

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.

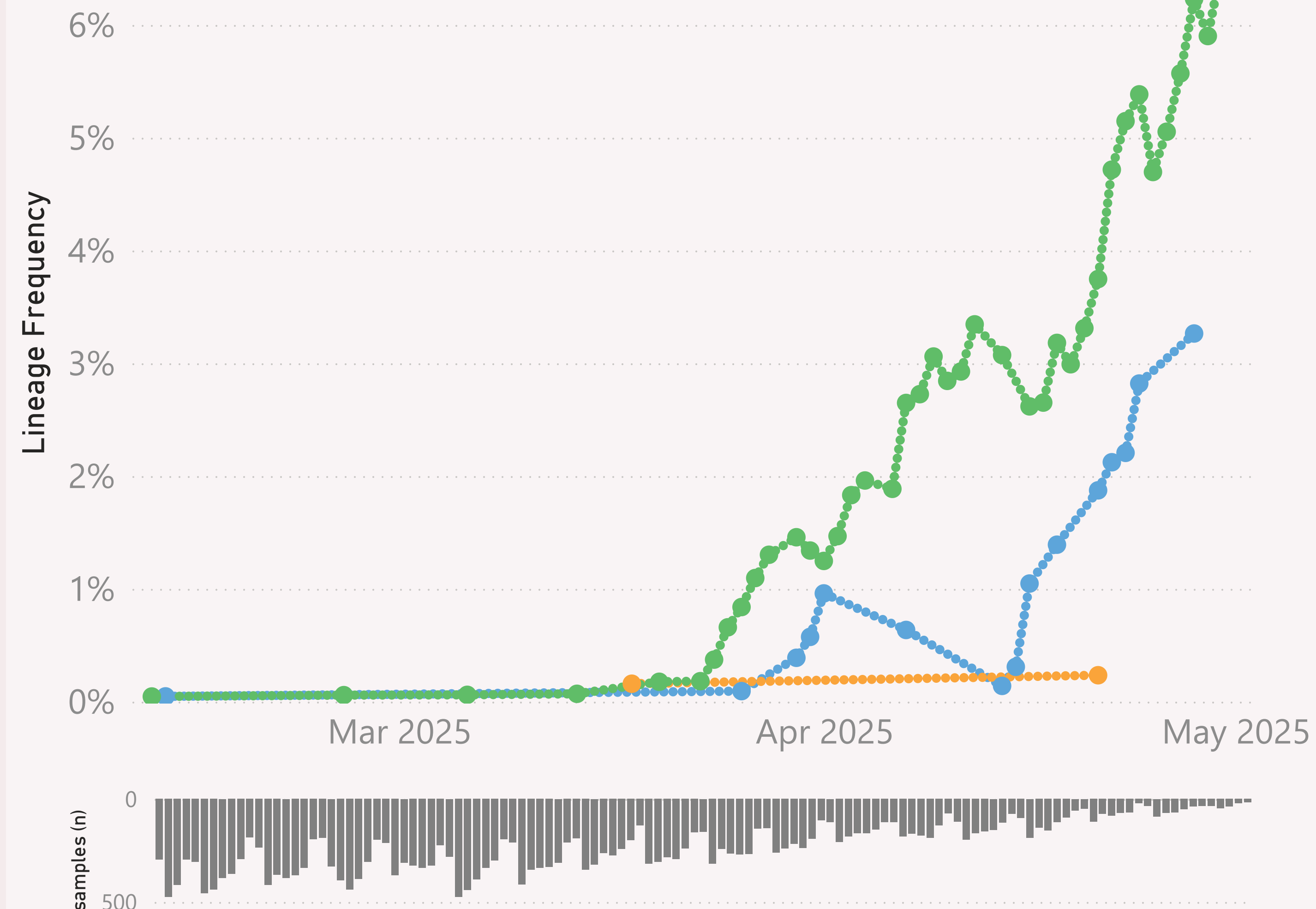
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

