n=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

United States

● BA.2.86.*   ● JN.1.* +DeFL...   ● JN.1.* +FLiRT   ● LP.8.1.*   ● NB.1.8.1.* ...   ● XEC.*   ● XFG.*

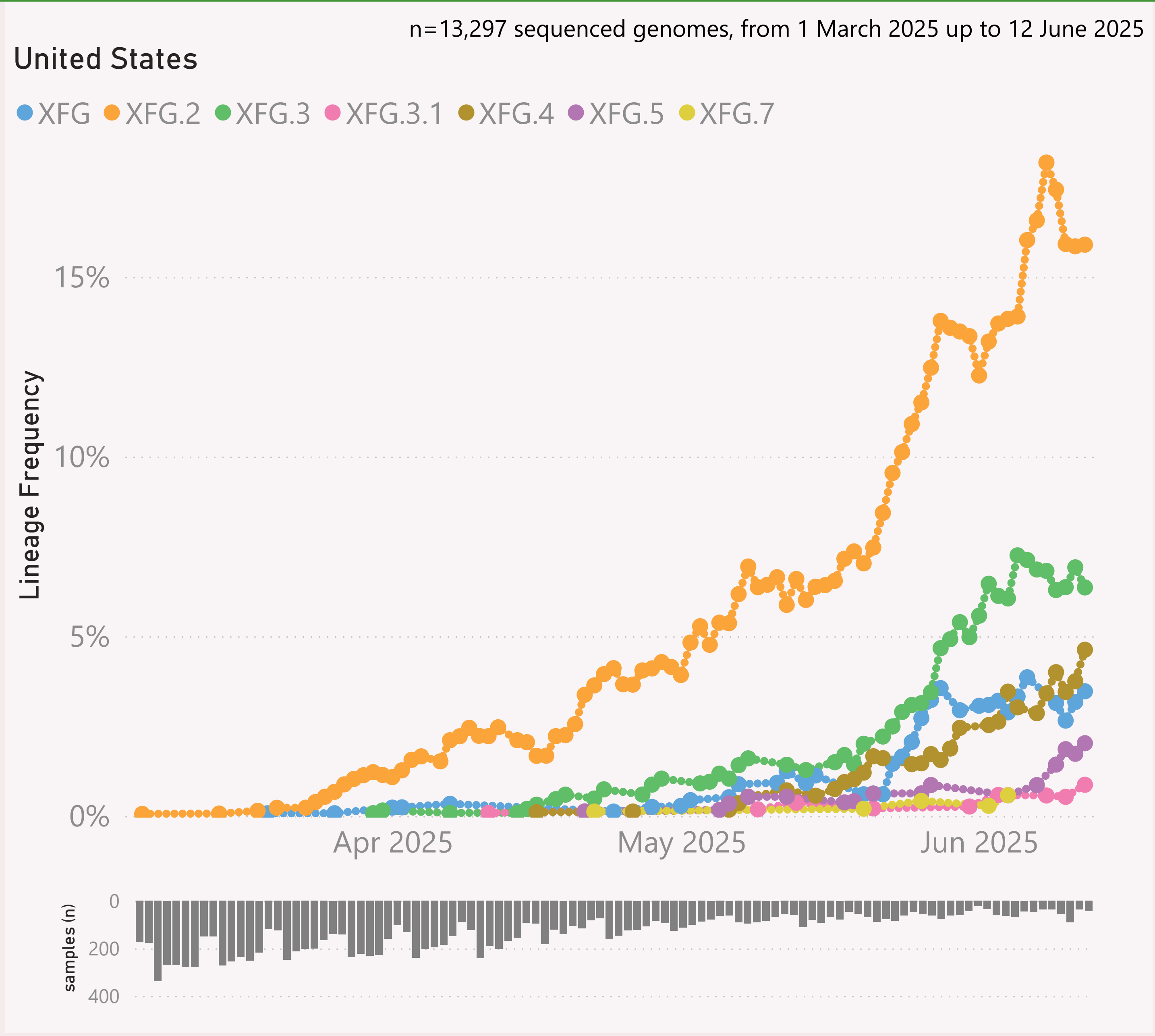This page shows the frequency of the top 7 "L2" lineages, across recent months.

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.

n=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

United States

●XFG ●XFG.2 ●XFG.3 ●XFG.3.1 ●XFG.4 ●XFG.5 ●XFG.7

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.*.

