n=42,361 sequenced genomes, from 1 April 2025 up to 20 July 2025

Global

● JN.1.* +DeFLuQE　● JN.1.* +FLiRT　● LP.8.1.*　● NB.1.8.1.* Nimbus　● XEC.*　● XFG.*

This page shows the frequency of the top 6 "L2" lineages, across recent months.
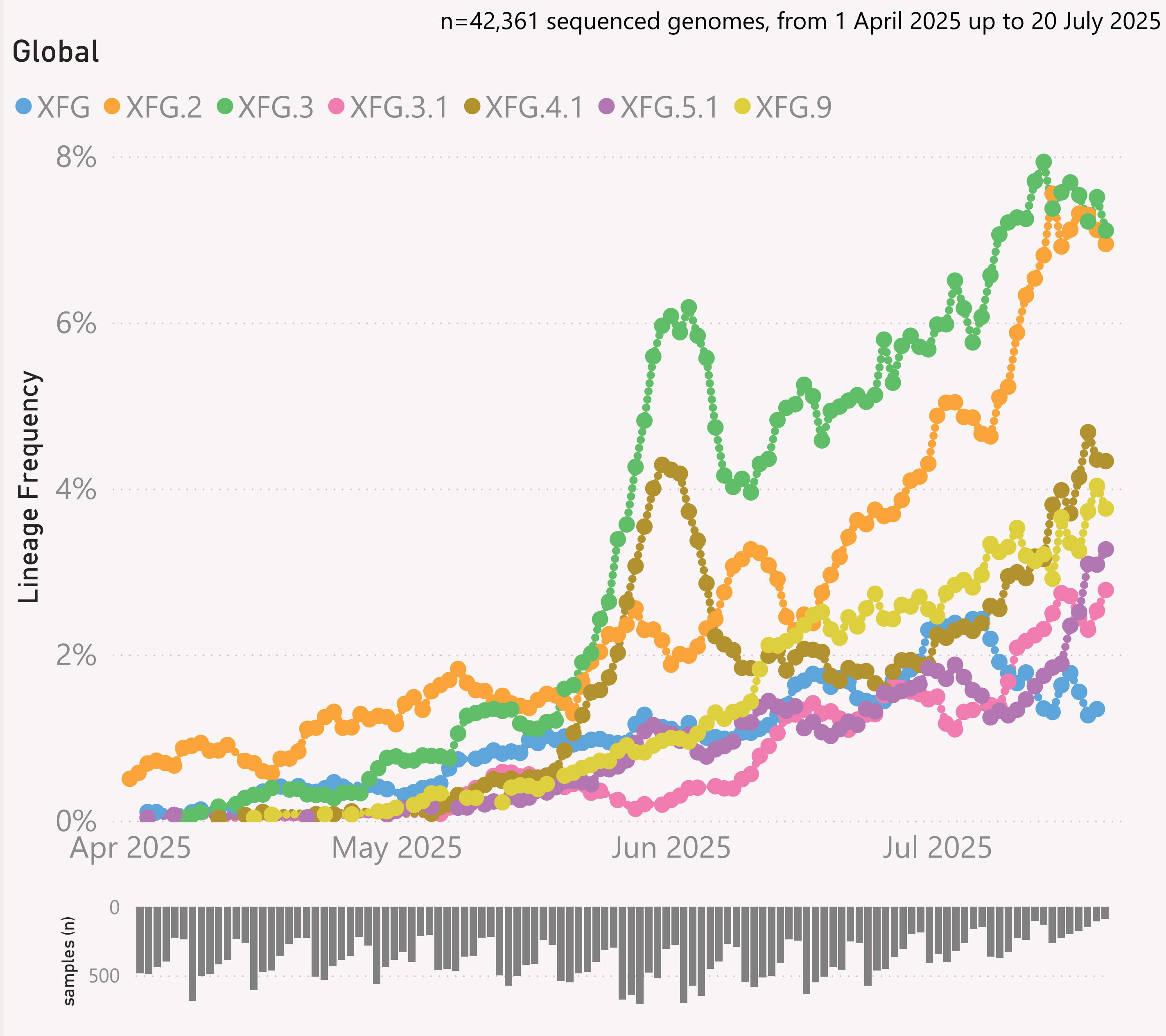
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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.

