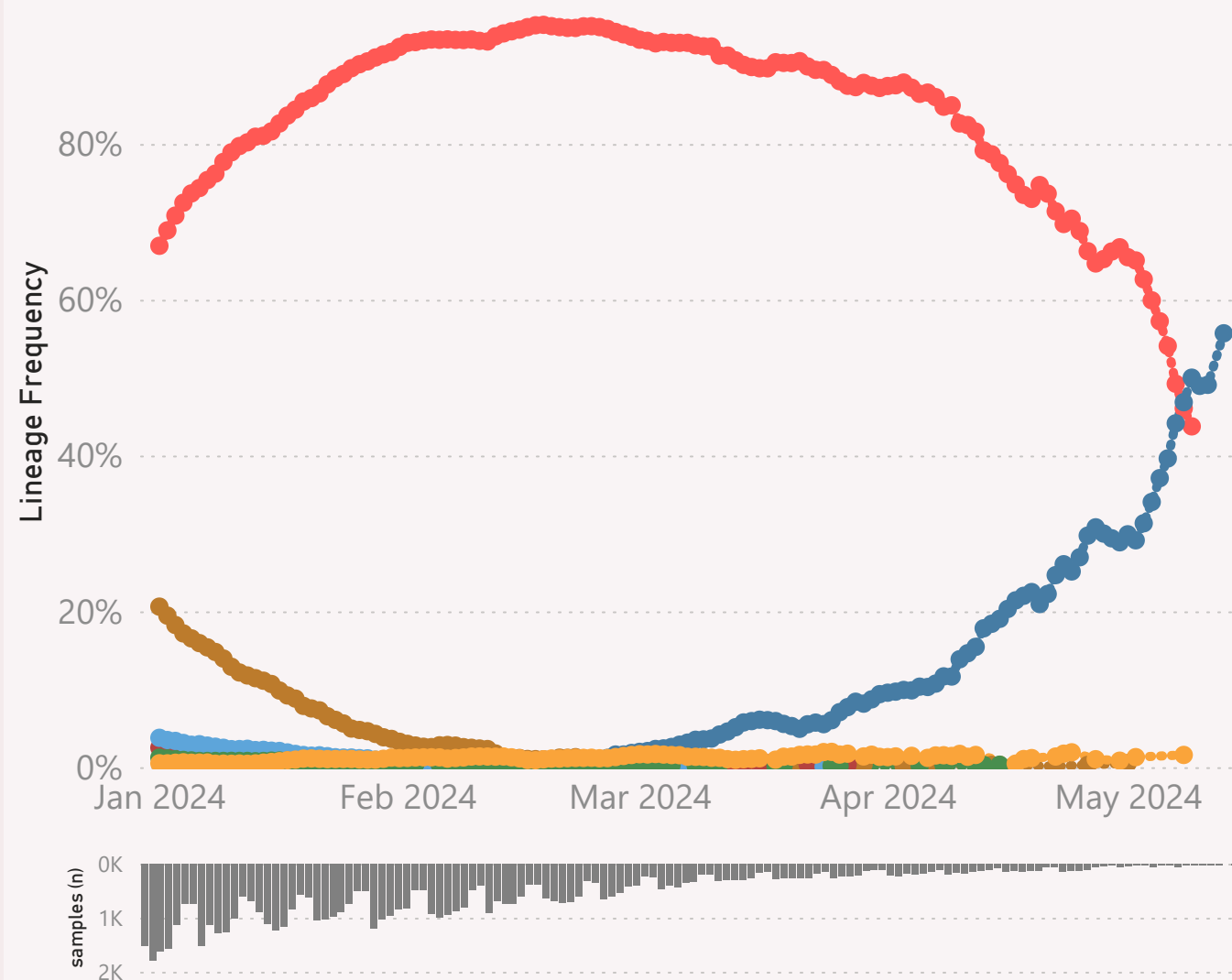


United States

n=62,594 sequenced genomes, up to 13 May 2024

● BA.2.86.* ● EG.5.* ● JN.1.* + FLiRT ● XBB.1.16.* ● XBB.1.5.* ● XBB.2.3.* ● XDP.*



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 its 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.

