

# Respiratory Viruses in Luxembourg (ReViLux)

## Report – Sentinel Week 46 and Sequencing Update

### Summary

At the end of week **2024/46**, the sentinel network detected a baseline epidemic activity, based on **3.9%** of consultations being associated with influenza-like illness. Among the specimens collected by the sentinel network over the last week, the percentage of positive tests for **Human rhinovirus** was **29.2%**, **9.9%** for **SARS-CoV-2** and **7.7%** for **Adenovirus**.

During the week **2024/46**, the network detected an increase in **RSV activity** with a positivity of **7.7%** and low circulation of Influenza with a positivity of **1.4%** for **Influenza A** and **Influenza B** in the sentinel network.

In total, this season (24/25) 409 samples were tested with 7 Influenza positive samples (4 Influenza B and 3 Influenza A). Two Influenza A samples have been subtyped as A(H1) virus. Among those RSV subtyped (N=4), there was a mixture of RSV- A (75%) and RSV-B (25%).

Regarding SARS-CoV-2 genomic surveillance in Luxembourg, starting from week 48 of 2023, the most common variant seen was JN.1, a sub-variant of BA.2.86 designated as a variant of concern (VOI). Since beginning of April 2024, several sub-variants of JN.1 have been circulating in Luxembourg. The estimated distribution for KP.3 was 56.4% (95%CI: 46.6-65.8%), and 35.4% (95%CI: 26.6 -45.2%) for XEC during the weeks 2024/41-2024/43.

### Currently circulating variants

Sub-variant	Genetic features	First detected in Luxembourg	Estimated prevalence (2024/41-43)
JN.1*	BA.2.86 + S:L455S	25.08.2023	5.5%
KP.3	JN.1 + S:F456L, S:Q493E, S:V1104L	03.04.2024	56.4%
KP.2	JN.1 + S:R346T, S:F456L, S:V1104L	08.04.2024	1.8%
JN.1.7	JN.1 + S:T572I, S:E1150D	10.01.2024	0.0%
JN.1.18	JN.1 + S:R346T	10.01.2024	0.0%
LB.1	JN.1+ S:S31-, S:Q183H, S:R346T, S:F456L	22.05.2024	0.9%
XEC	JN.1 + S:T22N, S:F59S, S:F456L, S:Q493E, S:V1104L	19.07.2024	35.4%

*\*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 usually called inter-season.

### Clinical results

Last week (**end of week 2024/46**), **3.9%** of the consultations were reported as ILI, representing a baseline epidemic activity for Luxembourg, according to ECDC and the Moving Epidemic Method. Over the past few weeks baseline ILI rates have been observed, but latest rate shows increasing trend. 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	%	
2024/43	22	14.38	4	2.61	153
2024/44	29	16.96	4	2.34	171
2024/45	19	8.64	5	2.27	220
2024/46	34	13.33	10	3.92	255

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

### Laboratory results

Over the last week, the most frequently detected viruses (according to positivity rates) were **Human rhinovirus (29.2%)**, followed by **SARS-CoV-2 (9.9%)** and **Adenovirus (7.7%)**. In week 2024/46, positivity for **RSV** was **7.7%** and **1.4%** for **Influenza A** and **B** in the sentinel network. RSV activity increased from 4.3 (2024/45) to 7.7% (week 2024/46), but not all samples have

been consolidated yet. So far this season (24/25), nine RSV cases have been detected, including three RSV-A and one RSV-B. All cases were between 1 to 3 years (median 1 year).

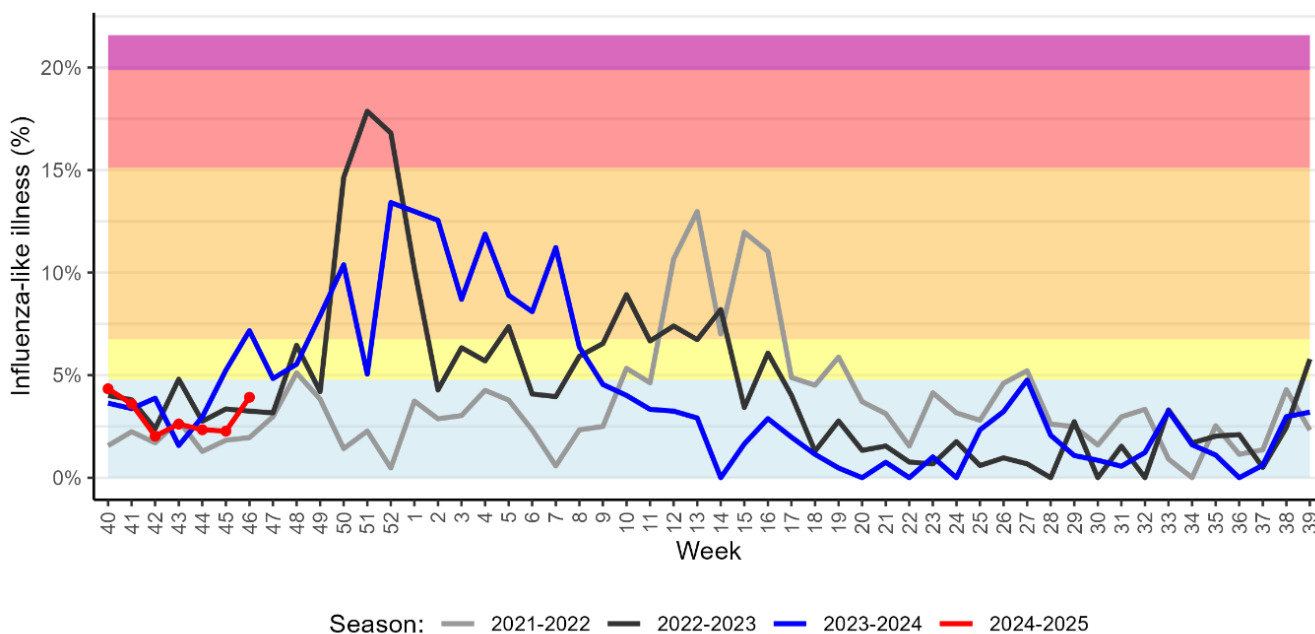


Figure 1. Percentage of patients with influenza-like illness over the last three seasons  
Background colours according to intensity of circulation: baseline, low, medium, high, very high.

