

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

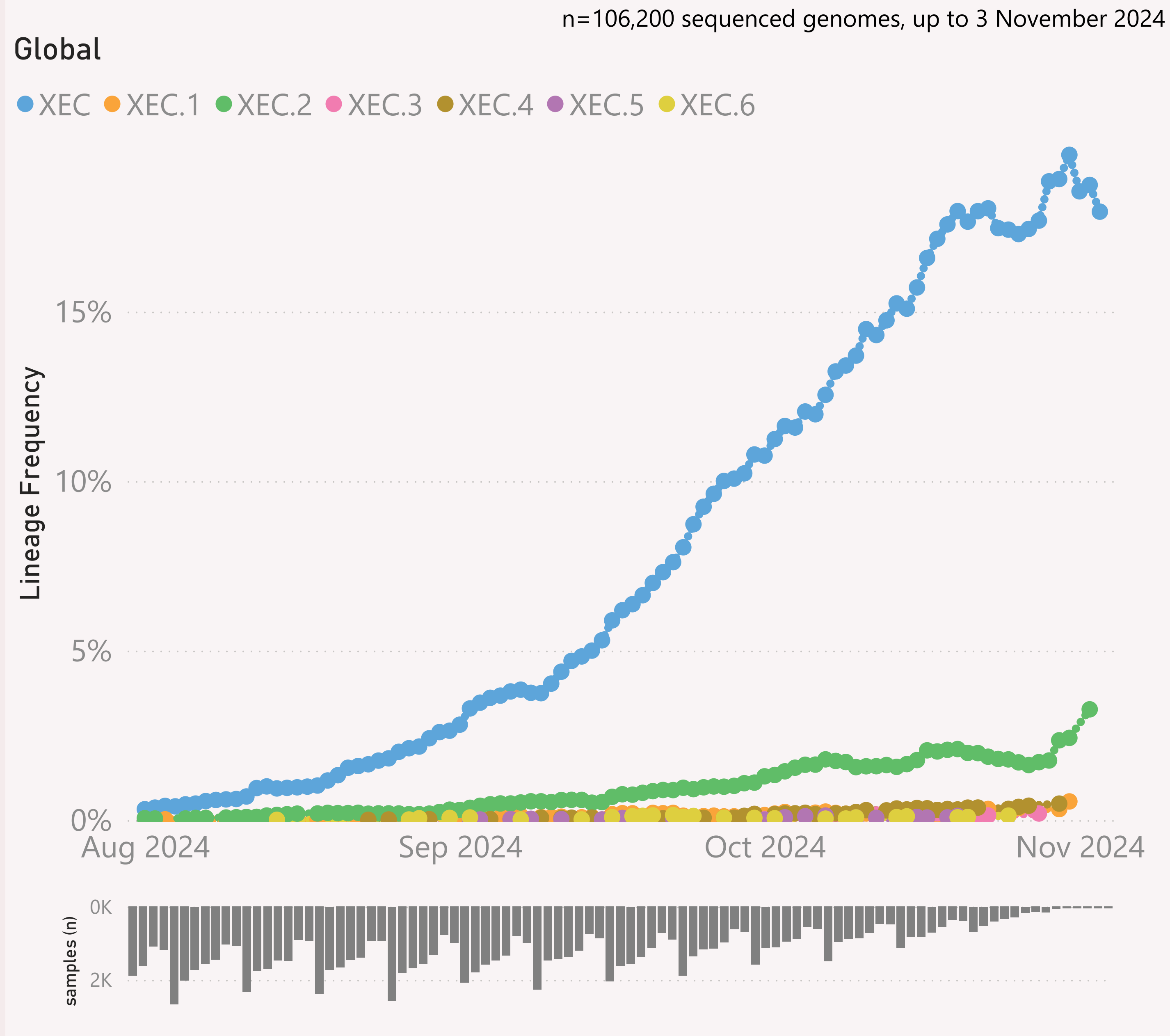
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



