

This page shows the frequency of the top 6 "L2" lineages, across recent months.

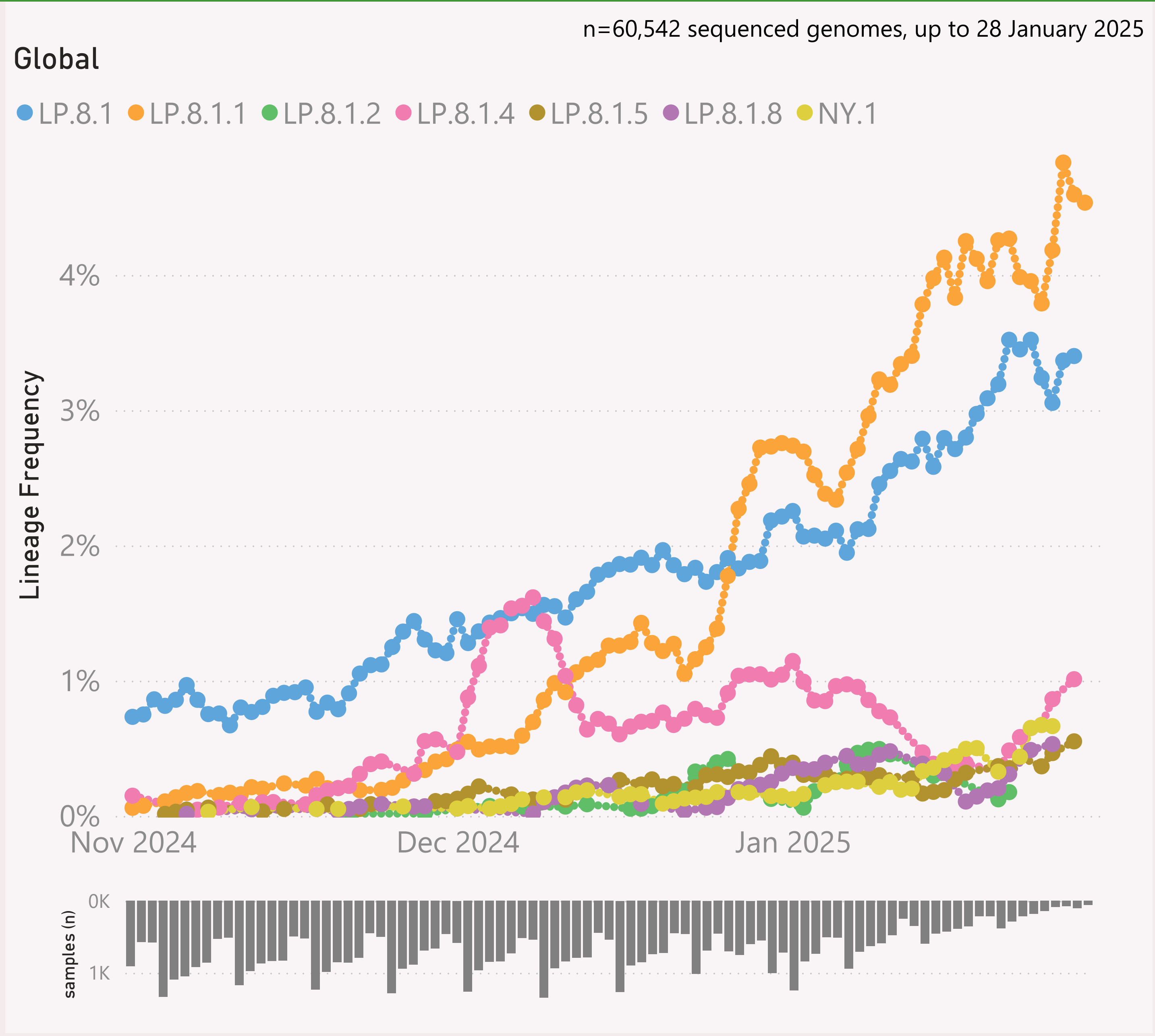
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



