n=18,340 sequenced genomes, up to 28 April 2025

Global

- BA.2.86.*
- JN.1.* +DeFLuQE
- JN.1.* +FLiRT
- LP.8.1.*
- XDV.*
- XEC.*

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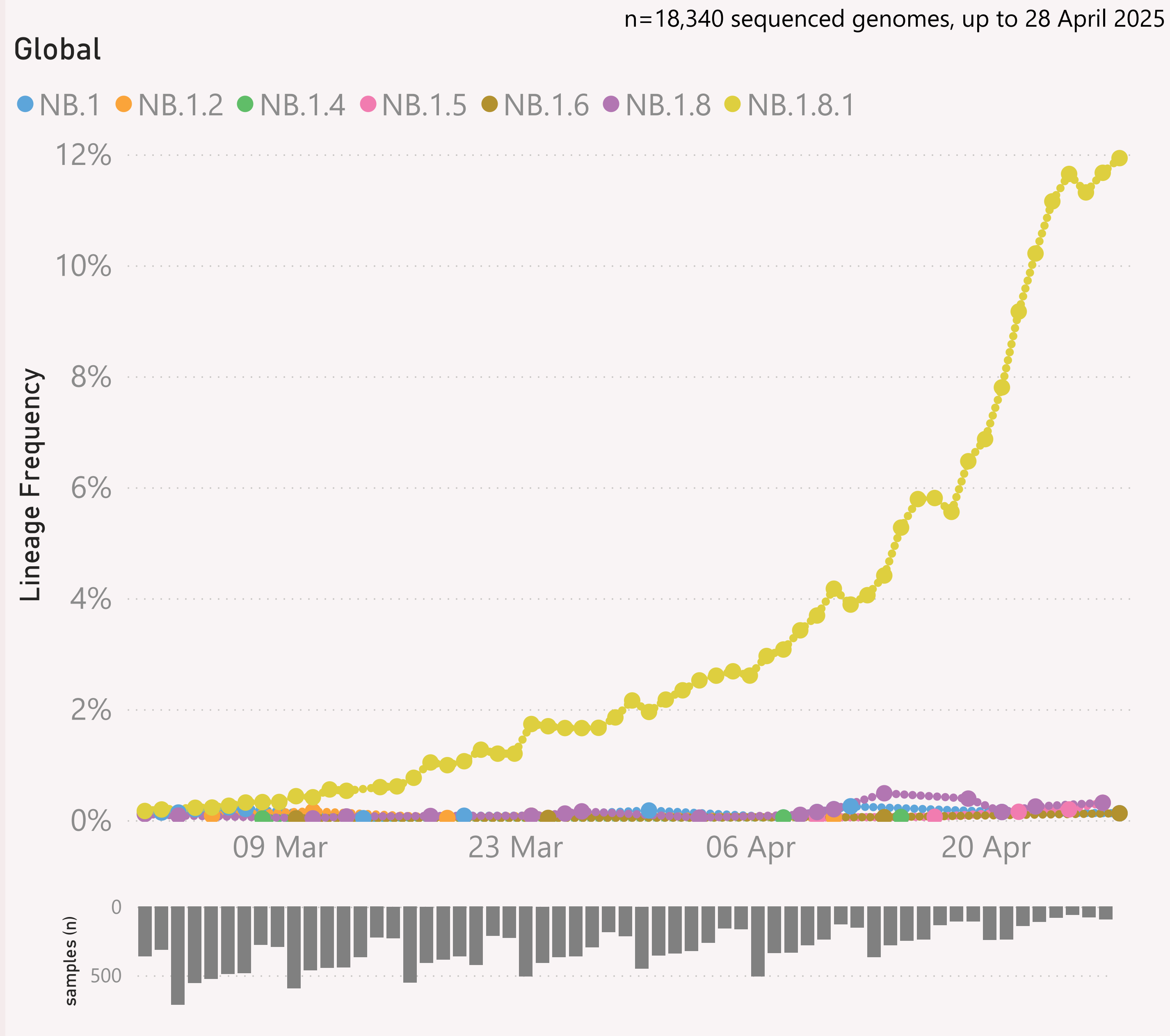
The detailed Lineage classifications are provided by Nextclade. I roll those up into "L2" groups, which roughly follow the WHO Variant definitions. For example, my "BA.2.86.*" group includes BA.2.86 and all it's descendants, e.g. the JN.* lineages.

