

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

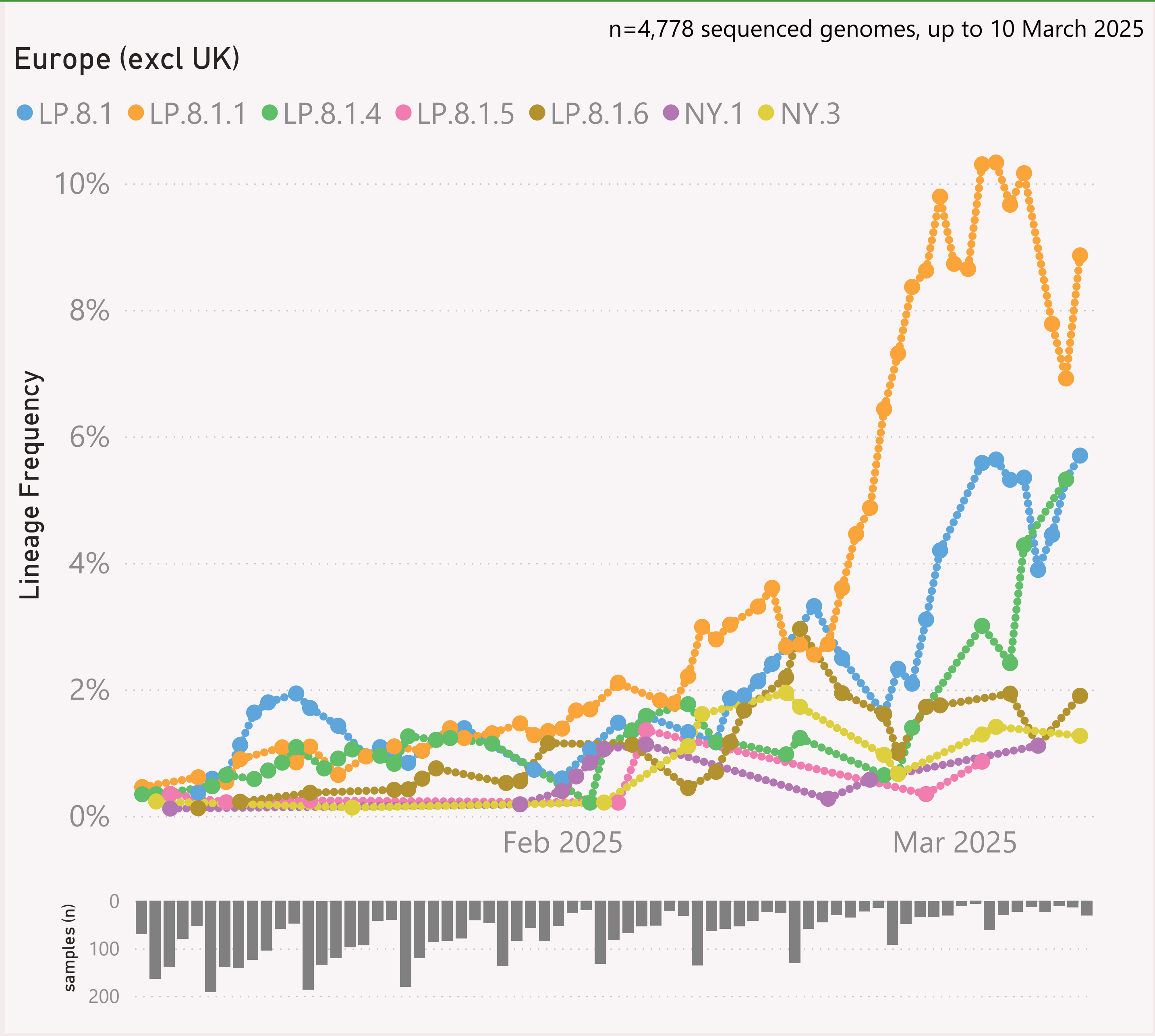
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.