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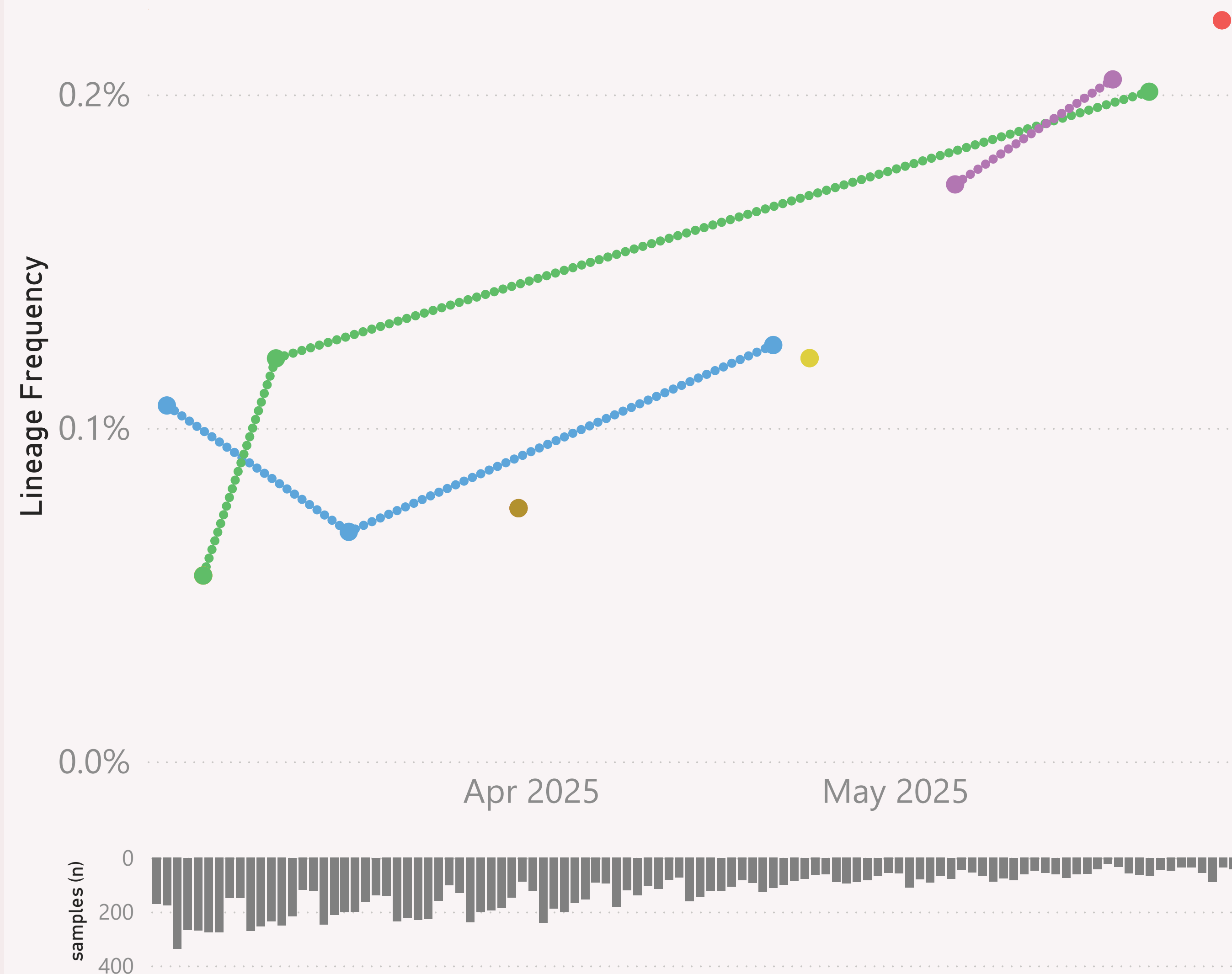
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