United States

● XFG ● XFG.1 ● XFG.2

n=26,693 sequenced genomes, up to 1 May 2025



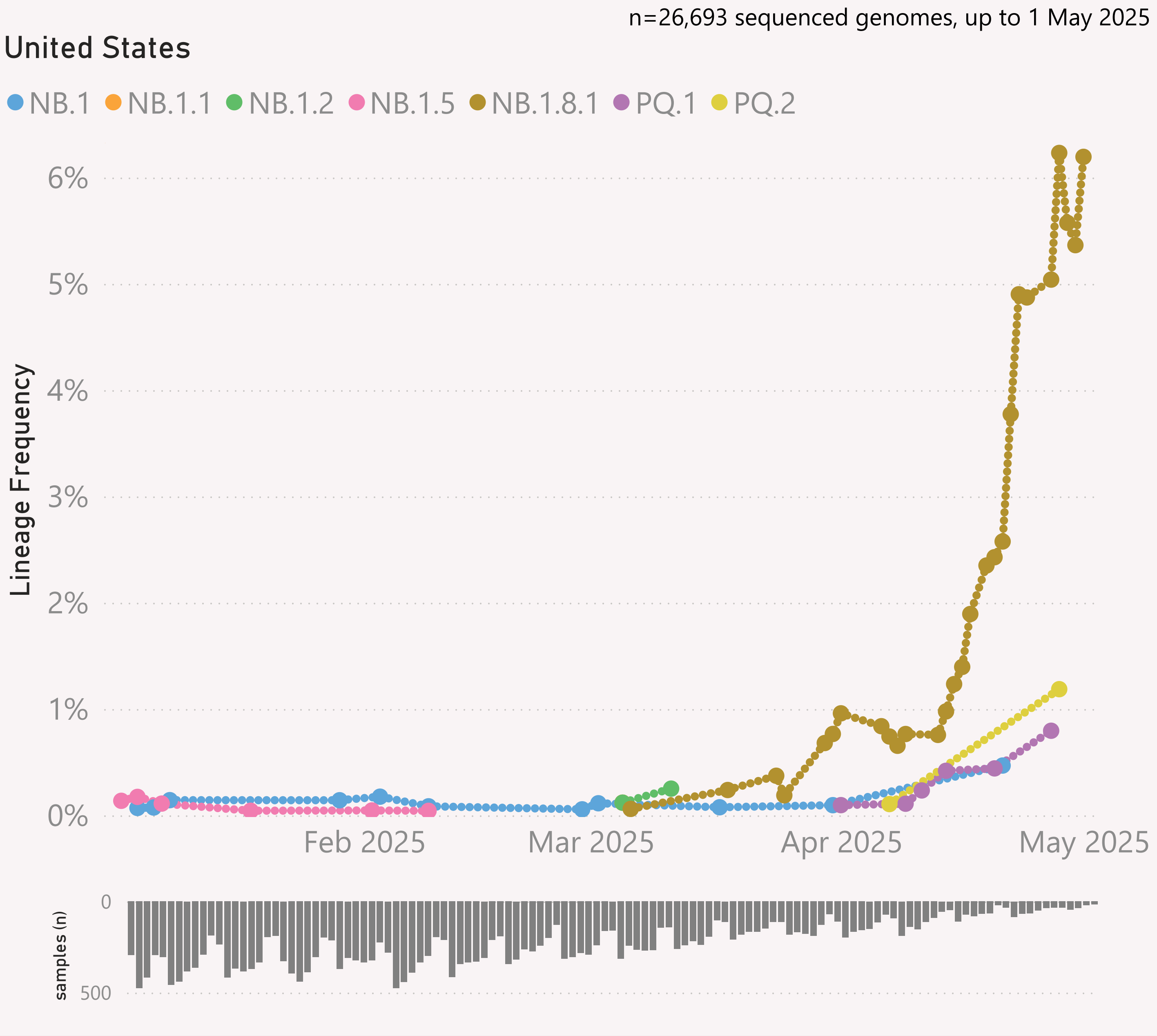
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "XFG.*".

