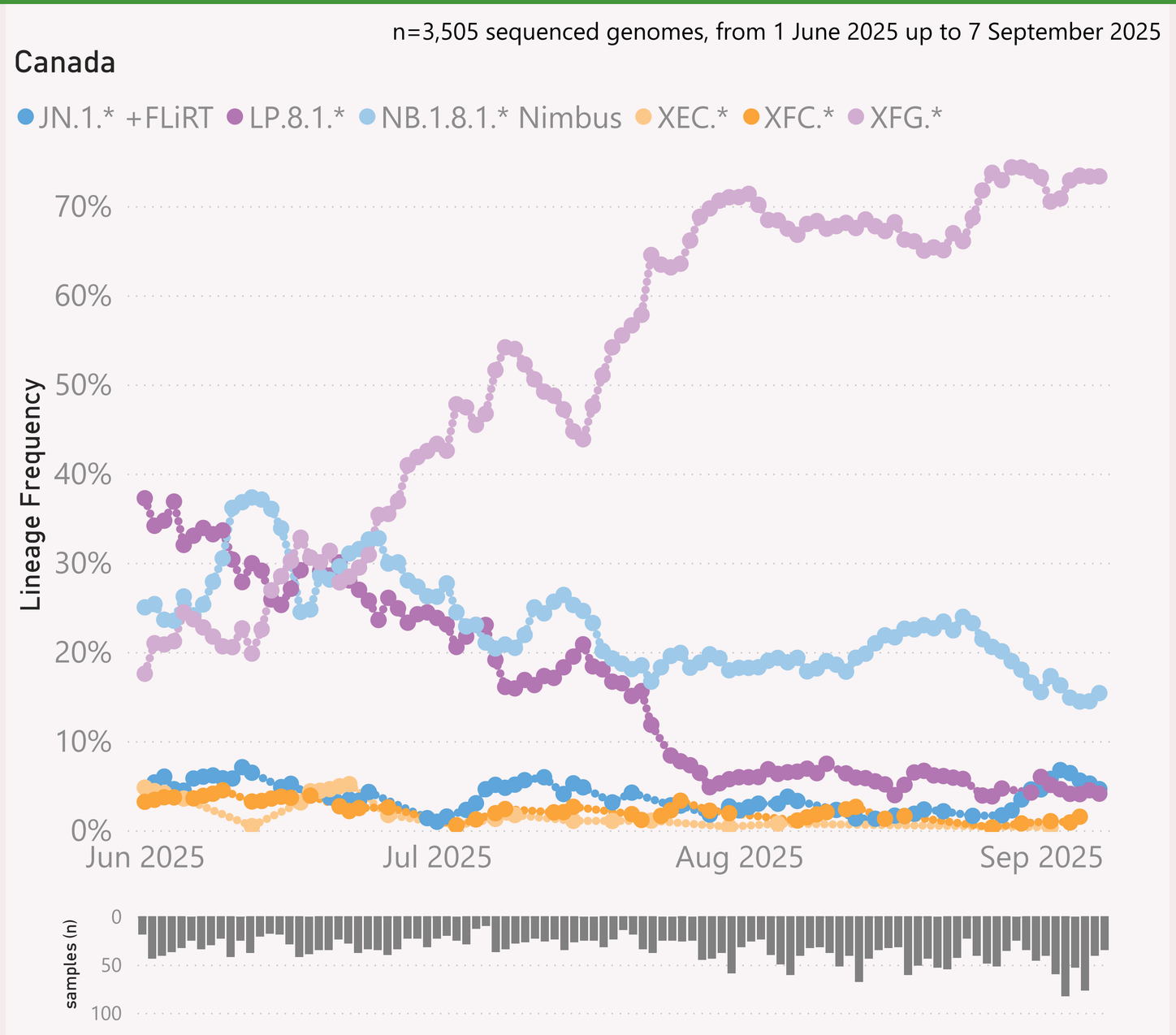
n=3,505 sequenced genomes, from 1 June 2025 up to 7 September 2025




Linear | Log

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.