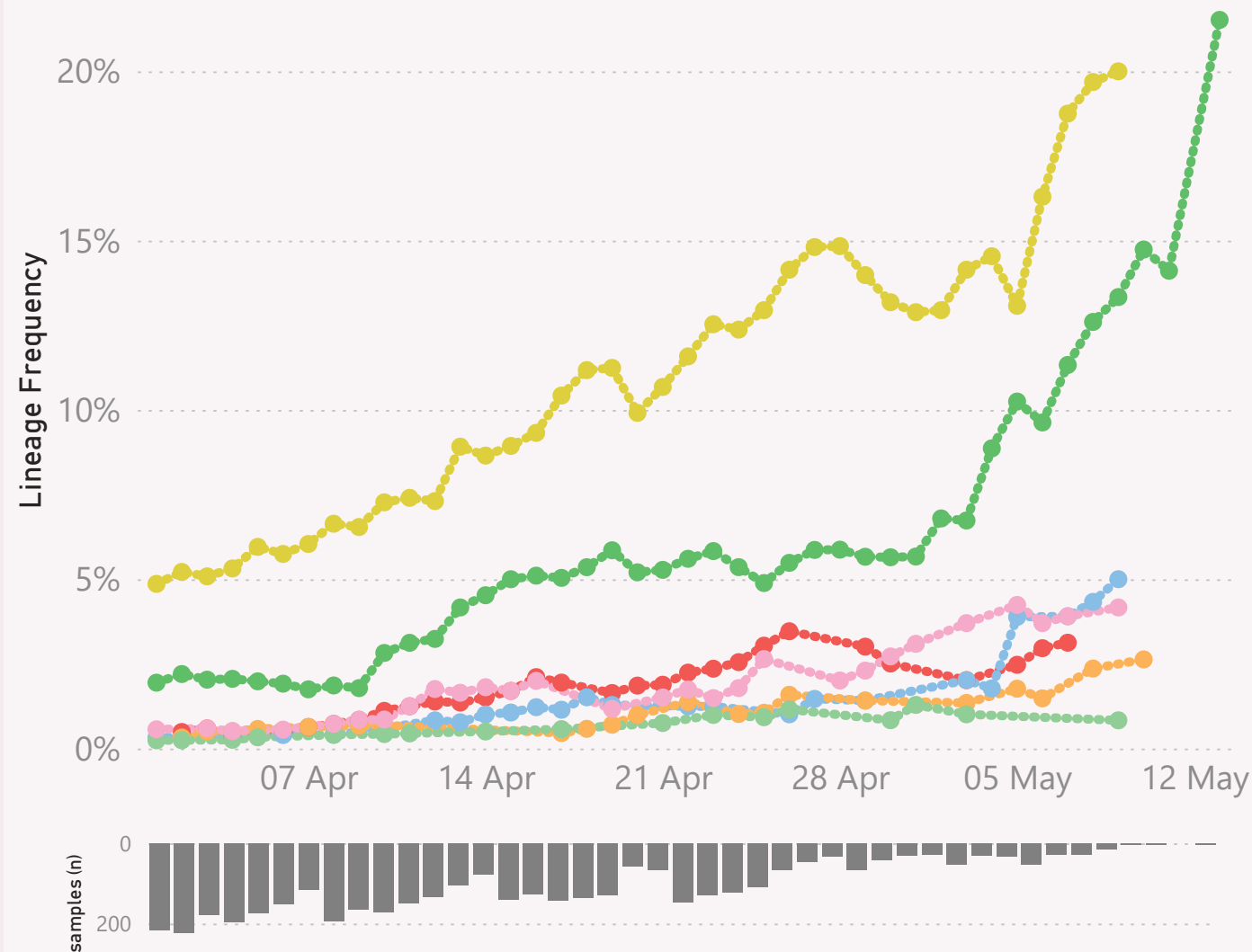
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

United States

n=4,109 sequenced genomes, up to 13 May 2024

● JN.1.16.1 ● KP.1.1 ● KP.1.1.1 ● KP.2 ● KP.2.2 ● KR.1 ● KS.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 "JN.1.* + FLiRT".

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.

