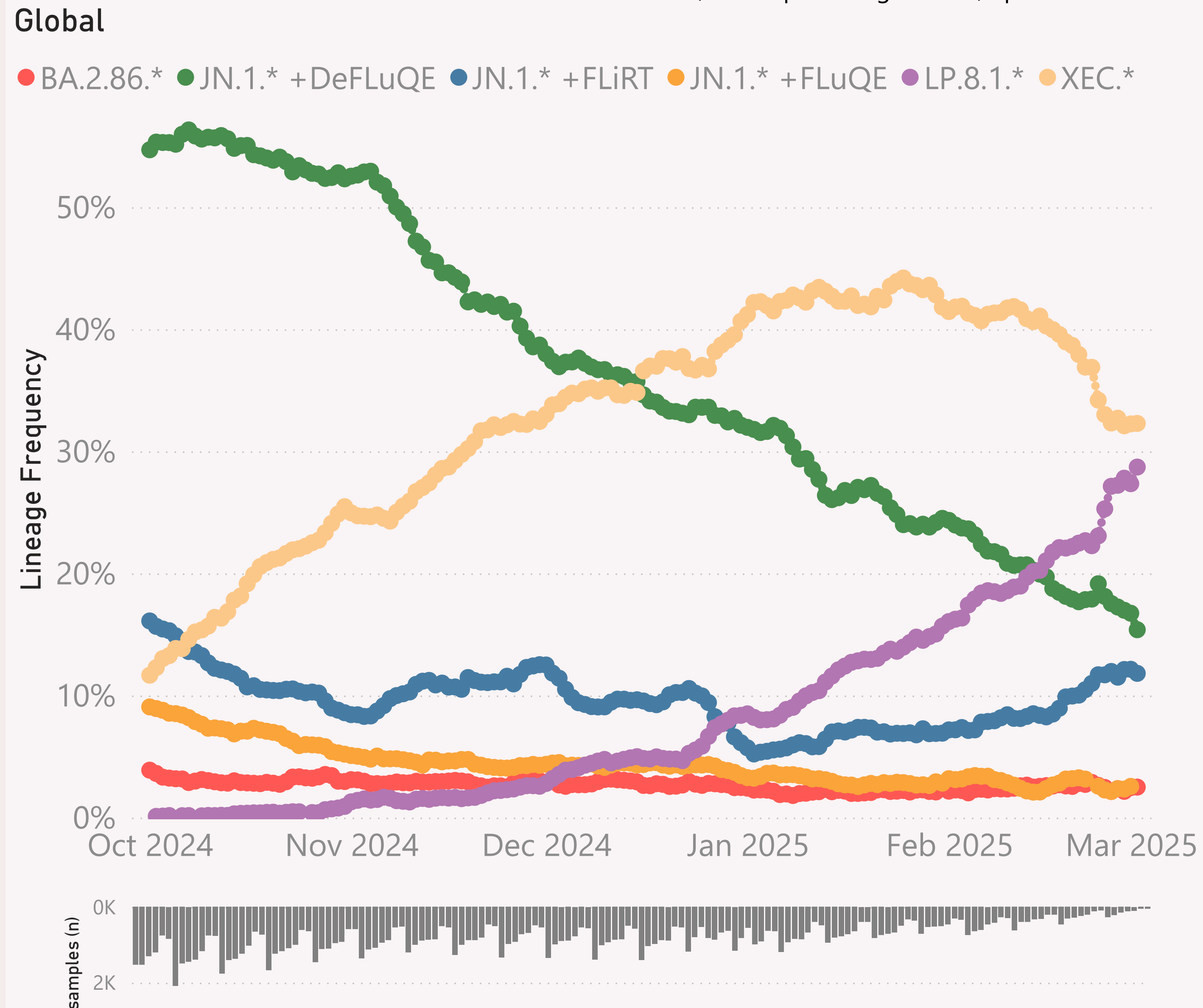


n=118,253 sequenced genomes, up to 2 March 2025



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