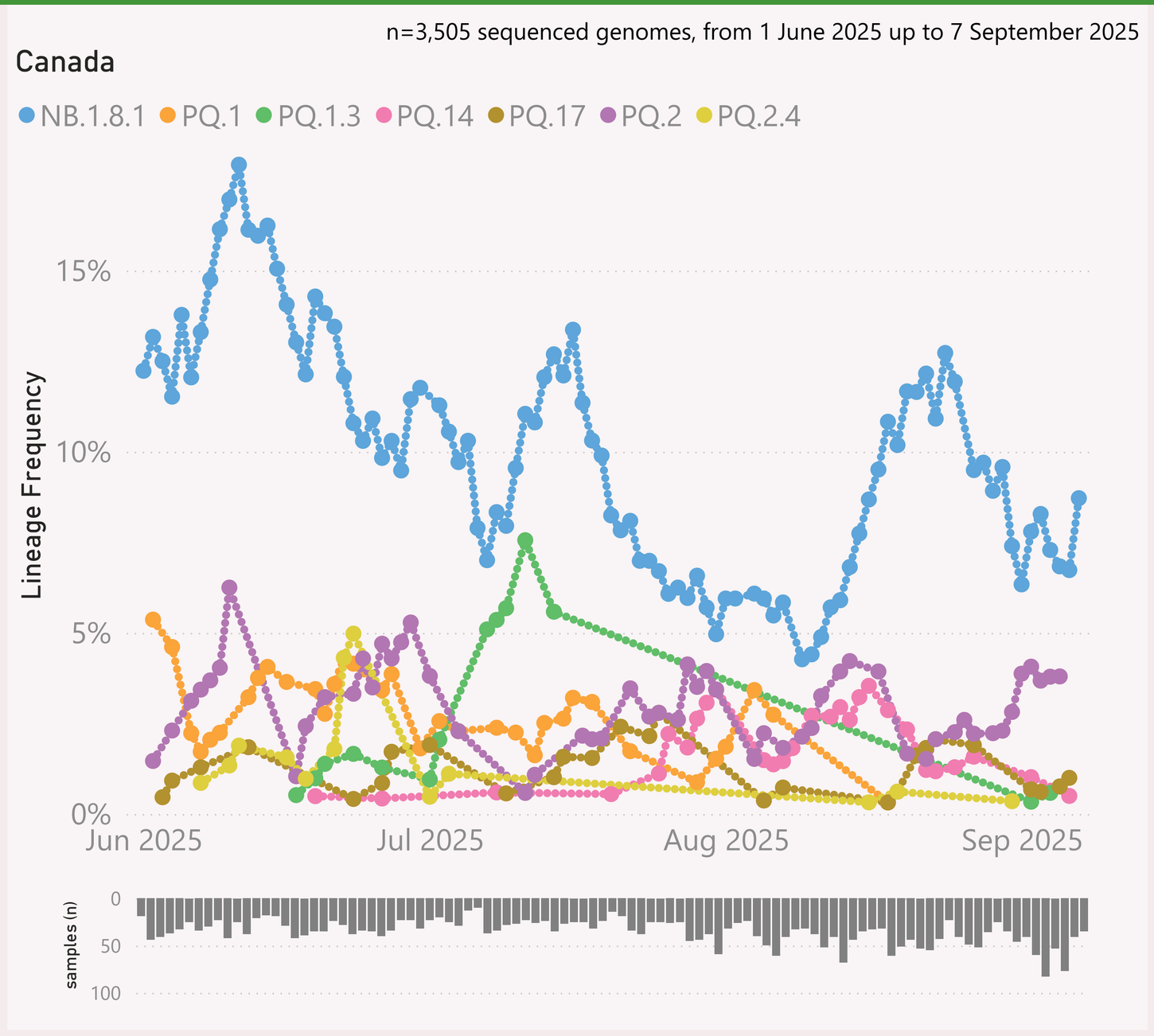
The detailed Lineage classifications are quite numerous and dynamic, so the "Lineage L2" groups give a simpler and more stable basis for analysis and comparison.

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=3,505 sequenced genomes, from 1 June 2025 up to 7 September 2025




Linear Log

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 NB.1.8.1.* "Nimbus'.

