

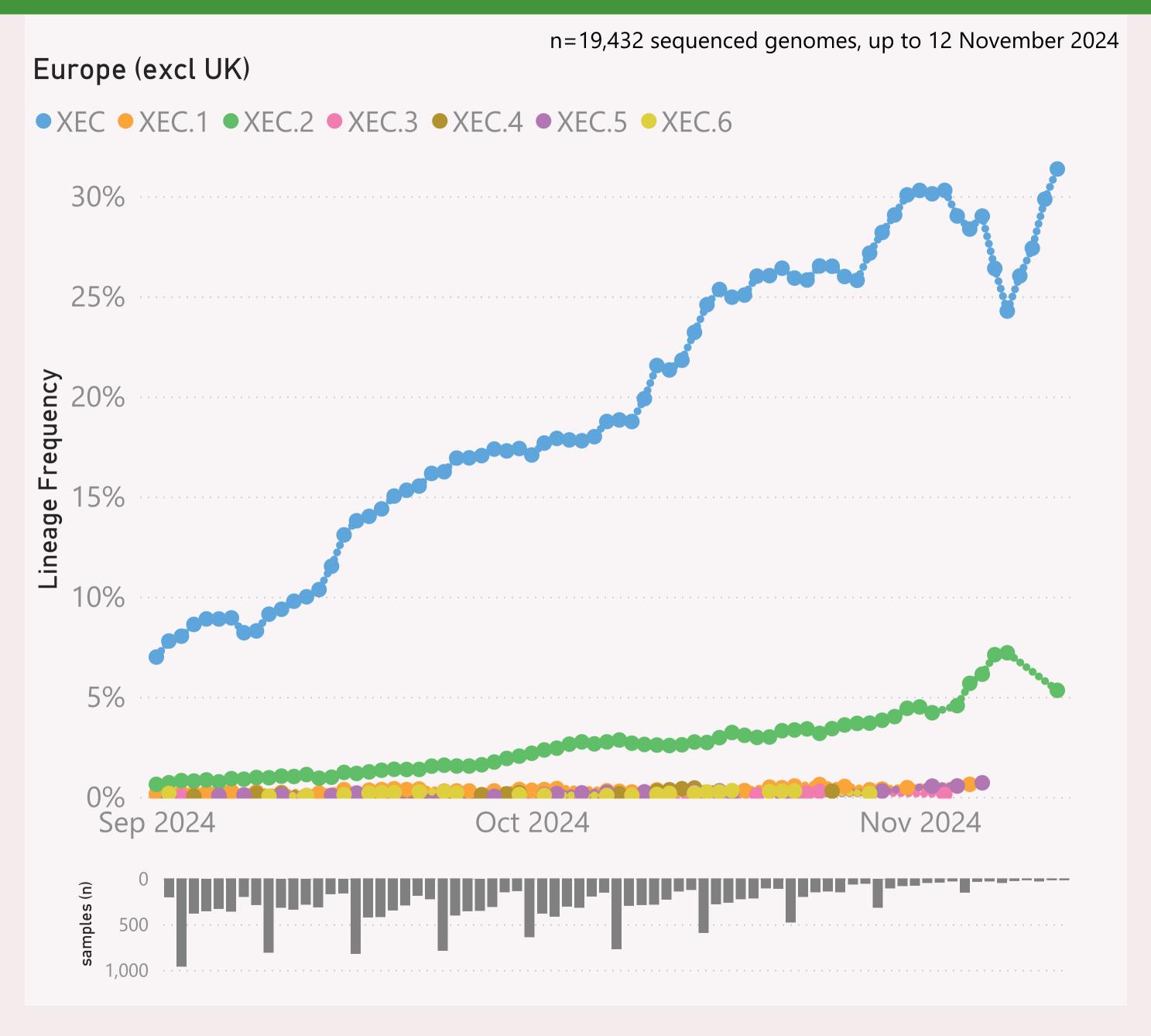
This page shows the frequency of the top 6 "L2" lineages, across recent months.

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.

