n=200,325 sequenced genomes, up to 4 December 2024

Global

- ● BA.2.86.*
- ● JN.1.* +DeFLuQE
- ● JN.1.* +FLiRT
- ● JN.1.* +FLuQE
- ● XDV.*
- ● XEC.*

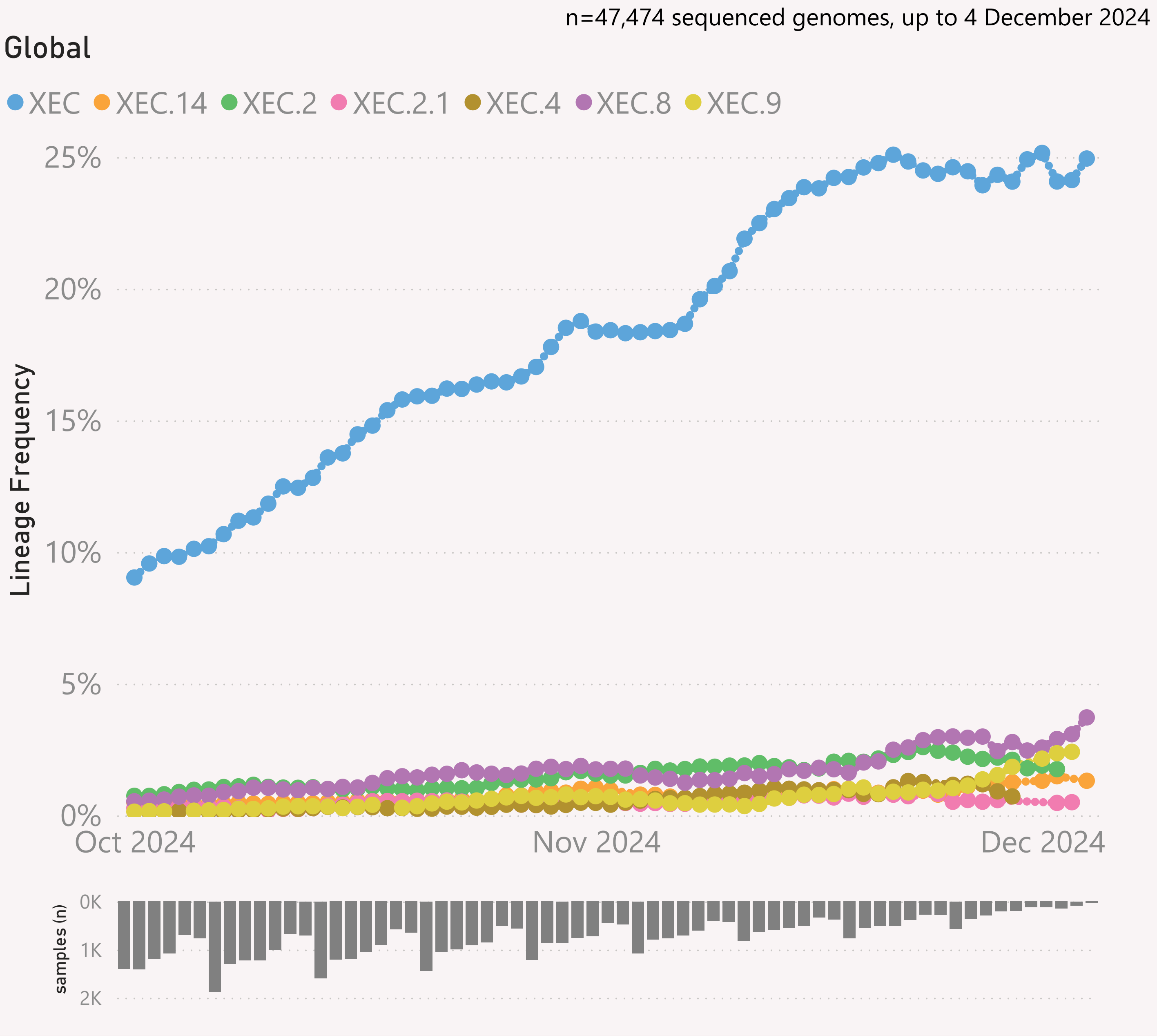This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.

