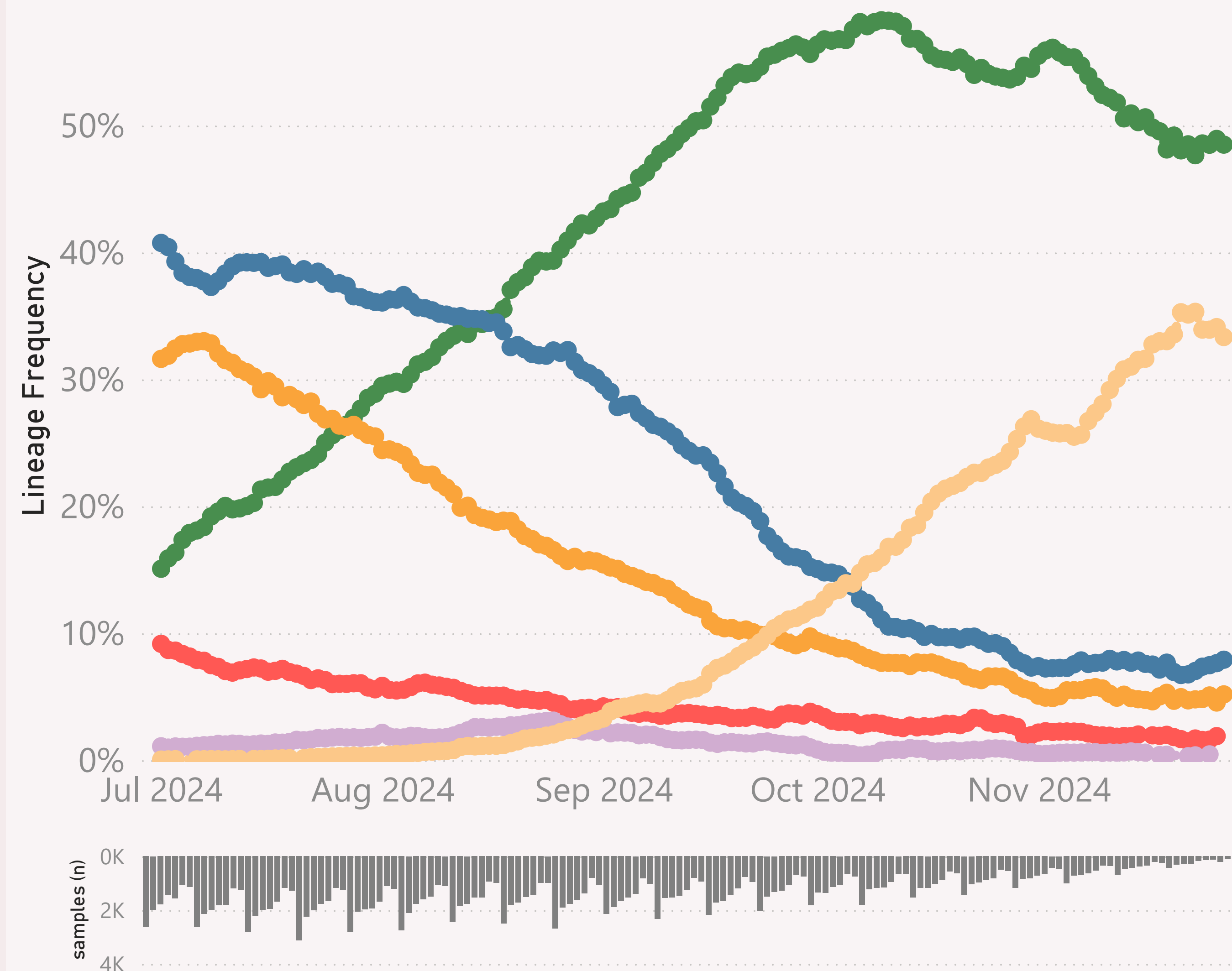n=191,068 sequenced genomes, up to 27 November 2024

