

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

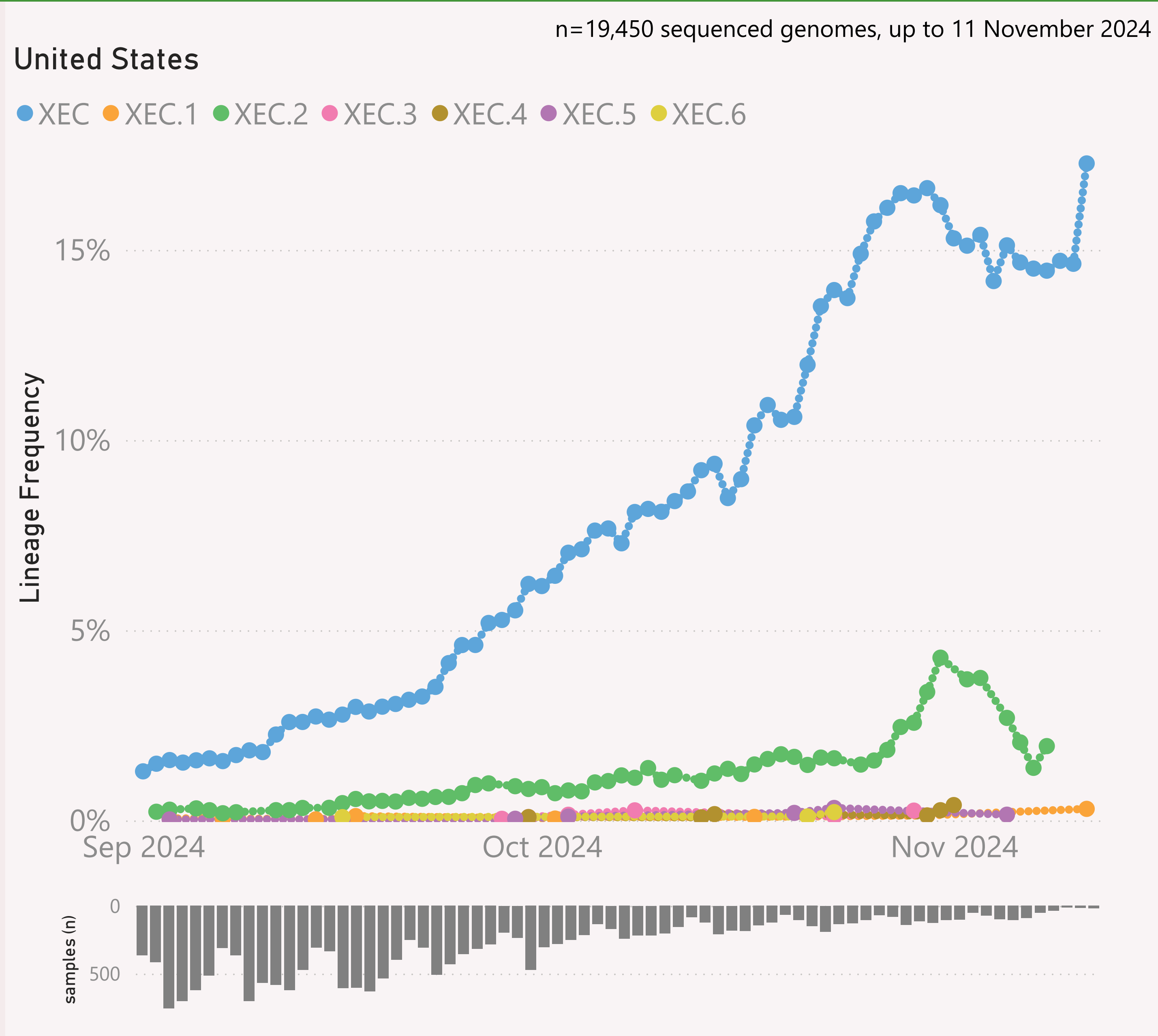
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all it's descendants, e.g. the JN.\* lineages.

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.



