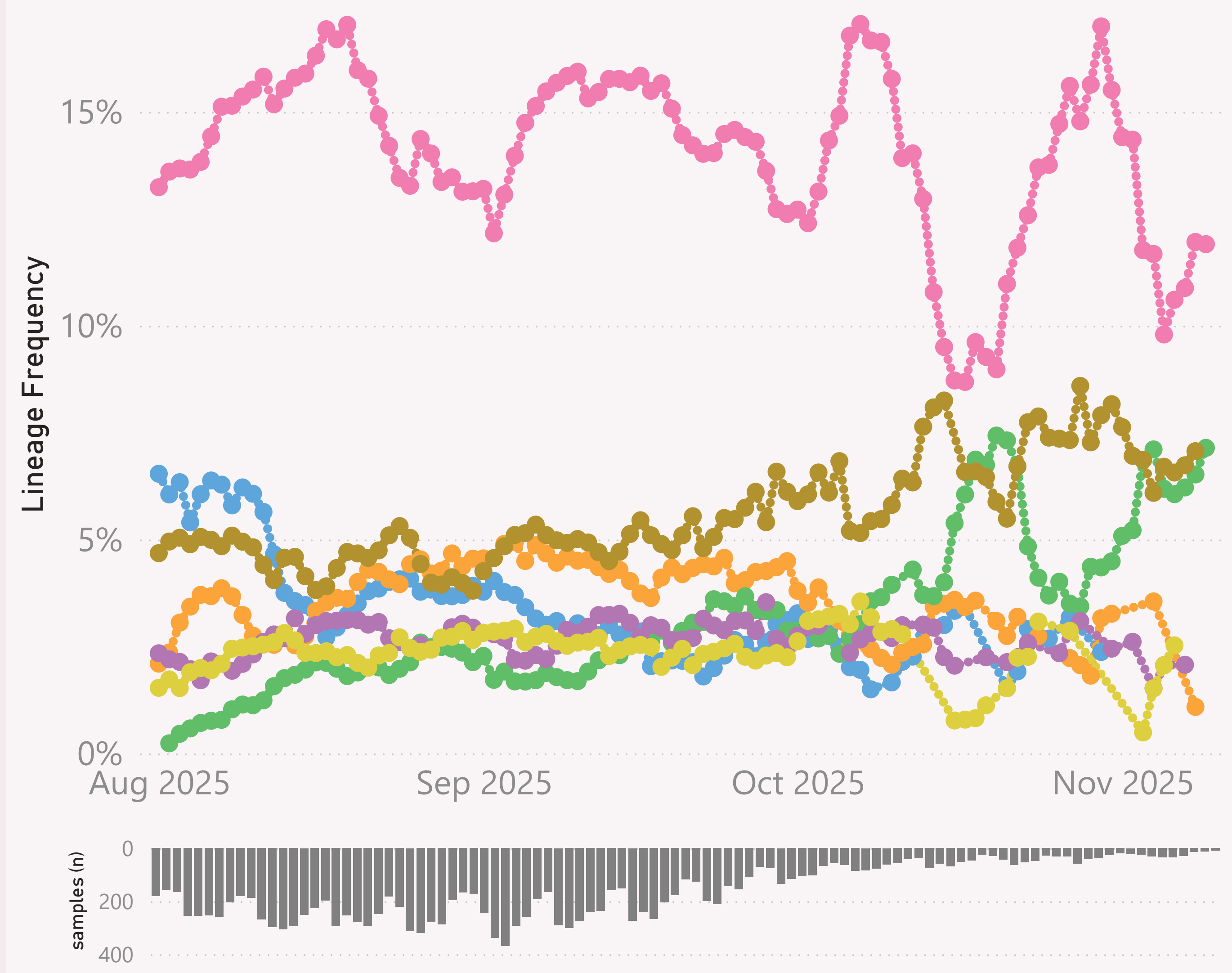
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

United States

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



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.