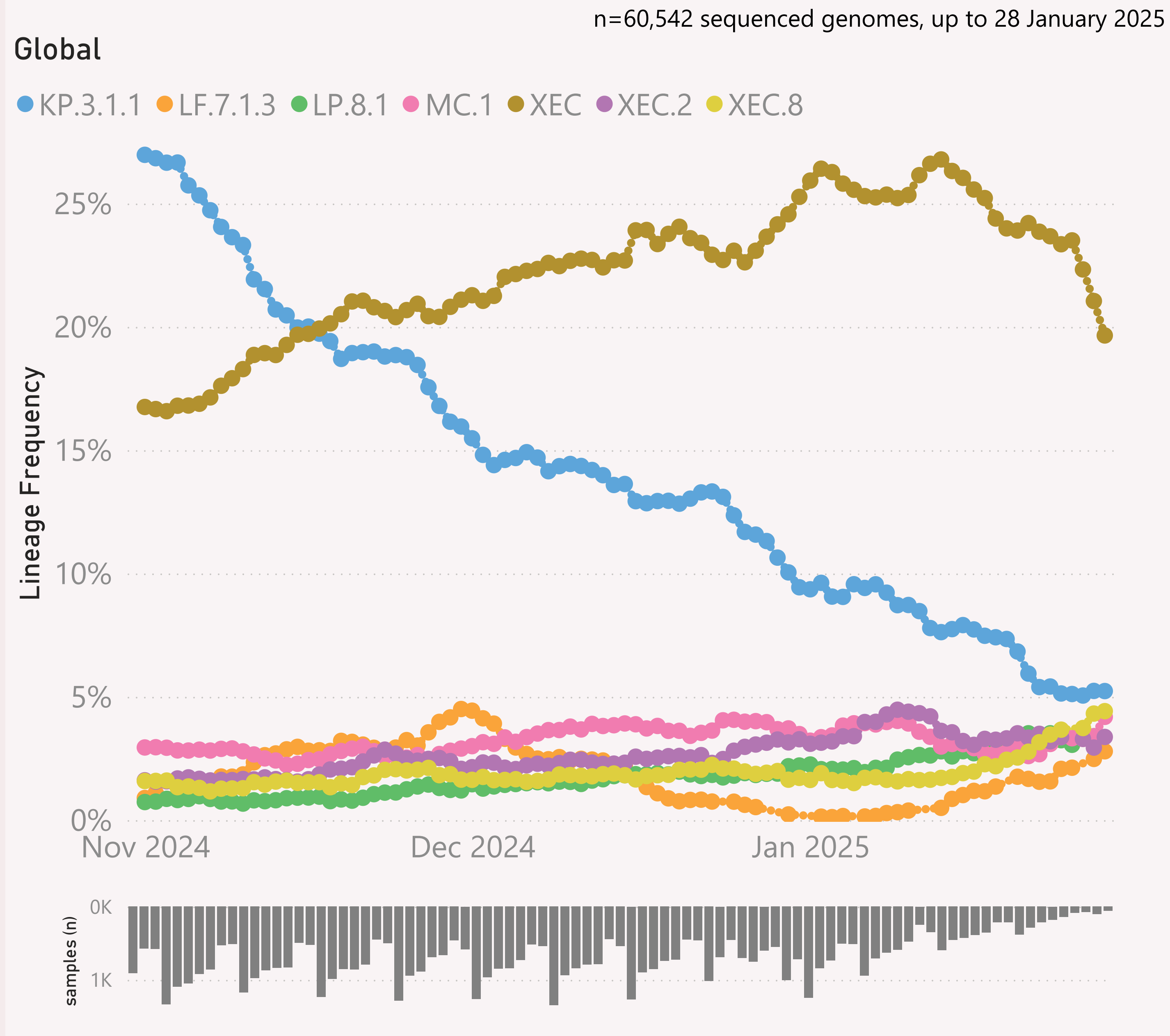
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently LP.8.1.*.