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=18,340 sequenced genomes, up to 28 April 2025

Global

- NB.1
- NB.1.2
- NB.1.4
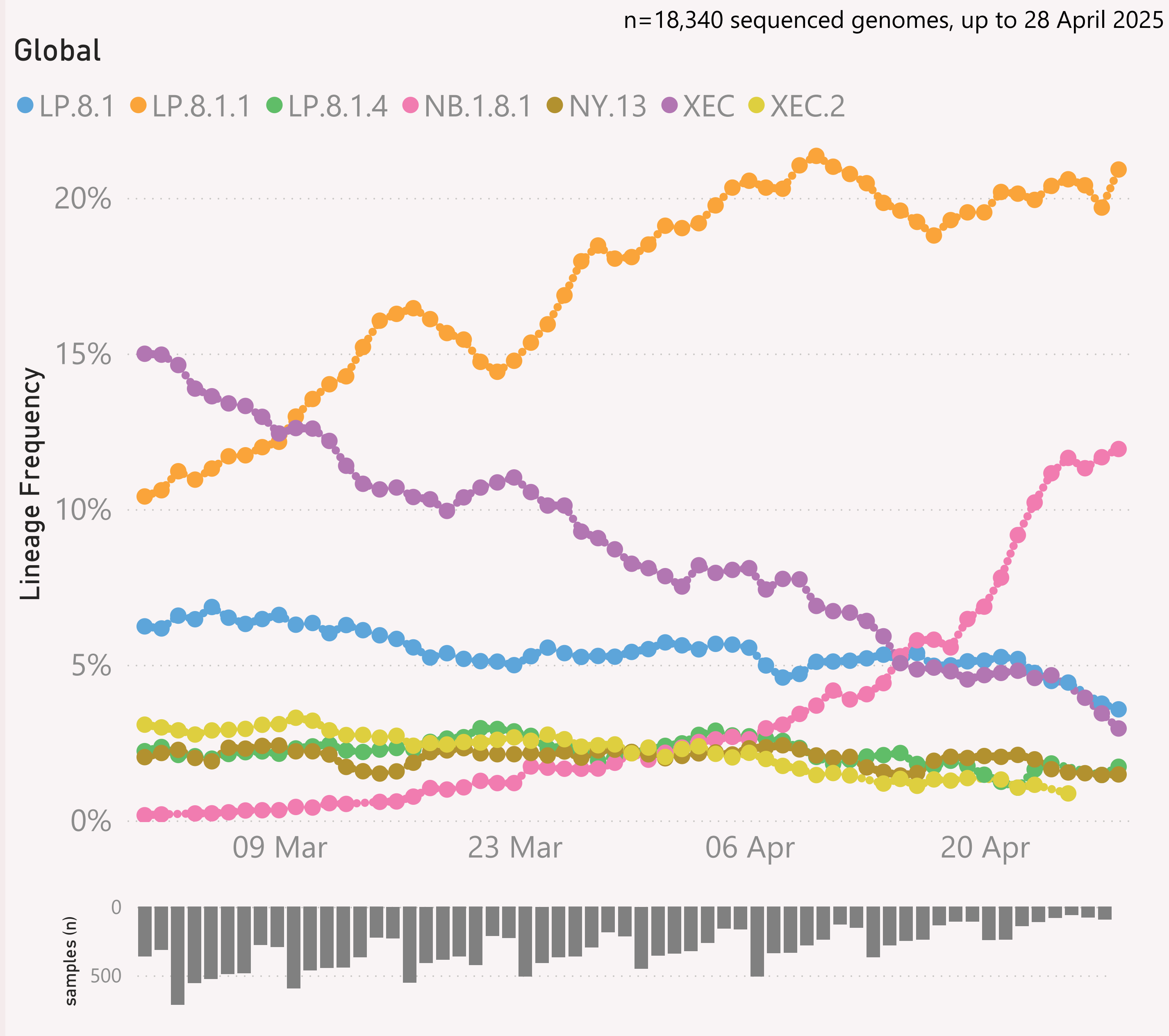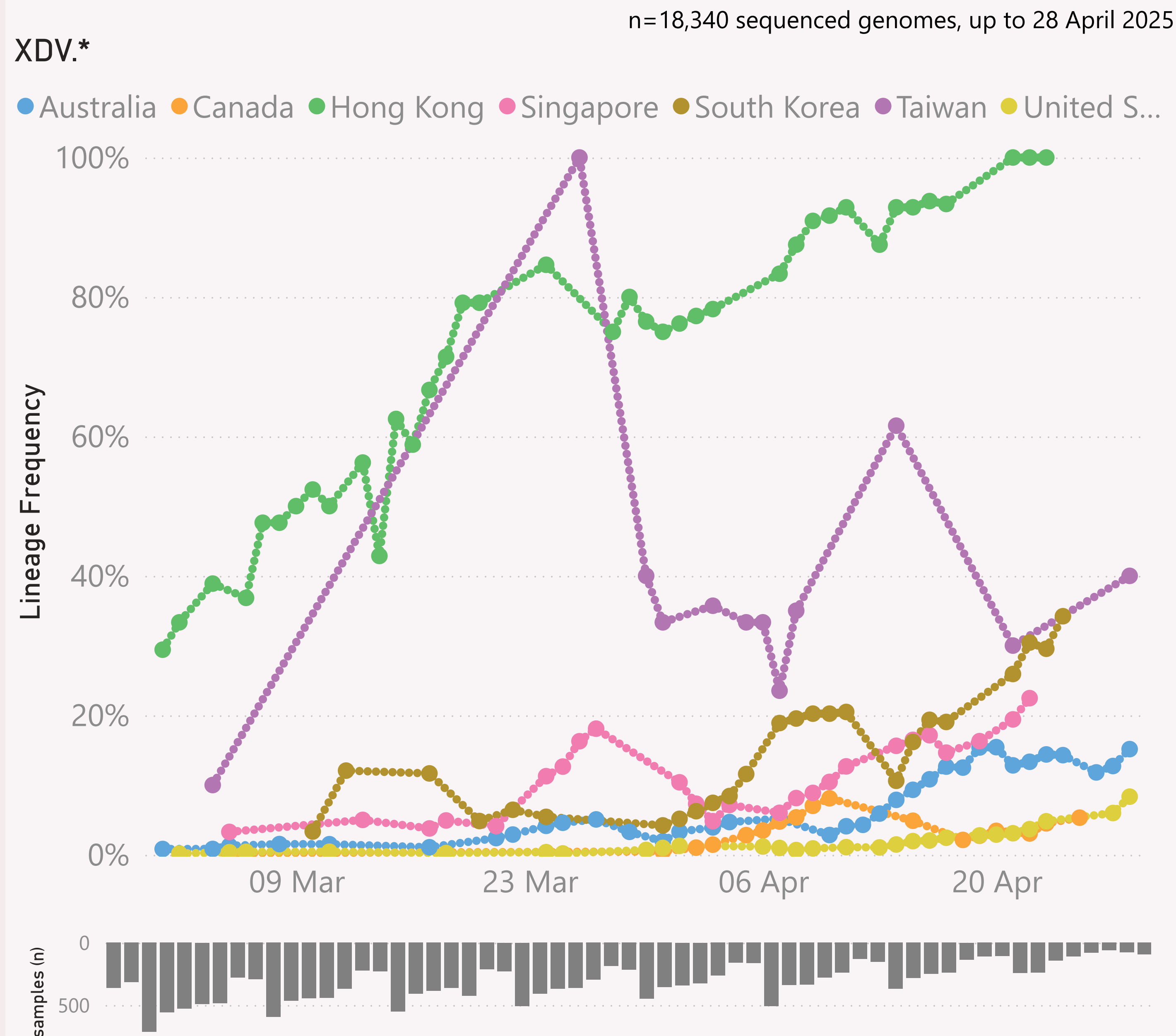- NB.1.5
- NB.1.6
- NB.1.8
- NB.1.8.1