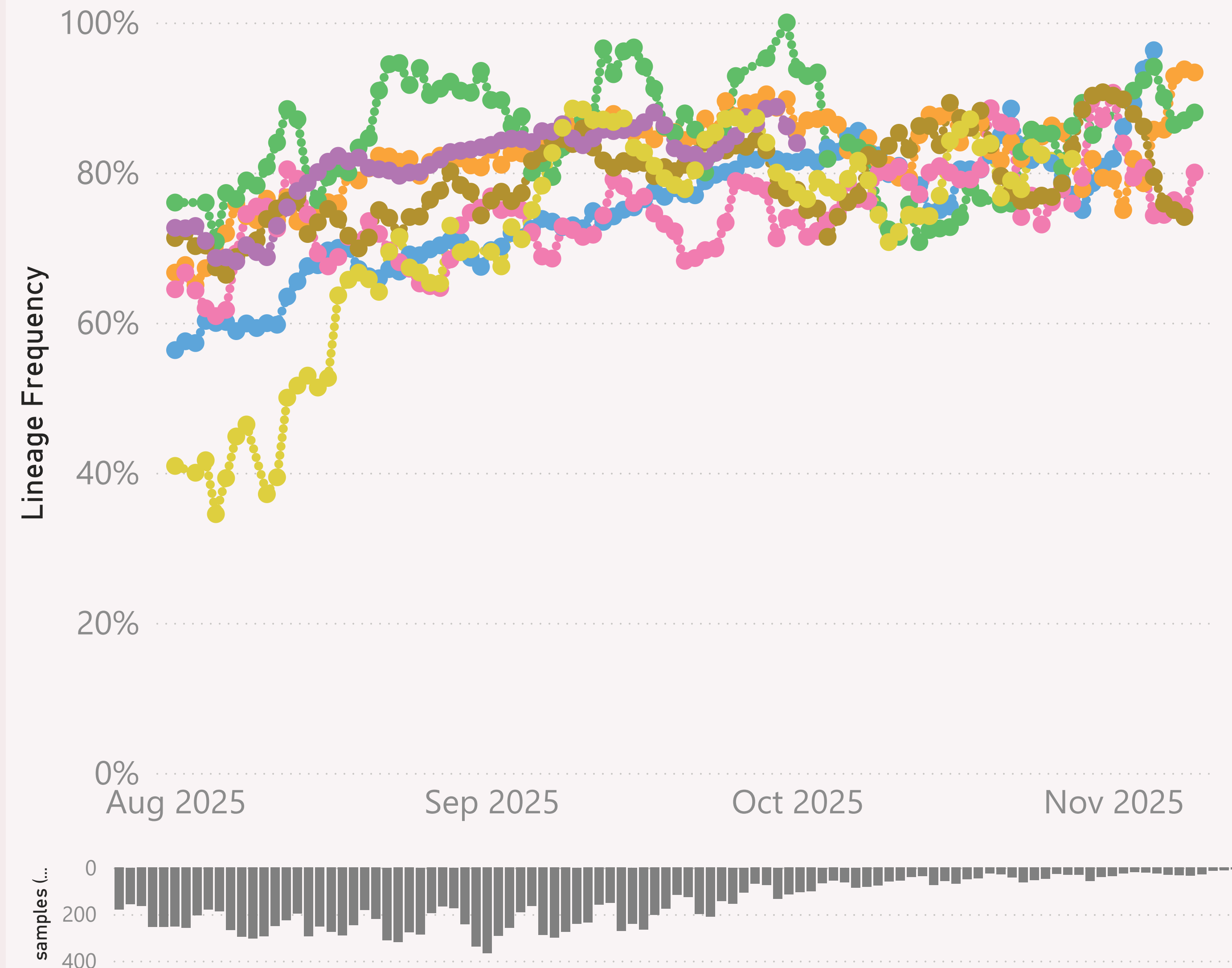
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

XFG.*

● California ● Colorado ● Maryland ● 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 it's 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.

