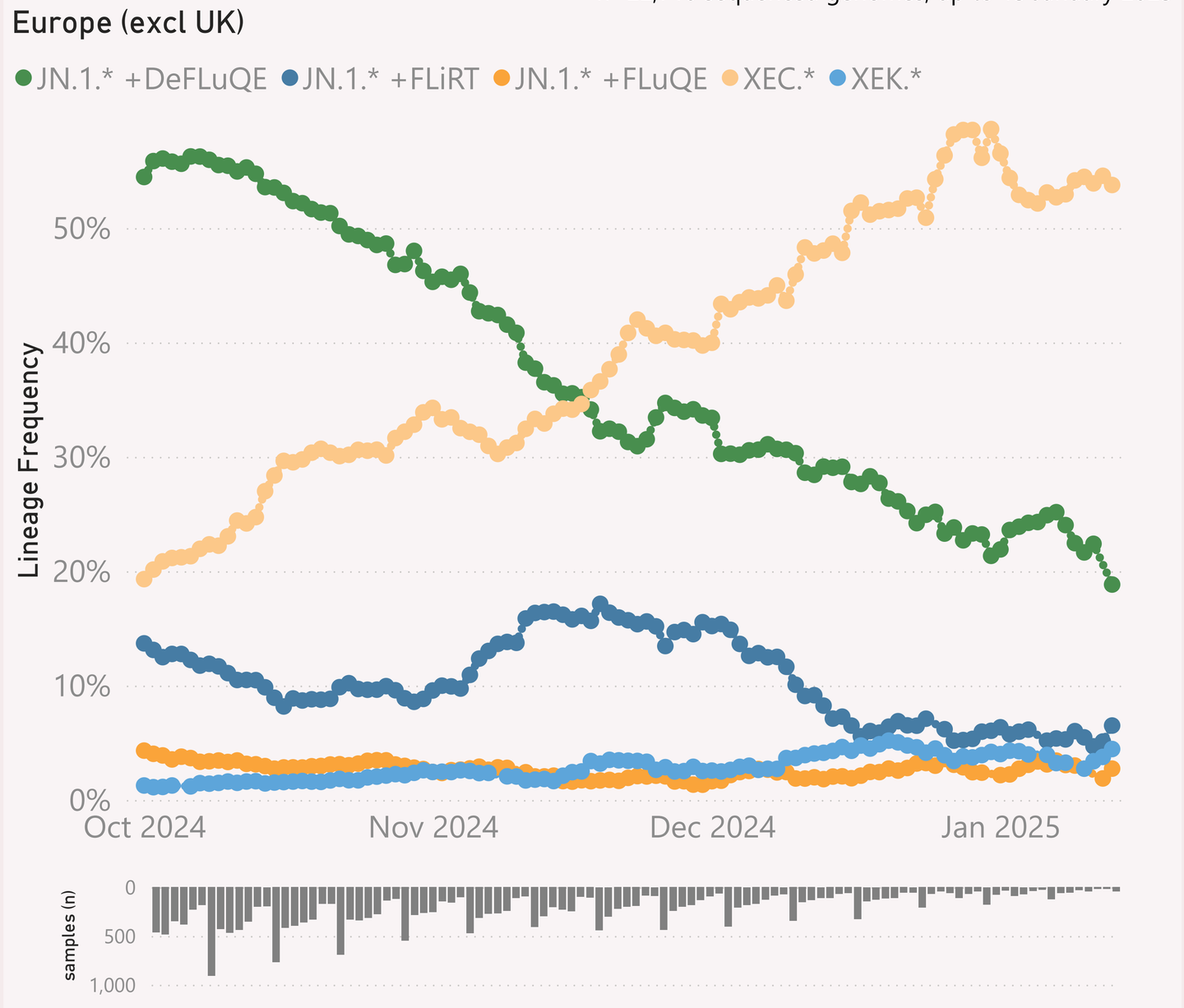
n=22,710 sequenced genomes, up to 13 January 2025



This page shows the frequency of the top 5 "L2" lineages, across recent months.