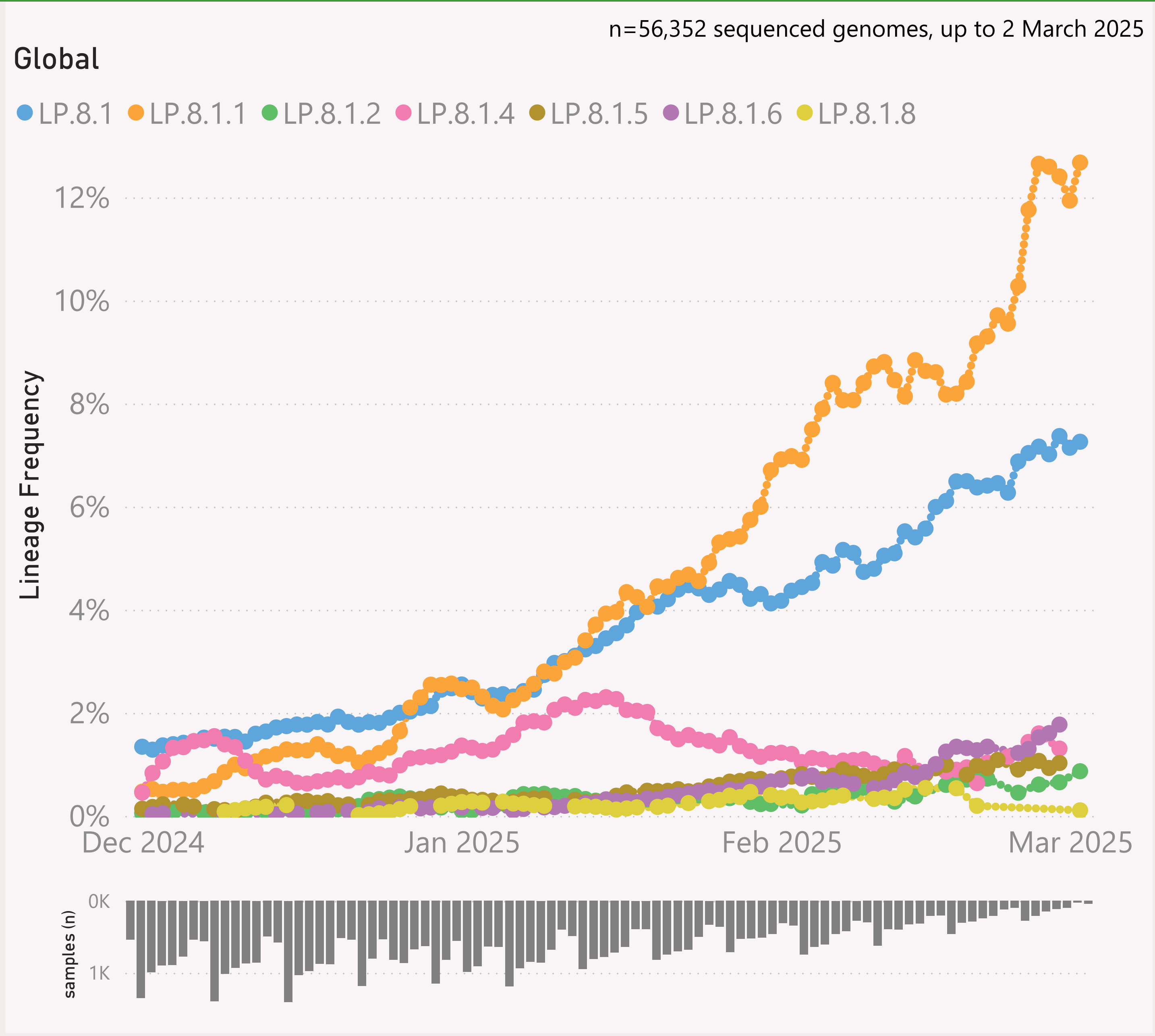
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



