

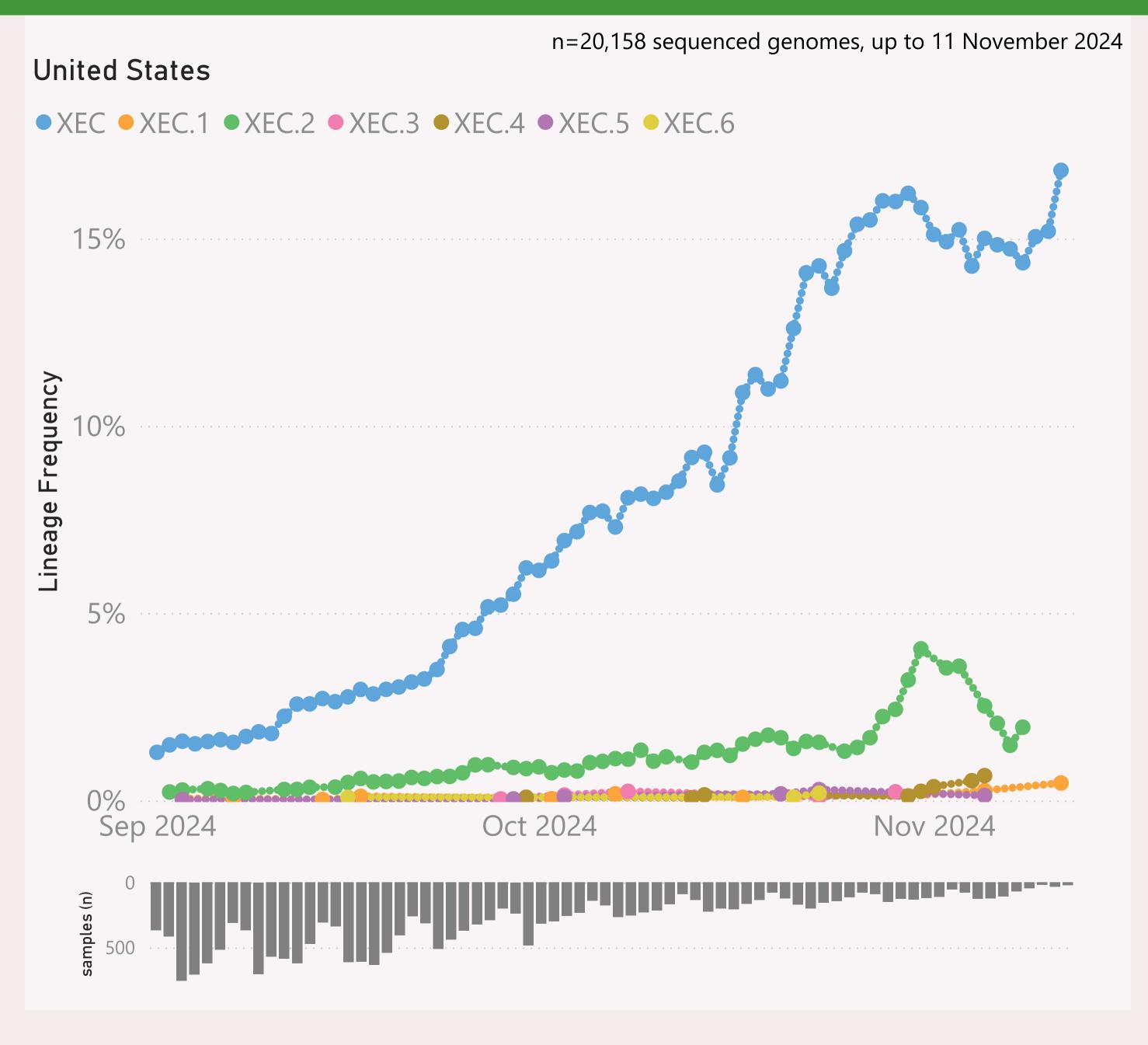
This page shows the frequency of the top 7 "L2" lineages, across recent months.