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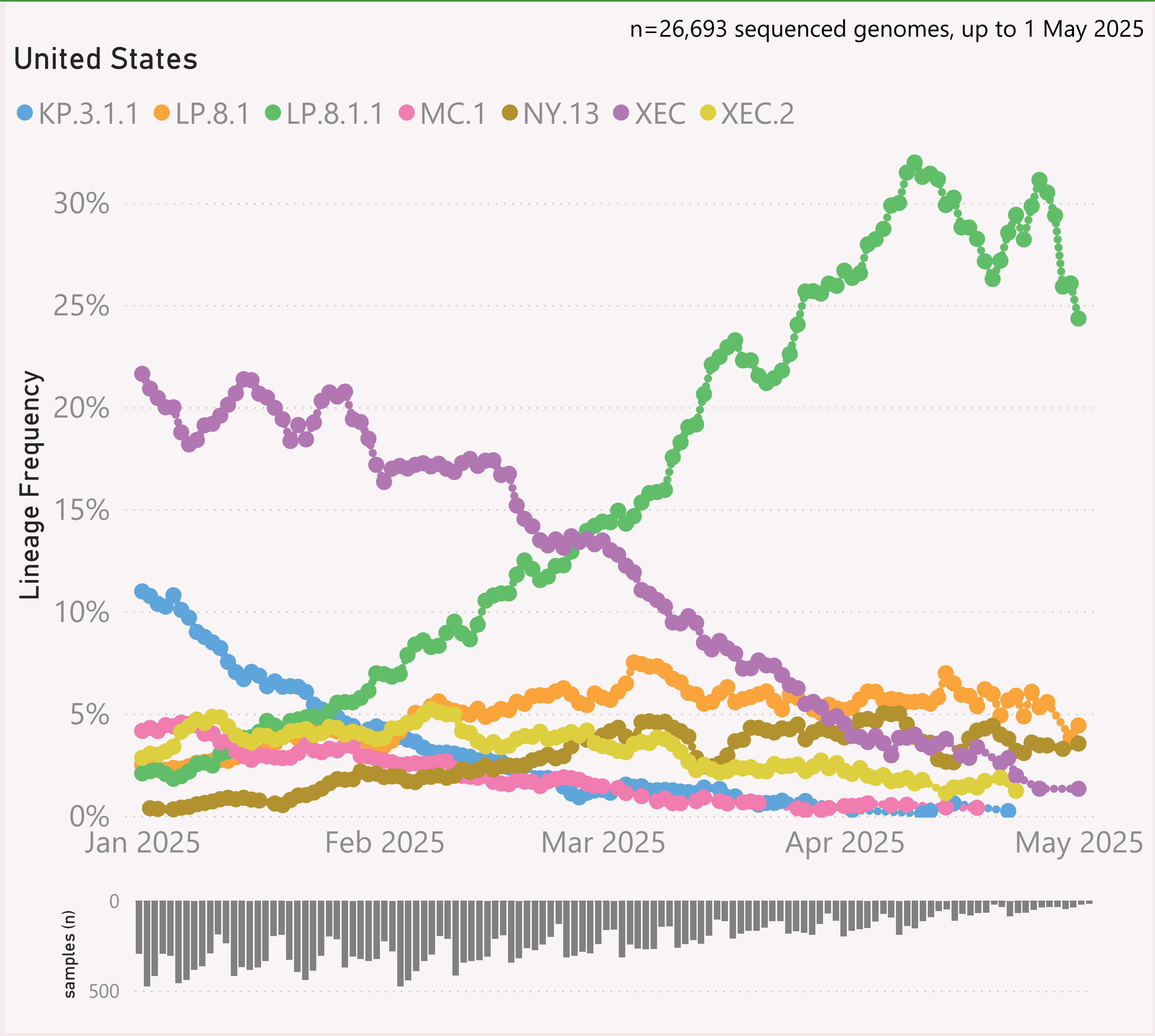
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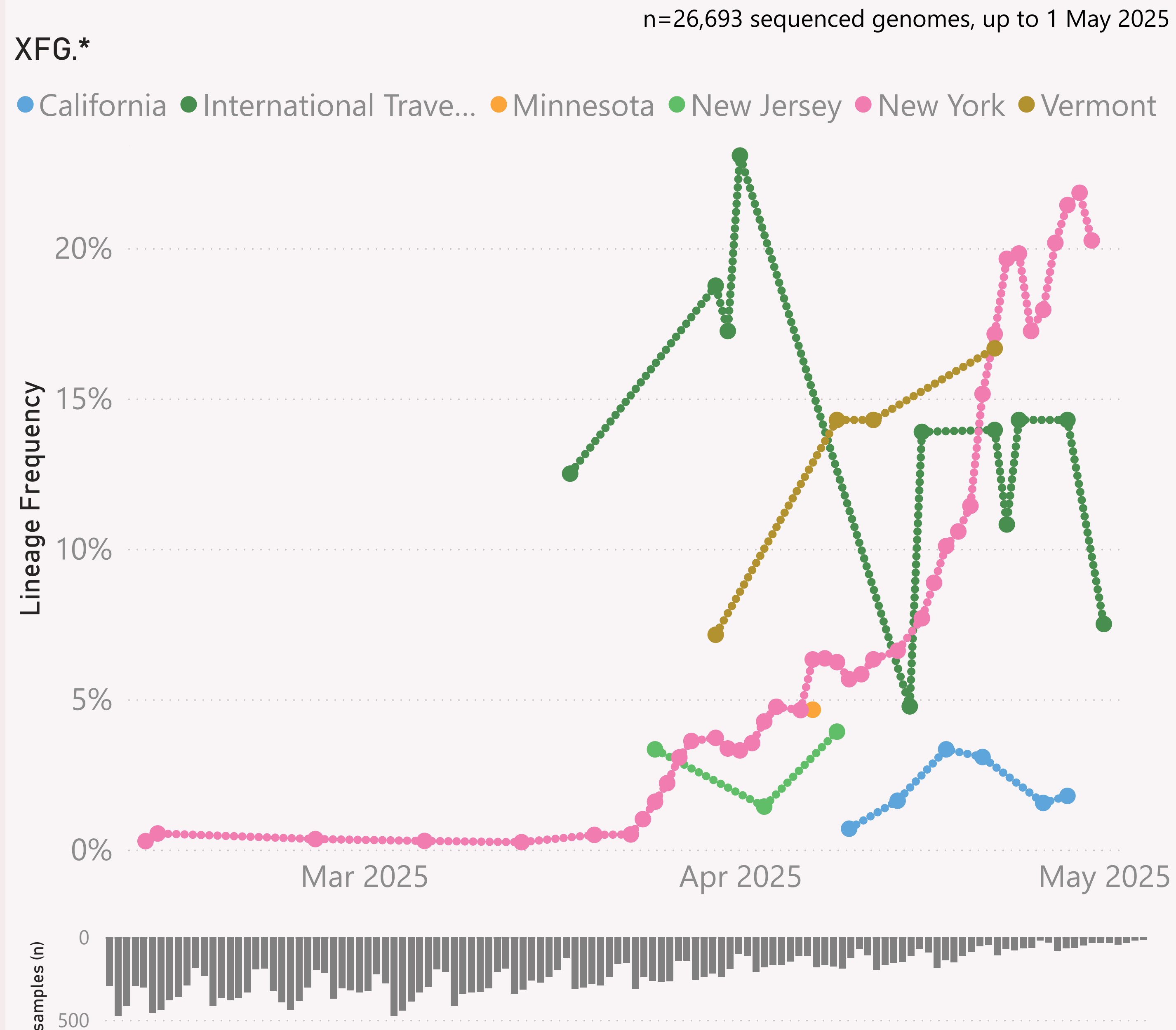
This page shows the frequency of the top 7 lineages, across recent months.

