n=187,130 sequenced genomes, up to 21 October 2024

Global

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

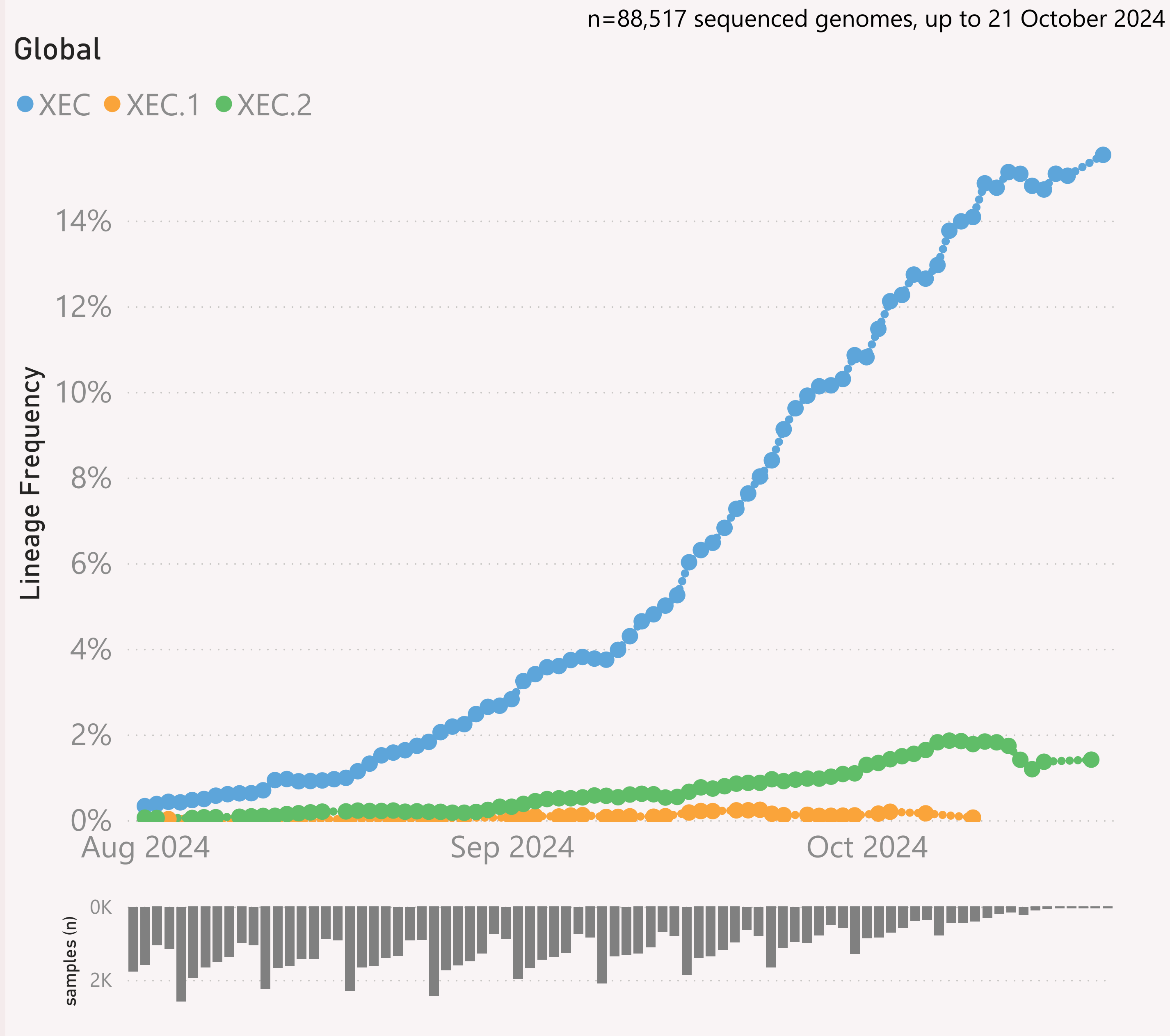This page shows the frequency of the top 6 "L2" lineages, across recent months.