United States

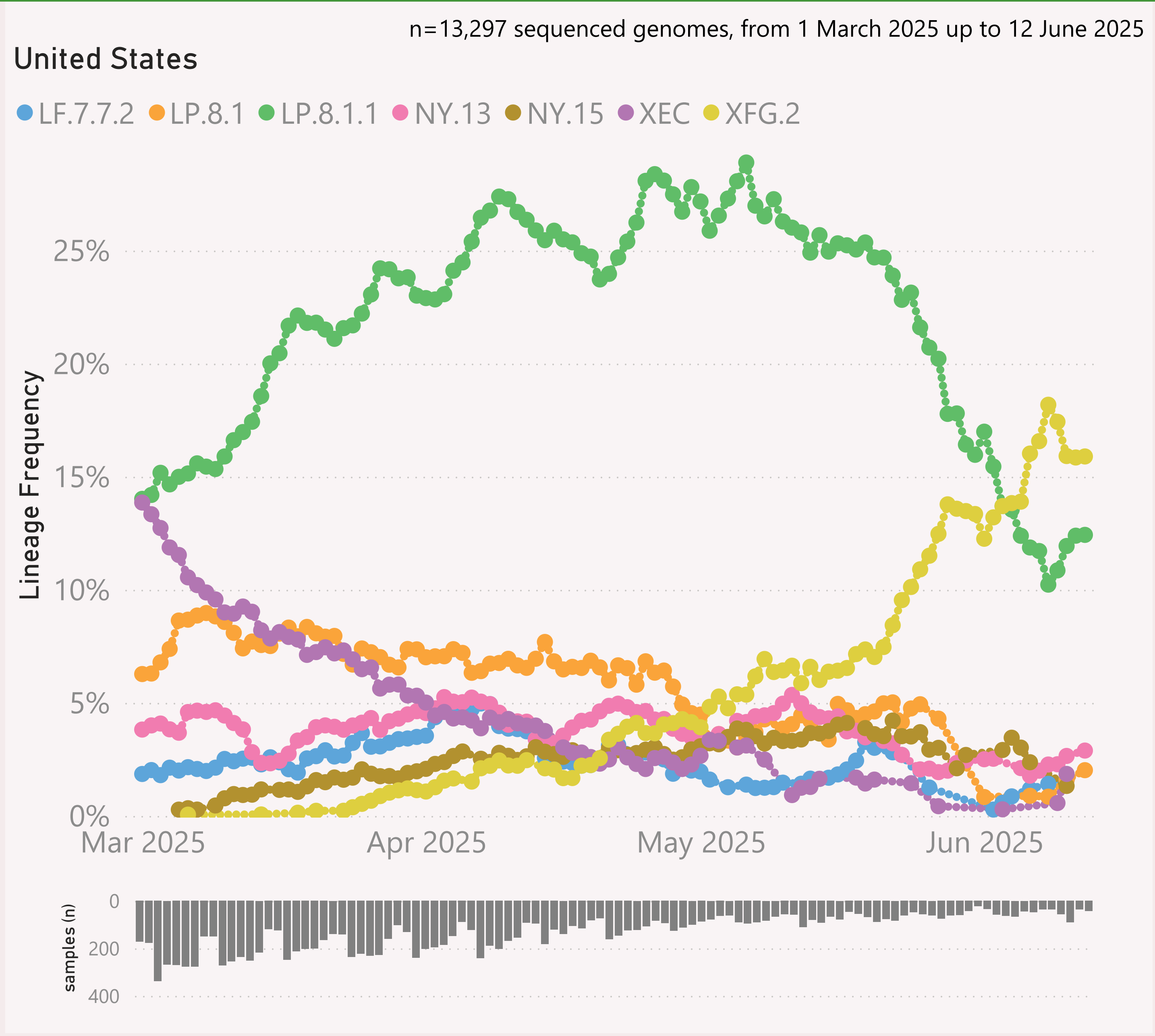● NB.1　● NB.1.1　● NB.1.2　● NB.1.2.1　● NB.1.6　● NB.1.8　● XDV　● XDV.1.5.1

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 NB.1.8.1.* "Nimbus".

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=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

United States

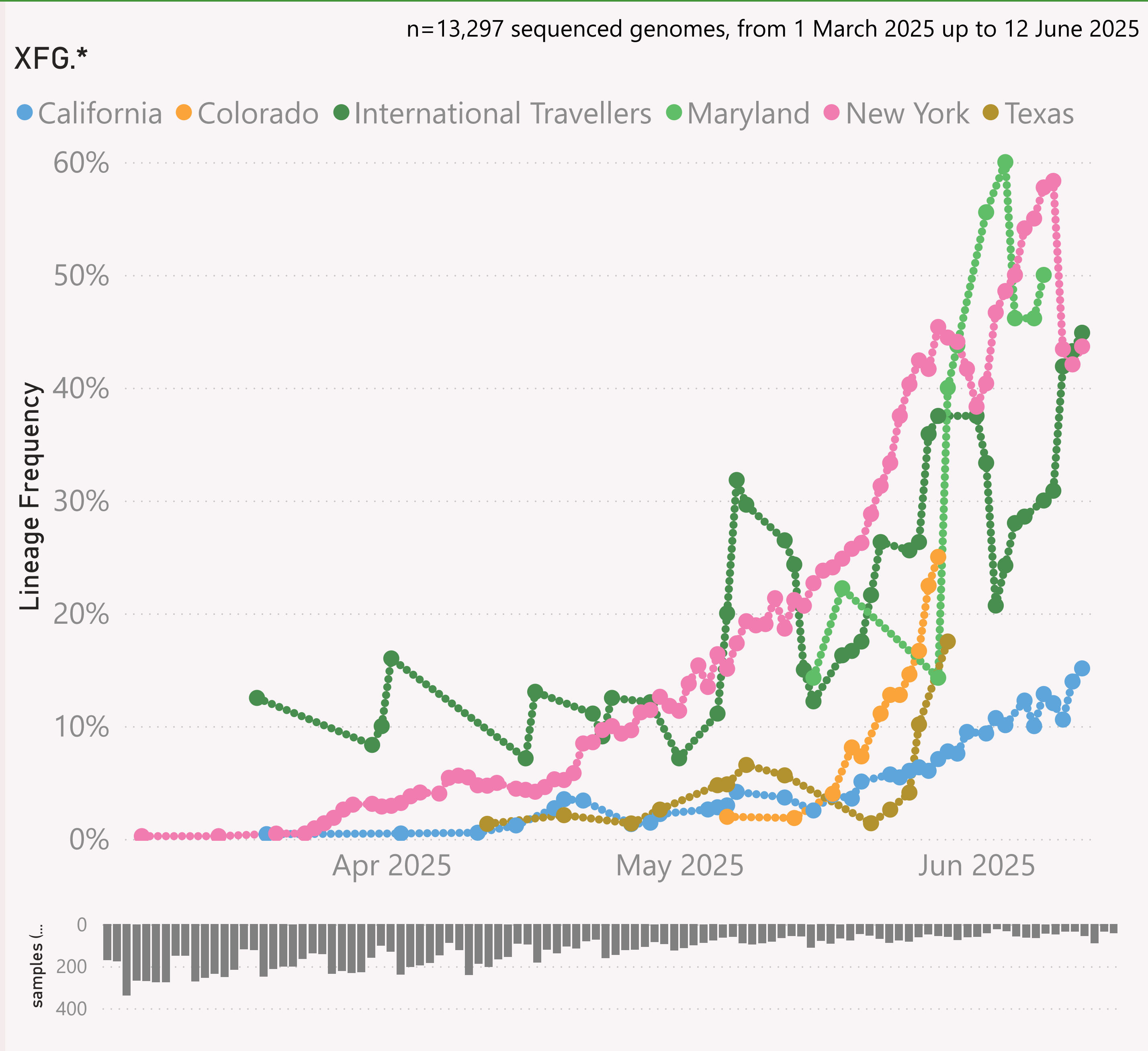● LF.7.7.2 ● LP.8.1 ● LP.8.1.1 ● NY.13 ● NY.15 ● XEC ● XFG.2