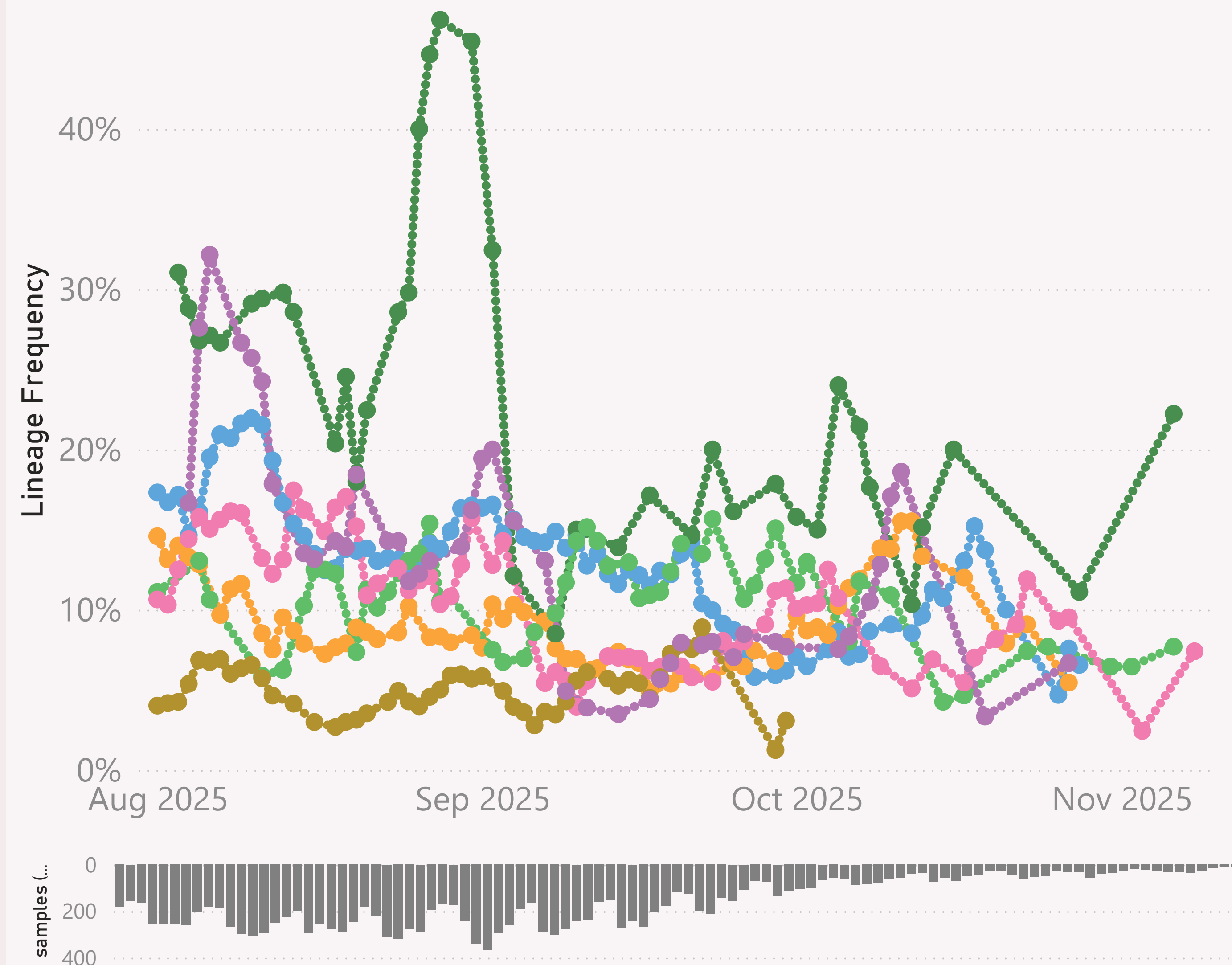
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

NB.1.8.1.* Nimbus

● California ● Colorado ● Internation... ● 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 it's 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.