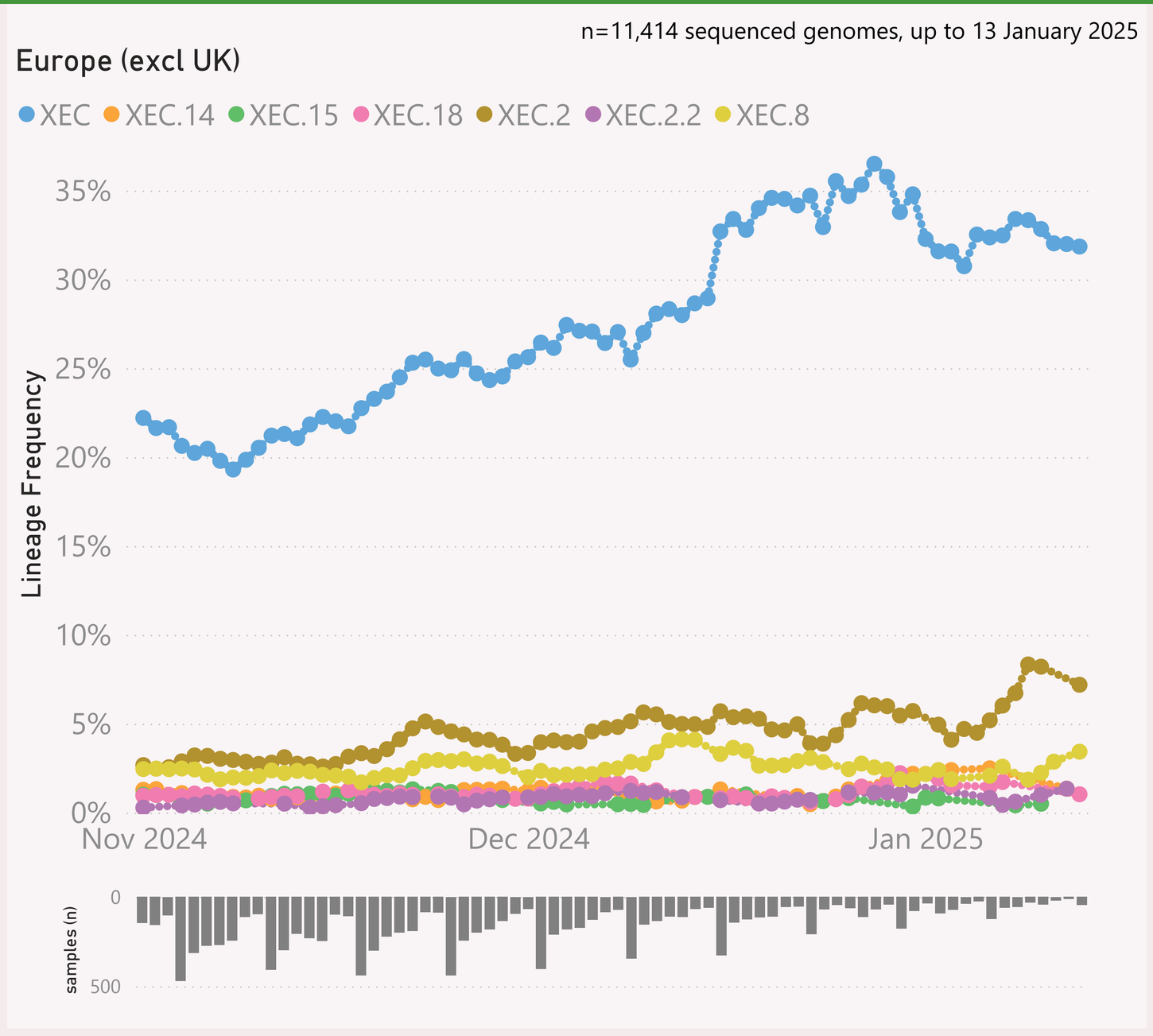
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.*".

