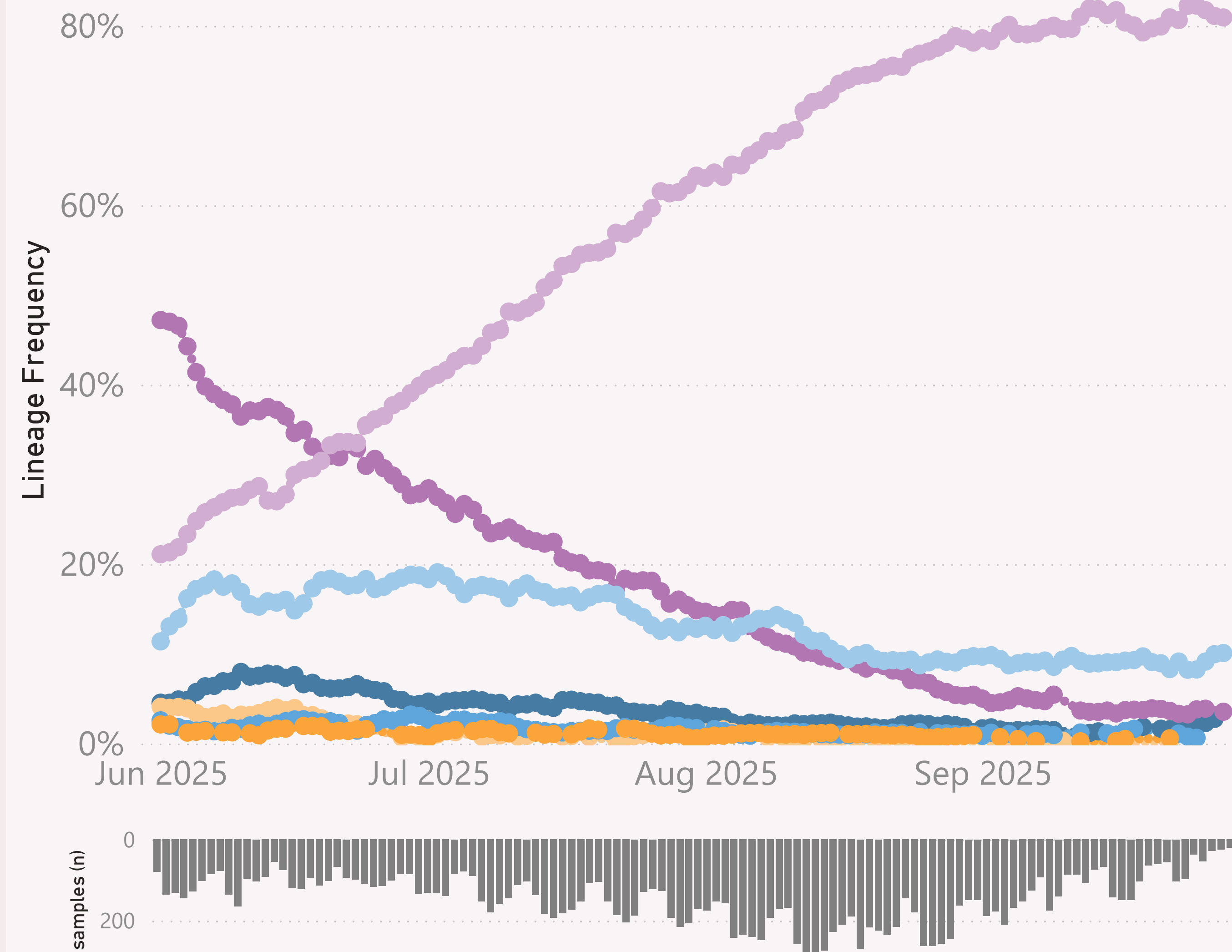


n=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025

United States

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



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.