Global

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

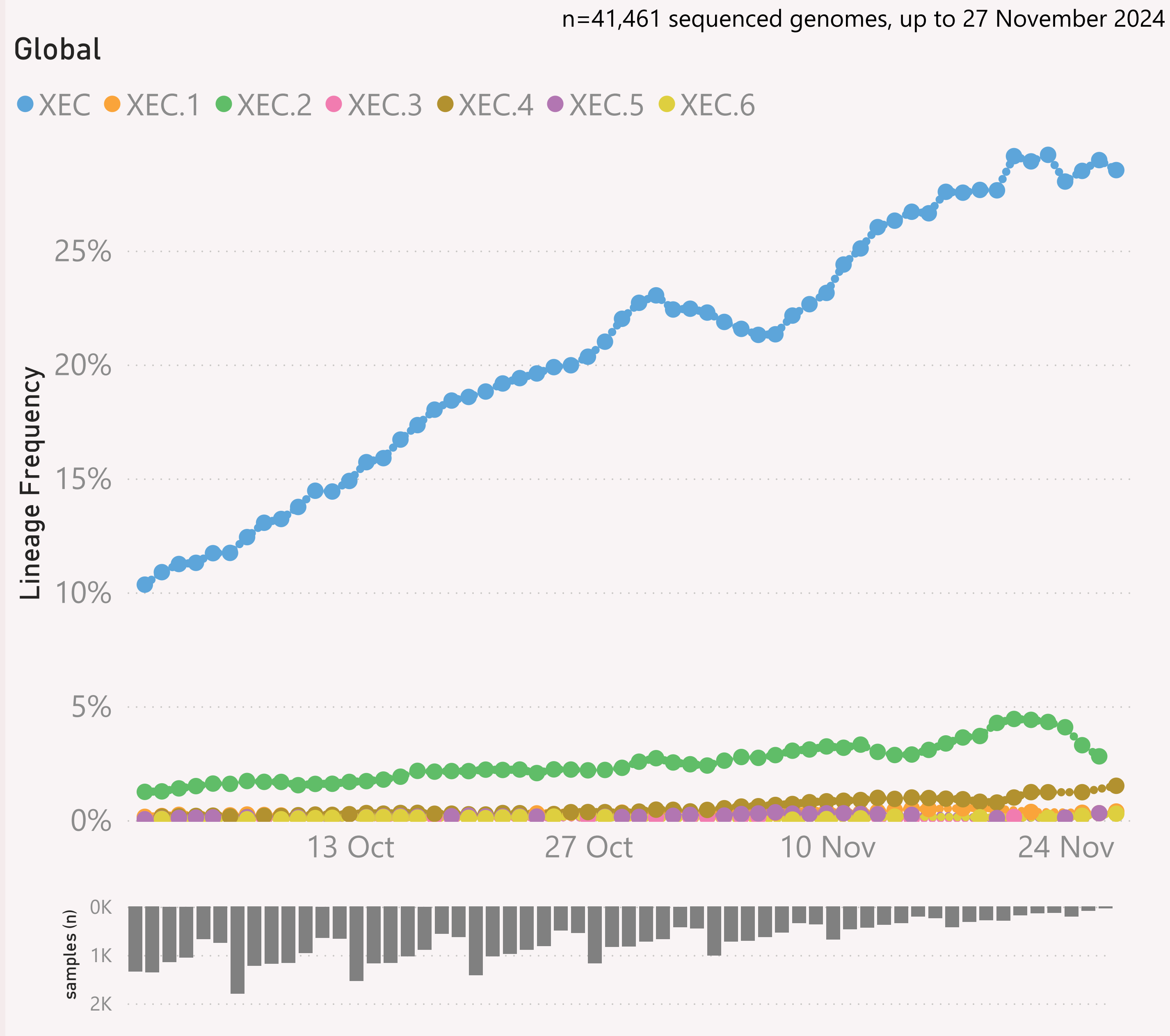This page shows the frequency of the top 6 "L2" lineages, across recent months.

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=41,461 sequenced genomes, up to 27 November 2024