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.

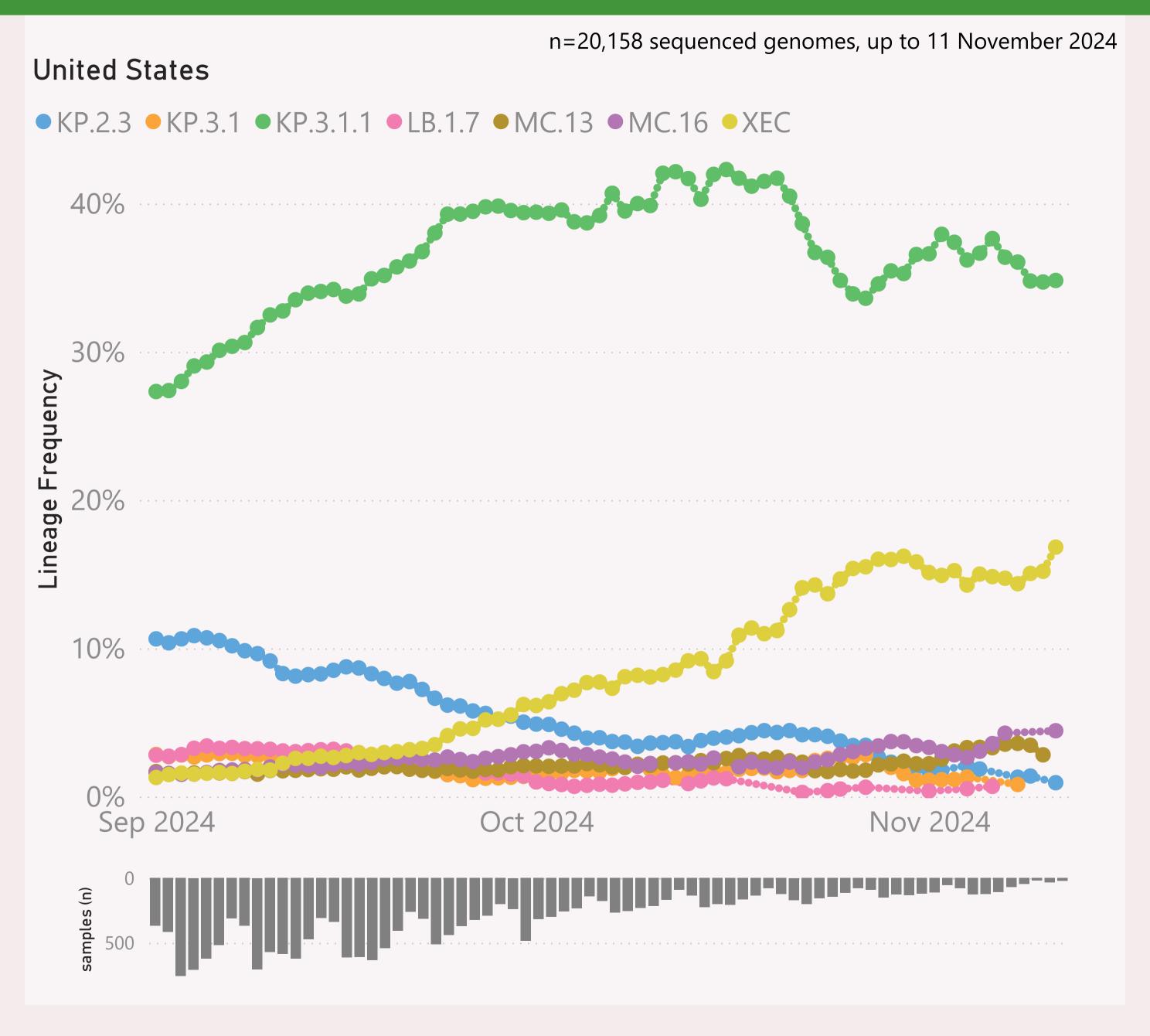


This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "XEC.\*.