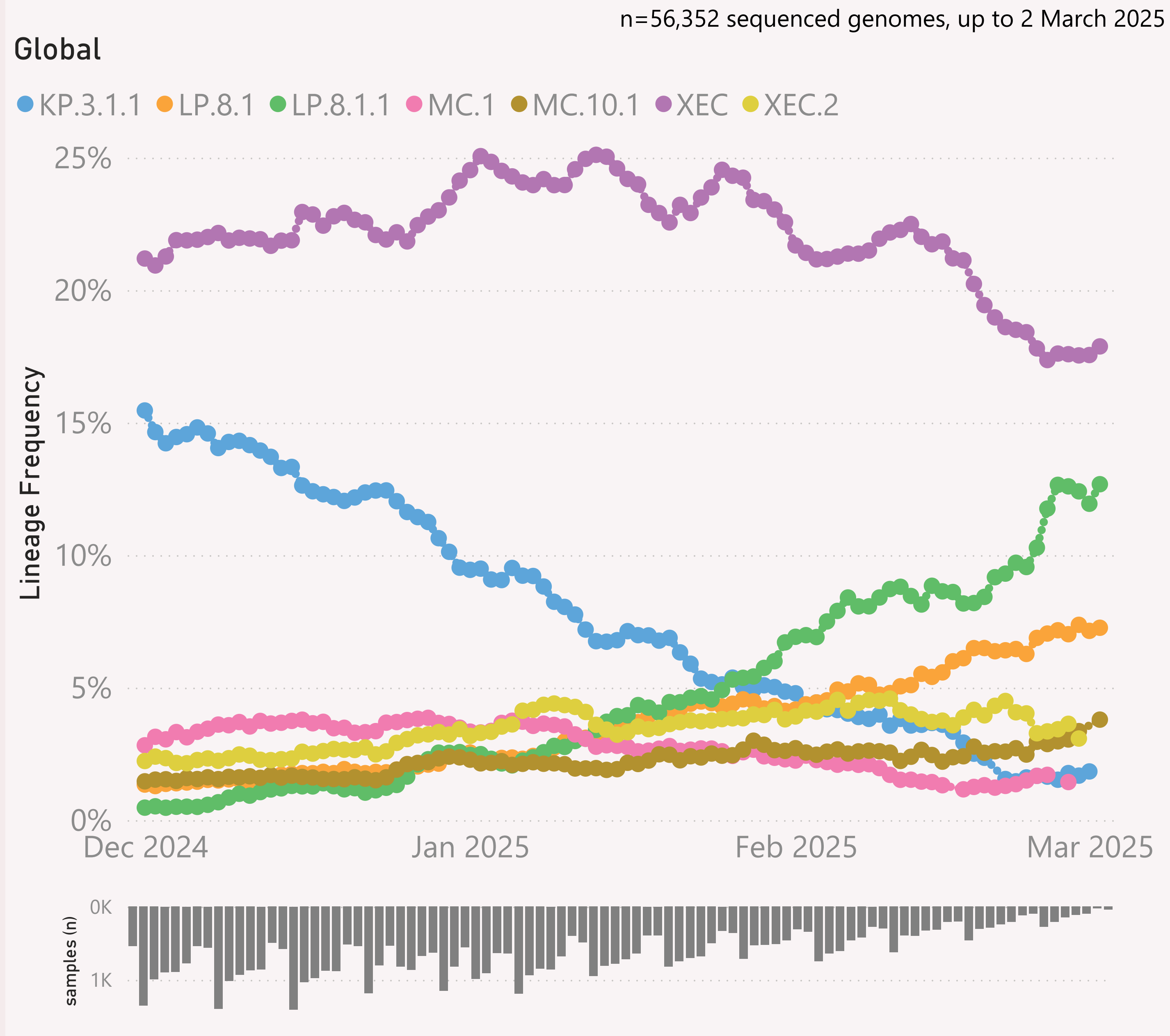
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently LP.8.1.*.

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.