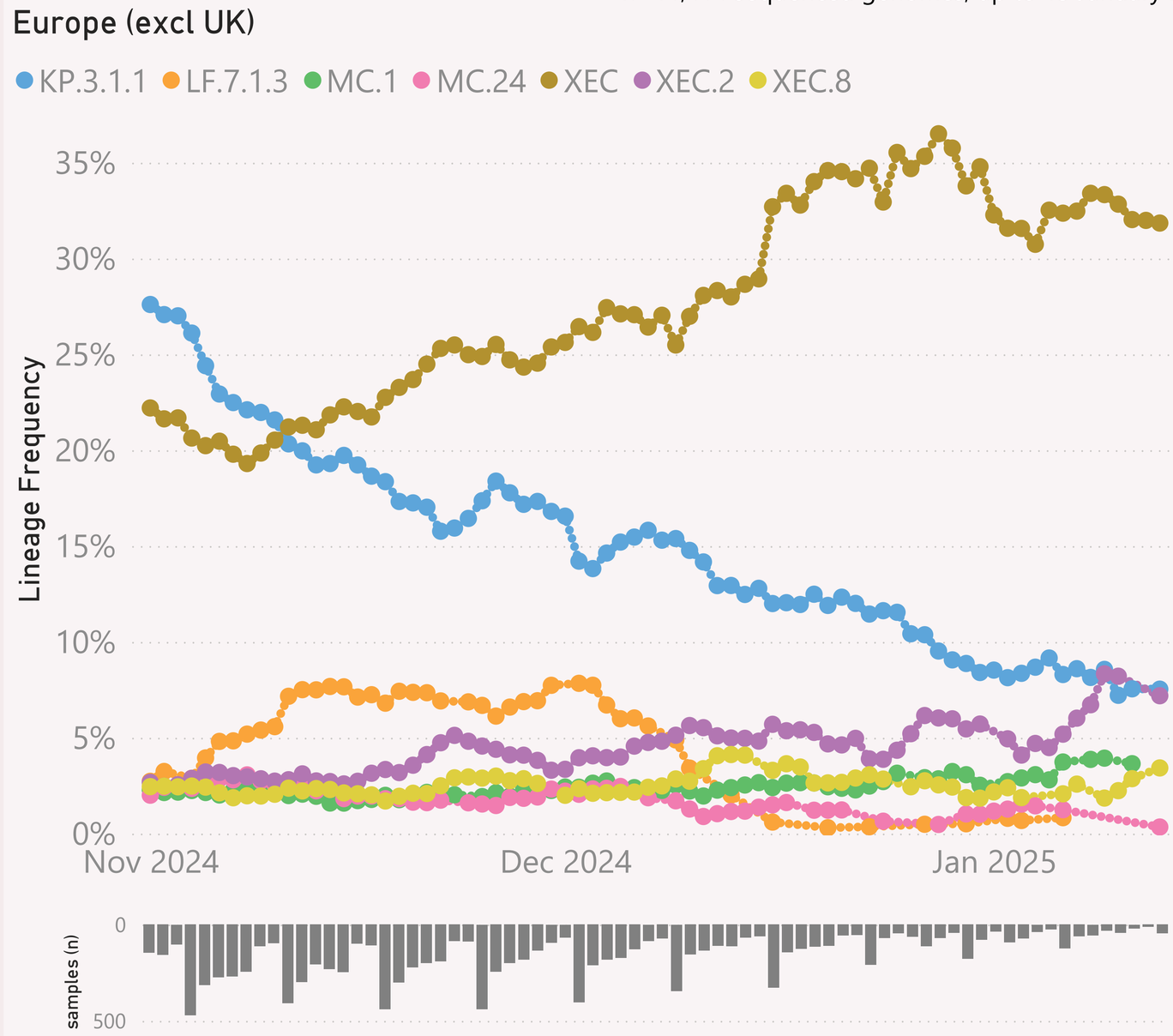
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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.