The Lineage classifications are provided by Nextclade. The colour assignments are random.

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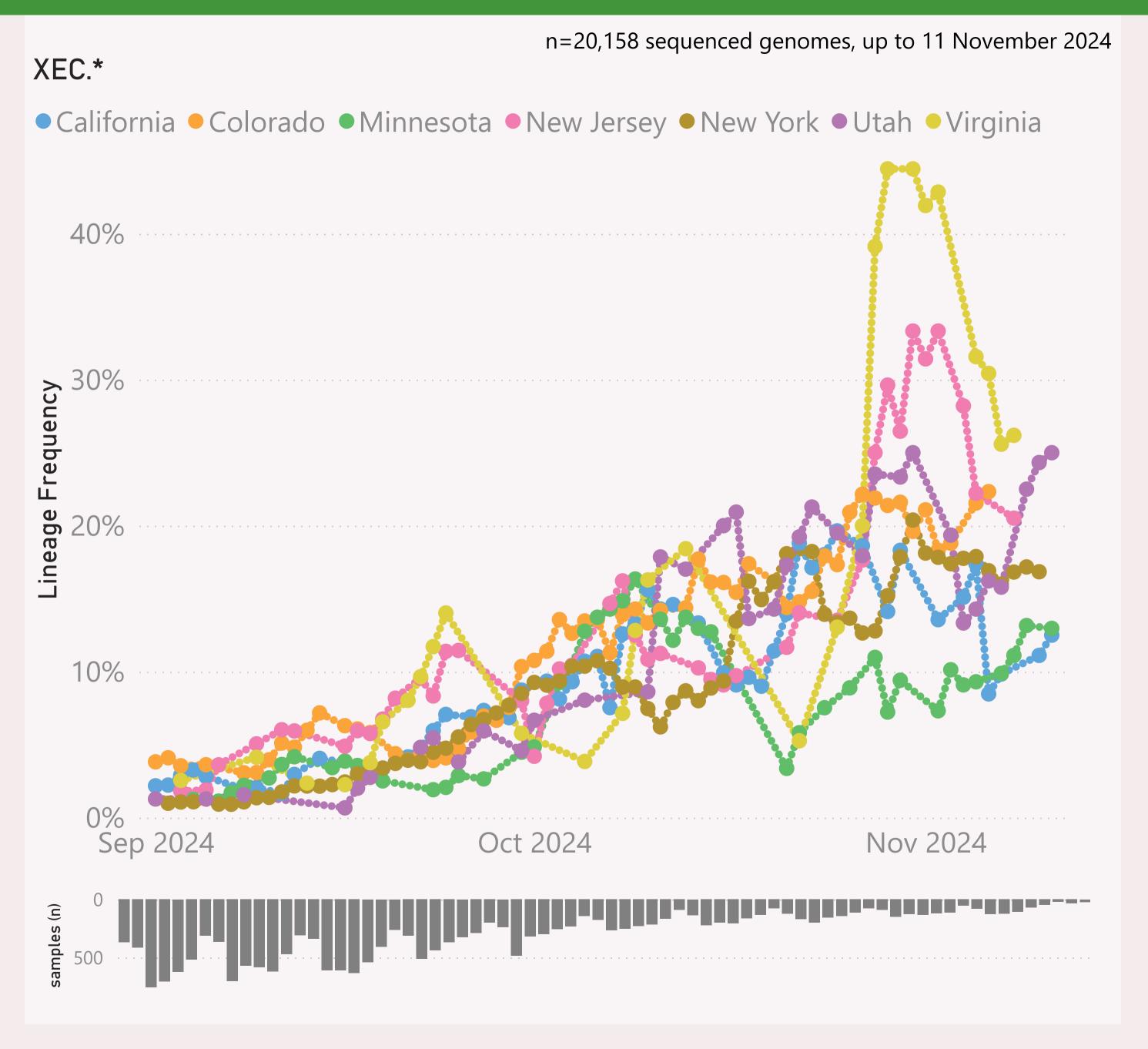


