

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

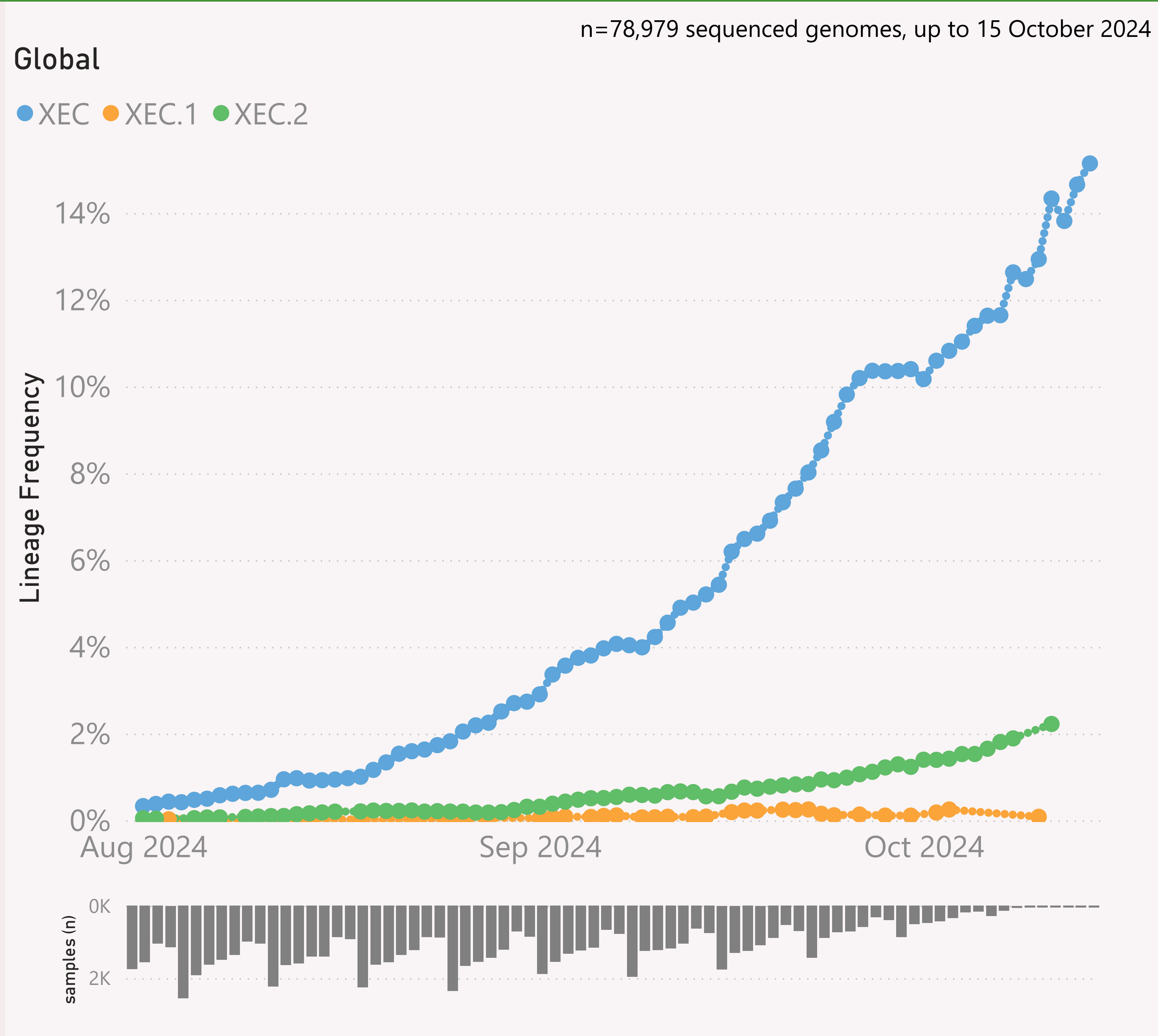
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