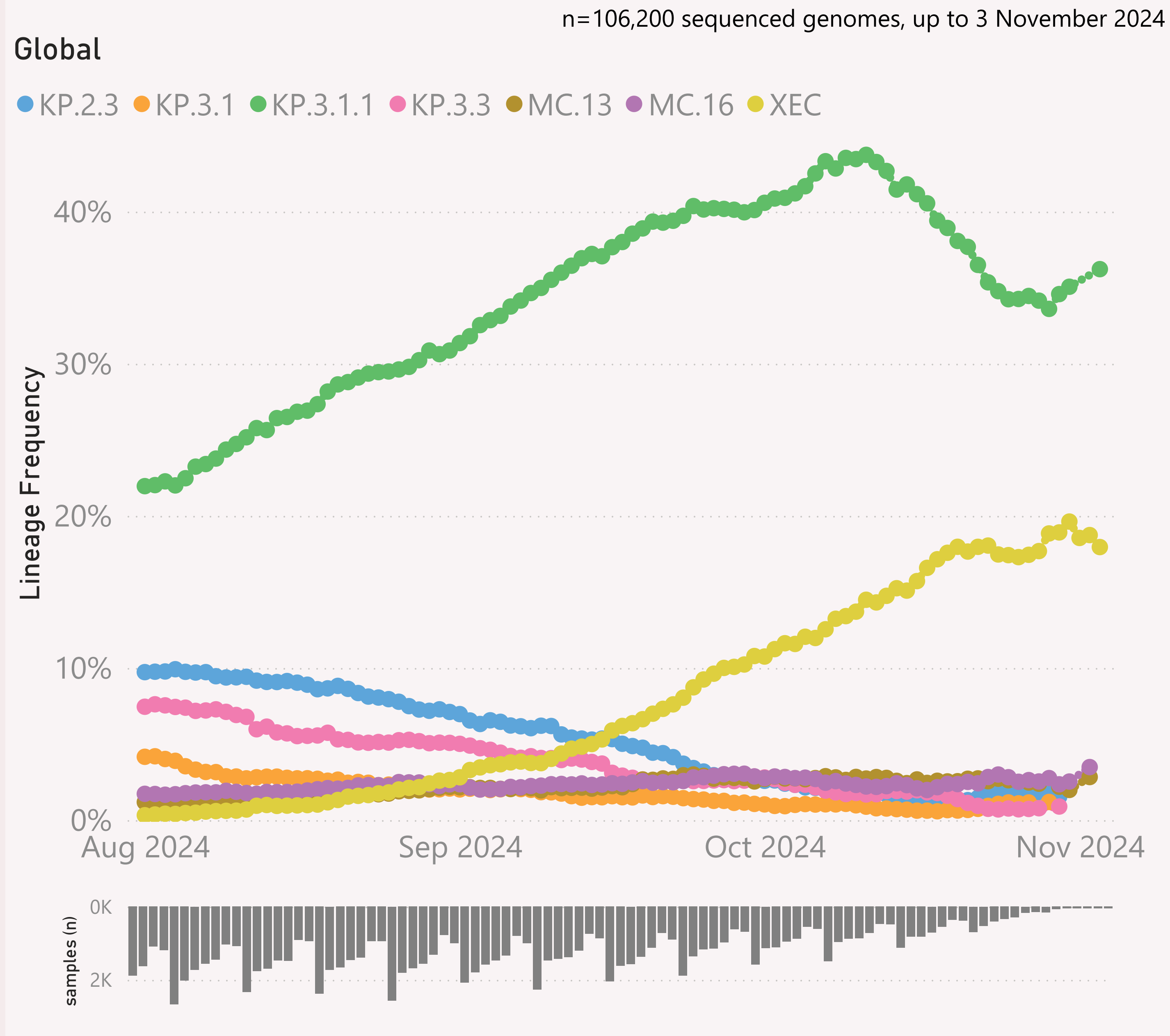
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently XEC.*.

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.

