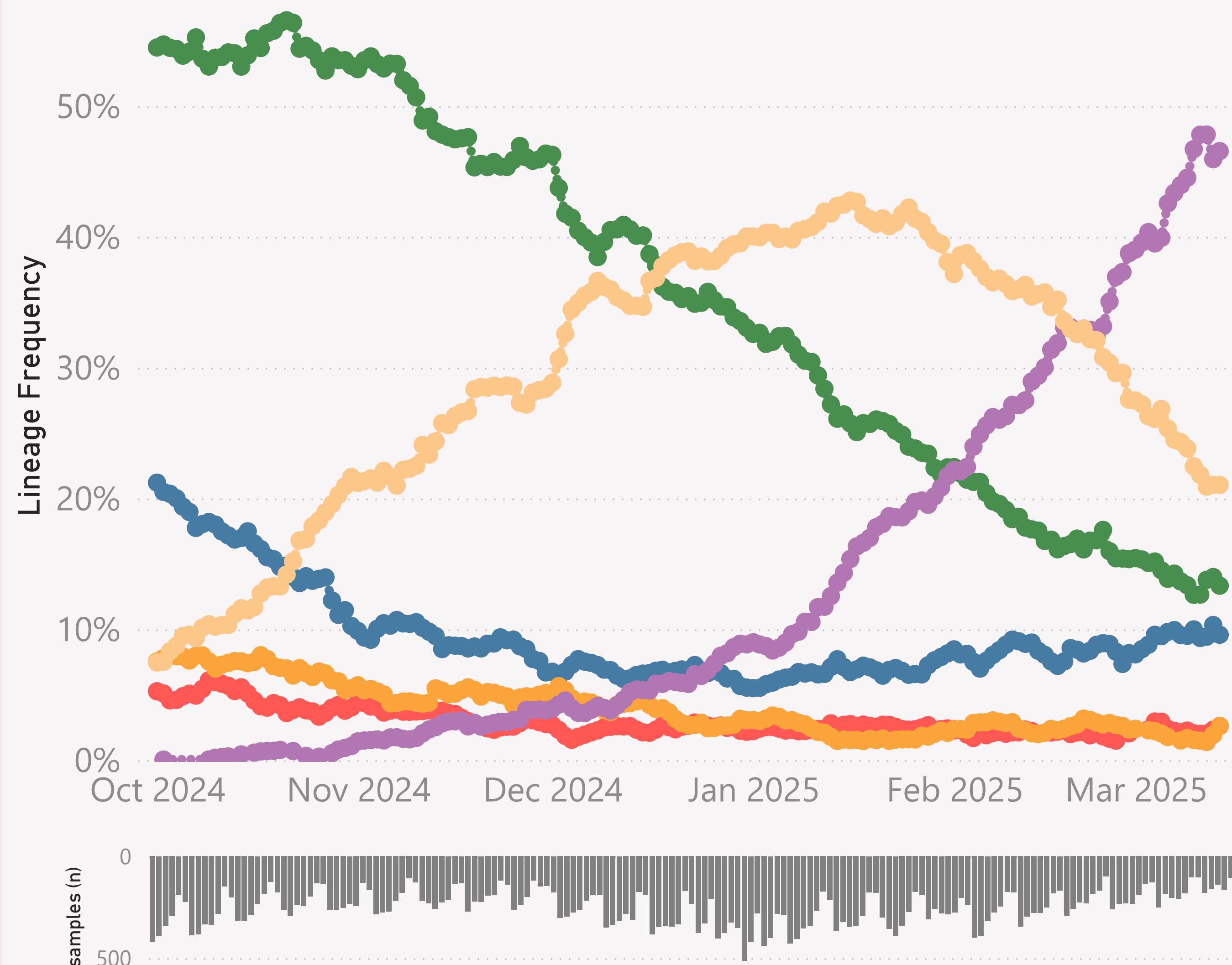


n=41,873 sequenced genomes, up to 14 March 2025

United States

● BA.2.86.* ● JN.1.* + DeFLuQE ● JN.1.* + FLiRT ● JN.1.* + FLuQE ● LP.8.1.* ● XEC.*



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