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



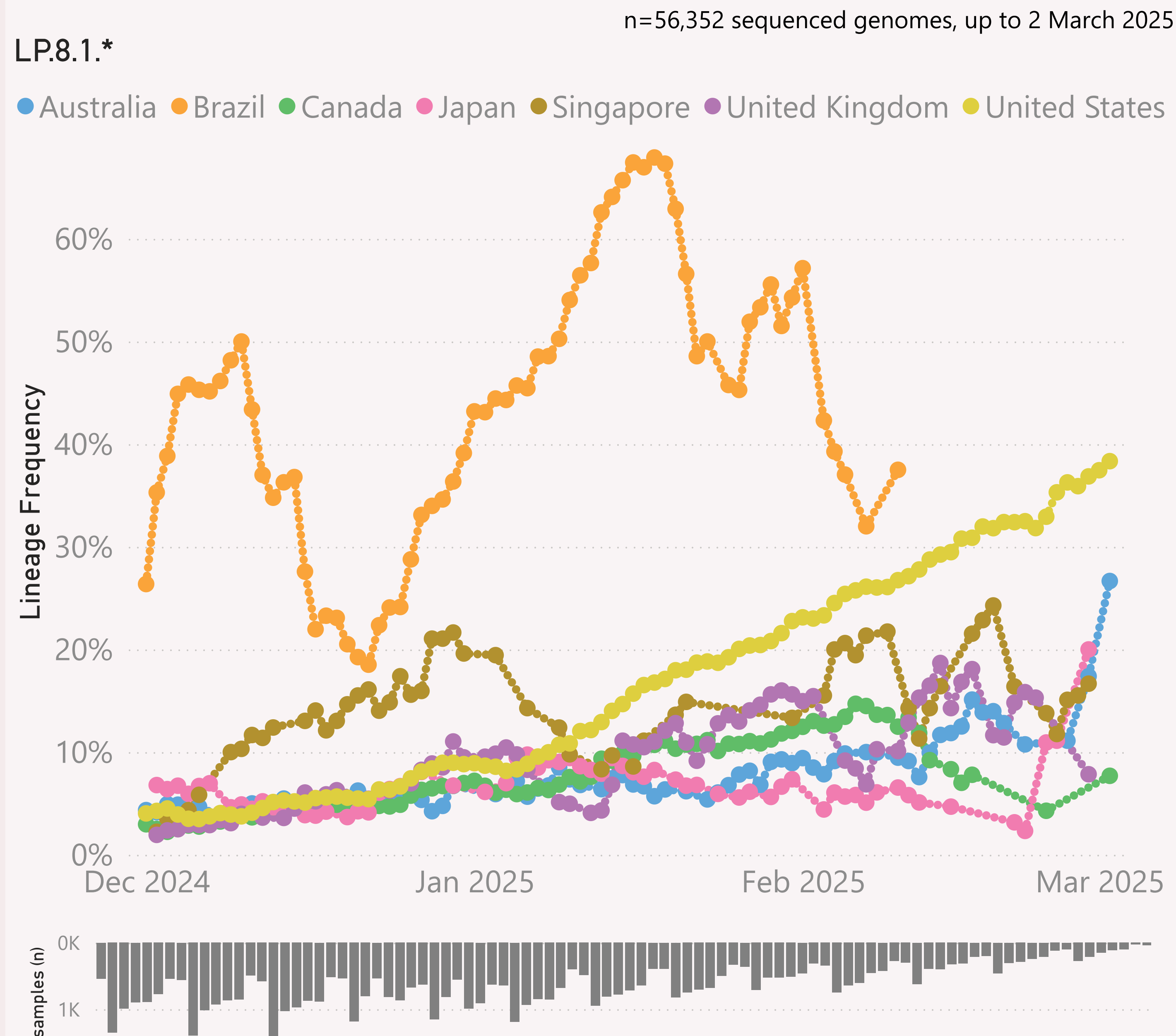
This page shows the frequency of the top 7 lineages, across recent months.