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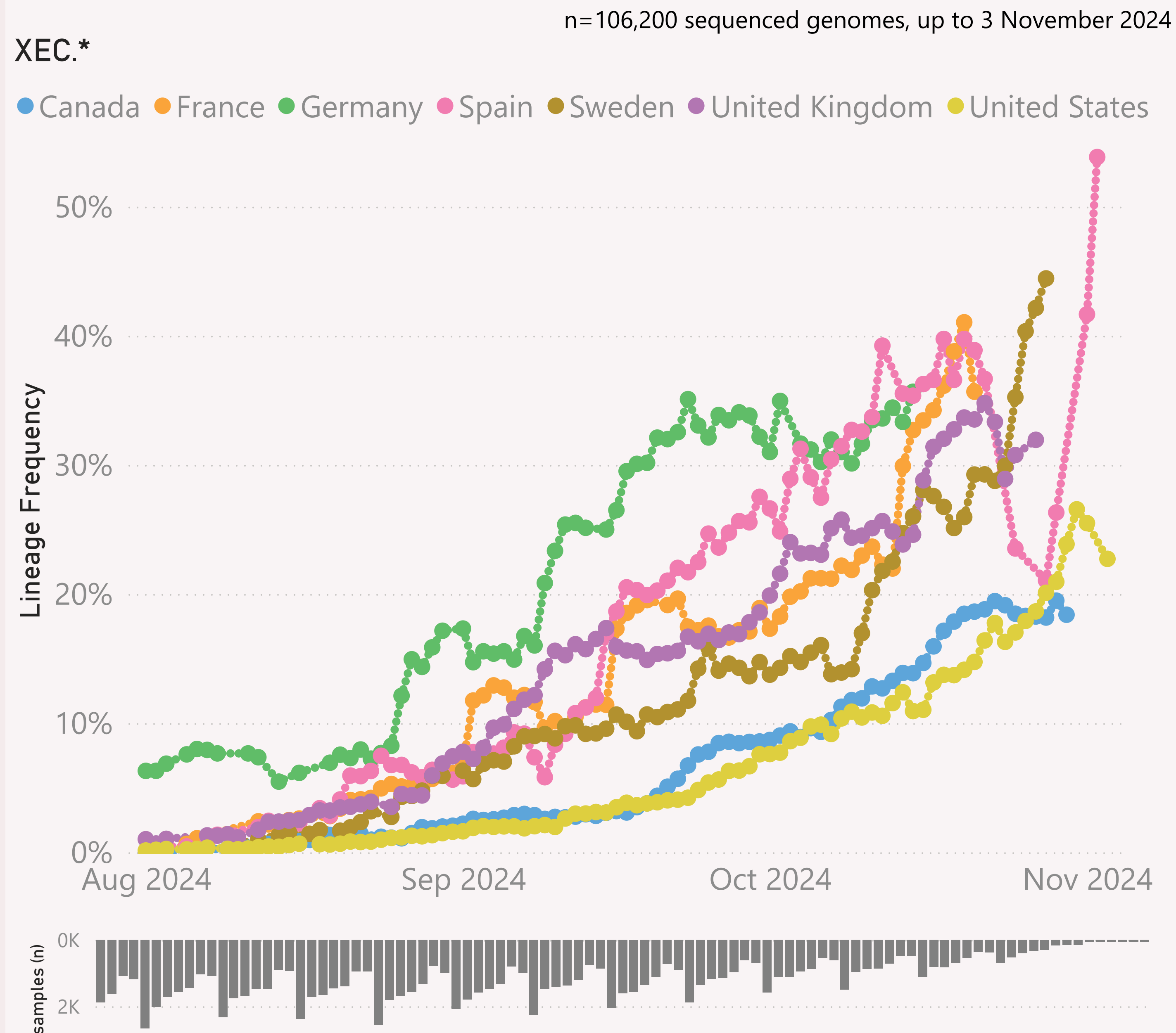
This page shows the frequency of the top 7 lineages, across recent months.

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.