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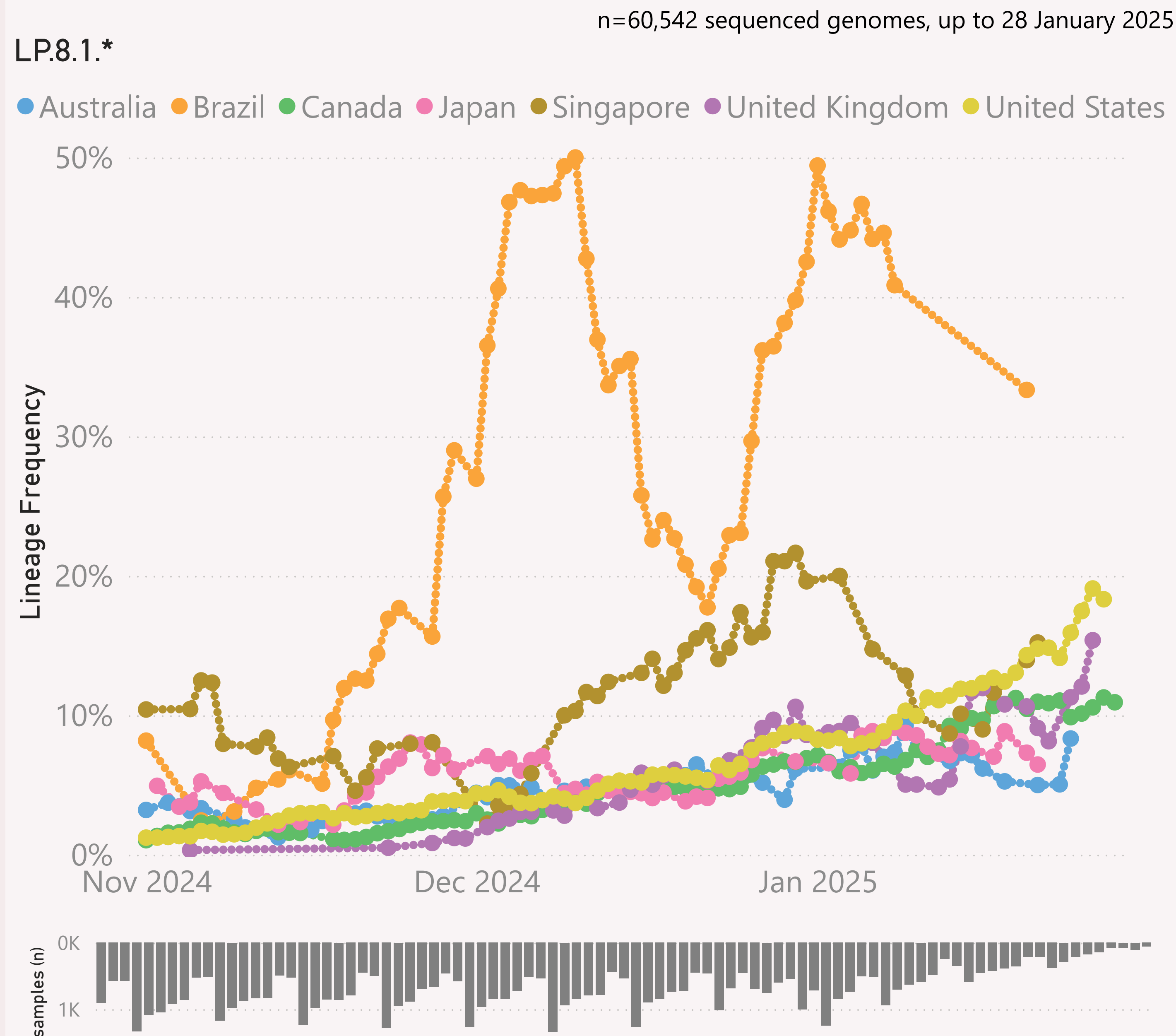
This page shows the frequency of the top 7 lineages, across recent months.

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, for the 7 countries reporting the most samples over recent months.