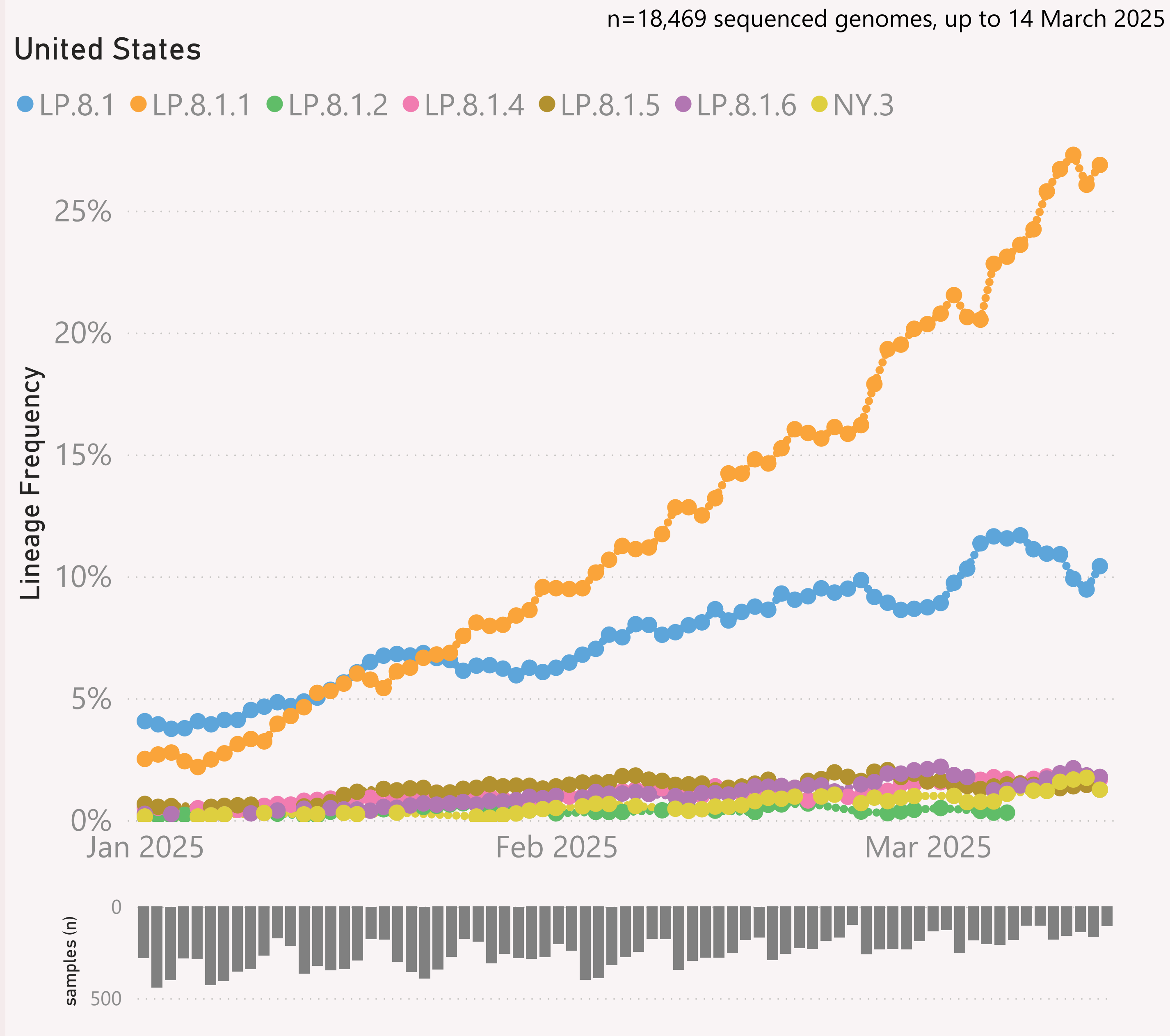
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



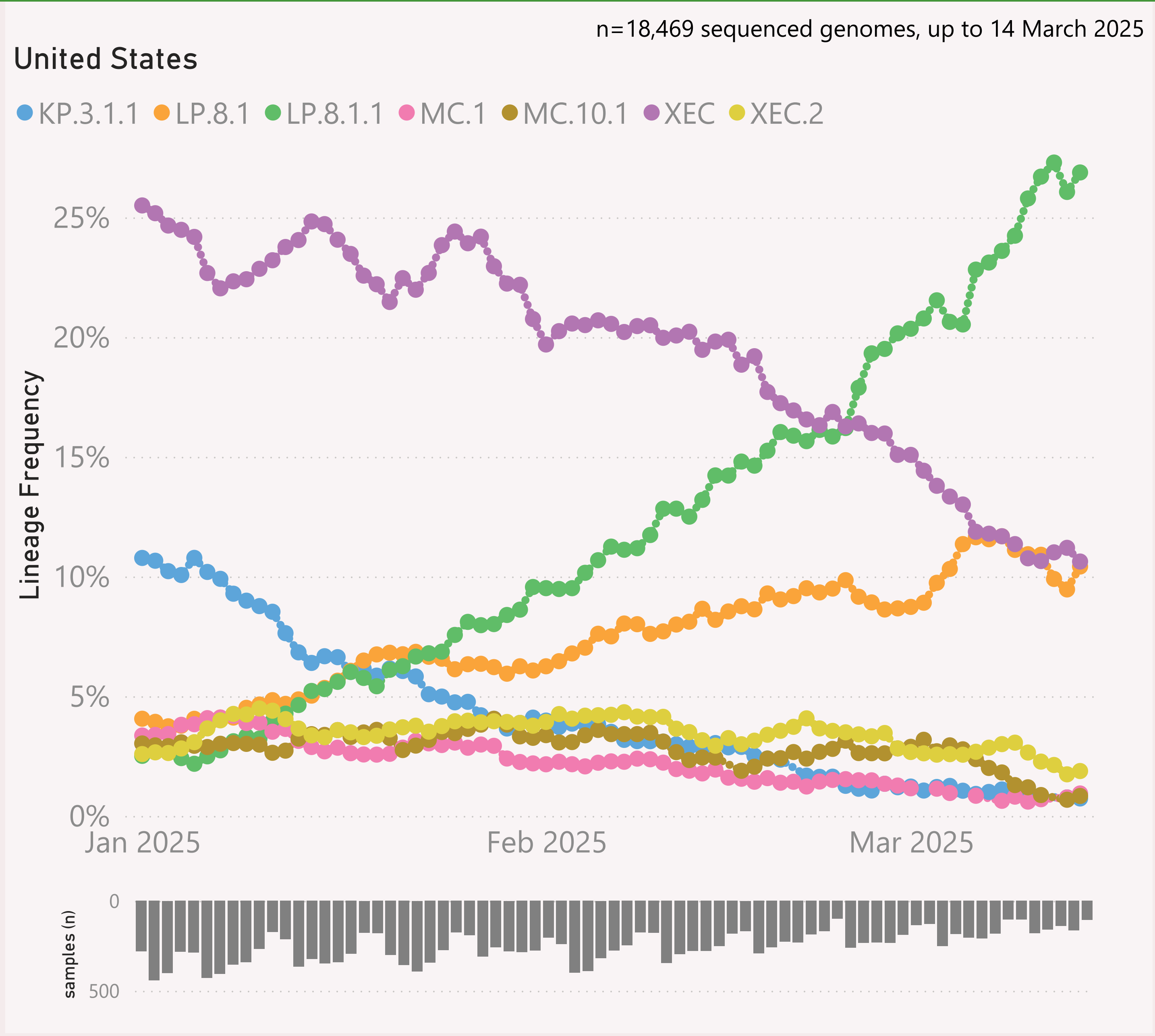
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "LP.8.1.*".