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.

COVID-19 Genomic Sequencing analysis - top Locations for a Lineage. Data from gisaid.org, with nextclade lineages Source files and info on github.

Last Update: 2025-07-05 06:12 (UTC)

n=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

XFG.*

- California
- Colorado
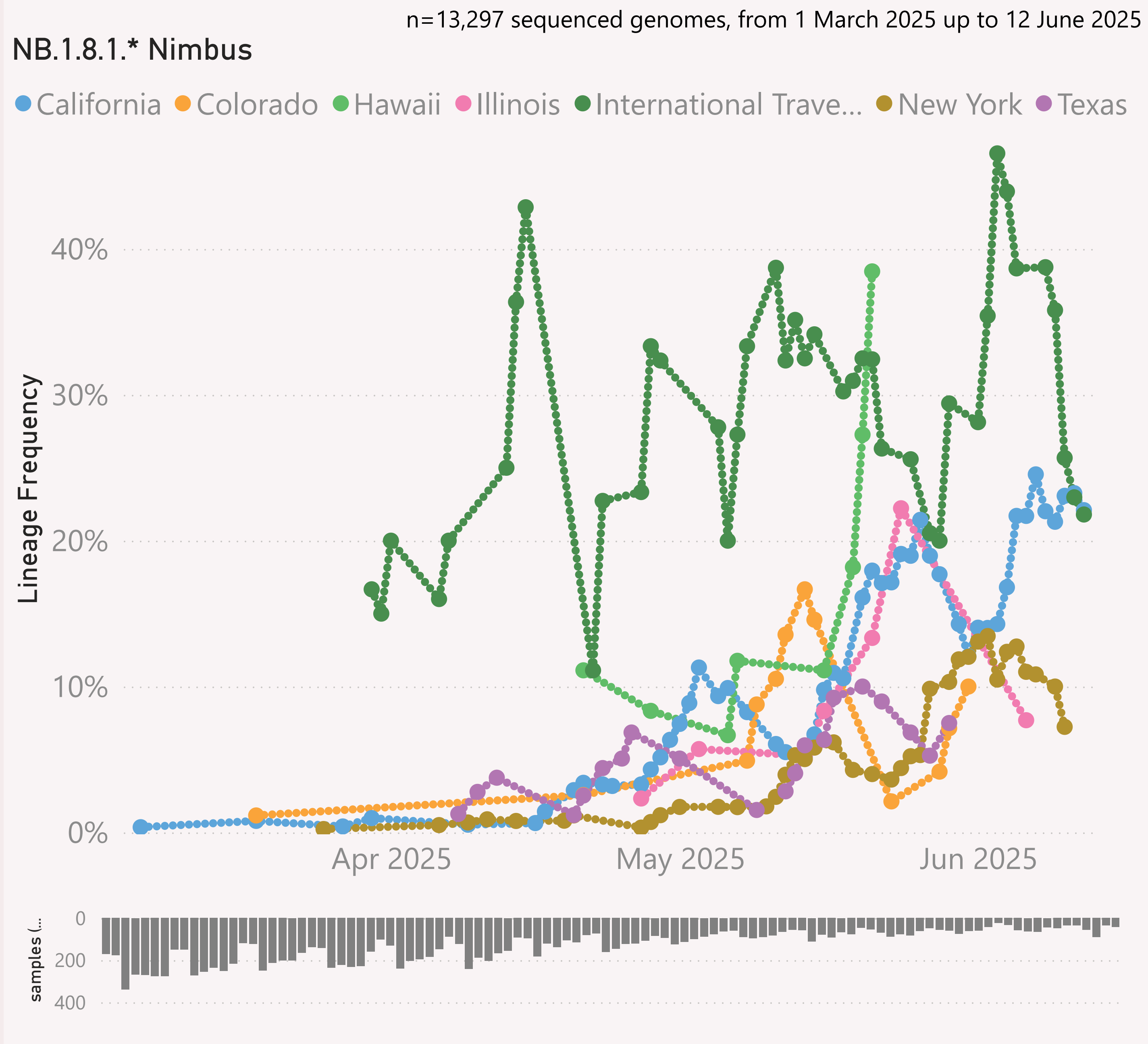- International Travellers
- Maryland
- New York
- Texas