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=88,517 sequenced genomes, up to 21 October 2024
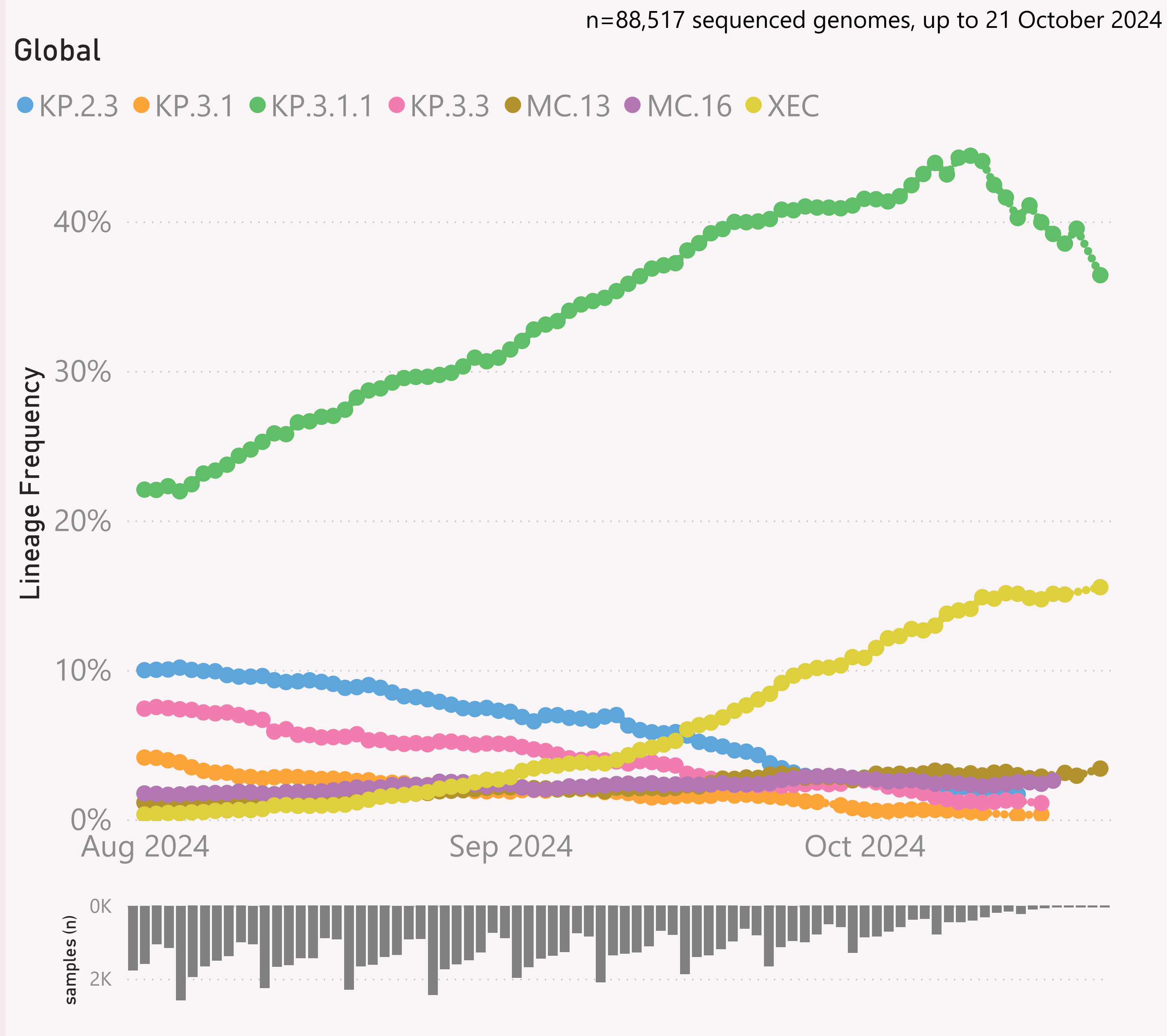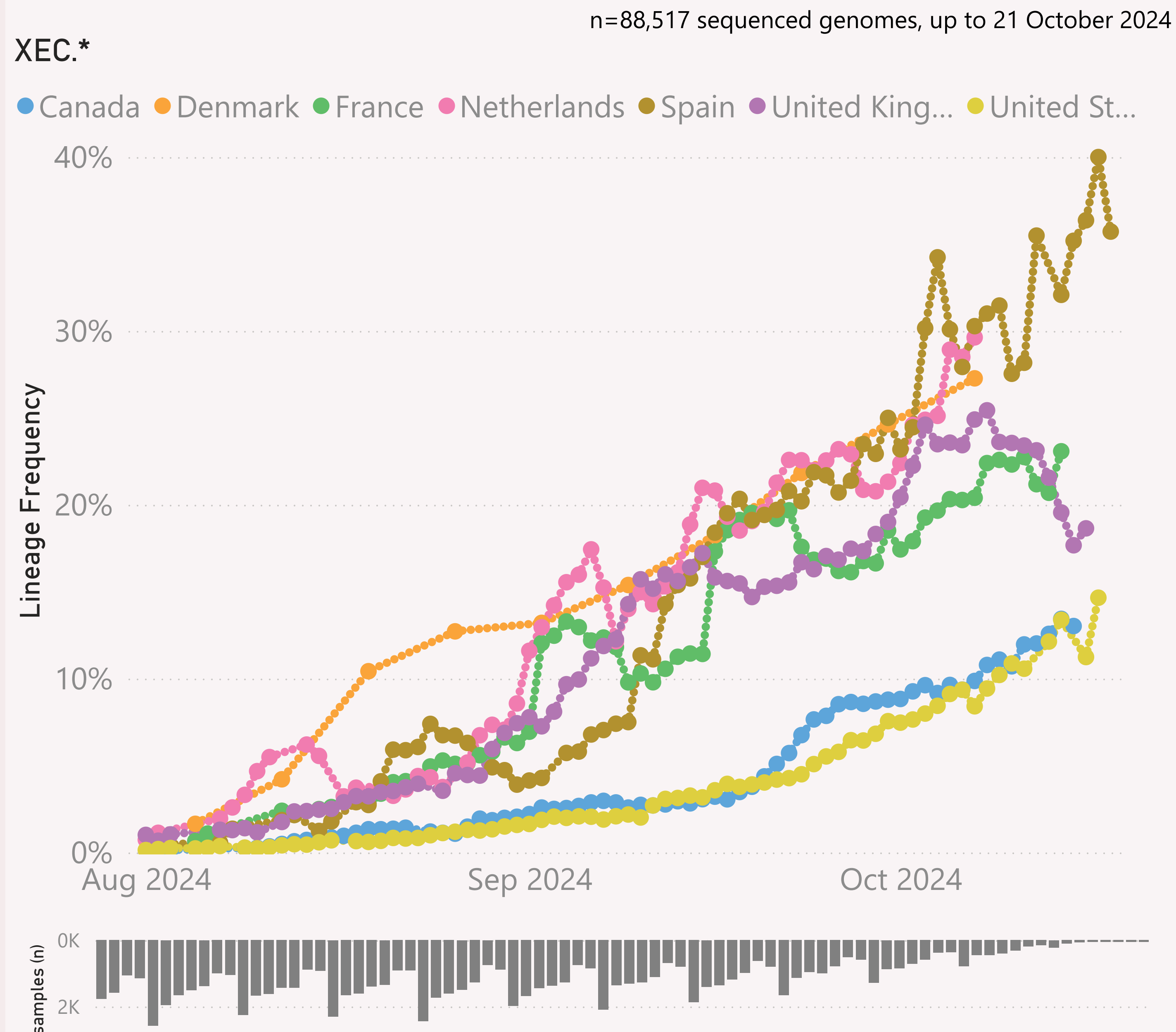