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

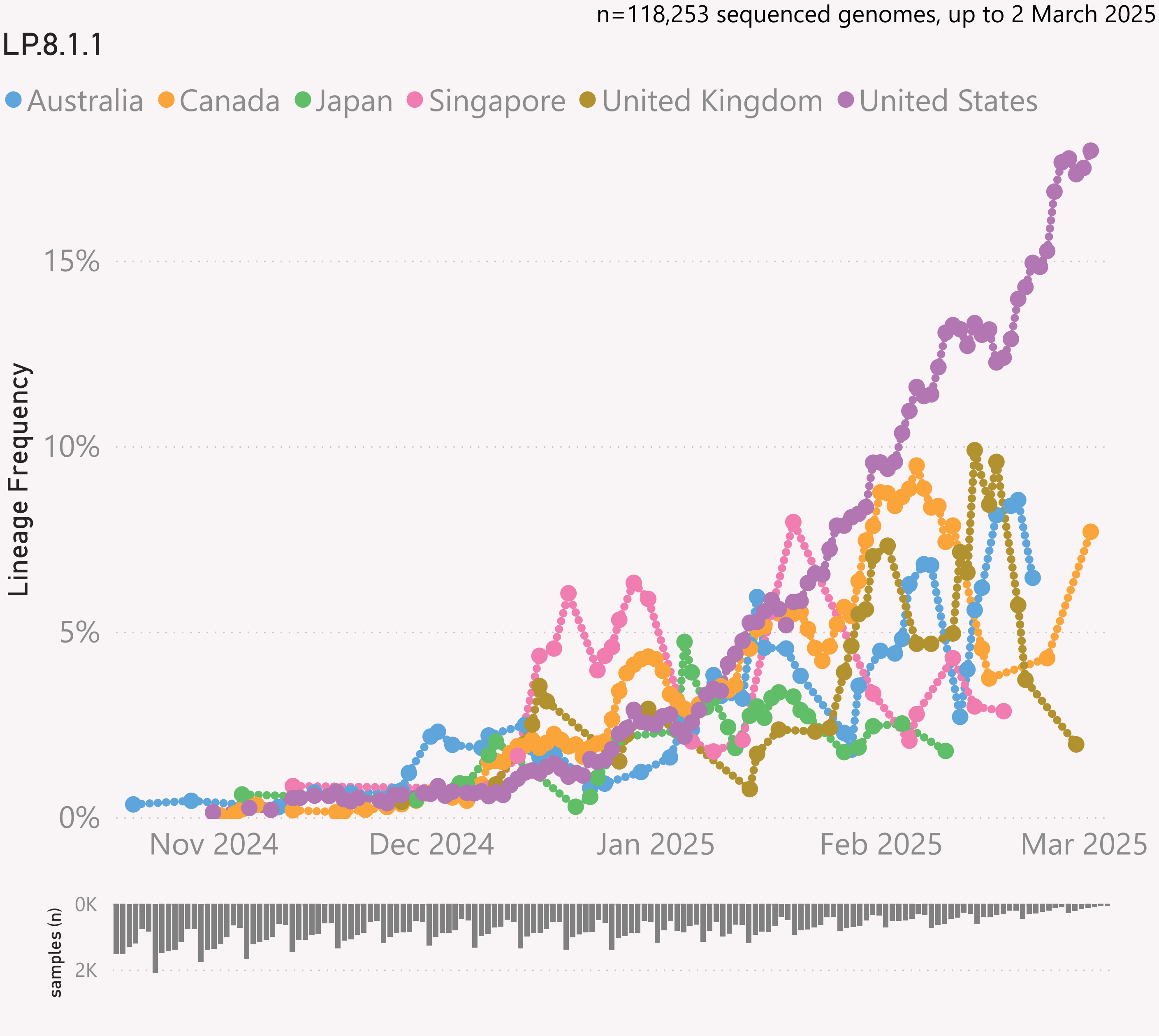
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.