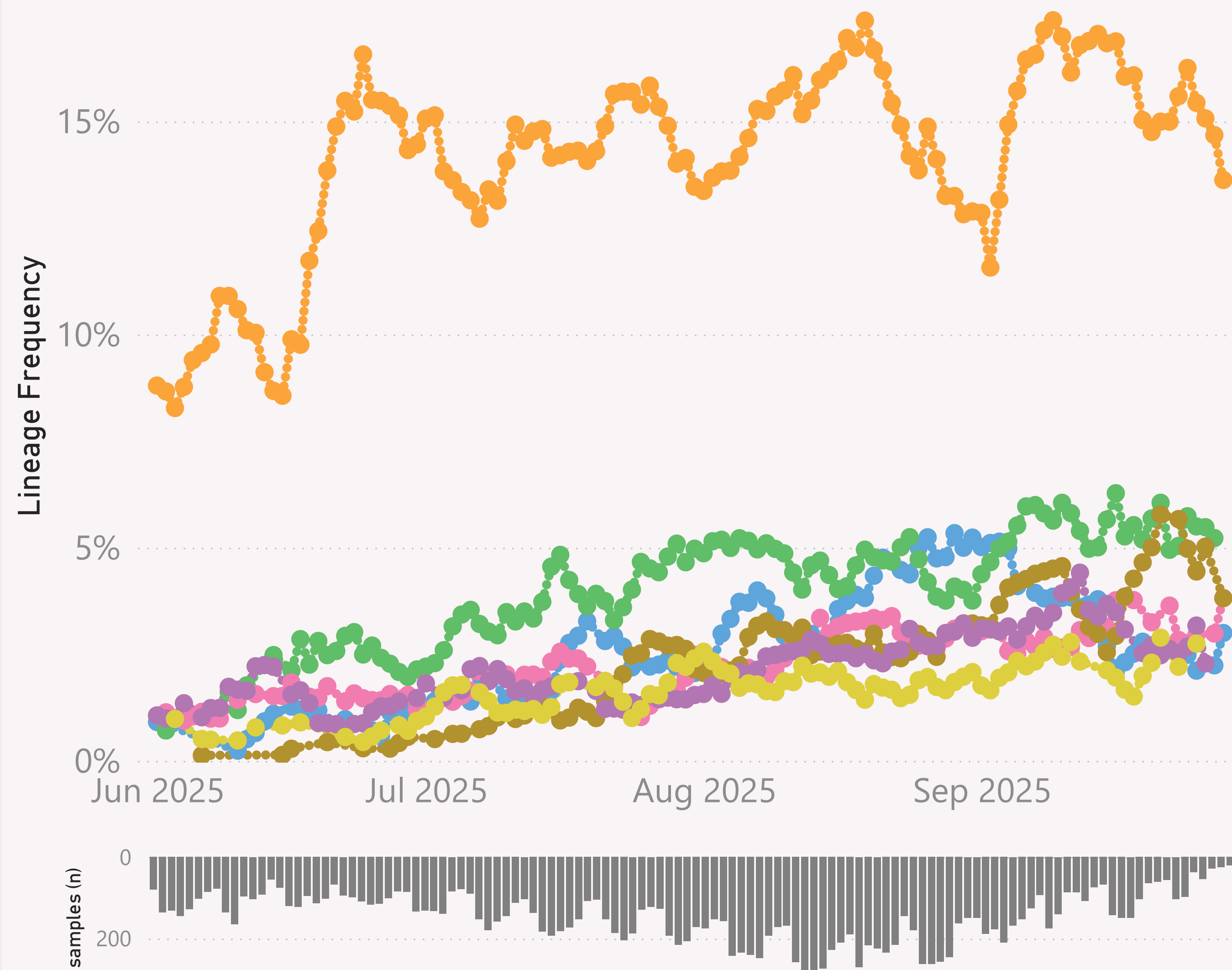
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025

United States

● XFG ● XFG.2 ● XFG.3 ● XFG.3.15 ● XFG.3.4.1 ● 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.

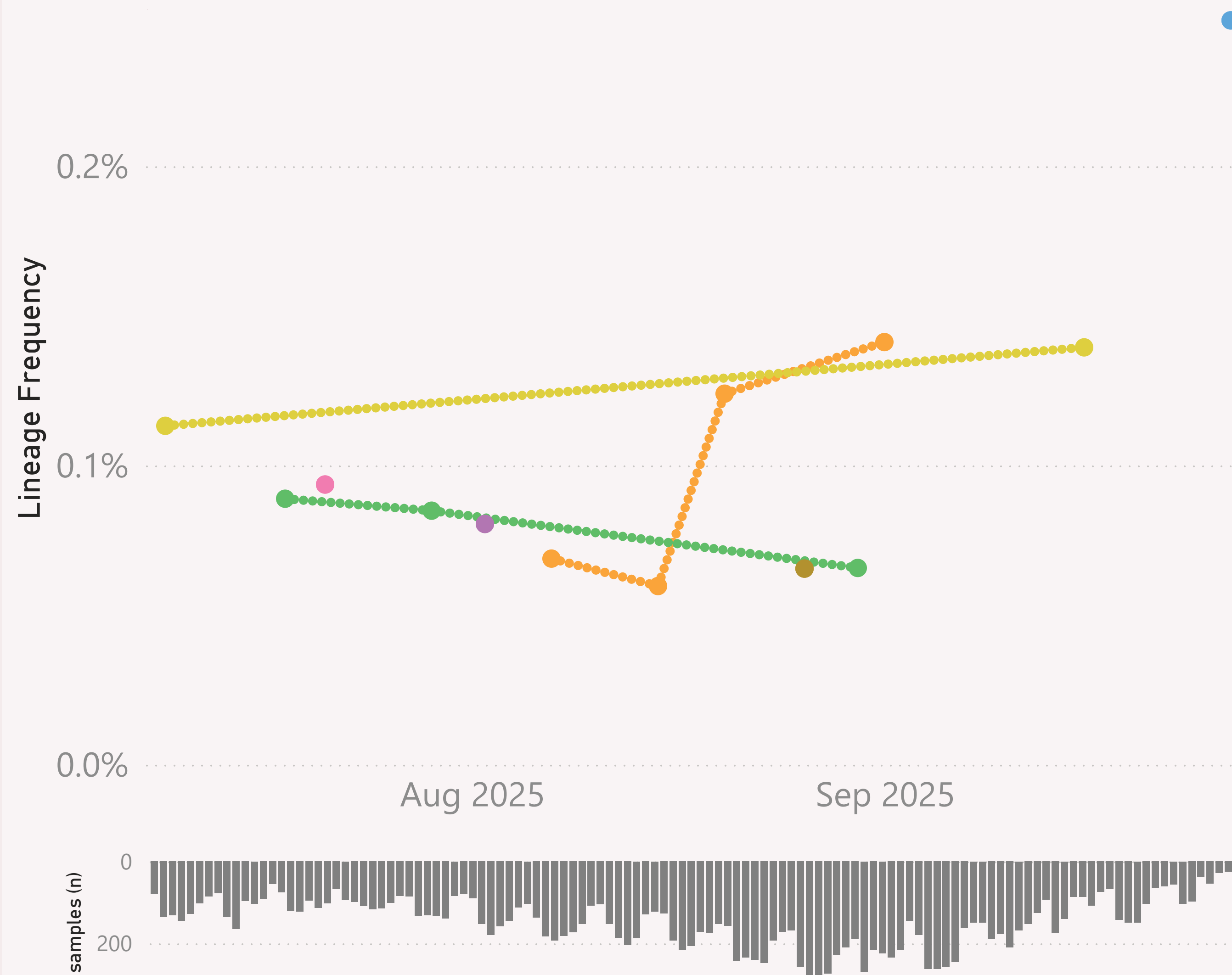
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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n=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025