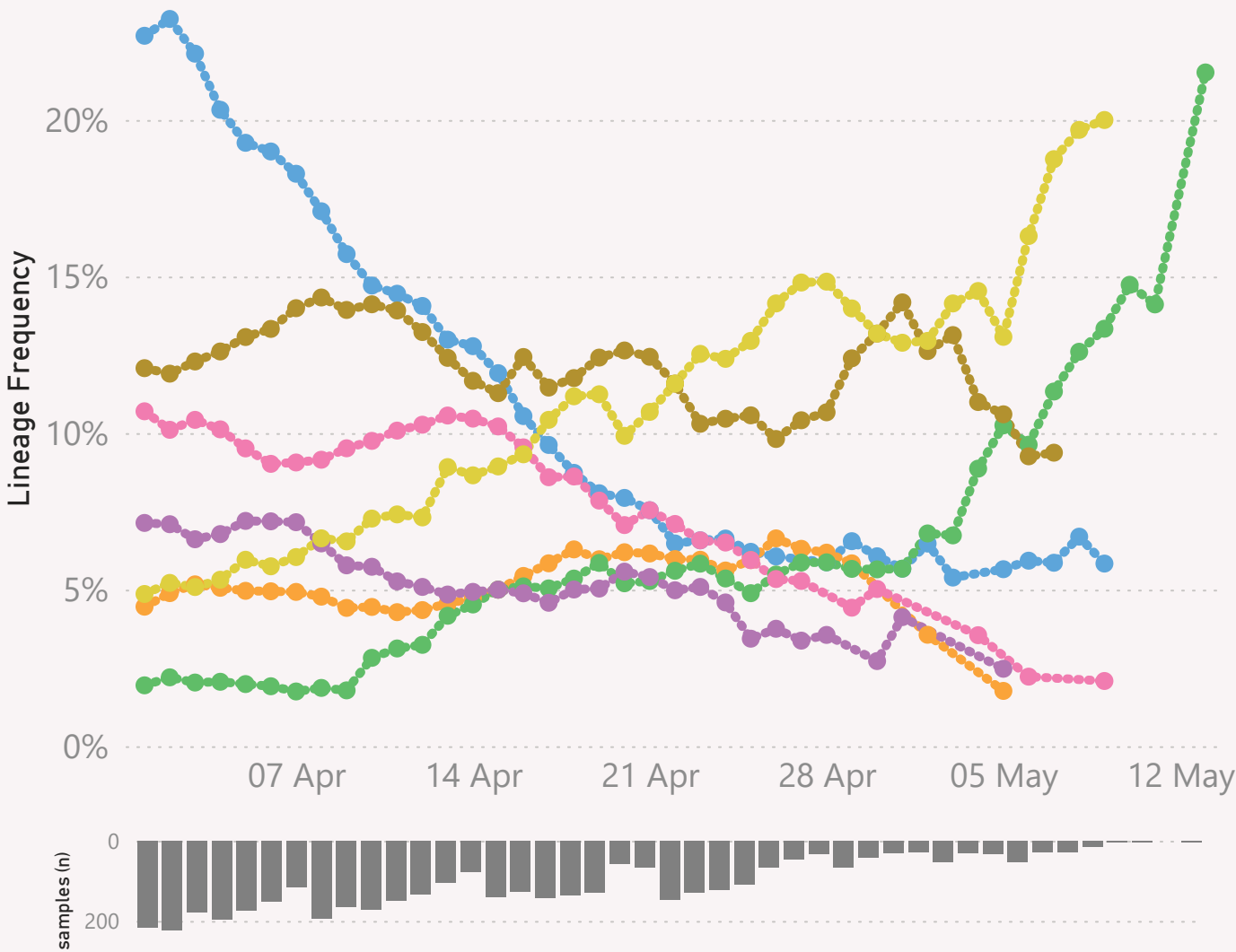
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=4,109 sequenced genomes, up to 13 May 2024

United States

JN.1 JN.1.13.1 JN.1.16.1 JN.1.4 JN.1.7 JN.1.8.1 KP.2



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.