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This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

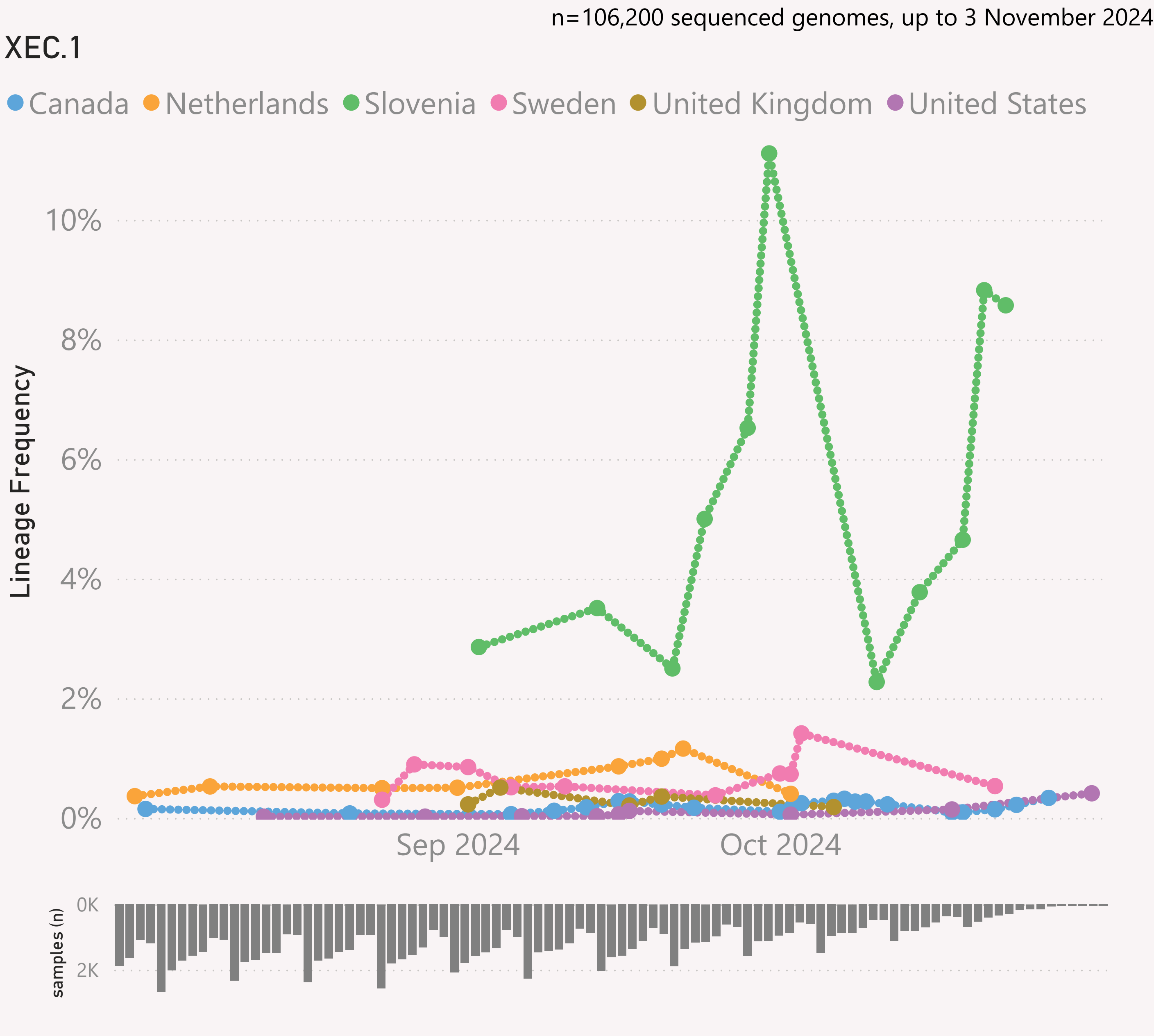
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