United States

● NB.1.6 ● NB.1.7 ● NB.1.8 ● QL.1 ● XDV ● XDV.1.5 ● XDV.1.5.1



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 NB.1.8.1.* "Nimbus".

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.

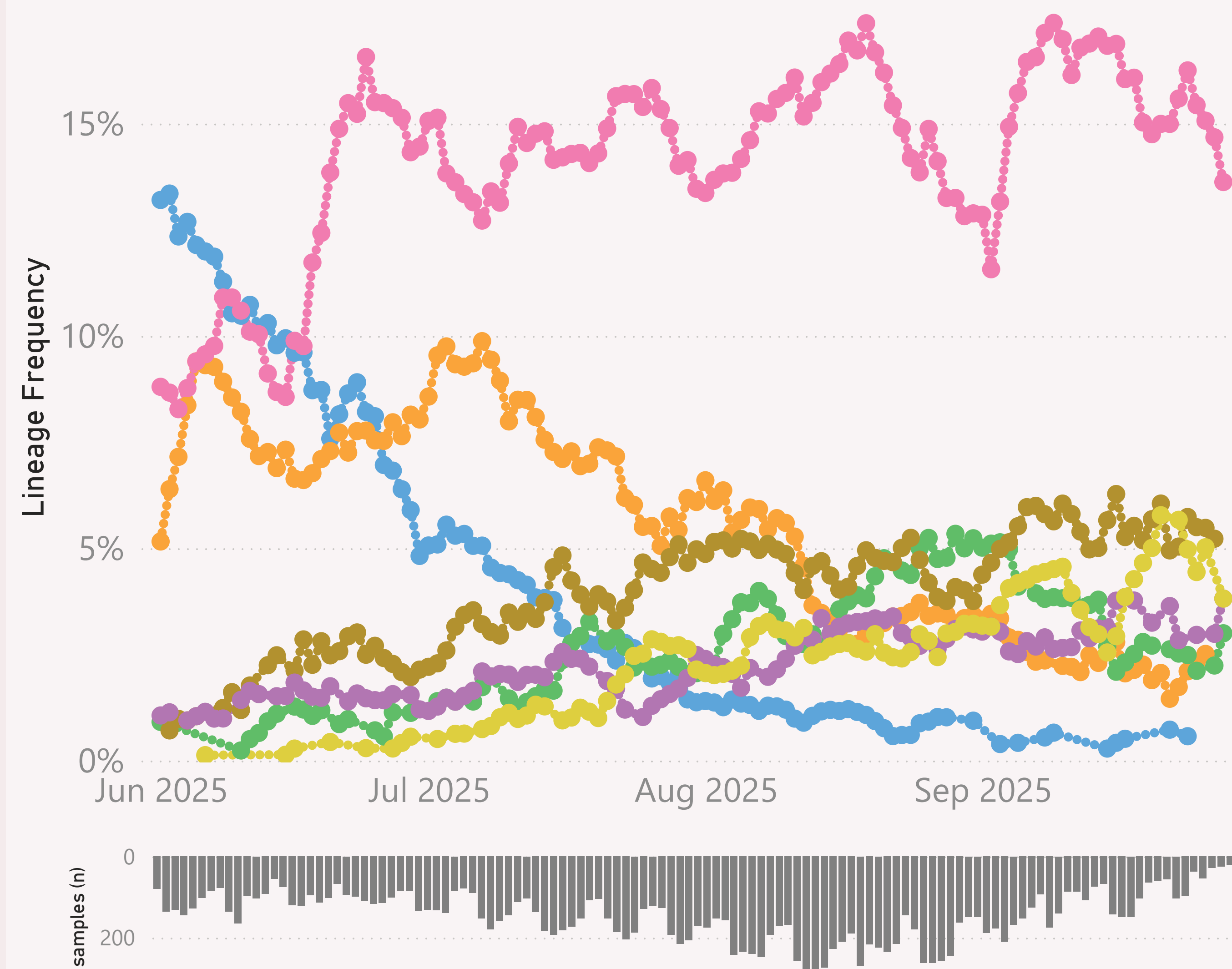
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025