n=42,361 sequenced genomes, from 1 April 2025 up to 20 July 2025

Global

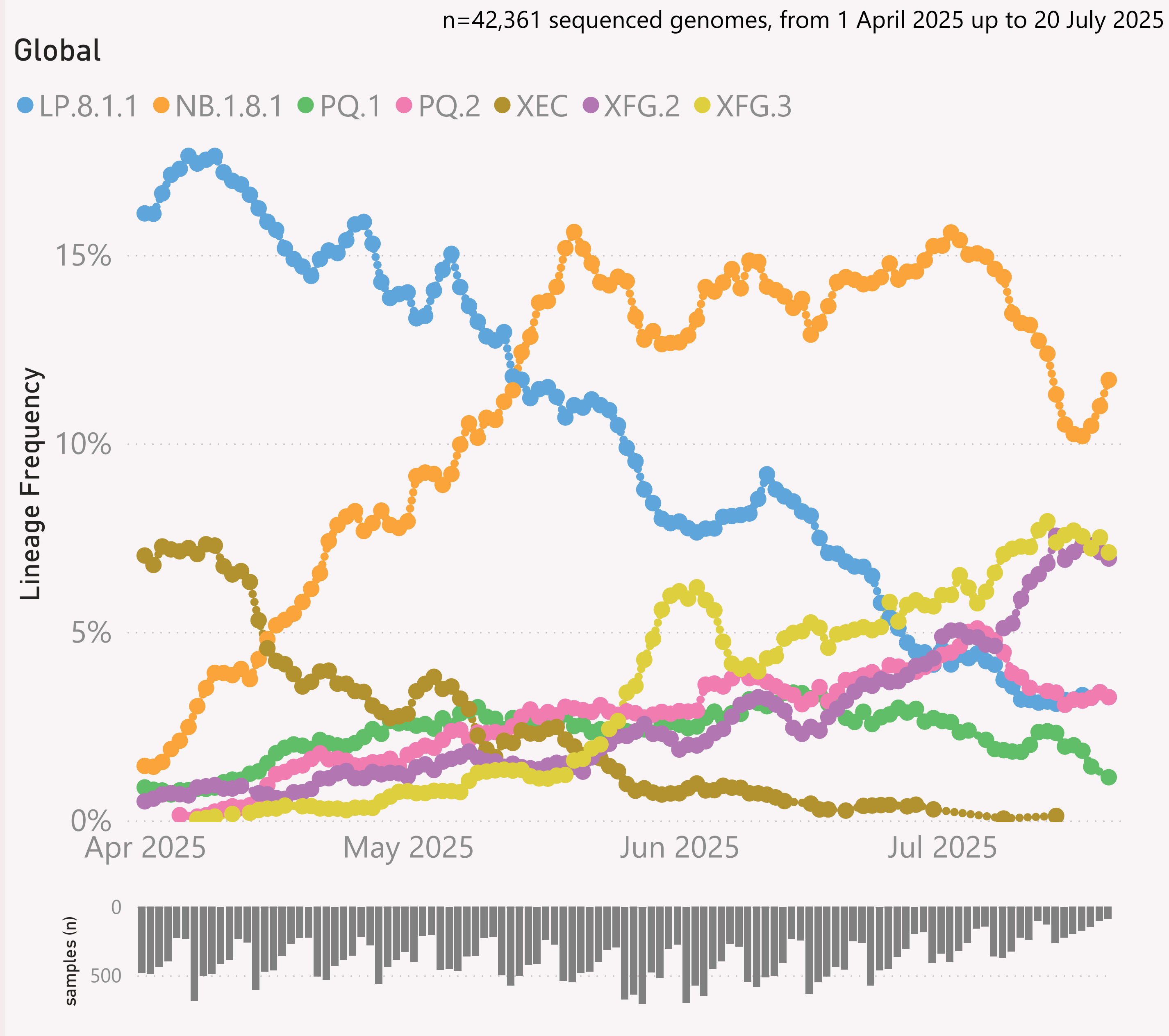● XFG ● XFG.2 ● XFG.3 ● XFG.3.1 ● XFG.4.1 ● XFG.5.1 ● XFG.9

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 XFG.* Stratus.

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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Global