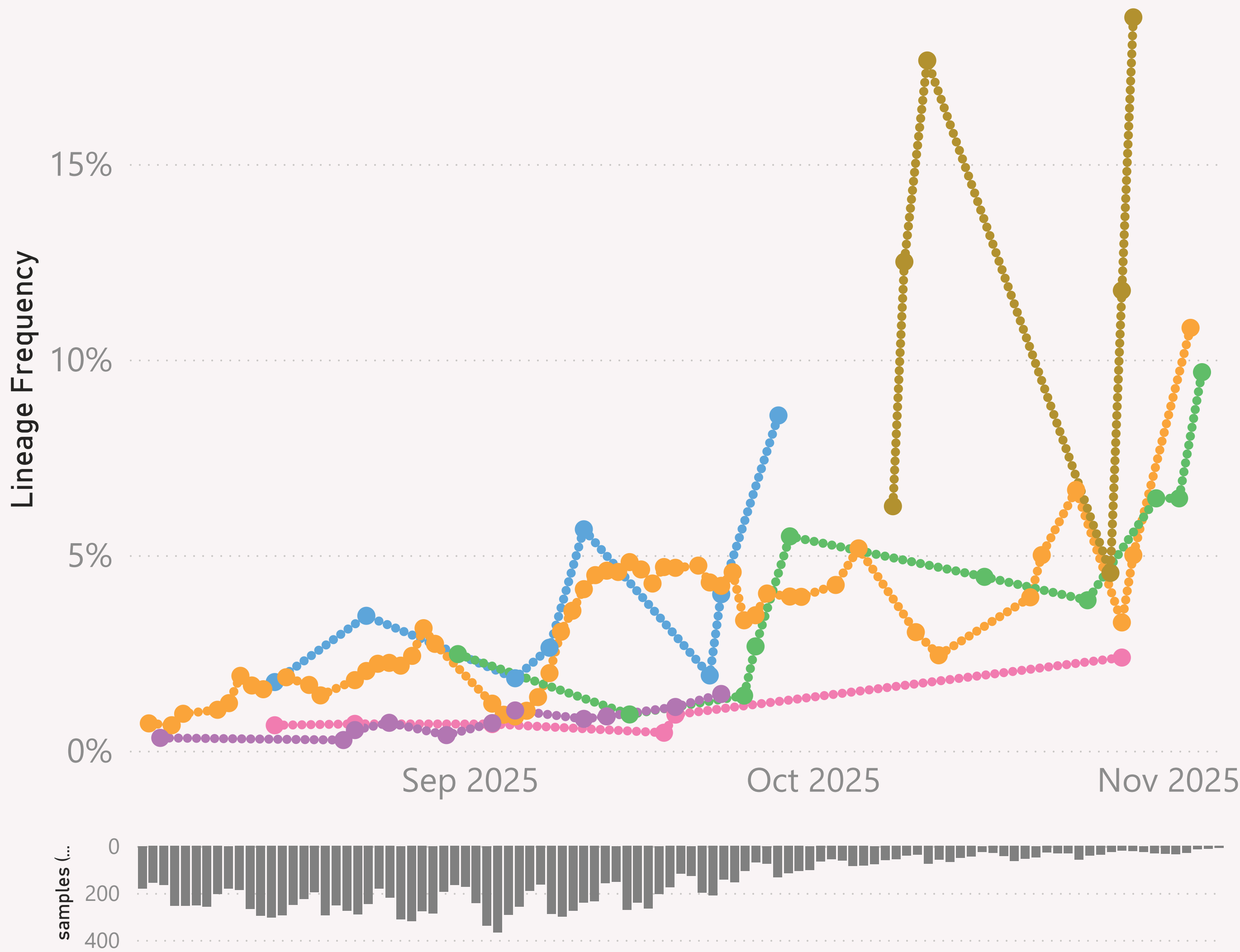
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

XFG.1.1

● Arizona ● California ● Minnesota ● New York ● Oregon ● 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.