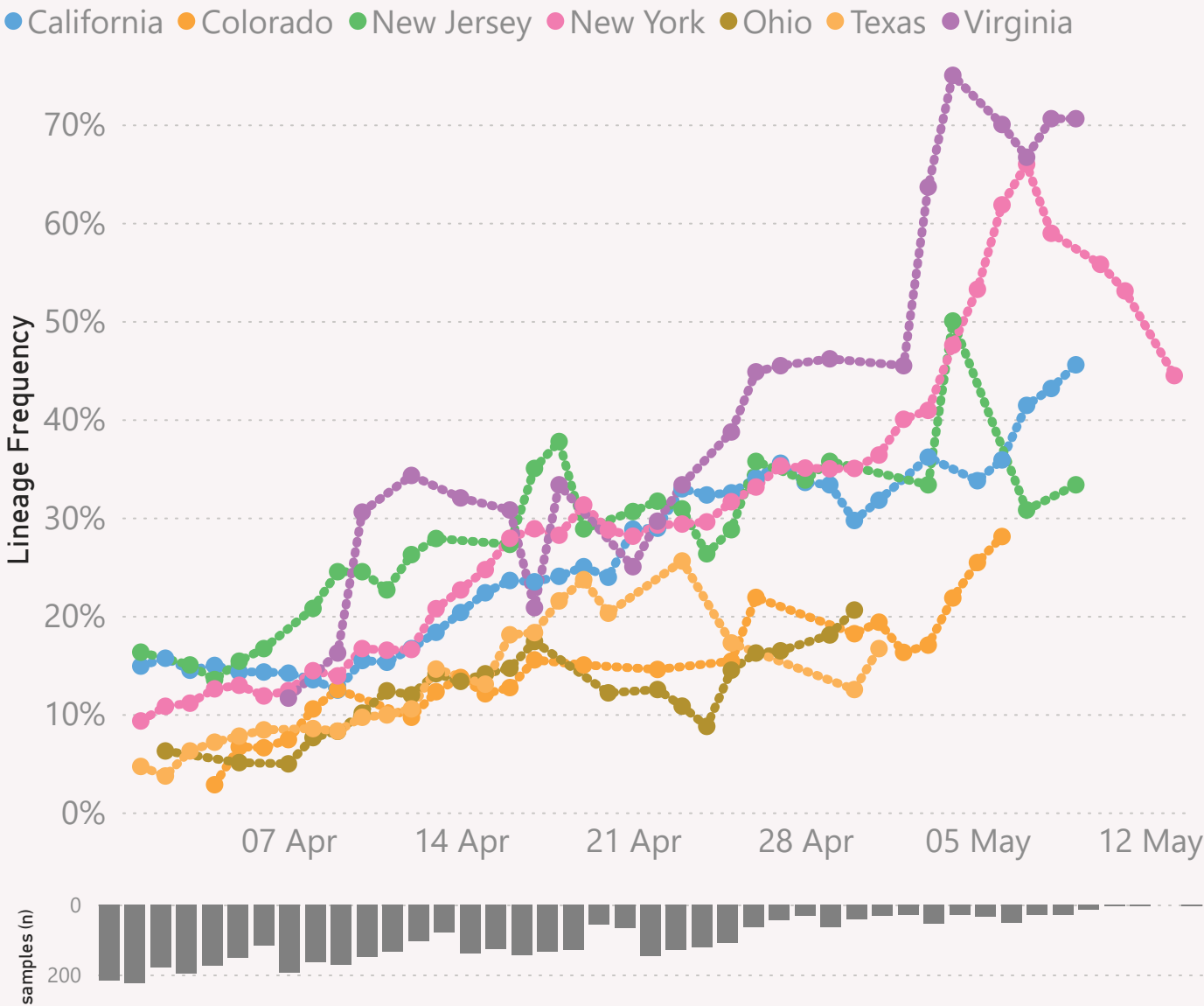
The frequency shown at each point is based on the 7-day rolling average across all lineages.

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=4,109 sequenced genomes, up to 13 May 2024

JN.1.* +FLiRT



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.