United States

● LP.8.1.1 ● NB.1.8.1 ● XFG ● XFG.2 ● XFG.3 ● XFG.3.15 ● XFG.3.4.1



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

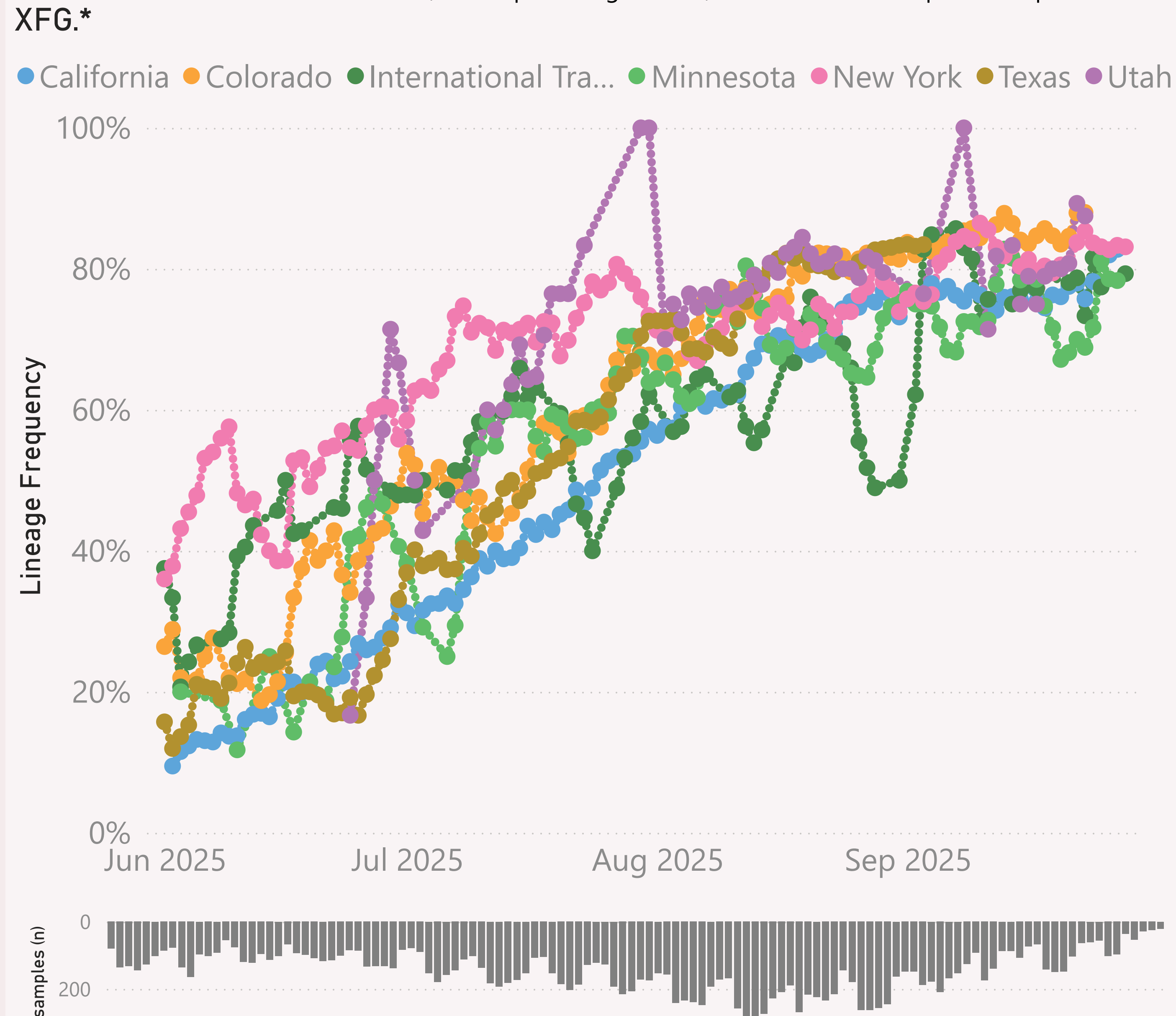
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025



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.