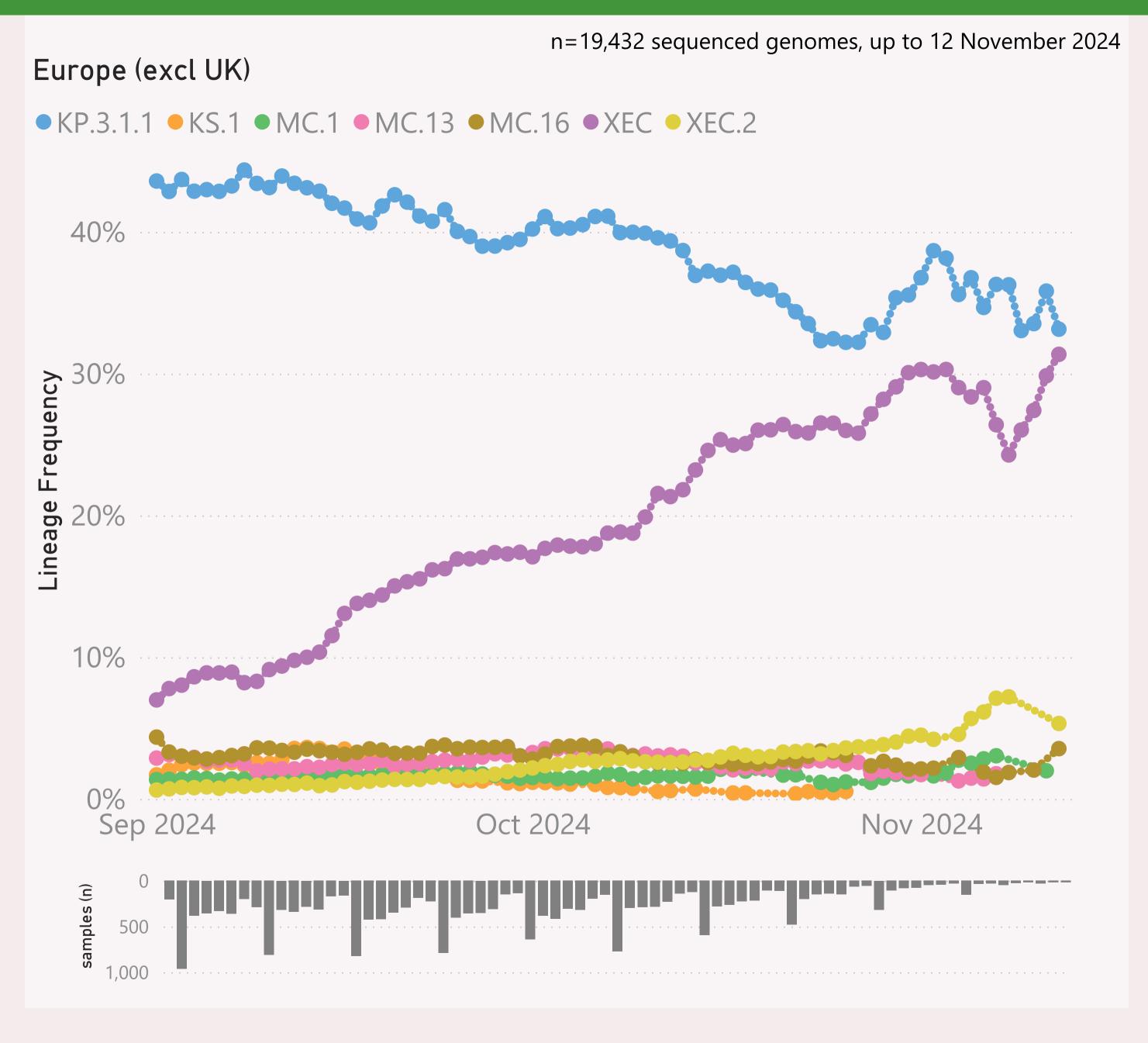


This page shows the frequency of the top 7 lineages, across recent months. The lineages are filtered for a "Lineage L2" group of interest, currently "XEC.*".

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.