n=11,414 sequenced genomes, up to 13 January 2025



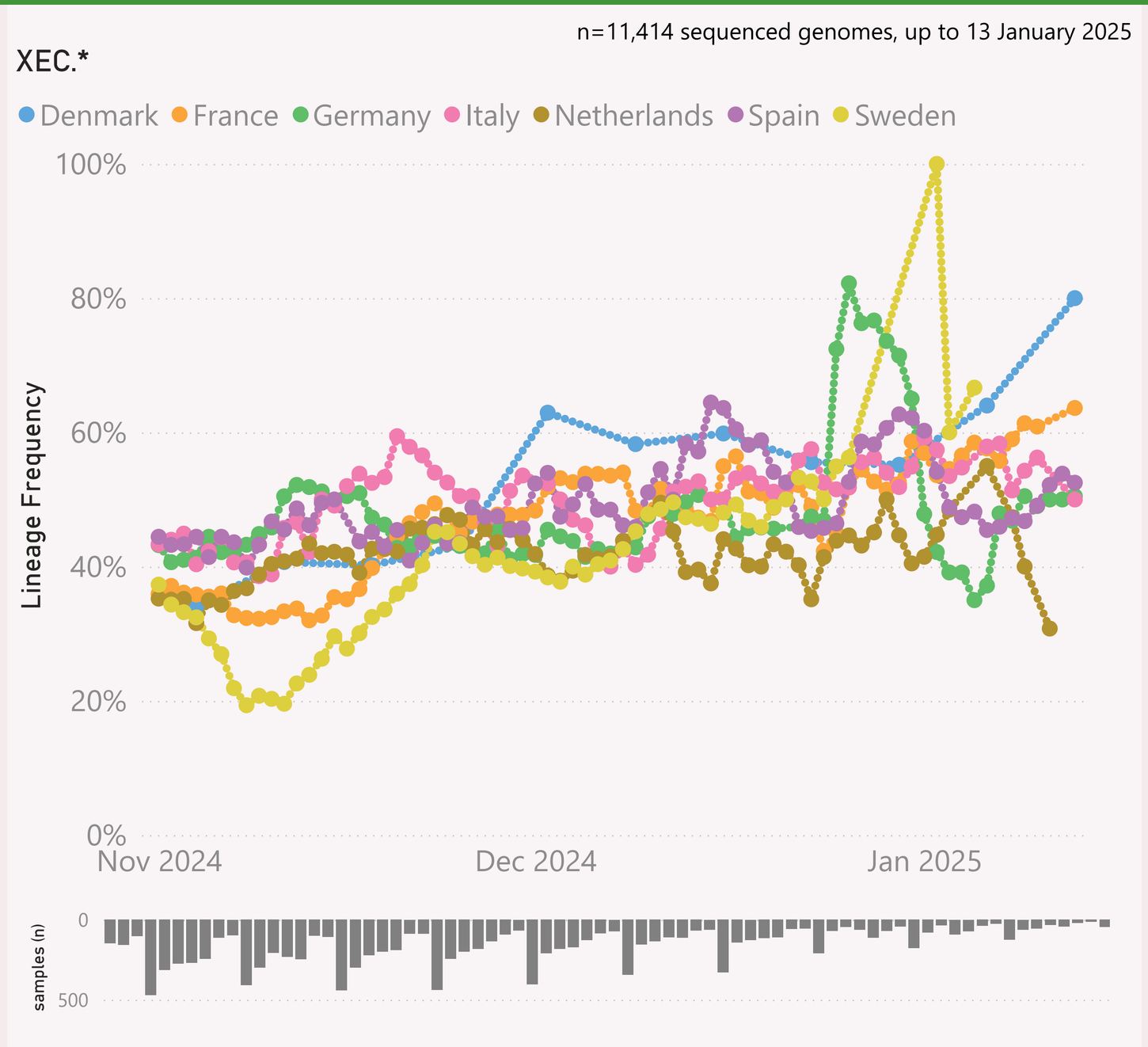
This page shows the frequency of the top 7 lineages, across recent months.

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.