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 XDV.*.

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=18,340 sequenced genomes, up to 28 April 2025

Global

● LP.8.1 ● LP.8.1.1 ● LP.8.1.4 ● NB.1.8.1 ● NY.13 ● XEC ● XEC.2

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.

n=18,340 sequenced genomes, up to 28 April 2025

XDV.*

● Australia　● Canada　● Hong Kong　● Singapore　● South Korea　● Taiwan　● United S...

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.

n=59,704 sequenced genomes, up to 28 April 2025

NB.1.8.1

● Australia ● Canada ● Hong Kong ● Singapore ● South Korea ● United States
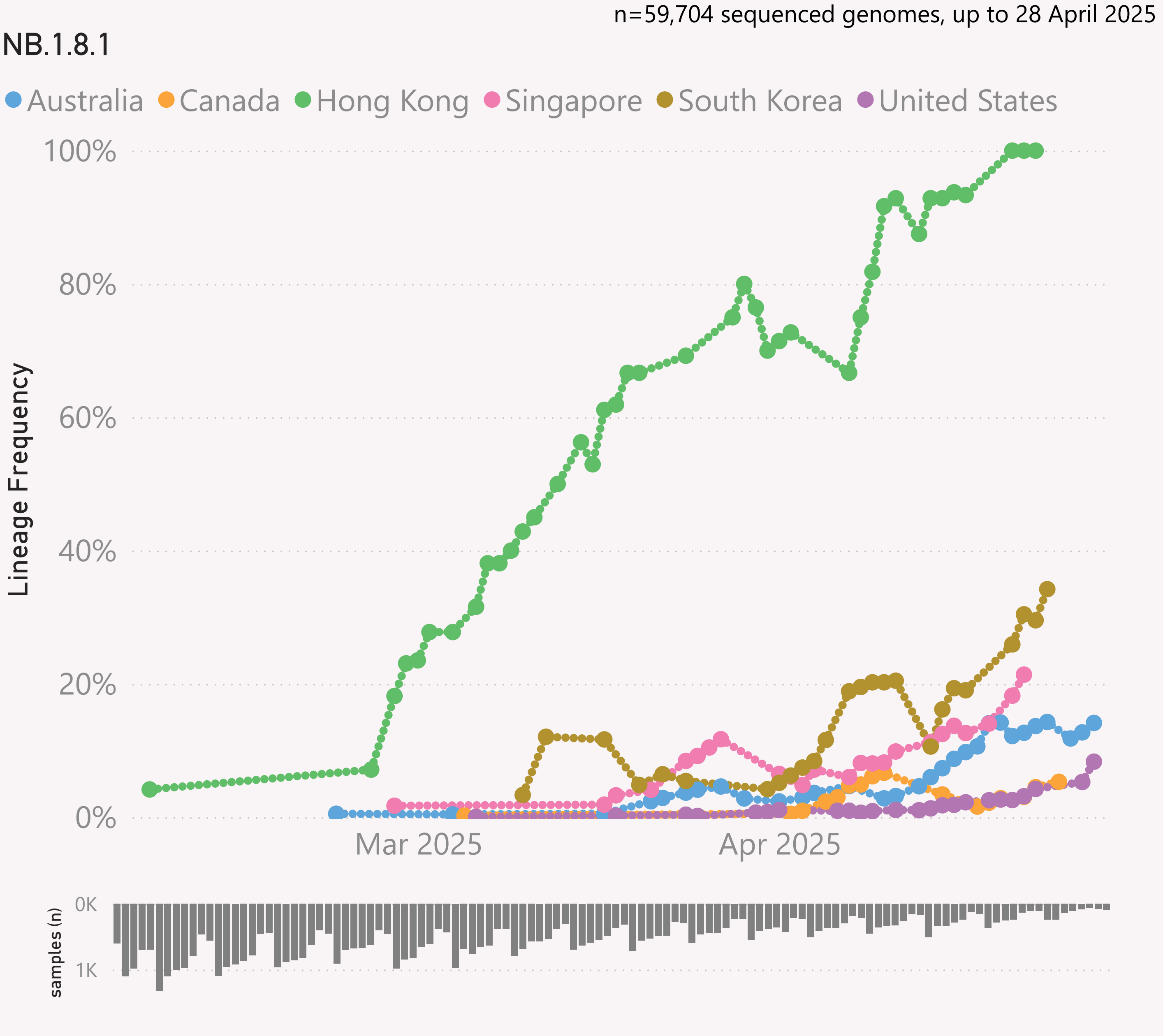
This page shows the frequency of a selected Lineage of interest, for the 6 countries reporting the most samples over recent months.