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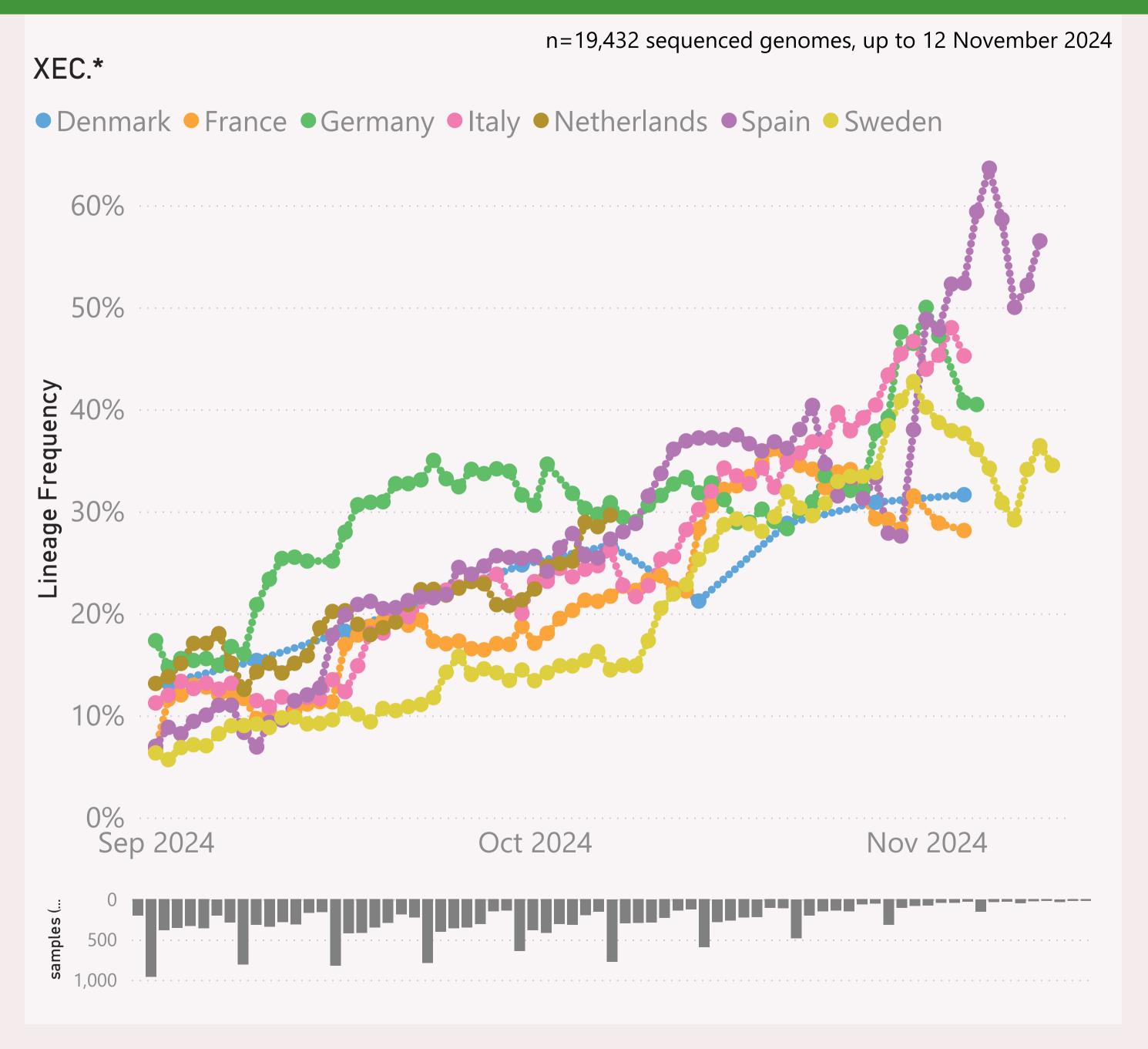


This page shows the frequency of the top 7 lineages, across recent months.