Global

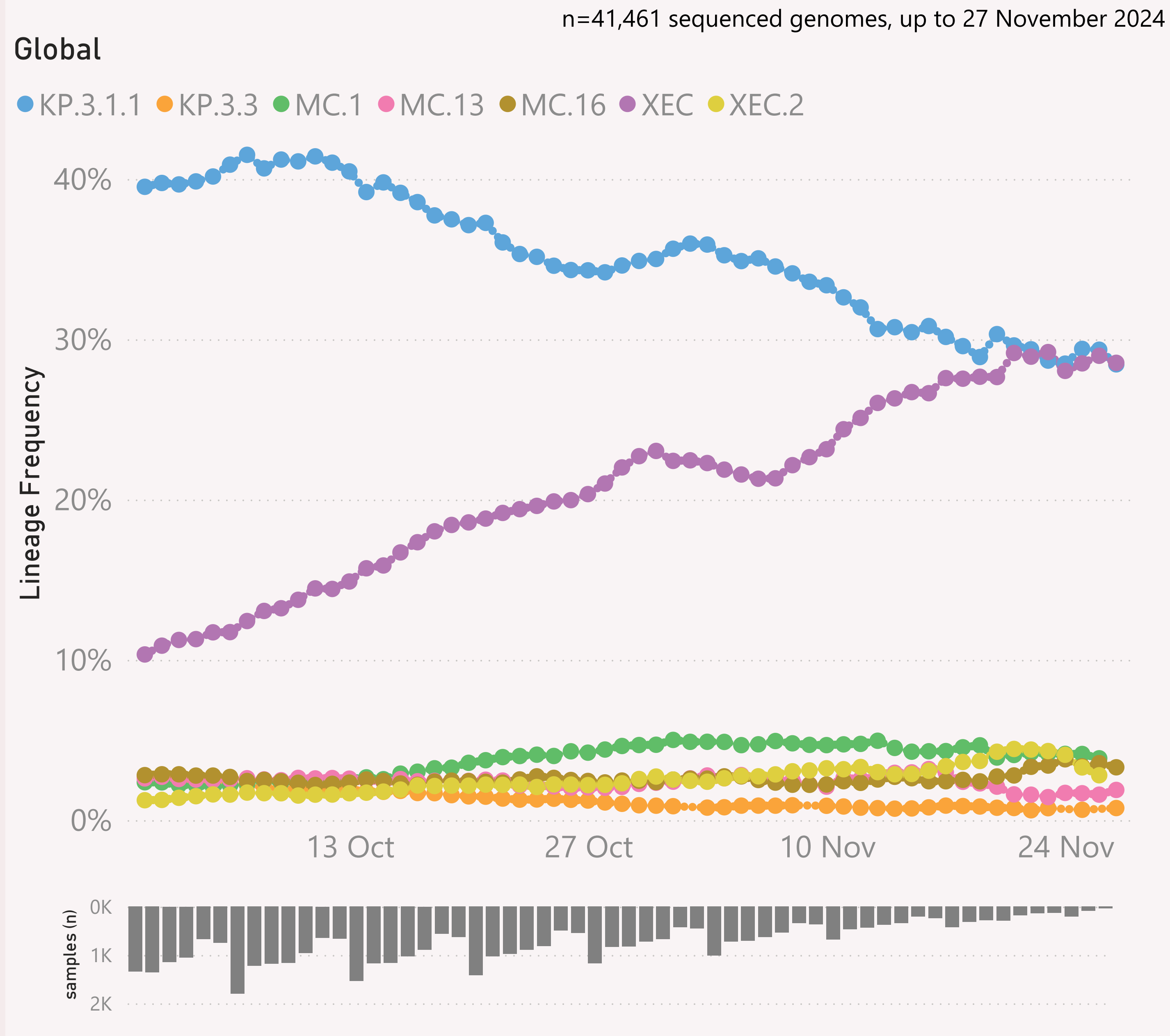● XEC ● XEC.1 ● XEC.2 ● XEC.3 ● XEC.4 ● XEC.5 ● XEC.6

