

Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 28 and Sequencing Update

Summary

Over the past two weeks (2025/27-28), the sentinel network detected a baseline activity, based on **less than 2%** of consultations being associated with influenza-like illness. Among the specimens collected by the sentinel network over the past two weeks, the percentage of positive tests for **human rhinovirus** and **parainfluenza** were each **22.5%** and **10.0%** for **adenovirus**, while **SARS-CoV-2** activity remained stable at **7.0%**.

Regarding SARS-CoV-2 genomic surveillance, several sub-lineages and recombinant lineages of JN.1 circulate in Luxembourg and globally.

Over the past 4 weeks, the estimated distribution for **XFG** was **28.1%** (95%CI: 20.1 – 37.3%) and **23.7%** (95%CI: 16.2 – 32.6%) for each **NB.1.8.1** and **LP.8.1**.

Variants under monitoring

| Sub-variant | Genetic features | First detected in Luxembourg | Estimated prevalence (2025/24-2025/27) |
|-------------|---|------------------------------|--|
| JN.1* | BA.2.86 + S:L455S | 25.08.2023 | 7.9% |
| KP.3 | JN.1 + S:F456L, S:Q493E, S:V1104L | 03.04.2024 | 0.0% |
| XEC | JN.1 + S:T22N, S:F59S, S:F456L, S:Q493E, S:V1104L | 19.07.2024 | 0.9% |
| LP.8.1 | JN.1 + S:S31-, S:F186L, S:R190S, S:R346T, S:V445R, S:F456L, S:Q493E, S:K1086R, S:V1104L | 05.11.2024 | 23.7% |
| NB.1.8.1 | JN.1 + S:T22N, S:F59S, S:G184S, S:A435S, S:F456L, S:T478I, S:Q493E | 07.04.2025 | 23.7% |
| XFG | JN.1 + S:T22N, S:S31P, S:K182R, S:R190S, S:R346T, S:K444R, S:V445R, S:F456L, S:N487D, S:Q493E, S:T572I | 13.03.2025 | 28.1% |

*JN.1 excludes sub-variants listed in table

Sentinel Surveillance Network

The Sentinel Surveillance aims at monitoring the circulating respiratory viruses, from traditional ones like Influenza to more recent ones like SARS-CoV-2, and hence underpin public health actions. The Sentinel Network is a group of general practitioners and paediatricians spread across the country. They report the weekly number of patients showing symptoms suggestive of acute respiratory infection (ARI) and influenza-like illness (ILI), and those patients are then sampled and tested for a panel of respiratory viruses. The circulation of respiratory viruses in the north hemisphere is generally monitored by seasons that go from week 40 to week 20. The period between weeks 20 and 40 is called inter-season and monitoring is done on a voluntary basis.

Clinical results

Last week (**end of week 2025/28**), **1.7%** of the consultations were reported as ILI, representing a baseline activity for Luxembourg, according to ECDC and the Moving Epidemic Method. Over the past 7 weeks, the network has reported baseline ILI rates, indicating low activity. The history of ILI consultations is displayed in figure 1, and a detailed summary of the number of ARI and ILI cases during the last four weeks is included in table 1.

Table 1. Syndromic surveillance over the last 4 weeks

| Week | ARI | | ILI | | Total consultations |
|---------|-----|------|-----|------|---------------------|
| | N | % | N | % | |
| 2025/25 | 21 | 8.90 | 4 | 1.69 | 236 |
| 2025/26 | 7 | 5.04 | 4 | 2.88 | 139 |
| 2025/27 | 14 | 7.41 | 3 | 1.59 | 189 |
| 2025/28 | 14 | 5.86 | 4 | 1.67 | 239 |

ARI: Acute Respiratory Infections; ILI: Influenza-Like Illness.

