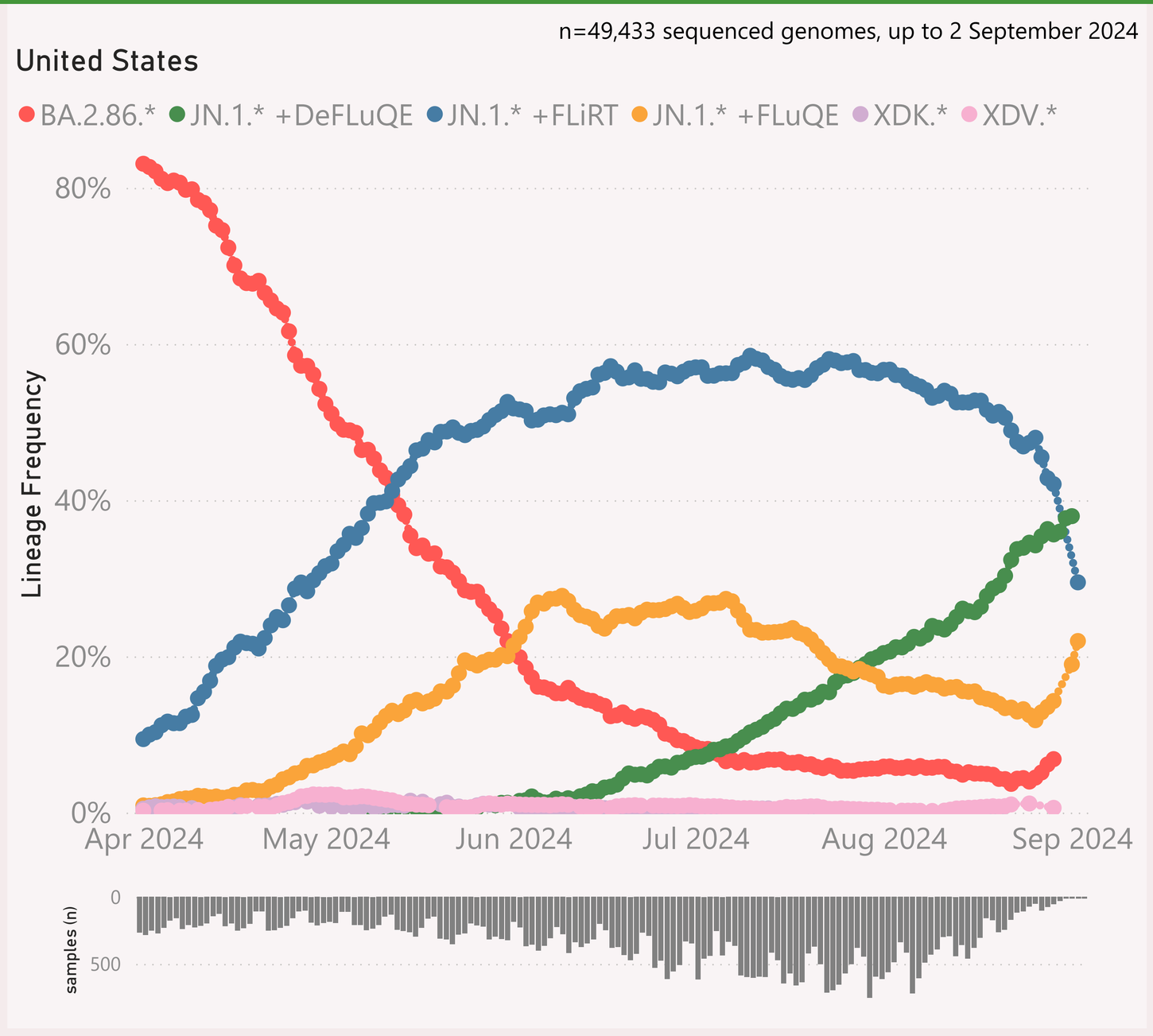


This page shows the frequency of the top 7 "L2" lineages, across recent months.