- LP.8.1.1
- NB.1.8.1
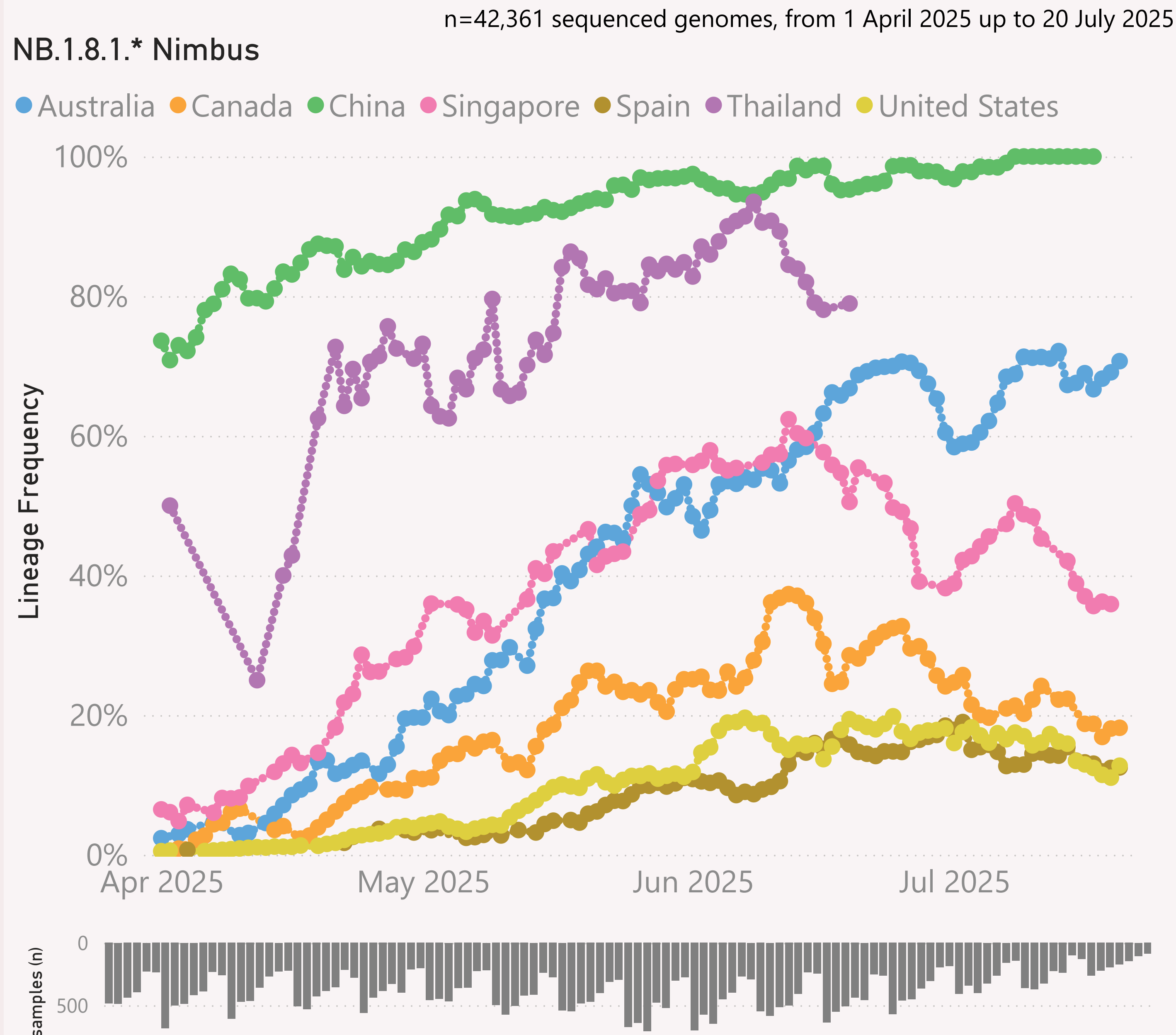- PQ.1
- PQ.2
- XEC
- XFG.2
- XFG.3

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.

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n=42,361 sequenced genomes, from 1 April 2025 up to 20 July 2025