n=47,474 sequenced genomes, up to 4 December 2024

Global

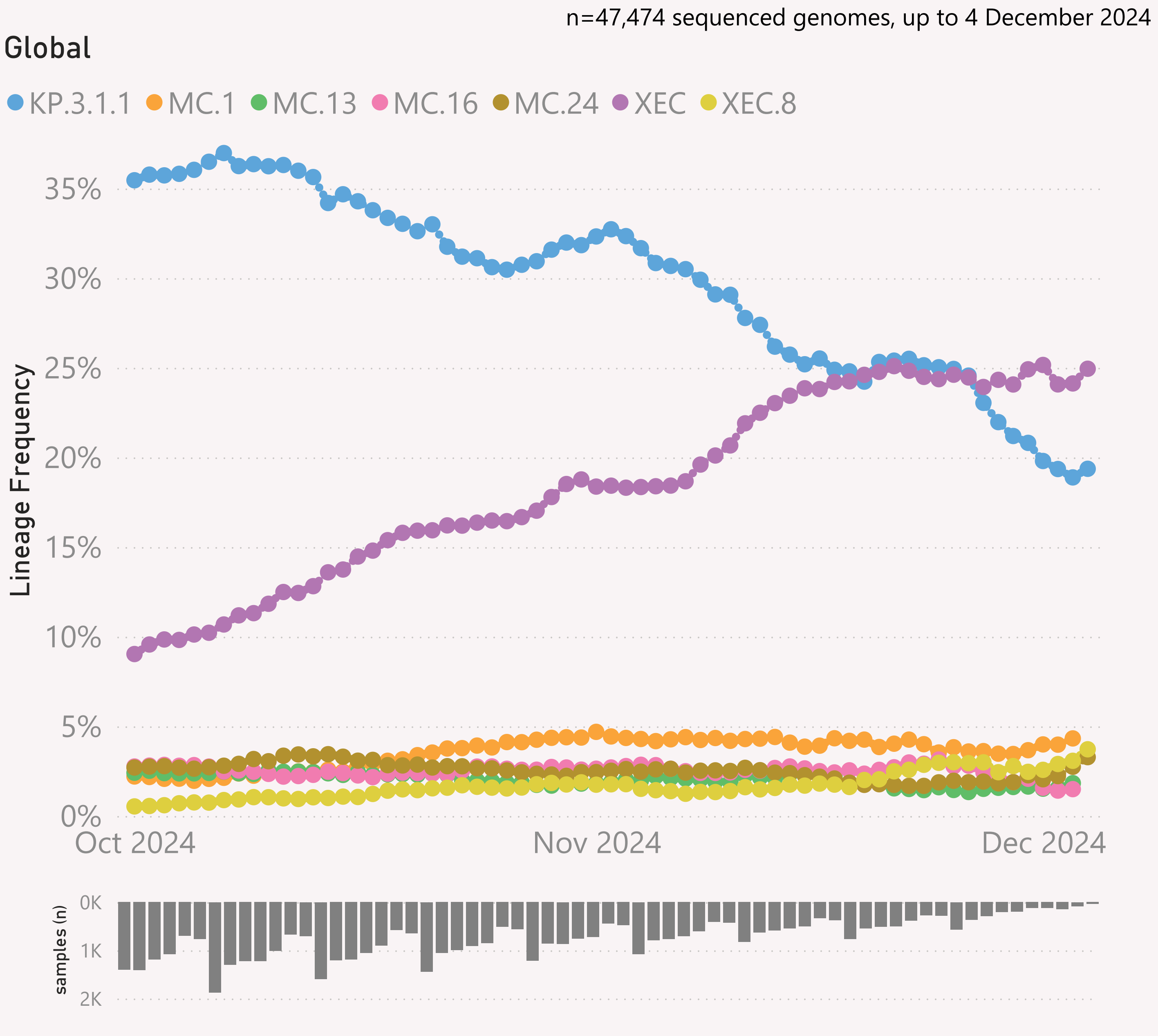