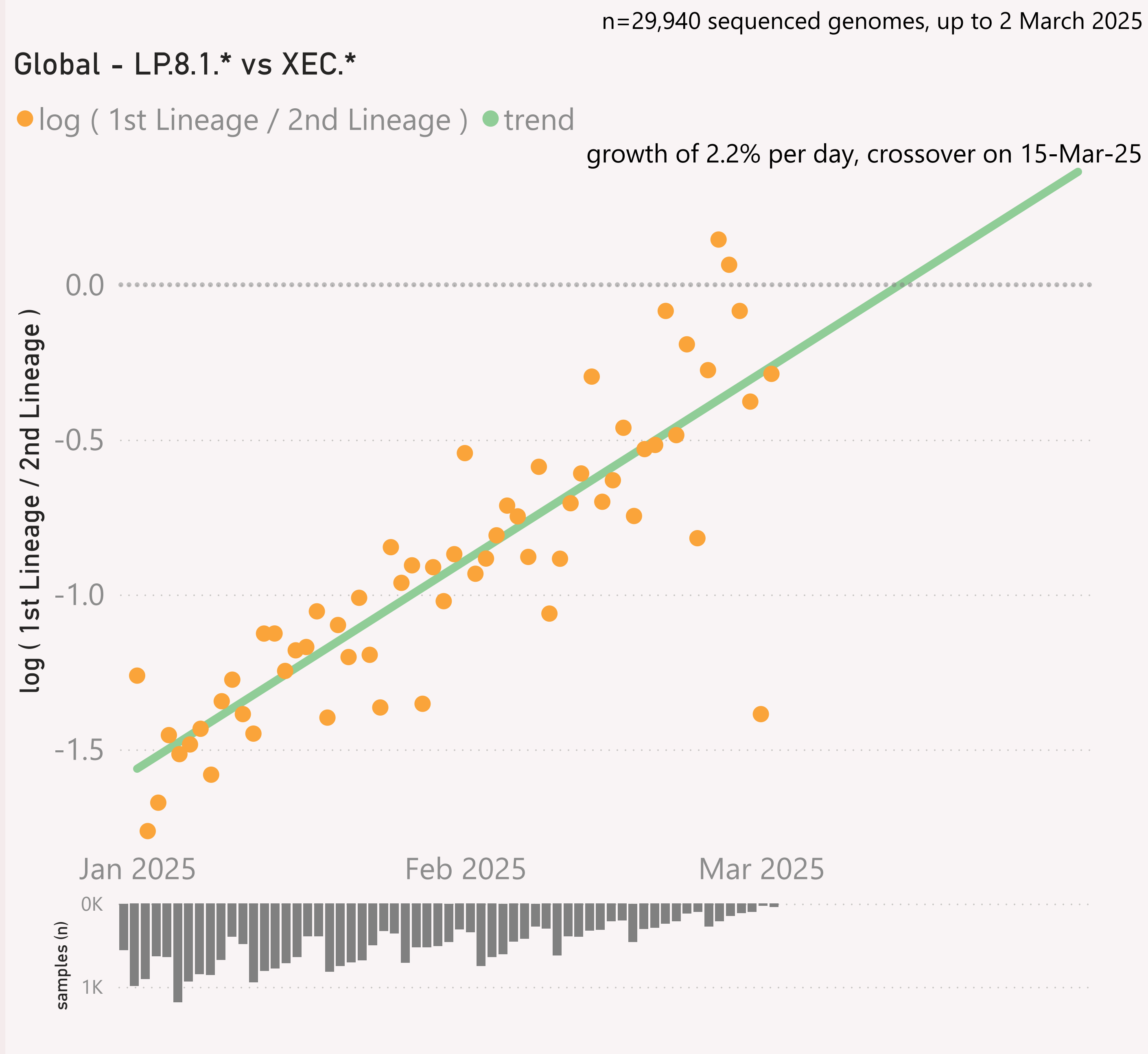
This page shows the frequency of a selected Lineage of interest, for the 6 countries reporting the most samples over recent months.

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.