NB.1.8.1.* Nimbus

● Australia ● Canada ● China ● Singapore ● Spain ● Thailand ● United States

Lineage Frequency

100%
80%
60%
40%
20%
0%

Apr 2025　　May 2025　　Jun 2025　　Jul 2025

samples (n)
0
500

This page shows the frequency of a selected "Lineage L2" group of interest, for the 7 countries reporting the most samples over recent months.
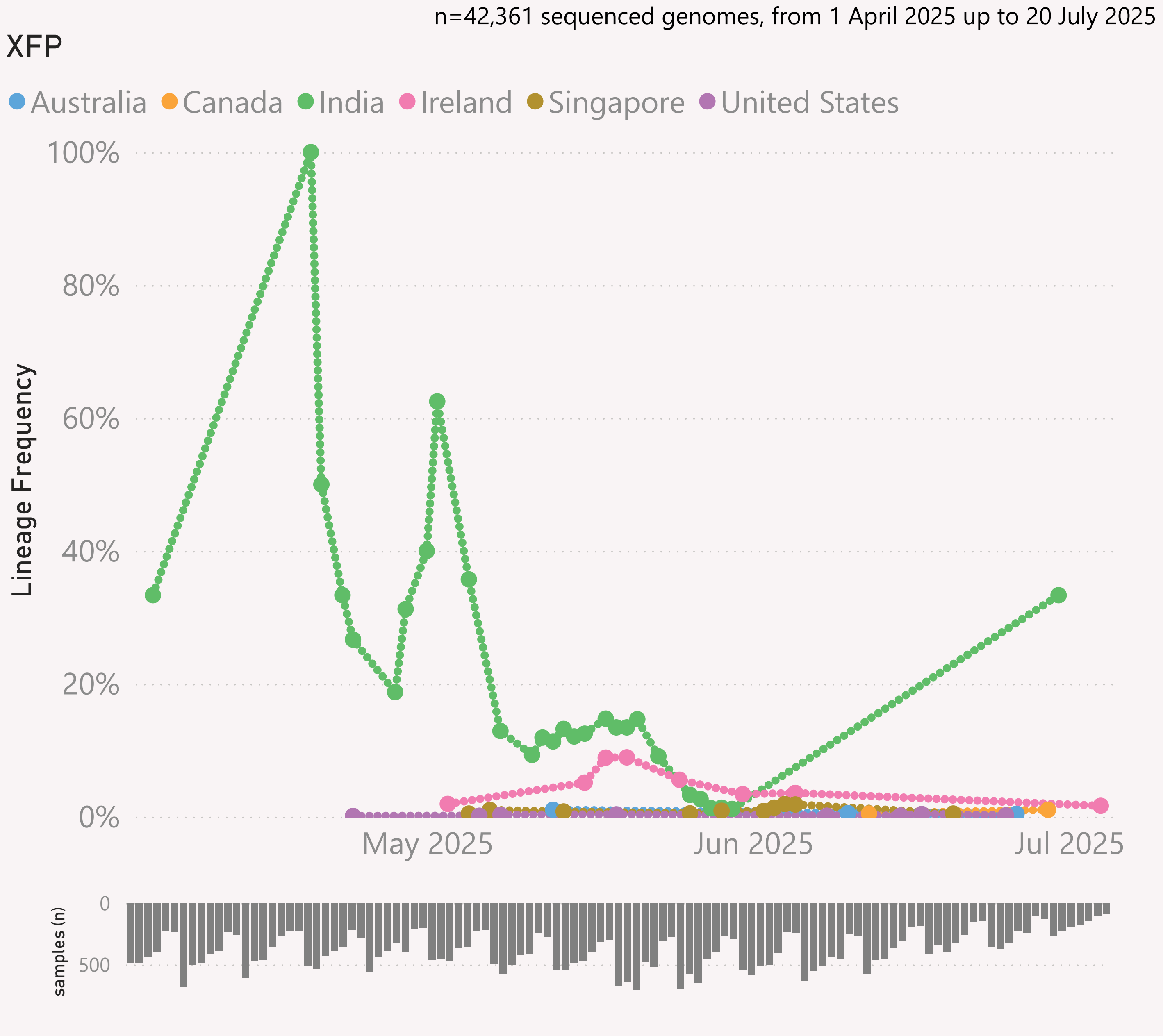
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "JN.1.* +FLiRT" group includes the descendants of JN.1.* with the mutations: F456L & R346T.

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.

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n=42,361 sequenced genomes, from 1 April 2025 up to 20 July 2025

XFG.*

Canada　France　India　Singapore　Spain　United Kingdom　United States

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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.

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n=42,361 sequenced genomes, from 1 April 2025 up to 20 July 2025

XFP

● Australia ● Canada ● India ● Ireland ● Singapore ● United States

Date	
01/01/2025	31/12/2025

Host

Human

Continent, Country, Location

All

Lineage L2, Lineage (nextclade)

XFP.* (Lineage L2) + XFP (Lineage (nextclad...

Samples Sequenced (gisaid)

85

Country	Location	Addi...	Collection date	Lineage L2	Lineage (nextc
Japan		Quar...	15/07/2025	XFP.*	XFP
Ireland	Dublin		04/07/2025	XFP.*	XFP
India	Maharashtra		30/06/2025	XFP.*	XFP
Canada	Ontario		29/06/2025	XFP.*	XFP
Germany	Rhineland-Pala...		27/06/2025	XFP.*	XFP
United Kingdom	Wales		27/06/2025	XFP.*	XFP
Australia	Victoria		26/06/2025	XFP.*	XFP
USA	Minnesota		25/06/2025	XFP.*	XFP
France	Provence-Alpe...		21/06/2025	XFP.*	XFP
Singapore			20/06/2025	XFP.*	XFP
USA	Minnesota		17/06/2025	XFP.*	XFP
USA	International Tr...		15/06/2025	XFP.*	XFP
Canada	Ontario		12/06/2025	XFP.*	XFP
Poland	Warminsko-M...		12/06/2025	XFP.*	XFP
Australia	Western Austr...		10/06/2025	XFP.*	XFP
USA	International Tr...		08/06/2025	XFP.*	XFP
Netherlands	Gelderland		07/06/2025	XFP.*	XFP
Singapore			05/06/2025	XFP.*	XFP
Ireland	Dublin		05/06/2025	XFP.*	XFP
Singapore			04/06/2025	XFP.*	XFP
Singapore			03/06/2025	XFP.*	XFP
Finland			02/06/2025	XFP.*	XFP