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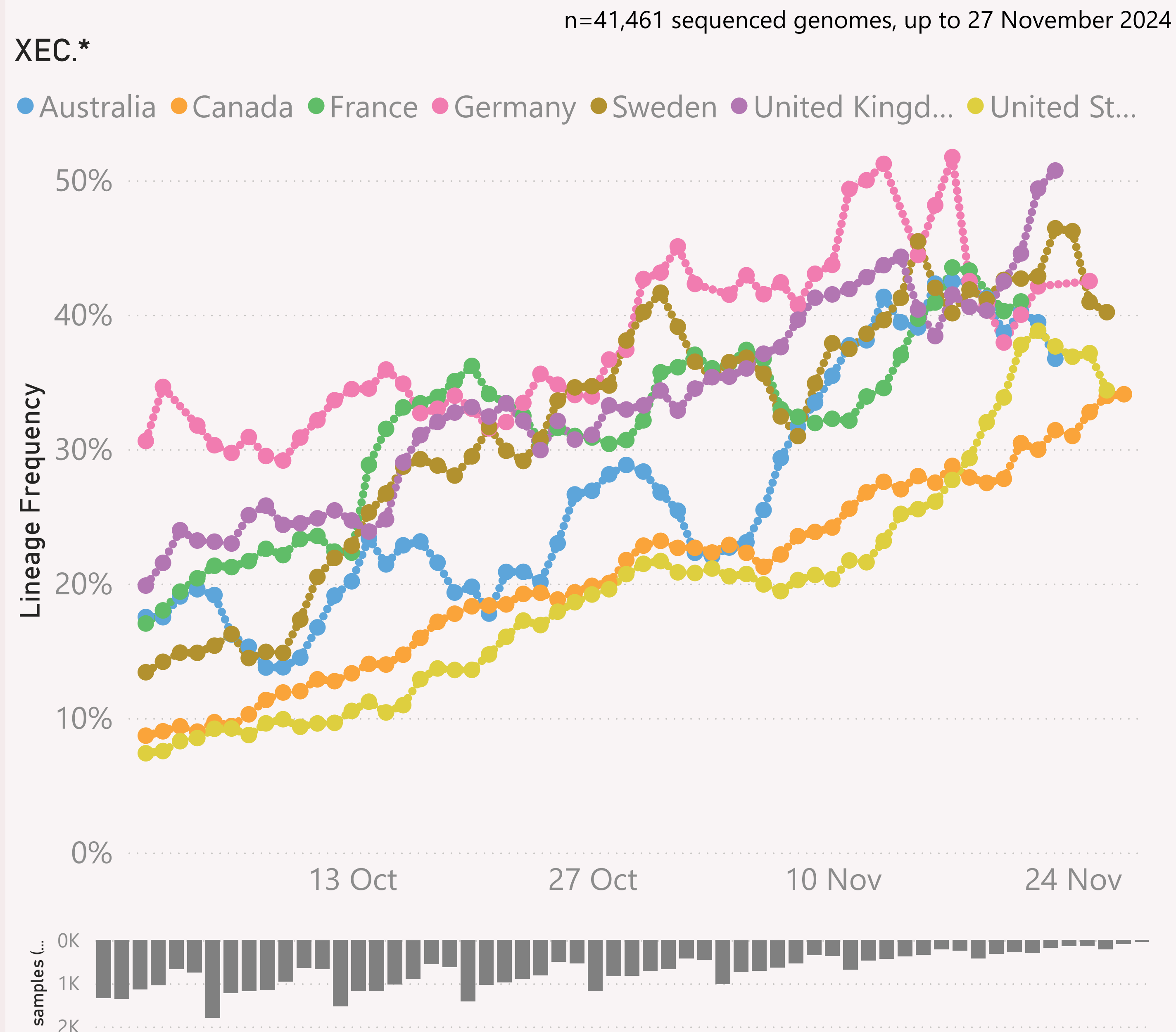
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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.
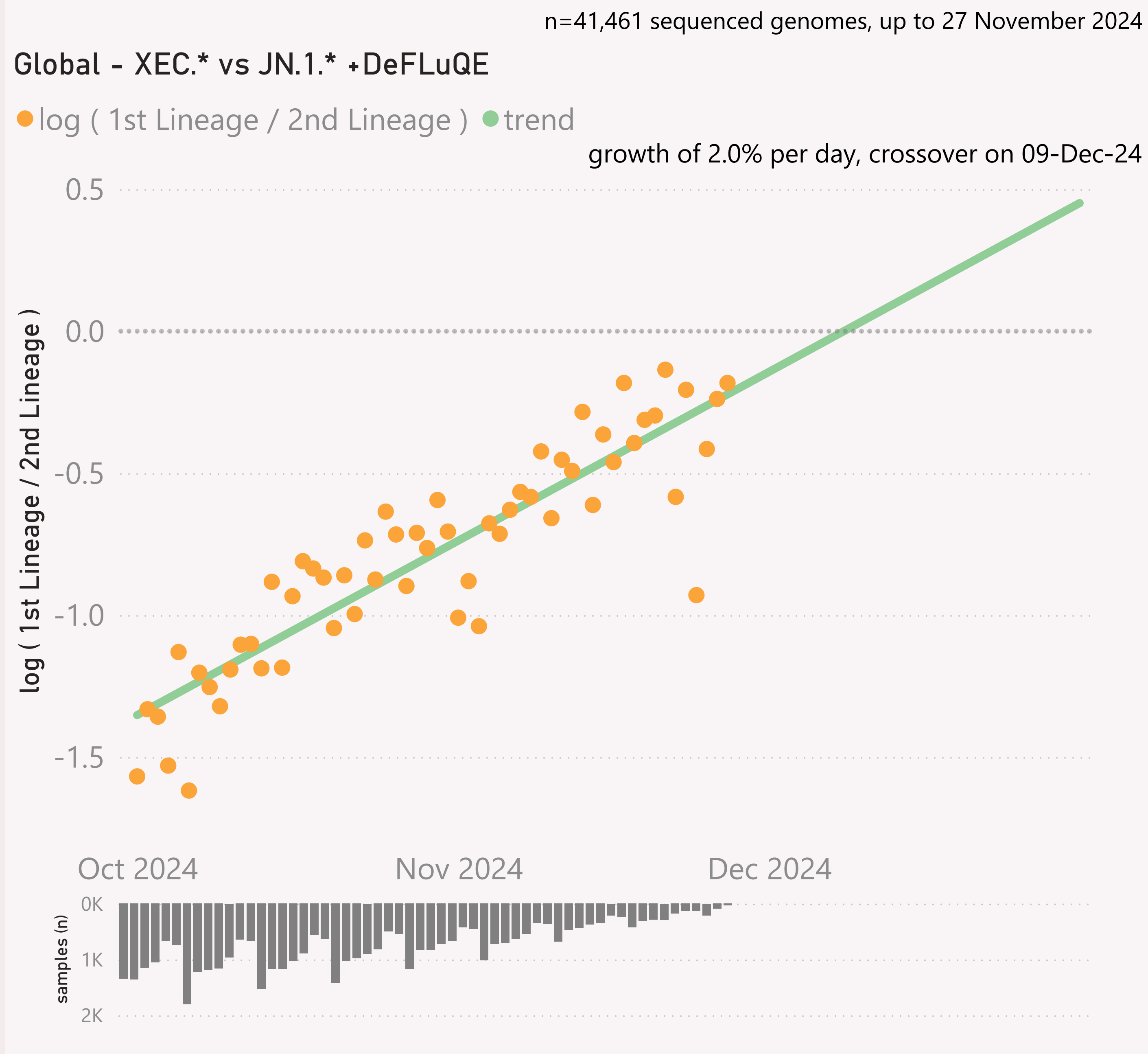
n=41,461 sequenced genomes, up to 27 November 2024