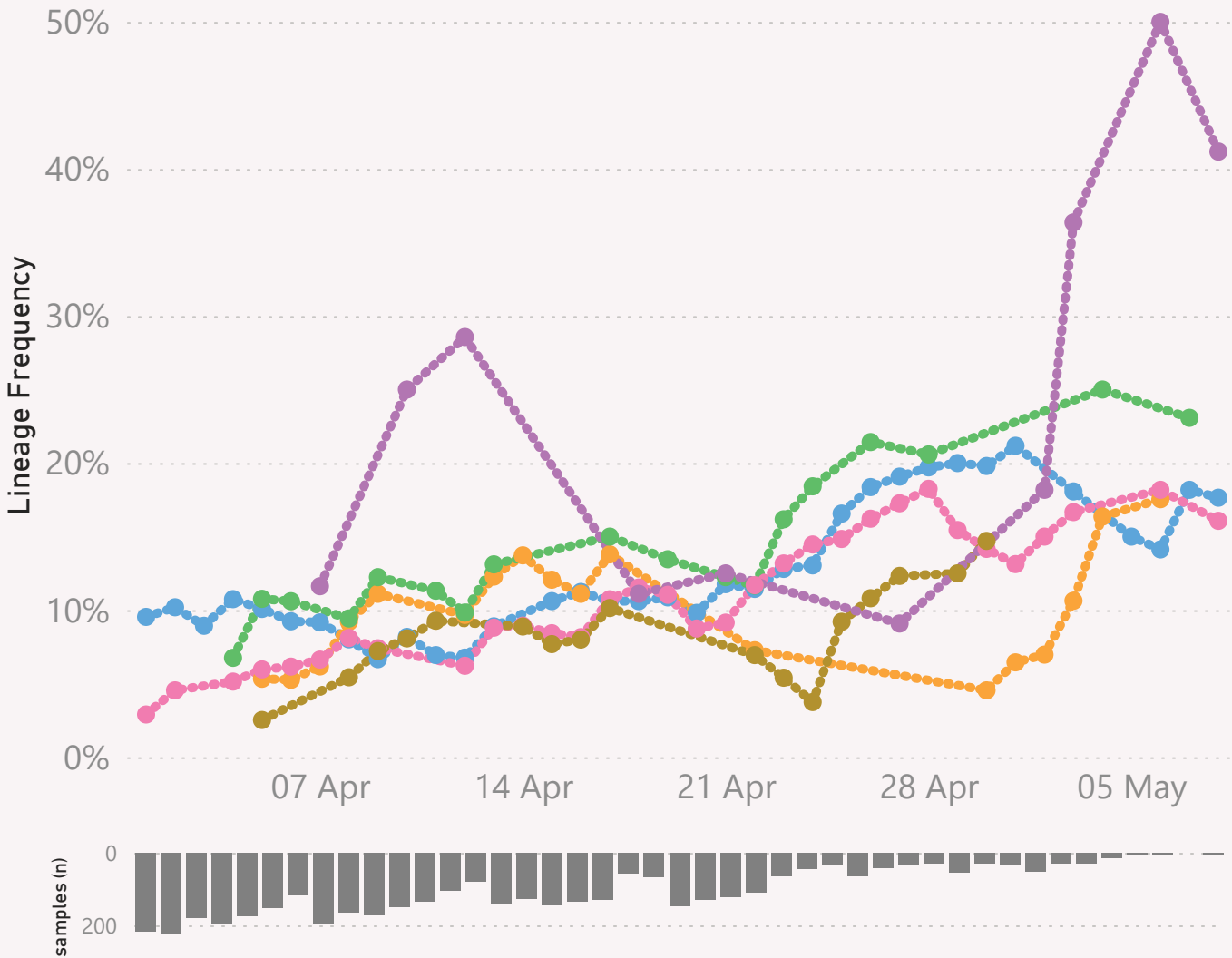
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=4,109 sequenced genomes, up to 13 May 2024

KP.2

California Colorado New Jersey New York Ohio Virginia



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.