Laboratory results

From week 2025/27 to week 2025/28, respiratory viruses were identified in a total of 23 samples (53.5%) of the 43 sentinel samples sent to LNS. **Human rhinovirus (22.5%)** and **parainfluenza (22.5%)** were the most prevalent circulating viruses, followed by **adenovirus** with **10.0%**.

Over the past 4 weeks SARS-CoV-2 positivity remained below 10%, indicating stable activity in the network. More than half of cases (57.1%) were detected in patients aged between the ages of 18 and 64.

Over the last 4 weeks, more than 90% of adenovirus and nearly 75% of the parainfluenza virus cases were identified in children below 10 years, while human rhinovirus was detected across all age-groups.

Overall, no new RSV cases were detected in the network during the inter-season and no influenza activity was detected in the last two weeks. However, low-level influenza activity was detected across Europe and, if subtyped, identified as A(H1) pdm09. An overview of the submitted samples and circulating viral pathogens during the inter-season and previous inter-season can be found in table 2, figure 2 and figure 3.

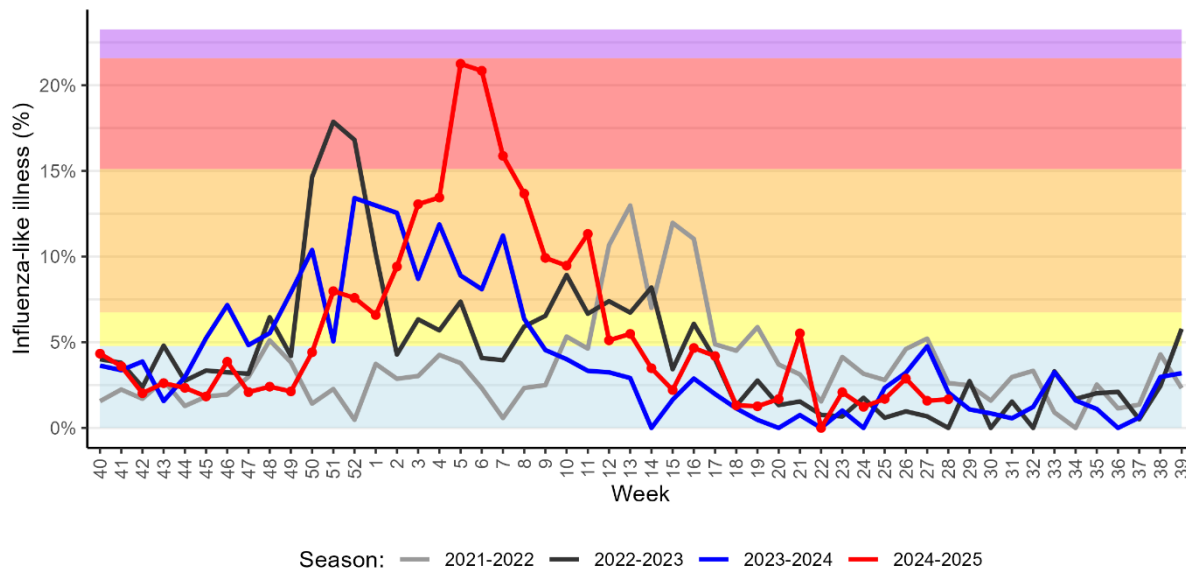


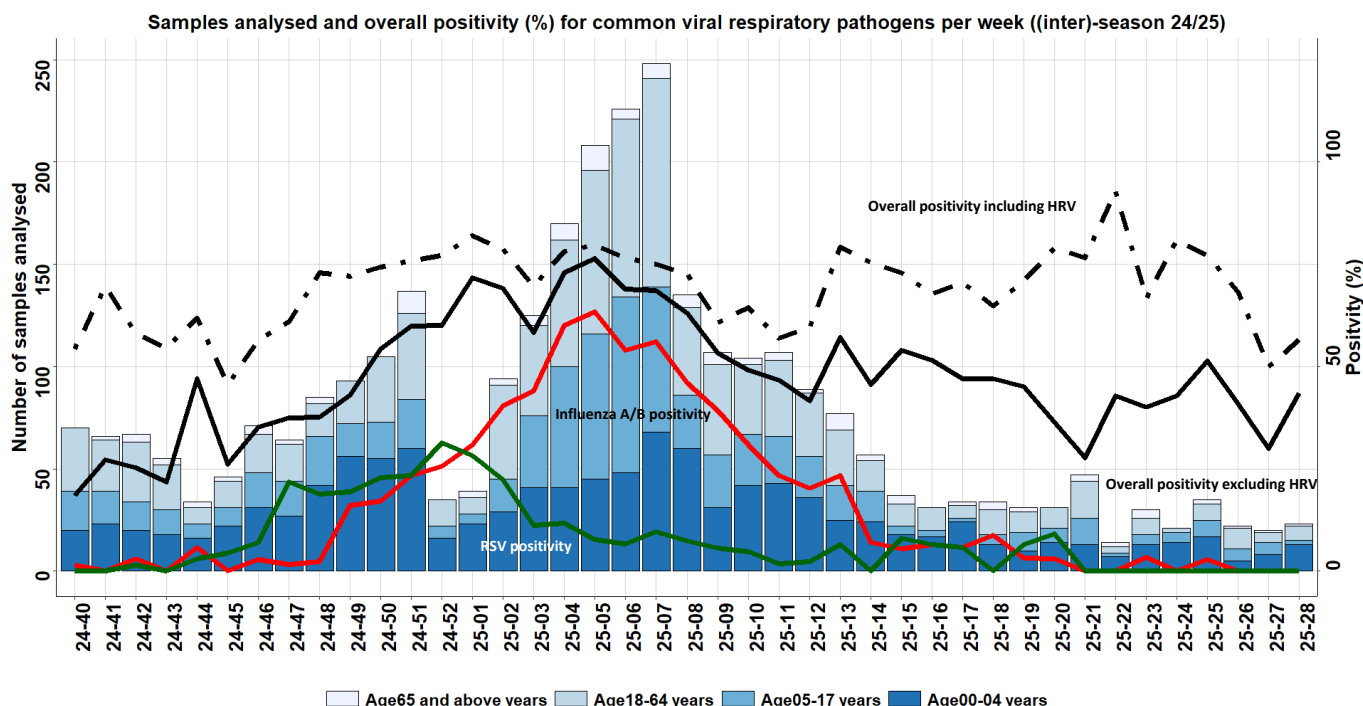
Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

Table 2. Distribution of respiratory viruses detected in the Sentinel Network over the last 8 weeks compared to the previous year.

| Virus | Inter-season 2024/25 | | | | Inter-season 2023/24 | |
|-----------------------------|----------------------|--------|--------|--------|----------------------|--------|
| | Positivity Rate in % | | | | | |
| | W21/22 | W23/24 | W25/26 | W27/28 | W25/26 | W27/28 |
| Human rhinovirus | 52.5 | 36.0 | 38.6 | 22.5 | 28.5 | 48.3 |
| Parainfluenzavirus | 9.8 | 16.0 | 24.6 | 22.5 | 12.5 | 8.3 |
| Adenovirus | 1.6 | 12.0 | 17.5 | 10.0 | 8.9 | 18.3 |
| SARS-CoV-2 | 6.6 | 9.8 | 7.0 | 7.0 | 21.3 | 9.8 |
| Metapneumovirus | 14.8 | 2.0 | 0.0 | 2.5 | 3.6 | 3.3 |
| Influenzavirus A | 0.0 | 2.0 | 1.8 | 0.0 | 0.0 | 0.0 |
| Respiratory syncytial virus | 0.0 | 0.0 | 0.0 | 0.0 | 0.0 | 1.6 |
| Influenzavirus B | 0.0 | 0.0 | 0.0 | 0.0 | 4.9 | 0.0 |