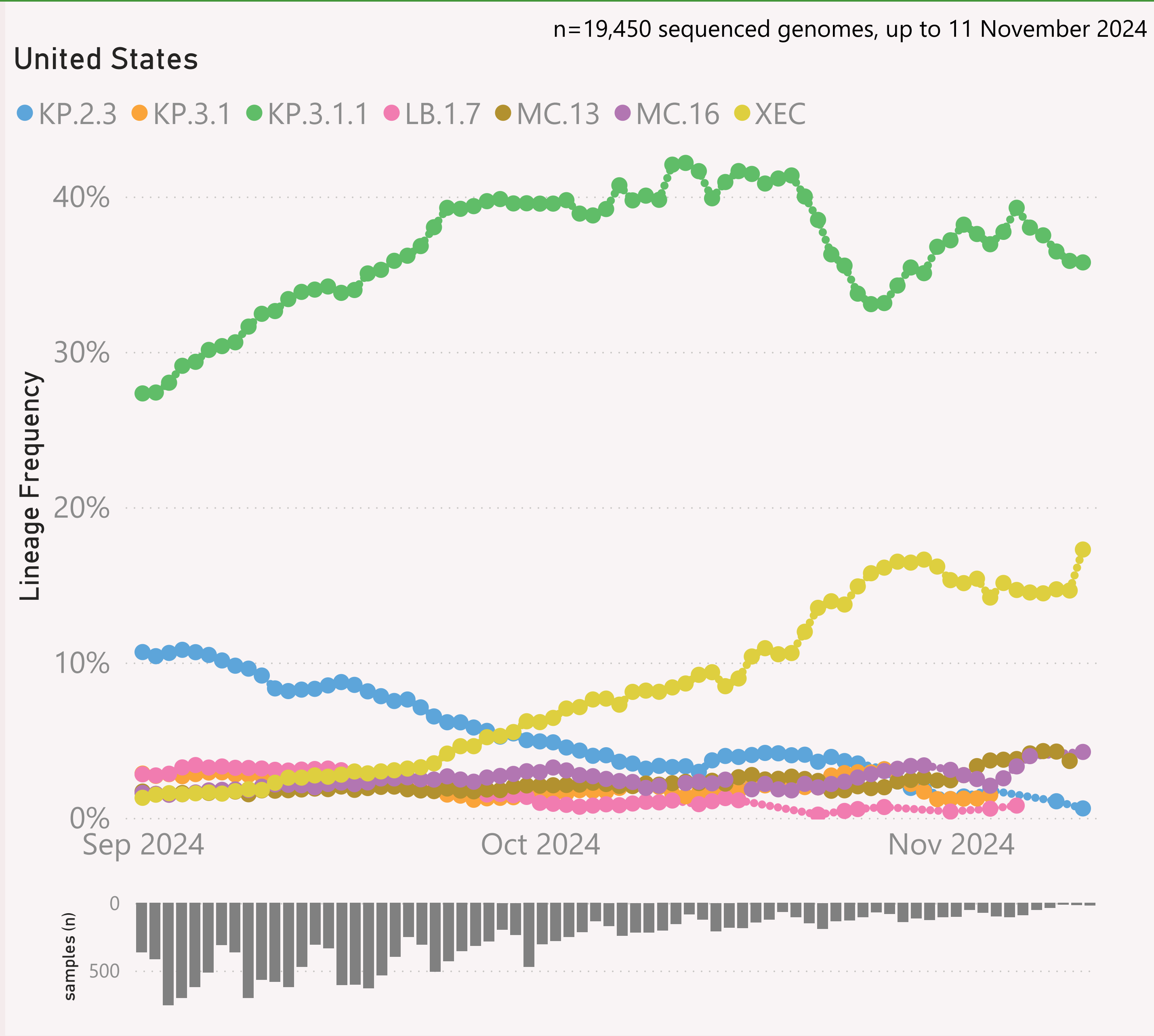
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "XEC.\*".