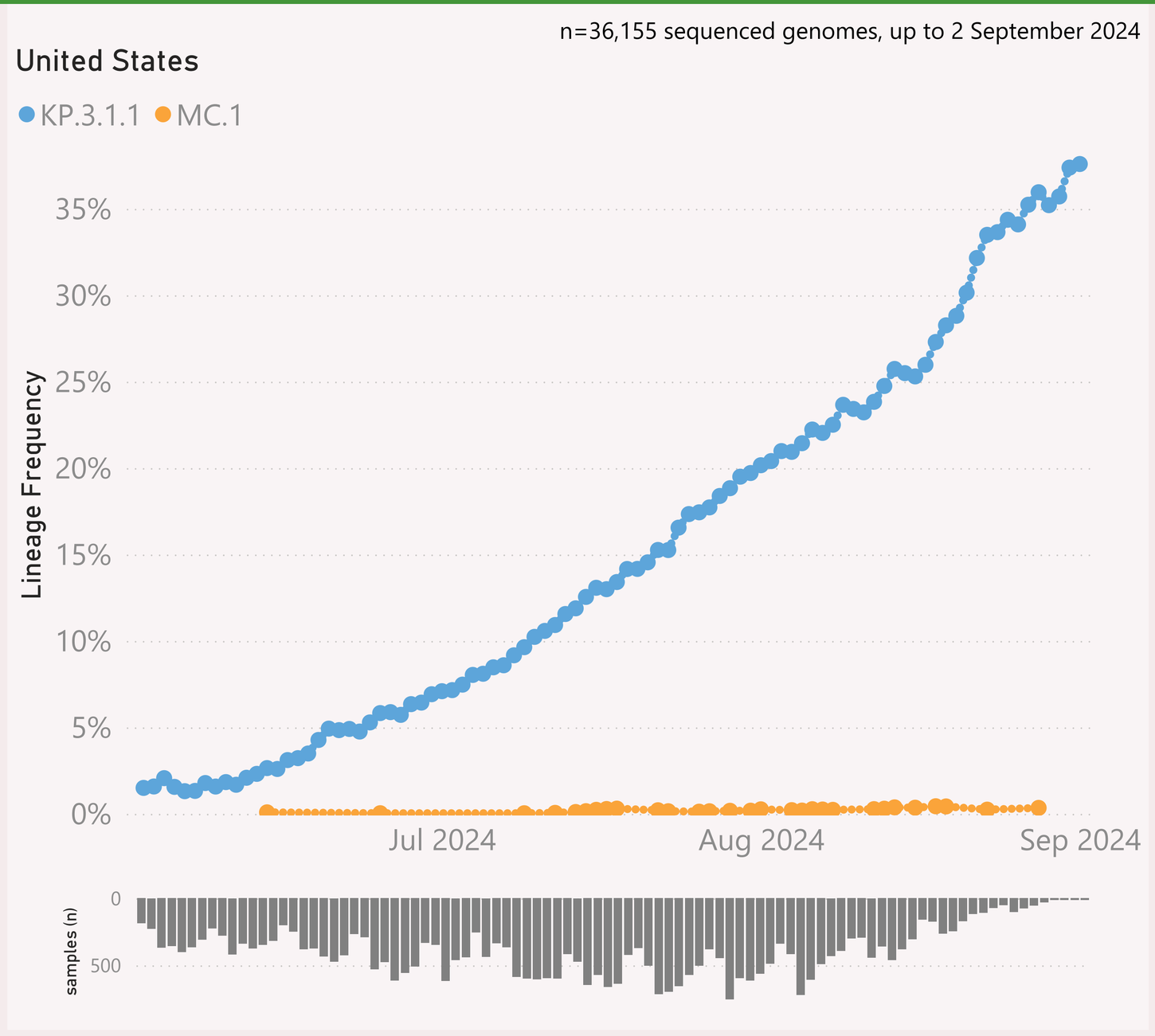
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