*Co-detection is counted once for each virus detected. Data is displayed in two-week intervals due to low case count during inter-season. All data is provisional, taking into account possible late reporting

Figure 2. Displays number of sentinel samples received weekly by age-group, including overall positivity of the samples: including Human rhinovirus (HRV: dotted line); excluding HRV (black line); influenza (red) and RSV (green); secondary axis corresponds to positivity



Circulation of common viral respiratory pathogens in sentinel network ((inter)-seasons 23/24 and 24/25)

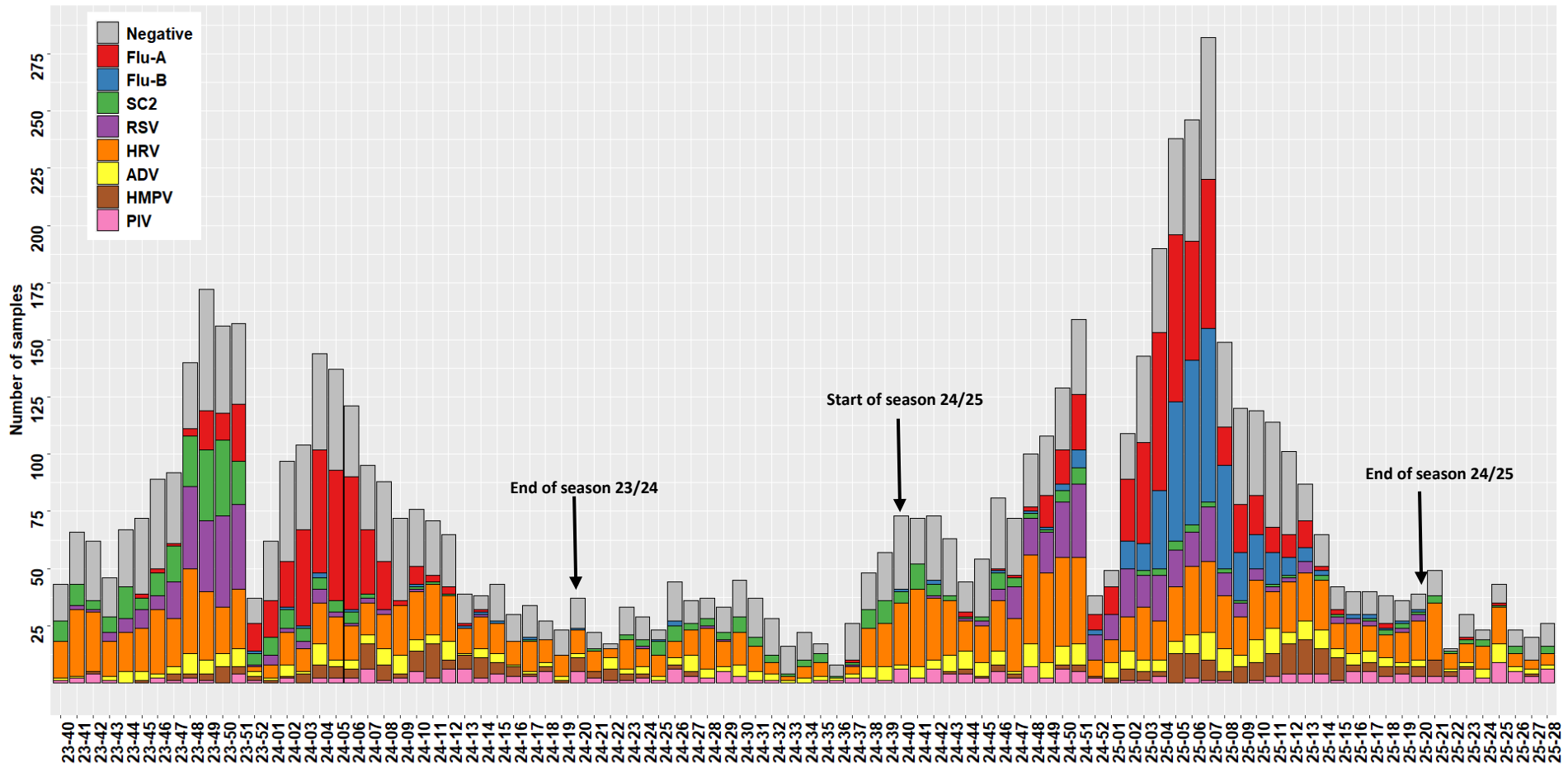


Figure 3. Distribution of respiratory viruses detected within the Sentinel Network by calendar week; results from last week are not yet fully consolidated.
 FLU-A: influenza A; FLU-B: influenza B; PIV: parainfluenza virus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: human rhinovirus; SC2: SARS-CoV-2

SARS-CoV-2 Genomic Surveillance

The LNS receives positive specimens (nasopharyngeal or oropharyngeal swabs analysed by RT-PCR) from the national network of laboratories. A selection of hospital specimens are sequenced, as well as a representative selection of community specimens. Illumina devices are used. Bioinformatic analyses are based on a standardised pipeline and lineage assignment is performed through the Pangolin software (Pangolin: 4.3.1; 1.34 mode USHER).

Sequencing activity