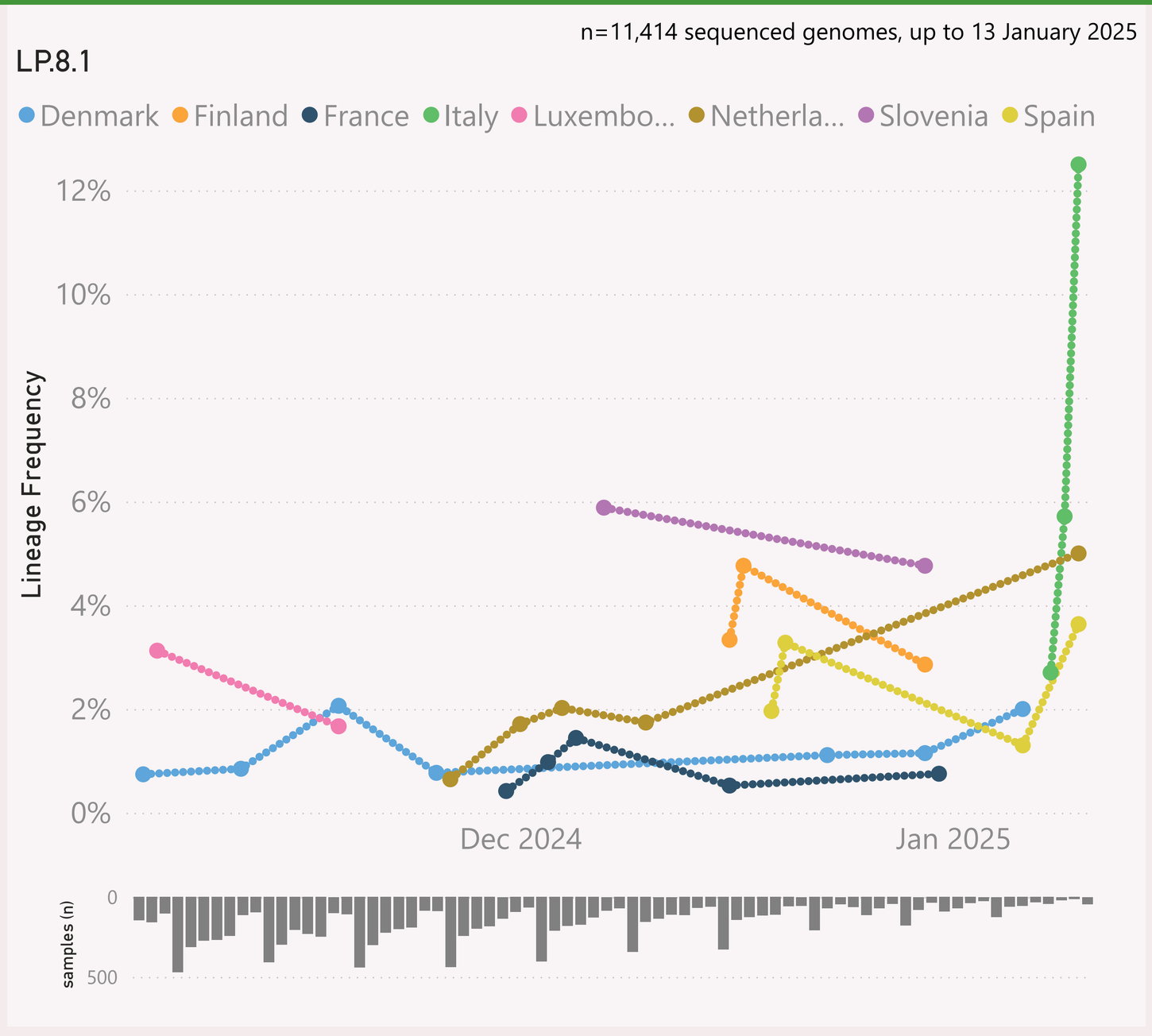
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