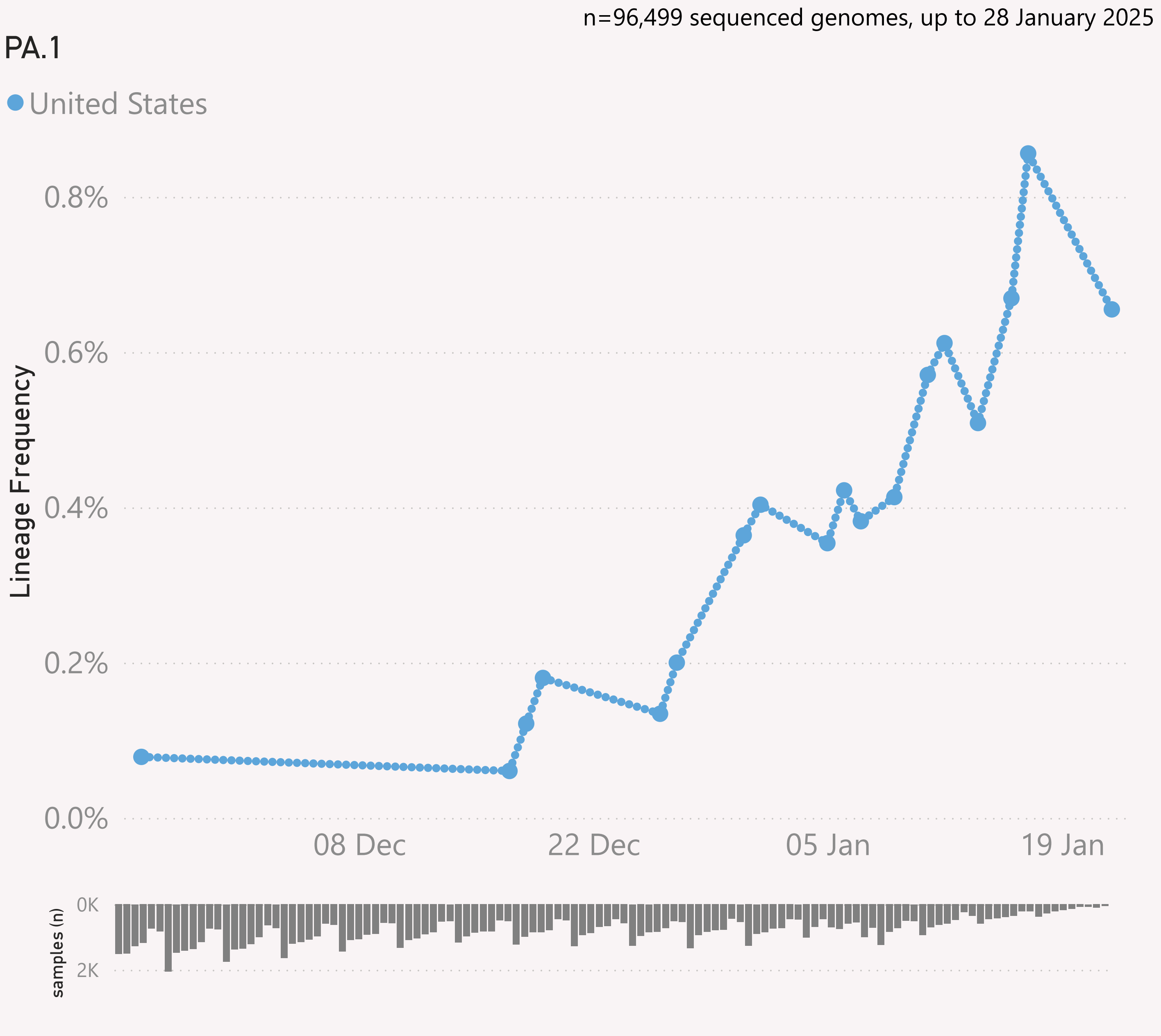
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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, for that country.

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, for the 6 countries reporting the most samples over recent months.

The Lineage classifications are provided by Nextclade.