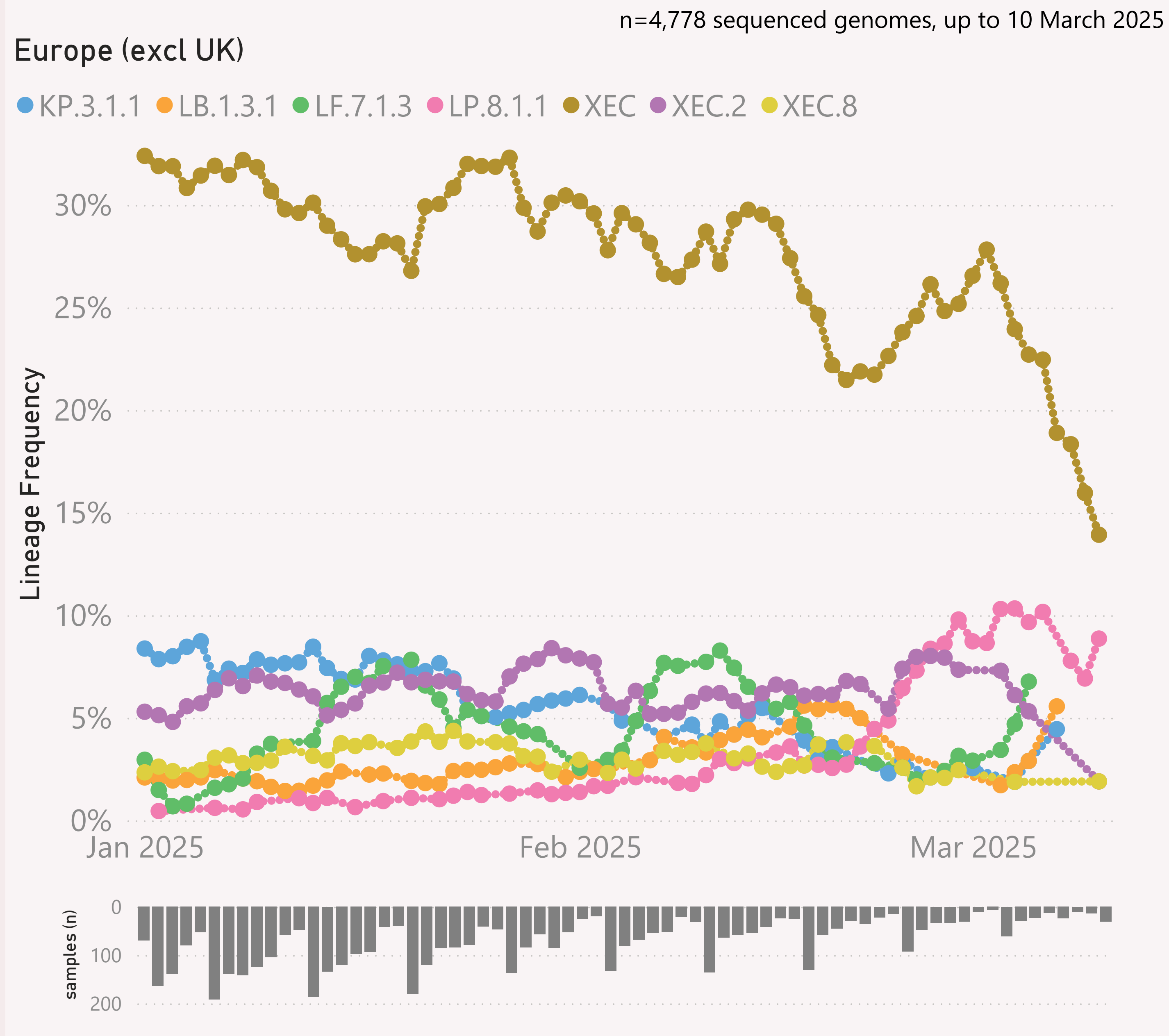
This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "LP.8.1.*".

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.