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=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

NB.1.8.1.* Nimbus

● California ● Colorado ● Hawaii ● Illinois ● International Trave... ● New York ● Texas

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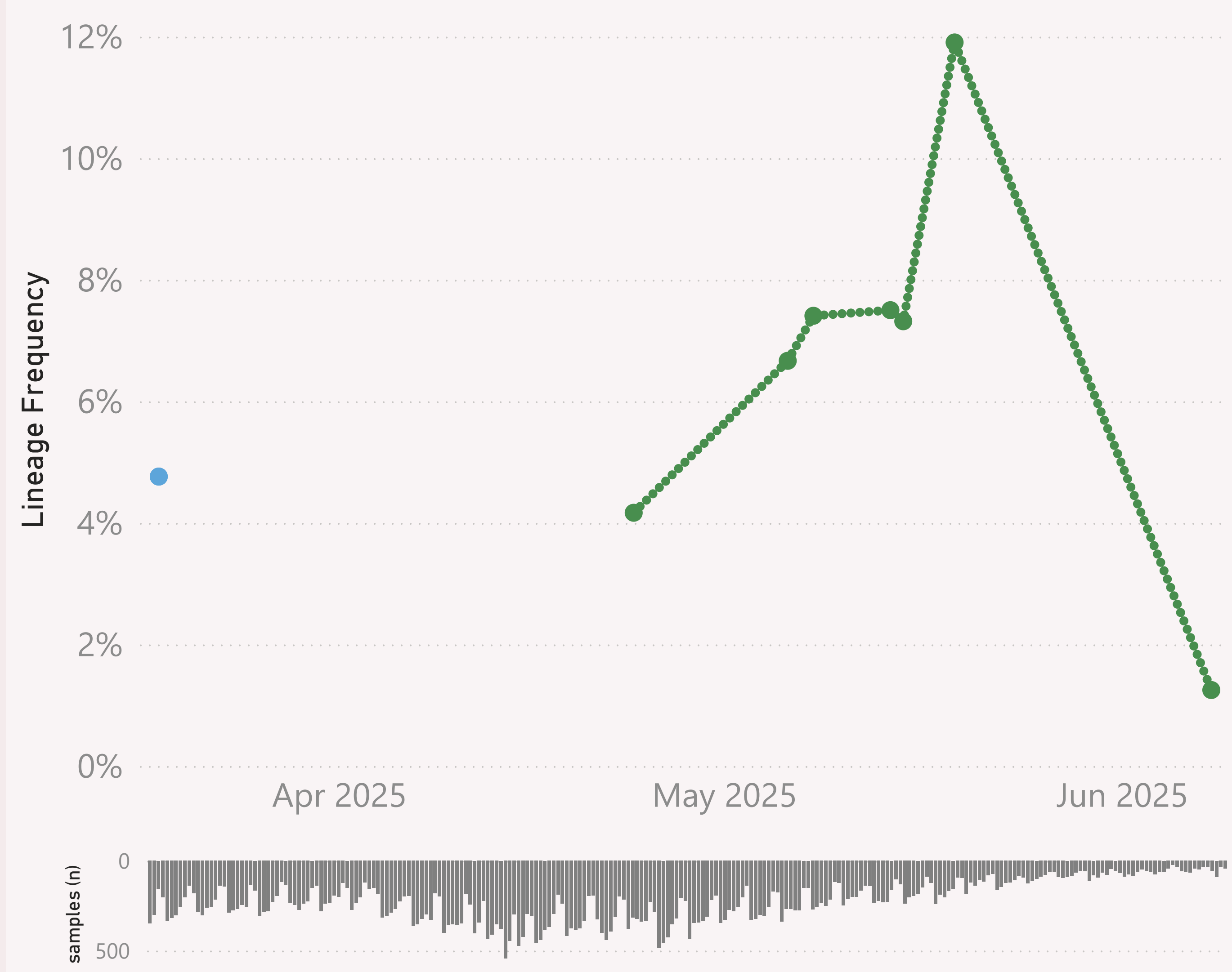
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=53,737 sequenced genomes, from 10 October 2024 up to 12 June 2025