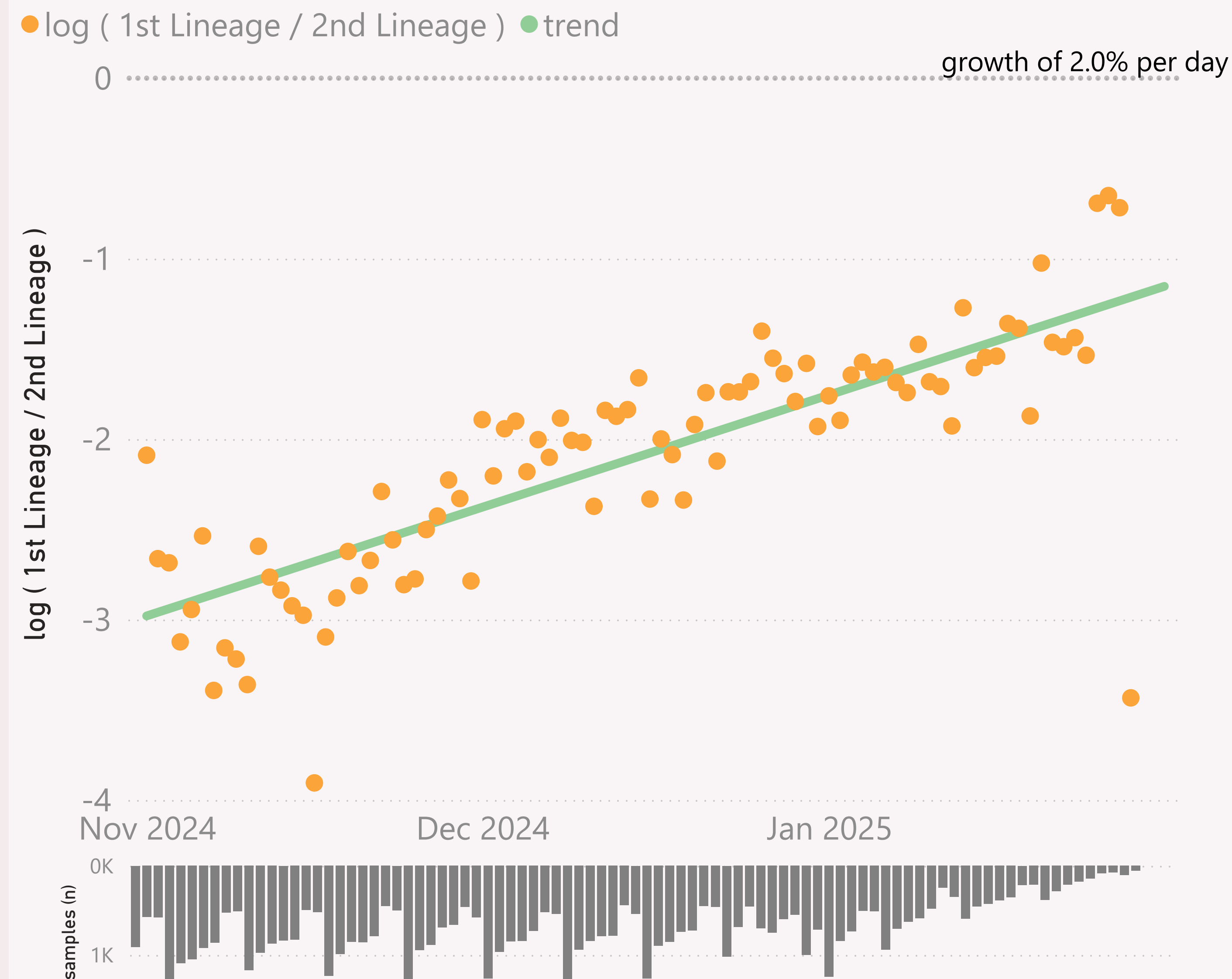
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

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=60,542 sequenced genomes, up to 28 January 2025

Global - LP.8.1.* vs XEC.*



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".