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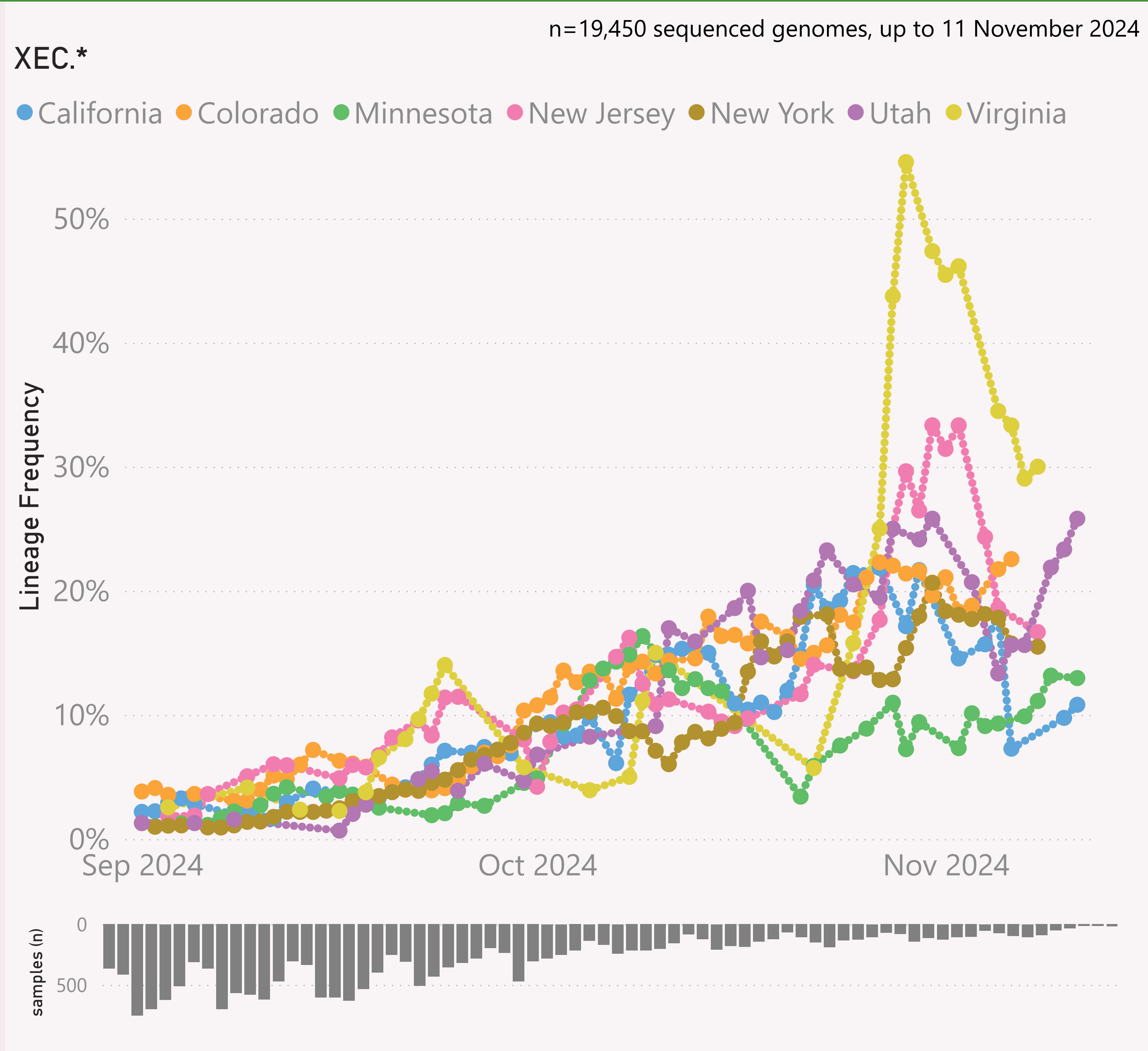
This page shows the frequency of the top 7 lineages, across recent months.

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.