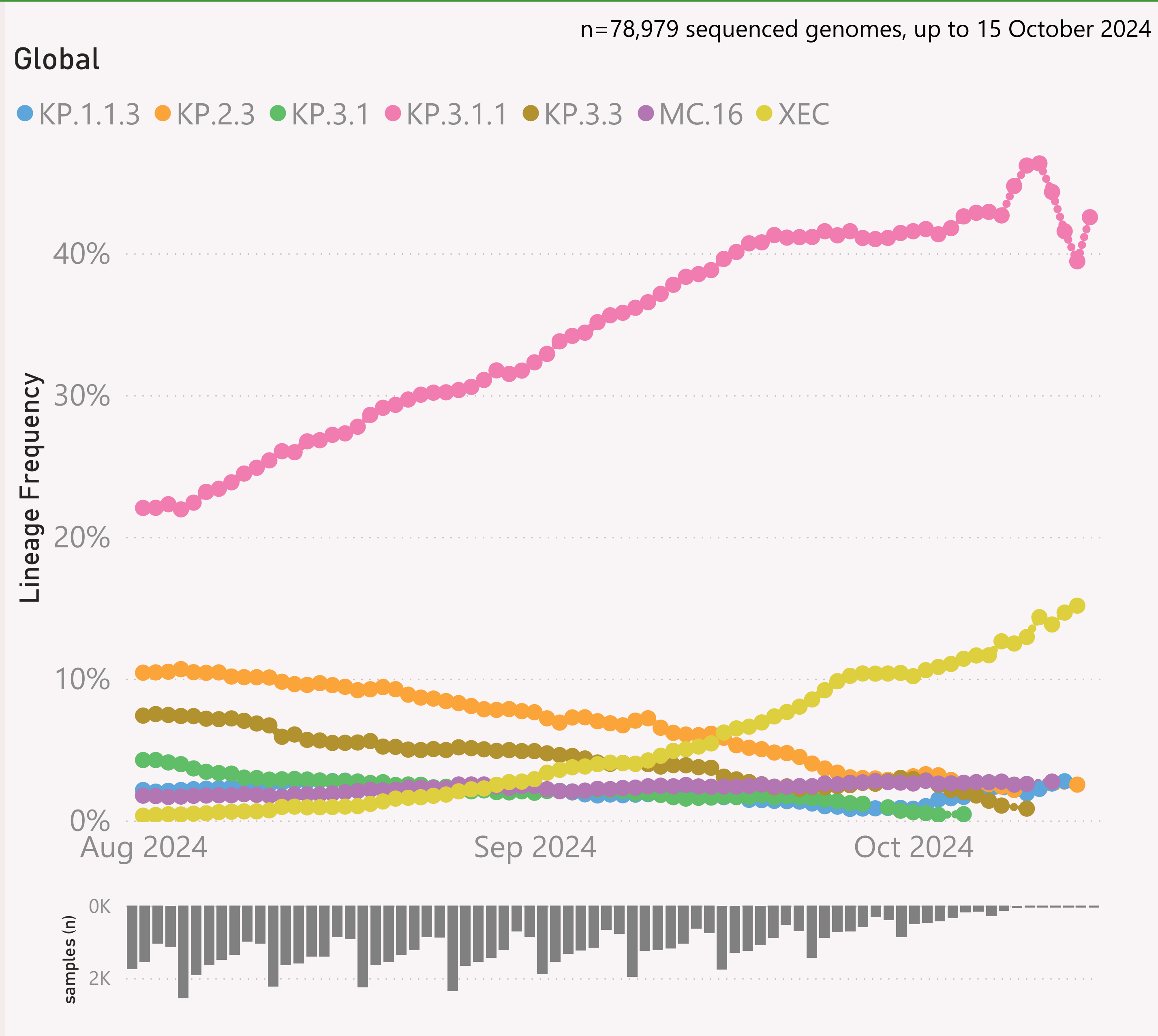
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently XEC.*.

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.