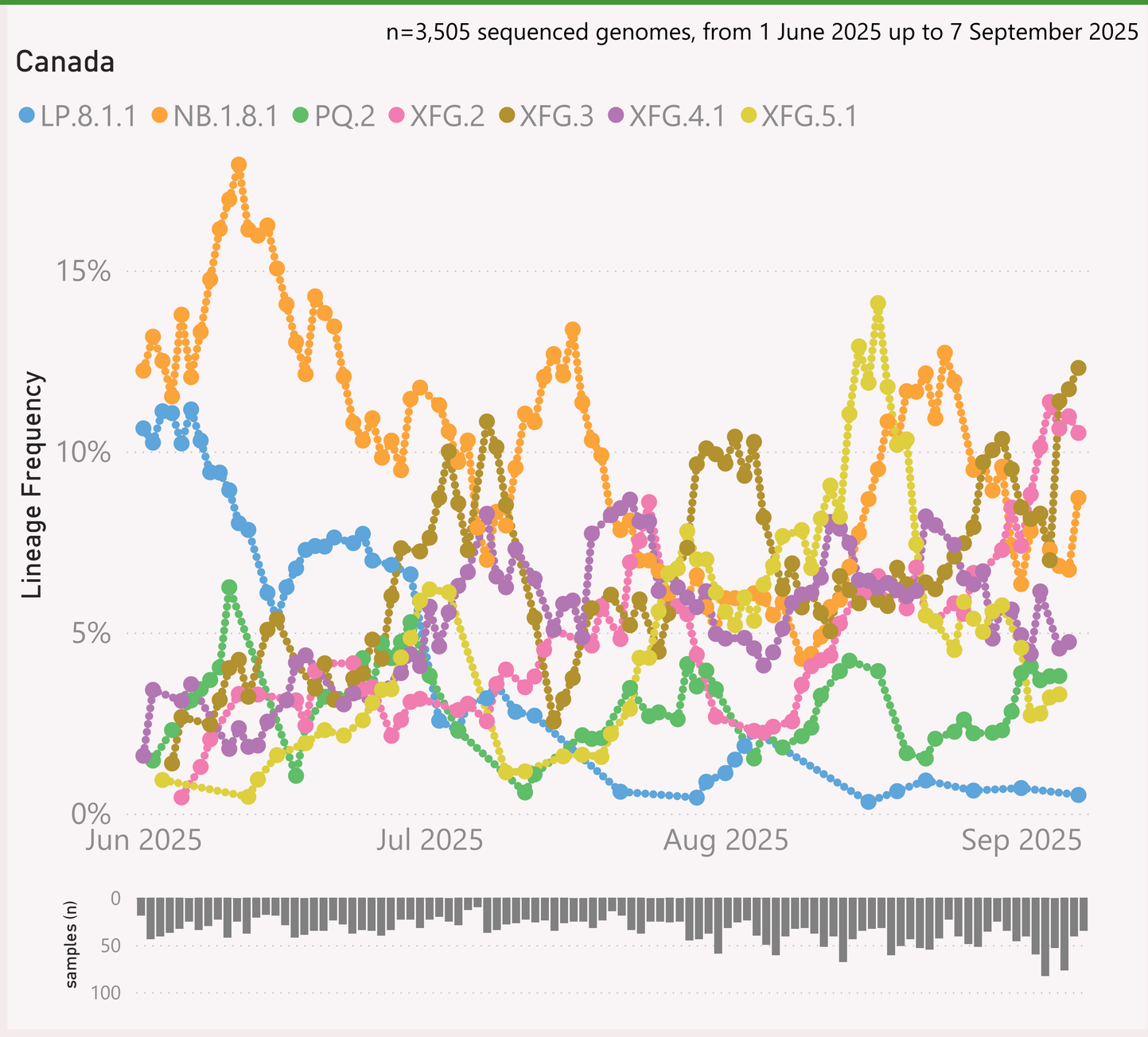
The Lineage classifications are provided by Nextclade. The colour assignments are random.

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=3,505 sequenced genomes, from 1 June 2025 up to 7 September 2025




Linear Log

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.