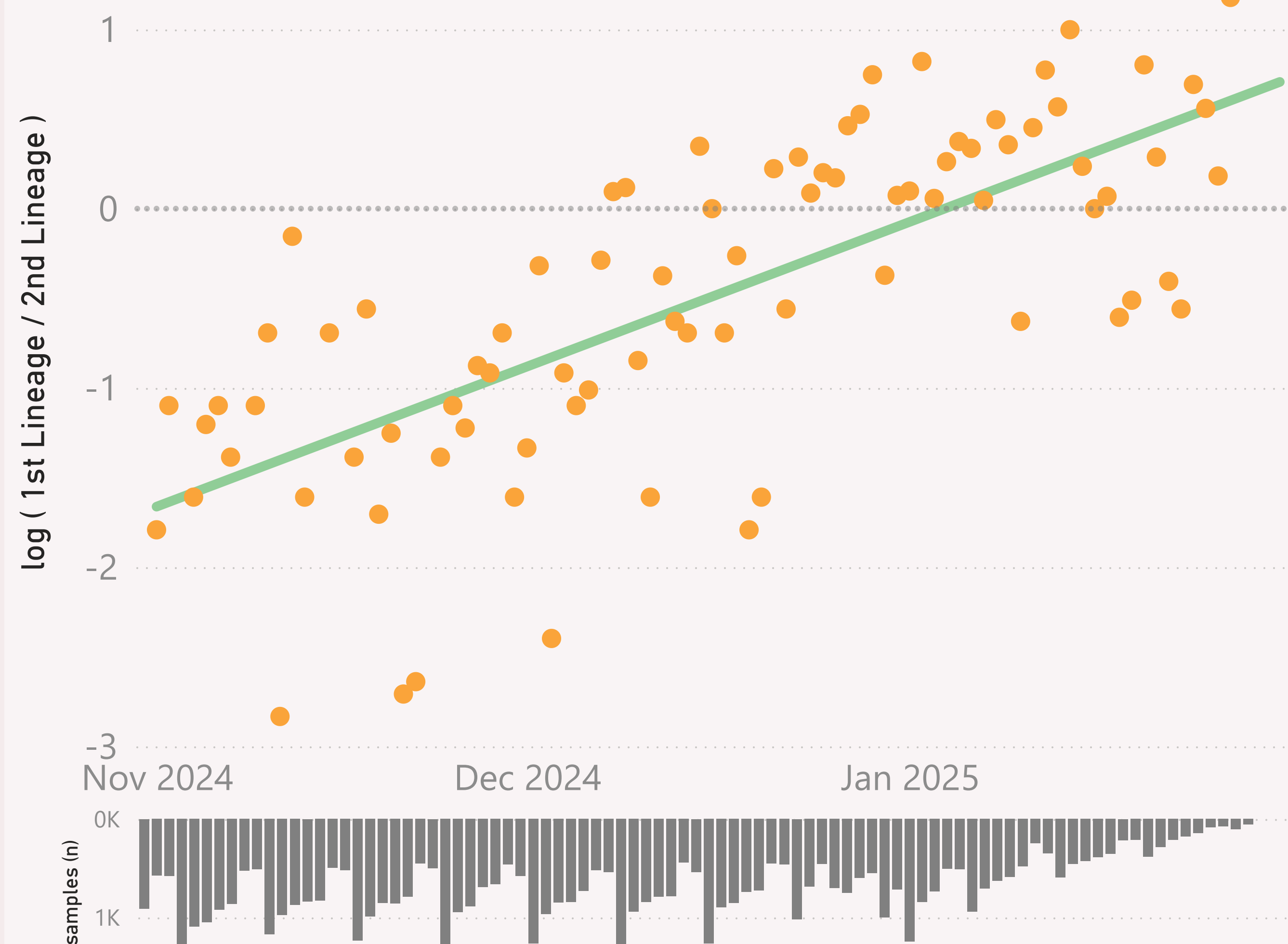
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

n=60,542 sequenced genomes, up to 28 January 2025

Global - LP.8.1.1 vs LP.8.1

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

growth of 2.6% per day, crossover on 04-Jan-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.