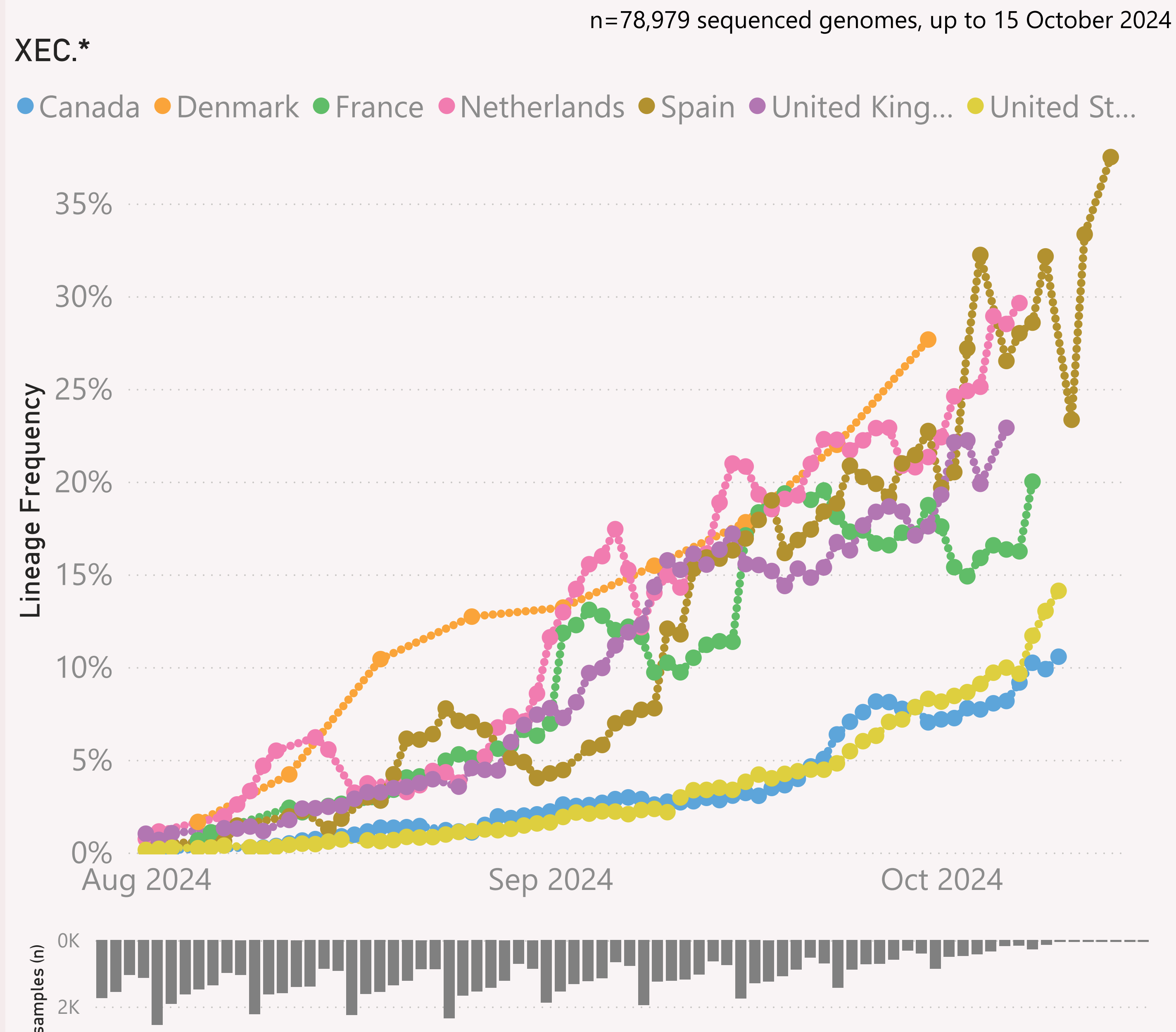
This page shows the frequency of the top 7 lineages, across recent months.

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.