Global

● XEC ● XEC.1 ● XEC.2

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=88,517 sequenced genomes, up to 21 October 2024

Global

● KP.2.3   ● KP.3.1   ● KP.3.1.1   ● KP.3.3   ● MC.13   ● MC.16   ● XEC

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=88,517 sequenced genomes, up to 21 October 2024

XEC.*

● Canada　● Denmark　● France　● Netherlands　● Spain　● United King...　● 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=88,517 sequenced genomes, up to 21 October 2024

XEC.1

● Canada ● Netherlands ● Slovenia ● Sweden ● United Kingdom ● United States
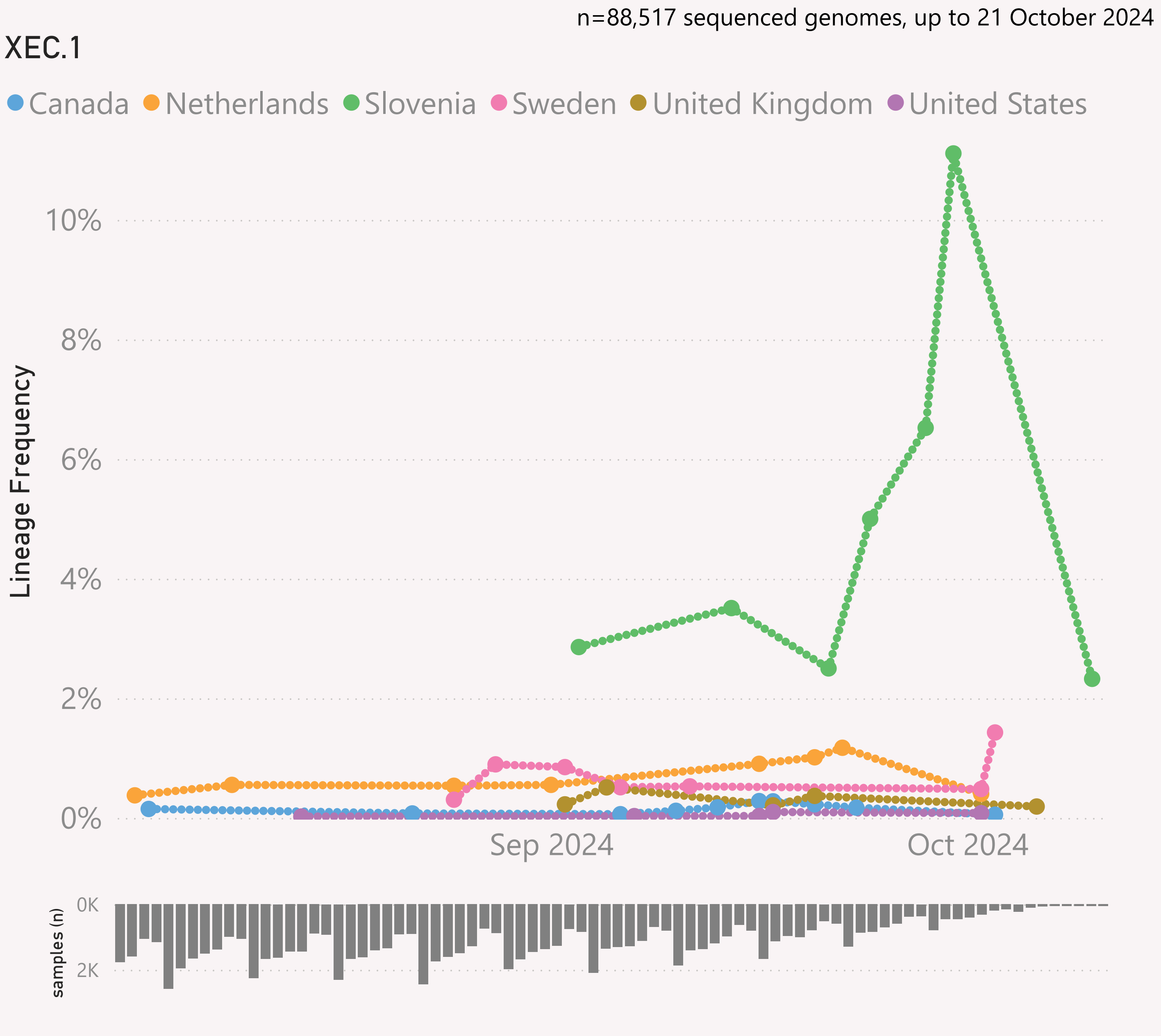
This page shows the frequency of a selected Lineage of interest, for the 6 countries reporting the most samples over recent months.