XFP

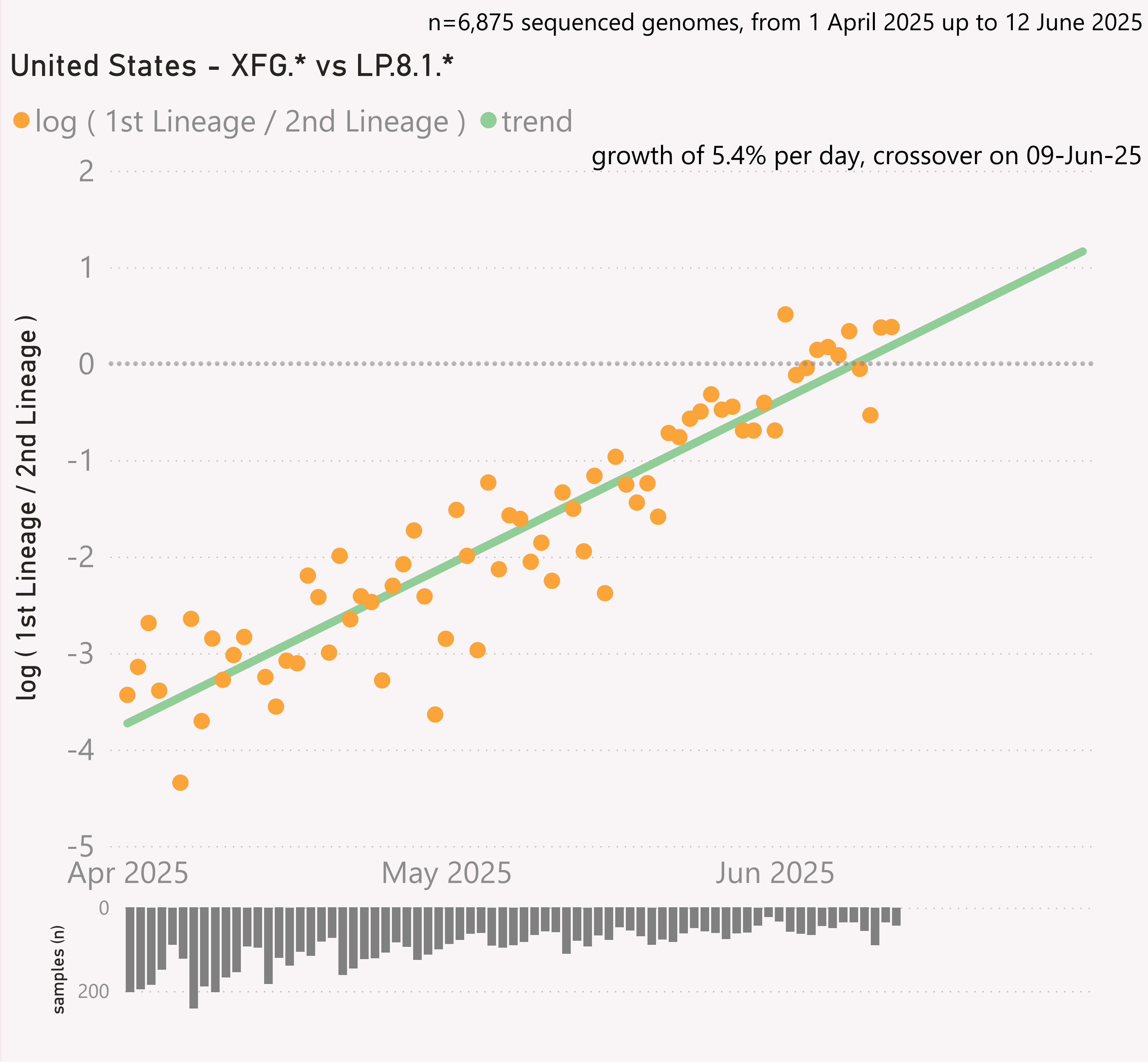● District of Columbia   ● International Travellers

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=6,875 sequenced genomes, from 1 April 2025 up to 12 June 2025