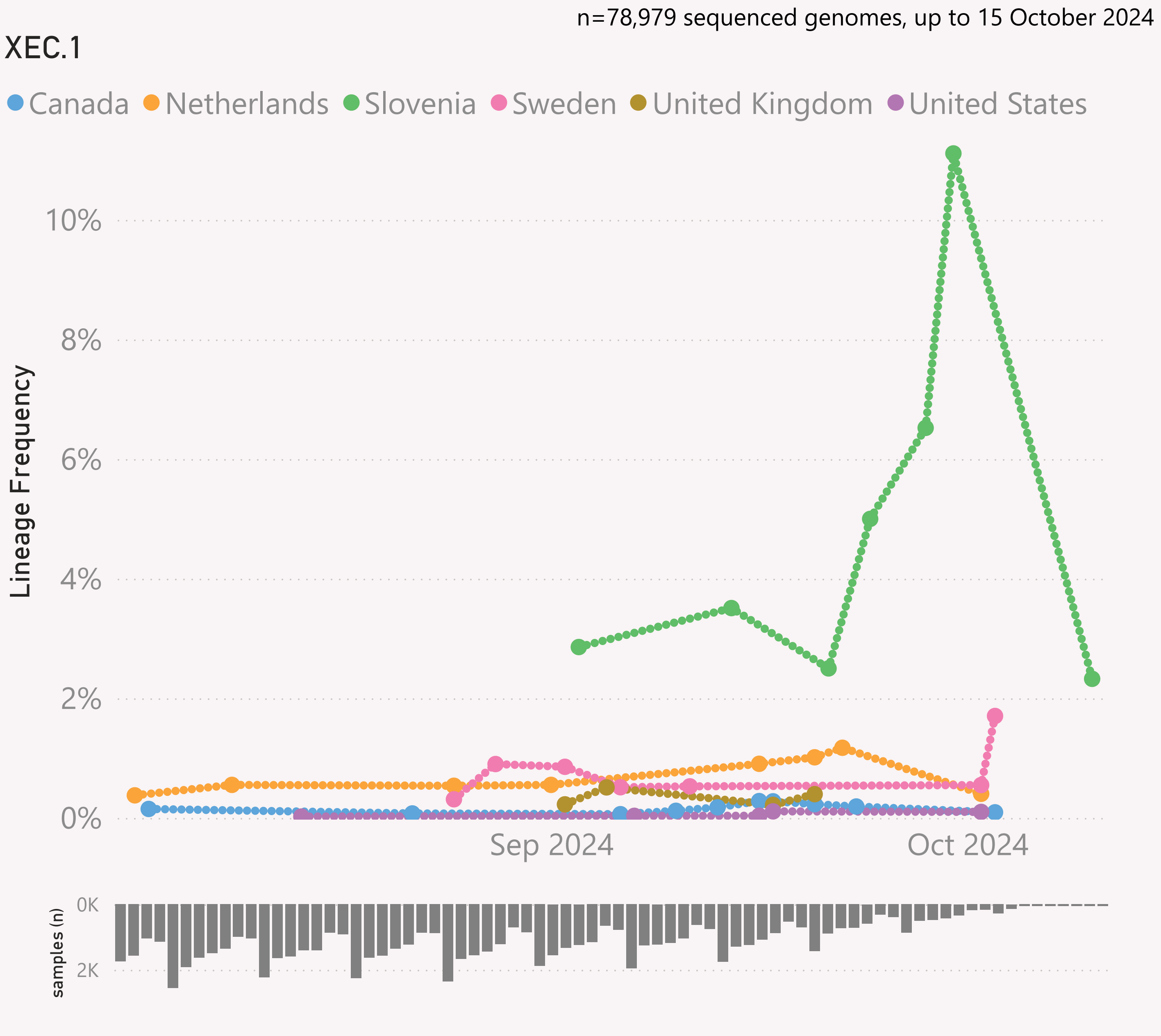
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