Total

n=30,368 sequenced genomes, from 1 May 2025 up to 20 July 2025

Global – XFG.* vs NB.1.8.1.* Nimbus

● log (1st Lineage / 2nd Lineage)　　● trend

growth of 2.5% per day, crossover on 21-Jun-25
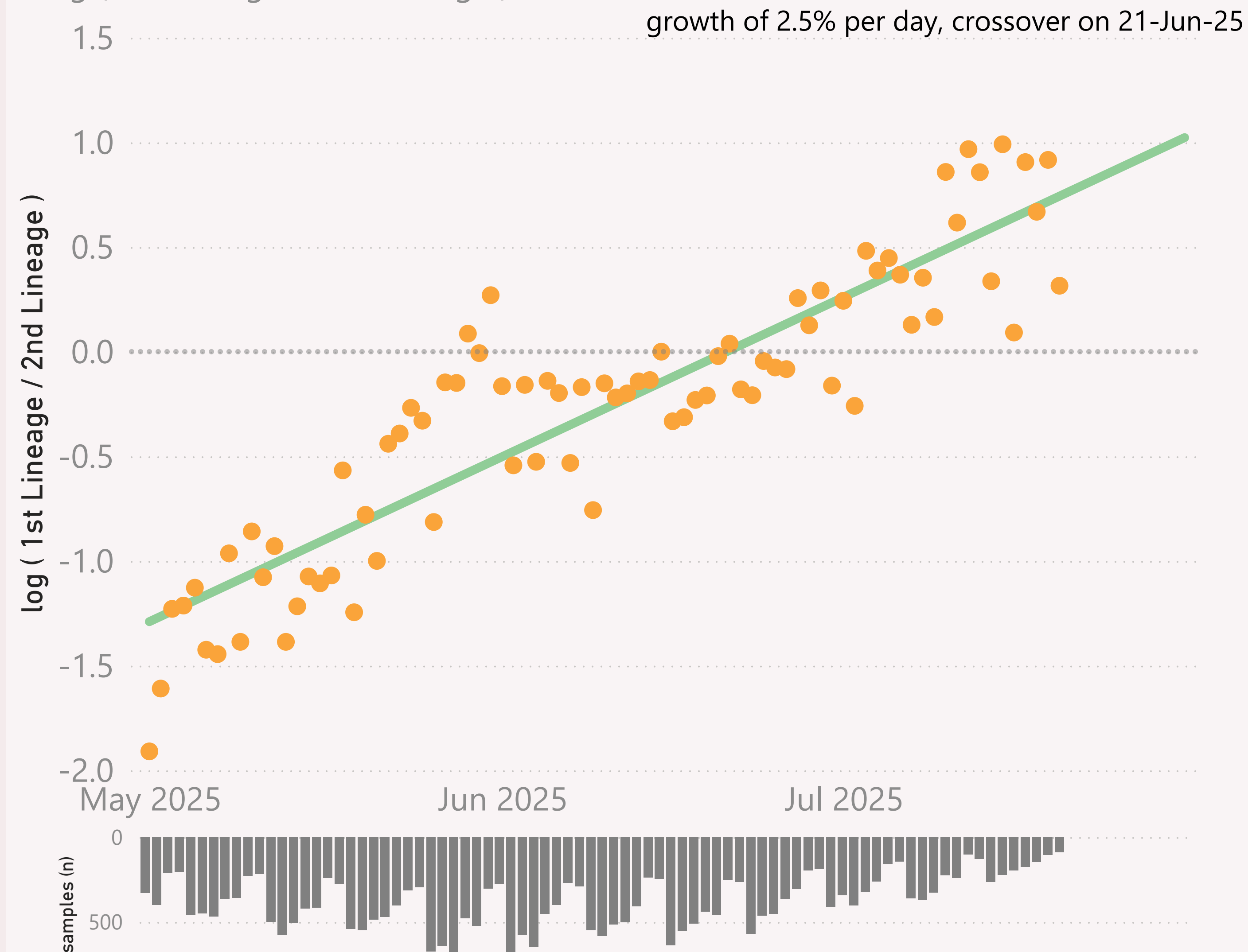
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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=30,368 sequenced genomes, from 1 May 2025 up to 20 July 2025