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=42,069 sequenced genomes, up to 21 October 2024

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

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

growth of 3.6% per day, crossover on 11-Nov-24
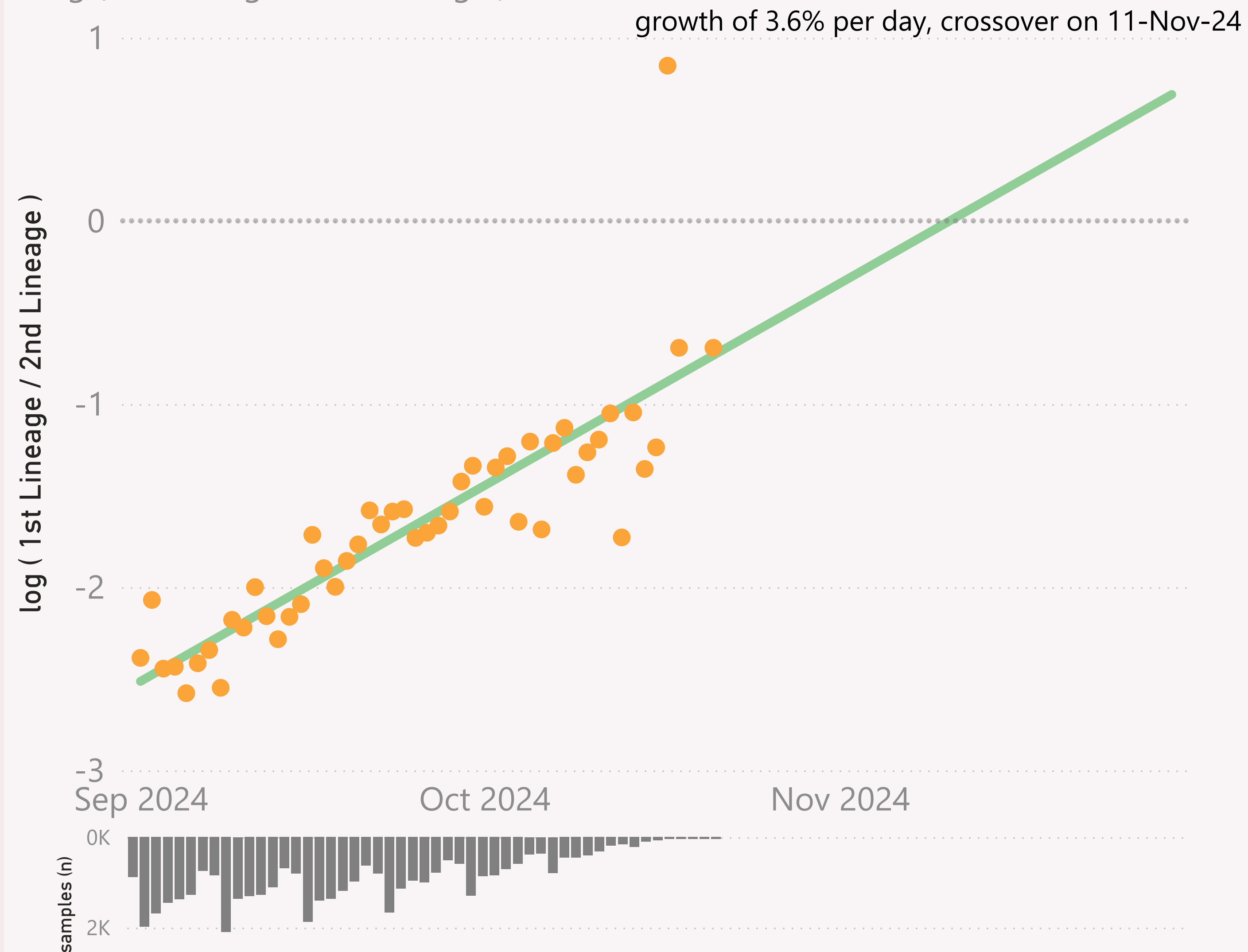
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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=42,069 sequenced genomes, up to 21 October 2024