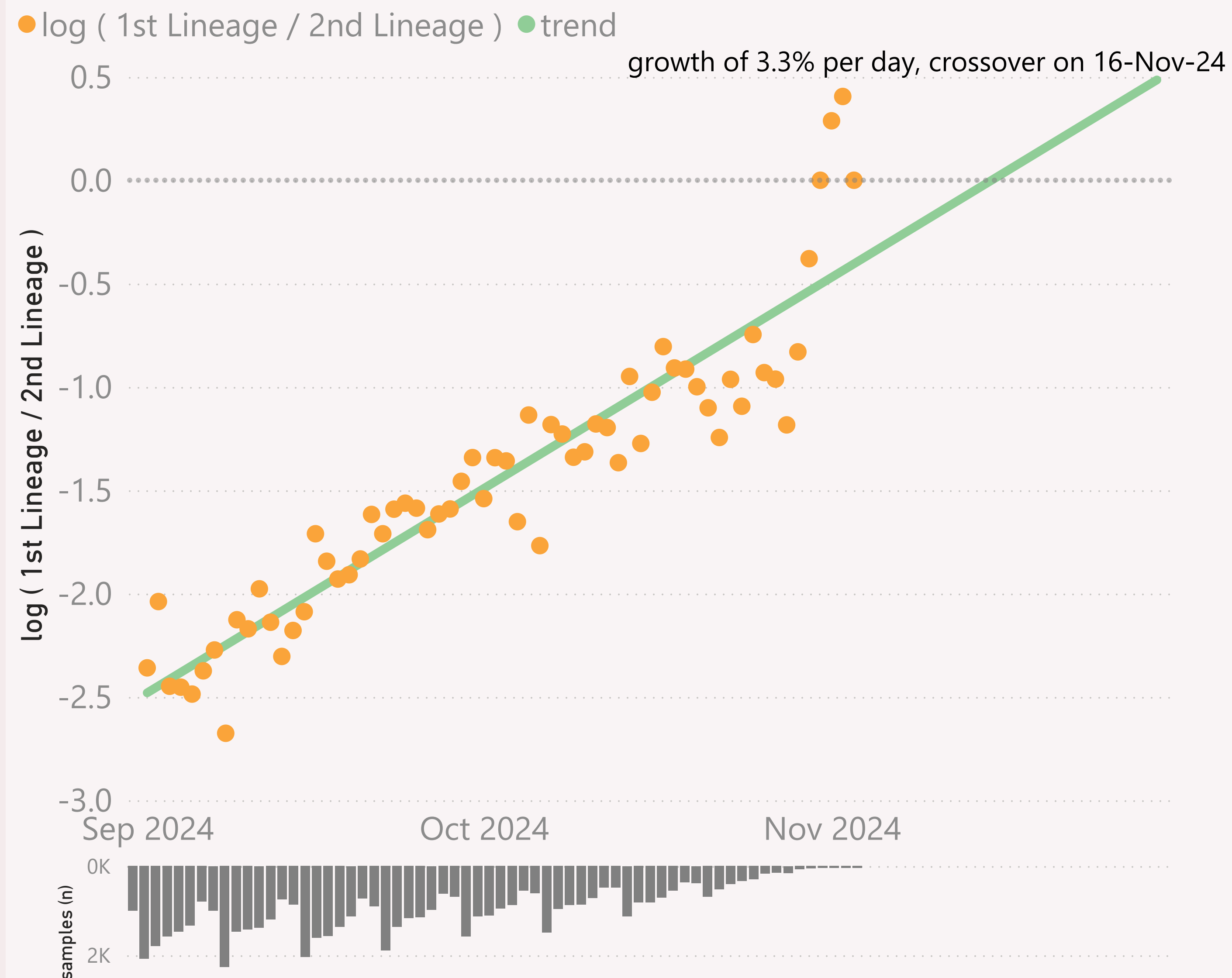
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that country.

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=58,011 sequenced genomes, up to 3 November 2024

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



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.