United States – XFG.* vs LP.8.1.*

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

growth of 5.4% per day, crossover on 09-Jun-25

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.
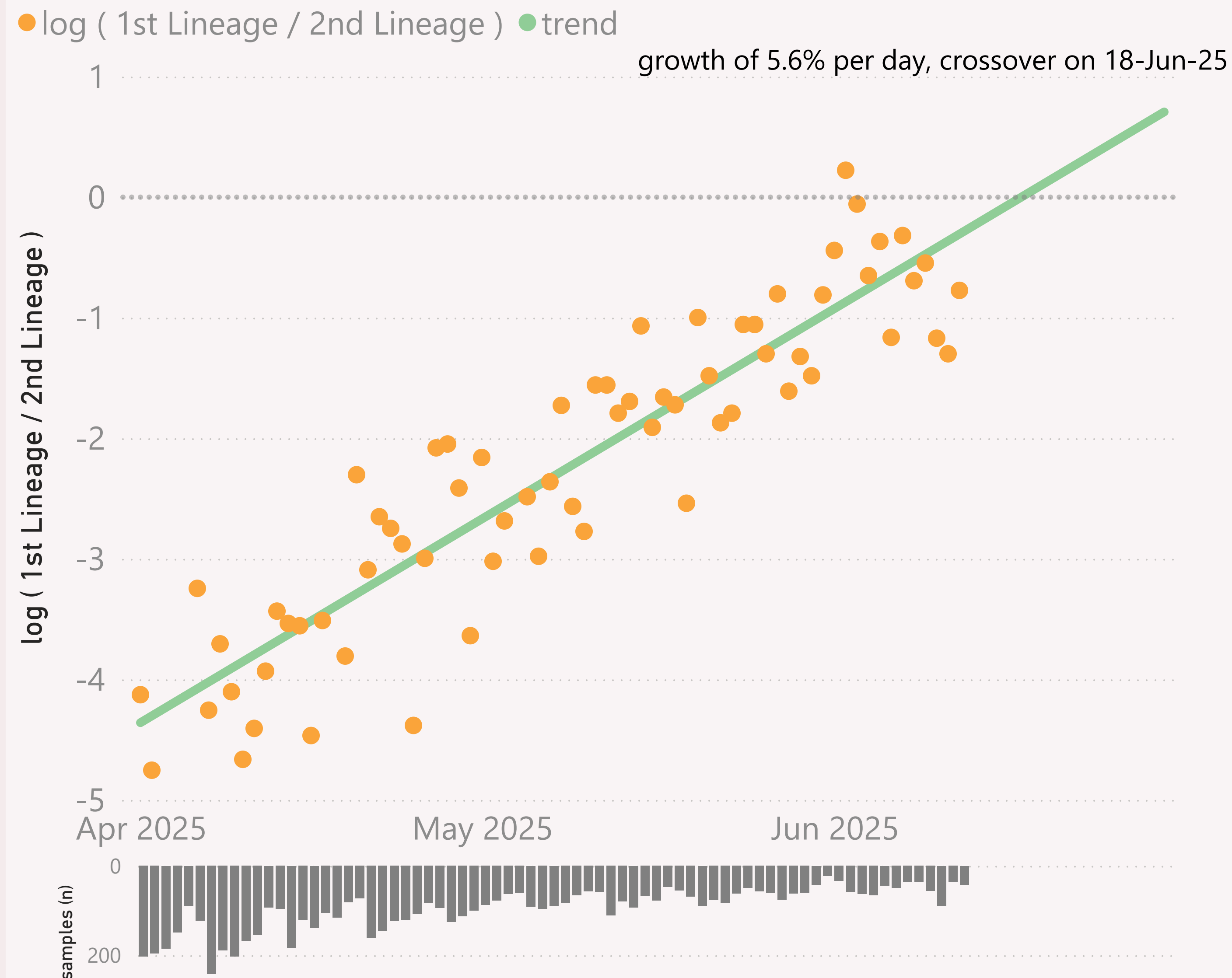
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage L2 is considered to have "crossed over" or taken over dominance from the 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=6,875 sequenced genomes, from 1 April 2025 up to 12 June 2025