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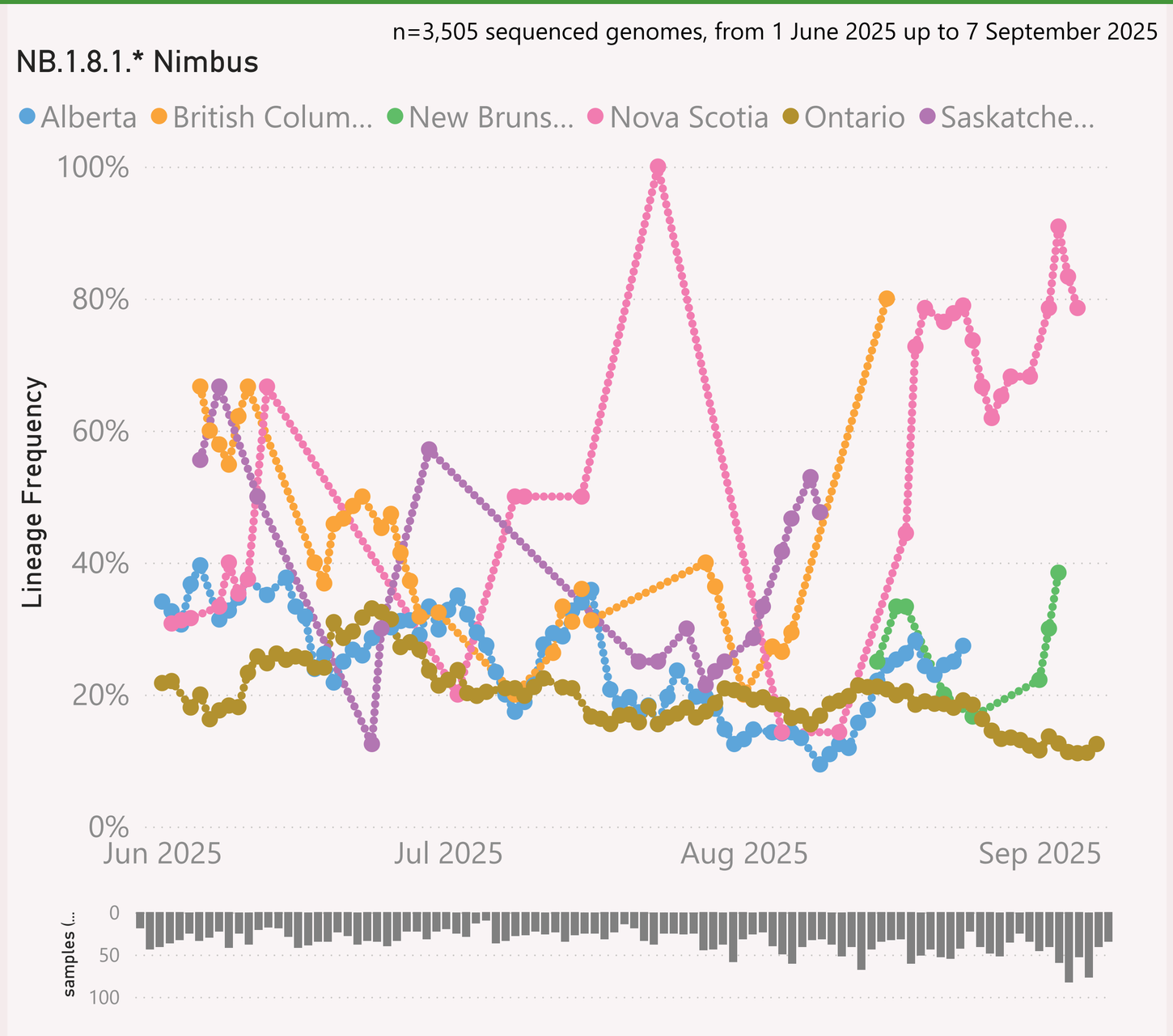
n=3,505 sequenced genomes, from 1 June 2025 up to 7 September 2025




Linear | Log

This page shows the frequency of a selected Lineage L2 of interest, across the provinces of Canada, over recent months.

The Lineage classifications are provided by Nextclade.