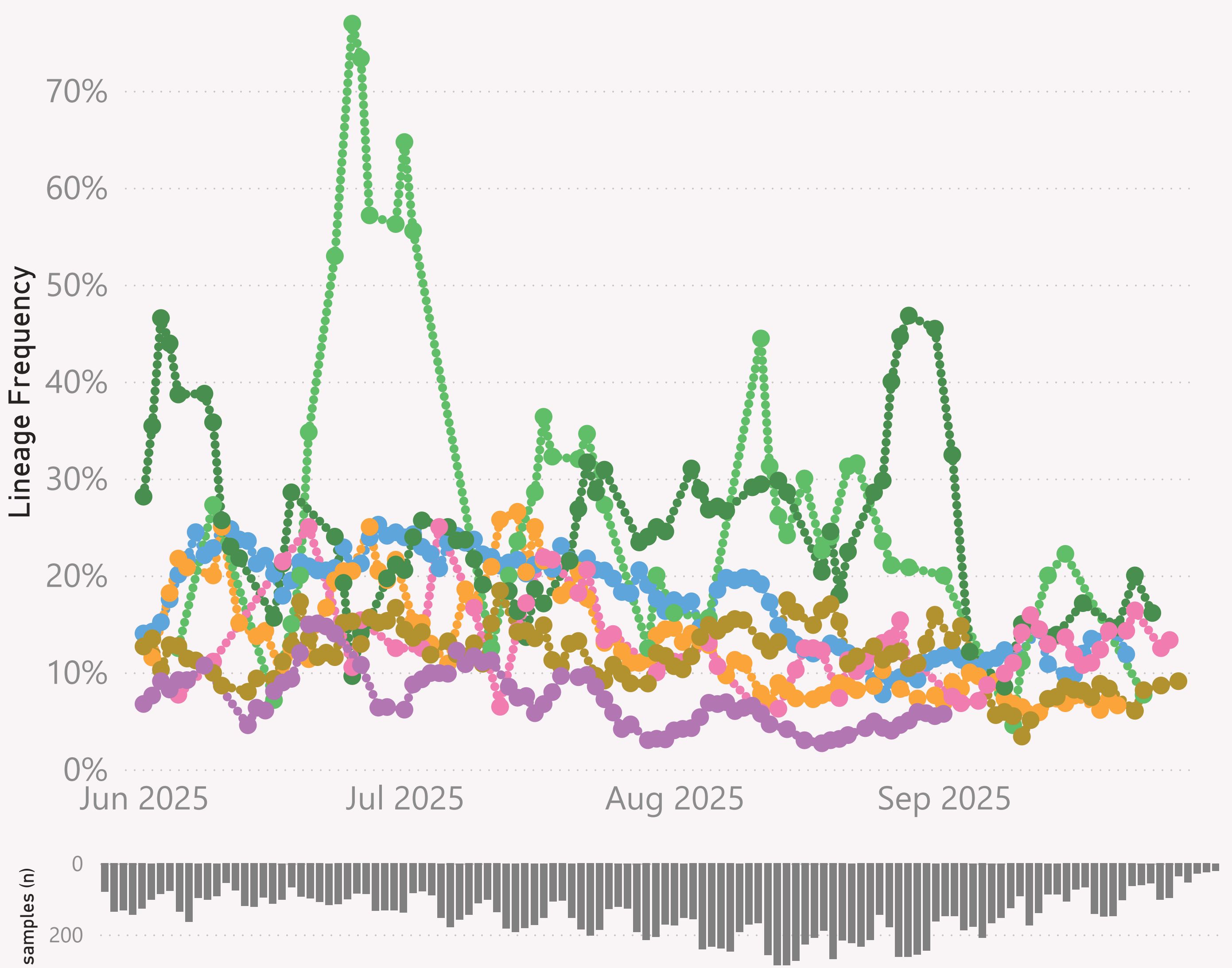
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025

NB.1.8.1.* Nimbus

● California ● Colorado ● Hawaii ● International T... ● Minnesota ● New York ● Texas



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.