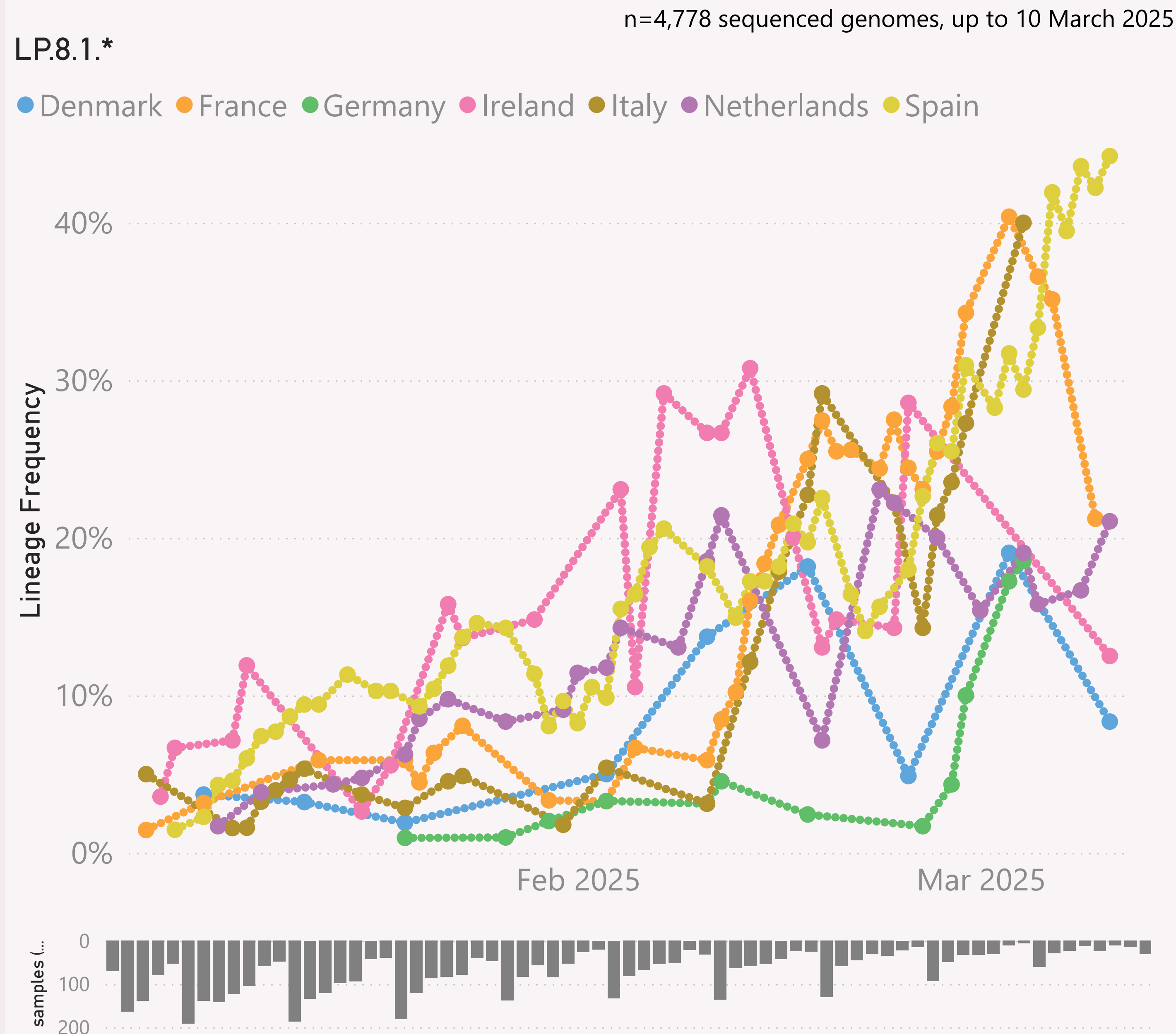
This page shows the frequency of the top 7 lineages, across recent months.

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.