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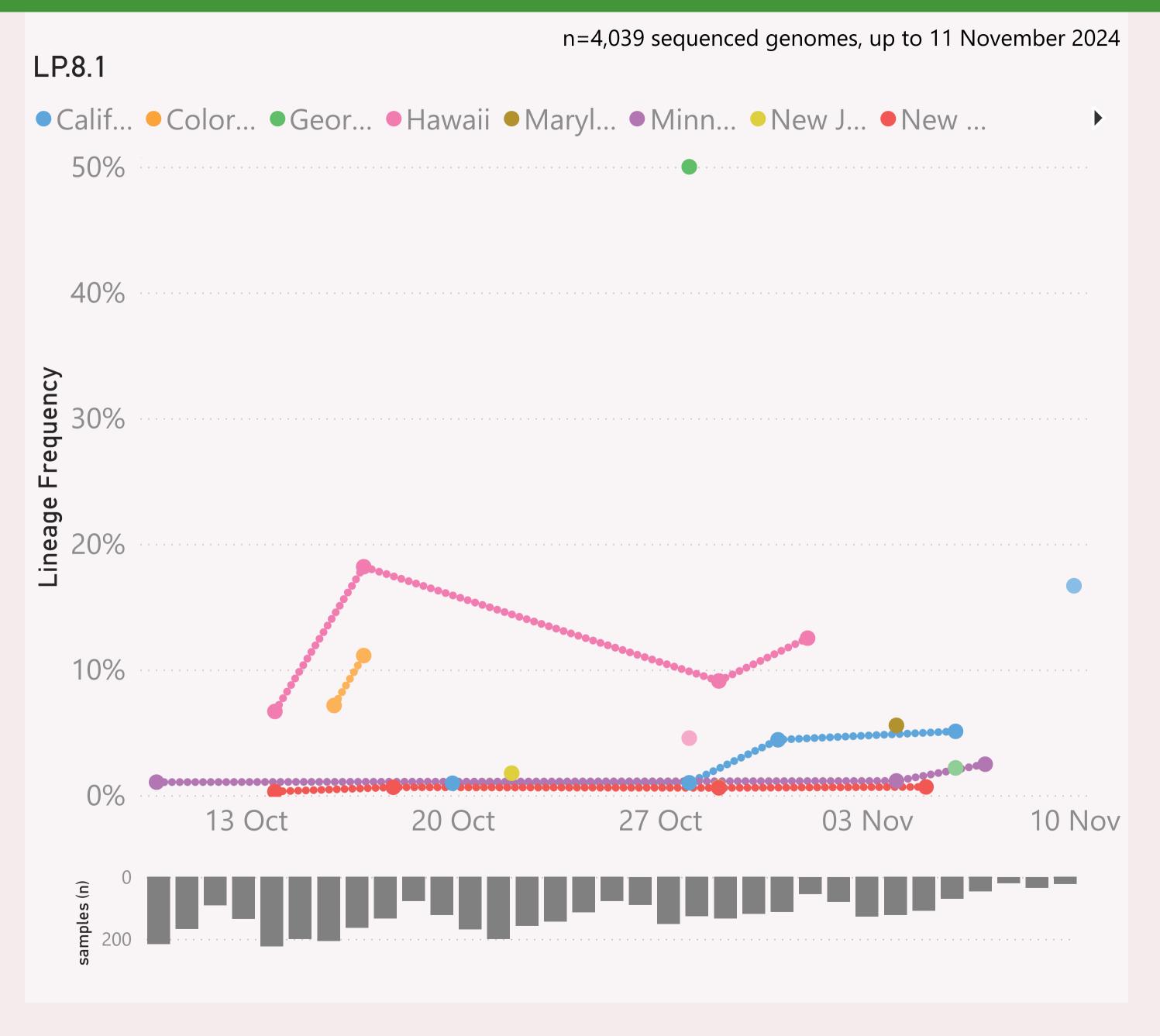


This page shows the frequency of a selected "Lineage L2" group of interest, across the leading States, over recent months.