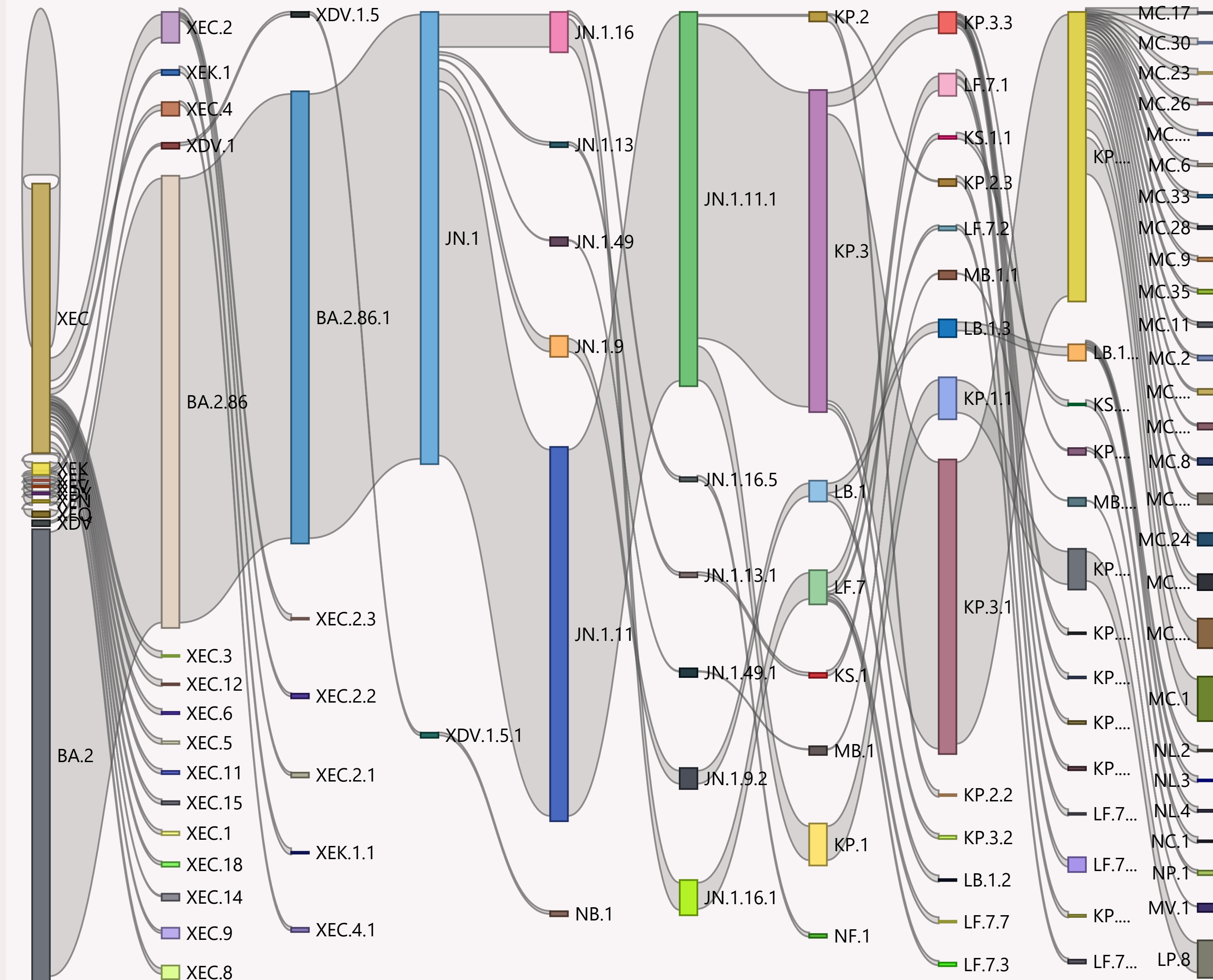
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the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

Global

n=60,736 sequenced genomes, up to 28 January 2025



This page shows the hierarchy of the significant Lineages, over recent months.