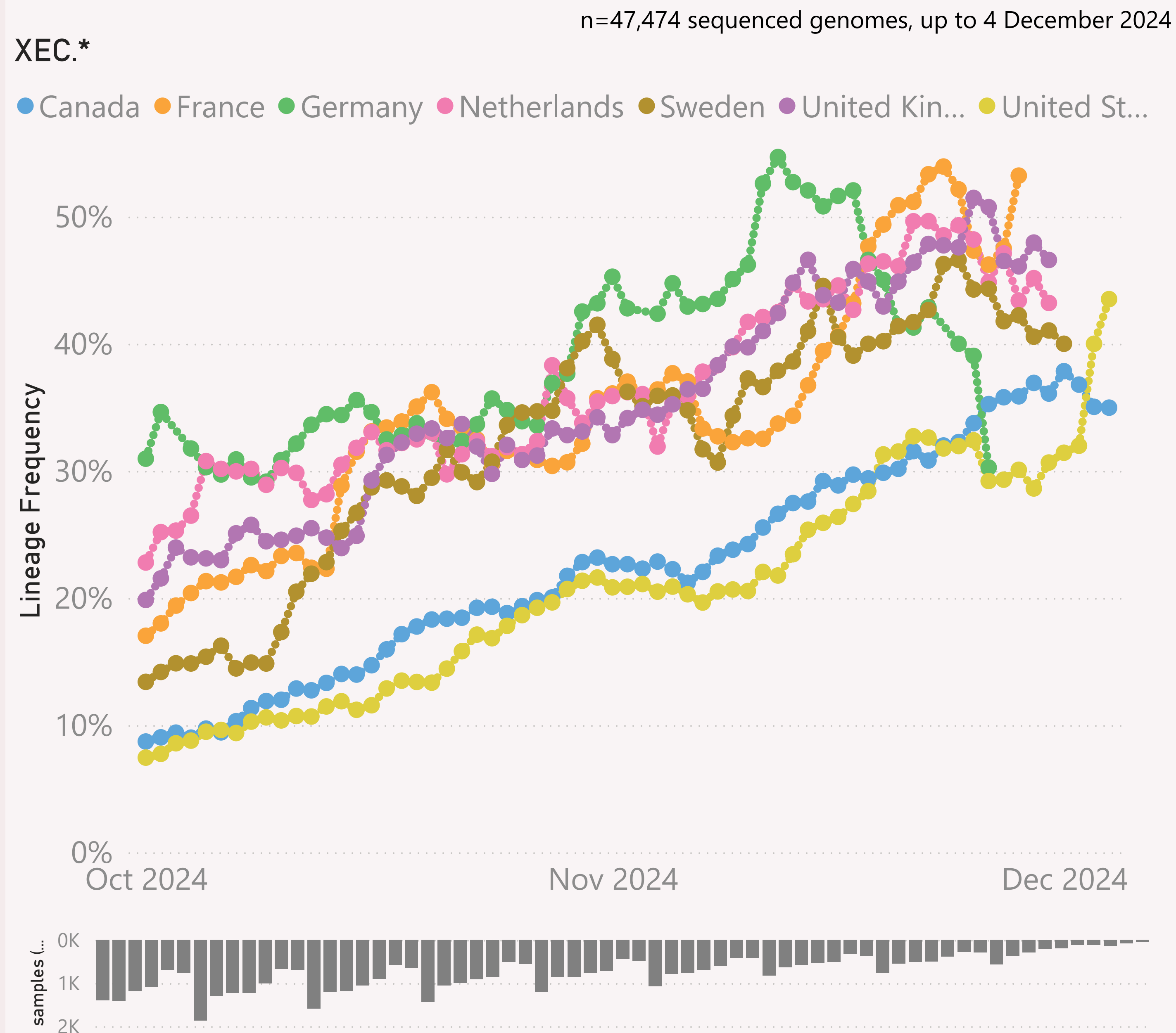● XEC ● XEC.14 ● XEC.2 ● XEC.2.1 ● XEC.4 ● XEC.8 ● XEC.9