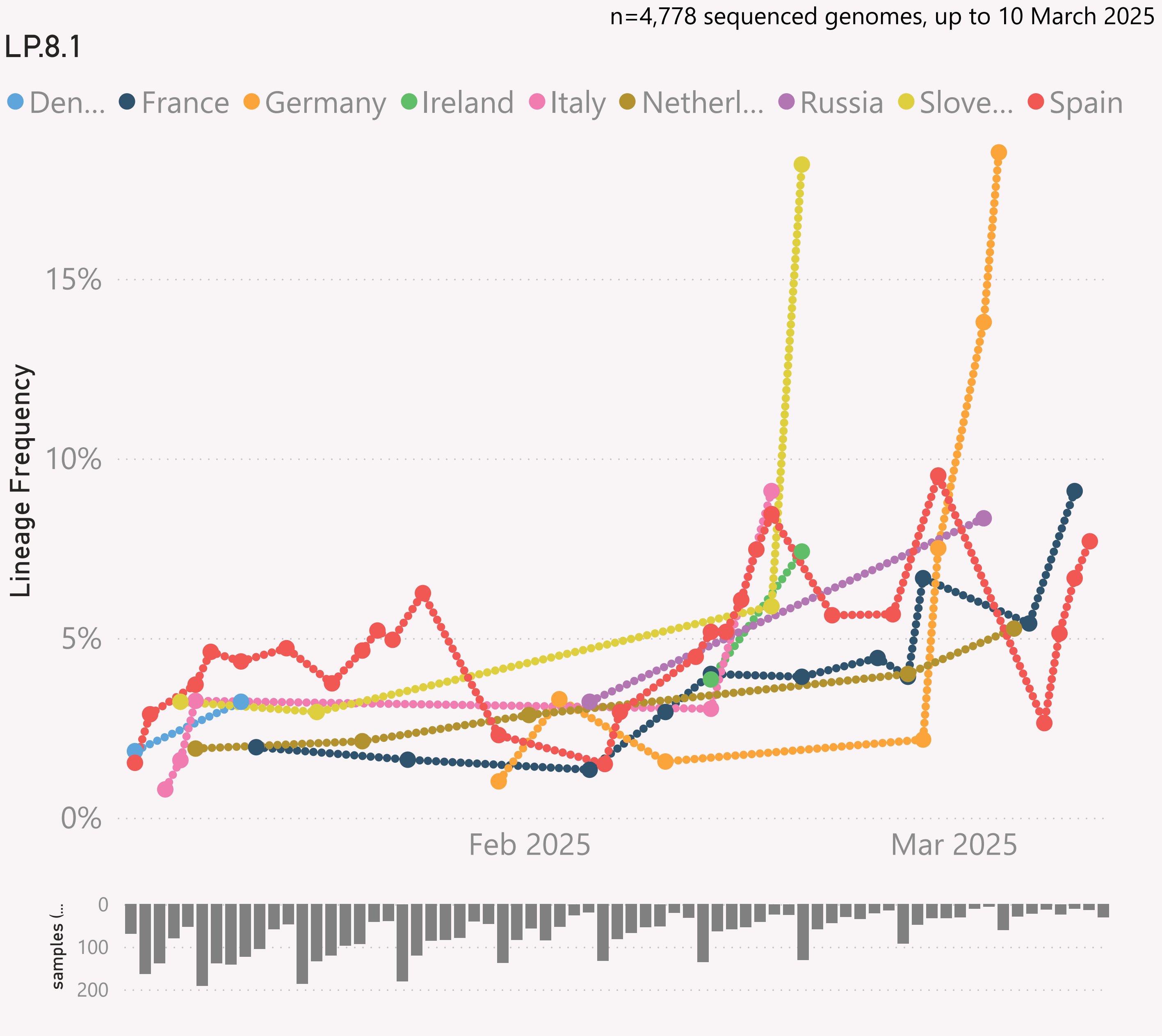
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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 7 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.