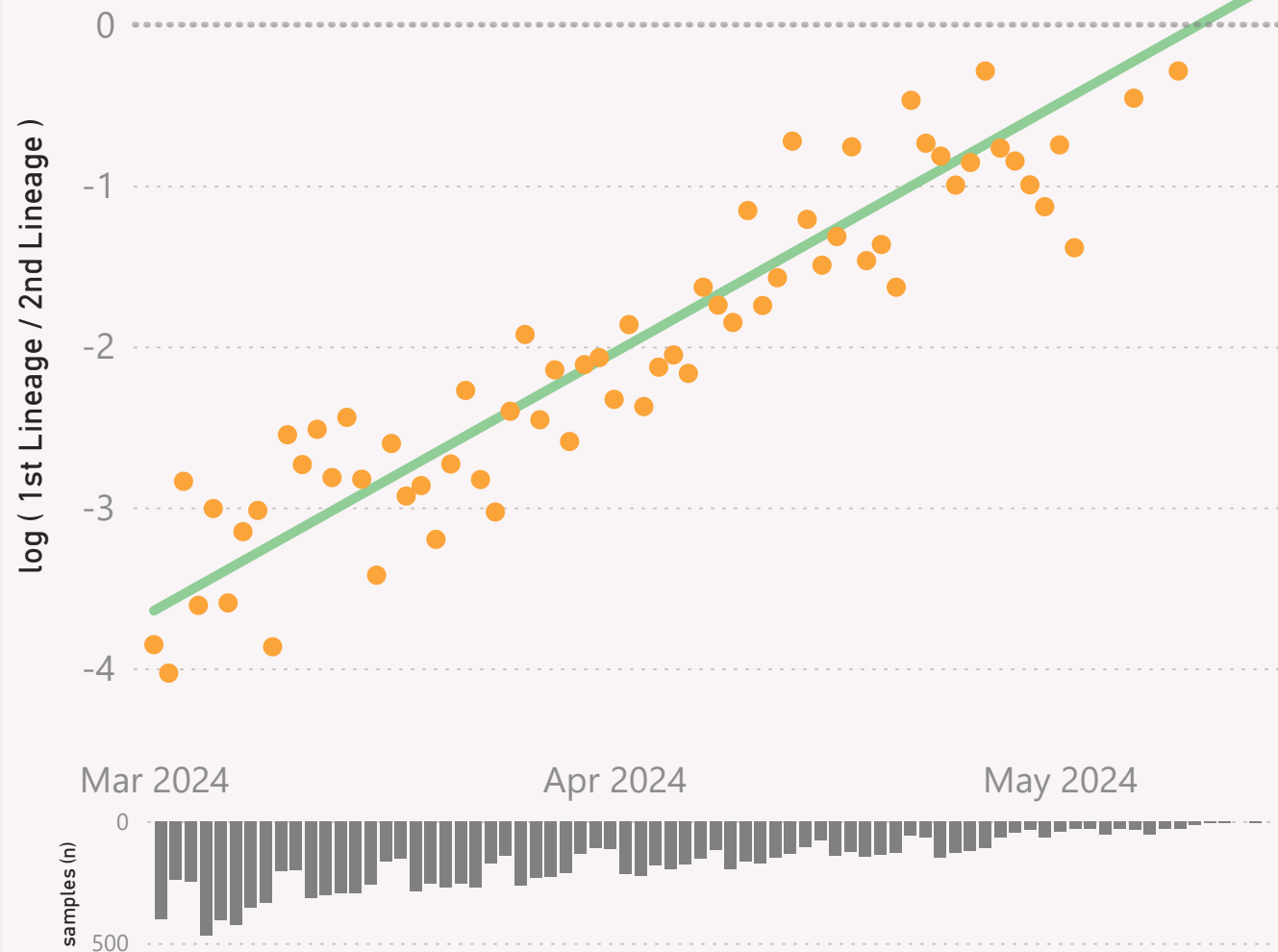
The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=12,083 sequenced genomes, up to 13 May 2024

United States - JN.1.* +FLiRT vs BA.2.86.*

● log (1st Lineage / 2nd Lineage) ● trend

growth of 5.2% per day, crossover on 11-May-24



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".