Global - XEC.1 vs XEC

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

decline of -2.3% per day
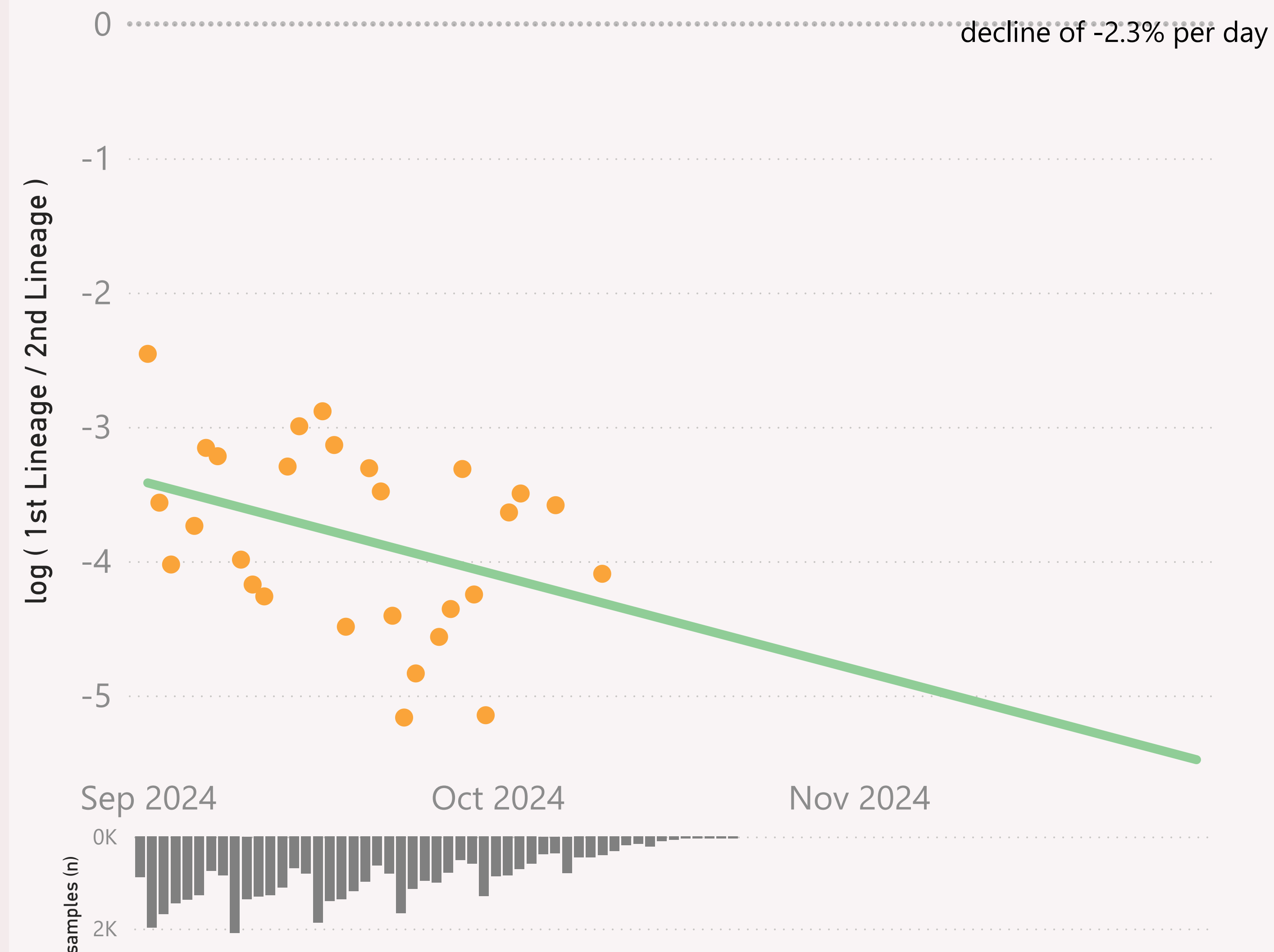
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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
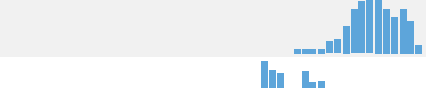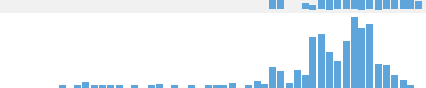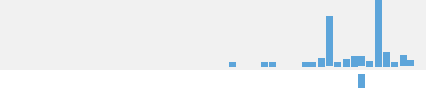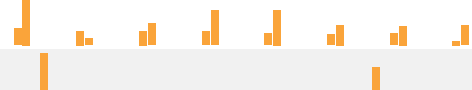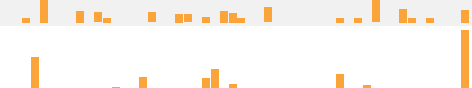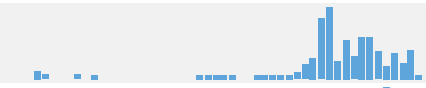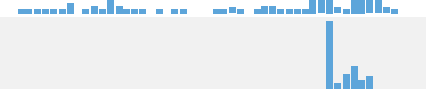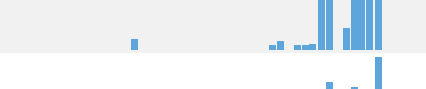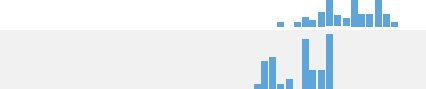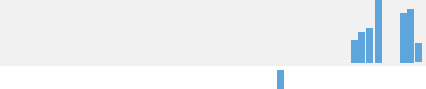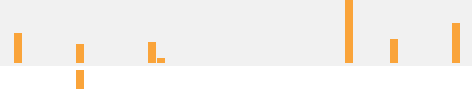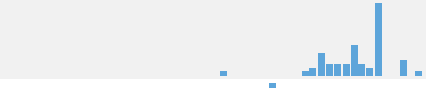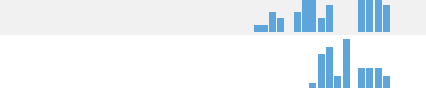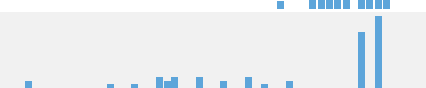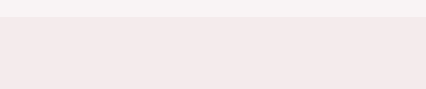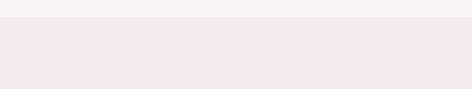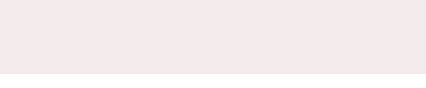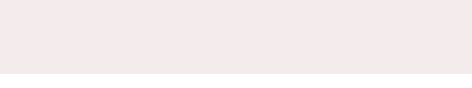
The Lineage classifications are provided by Nextclade.