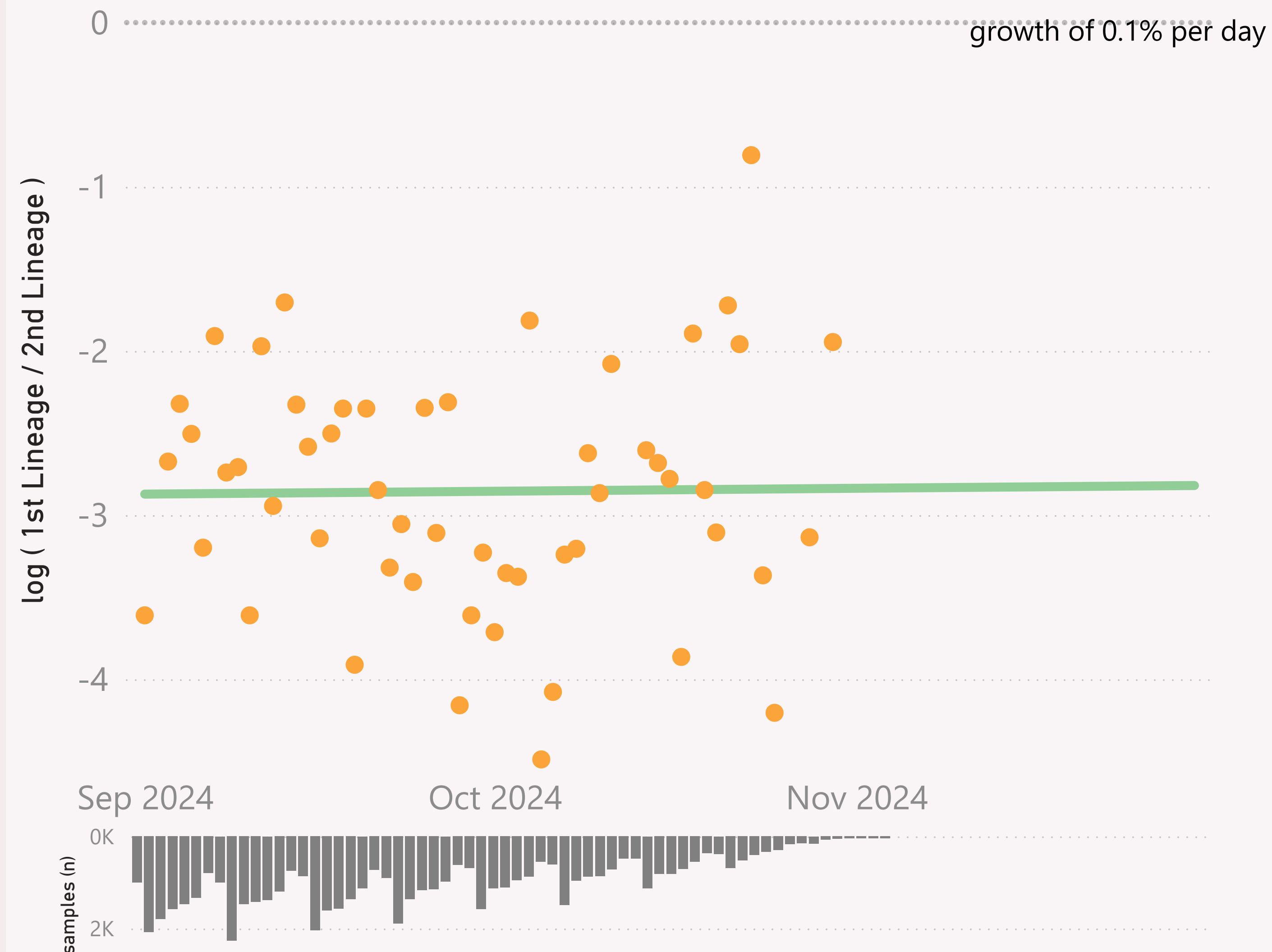
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=58,011 sequenced genomes, up to 3 November 2024