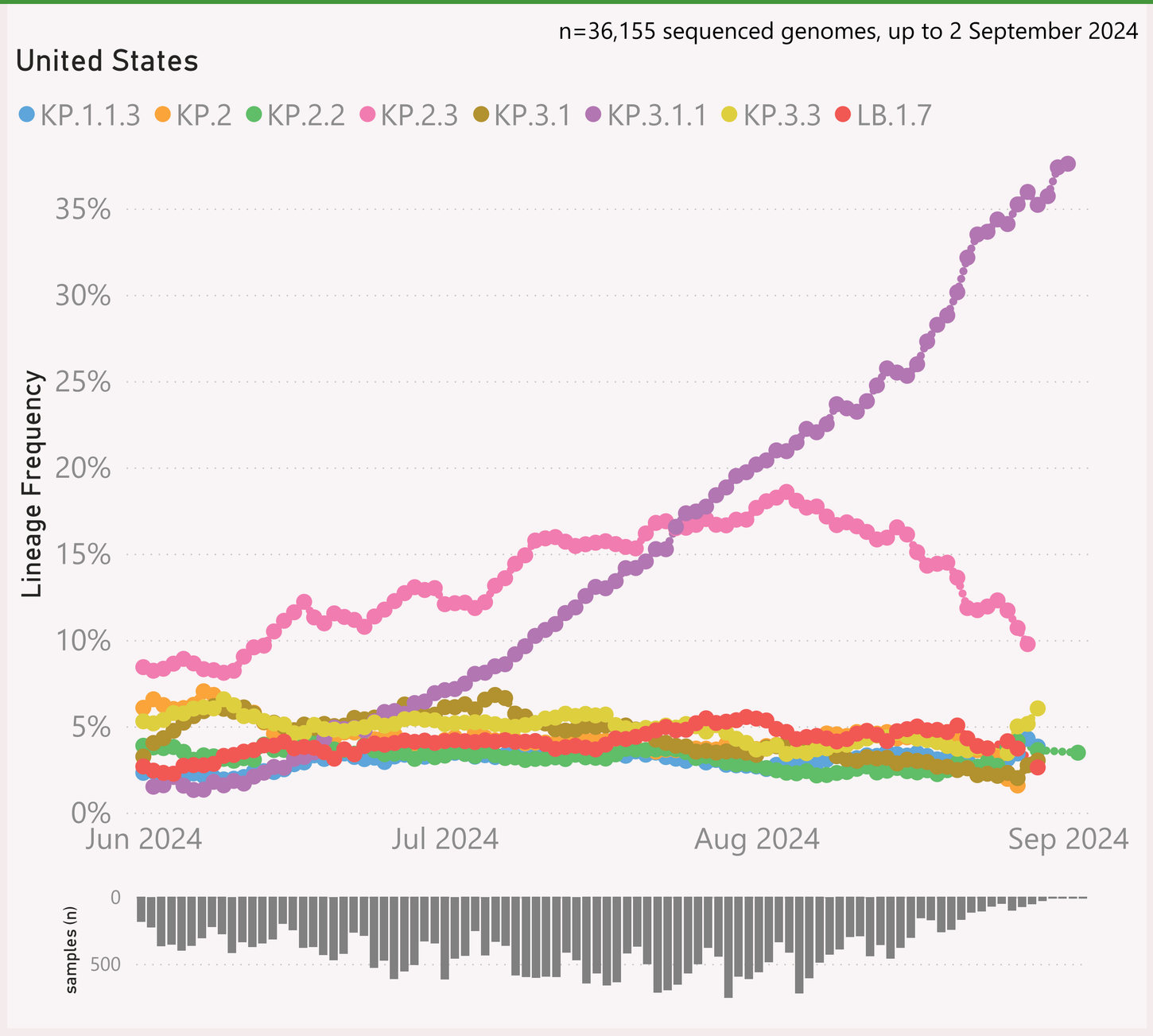
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "JN.1.* + DeFLuQE".

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.