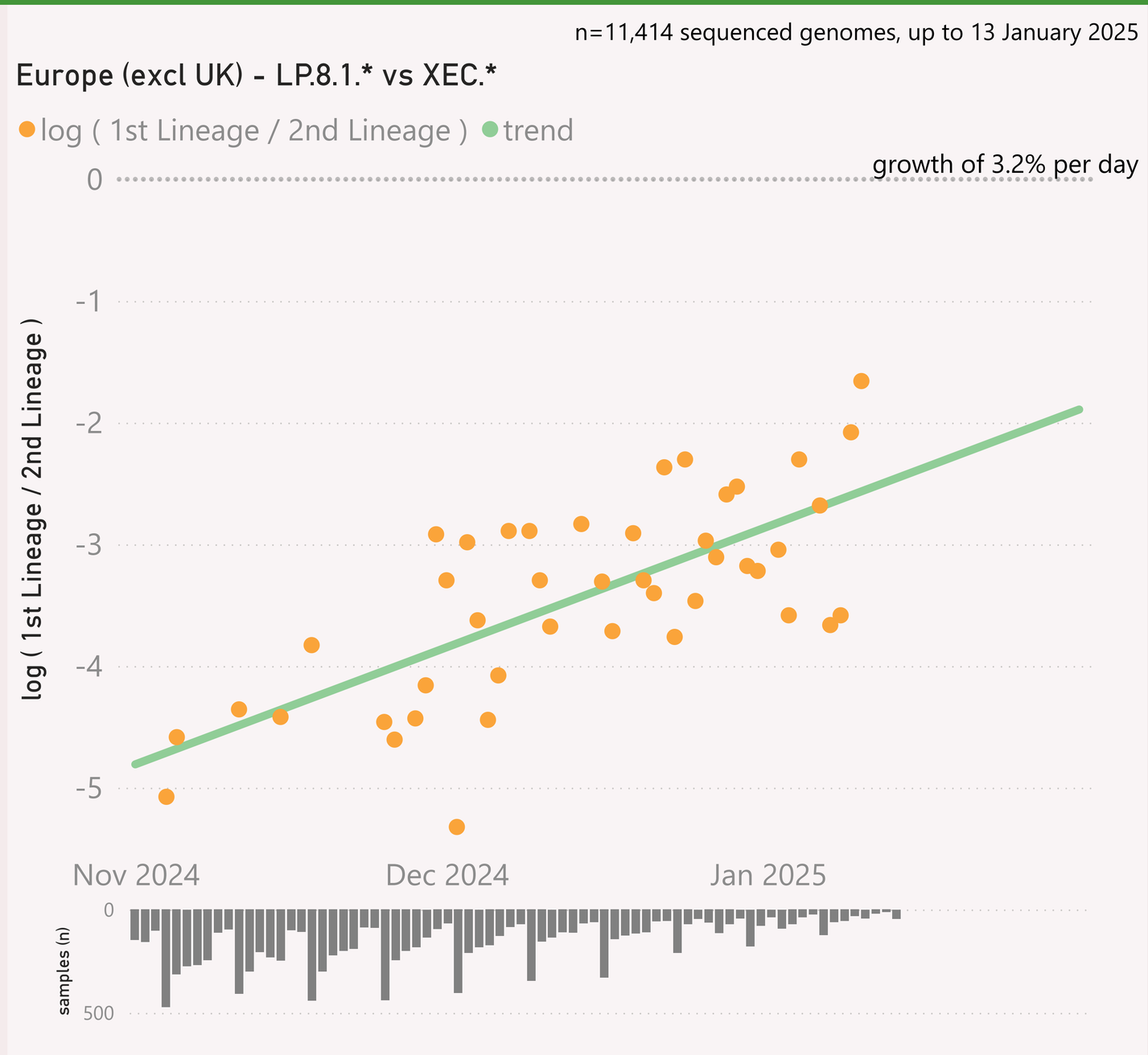
The Lineage classifications are provided by Nextclade.

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=11,414 sequenced genomes, up to 13 January 2025