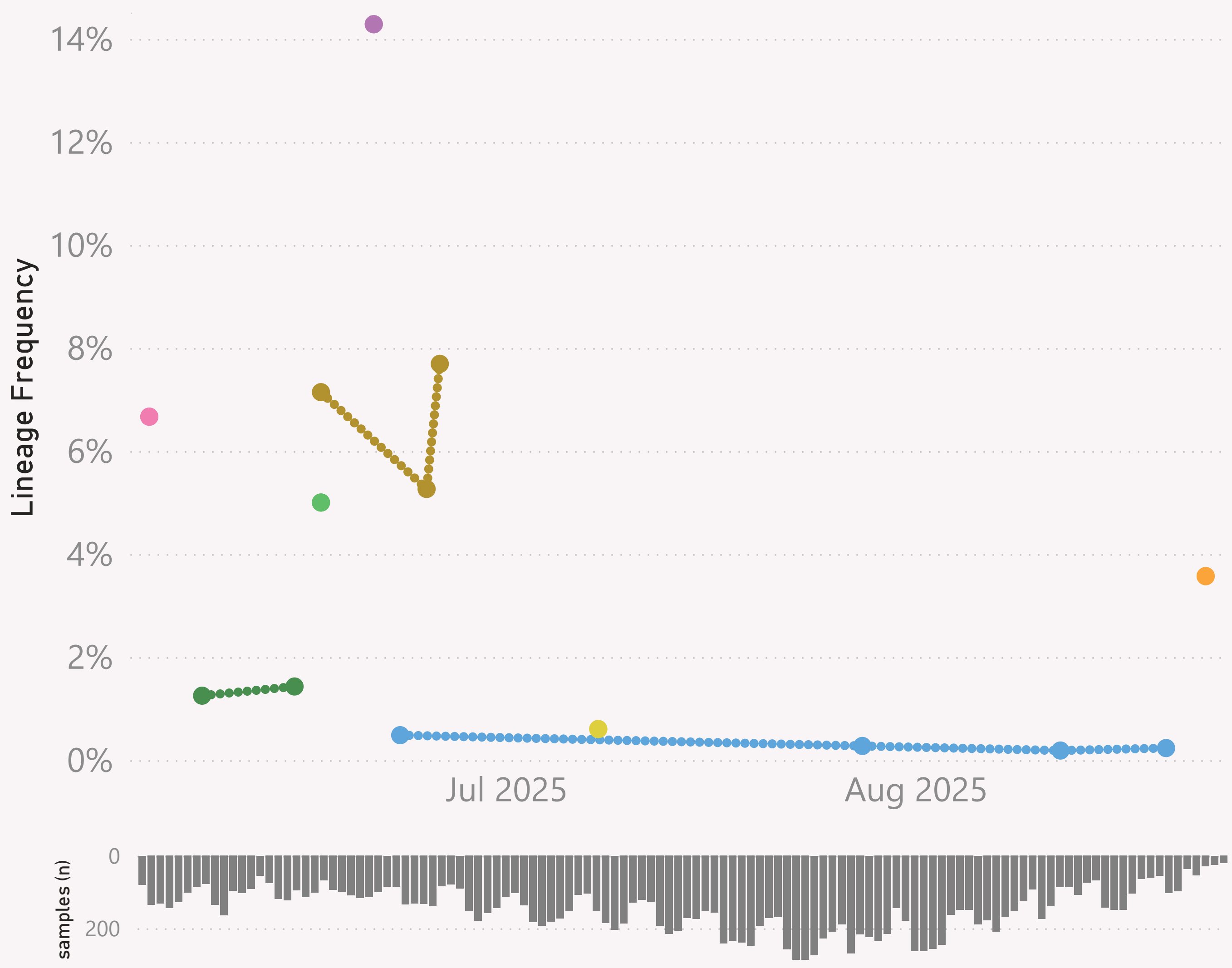
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=17,458 sequenced genomes, from 1 June 2025 up to 28 September 2025

XFP

●Califor... ●Illinois ●Intern... ●Massa... ●Michigan ●Minnes... ●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.

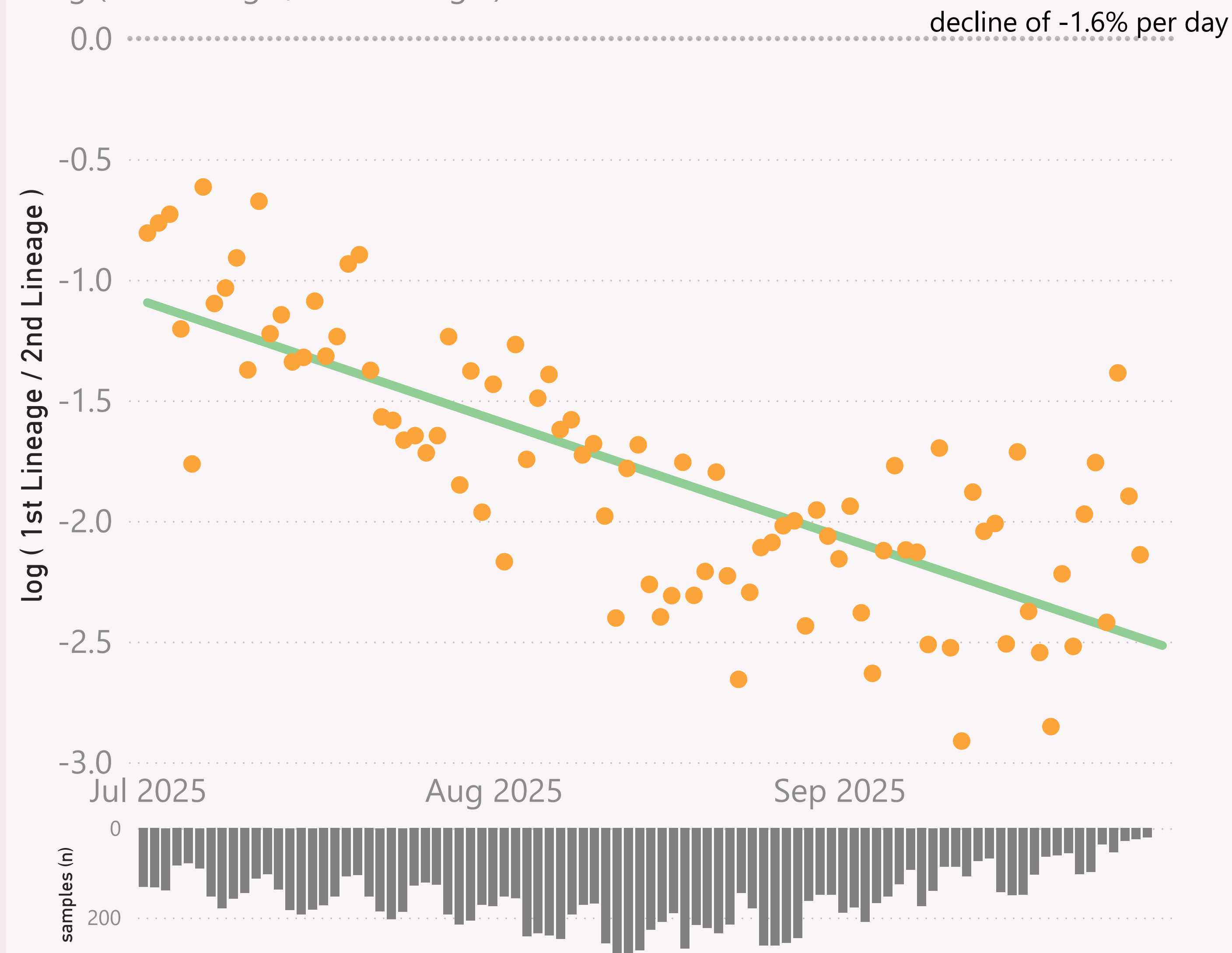
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=14,284 sequenced genomes, from 1 July 2025 up to 28 September 2025