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

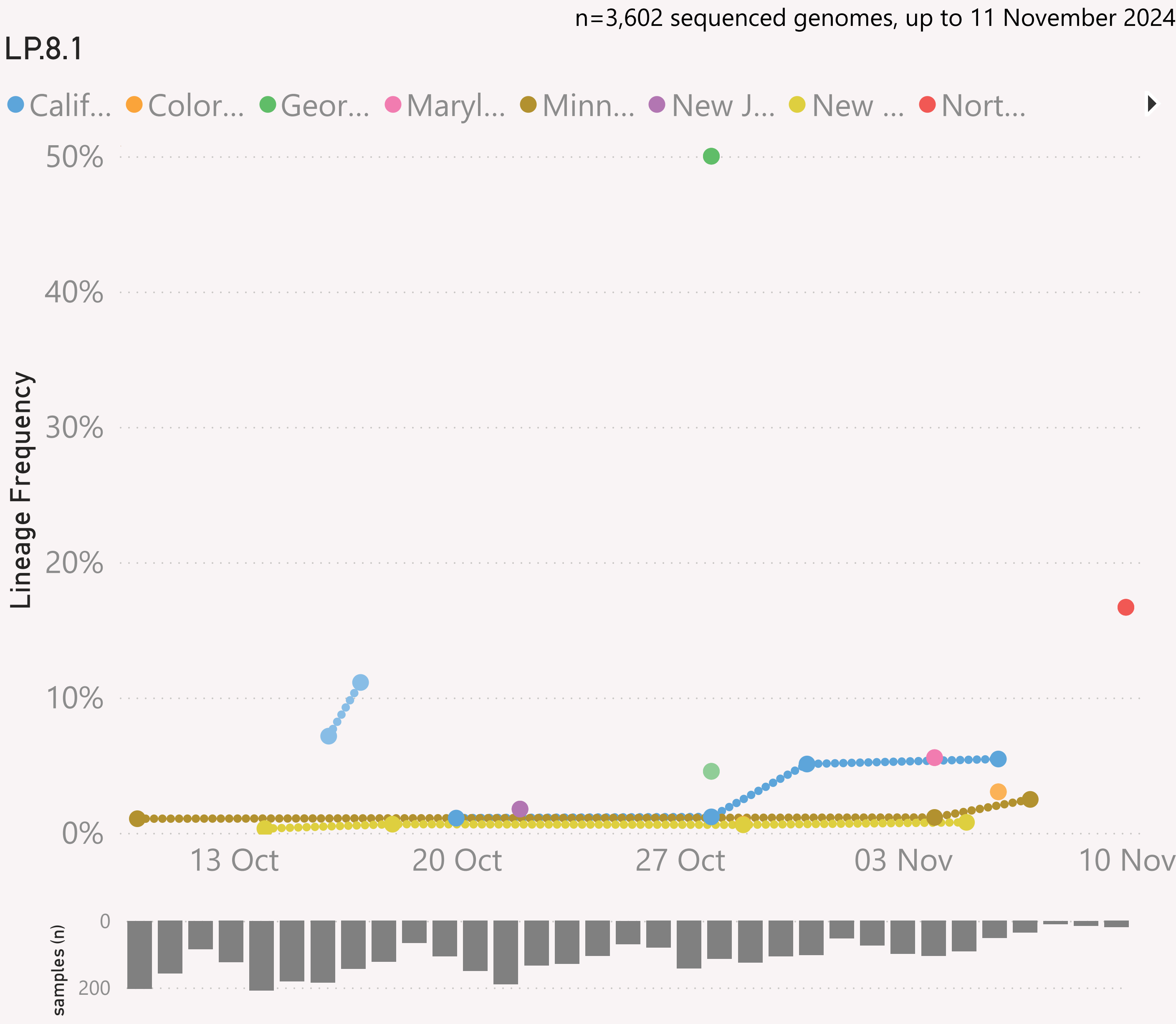
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.\*" group includes BA.2.86 and all it's descendants, e.g. the JN.\* lineages.

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.