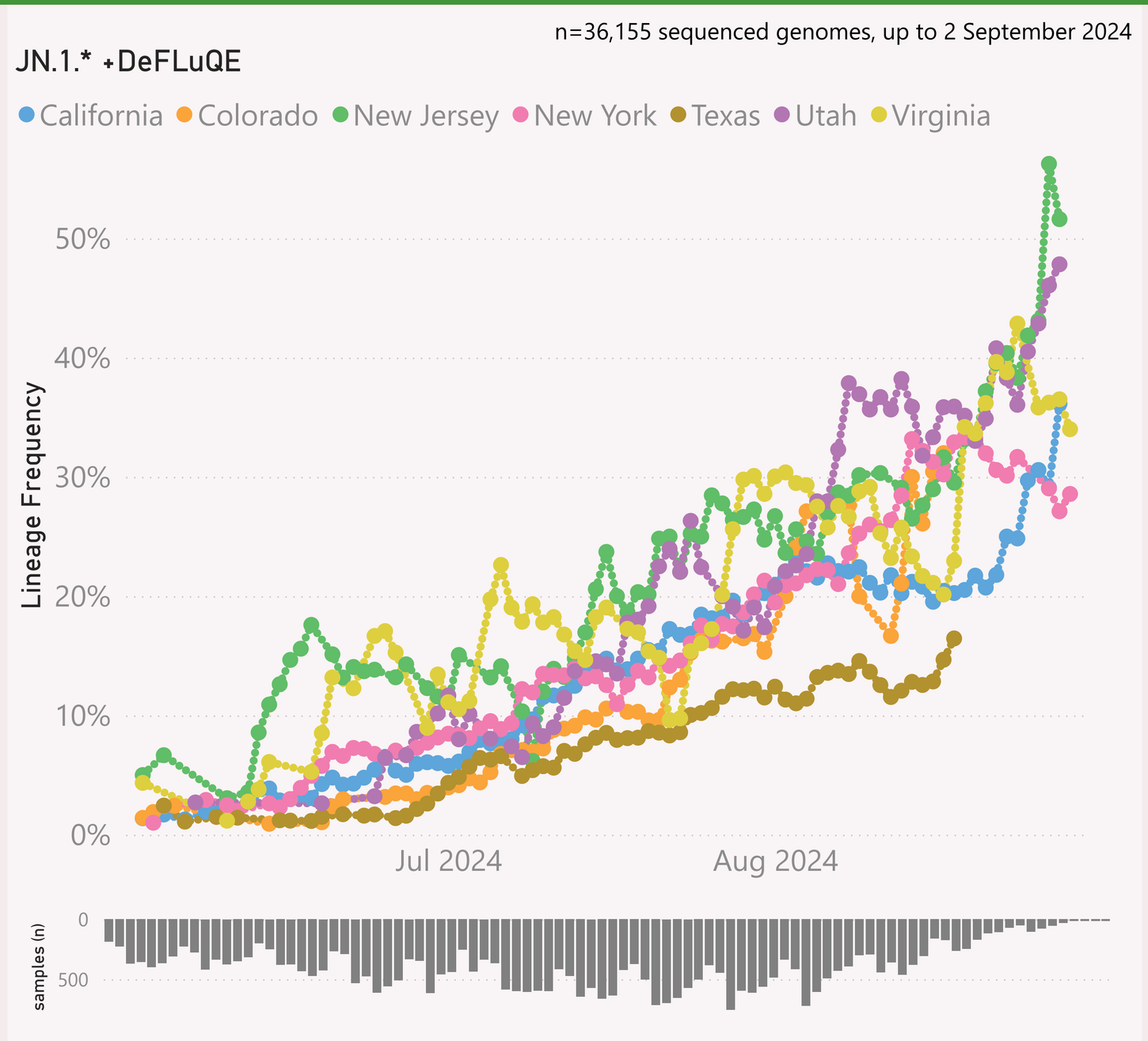
This page shows the frequency of the top 7 lineages, across recent months.

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.