Global - MV.1 vs XEC

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

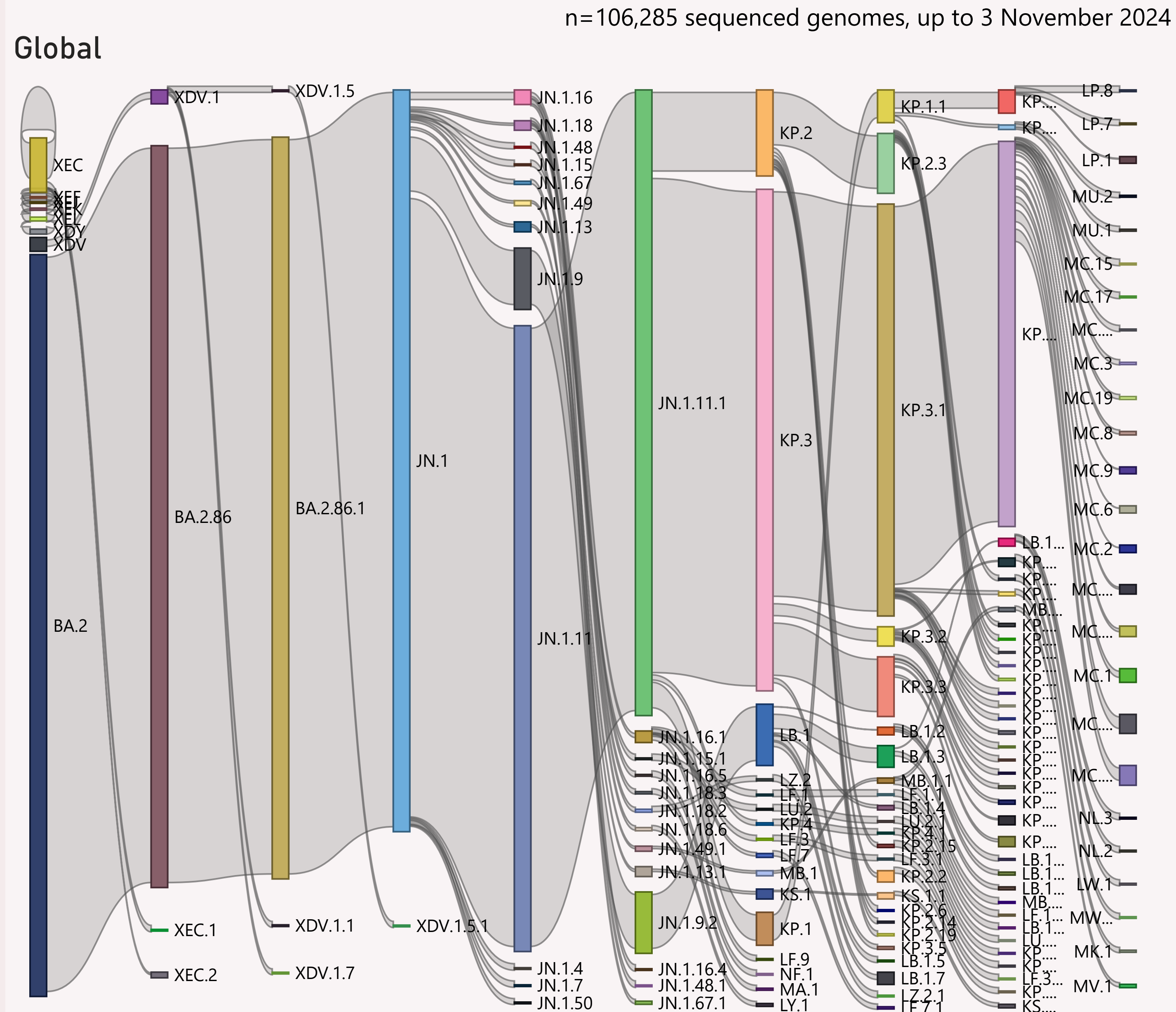


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.



This page shows the hierarchy of the significant Lineages, over recent months.