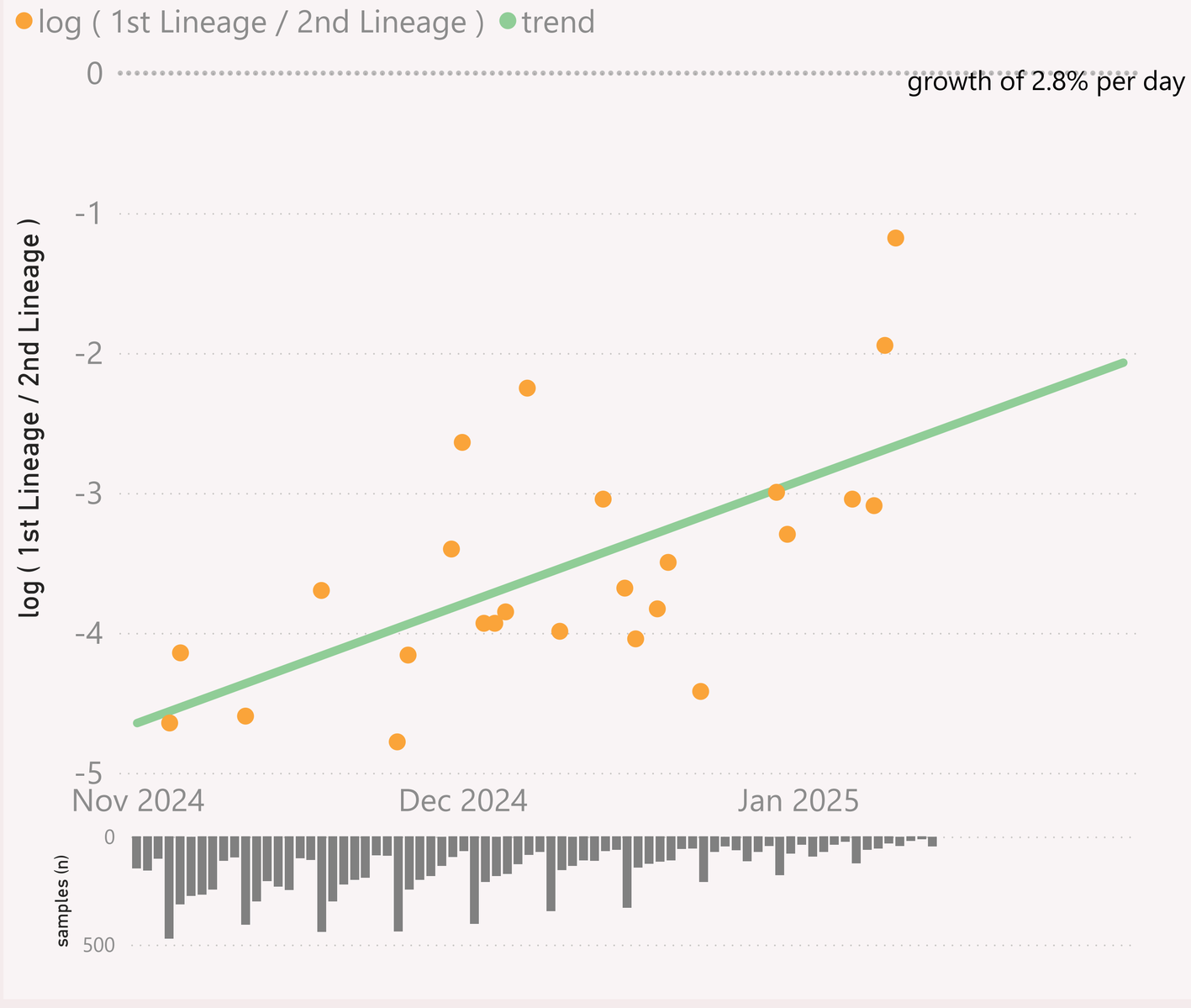
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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=11,414 sequenced genomes, up to 13 January 2025