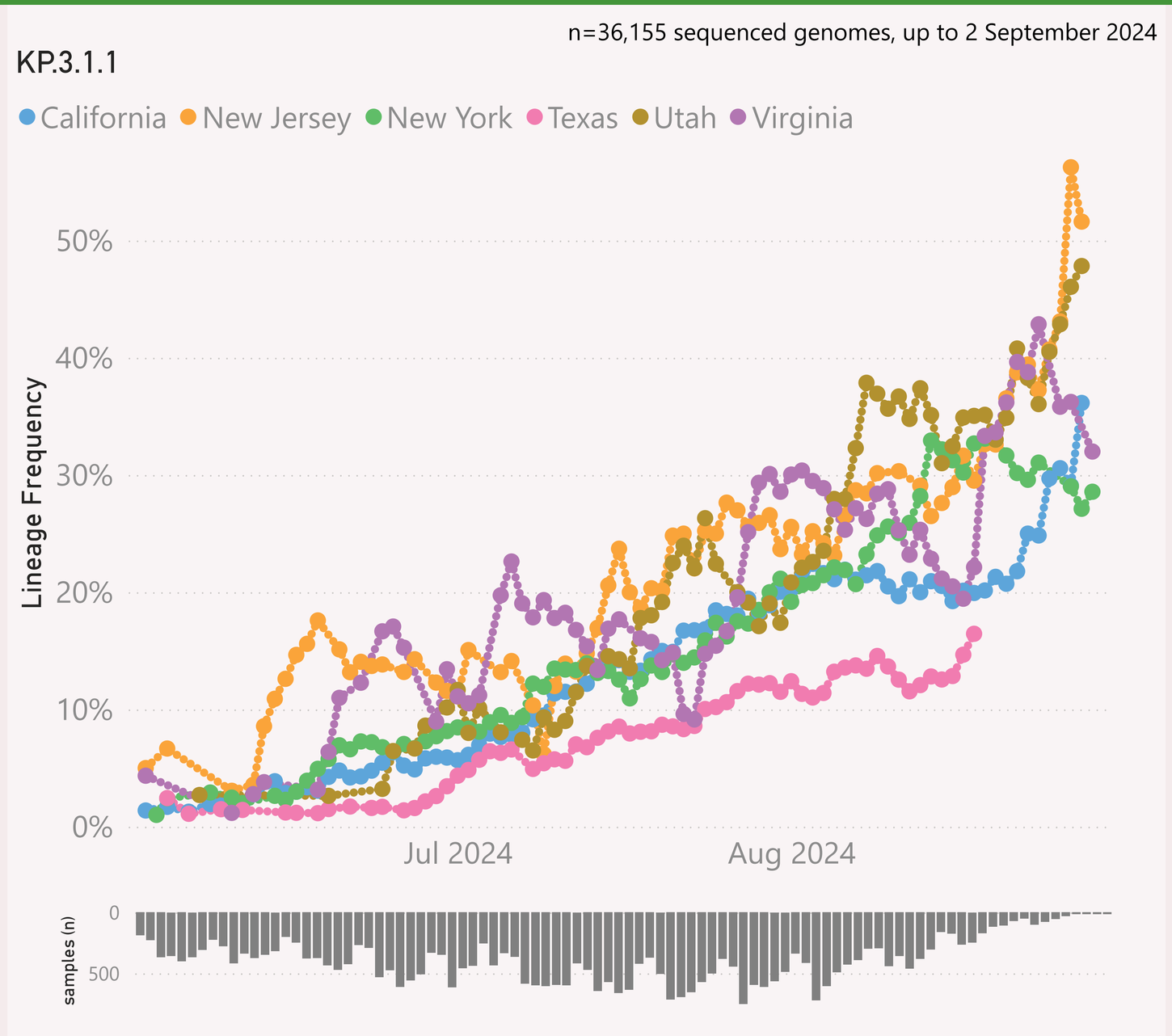
This page shows the frequency of a selected "Lineage L2" group of interest, across the leading States, over recent months.

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.