114 samples from 209 cases (54.5%) reported in Luxembourg were sequenced with specimen dates between week 2025/24 and 2025/27. About 20 % (N=22) were hospital samples and the remaining samples were community samples (80%; N=92). We prioritized sequencing the most recent samples and hospital samples. Any low coverage will be addressed in future sequencing runs.

Variant circulation

In recent weeks, several SARS-CoV-2 variants have co-circulated in Luxembourg and worldwide. In the beginning of May, SARS-CoV-2 reported cases increased nationwide with peak at the end of May (2025/23), but have remained stable over the last two weeks. Multiple JN.1 sub-variants such as **NB.1.8.1** and **XFG** have emerged. Both exhibit a growth advantage over other sub-lineages from JN.1 and have been classified as variant under monitoring (VUM) by the World Health Organisation. Over the past 4 weeks, the estimated proportion of **XFG** almost doubled from **15.7%** (weeks 2025/20-23) to **28.1%** (weeks 2025/24-27) and was detected in all age-groups. The proportion of **LP.8.1** (previously dominant) decreased slightly to below **25%** and **NB.1.8.1** remained stable at around **24%**. All circulating variants identified in the selected sample are presented in table 3 and figure 7.

During weeks 2025/20 to 2025/27, 50 (24.6%) samples from hospital laboratories and 153 (75.4%) specimens from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting and variants.

Table 4. Comparison of the three dominant sub-variants by sampling setting (weeks 2025/20-2025/27)