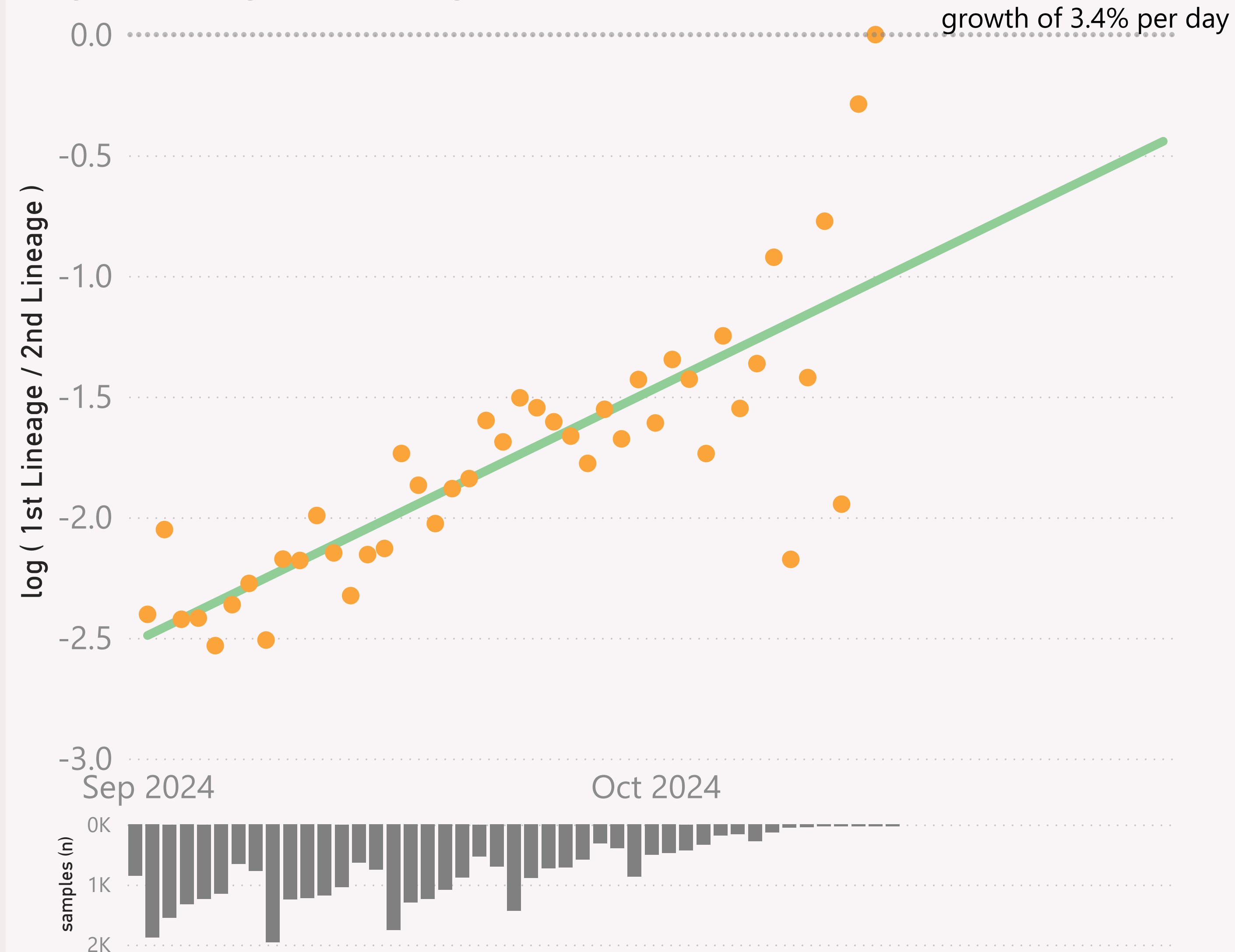
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=33,664 sequenced genomes, up to 15 October 2024

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

● $\log (1st \text{ Lineage} / 2nd \text{ Lineage})$ ● trend



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.