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

● log (1st Lineage / 2nd 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.

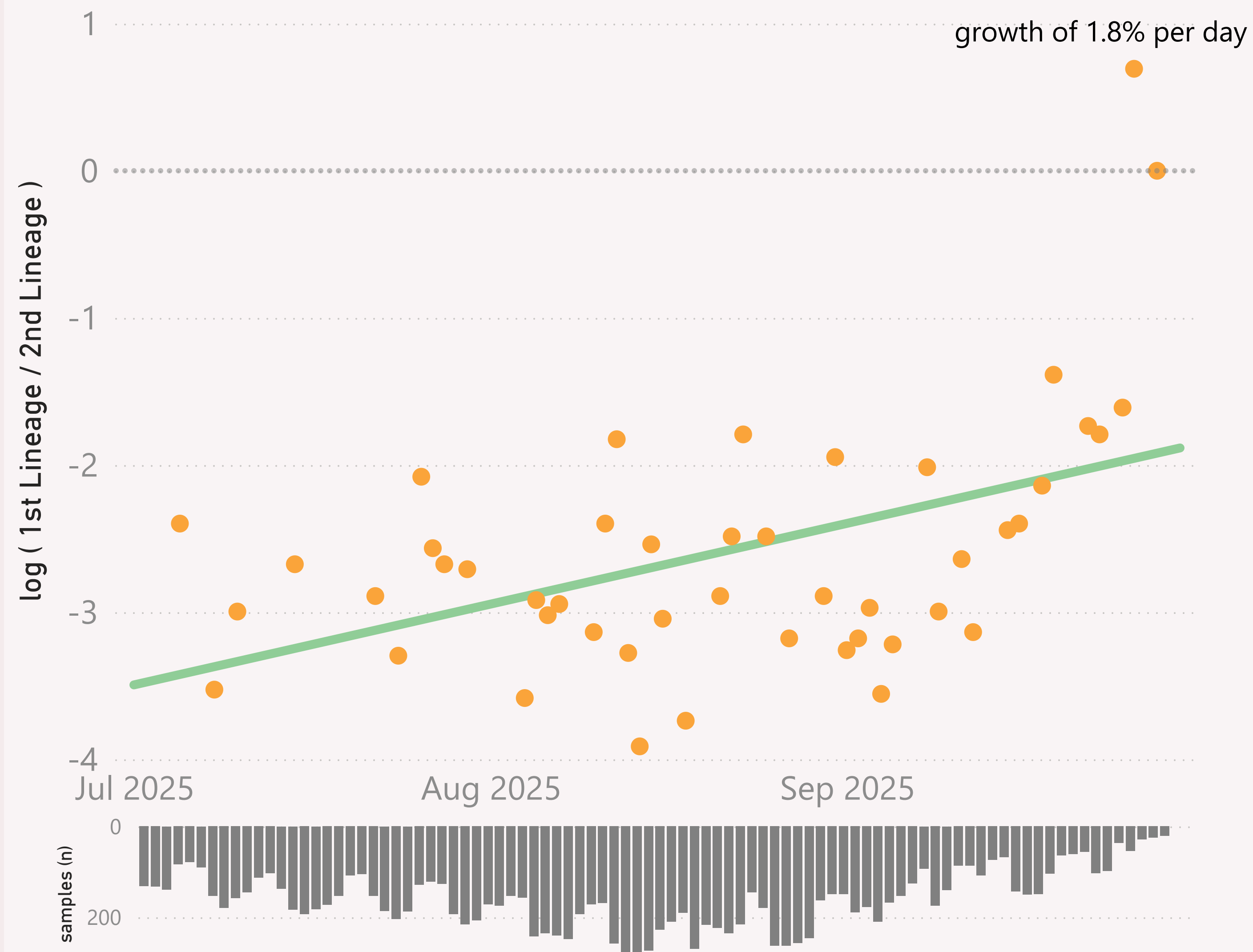
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=14,284 sequenced genomes, from 1 July 2025 up to 28 September 2025