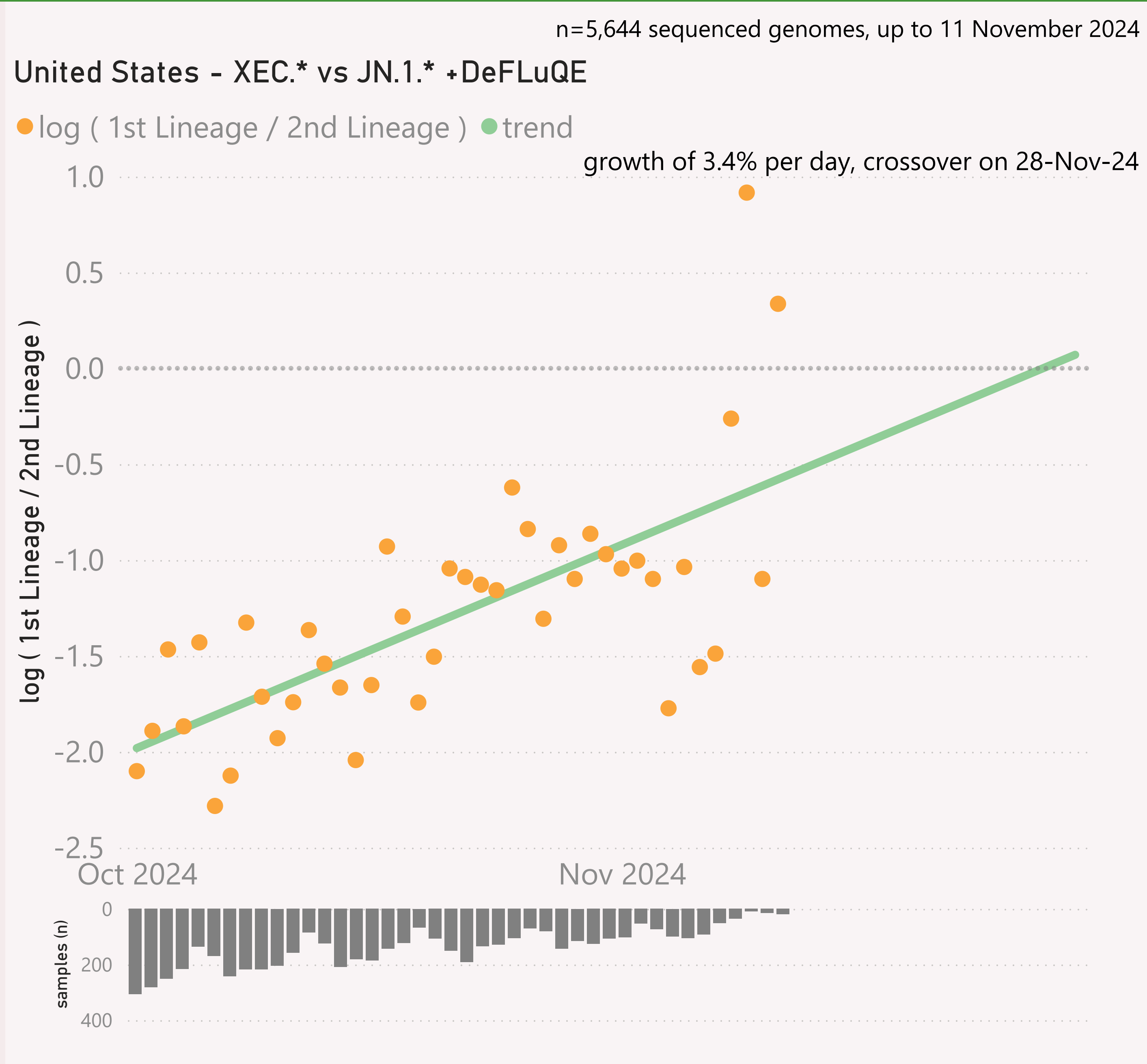
This page shows the frequency of a selected Lineage of interest, across the leading States, over recent months.

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.