Global

● KP.3.1.1　● KP.3.3　● MC.1　● MC.13　● MC.16　● XEC　● XEC.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.

n=41,461 sequenced genomes, up to 27 November 2024

XEC.*

● Australia ● Canada ● France ● Germany ● Sweden ● United Kingd... ● 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=41,461 sequenced genomes, up to 27 November 2024

LP.8.1

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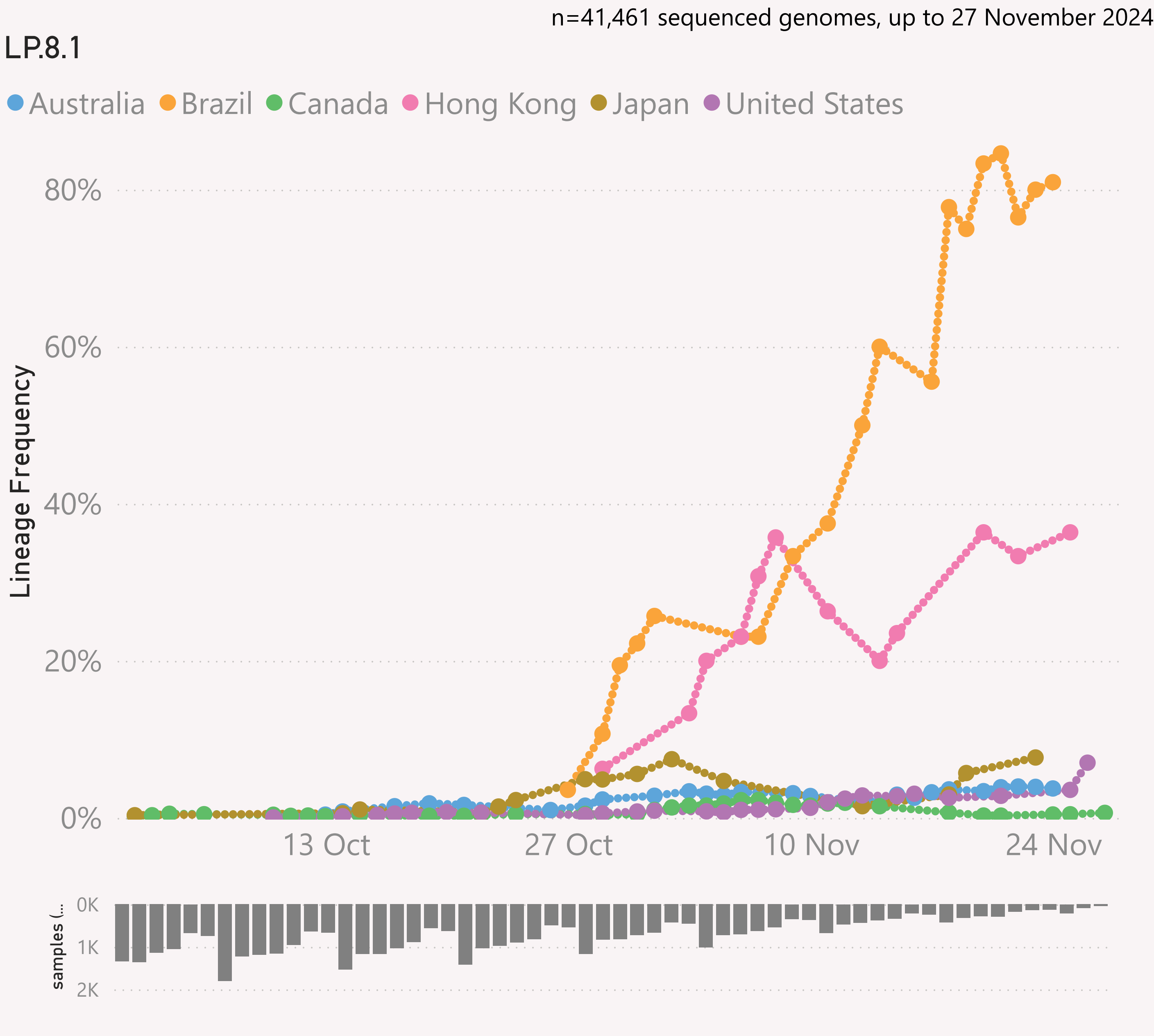
This page shows the frequency of a selected Lineage of interest, for the 6 countries reporting the most samples over recent months.