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.



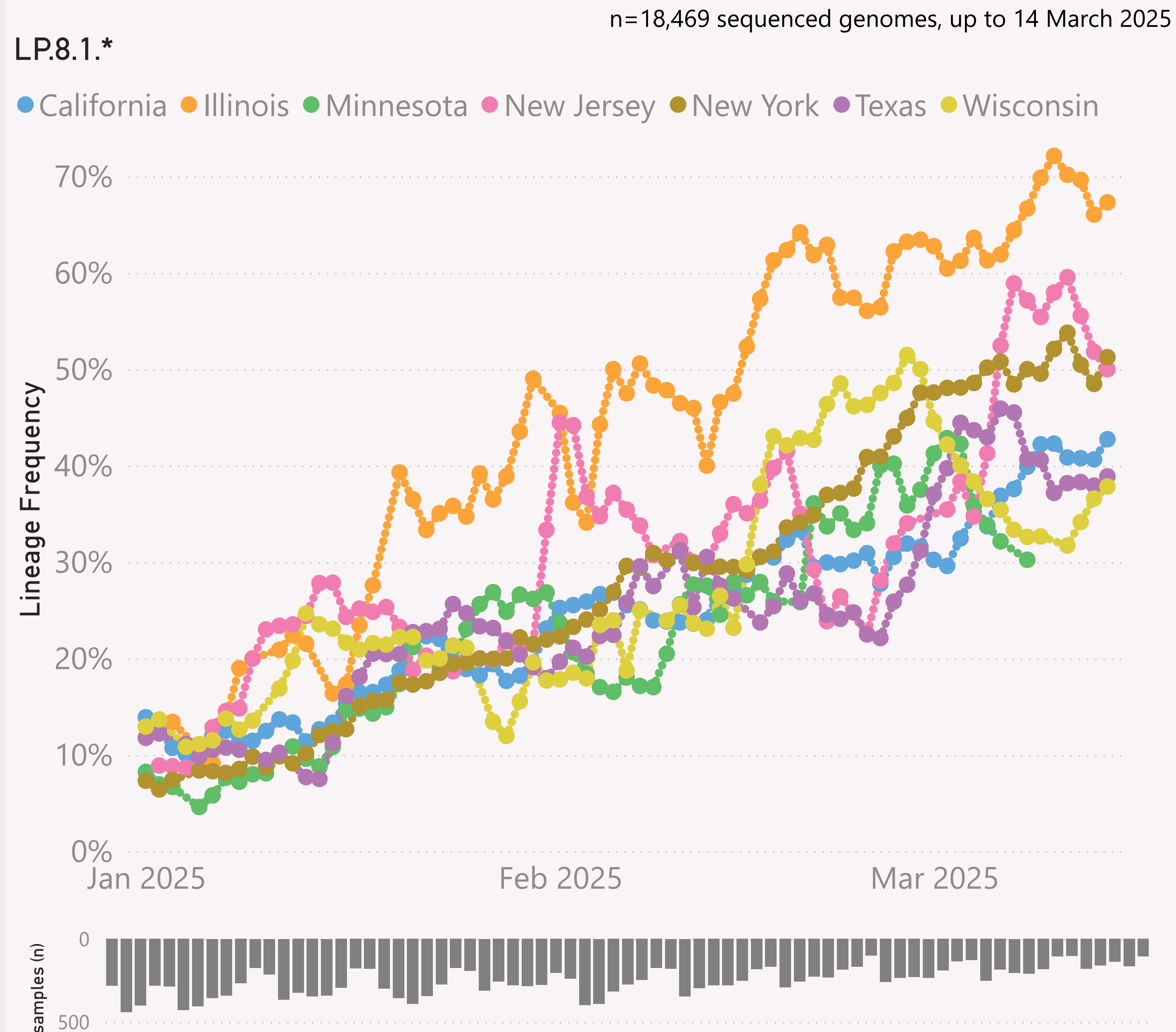
This page shows the frequency of the top 7 lineages, across recent months.

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.