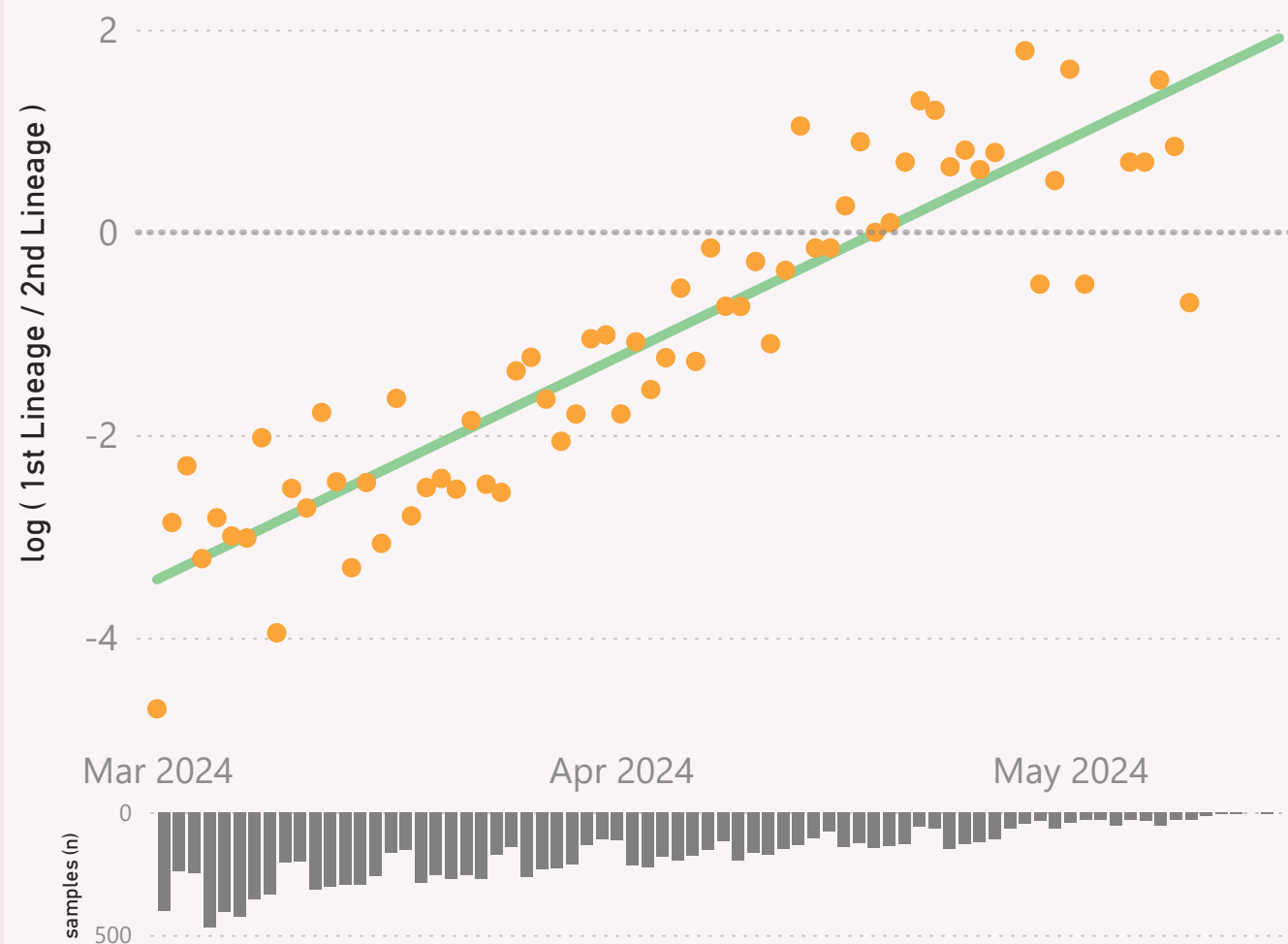
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=12,083 sequenced genomes, up to 13 May 2024