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

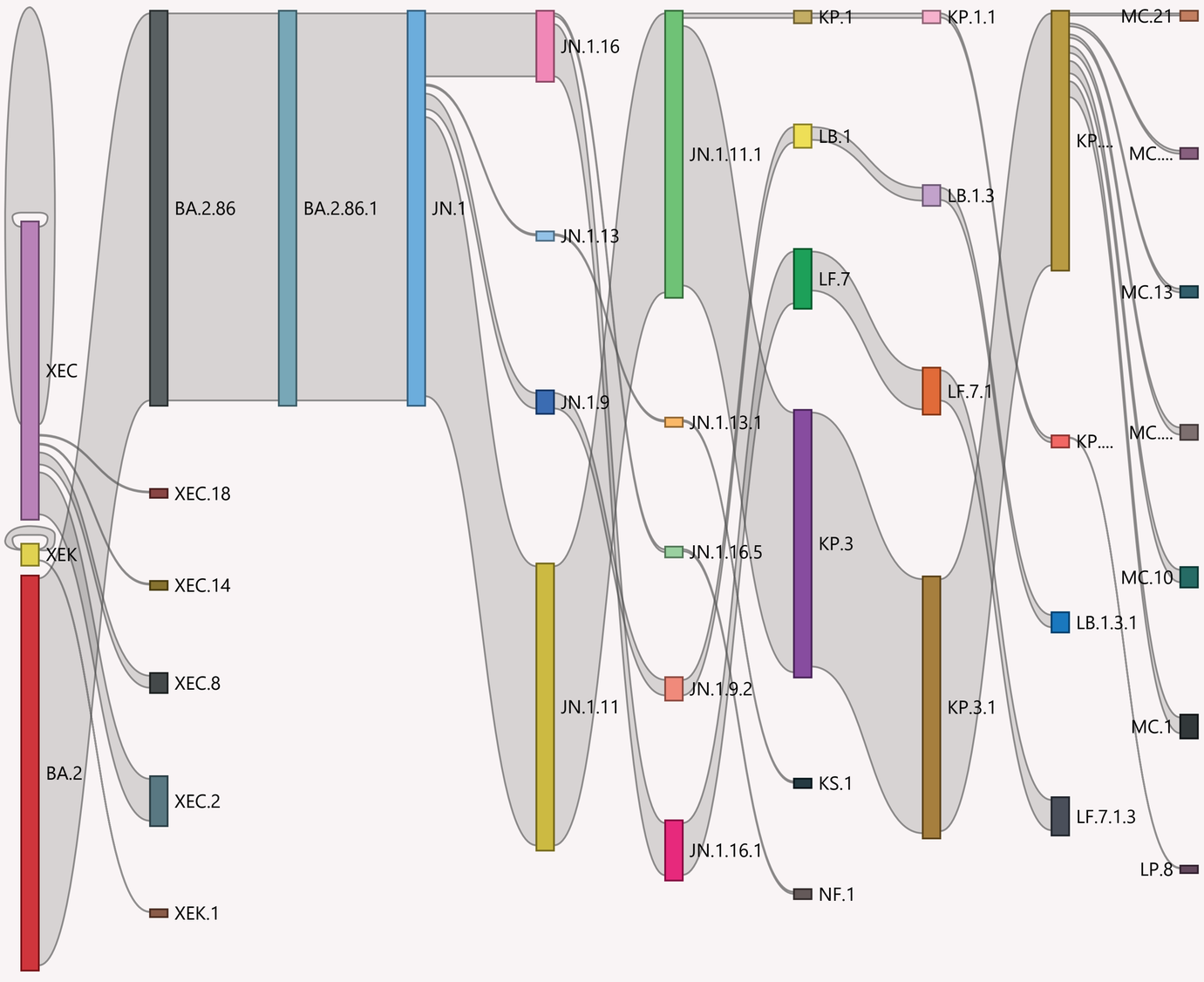
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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=11,576 sequenced genomes, up to 13 January 2025

Europe (excl UK)



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: 2025-02-02 05:19 (UTC)

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
France	1,543	13/01/2025		23/01/2025	
Spain	1,514	13/01/2025		23/01/2025	
Russia	1,288	20/12/2024		20/01/2025	
Germany	1,203	13/01/2025		23/01/2025	
Sweden	961	06/01/2025		23/01/2025	
Netherlands	807	13/01/2025		23/01/2025	
Slovenia	799	13/01/2025		23/01/2025	
Denmark	758	13/01/2025		23/01/2025	
Italy	710	13/01/2025		23/01/2025	
Greece	453	17/12/2024		23/01/2025	
Finland	394	31/12/2024		17/01/2025	
Luxembourg	268	01/01/2025		23/01/2025	
Ireland	238	13/01/2025		23/01/2025	
Poland	156	10/01/2025		21/01/2025	
Hungary	147	02/12/2024		13/01/2025	
Switzerland	147	12/01/2025		23/01/2025	
Estonia	131	25/09/2024		09/01/2025	
Bulgaria	95	09/12/2024		29/12/2024	
Norway	88	27/12/2024		14/01/2025	
Ukraine	81	04/12/2024		03/01/2025	
Slovakia	71	02/12/2024		16/01/2025	
Portugal	68	01/01/2025		20/01/2025	
Czechia	63	21/10/2024		16/01/2025	
Montenegro	27	28/11/2024		18/01/2025	
Croatia	26	03/01/2025		13/01/2025	
Belgium	15	28/11/2024		11/12/2024	
Romania	10	04/01/2025		23/01/2025	
Austria	5	07/01/2025		16/01/2025	
Total	**12,070**	**13/01/2025**		**23/01/2025**	

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.