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=41,461 sequenced genomes, up to 27 November 2024

Global - XEC.* vs JN.1.* +DeFLuQE

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

growth of 2.0% per day, crossover on 09-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=41,461 sequenced genomes, up to 27 November 2024

Global – LP.8.1 vs XEC

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

growth of 4.0% per day
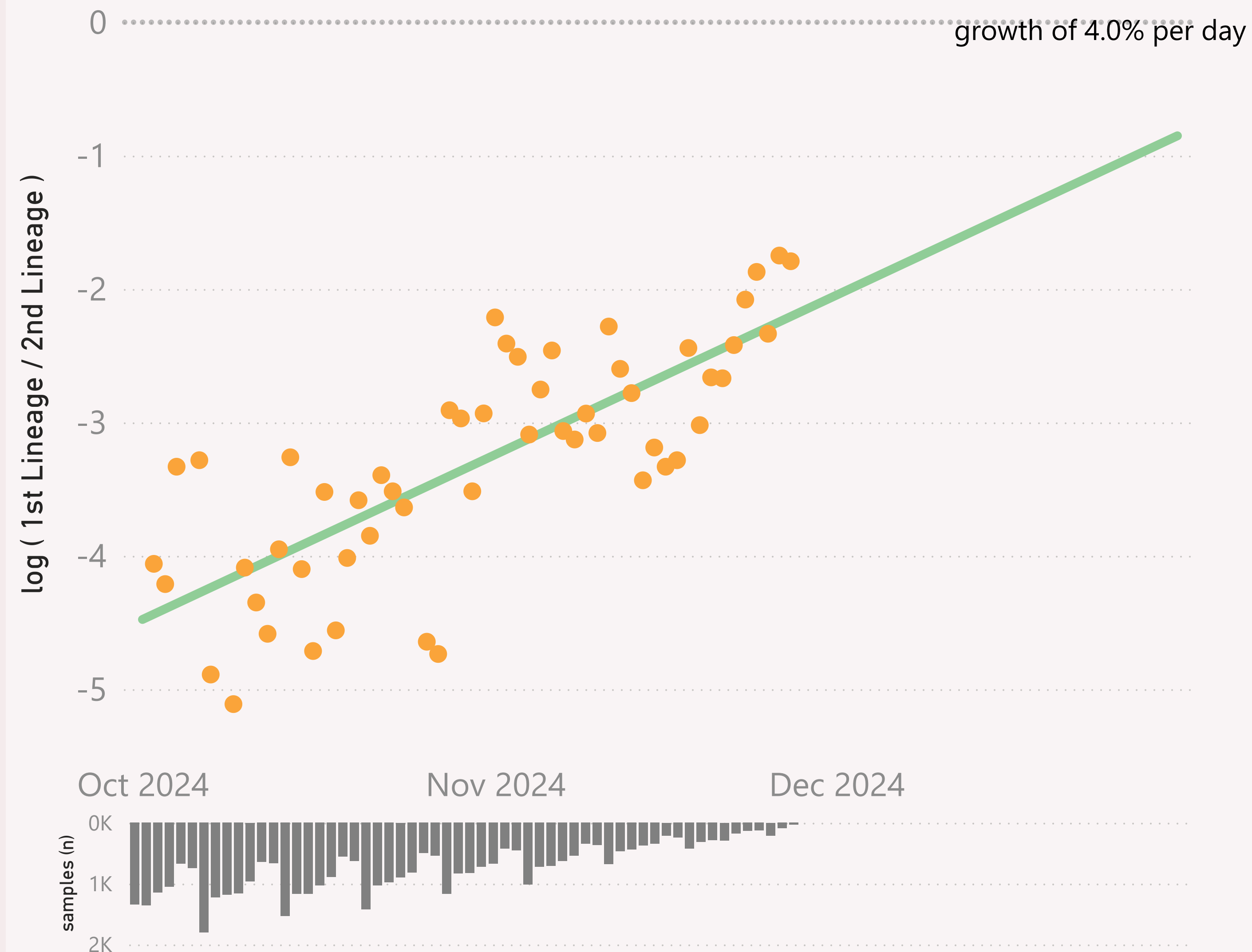
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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=41,477 sequenced genomes, up to 27 November 2024
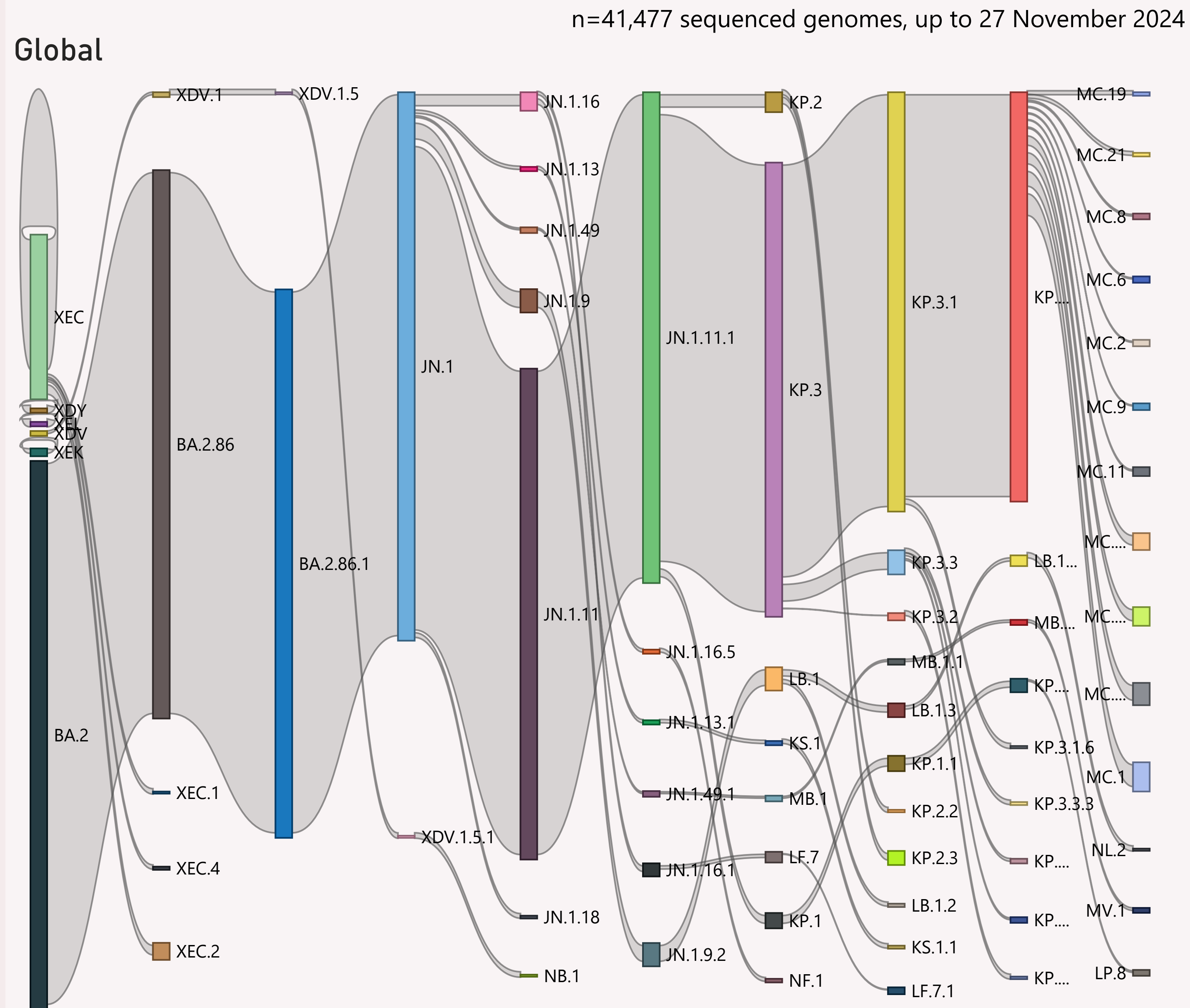
This page shows the hierarchy of the significant Lineages, over recent months.