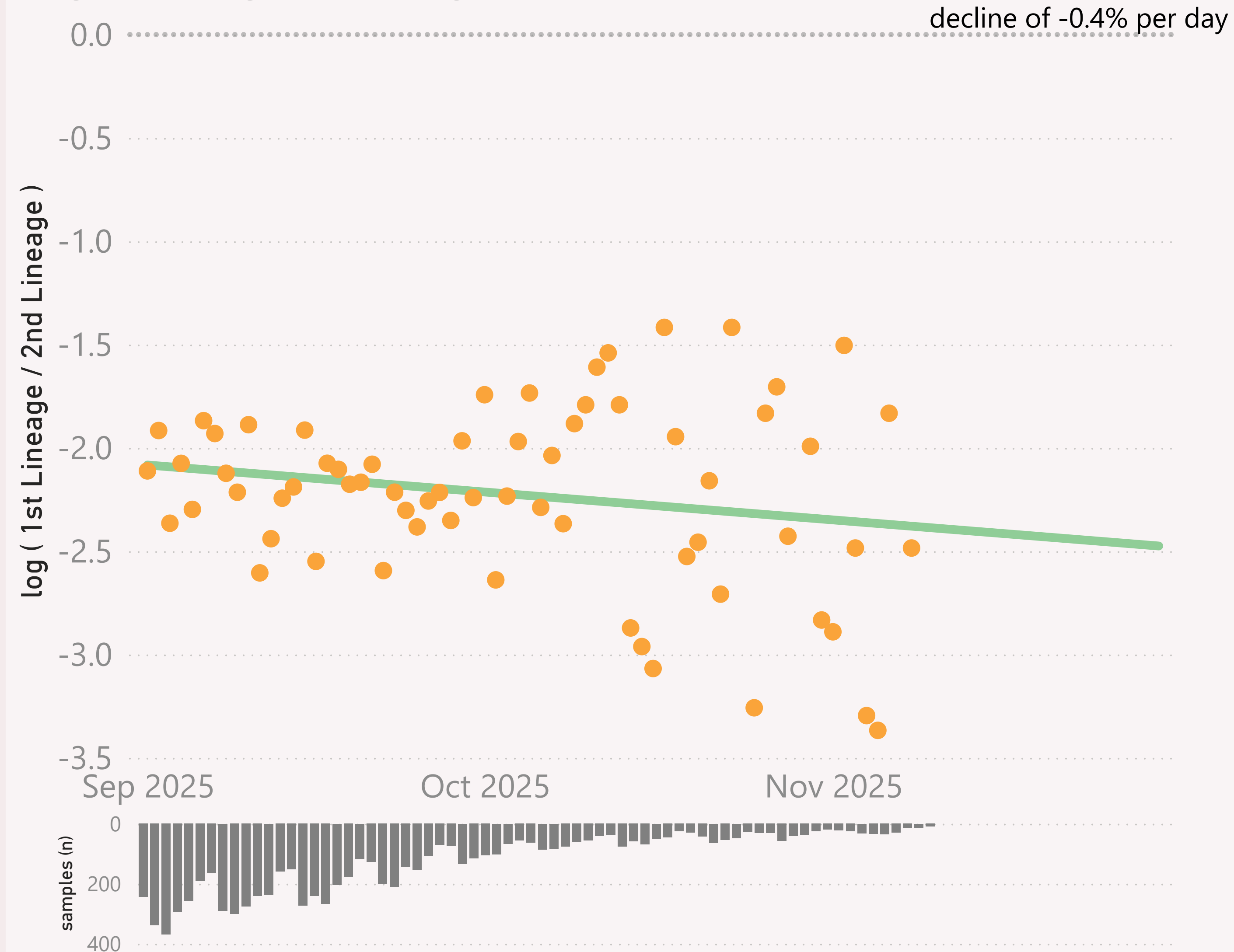
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=8,024 sequenced genomes, from 1 September 2025 up to 9 November 2025