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=18,340 sequenced genomes, up to 28 April 2025

Global - XDV.* vs LP.8.1.*

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

growth of 5.1% per day, crossover on 24-May-25
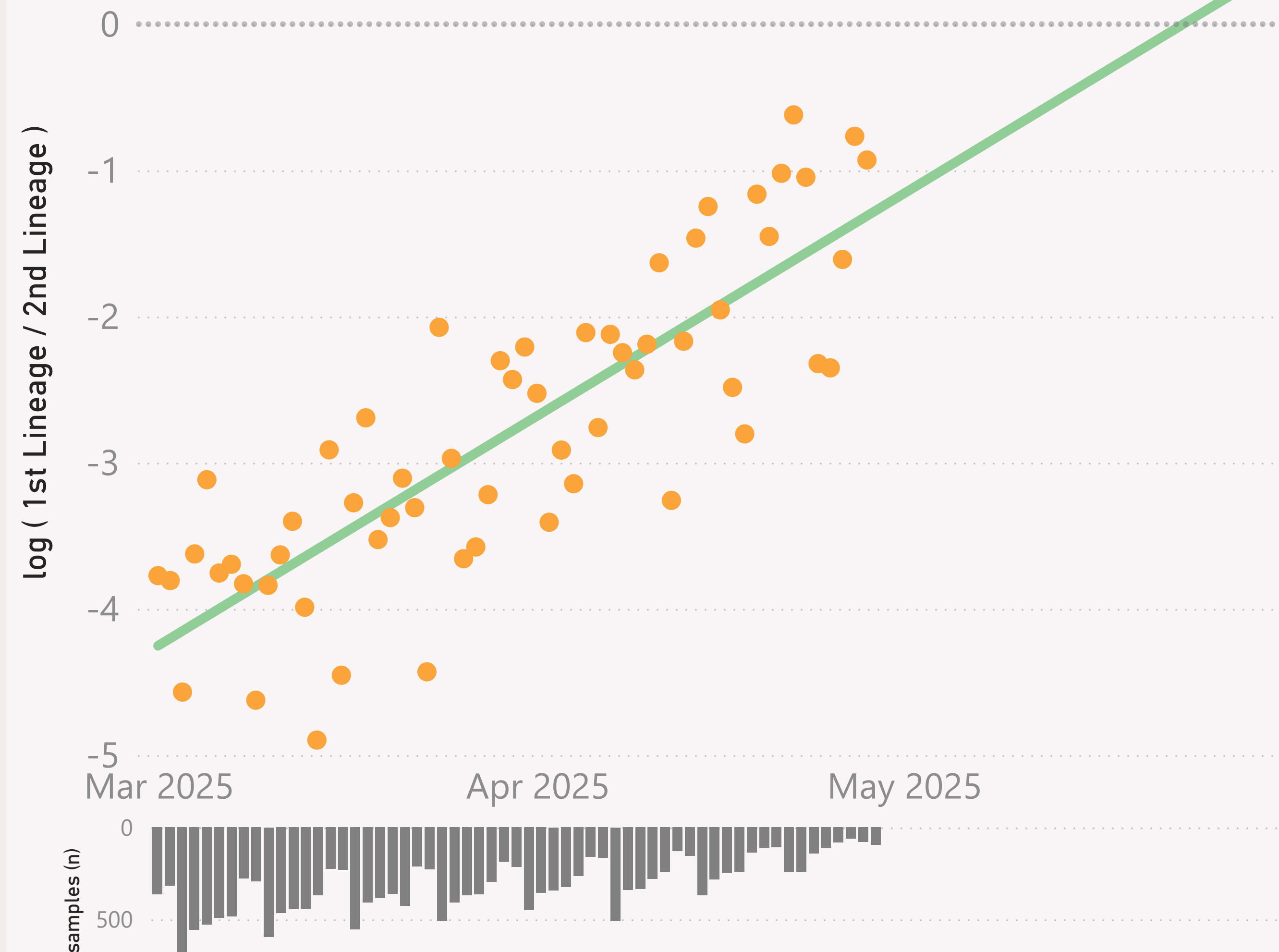
This page compares the relative frequency of 2 selected "Lineage L2" groups, over recent months. A challenging Lineage L2 is selected first, and compared to the incumbent.