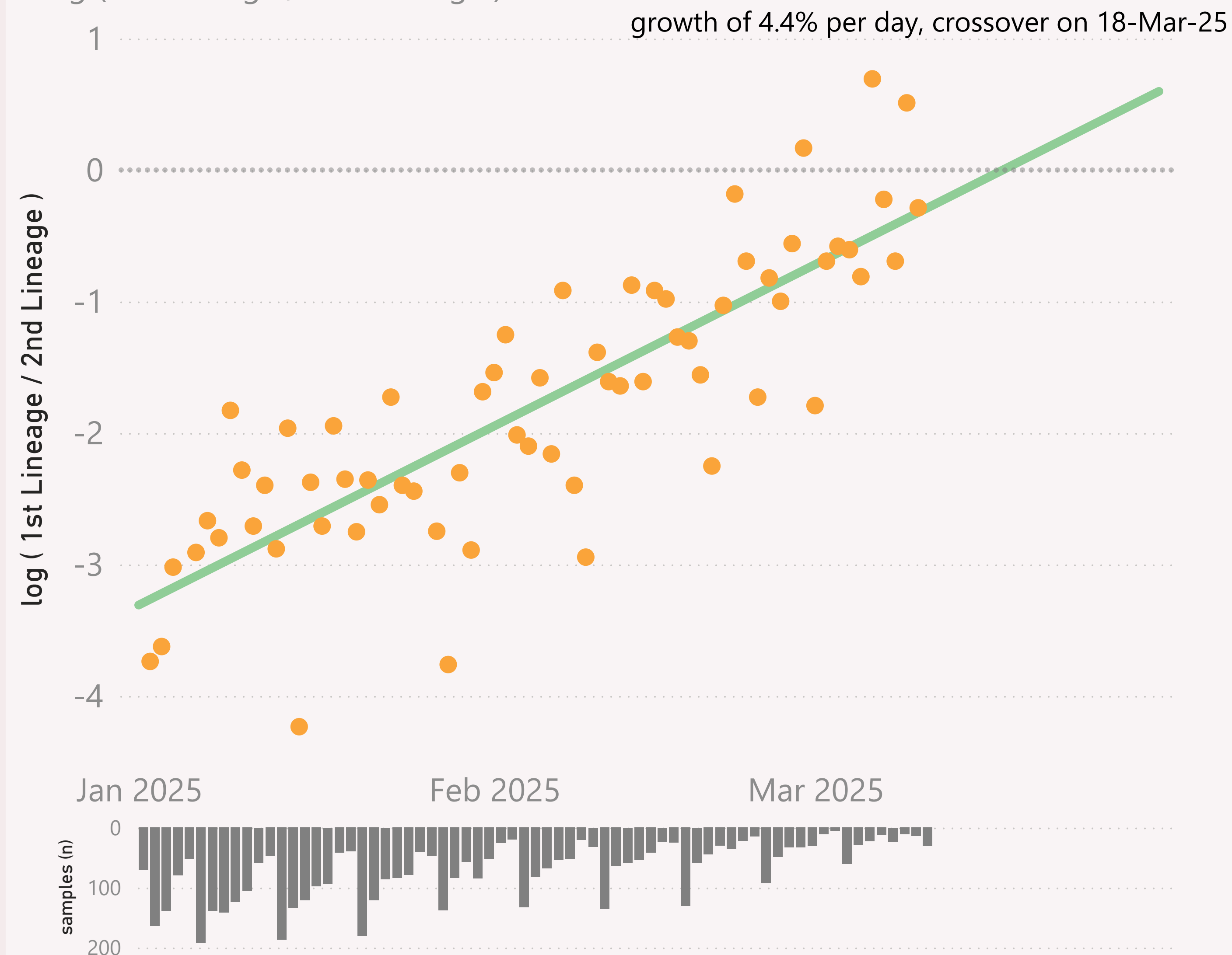
The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