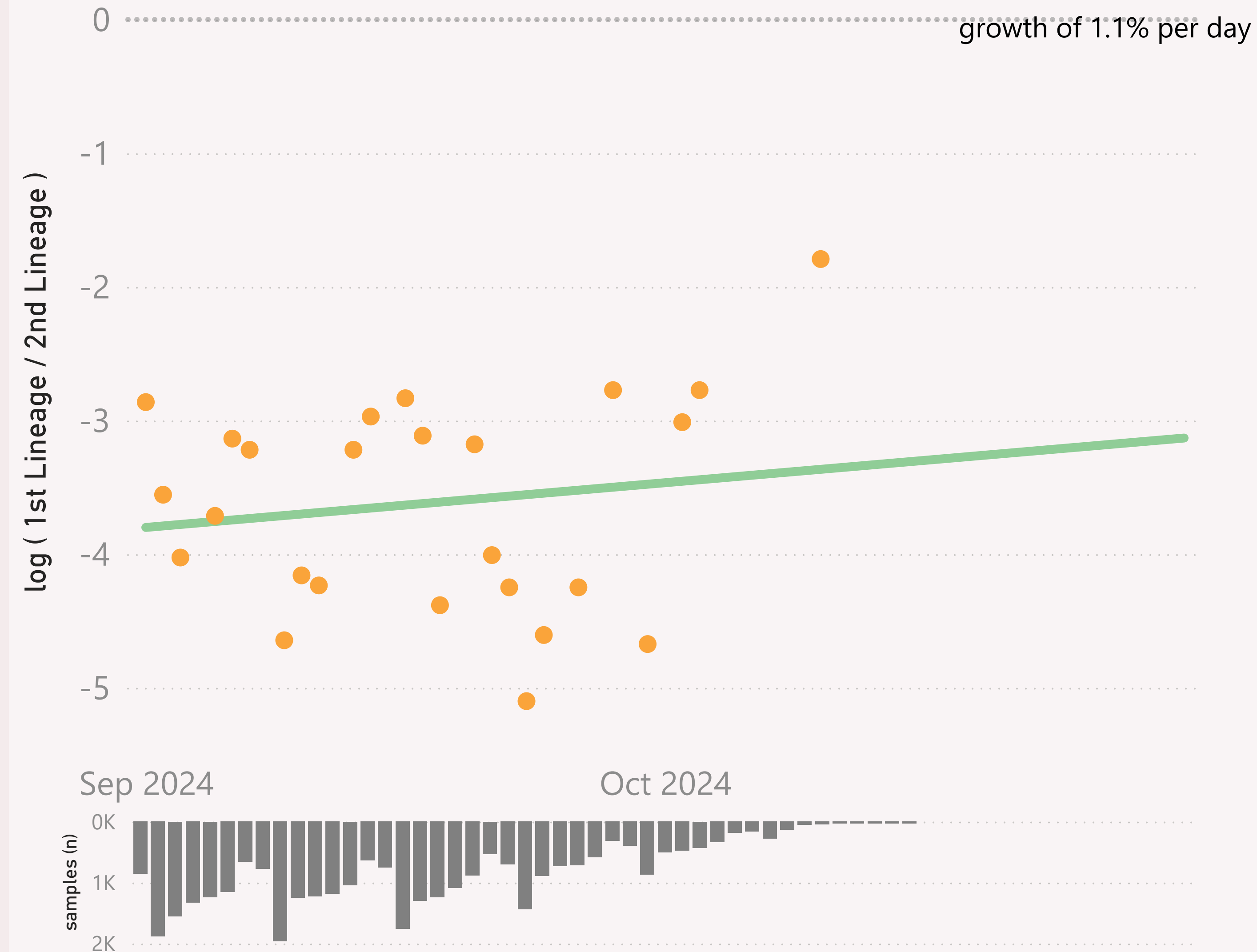
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=33,664 sequenced genomes, up to 15 October 2024