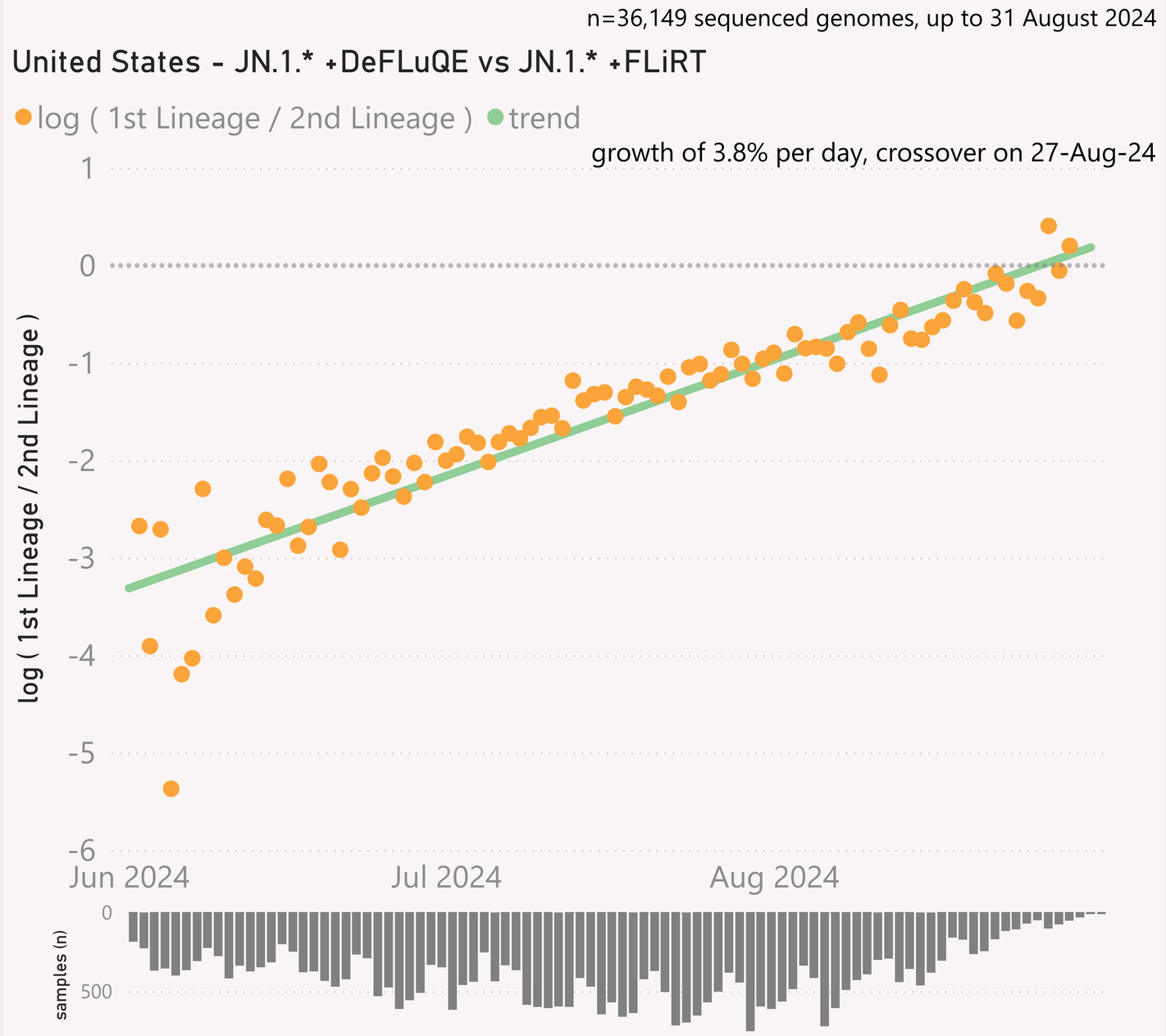
This page shows the frequency of a selected Lineage of interest, across the leading States, over recent months.

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.