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.

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.
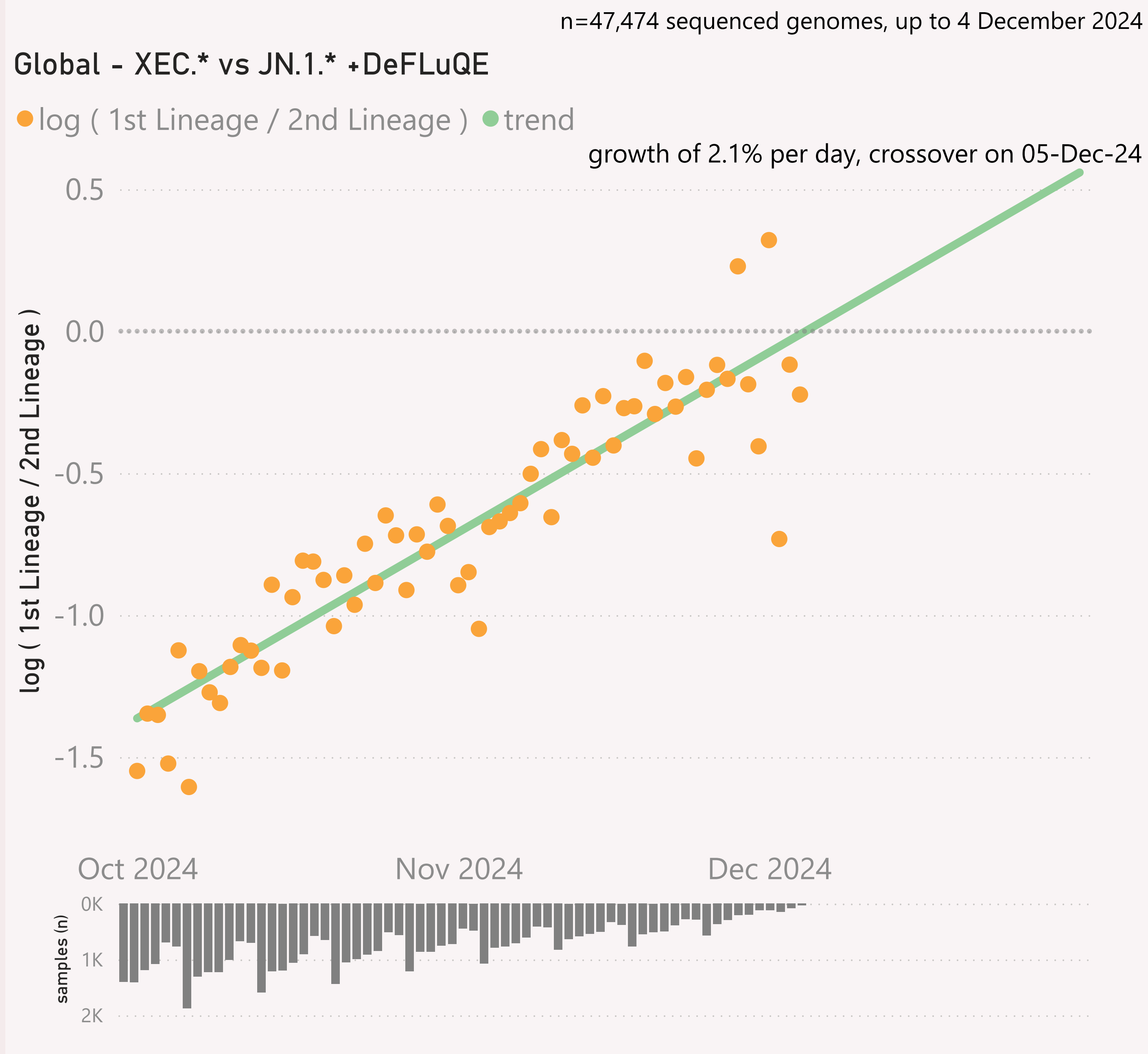
n=47,474 sequenced genomes, up to 4 December 2024

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=47,474 sequenced genomes, up to 4 December 2024

XEC.*

● Canada ● France ● Germany ● Netherlands ● Sweden ● United Kin... ● United St...

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.