United States - KP.2 vs JN.1

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

growth of 7.1% per day, crossover on 19-Apr-24



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

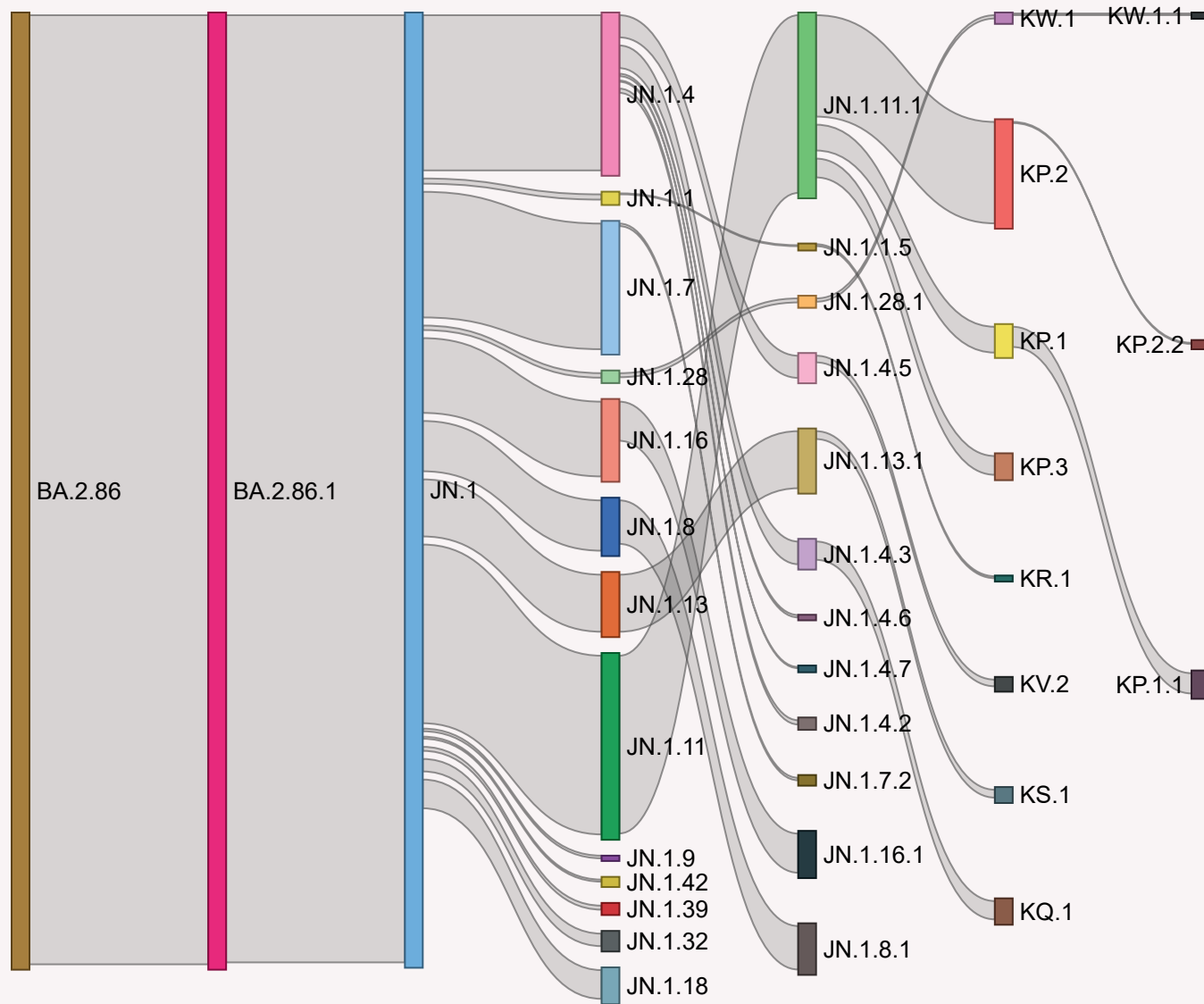
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

n=4,109 sequenced genomes, up to 13 May 2024



Show most significant labels

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 its 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>	23,599	13/05/2024		11/05/2024	
California	5,723	9/05/2024		11/05/2024	
New York	4,580	13/05/2024		11/05/2024	
Wisconsin	1,739	8/04/2024		26/04/2024	
Tennessee	1,736	10/04/2024		1/05/2024	
Texas	1,230	2/05/2024		11/05/2024	
Colorado	758	7/05/2024		11/05/2024	
Ohio	691	30/04/2024		11/05/2024	
New Jersey	640	9/05/2024		11/05/2024	
Illinois	608	29/04/2024		11/05/2024	
Virginia	547	9/05/2024		11/05/2024	
Hawaii	528	30/04/2024		11/05/2024	
Connecticut	423	25/04/2024		11/05/2024	
Minnesota	420	24/04/2024		6/05/2024	
Oregon	406	18/04/2024		11/05/2024	
New Hampshire	342	10/04/2024		25/04/2024	
Utah	315	25/04/2024		11/05/2024	
Louisiana	265	26/04/2024		8/05/2024	
Delaware	245	27/04/2024		8/05/2024	
Washington	225	9/05/2024		11/05/2024	
Georgia	222	8/04/2024		8/05/2024	
Massachusetts	211	25/04/2024		11/05/2024	
Pennsylvania	200	26/04/2024		9/05/2024	
Arizona	193	7/05/2024		11/05/2024	
Nevada	151	30/04/2024		9/05/2024	
Florida	128	7/05/2024		11/05/2024	
Iowa	127	9/05/2024		11/05/2024	
New Mexico	107	18/04/2024		8/05/2024	
Total	23,599	13/05/2024		11/05/2024	

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.