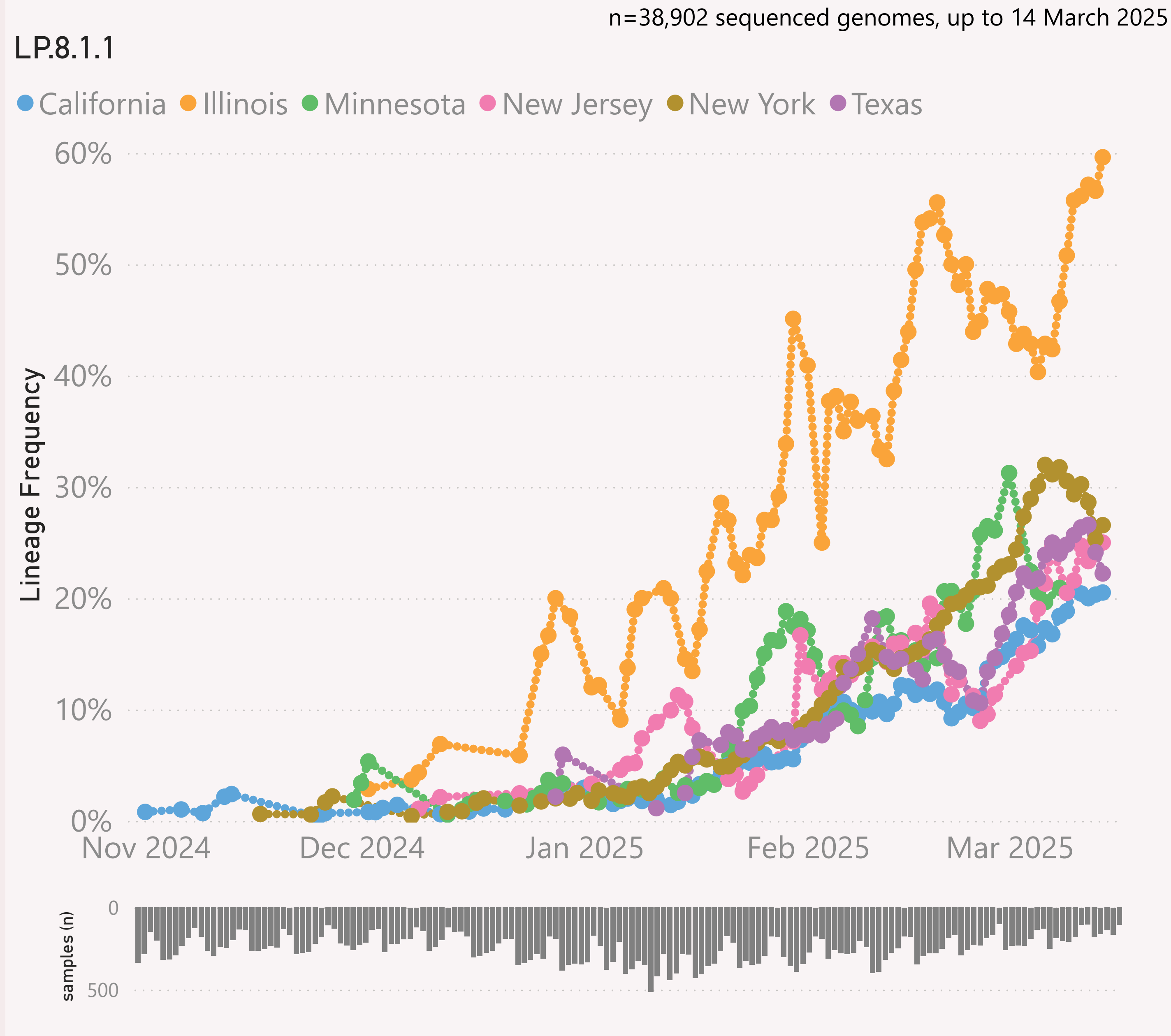
This page shows the frequency of a selected "Lineage L2" group of interest, across the leading States, over recent months.

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.



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.