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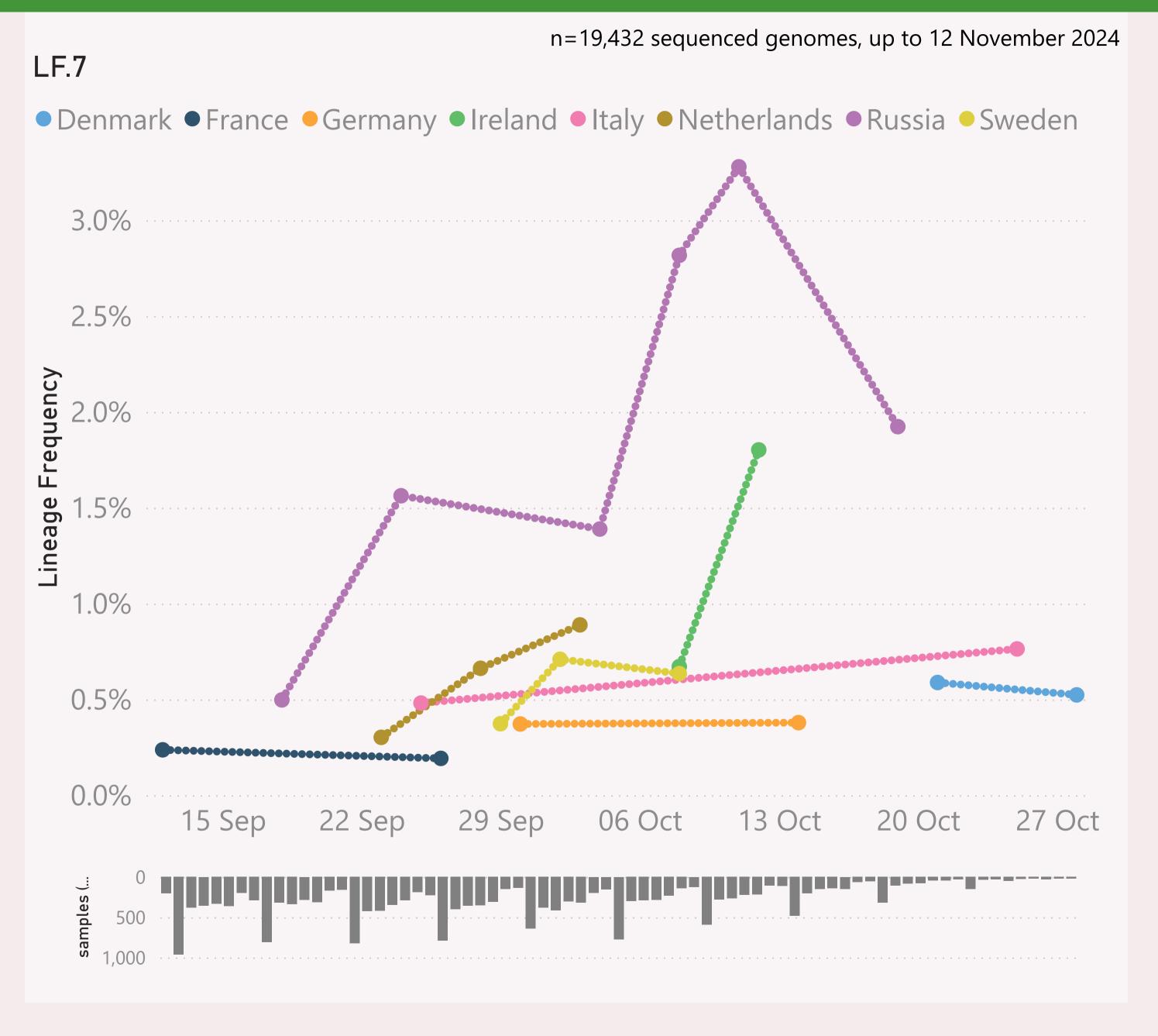
This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.

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.