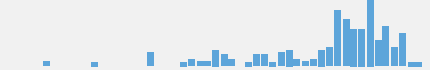





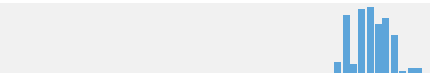









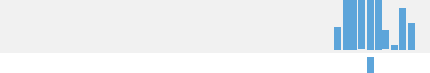
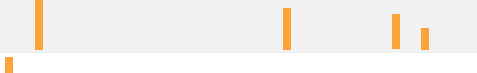




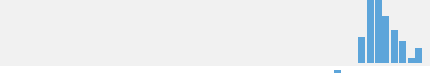

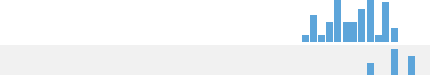
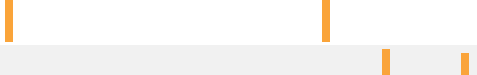


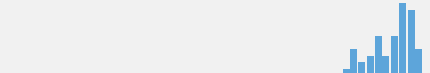



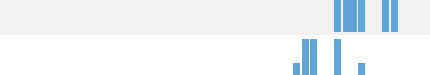


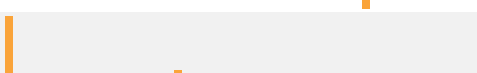


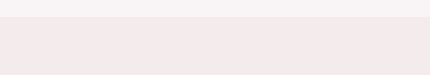
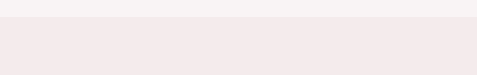
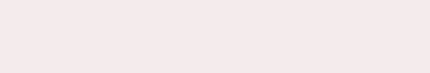
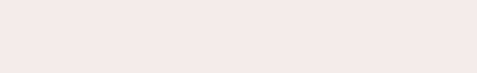
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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
<div>+ United States</div>	21,153	28/01/2025		31/01/2025	
<div>+ Canada</div>	10,558	28/01/2025		31/01/2025	
<div>+ Japan</div>	2,903	28/01/2025		31/01/2025	
<div>+ Russia</div>	2,178	28/01/2025		31/01/2025	
<div>+ Australia</div>	1,827	27/01/2025		31/01/2025	
<div>+ Brazil</div>	1,613	20/01/2025		31/01/2025	
<div>+ Spain</div>	1,518	28/01/2025		31/01/2025	
<div>+ Singapore</div>	1,361	22/01/2025		31/01/2025	
<div>+ United Kingdom</div>	1,345	27/01/2025		31/01/2025	
<div>+ France</div>	1,307	25/01/2025		31/01/2025	
<div>+ China</div>	1,040	20/01/2025		23/01/2025	
<div>+ Germany</div>	969	22/01/2025		31/01/2025	
<div>+ Slovenia</div>	810	21/01/2025		24/01/2025	
<div>+ Sweden</div>	799	27/01/2025		31/01/2025	
<div>+ Peru</div>	754	04/01/2025		31/01/2025	
<div>+ New Zealand</div>	734	18/01/2025		27/01/2025	
<div>+ Italy</div>	664	26/01/2025		31/01/2025	
<div>+ Denmark</div>	646	13/01/2025		29/01/2025	
<div>+ Greece</div>	628	17/12/2024		31/01/2025	
<div>+ Netherlands</div>	567	21/01/2025		31/01/2025	
<div>+ Finland</div>	394	31/12/2024		17/01/2025	
<div>+ Ireland</div>	358	19/01/2025		31/01/2025	
<div>+ Chile</div>	344	30/12/2024		16/01/2025	
<div>+ Israel</div>	337	20/01/2025		31/01/2025	
<div>+ South Korea</div>	318	20/01/2025		31/01/2025	
<div>+ Luxembourg</div>	268	01/01/2025		29/01/2025	
<div>+ Argentina</div>	252	19/12/2024		21/01/2025	
<div>+ Thailand</div>	249	13/01/2025		29/01/2025	
<div>— Total</div>	58,506	28/01/2025		31/01/2025	

This page shows the volume and currency/timeliness of the genomic sequencing data shared via GISAID, over the last 8 weeks, for the countries sharing the most samples.

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.