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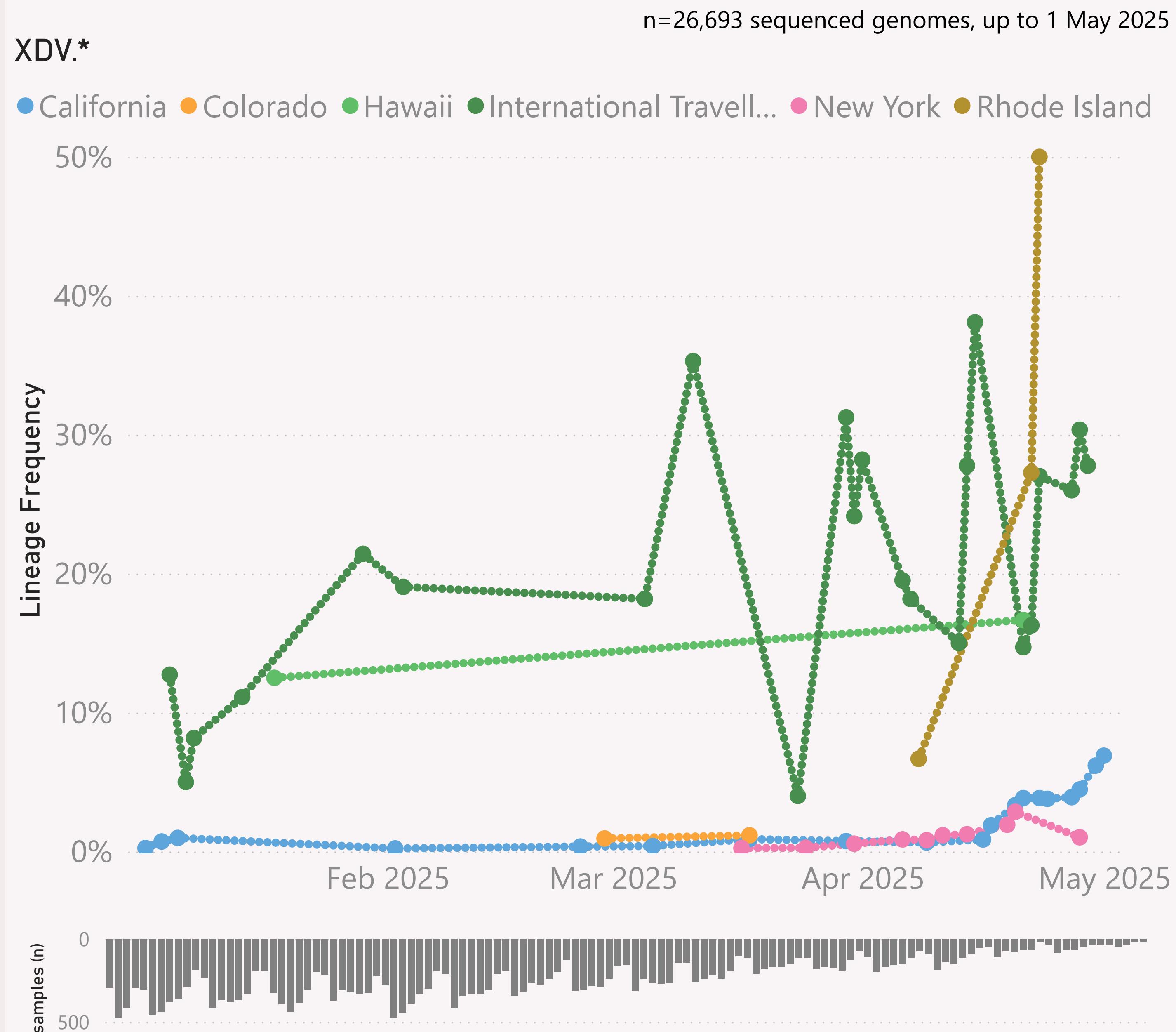
This page shows the frequency of a selected "Lineage L2" group of interest, across the leading States, over recent months.