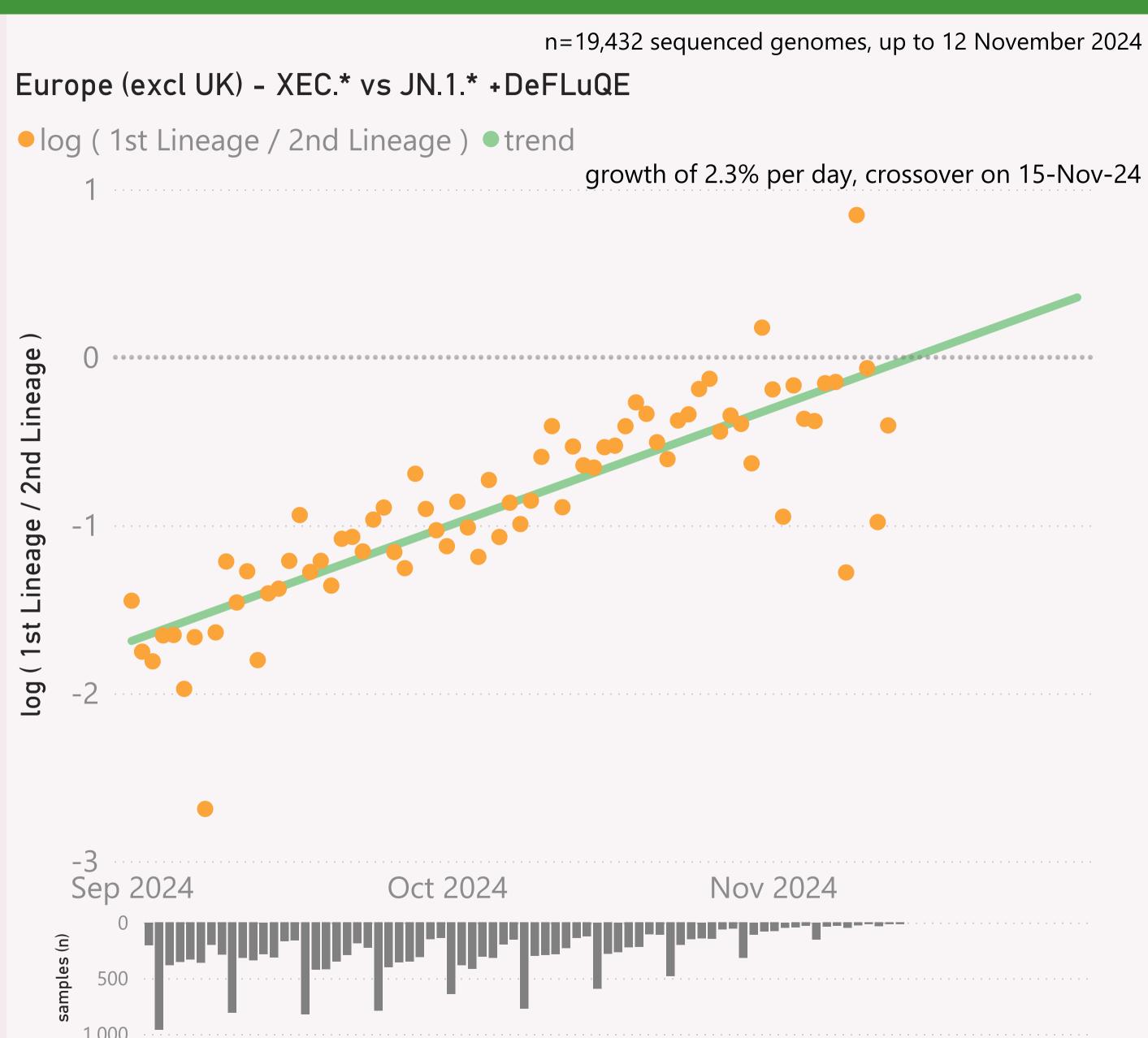


This page shows the frequency of a selected Lineage of interest, for the 7 countries reporting the most samples over recent months.

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.