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.



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

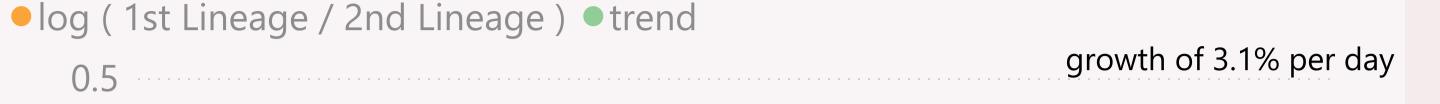
The Lineage classifications are provided by Nextclade.

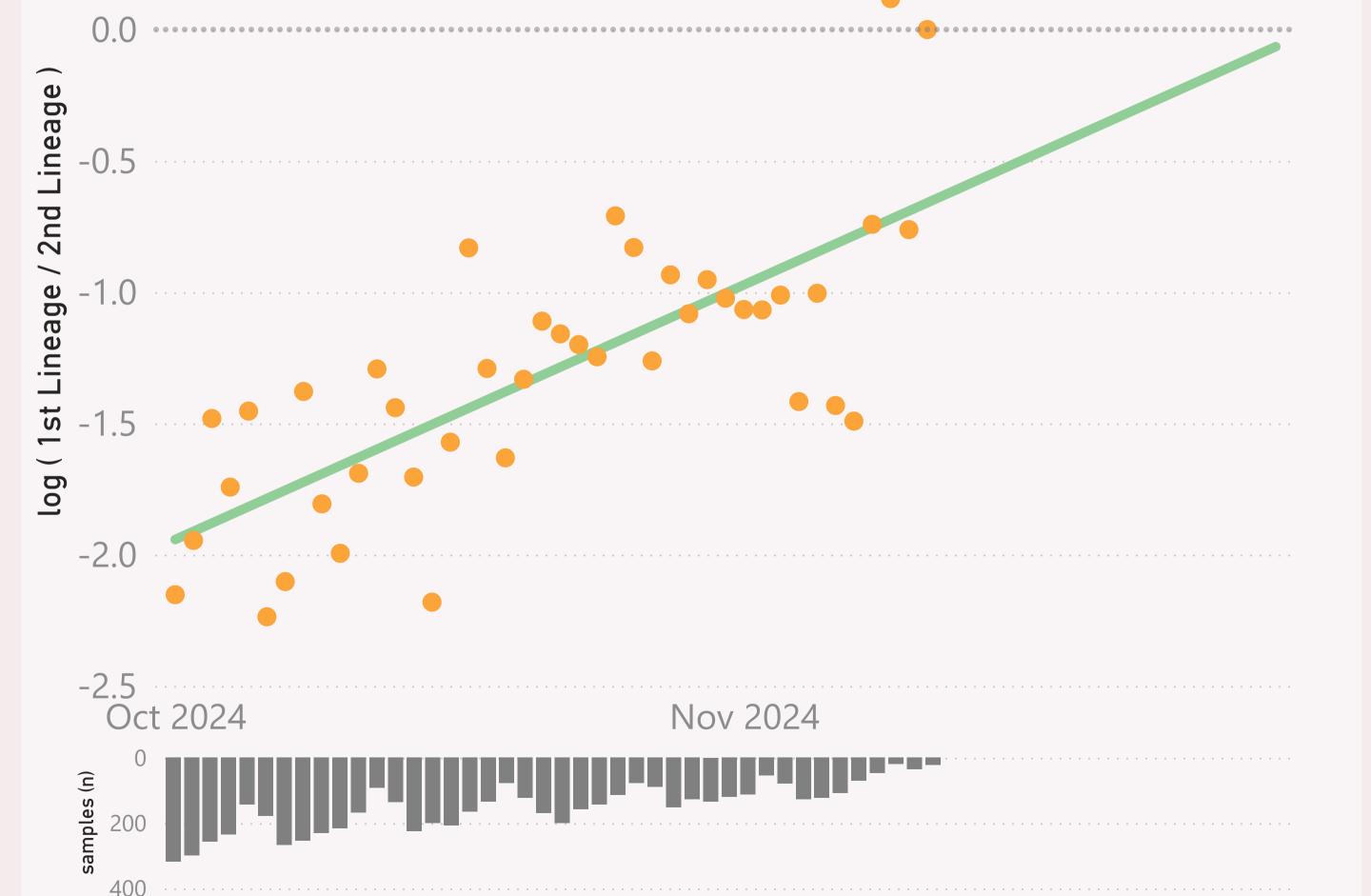
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that state.