Global - XFN vs XFG.3

● log (1st Lineage / 2nd Lineage) ● trend

decline of -0.1% per day
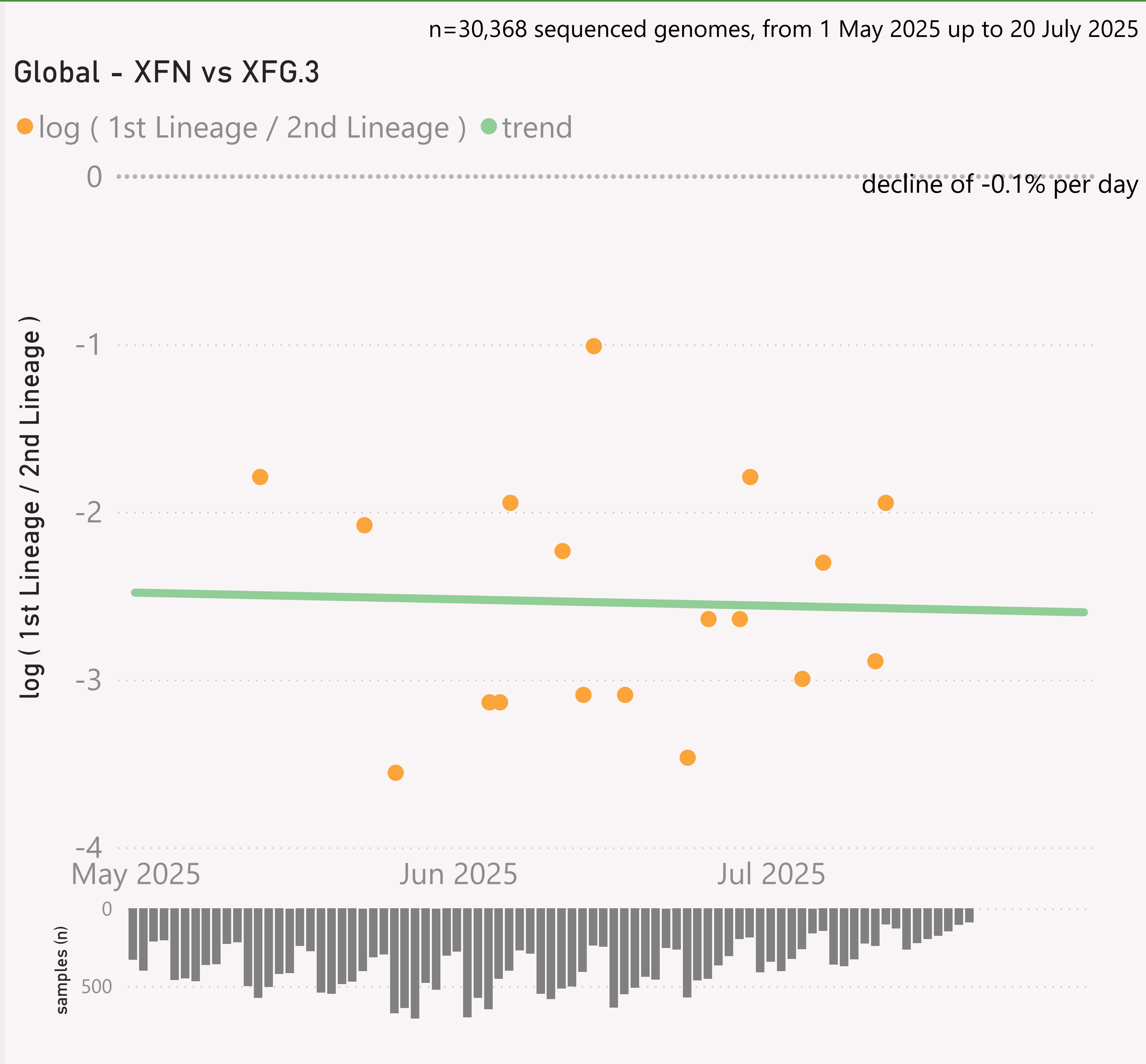
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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.

COVID-19 Genomic Sequencing sankey diagram. Data from gisaid.org, with nextclade lineages. Source files and more info on github.

Last Update: 2025-08-08 22:27 (UTC)

n=42,361 sequenced genomes, from 1 April 2025 up to 20 July 2025
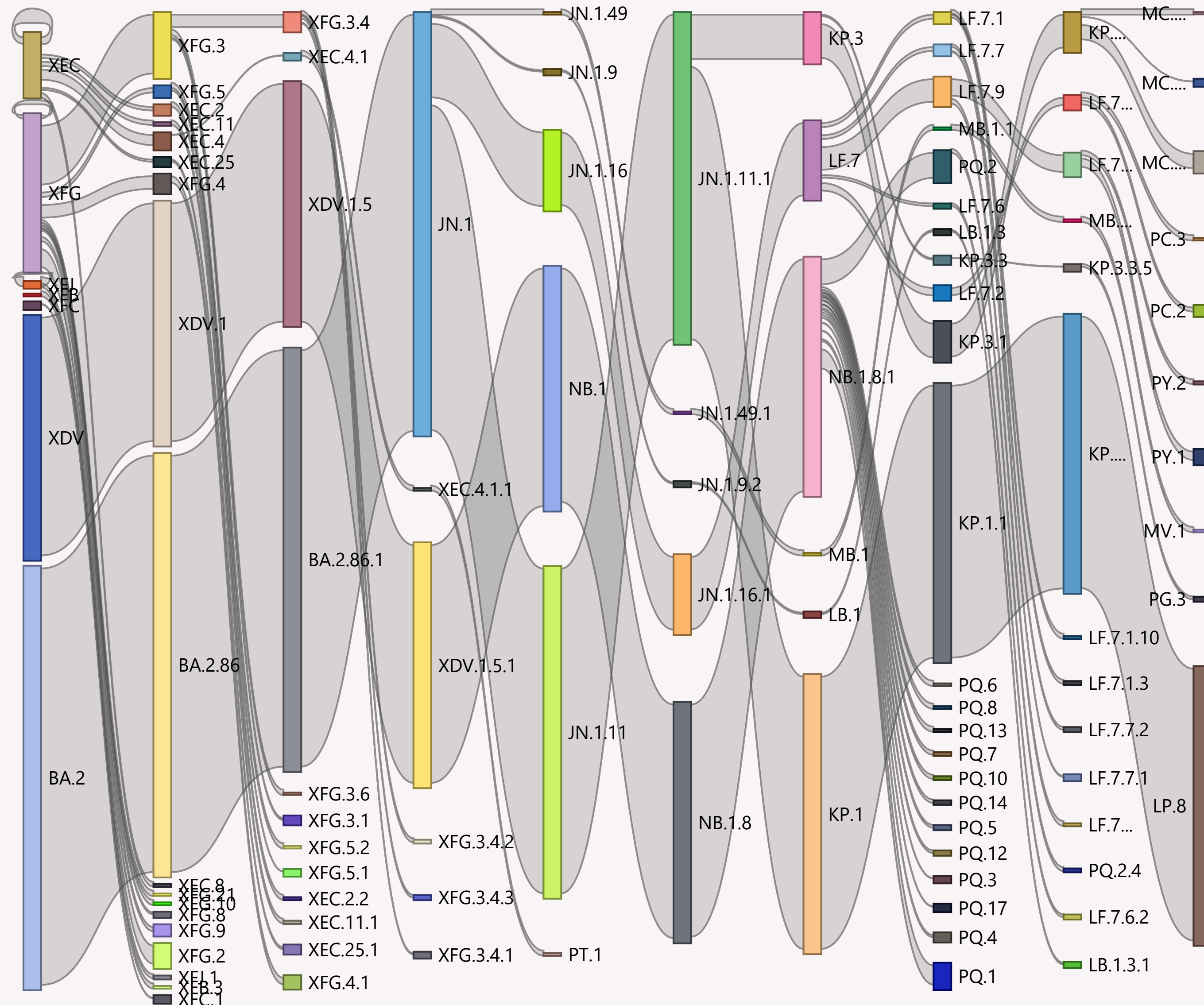
This page shows the hierarchy of the significant Lineages, over recent months.