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

n=4,778 sequenced genomes, up to 10 March 2025

Europe (excl UK) - LP.8.1.* vs XEC.*

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

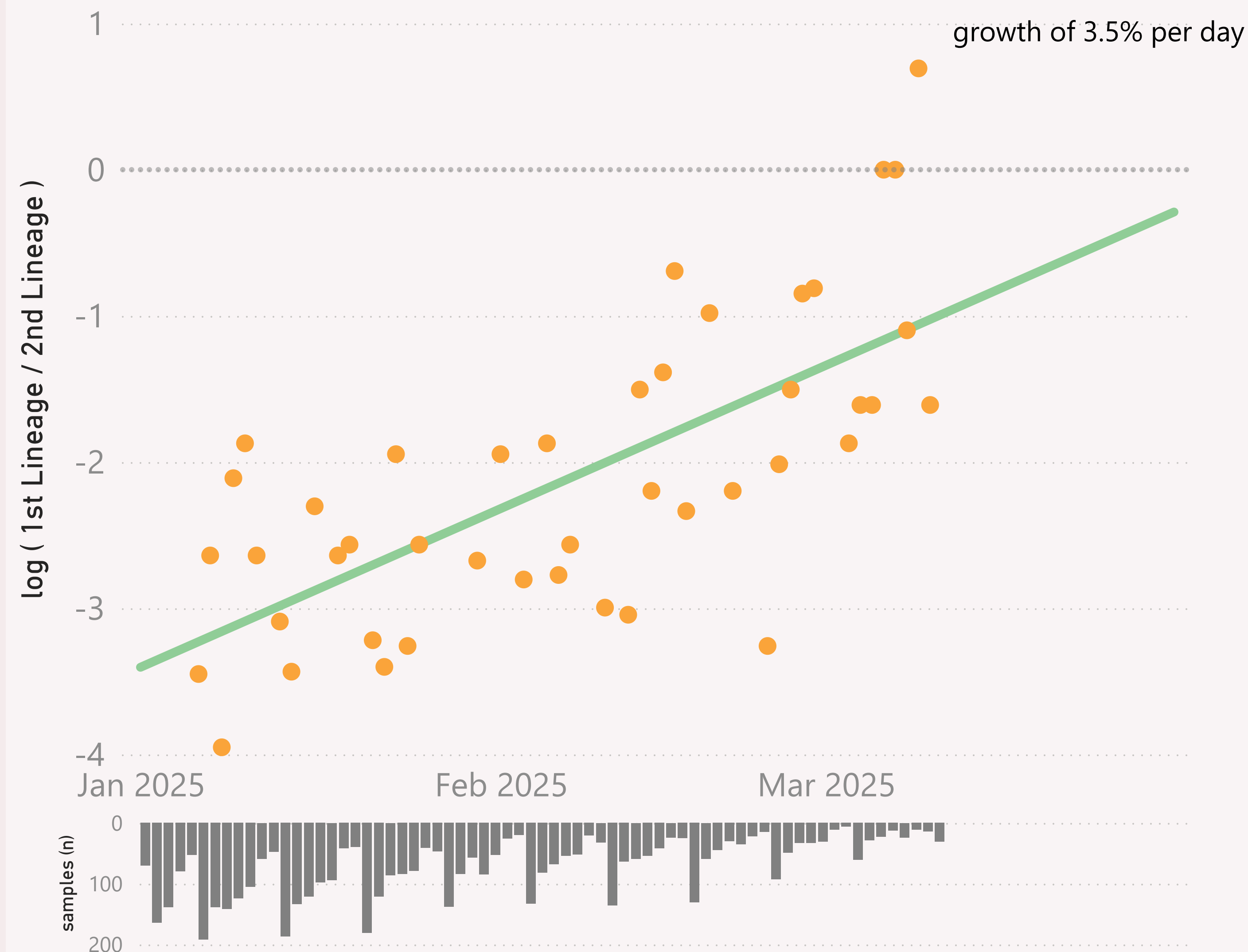
The Lineage classifications are provided by Nextclade. I add the "Lineage L2" groups, typically following common variant groupings, but occasionally being "creative".

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=4,778 sequenced genomes, up to 10 March 2025