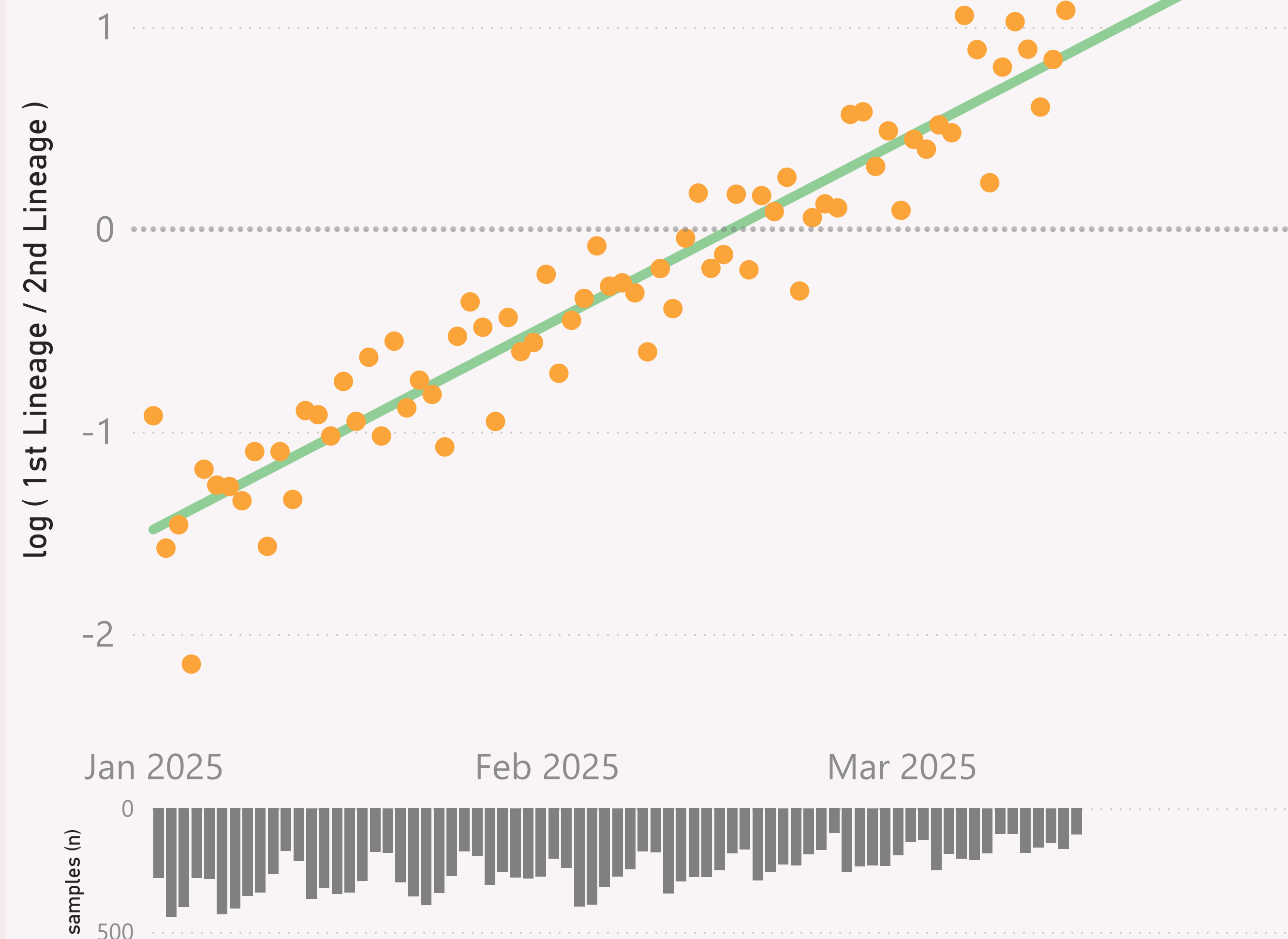
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

United States - LP.8.1.* vs XEC.*

n=18,469 sequenced genomes, up to 14 March 2025

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

growth of 3.3% per day, crossover on 16-Feb-25



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.

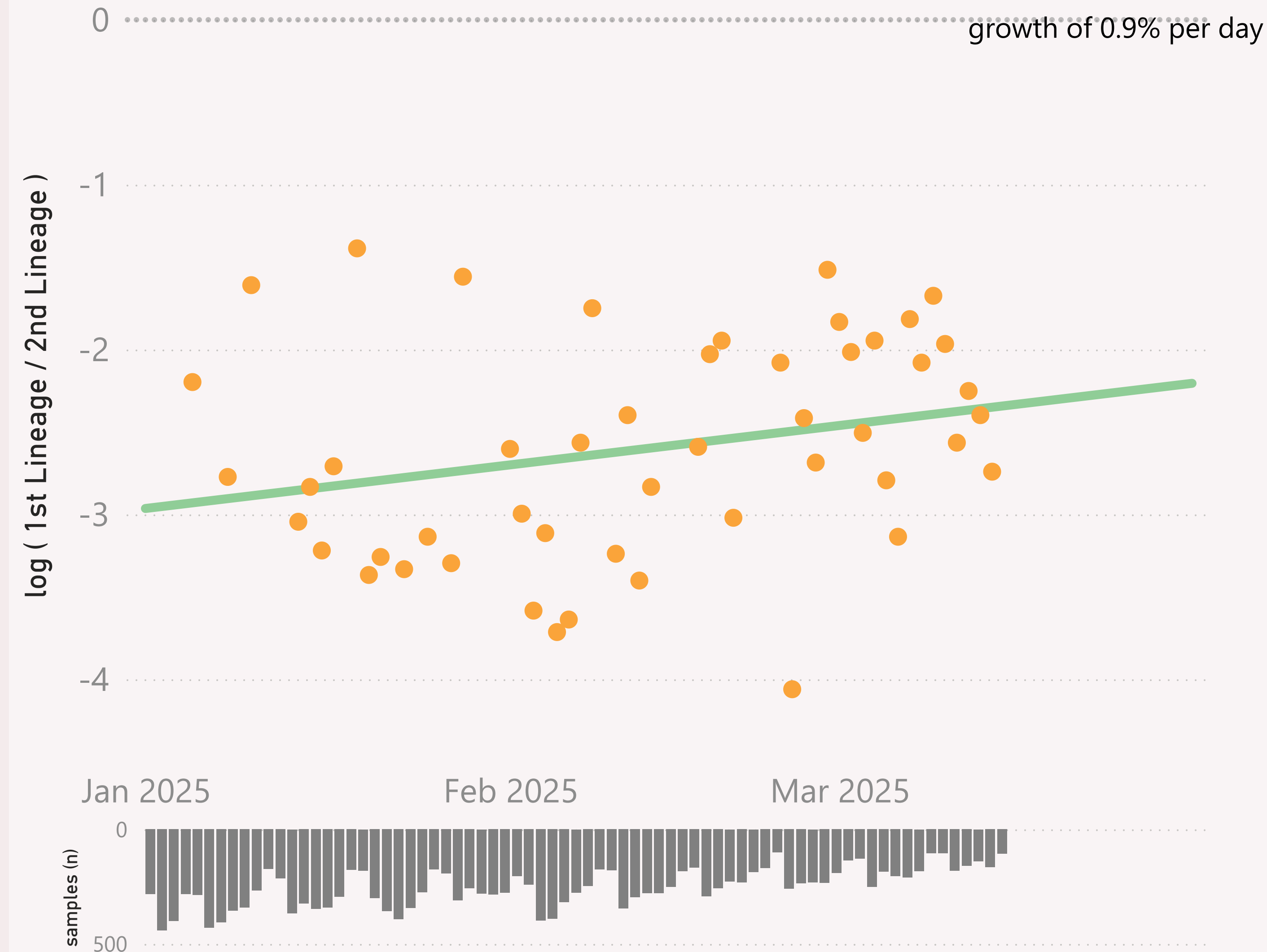
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=18,469 sequenced genomes, up to 14 March 2025