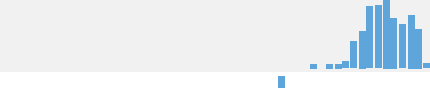The frequency results calculated for the most recent dates might not be representative, due to those lower sample sizes.

n=47,474 sequenced genomes, up to 4 December 2024

LP.8.1

● Australia ● Brazil ● Canada ● Hong Kong ● Japan ● Singapore ● United States
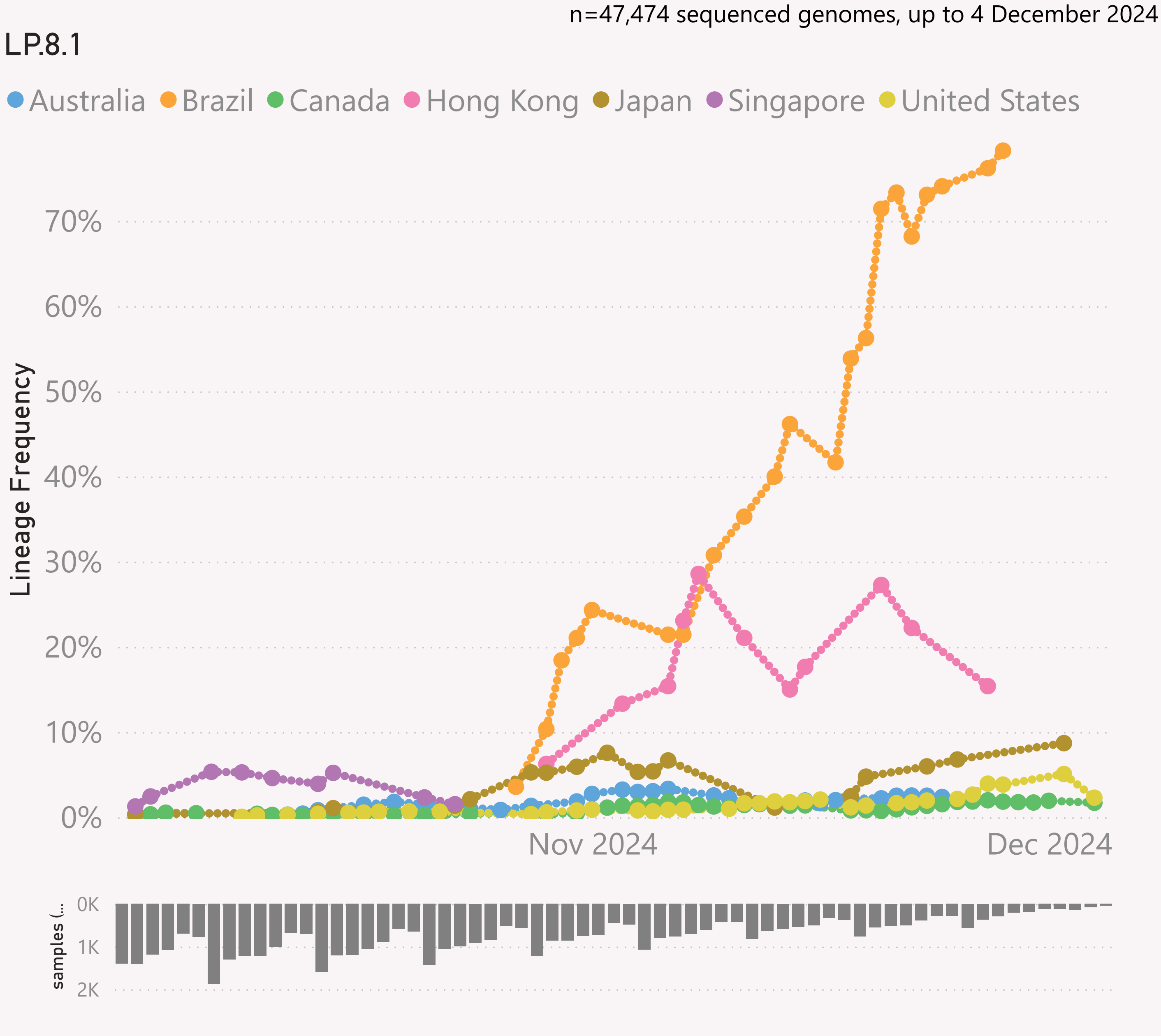
This page shows the frequency of a selected Lineage of interest, for the 6 countries reporting the most samples over recent months.