United States – NB.1.8.1.* Nimbus vs LP.8.1.*

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

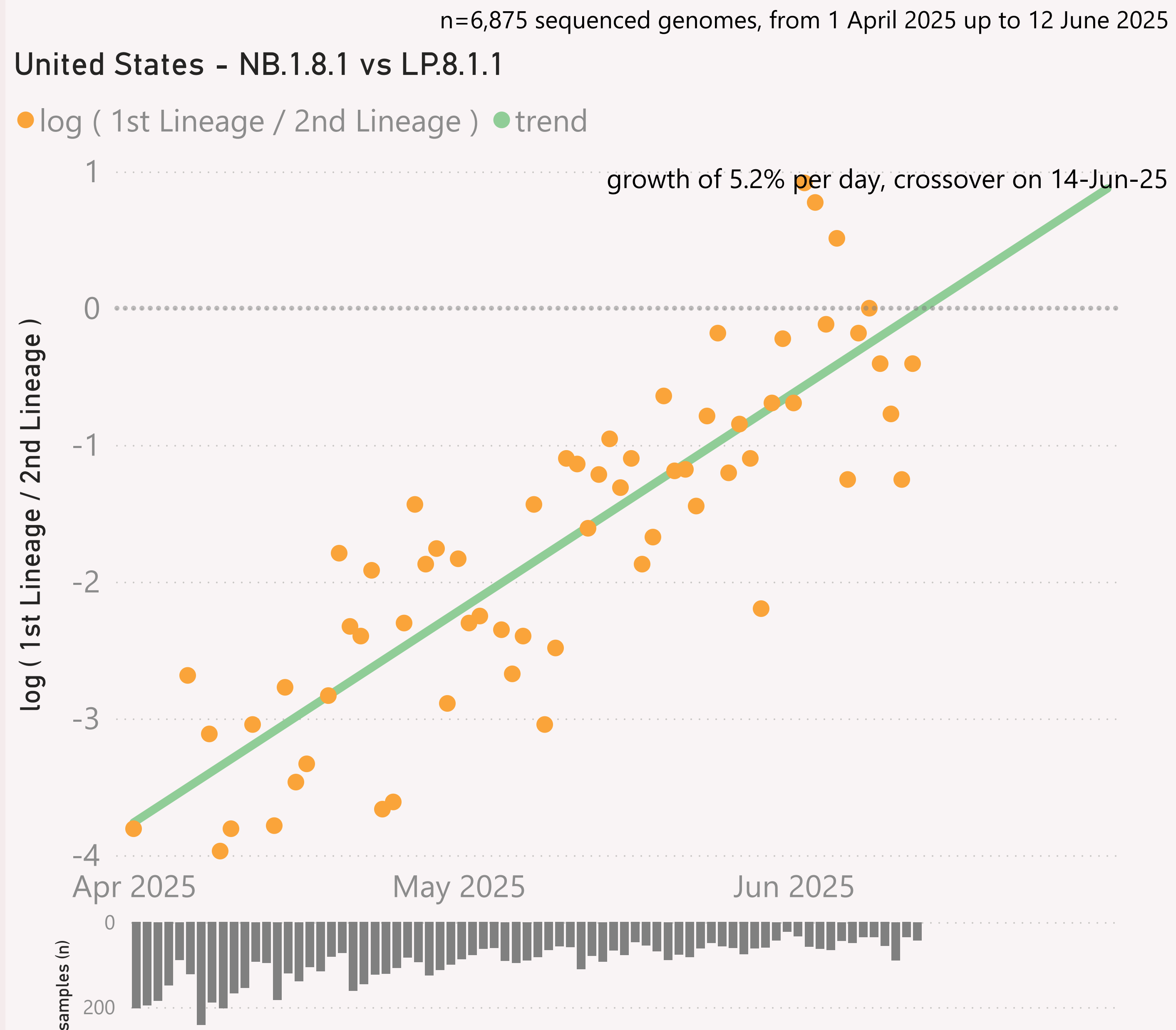growth of 5.6% per day, crossover on 18-Jun-25

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=6,875 sequenced genomes, from 1 April 2025 up to 12 June 2025

United States – NB.1.8.1 vs LP.8.1.1

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

growth of 5.2% per day, crossover on 14-Jun-25

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.

COVID-19 Genomic Sequencing sankey diagram. Data from gisaid.org, with nextclade lineages. Source files and more info on github.

Last Update: 2025-07-05 06:12 (UTC)

n=13,297 sequenced genomes, from 1 March 2025 up to 12 June 2025

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: 2025-07-05 06:12 (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**	**7,326**	**12/06/2025**		**22/06/2025**	
New York	1,805	12/06/2025		22/06/2025	
California	1,433	12/06/2025		22/06/2025	
Michigan	1,139	30/05/2025		22/06/2025	
Texas	788	29/05/2025		20/06/2025	
Colorado	348	31/05/2025		20/06/2025	
International Travellers	302	12/06/2025		22/06/2025	
Illinois	216	10/06/2025		22/06/2025	
New Mexico	149	10/05/2025		22/06/2025	
New Jersey	143	10/06/2025		22/06/2025	
Connecticut	140	11/05/2025		22/06/2025	
Wisconsin	137	28/05/2025		22/06/2025	
Massachusetts	97	03/05/2025		30/05/2025	
Utah	77	05/05/2025		20/06/2025	
Oregon	72	02/06/2025		22/06/2025	
Rhode Island	71	15/05/2025		22/06/2025	
Hawaii	65	21/05/2025		06/06/2025	
Maryland	60	12/06/2025		20/06/2025	
District of Columbia	49	04/06/2025		22/06/2025	
South Carolina	38	19/05/2025		04/06/2025	
Vermont	33	03/06/2025		22/06/2025	
Nevada	32	12/06/2025		22/06/2025	
Nebraska	29	10/06/2025		22/06/2025	
Wyoming	15	13/05/2025		22/06/2025	
Pennsylvania	12	05/05/2025		05/06/2025	
Arizona	11	18/05/2025		20/06/2025	
North Dakota	10	20/05/2025		11/06/2025	
Florida	9	05/05/2025		03/06/2025	
Total	**7,326**	**12/06/2025**		**22/06/2025**	

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.