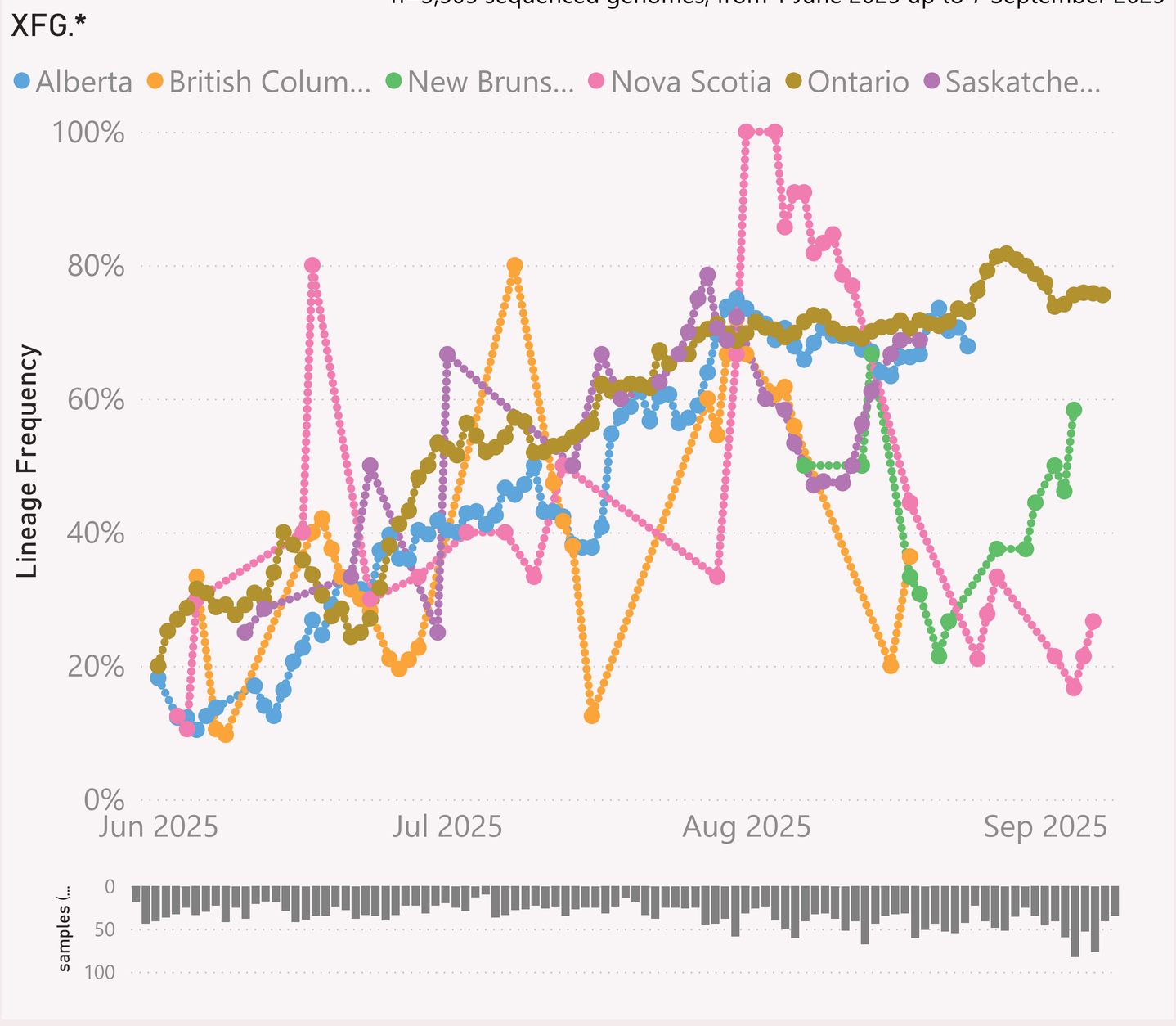
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that state.

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.

COVID-19 Genomic Sequencing analysis - selected Lineage by Province. Data from gisaid.org, with nextclade lineages Source files and info on github. Last Update: 2025-09-26 22:42 (UTC)

n=3,505 sequenced genomes, from 1 June 2025 up to 7 September 2025




Linear | Log

This page shows the frequency of a selected Lineage L2 of interest, across the provinces of Canada, over recent months.

The Lineage classifications are provided by Nextclade.