The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.
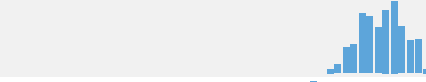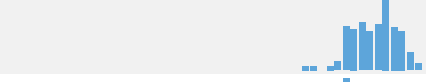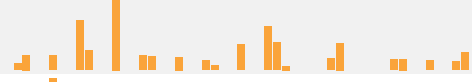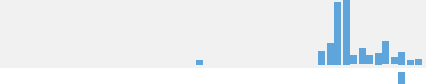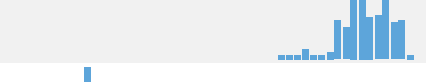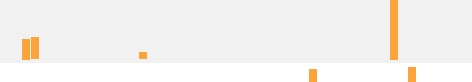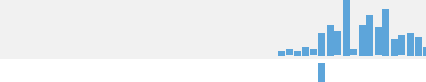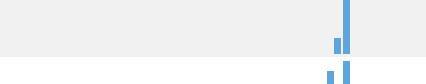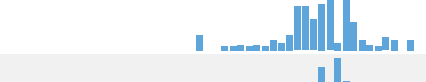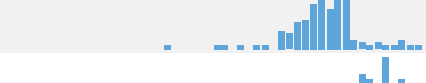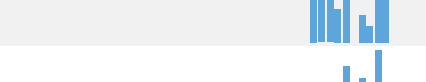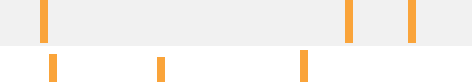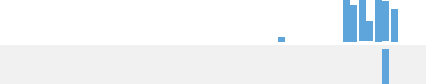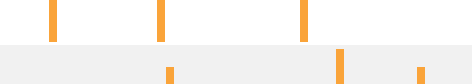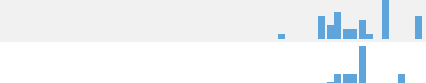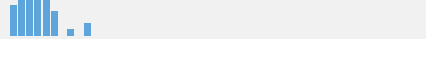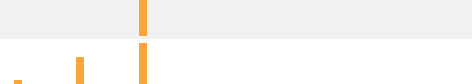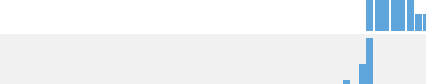
The vertical height of each bar segment represents the relative volume of all the samples of that specific Lineage, as well as all it's descendants.

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: 2024-12-07 21:19 (UTC)

Data Submitted in the last 8 weeks

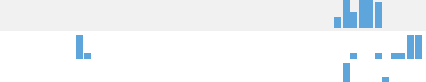| Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ United States	18,226	26/11/2024		03/12/2024	
⊞ Canada	15,610	27/11/2024		03/12/2024	
⊞ Spain	3,707	26/11/2024		03/12/2024	
⊞ United Kingdom	3,210	23/11/2024		03/12/2024	
⊞ France	2,757	21/11/2024		03/12/2024	
⊞ Japan	2,750	27/11/2024		03/12/2024	
⊞ Sweden	2,519	27/11/2024		03/12/2024	
⊞ Germany	2,110	25/11/2024		03/12/2024	
⊞ Australia	1,900	24/11/2024		03/12/2024	
⊞ Netherlands	1,787	14/11/2024		25/11/2024	
⊞ Mexico	1,674	22/08/2024		27/11/2024	
⊞ Italy	1,594	27/11/2024		03/12/2024	
⊞ Russia	1,420	12/11/2024		30/11/2024	
⊞ Denmark	1,372	18/11/2024		03/12/2024	
⊞ China	1,312	25/11/2024		02/12/2024	
⊞ Brazil	1,184	24/11/2024		03/12/2024	
⊞ Ireland	649	27/11/2024		03/12/2024	
⊞ South Korea	618	25/11/2024		03/12/2024	
⊞ Greece	492	04/10/2024		31/10/2024	
⊞ Luxembourg	481	30/10/2024		27/11/2024	
⊞ New Zealand	438	03/11/2024		15/11/2024	
⊞ Poland	361	20/11/2024		28/11/2024	
⊞ Israel	330	12/11/2024		03/12/2024	
⊞ Cyprus	309	28/02/2024		28/10/2024	
⊞ Singapore	301	23/10/2024		28/10/2024	
⊞ Thailand	281	21/11/2024		29/11/2024	
⊞ Slovenia	269	27/11/2024		03/12/2024	
⊞ Chile	258	23/10/2024		18/11/2024	
Total	**71,449**	**27/11/2024**		**03/12/2024**	

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.