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

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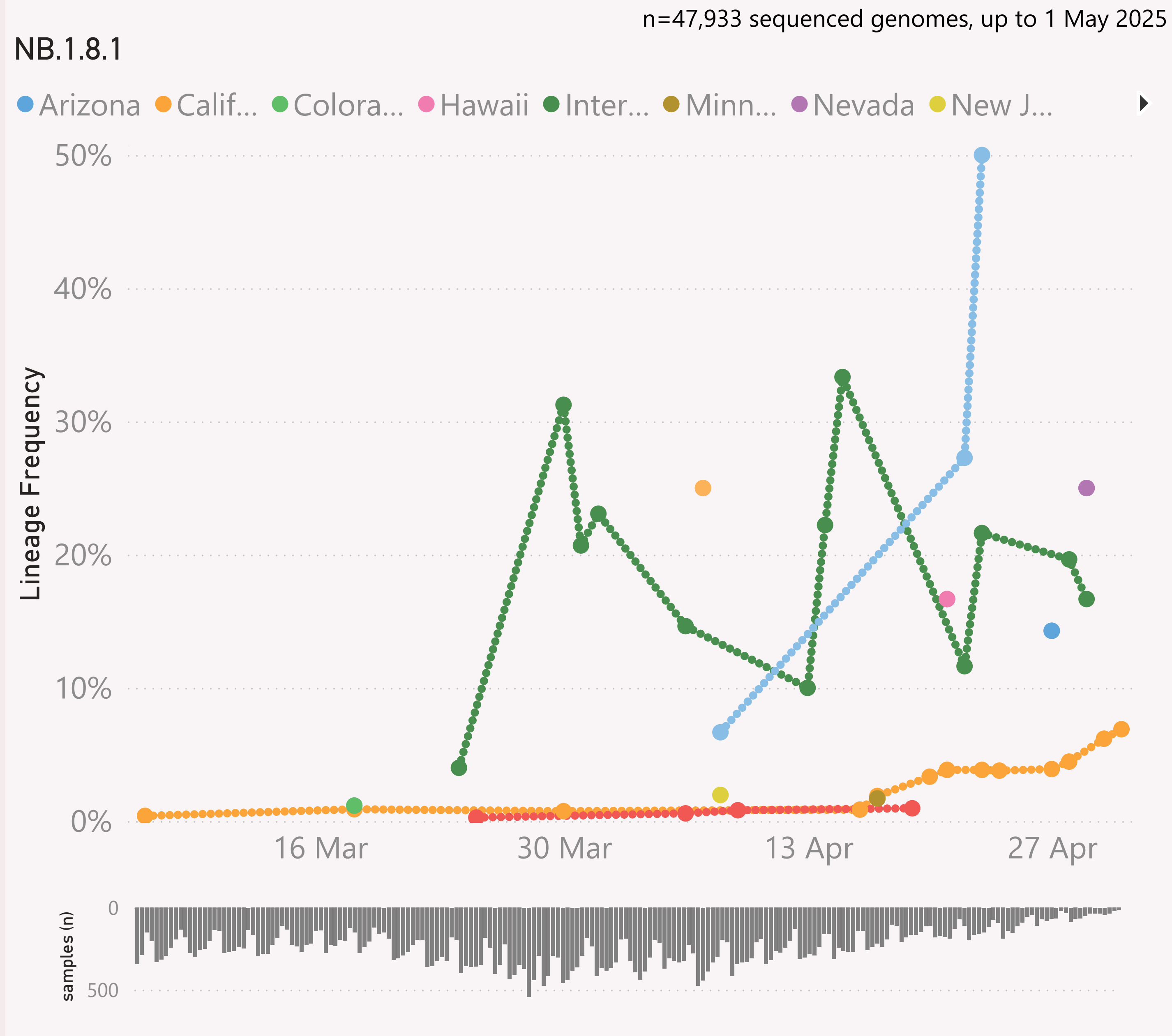
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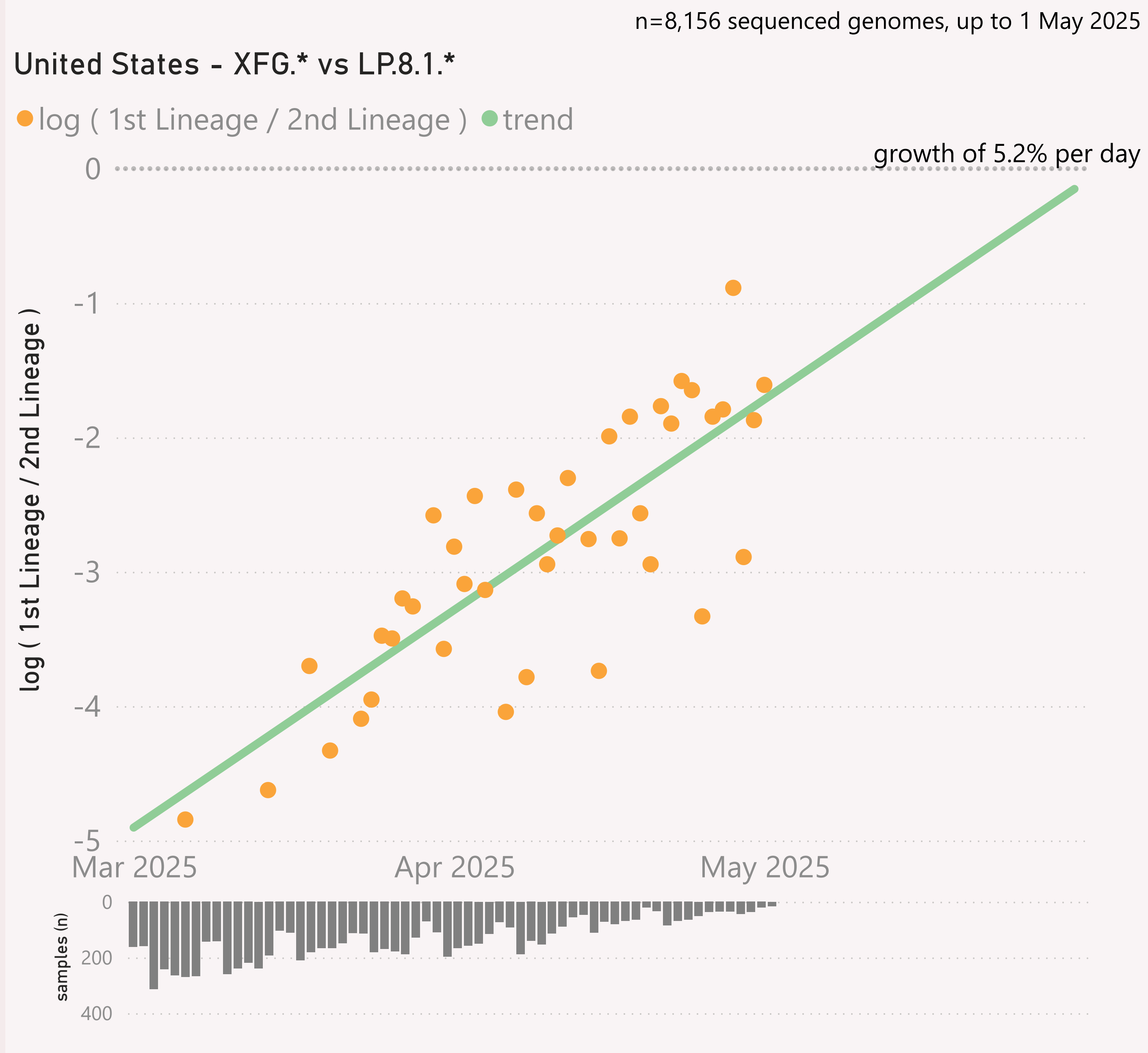
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The frequency shown at each point is based on the 7-day rolling average across all lineages, for that state.