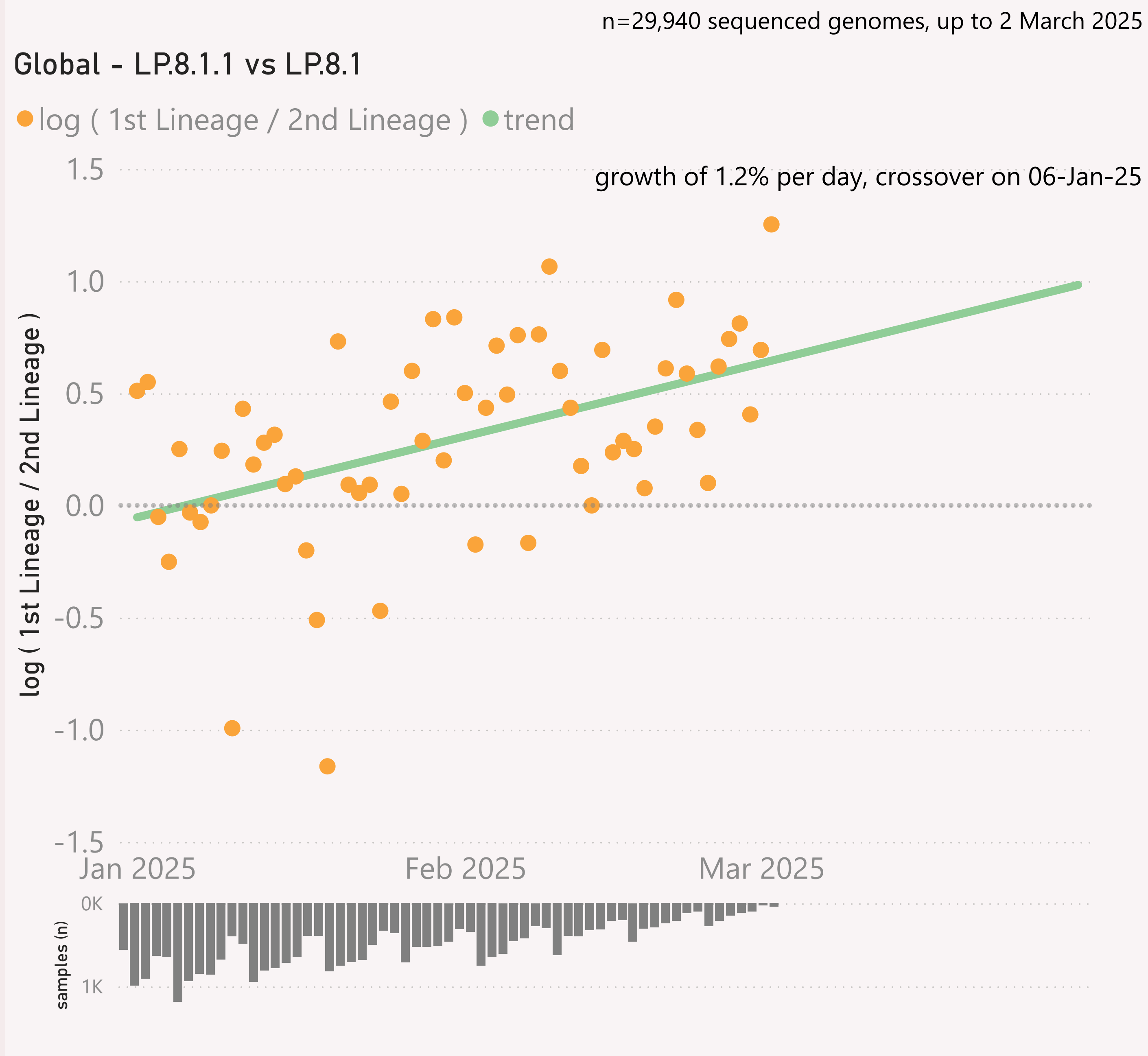


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.