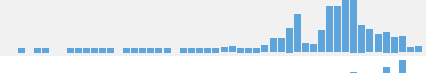



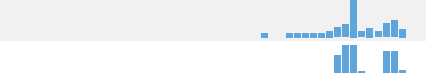





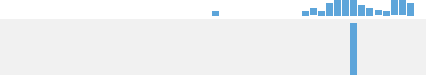



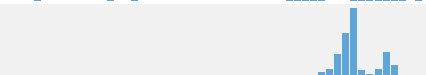



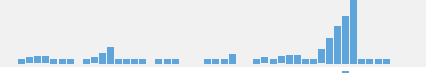





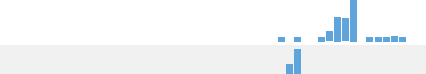



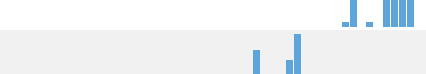



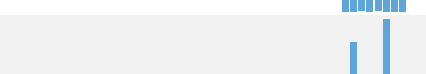




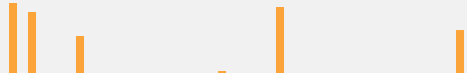


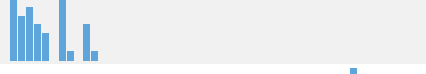
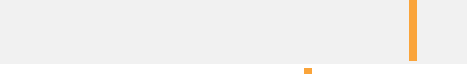






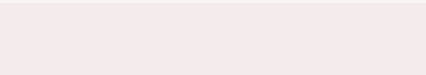
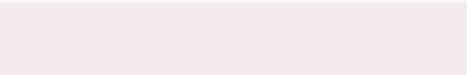
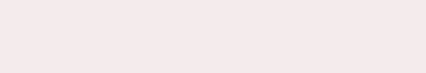
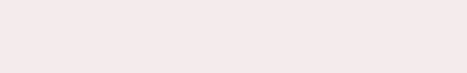
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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

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	29,426	03/11/2024		02/11/2024	
<div>+ </div> Canada	15,487	30/10/2024		02/11/2024	
<div>+ </div> Spain	4,652	02/11/2024		02/11/2024	
<div>+ </div> Japan	3,976	30/10/2024		02/11/2024	
<div>+ </div> United Kingdom	3,887	27/10/2024		02/11/2024	
<div>+ </div> France	3,392	21/10/2024		02/11/2024	
<div>+ </div> Sweden	2,591	28/10/2024		02/11/2024	
<div>+ </div> Australia	2,235	28/10/2024		02/11/2024	
<div>+ </div> China	1,816	24/10/2024		02/11/2024	
<div>+ </div> Denmark	1,648	21/10/2024		02/11/2024	
<div>+ </div> Italy	1,560	31/10/2024		02/11/2024	
<div>+ </div> Germany	1,550	17/10/2024		02/11/2024	
<div>+ </div> Netherlands	1,537	08/10/2024		28/10/2024	
<div>+ </div> Brazil	1,439	18/10/2024		02/11/2024	
<div>+ </div> Russia	994	01/10/2024		25/10/2024	
<div>+ </div> Ireland	912	02/11/2024		02/11/2024	
<div>+ </div> South Korea	782	17/10/2024		02/11/2024	
<div>+ </div> Greece	664	08/09/2024		31/10/2024	
<div>+ </div> Singapore	554	23/10/2024		28/10/2024	
<div>+ </div> Costa Rica	551	23/09/2024		02/11/2024	
<div>+ </div> New Zealand	477	20/10/2024		30/10/2024	
<div>+ </div> Poland	440	25/10/2024		02/11/2024	
<div>+ </div> Bahrain	386	26/08/2024		09/10/2024	
<div>+ </div> Taiwan	348	30/10/2024		02/11/2024	
<div>+ </div> Israel	314	09/10/2024		27/10/2024	
<div>+ </div> Cyprus	309	28/02/2024		28/10/2024	
<div>+ </div> Slovenia	307	27/10/2024		30/10/2024	
<div>+ </div> Thailand	274	24/10/2024		02/11/2024	
<div>+ </div> Total	87,040	03/11/2024		02/11/2024	

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.