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=47,474 sequenced genomes, up to 4 December 2024

Global – XEC.* vs JN.1.* +DeFLuQE

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

growth of 2.1% per day, crossover on 05-Dec-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=47,474 sequenced genomes, up to 4 December 2024

Global - LP.8.1 vs XEC

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

growth of 3.2% per day
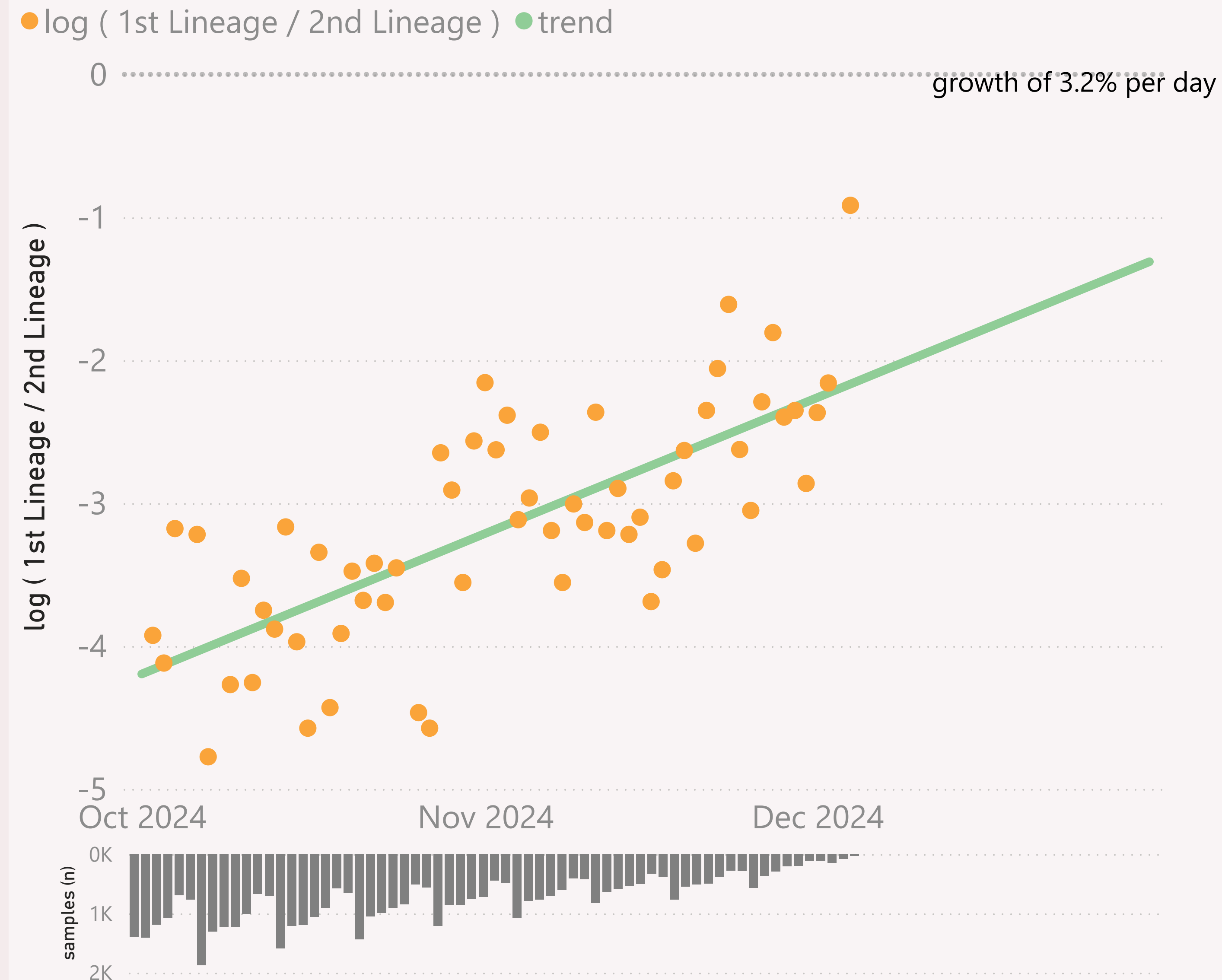
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