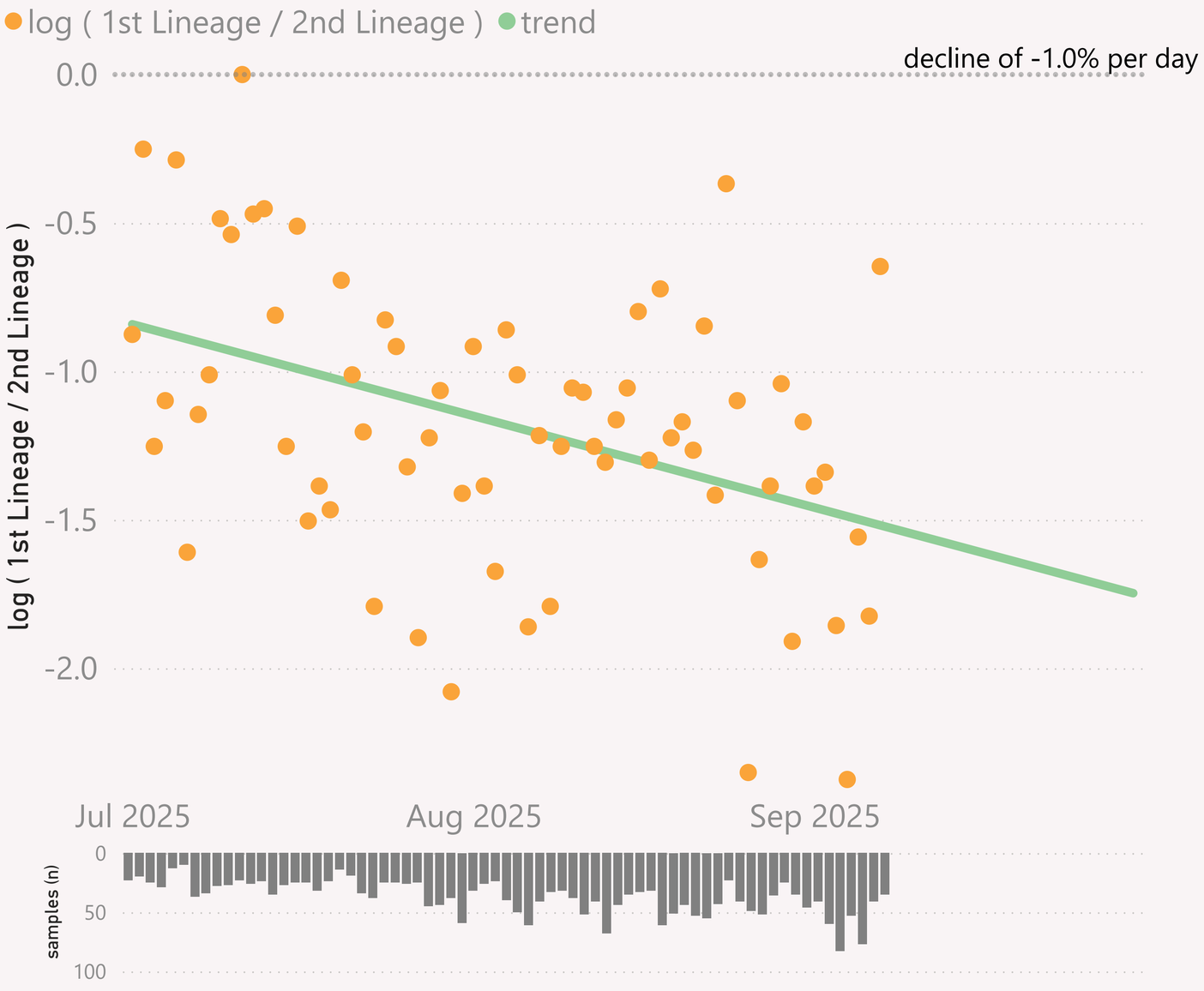
The frequency shown at each point is based on the 7-day rolling average across all lineages, for that state.

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=2,565 sequenced genomes, from 1 July 2025 up to 7 September 2025

## Canada - NB.1.8.1.* Nimbus vs XFG.*




Date: 01/07/2025 – 30/09/2025

Continent, Country, Location: North America (Continent) + Canada (Coun...