Europe (excl UK) - LP.8.1 vs XEC

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



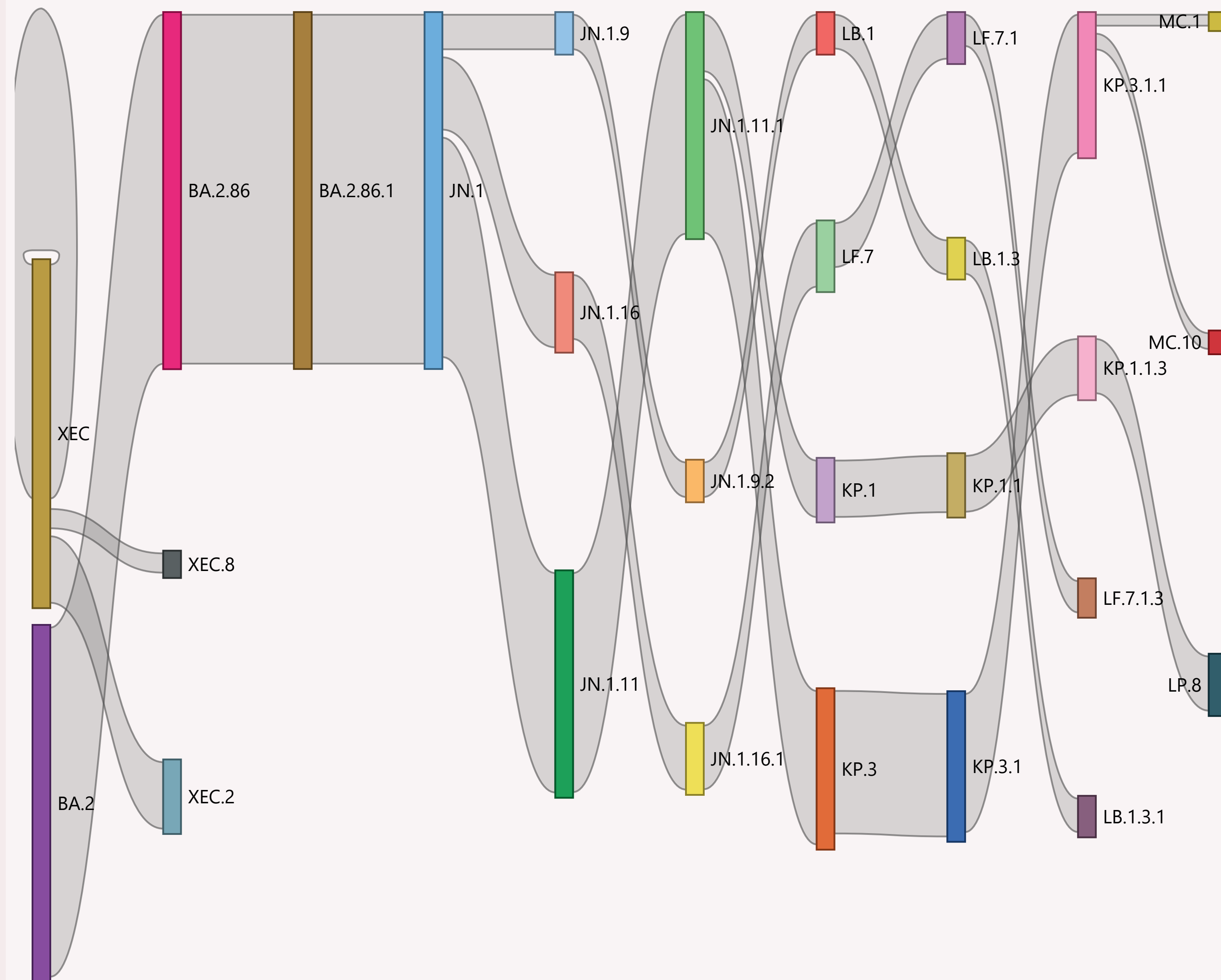
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.