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.

n=839 sequenced genomes, from 1 April 2025 up to 20 July 2025

Global

- JN.1.* +FLiRT
- LP.8.1.*
- NB.1.8.1.* Nimbus
- XEC.*
- XFC.*
- XFG.*
- XFP.*
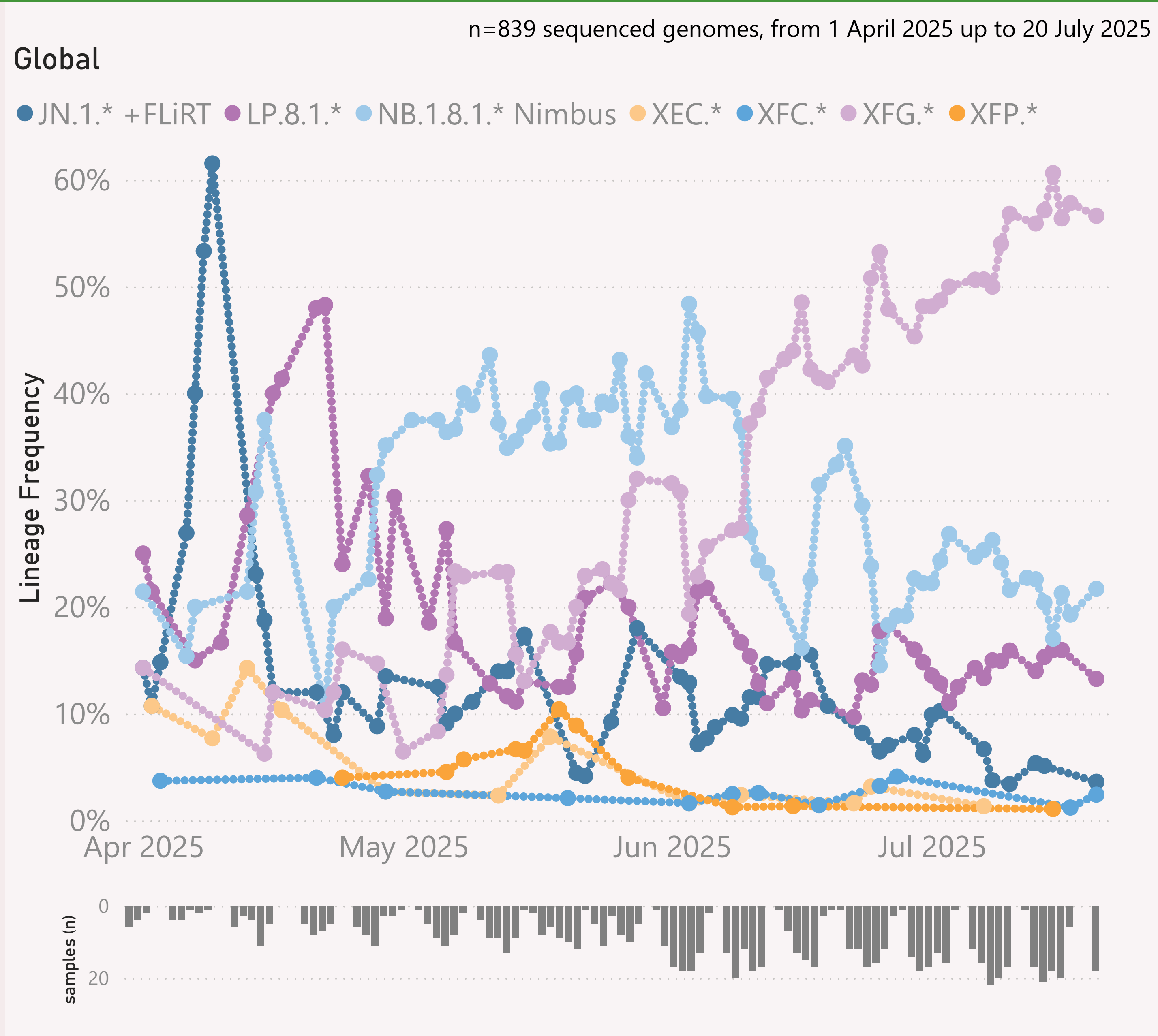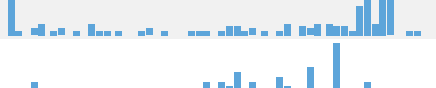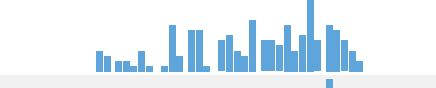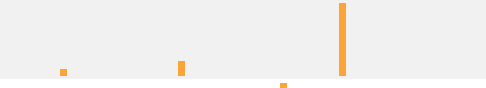
This page shows the frequency of the top 6 "L2" lineages, across recent months, for "International Traveller" samples.