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=18,340 sequenced genomes, up to 28 April 2025

Global – NB.1.8.1 vs LP.8.1.1

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

growth of 5.4% per day, crossover on 11-May-25
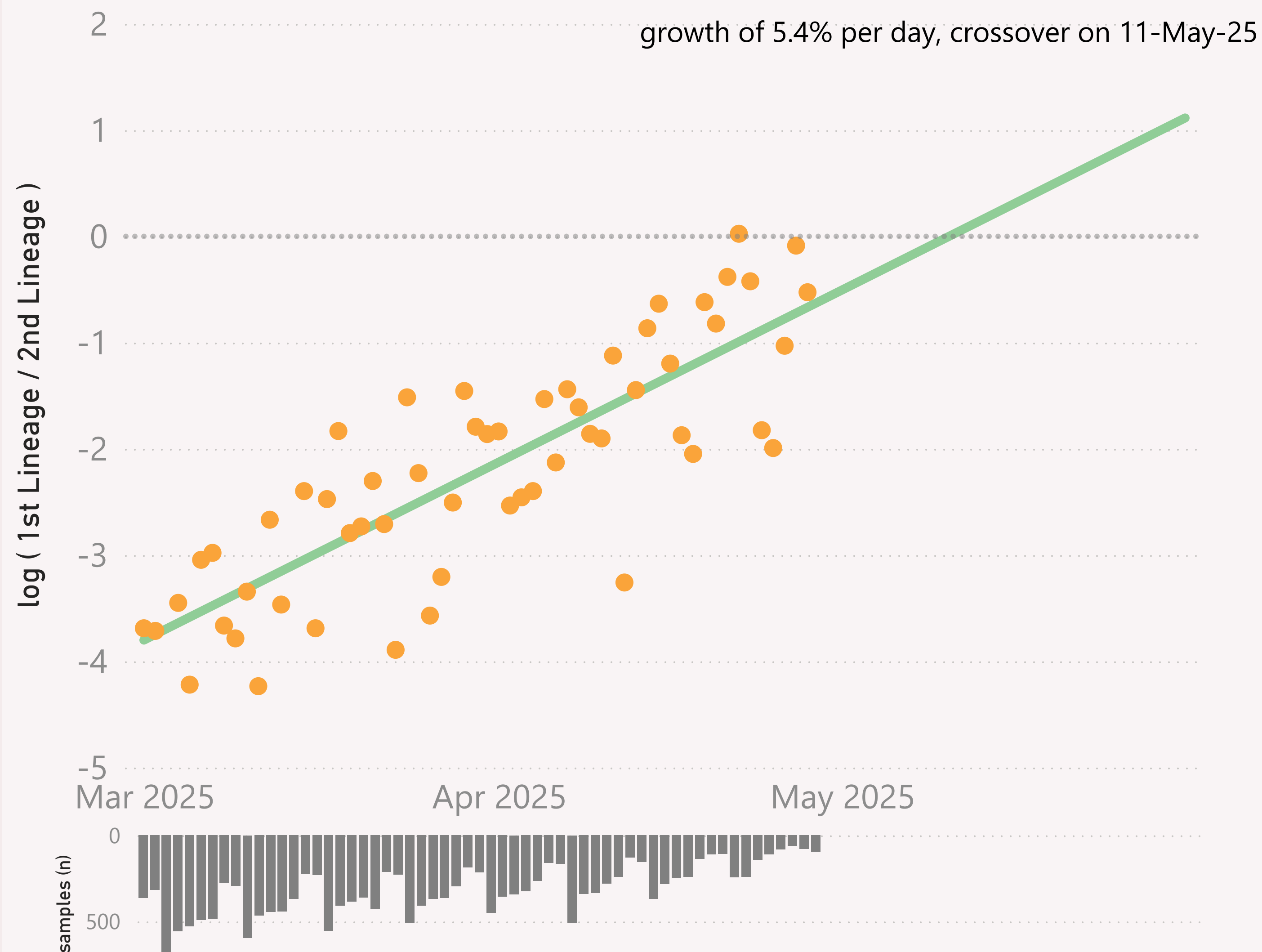
This page compares the relative frequency of 2 selected Lineages, over recent months. A challenging Lineage is selected first, and compared to the incumbent.