Lineage L2: NB.1.8.1.* Nimbus

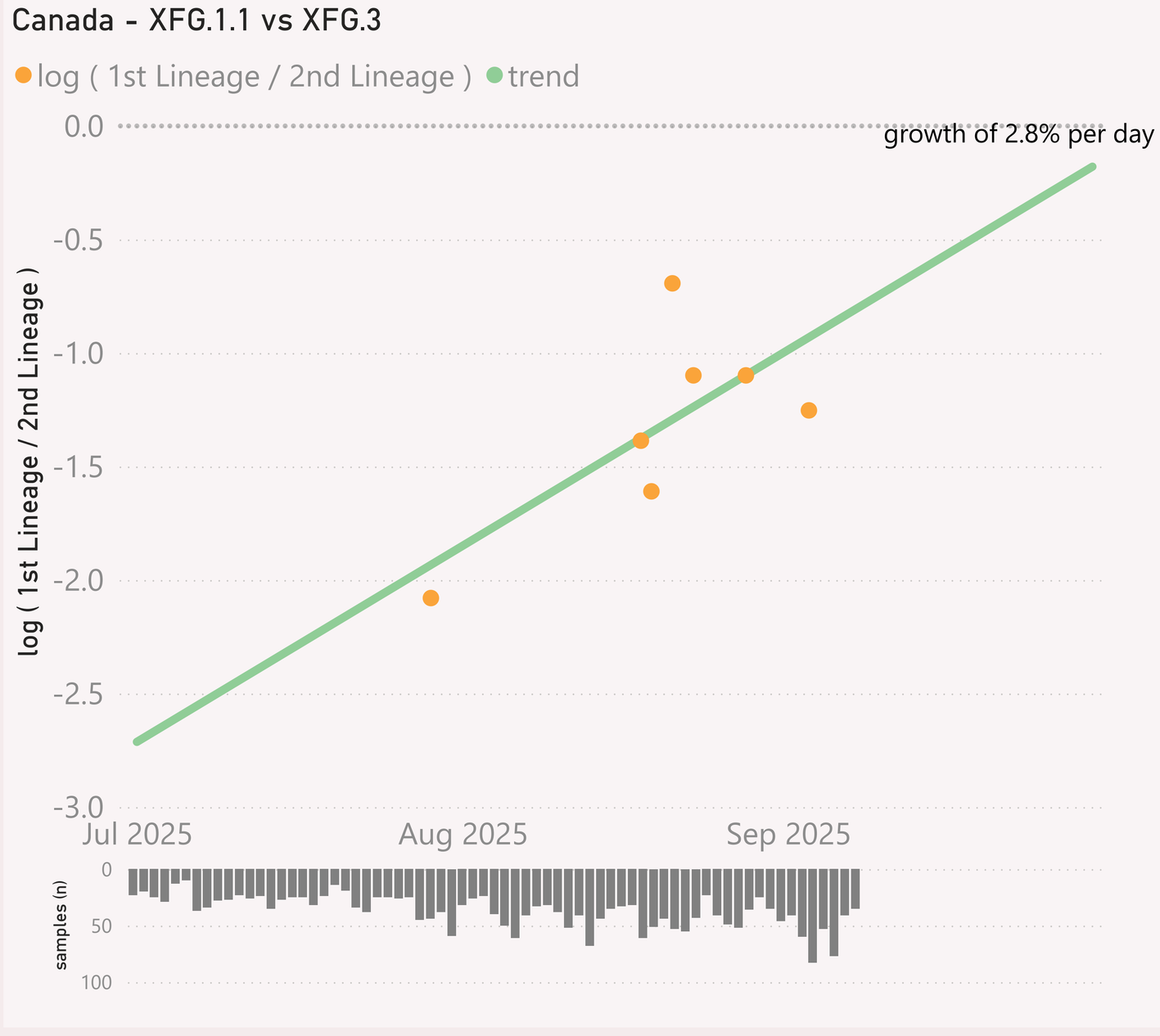
Host: Human

vs Lineage L2 (nextclade): XFG.*

| Country | Location | Addi... | Collection date | Lineage L2 | Lineage (nextcla |
|---|---|---|---|---|---|
| Canada | Ontario | | 07/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Ontario | | 06/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Ontario | | 06/09/2025 | NB.1.8.1.... | PQ.13.1 |
| Canada | Ontario | | 06/09/2025 | NB.1.8.1.... | PQ.14 |
| Canada | Ontario | | 06/09/2025 | NB.1.8.1.... | PQ.17 |
| Canada | Nova Scotia | | 05/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Nova Scotia | | 05/09/2025 | NB.1.8.1.... | PQ.2 |
| Canada | Nova Scotia | | 05/09/2025 | NB.1.8.1.... | PQ.2.5 |
| Canada | Ontario | | 05/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Ontario | | 05/09/2025 | NB.1.8.1.... | PQ.1.3 |
| Canada | Ontario | | 05/09/2025 | NB.1.8.1.... | PQ.15 |
| Canada | Ontario | | 05/09/2025 | NB.1.8.1.... | PQ.17 |
| Canada | Ontario | | 05/09/2025 | NB.1.8.1.... | PQ.2 |
| Canada | Ontario | | 05/09/2025 | NB.1.8.1.... | PQ.9 |
| Canada | Nova Scotia | | 04/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Ontario | | 04/09/2025 | NB.1.8.1.... | PQ.1.3 |
| Canada | Ontario | | 04/09/2025 | NB.1.8.1.... | PQ.2 |
| Canada | New Brunswick | | 03/09/2025 | NB.1.8.1.... | PQ.1.2 |
| Canada | New Brunswick | | 03/09/2025 | NB.1.8.1.... | PQ.2 |
| Canada | Nova Scotia | | 03/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Ontario | | 03/09/2025 | NB.1.8.1.... | NB.1.8.1 |
| Canada | Ontario | | 03/09/2025 | NB.1.8.1.... | PQ.17 |

**Total**

n=2,565 sequenced genomes, from 1 July 2025 up to 7 September 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.