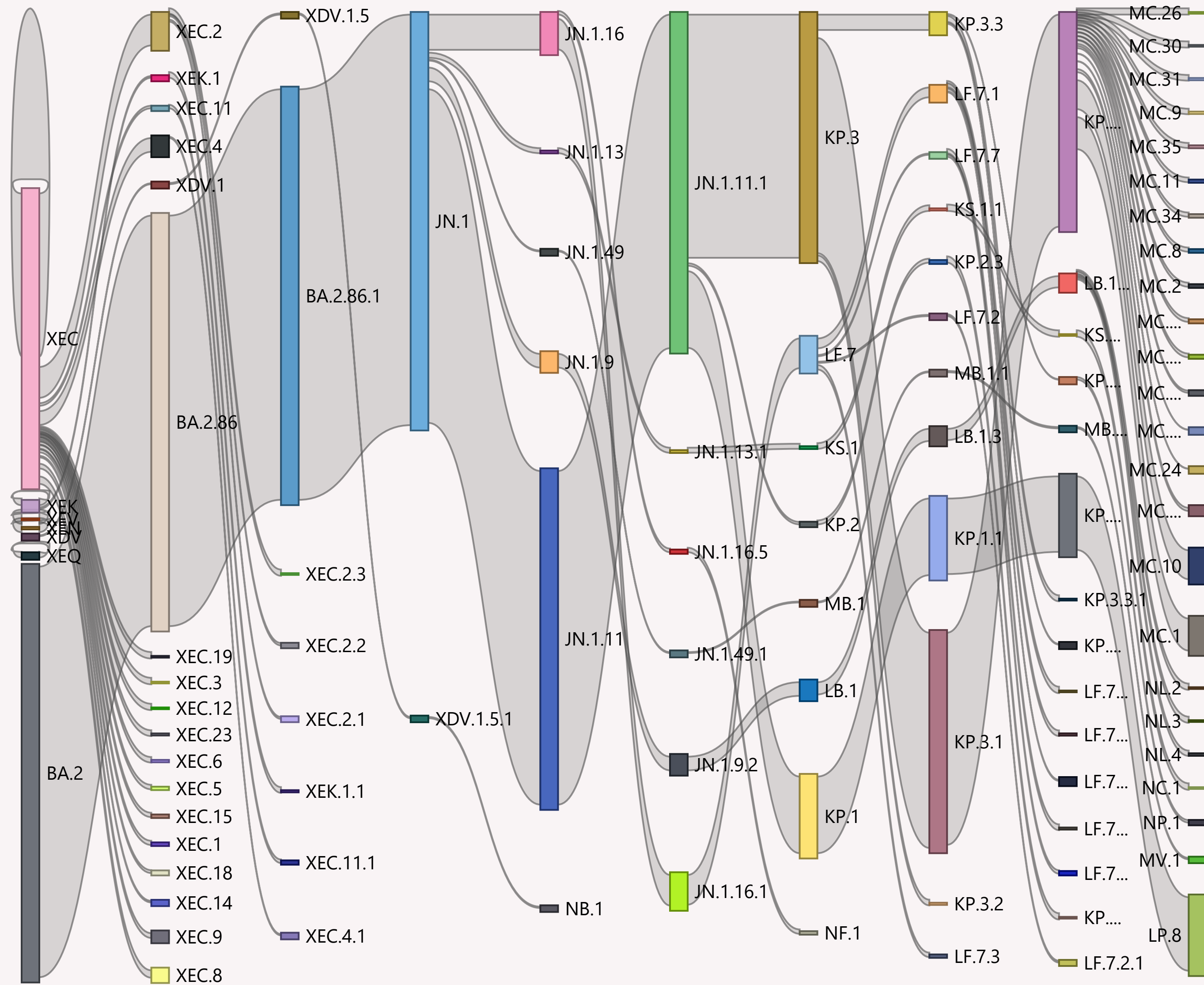
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

Global



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	18,910	02/03/2025		02/03/2025	
Canada	6,228	02/03/2025		02/03/2025	
Japan	2,916	28/02/2025		02/03/2025	
Australia	1,904	02/03/2025		02/03/2025	
Brazil	1,248	10/02/2025		02/03/2025	
Spain	1,206	02/03/2025		02/03/2025	
United Kingdom	1,180	02/03/2025		02/03/2025	
Russia	1,168	28/01/2025		02/03/2025	
Germany	862	26/02/2025		02/03/2025	
Peru	852	04/01/2025		02/03/2025	
France	758	28/02/2025		02/03/2025	
Greece	633	07/02/2025		02/03/2025	
Italy	593	28/02/2025		02/03/2025	
New Zealand	534	23/02/2025		02/03/2025	
Singapore	484	01/03/2025		02/03/2025	
Chile	482	26/02/2025		02/03/2025	
Denmark	419	24/02/2025		02/03/2025	
Slovenia	400	28/02/2025		02/03/2025	
South Korea	330	20/02/2025		02/03/2025	
Ireland	307	02/03/2025		02/03/2025	
Netherlands	305	23/02/2025		02/03/2025	
Sweden	258	21/02/2025		02/03/2025	
Argentina	252	19/12/2024		21/01/2025	
Israel	249	20/01/2025		02/02/2025	
China	248	01/03/2025		02/03/2025	
Ghana	211	19/12/2024		02/03/2025	
Austria	184	27/01/2025		24/02/2025	
South Africa	156	18/02/2025		02/03/2025	
Total	45,530	02/03/2025		02/03/2025	

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.