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n=6,222 sequenced genomes, up to 11 November 2024





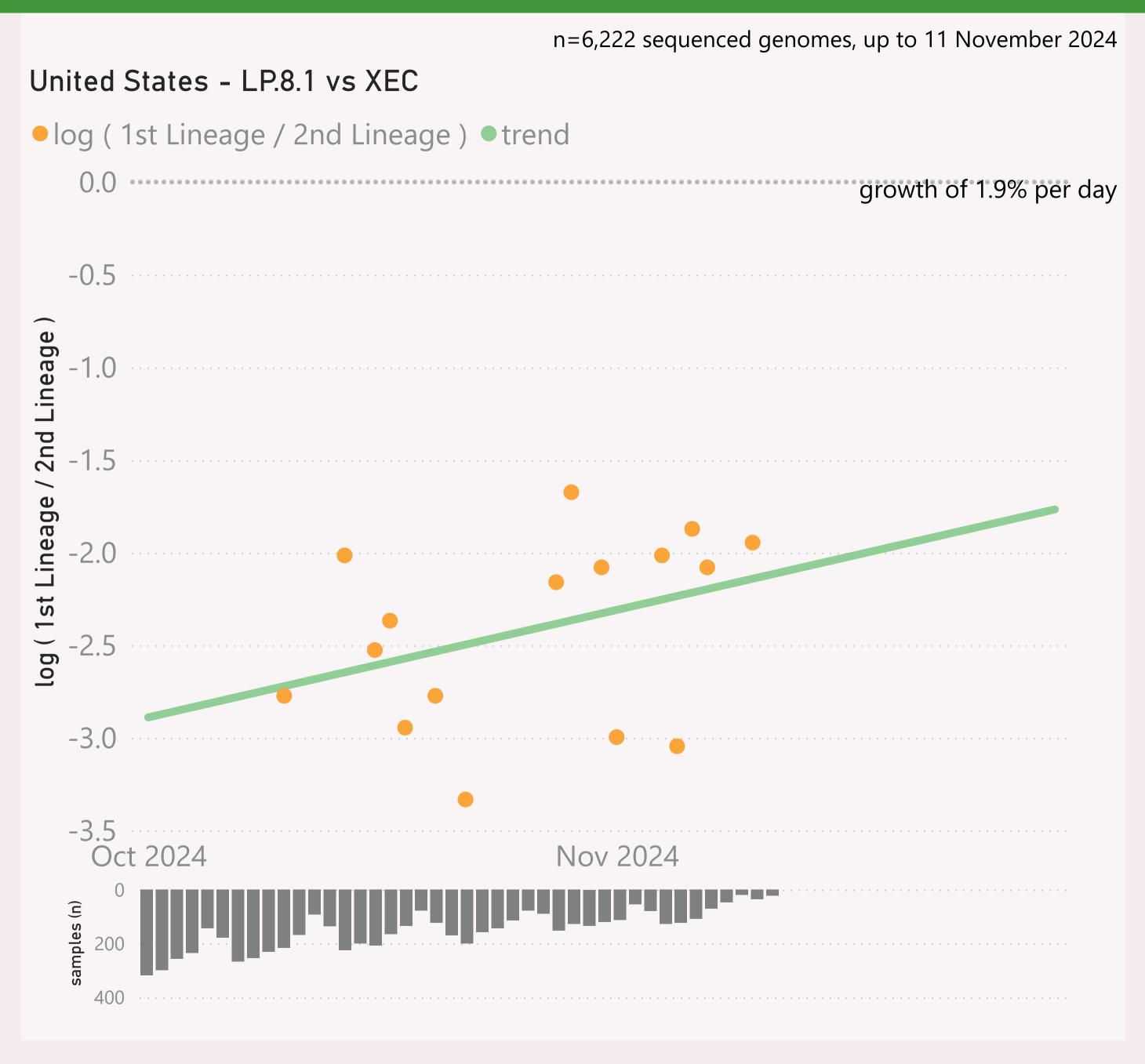


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

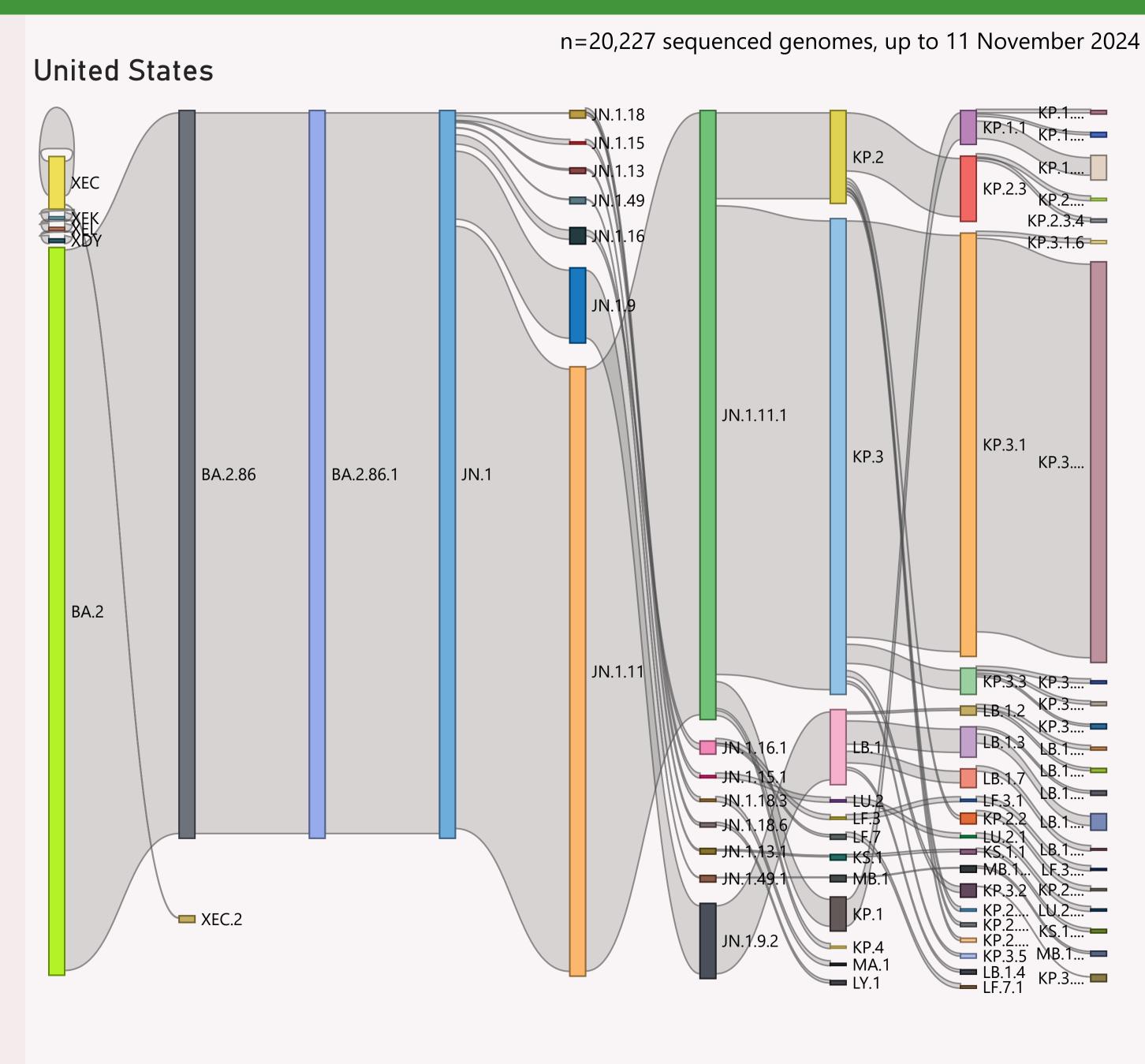


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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

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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
□ United States	19,597	11/11/2024		22/11/2024	المدامر الباليمين عامر وبالبالما
New York	2,744	11/11/2024		22/11/2024	a bone at an interest
Colorado	2,483	07/11/2024	- Marie	22/11/2024	المالية الأراب
California	2,326	11/11/2024	المطالب السار	22/11/2024	delle atrode assistant consis