n=47,490 sequenced genomes, up to 4 December 2024

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.
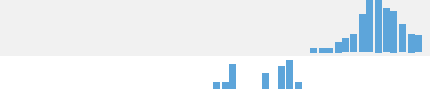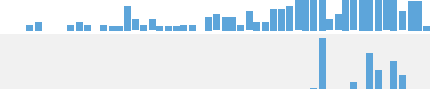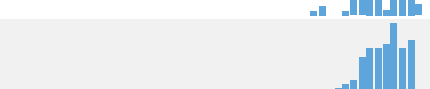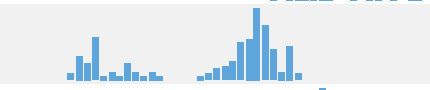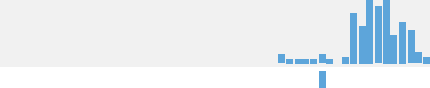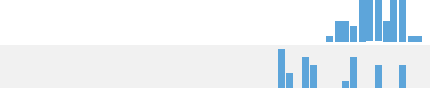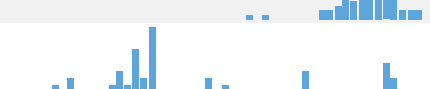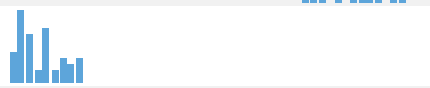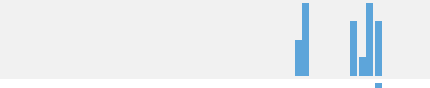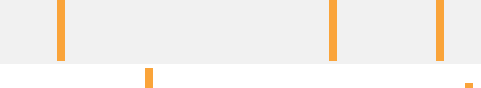
The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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: 2024-12-15 12:53 (UTC)

Data Submitted in the last 8 weeks

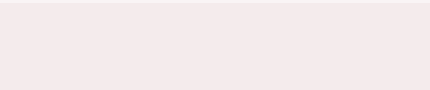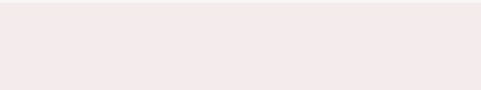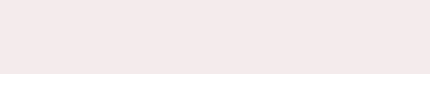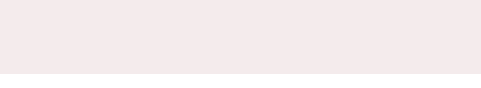| Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
United States	18,294	04/12/2024		08/12/2024	
Canada	14,258	04/12/2024		08/12/2024	
Spain	3,145	03/12/2024		08/12/2024	
United Kingdom	2,844	03/12/2024		08/12/2024	
China	2,823	01/12/2024		08/12/2024	
Sweden	2,443	02/12/2024		08/12/2024	
Japan	2,366	04/12/2024		08/12/2024	
Germany	2,305	26/11/2024		08/12/2024	
France	2,301	28/11/2024		08/12/2024	
Australia	2,131	27/11/2024		08/12/2024	
Netherlands	1,515	02/12/2024		08/12/2024	
Mexico	1,458	22/08/2024		27/11/2024	
Russia	1,420	12/11/2024		30/11/2024	
Italy	1,333	04/12/2024		08/12/2024	
Denmark	1,313	25/11/2024		08/12/2024	
Brazil	1,163	28/11/2024		08/12/2024	
Chile	598	27/11/2024		08/12/2024	
South Korea	563	02/12/2024		08/12/2024	
Greece	492	04/10/2024		31/10/2024	
Ireland	467	02/12/2024		05/12/2024	
Thailand	408	21/11/2024		08/12/2024	
Poland	369	20/11/2024		08/12/2024	
Cyprus	309	28/02/2024		28/10/2024	
Luxembourg	299	30/10/2024		27/11/2024	
New Zealand	292	03/11/2024		15/11/2024	
Israel	252	12/11/2024		05/12/2024	
Costa Rica	196	09/11/2024		08/12/2024	
Slovenia	187	29/11/2024		03/12/2024	
Total	**68,479**	**04/12/2024**		**08/12/2024**	

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.