This is probably a more randomised sample than the "Global" aggregate of all samples submitted to GISAID, as those are dominated by the US and Canada

These samples are mainly collected from arrivals into the US and Japan.

COVID-19 Genomic Sequencing analysis - Data Currency. Data from gisaid.org. Source files and info on github.

Last Update: 2025-08-08 22:27 (UTC)

Data Submitted in the last 8 weeks

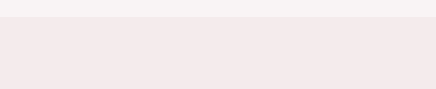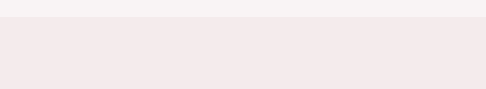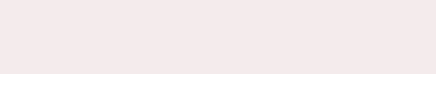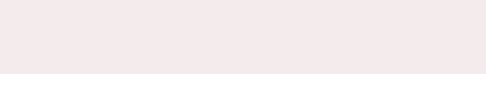| Country	# Samples Sequenced	Latest Collection date	by Collection date	Latest Submission date	by Submission date
⊞ United States	5,175	20/07/2025		08/08/2025	
⊞ Spain	3,513	20/07/2025		08/08/2025	
⊞ United Kingdom	1,692	20/07/2025		08/08/2025	
⊞ Canada	1,657	20/07/2025		06/08/2025	
⊞ China	1,591	17/07/2025		01/08/2025	
⊞ Australia	1,363	20/07/2025		06/08/2025	
⊞ Singapore	1,350	19/07/2025		28/07/2025	
⊞ France	870	20/07/2025		31/07/2025	
⊞ India	592	02/07/2025		07/08/2025	
⊞ New Zealand	520	20/07/2025		04/08/2025	
⊞ Ireland	519	20/07/2025		07/08/2025	
⊞ Brazil	360	17/07/2025		07/08/2025	
⊞ Luxembourg	351	07/07/2025		18/07/2025	
⊞ Malaysia	343	18/07/2025		31/07/2025	
⊞ Portugal	327	01/07/2025		29/07/2025	
⊞ Costa Rica	321	11/07/2025		04/08/2025	
⊞ South Korea	292	09/07/2025		01/08/2025	
⊞ Taiwan	271	16/07/2025		01/08/2025	
⊞ Germany	262	20/07/2025		07/08/2025	
⊞ Japan	262	19/07/2025		07/08/2025	
⊞ Netherlands	254	08/07/2025		25/07/2025	
⊞ Mexico	244	18/06/2025		22/07/2025	
⊞ Thailand	235	19/06/2025		14/07/2025	
⊞ Russia	212	01/07/2025		24/07/2025	
⊞ Puerto Rico	203	18/07/2025		08/08/2025	
⊞ Kazakhstan	146	28/05/2025		04/07/2025	
⊞ Denmark	140	30/06/2025		18/07/2025	
⊞ Hong Kong	137	17/07/2025		01/08/2025	
Total	**24,471**	**20/07/2025**		**08/08/2025**	

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.