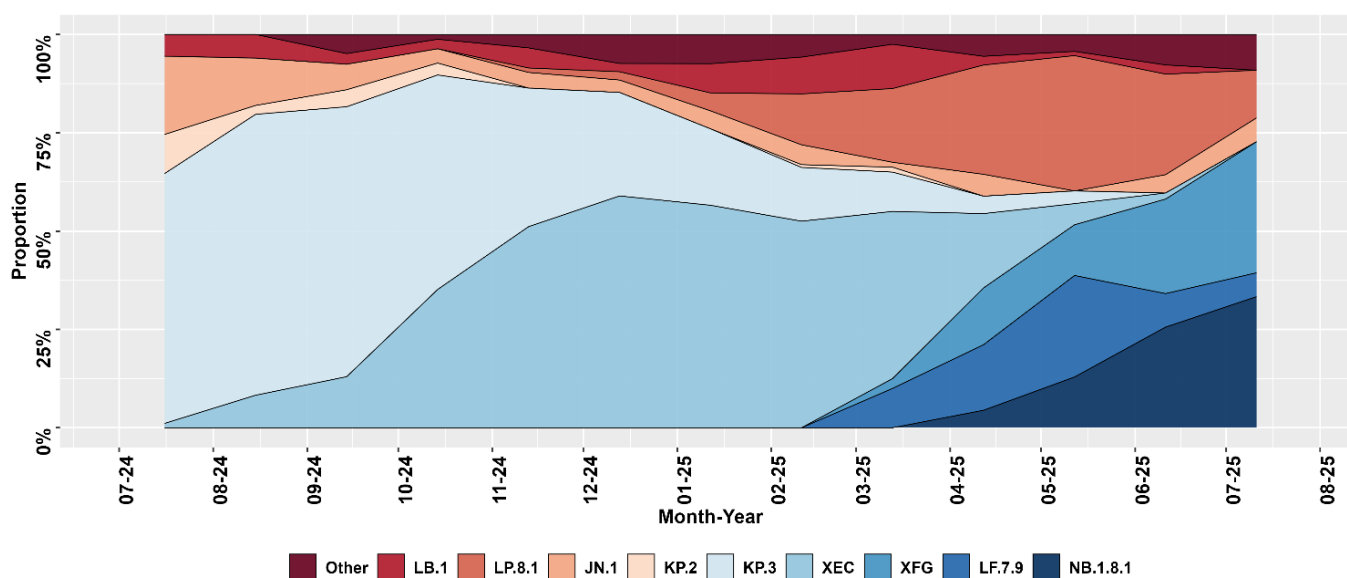
| Lineage | Community | | | Hospital | | |
|-----------------|---------------|---------------|---------------|---------------|---------------|---------------|
| | Women | Men | Total | Women | Men | Total |
| NB.1.8.1 | 32.4% | 29.2% | 34.5% | 27.8% | 58.3% | 40.0% |
| LP.8.1 | 30.9% | 39.6% | 31.0% | 44.4% | 33.3% | 40.0% |
| XFG | 36.8% | 31.3% | 34.5% | 27.8% | 8.3% | 20.0% |
| Total | 100.0% | 100.0% | 100.0% | 100.0% | 100.0% | 100.0% |

Table 3. Distribution of SARS-CoV-2 lineages detected during weeks 2025/20 to 2025/27. Previously reported cases might be updated by retrospective analysis; samples from isolated transmission event have been excluded

*JN.1 excludes sub-variants listed in table. Variants under monitoring in bold letters.

| Lineage | weeks 20-23 (N=89) | | weeks 24-27 (N=114) | |
|-----------------|--------------------|-------------|---------------------|-------------|
| | % | CI % | % | CI % |
| XFG | 15.7 | 8.9 – 25.0 | 28.1 | 20.1 – 37.3 |
| LP.8.1 | 28.1 | 19.1 – 38.6 | 23.7 | 16.2 – 32.6 |
| NB.1.8.1 | 23.6 | 15.2 – 33.8 | 23.7 | 16.2 – 32.6 |
| JN.1* | 3.4 | 0.7 – 9.5 | 7.9 | 3.7 – 14.5 |
| LF.7.9 | 16.9 | 9.8 – 26.3 | 7.9 | 3.7 – 14.5 |
| Other | 7.9 | 3.2 – 15.5 | 7.9 | 3.7 – 14.5 |
| XEC | 4.5 | 1.2 – 11.1 | 0.9 | 0.0 – 4.8 |

Figure 6. Proportion of each variant circulating in Luxembourg over the last 12 months. All displayed variants include descendant lineages, except those specified on the legend