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=88,602 sequenced genomes, up to 21 October 2024

Global

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: 2024-10-26 11:56 (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	33,092	10/18/2024		10/22/2024	
⊞ Canada	12,941	10/16/2024		10/22/2024	
⊞ Spain	4,898	10/21/2024		10/22/2024	
⊞ United Kingdom	4,383	10/16/2024		10/22/2024	
⊞ Japan	4,210	10/17/2024		10/22/2024	
⊞ France	3,847	10/14/2024		10/22/2024	
⊞ Sweden	2,840	10/14/2024		10/22/2024	
⊞ China	2,513	10/17/2024		10/22/2024	
⊞ Australia	2,253	10/21/2024		10/22/2024	
⊞ Italy	2,067	10/15/2024		10/22/2024	
⊞ Netherlands	2,003	10/8/2024		10/16/2024	
⊞ Denmark	1,783	10/7/2024		10/22/2024	
⊞ Brazil	1,408	10/2/2024		10/22/2024	
⊞ South Korea	1,120	10/2/2024		10/22/2024	
⊞ Ireland	1,094	10/21/2024		10/22/2024	
⊞ Russia	1,088	10/1/2024		10/22/2024	
⊞ Germany	992	10/1/2024		10/22/2024	
⊞ Costa Rica	589	9/9/2024		10/3/2024	
⊞ Greece	580	8/2/2024		9/23/2024	
⊞ Singapore	552	10/16/2024		10/21/2024	
⊞ Puerto Rico	530	10/3/2024		10/21/2024	
⊞ New Zealand	506	10/6/2024		10/18/2024	
⊞ Mexico	478	8/9/2024		10/15/2024	
⊞ Poland	445	10/15/2024		10/22/2024	
⊞ Bahrain	386	8/26/2024		10/9/2024	
⊞ Luxembourg	356	9/30/2024		10/17/2024	
⊞ Portugal	351	9/24/2024		10/8/2024	
⊞ Taiwan	320	10/7/2024		10/14/2024	
Total	**92,184**	**10/21/2024**		**10/22/2024**	

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.