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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.

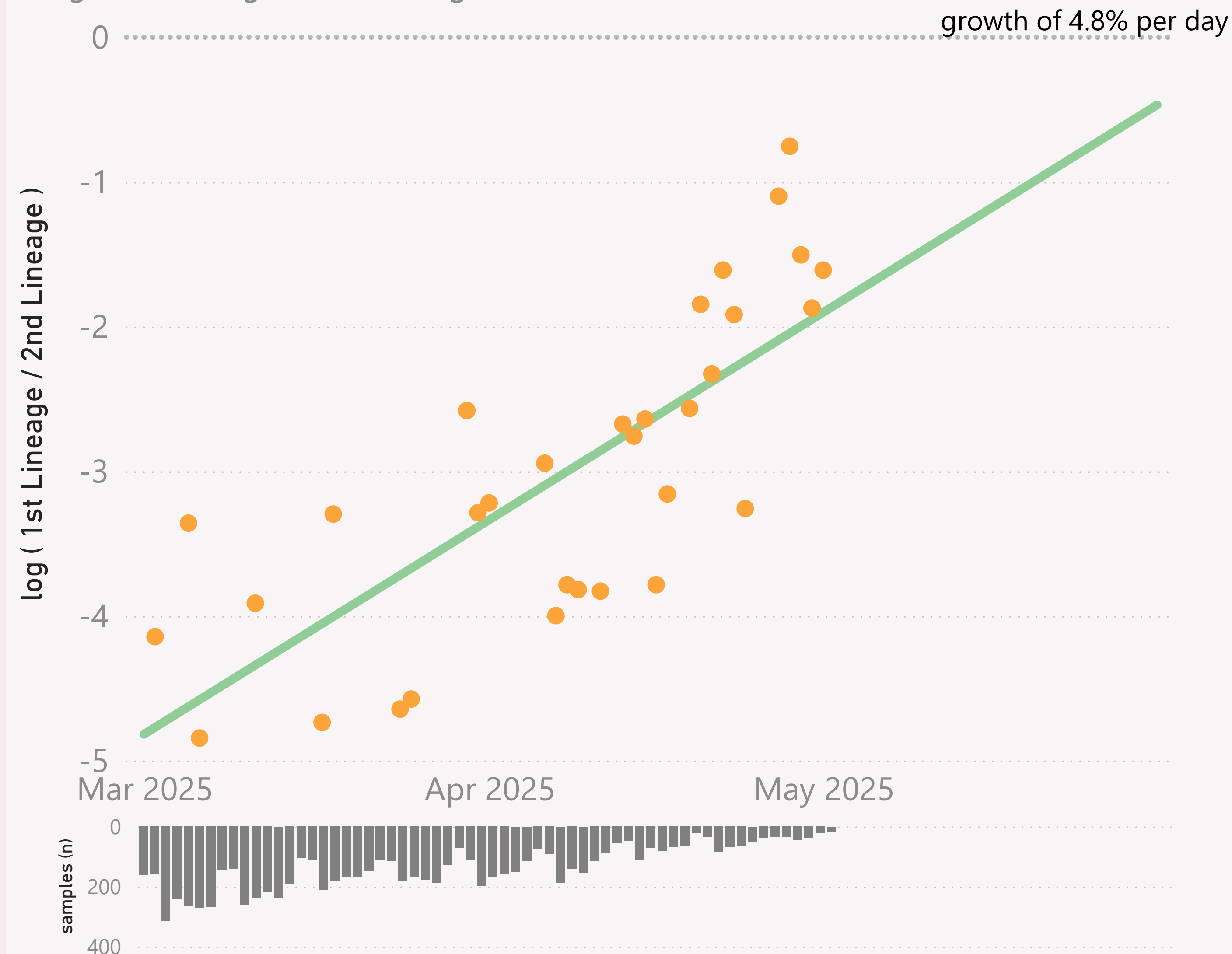
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=8,156 sequenced genomes, up to 1 May 2025