United States - LF.7.7.2 vs LP.8.1.1

● $\log (1st\ Lineage / 2nd\ Lineage)$ ● 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

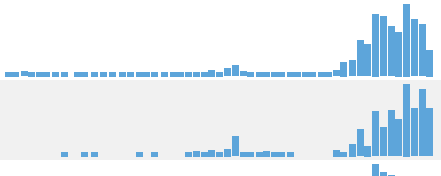
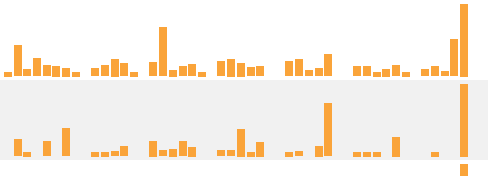
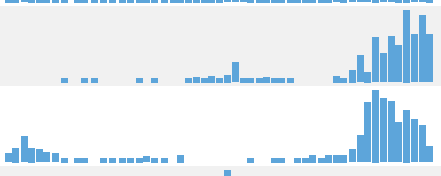
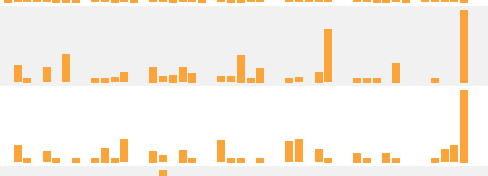
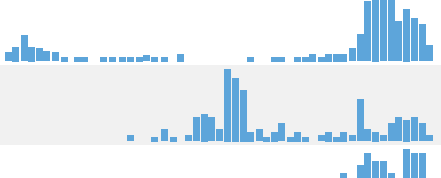
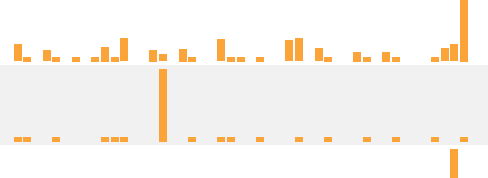
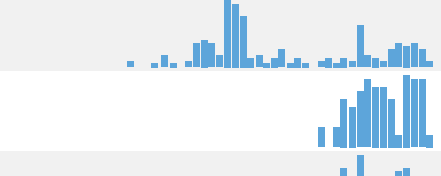
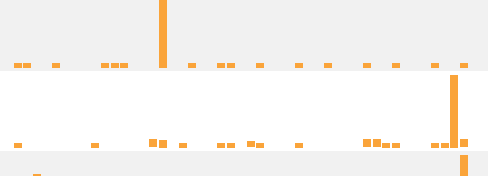
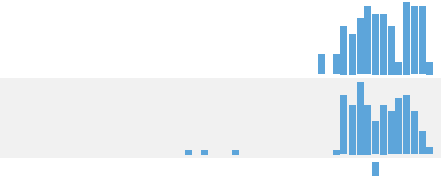
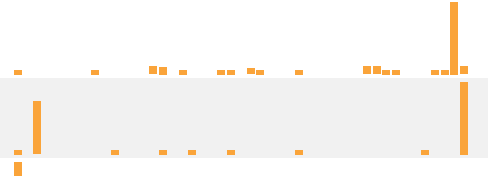
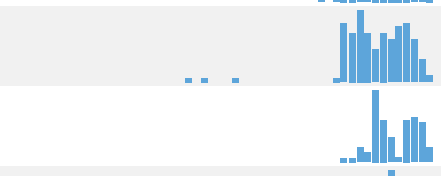