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

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

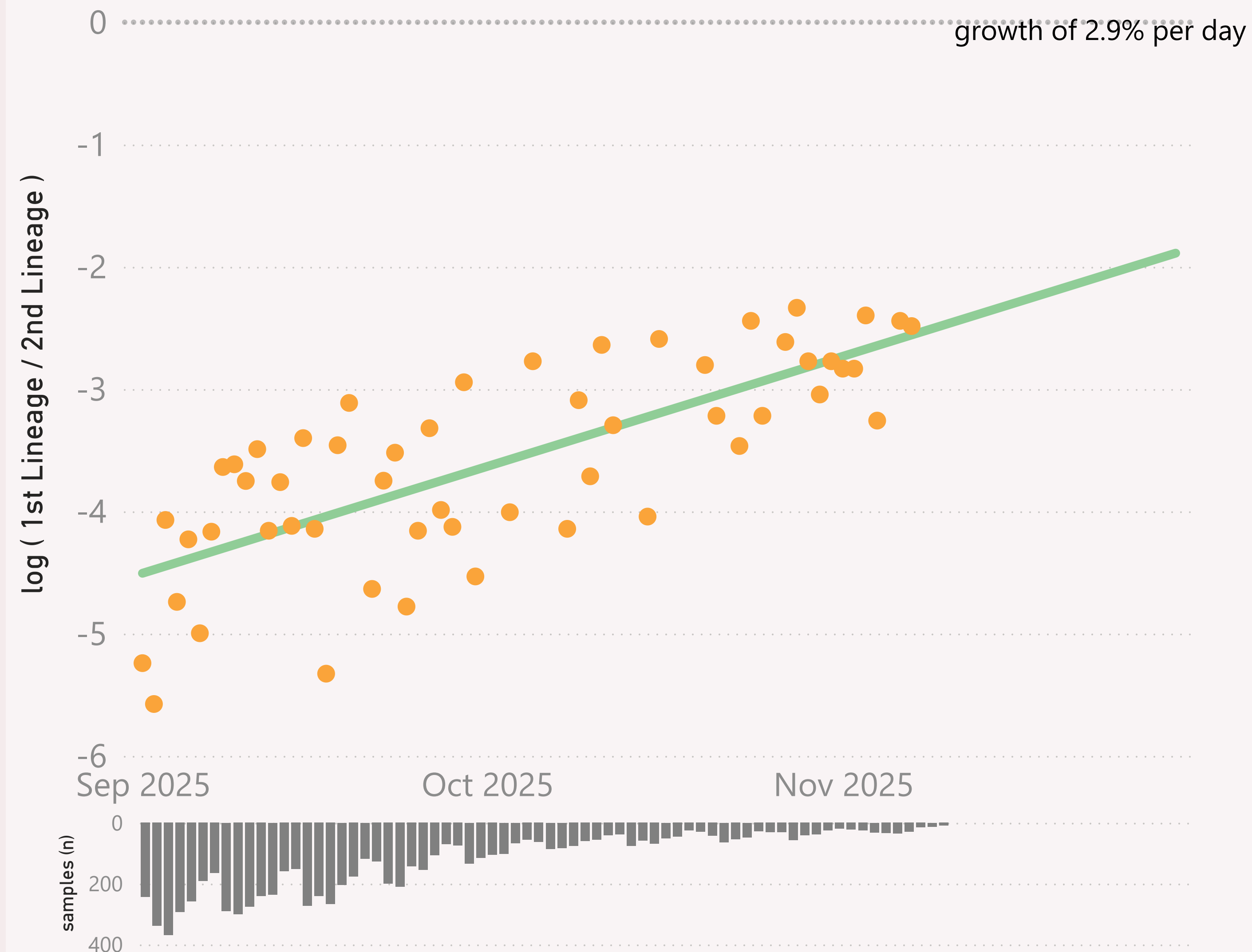
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=8,024 sequenced genomes, from 1 September 2025 up to 9 November 2025