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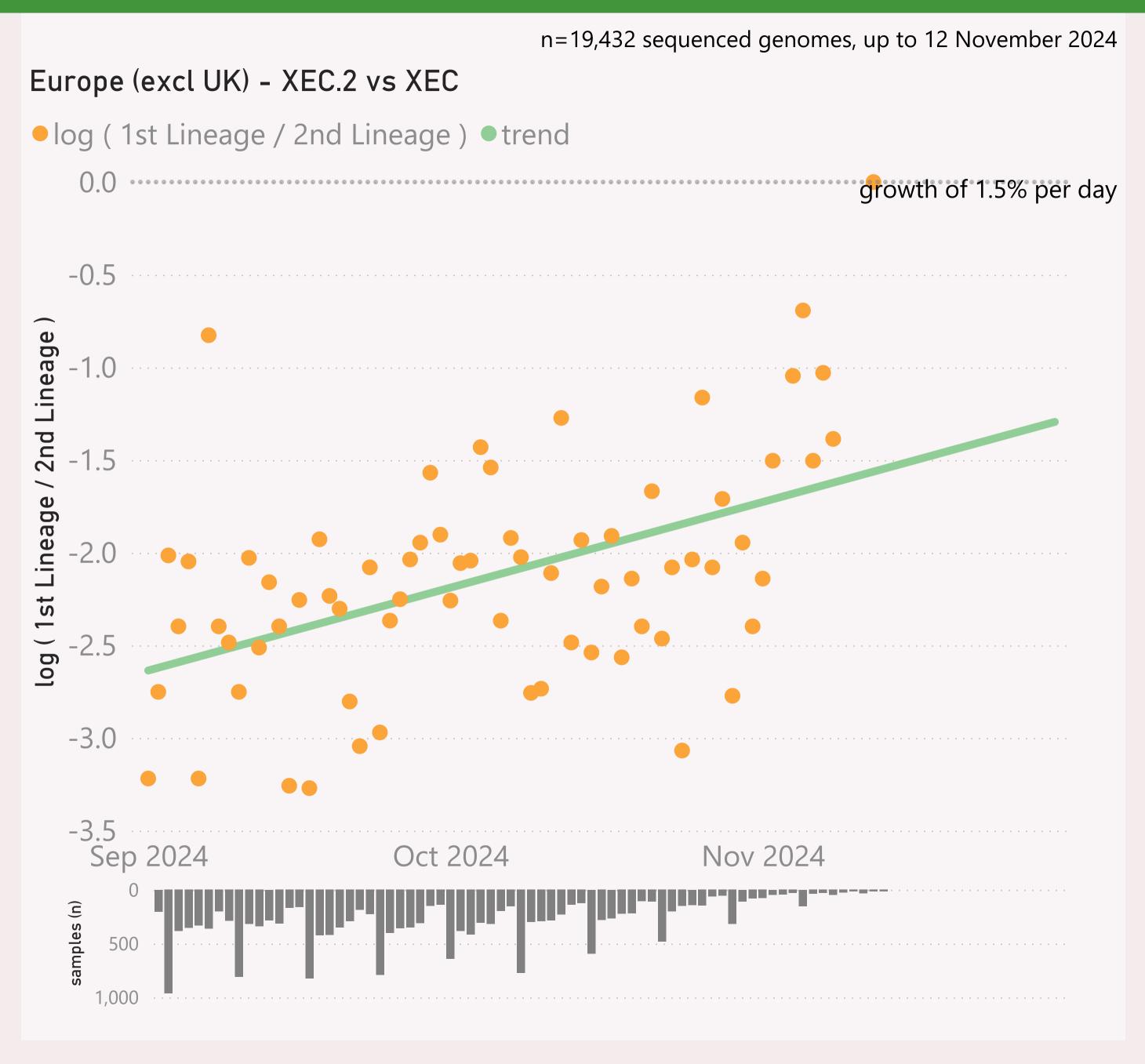


This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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.