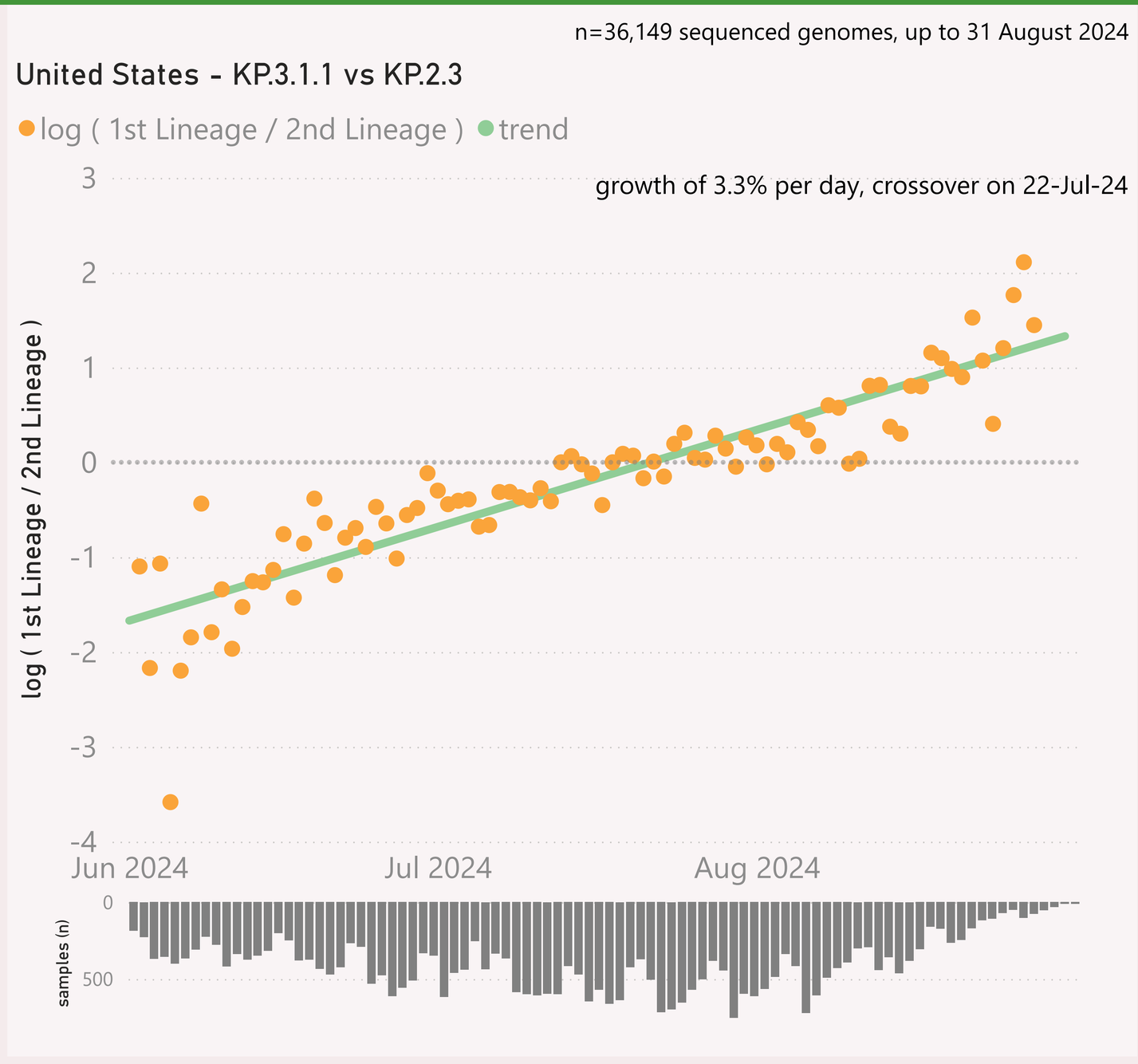


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

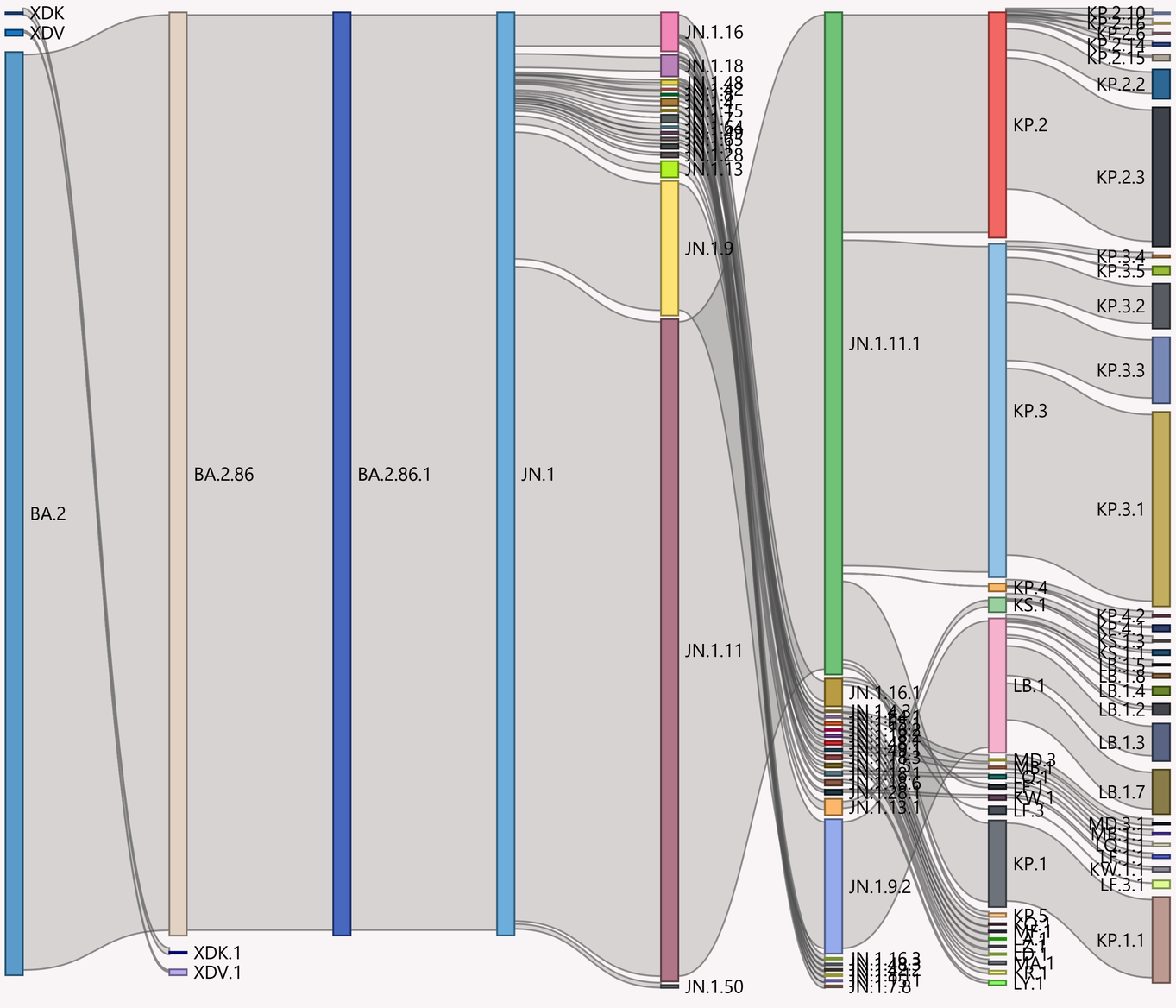
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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.

n=36,248 sequenced genomes, up to 2 September 2024

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.

COVID-19 Genomic Sequencing analysis - Data Currency. Data from gisaid.org. Source files and info on github.

Last Update: 2024-09-09 05:12 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
United States	**34,169**	**9/2/2024**		**9/4/2024**	
California	5,697	8/28/2024		9/4/2024	
Texas	5,160	8/18/2024		9/4/2024	
New York	4,635	8/29/2024		9/4/2024	
Colorado	1,774	8/17/2024		9/4/2024	
New Jersey	1,525	8/28/2024		9/4/2024	
Virginia	1,426	8/29/2024		9/4/2024	
Tennessee	1,046	8/22/2024		9/4/2024	
Hawaii	1,037	8/22/2024		9/4/2024	
Ohio	976	8/26/2024		9/4/2024	
Utah	957	8/28/2024		9/3/2024	
Florida	699	8/29/2024		9/4/2024	
Illinois	661	8/26/2024		9/4/2024	
Minnesota	613	8/12/2024		9/4/2024	
Maryland	599	8/26/2024		9/4/2024	
Pennsylvania	571	8/24/2024		9/4/2024	
Michigan	567	8/21/2024		9/4/2024	
Louisiana	529	8/28/2024		9/4/2024	
Washington	473	8/29/2024		9/4/2024	
Nevada	436	8/29/2024		9/4/2024	
Iowa	427	9/2/2024		9/4/2024	
Rhode Island	425	8/20/2024		9/3/2024	
North Carolina	423	8/26/2024		9/4/2024	
Arizona	407	8/19/2024		9/4/2024	
Nebraska	391	8/28/2024		9/4/2024	
Delaware	388	8/20/2024		9/4/2024	
Georgia	361	8/24/2024		9/4/2024	
New Mexico	300	8/2/2024		9/4/2024	
Total	**34,169**	**9/2/2024**		**9/4/2024**	

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.