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=18,349 sequenced genomes, up to 28 April 2025

Global
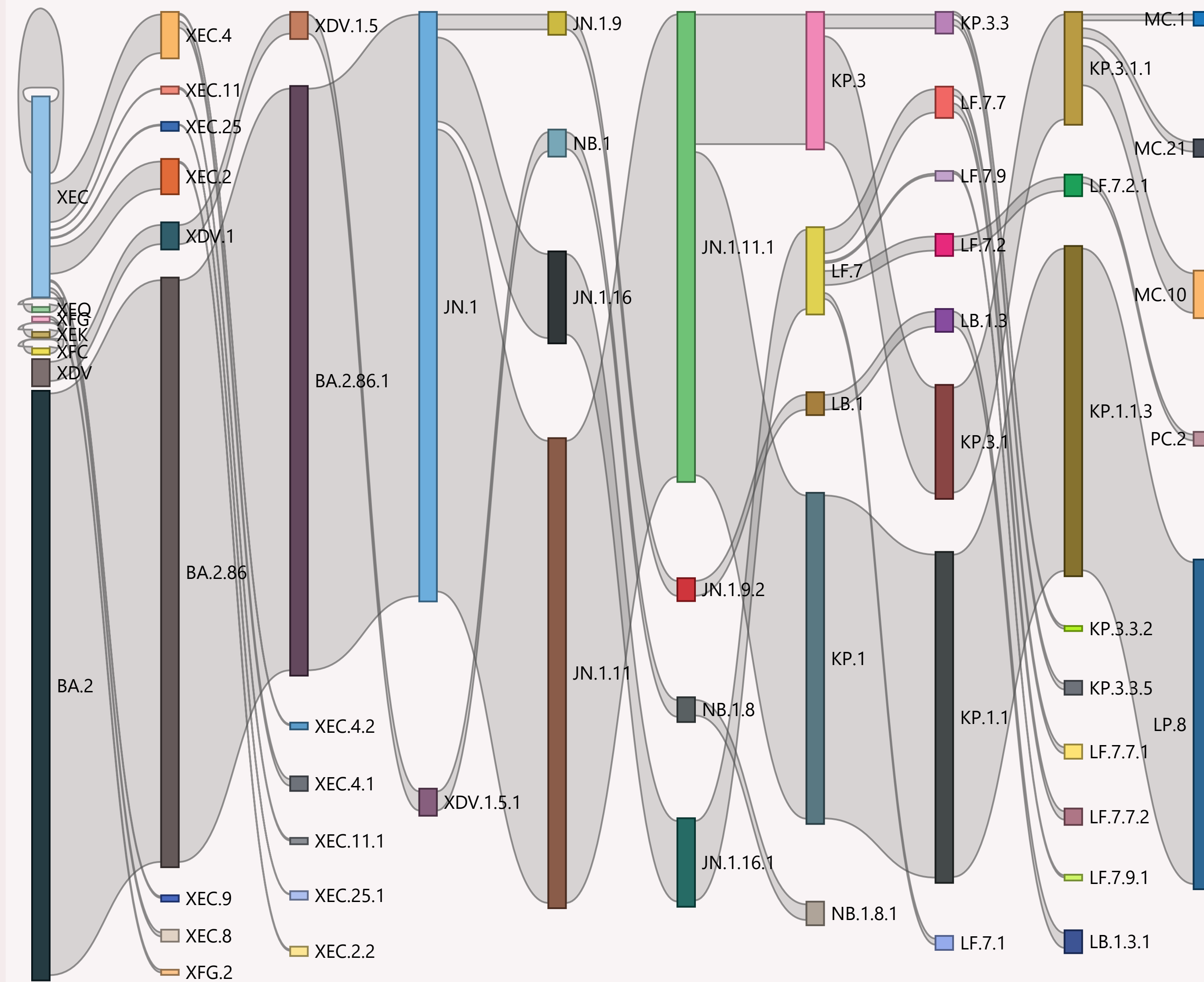
This page shows the hierarchy of the significant Lineages, over recent months.
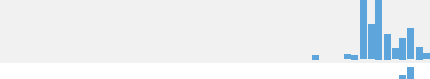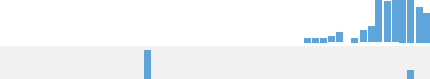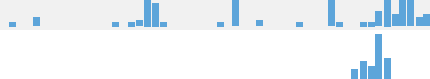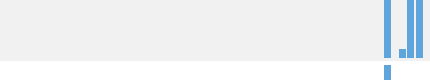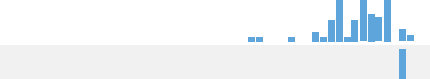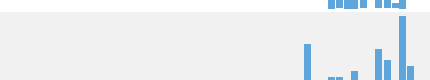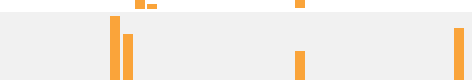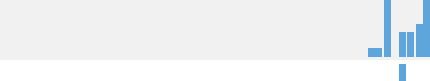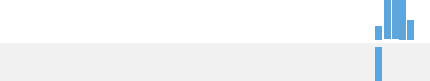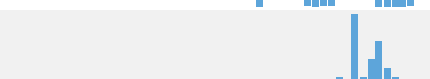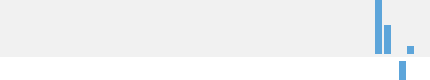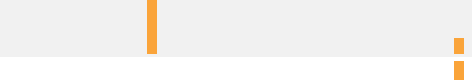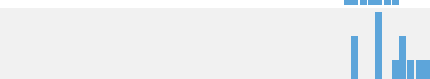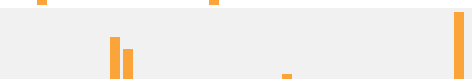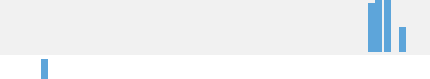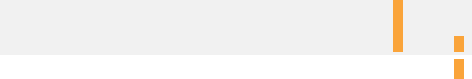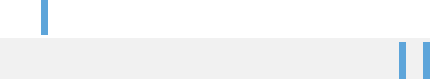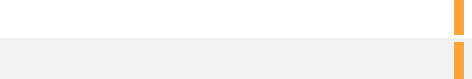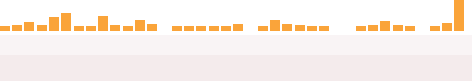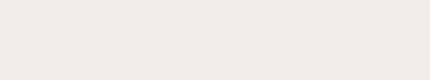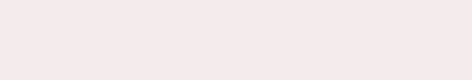
The hierarchy can be read from left to right, starting with the earliest/highest Lineages being broken down into more detailed child Lineages.