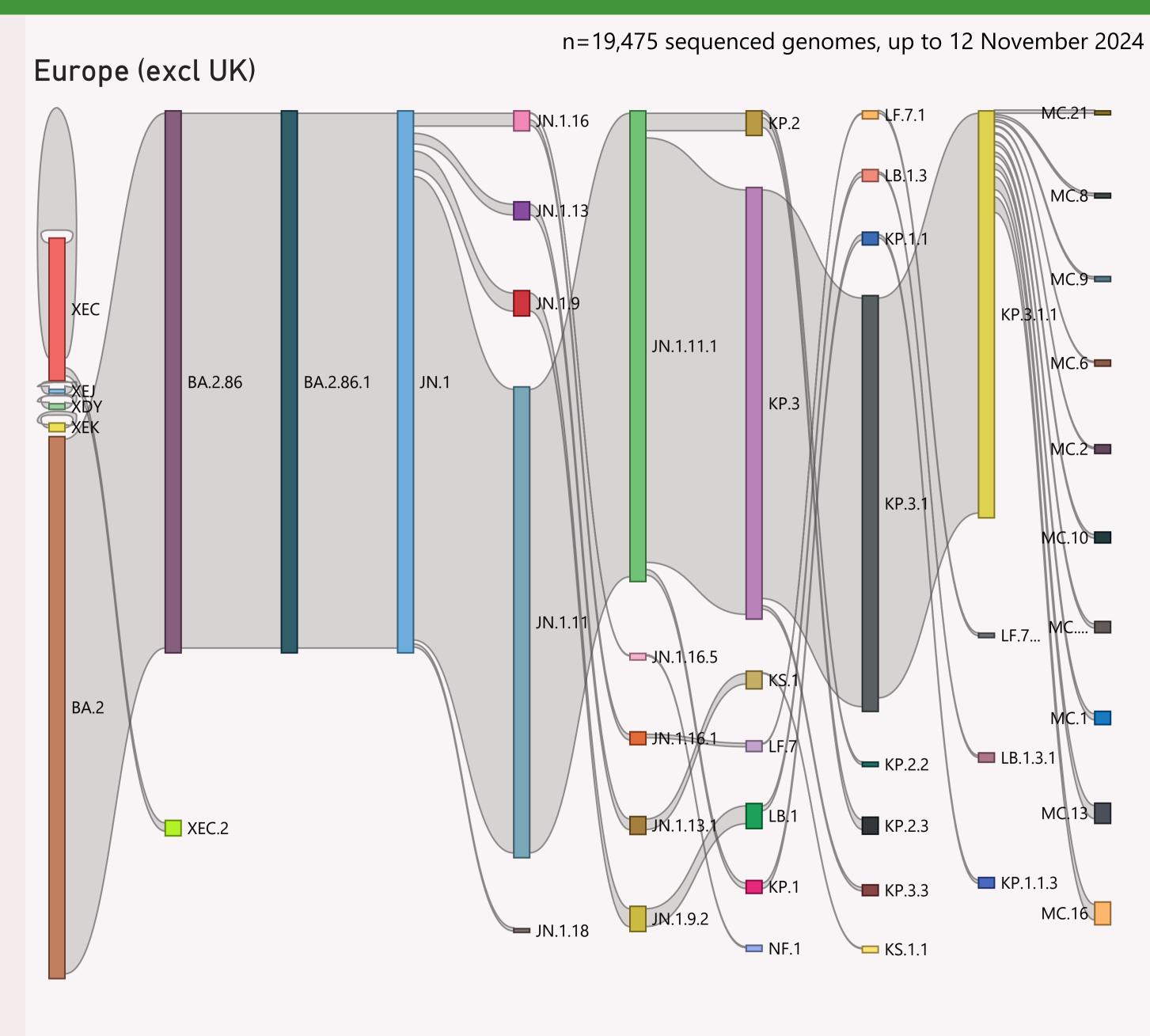


This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

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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.

Data Submitted in the last 8 weeks

Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
± Spain	4,125	12/11/2024	and did a	16/11/2024	المراجع المراجع المراجع المراجع المراجع المراجع المراجع المراجع
	2,670	04/11/2024		16/11/2024	and the desired of
± Sweden	2,600	11/11/2024		16/11/2024	da a a da di
H Germany	1,818	05/11/2024		16/11/2024	and a sale from
⊕ Denmark	1,697	04/11/2024	.	16/11/2024	.ur i i l .au
⊞ Italy	1,678	07/11/2024	علاله	16/11/2024	the late the cases and all
⊕ Russia	1,412	31/10/2024	س ىلى بىر	13/11/2024	
	1,289	08/10/2024		28/10/2024	11 11 1
⊞ Ireland	794	12/11/2024		16/11/2024	r Jack Latherna
 Greece	492	04/10/2024	ب الماد	31/10/2024	
⊕ Poland	421	04/11/2024		16/11/2024	
	359	30/10/2024	lok .	16/11/2024	
E Cyprus	309	28/02/2024	Mar.	28/10/2024	
	282	10/11/2024	. J al u	16/11/2024	1. l l i
	222	27/10/2024	وبلار	16/11/2024	ar di la
	214	22/10/2024	M.	04/11/2024	1
⊞ Slovakia	203	28/10/2024	and the	15/11/2024	4.0
	178	09/10/2024		16/11/2024	
⊕ Finland	166	07/10/2024	.41.	31/10/2024	
⊞ Belgium	125	14/10/2024	als:	05/11/2024	The state of the s
	122	06/11/2024	باللب	16/11/2024	- II n
Norway	94	20/10/2024		01/11/2024	
	80	12/08/2024		04/10/2024	
	79	29/10/2024	all	11/11/2024	
⊞ Hungary	68	27/09/2024	1	11/11/2024	
E Romania	4	26/08/2024		01/10/2024	
⊞ Bulgaria	1	26/09/2024		14/10/2024	
Total	21,502	12/11/2024	بأنائه رازان	16/11/2024	anataathaalchtlanaath

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.