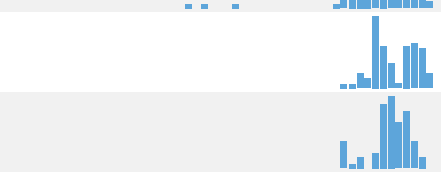
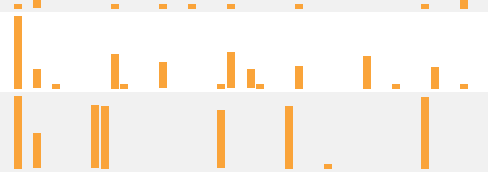
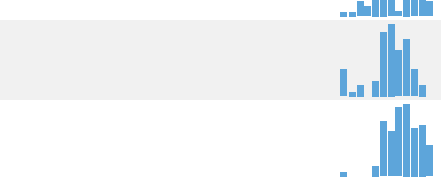

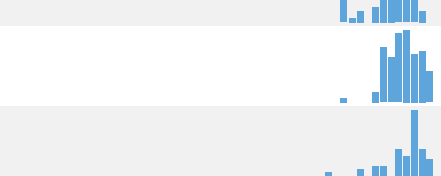
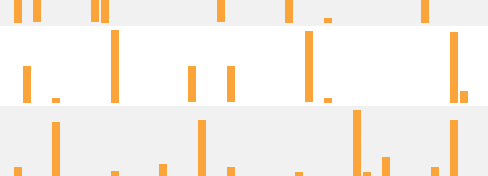
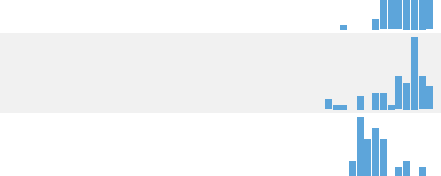

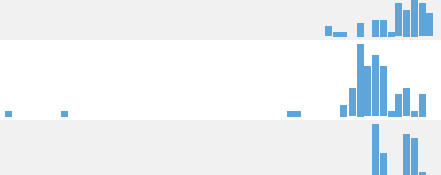
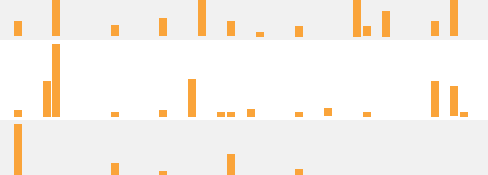
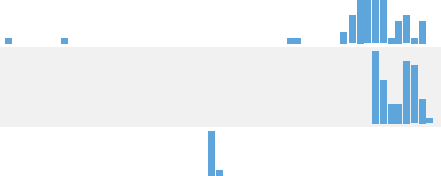

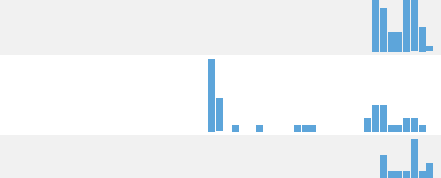
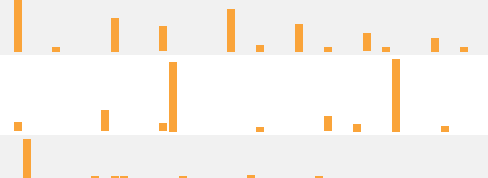
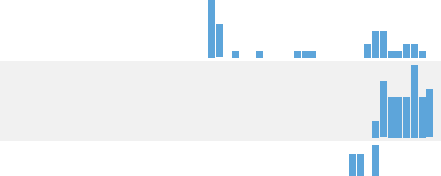

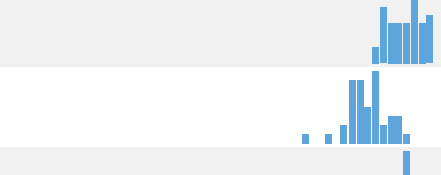
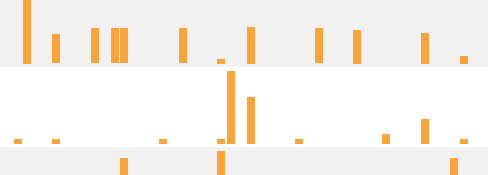
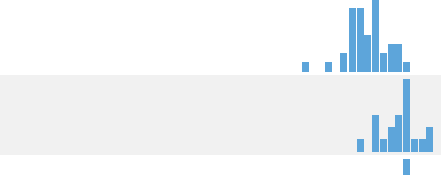
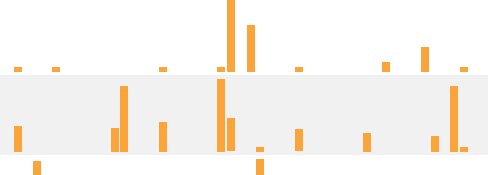
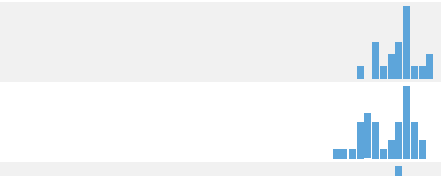