United States - XFG.1.1 vs XFG.*

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



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

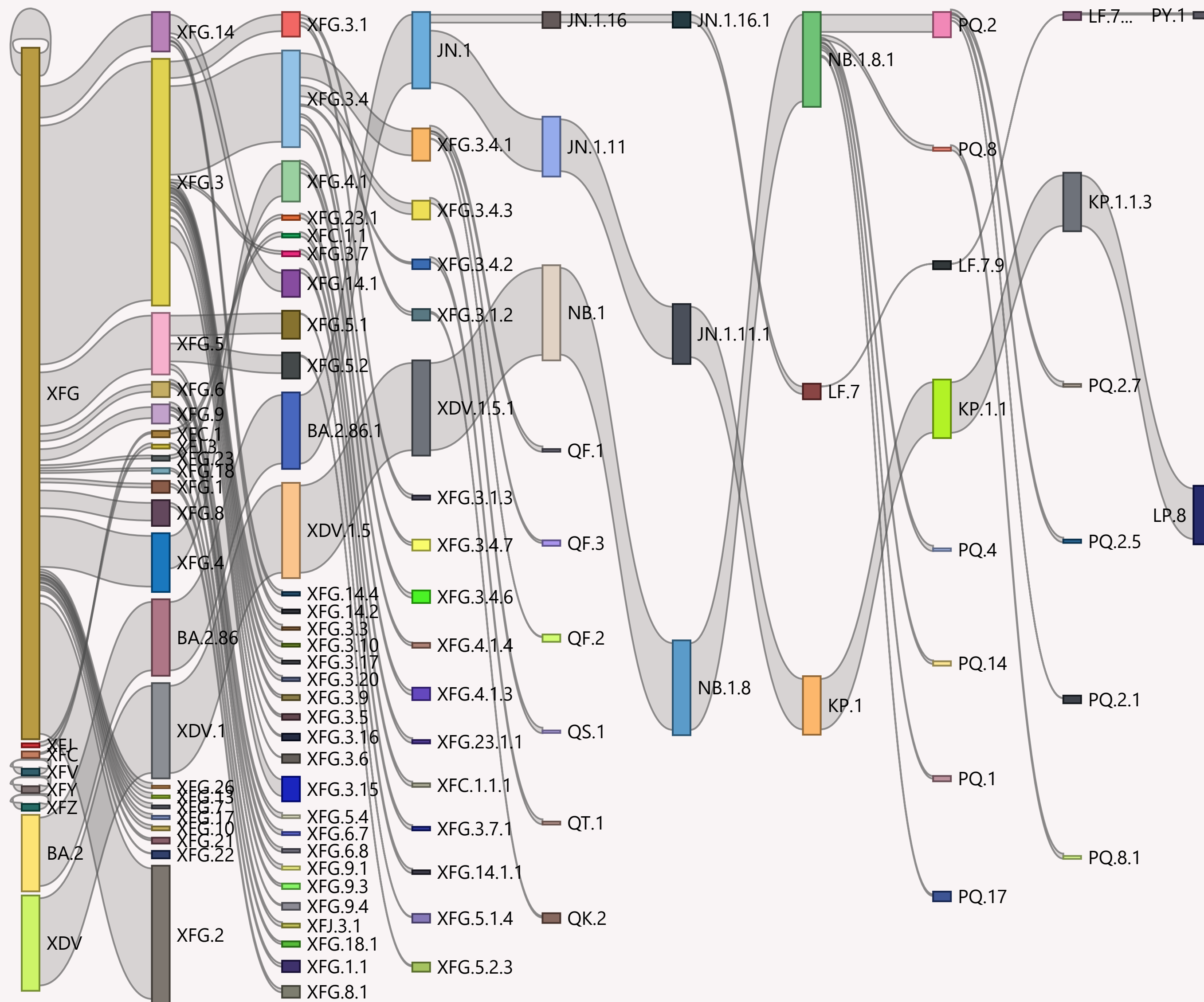
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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=15,471 sequenced genomes, from 1 August 2025 up to 9 November 2025

United States



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





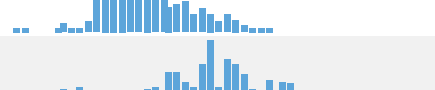
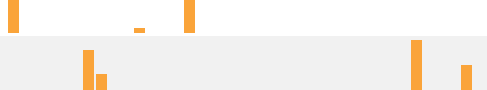
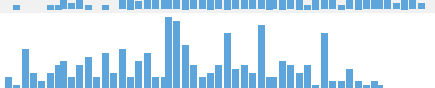








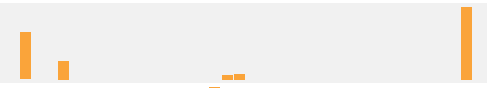





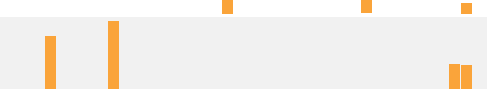
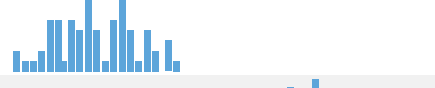