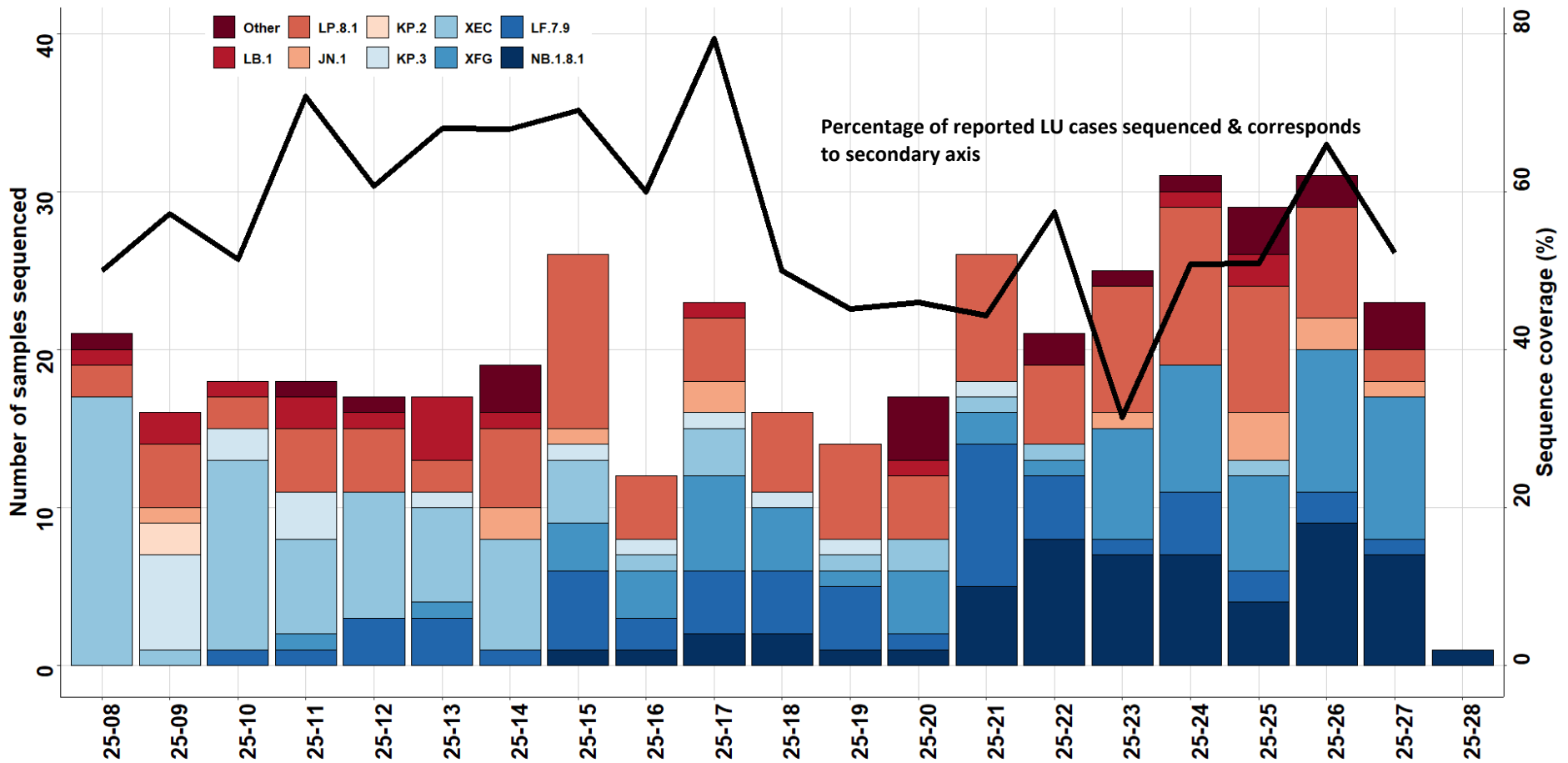


Figure 7. Distribution of lineages since 2025/08 (last 20 weeks).
 All displayed variants include descendant lineages- except those specified on the legend. Other: recent cases recombinant XFI, but diverse.

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