United States - XFG.1.1 vs XFG.2

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



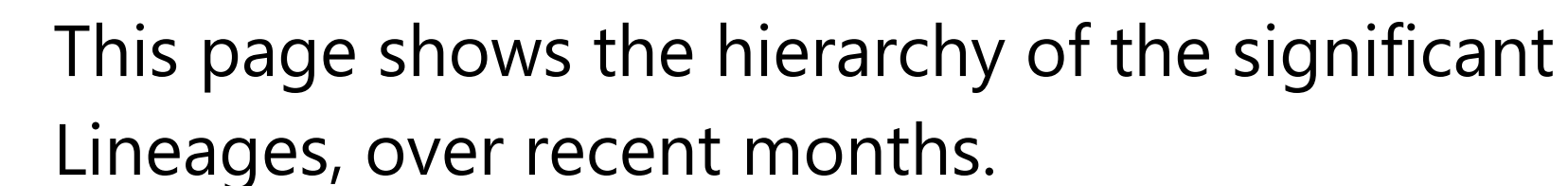
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

United States





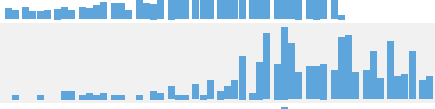

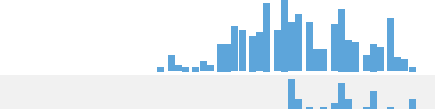

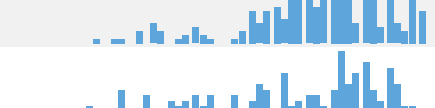

















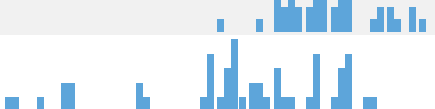



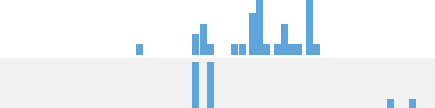




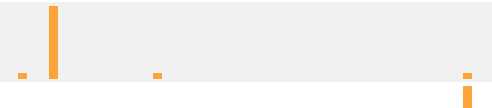
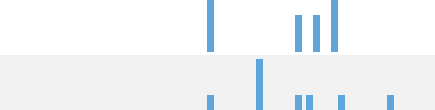
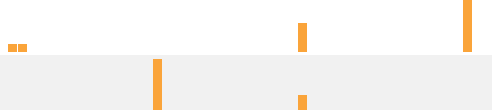



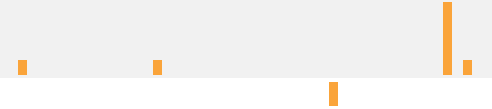


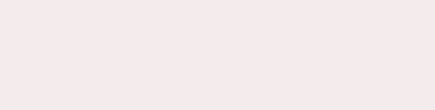
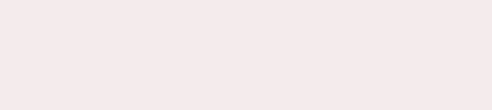
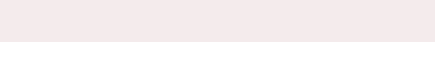
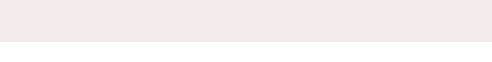


The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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>	12,549	28/09/2025		08/10/2025	
California	3,314	27/09/2025		08/10/2025	
Texas	3,010	03/09/2025		08/10/2025	
New York	1,174	28/09/2025		08/10/2025	
Colorado	1,100	23/09/2025		07/10/2025	
Minnesota	592	27/09/2025		08/10/2025	
Oregon	411	28/09/2025		08/10/2025	
Arizona	378	28/09/2025		08/10/2025	
Utah	345	25/09/2025		08/10/2025	
Massachusetts	260	25/09/2025		08/10/2025	
International Travellers	255	28/09/2025		07/10/2025	
Illinois	241	26/09/2025		08/10/2025	
Maryland	224	20/09/2025		08/10/2025	
Nebraska	208	23/09/2025		06/10/2025	
Connecticut	204	28/09/2025		08/10/2025	
New Jersey	174	28/09/2025		08/10/2025	
Hawaii	154	24/09/2025		08/10/2025	
Nevada	104	27/09/2025		08/10/2025	
Michigan	92	22/09/2025		06/10/2025	
New Mexico	88	08/09/2025		08/10/2025	
Virginia	62	09/09/2025		08/10/2025	
Alaska	25	25/09/2025		08/10/2025	
Washington	25	25/08/2025		22/09/2025	
Florida	17	04/08/2025		08/10/2025	
Georgia	16	09/09/2025		08/10/2025	
North Dakota	12	17/09/2025		06/10/2025	
Pennsylvania	10	15/09/2025		06/10/2025	
Oklahoma	8	12/09/2025		08/10/2025	
Total	12,549	28/09/2025		08/10/2025	

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.