Global - XEC.1 vs XEC









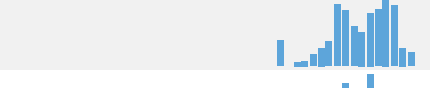





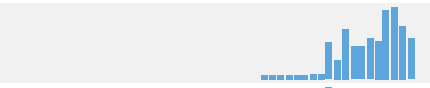












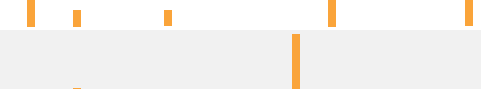








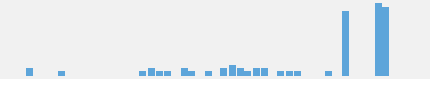



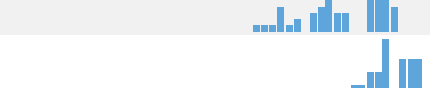





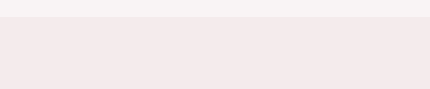
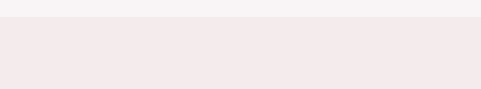
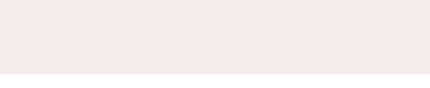
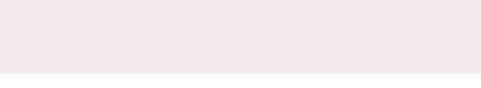
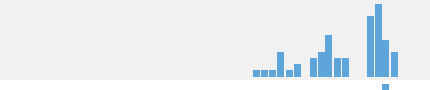
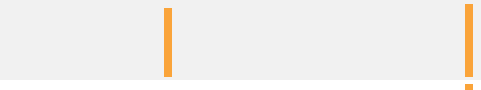



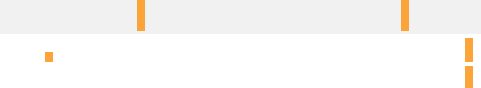


● $\log (1\text{st Lineage} / 2\text{nd Lineage})$ ● trend



Global



Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
<div>+ </div> United States	35,479	10/11/2024		10/15/2024	
<div>+ </div> Canada	11,974	10/13/2024		10/15/2024	
<div>+ </div> Spain	5,308	10/15/2024		10/15/2024	
<div>+ </div> Japan	4,572	10/12/2024		10/15/2024	
<div>+ </div> France	4,258	10/8/2024		10/15/2024	
<div>+ </div> United Kingdom	3,634	10/6/2024		10/15/2024	
<div>+ </div> Sweden	2,723	10/9/2024		10/15/2024	
<div>+ </div> China	2,662	10/14/2024		10/15/2024	
<div>+ </div> Italy	2,023	10/14/2024		10/15/2024	
<div>+ </div> Netherlands	2,003	10/8/2024		10/15/2024	
<div>+ </div> Australia	1,927	10/8/2024		10/15/2024	
<div>+ </div> Denmark	1,589	9/30/2024		10/15/2024	
<div>+ </div> South Korea	1,304	9/26/2024		10/15/2024	
<div>+ </div> Brazil	1,245	10/2/2024		10/15/2024	
<div>+ </div> Germany	1,211	9/30/2024		10/15/2024	
<div>+ </div> Ireland	1,094	10/13/2024		10/15/2024	
<div>+ </div> New Zealand	883	10/6/2024		10/15/2024	
<div>+ </div> Costa Rica	589	9/9/2024		10/3/2024	
<div>+ </div> Puerto Rico	589	9/23/2024		10/7/2024	
<div>+ </div> Greece	580	8/2/2024		9/23/2024	
<div>+ </div> Singapore	517	10/8/2024		10/14/2024	
<div>+ </div> Mexico	478	8/9/2024		10/15/2024	
<div>+ </div> Poland	441	10/2/2024		10/8/2024	
<div>+ </div> Taiwan	406	10/7/2024		10/14/2024	
<div>+ </div> Bahrain	386	8/26/2024		10/9/2024	
<div>+ </div> Luxembourg	356	9/30/2024		10/15/2024	
<div>+ </div> Slovenia	354	10/13/2024		10/15/2024	
<div>+ </div> Portugal	351	9/24/2024		10/8/2024	
<div>+ </div> Total	93,746	10/15/2024		10/15/2024	

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.