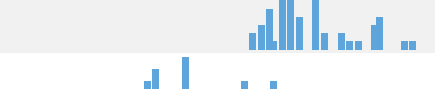

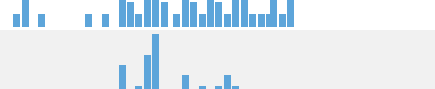
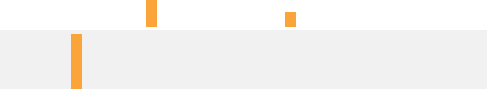
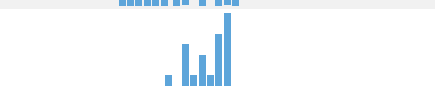




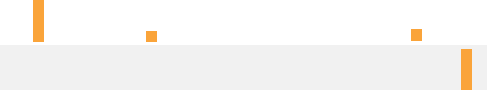
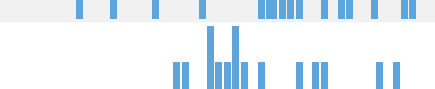

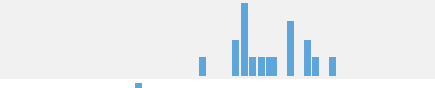
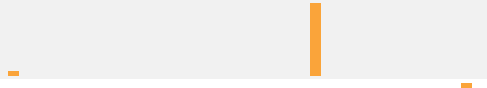


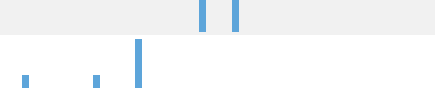

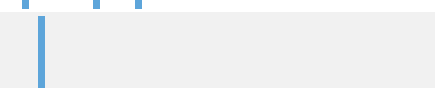
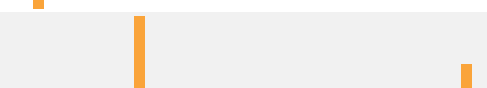
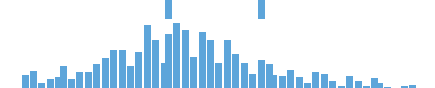

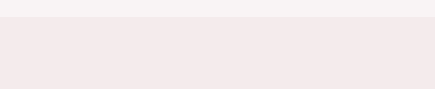
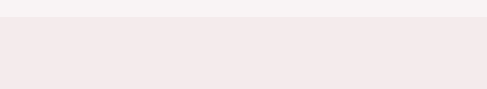
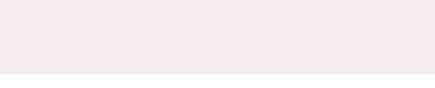
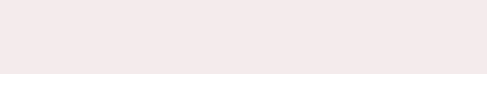
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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
<div><div></div>United States</div>	9,144	09/11/2025		11/11/2025	
California	3,093	05/11/2025		11/11/2025	
Texas	1,541	02/10/2025		20/10/2025	
New York	911	08/11/2025		11/11/2025	
Wisconsin	547	29/10/2025		11/11/2025	
Minnesota	531	09/11/2025		11/11/2025	
Colorado	521	09/11/2025		11/11/2025	
Maryland	245	09/11/2025		11/11/2025	
Illinois	228	07/11/2025		11/11/2025	
Oregon	183	09/11/2025		11/11/2025	
Massachusetts	180	01/10/2025		22/10/2025	
Arizona	177	27/10/2025		03/11/2025	
Kentucky	160	07/11/2025		11/11/2025	
Connecticut	135	09/11/2025		11/11/2025	
New Mexico	108	10/09/2025		10/11/2025	
International Travellers	106	06/11/2025		11/11/2025	
New Jersey	97	07/10/2025		28/10/2025	
Hawaii	66	24/09/2025		11/10/2025	
Utah	53	25/09/2025		09/10/2025	
Vermont	50	26/10/2025		10/11/2025	
Nevada	47	01/11/2025		07/11/2025	
New Hampshire	47	06/11/2025		11/11/2025	
Michigan	33	04/11/2025		11/11/2025	
Nebraska	25	22/10/2025		30/10/2025	
Wyoming	24	06/11/2025		11/11/2025	
Alaska	9	25/09/2025		16/10/2025	
Georgia	7	09/09/2025		08/10/2025	
Missouri	4	29/09/2025		11/11/2025	
Total	9,144	09/11/2025		11/11/2025	

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.