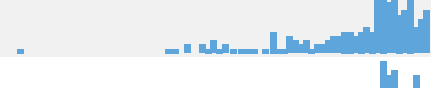





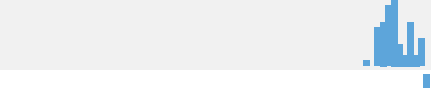

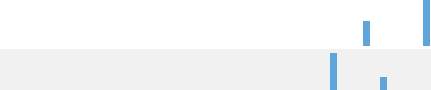



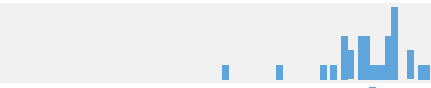





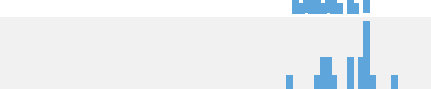



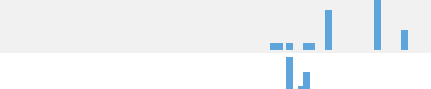

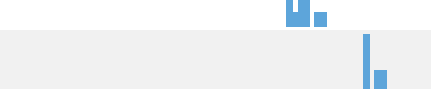
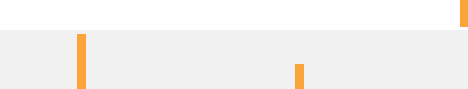


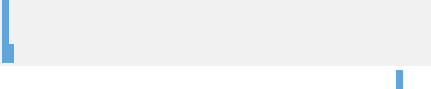

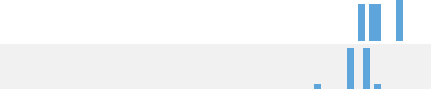



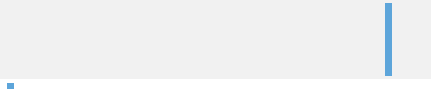
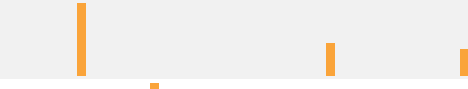




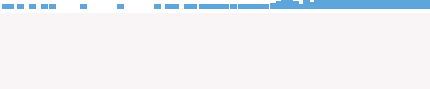



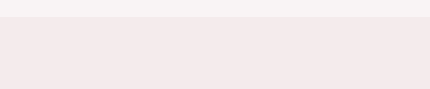
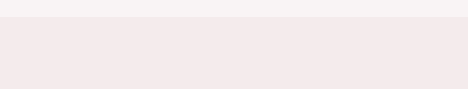
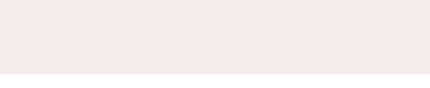
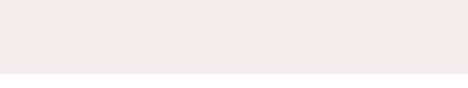




The grey column chart across the bottom shows the volume of sequences available by date. As there can be long sample and data processing times, it is quite routine for recent dates to show lower sample sizes.

Europe (excl UK)



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
⊕ Russia	1,277	05/03/2025		19/03/2025	
⊕ Spain	1,115	10/03/2025		19/03/2025	
⊕ France	590	10/03/2025		19/03/2025	
⊕ Italy	548	04/03/2025		19/03/2025	
⊕ Greece	505	01/03/2025		19/03/2025	
⊕ Germany	482	04/03/2025		19/03/2025	
⊕ Denmark	344	10/03/2025		19/03/2025	
⊕ Slovenia	343	10/03/2025		17/03/2025	
⊕ Netherlands	304	10/03/2025		19/03/2025	
⊕ Ireland	254	10/03/2025		19/03/2025	
⊕ Finland	236	22/02/2025		19/03/2025	
⊕ Sweden	234	07/03/2025		18/03/2025	
⊕ Austria	184	27/01/2025		24/02/2025	
⊕ Switzerland	87	28/02/2025		19/03/2025	
⊕ Norway	84	20/02/2025		07/03/2025	
⊕ Poland	84	25/02/2025		17/03/2025	
⊕ Czechia	74	09/12/2024		19/03/2025	
⊕ Portugal	35	16/02/2025		03/03/2025	
⊕ Ukraine	34	28/01/2025		20/02/2025	
⊕ Estonia	32	04/02/2024		01/03/2025	
⊕ Belgium	26	25/02/2025		17/03/2025	
⊕ Croatia	26	27/01/2025		11/03/2025	
⊕ Hungary	21	28/01/2025		19/03/2025	
⊕ Slovakia	20	01/02/2025		19/03/2025	
⊕ Lithuania	13	14/02/2025		13/03/2025	
⊕ Romania	13	03/03/2025		19/03/2025	
Total	6,965	10/03/2025		19/03/2025	

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.