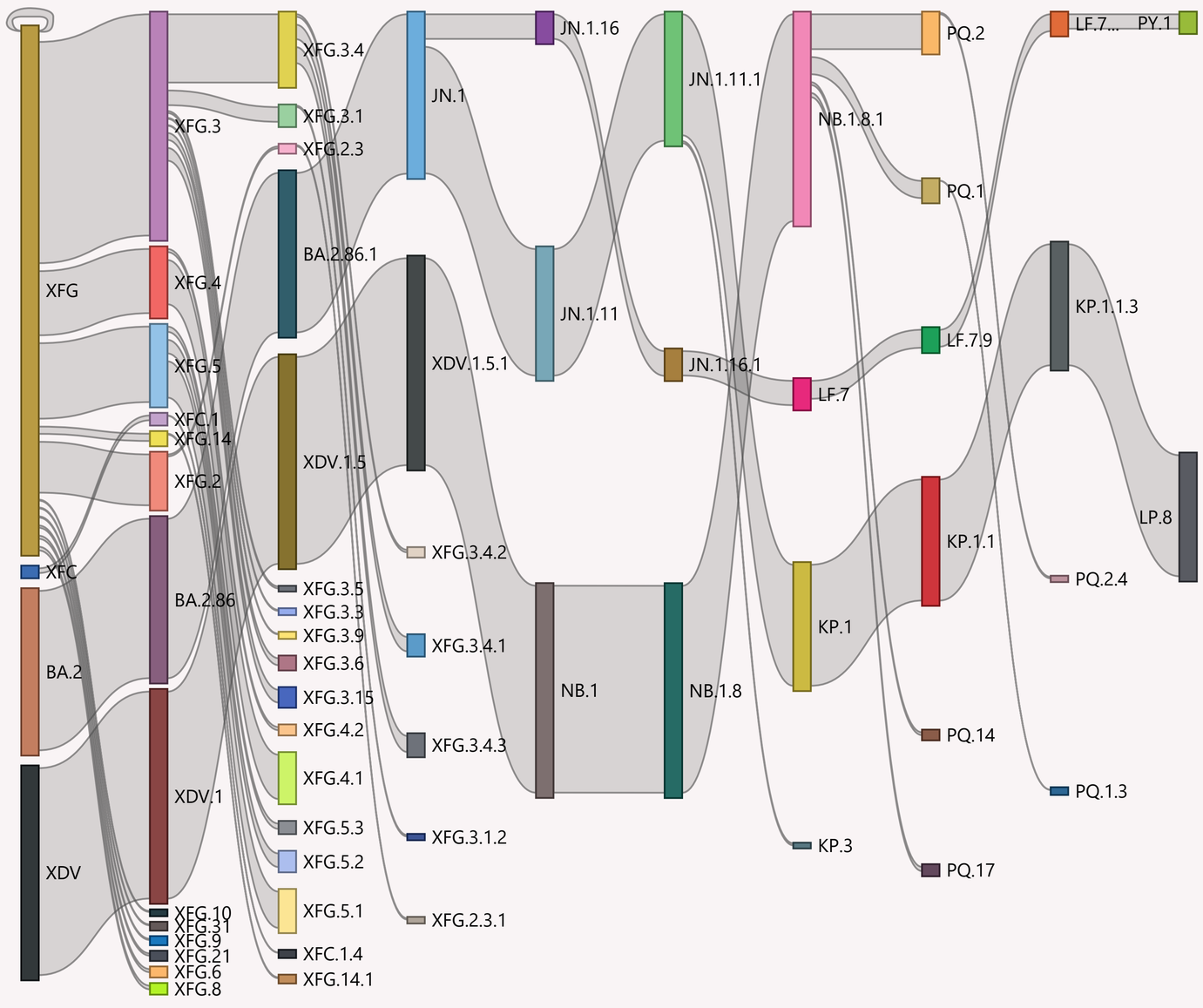
The trend is shown as a green line and expressed as a daily growth % advantage. If the green line crosses over the 0.0 line, the date when that occurred or is predicted to occur will be shown. At that point the challenging Lineage is considered to have "crossed over" or taken over dominance from the 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=3,505 sequenced genomes, from 1 June 2025 up to 7 September 2025

## Canada




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: 2025-09-26 22:42 (UTC)

## Data Submitted in the last 8 weeks

| Country | # Samples Sequenced | Latest Collection date | by Collection date | Latest Submission date | by Submission date |
|---|---|---|---|---|---|
| **Canada** | **2,383** | **07/09/2025** | | **17/09/2025** | |
| Alberta | 546 | 24/08/2025 | | 16/09/2025 | |
| British Columbia | 131 | 18/08/2025 | | 17/09/2025 | |
| New Brunswick | 40 | 04/09/2025 | | 11/09/2025 | |
| Newfoundland and Labrador | 9 | 06/08/2025 | | 03/09/2025 | |
| Nova Scotia | 120 | 06/09/2025 | | 17/09/2025 | |
| Ontario | 1,459 | 07/09/2025 | | 17/09/2025 | |
| Saskatchewan | 78 | 20/08/2025 | | 17/09/2025 | |
| **Total** | **2,383** | **07/09/2025** | | **17/09/2025** | |

This page shows the volume and currency/timeliness of the genomic sequencing data shared via GISAID, over the last 8 weeks. A breakdown by province is also shown.

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.