Texas	1,943	09/11/2024	عمالك بان	22/11/2024	بالمنا السال
Ohio	1,284	04/11/2024	a reliable	22/11/2024	atturn und minl
Minnesota	1,223	11/11/2024		22/11/2024	ala. Eli el III.
New Jersey	540	10/11/2024	عالله	22/11/2024	all la H.L. rancis.
Connecticut	531	29/10/2024	والمالية	22/11/2024	and the field
Utah	518	11/11/2024	عيناني .	22/11/2024	Landan Lan
Tennessee	485	05/11/2024	J dinta .	22/11/2024	
Virginia	461	11/11/2024	l Halian	22/11/2024	ara ar lar dhan ar 11
Maryland	415	08/11/2024	والمأفل	22/11/2024	ale anne al est eller
New Mexico	408	30/10/2024	عالمأان	19/11/2024	ar I a
Rhode Island	363	17/10/2024	<u>Life</u>	15/11/2024	
Illinois	353	10/11/2024	. 44.	22/11/2024	محالها للرما
Michigan	333	07/11/2024	ب التأملان	22/11/2024	Hlata a single
Hawaii	318	09/11/2024		22/11/2024	a II. I
Nevada	267	11/11/2024	riber -	22/11/2024	and a full of the control
North Carolina	253	11/11/2024	than a	22/11/2024	
Washington	252	06/11/2024	الملسانية التالية	22/11/2024	a Lacacar crack
Pennsylvania	225	08/11/2024	line.	22/11/2024	مصاحبا المالوال
Georgia	206	11/11/2024	allian, se	22/11/2024	
Arizona	202	09/11/2024		22/11/2024	والمنطا والمراجلا
Louisiana	202	10/11/2024	<b>≜</b> a.	22/11/2024	
Massachusetts	183	07/11/2024	والأربية والمراجع	22/11/2024	
Delaware	172	08/11/2024	Цı	19/11/2024	عال والمراعد
Nebraska	170	09/11/2024	. أويلا	20/11/2024	
Total	19,597	11/11/2024		22/11/2024	Haldin alcandal nat ad

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.