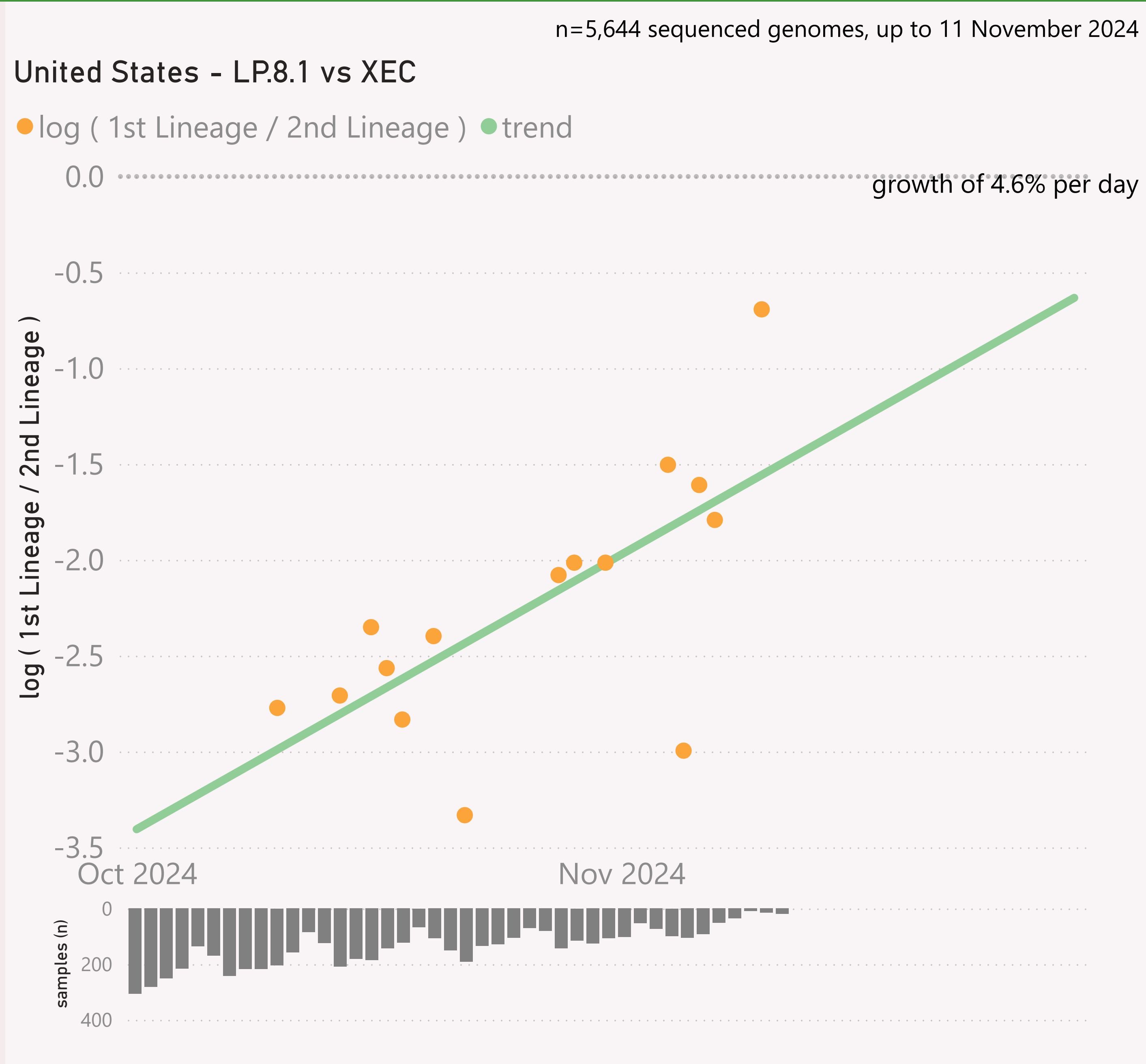


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.



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





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>	23,432	11/11/2024		16/11/2024	
New York	3,529	10/11/2024		16/11/2024	
California	3,214	11/11/2024		16/11/2024	
Colorado	2,938	07/11/2024		16/11/2024	
Texas	1,950	06/11/2024		16/11/2024	
Minnesota	1,459	11/11/2024		16/11/2024	
Ohio	1,422	04/11/2024		16/11/2024	
New Jersey	804	10/11/2024		16/11/2024	
Virginia	725	11/11/2024		16/11/2024	
Utah	558	11/11/2024		16/11/2024	
Illinois	506	08/11/2024		16/11/2024	
Maryland	506	08/11/2024		16/11/2024	
Tennessee	480	05/11/2024		16/11/2024	
Connecticut	459	29/10/2024		16/11/2024	
New Mexico	410	30/10/2024		16/11/2024	
Rhode Island	408	17/10/2024		15/11/2024	
Hawaii	360	22/10/2024		07/11/2024	
Pennsylvania	316	08/11/2024		16/11/2024	
Michigan	312	04/11/2024		16/11/2024	
North Carolina	283	11/11/2024		16/11/2024	
Nevada	265	11/11/2024		16/11/2024	
Georgia	254	11/11/2024		16/11/2024	
Delaware	246	08/11/2024		16/11/2024	
Nebraska	228	09/11/2024		16/11/2024	
Arizona	227	09/11/2024		16/11/2024	
Washington	214	06/11/2024		16/11/2024	
District of Columbia	177	28/10/2024		12/11/2024	
Iowa	173	11/11/2024		16/11/2024	
Total	23,432	11/11/2024		16/11/2024	

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.