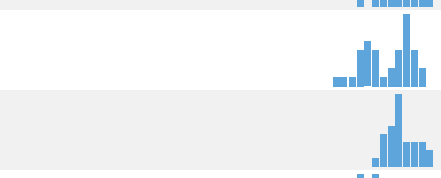



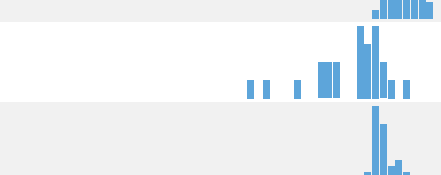

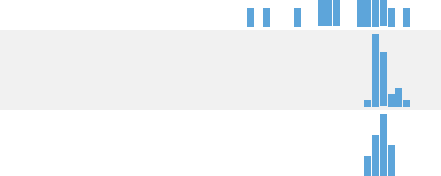
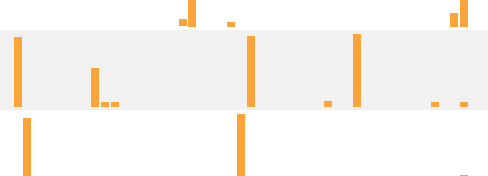
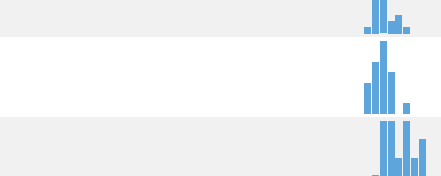
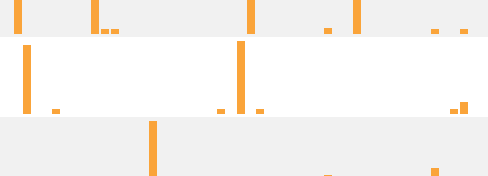
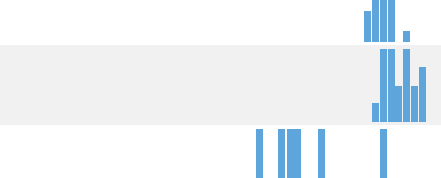


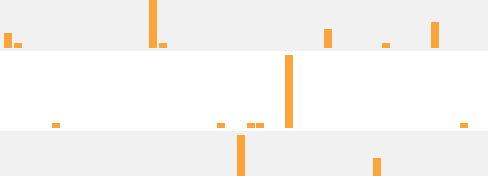


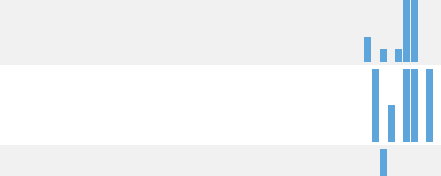
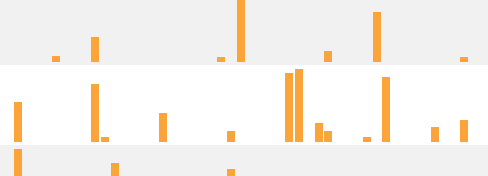
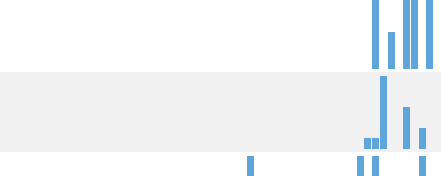
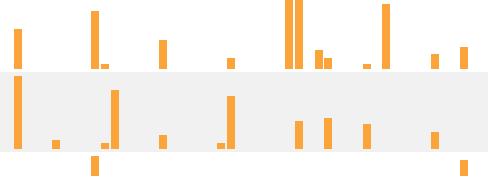
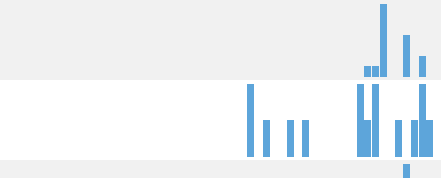

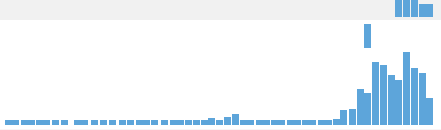
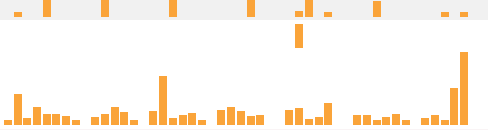


The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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>	19,726	14/03/2025		28/03/2025	
New York	3,782	14/03/2025		28/03/2025	
California	3,576	14/03/2025		28/03/2025	
Virginia	1,671	14/03/2025		28/03/2025	
Texas	1,314	14/03/2025		28/03/2025	
Wisconsin	1,167	14/03/2025		28/03/2025	
New Jersey	930	14/03/2025		28/03/2025	
Minnesota	880	09/03/2025		24/03/2025	
Colorado	865	14/03/2025		28/03/2025	
Illinois	661	14/03/2025		27/03/2025	
Massachusetts	597	12/03/2025		28/03/2025	
Pennsylvania	432	14/03/2025		28/03/2025	
Michigan	418	06/03/2025		26/03/2025	
Nebraska	319	14/03/2025		28/03/2025	
New Mexico	302	03/03/2025		28/03/2025	
Maryland	240	14/03/2025		28/03/2025	
District of Columbia	221	13/03/2025		28/03/2025	
Delaware	213	14/03/2025		28/03/2025	
Kentucky	191	05/03/2025		28/03/2025	
Connecticut	184	12/03/2025		28/03/2025	
Rhode Island	164	12/03/2025		28/03/2025	
Louisiana	152	13/03/2025		25/03/2025	
North Dakota	130	27/02/2025		28/03/2025	
Utah	124	03/03/2025		28/03/2025	
Arizona	115	14/03/2025		28/03/2025	
North Carolina	114	13/03/2025		25/03/2025	
Hawaii	105	14/03/2025		28/03/2025	
Iowa	101	14/03/2025		28/03/2025	
Total	19,726	14/03/2025		28/03/2025	

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.