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
United States	14,501	28/04/2025		29/04/2025	
Canada	3,324	28/04/2025		29/04/2025	
Australia	1,734	28/04/2025		29/04/2025	
France	1,393	28/04/2025		29/04/2025	
Japan	1,323	28/04/2025		29/04/2025	
United Kingdom	1,063	28/04/2025		29/04/2025	
Spain	936	28/04/2025		29/04/2025	
Singapore	711	22/04/2025		28/04/2025	
Brazil	707	24/04/2025		29/04/2025	
South Korea	568	24/04/2025		29/04/2025	
Luxembourg	390	01/04/2025		16/04/2025	
Germany	331	26/04/2025		29/04/2025	
Peru	325	01/04/2025		29/04/2025	
New Zealand	283	28/04/2025		29/04/2025	
Chile	246	22/04/2025		29/04/2025	
Denmark	235	21/04/2025		29/04/2025	
Italy	195	26/04/2025		29/04/2025	
Russia	192	29/03/2025		29/04/2025	
Netherlands	172	28/04/2025		29/04/2025	
Norway	149	18/04/2025		29/04/2025	
Ireland	146	28/04/2025		29/04/2025	
Mexico	139	09/04/2025		29/04/2025	
Finland	131	24/03/2025		09/04/2025	
Sweden	126	28/04/2025		29/04/2025	
Hong Kong	112	23/04/2025		29/04/2025	
Costa Rica	108	01/04/2025		29/04/2025	
Kazakhstan	95	07/02/2024		29/04/2025	
Taiwan	91	28/04/2025		29/04/2025	
Total	**30,941**	**28/04/2025**		**29/04/2025**	

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.