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

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

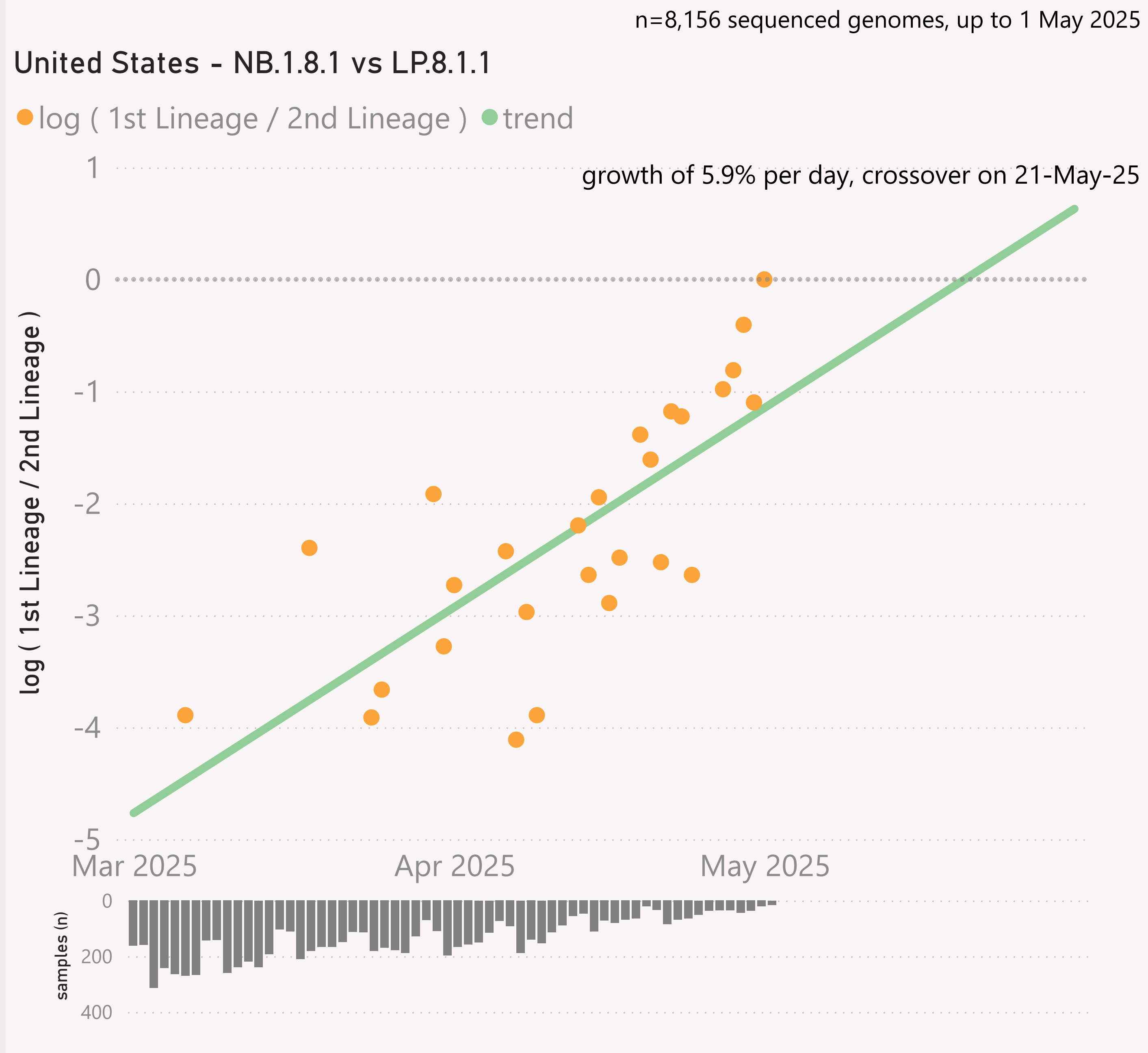


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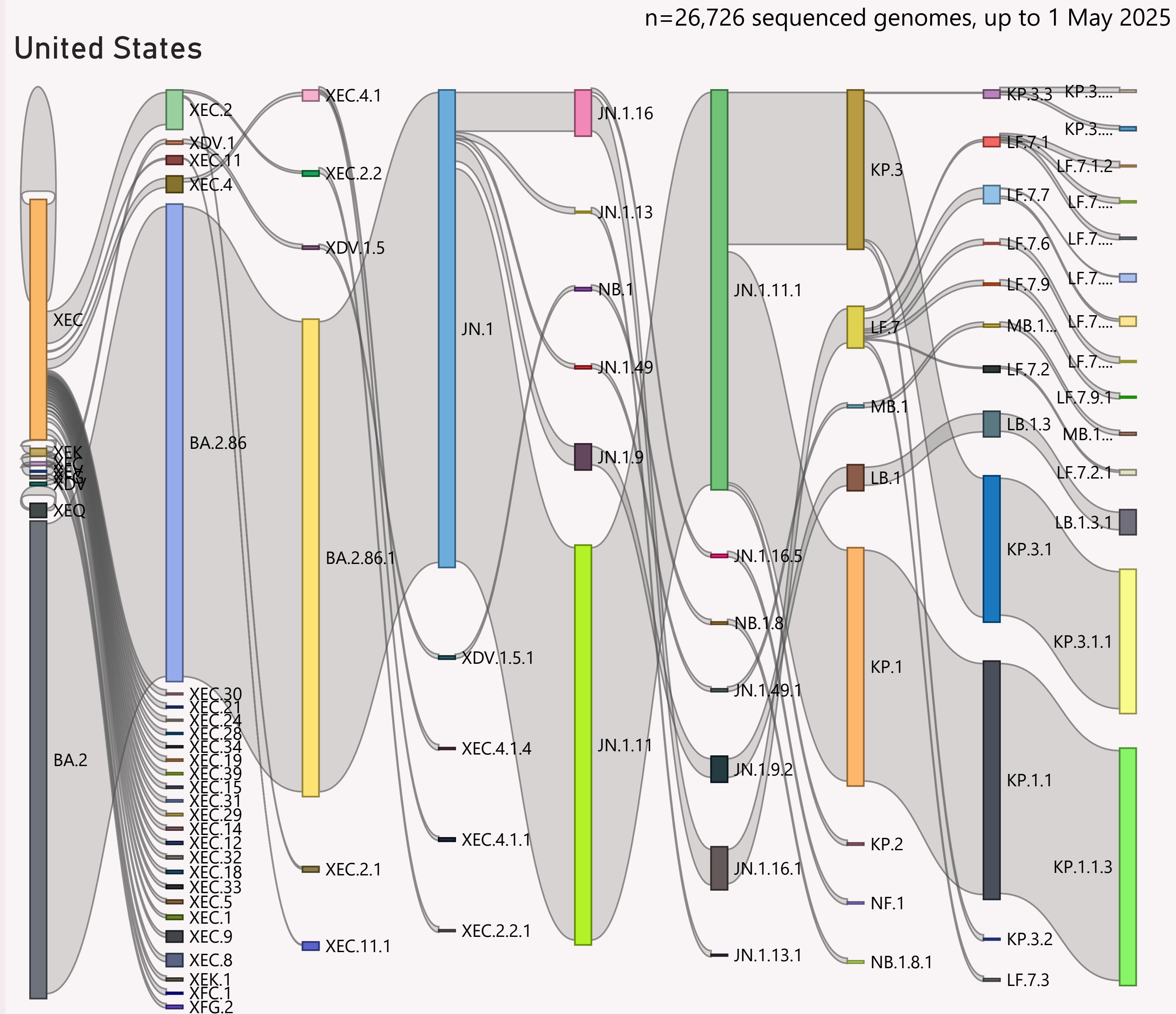


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

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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>	10,902	01/05/2025		02/05/2025	
California	2,700	01/05/2025		02/05/2025	
New York	2,331	01/05/2025		02/05/2025	
Illinois	1,095	23/04/2025		02/05/2025	
Michigan	559	28/04/2025		02/05/2025	
Wisconsin	533	10/04/2025		01/05/2025	
Minnesota	437	22/04/2025		02/05/2025	
Colorado	360	27/04/2025		02/05/2025	
New Jersey	273	11/04/2025		02/05/2025	
Tennessee	229	08/04/2025		02/05/2025	
Virginia	215	09/04/2025		02/05/2025	
Massachusetts	208	09/04/2025		02/05/2025	
International Travellers	196	01/05/2025		02/05/2025	
Louisiana	192	14/04/2025		02/05/2025	
Rhode Island	148	29/04/2025		02/05/2025	
Connecticut	135	08/04/2025		02/05/2025	
District of Columbia	124	11/04/2025		02/05/2025	
Pennsylvania	97	11/04/2025		02/05/2025	
New Mexico	95	09/04/2025		02/05/2025	
Nebraska	91	18/04/2025		01/05/2025	
Kentucky	82	05/03/2025		01/04/2025	
Utah	80	08/04/2025		02/05/2025	
Arizona	71	27/04/2025		02/05/2025	
Hawaii	70	23/04/2025		02/05/2025	
Vermont	70	25/04/2025		02/05/2025	
Oregon	61	01/05/2025		02/05/2025	
Georgia	48	10/04/2025		02/05/2025	
North Carolina	48	11/04/2025		02/05/2025	
Total	10,902	01/05/2025		02/05/2025	

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.