In total, 409 sentinel samples have been analysed with nearly 60% of samples belonging to age-group below 18 years (Figure 2) and with 52 % of female cases. Over the last 4 weeks, Human rhinovirus was detected in all age-groups whereas Adenovirus and Parainfluenza viruses have been primarily detected in children under the age of 5. In the sentinel network, nearly 60% of SARS-CoV-2 cases (N=12) were detected in age-group 18 to 65 years and 25% in patients above 65 years.

All Influenza B cases (N=4) were identified in children and teenagers. Over the last 4 weeks, approximately 80% (N=24) of all co-infections (N=30) were detected primarily in children below 5 years. The most commonly identified combination was Adenovirus with Human rhinovirus.

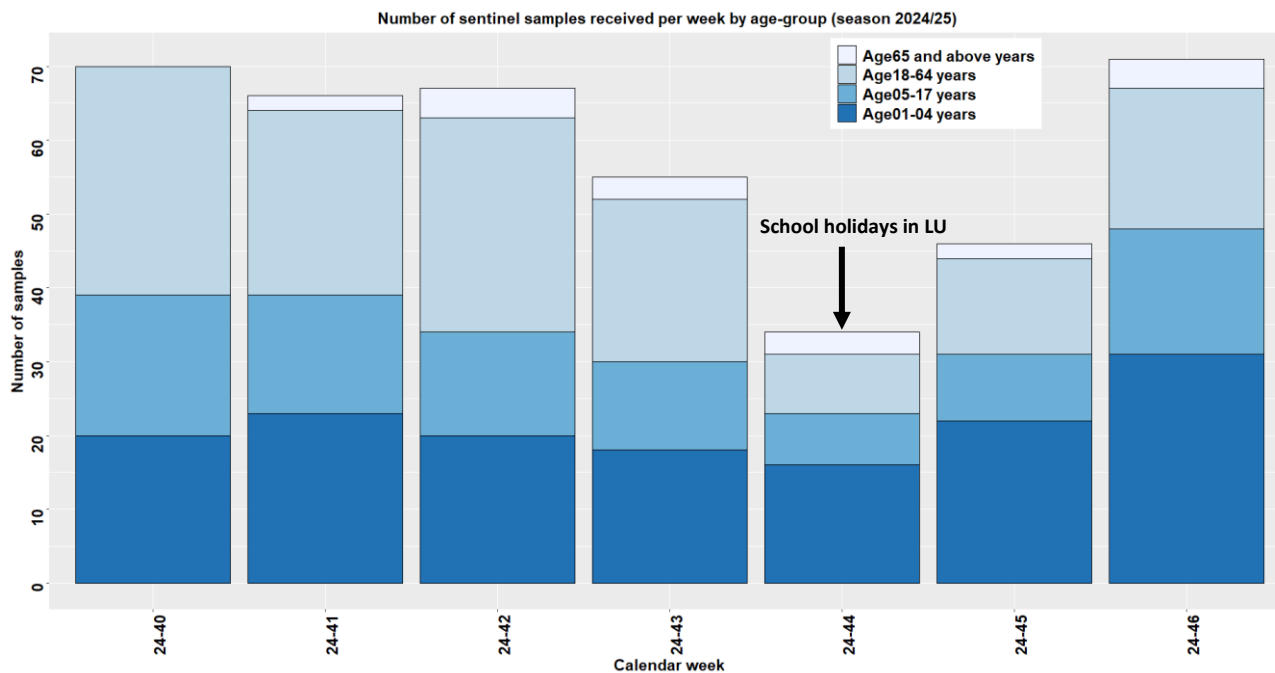
An overview of the circulating viral pathogens during the current and previous inter- season is displayed in Figure 3 and Table 2.

Table 2. Distribution of respiratory viruses detected within the Sentinel Network over the last 4 weeks compared to previous year.

Virus	Season 2024/25					Season 2023/24	
	Positivity Rate in %					W46	Total N (%)
	W43	W44	W45	W46	Total N (%)		
Human rhinovirus	46.2	39.4	34.8	29.2	160 (40.2)	32.9	572 (24.9)
SARS-CoV-2	3.6	2.9	4.3	9.9	33 (8.1)	11.6	227 (9.7)
Adenovirus	13.5	24.2	13.0	7.7	37 (9.3)	2.4	125 (5.4)
Parainfluenzavirus	7.7	12.1	4.3	7.7	29 (7.3)	2.4	77 (3.4)
Respiratory syncytial virus	0.0	3.0	4.3	7.7	9 (2.2)	7.1	212 (9.2)
Metapneumovirus	1.9	6.1	2.2	4.6	7 (1.8)	0.0	125 (5.4)
Influenzavirus A	0.0	5.9	0.0	1.4	3 (0.7)	2.3	388 (16.5)
Influenzavirus B	0.0	0.0	0.0	1.4	4 (1.0)	0.0	12 (0.5)

\*Co-detection counted once for each virus detected. All data is provisional as possibility of reporting delays.

Figure 2. Displays number of sentinel samples received per week by age-group. Data for week 2024/45 not yet completely consolidated



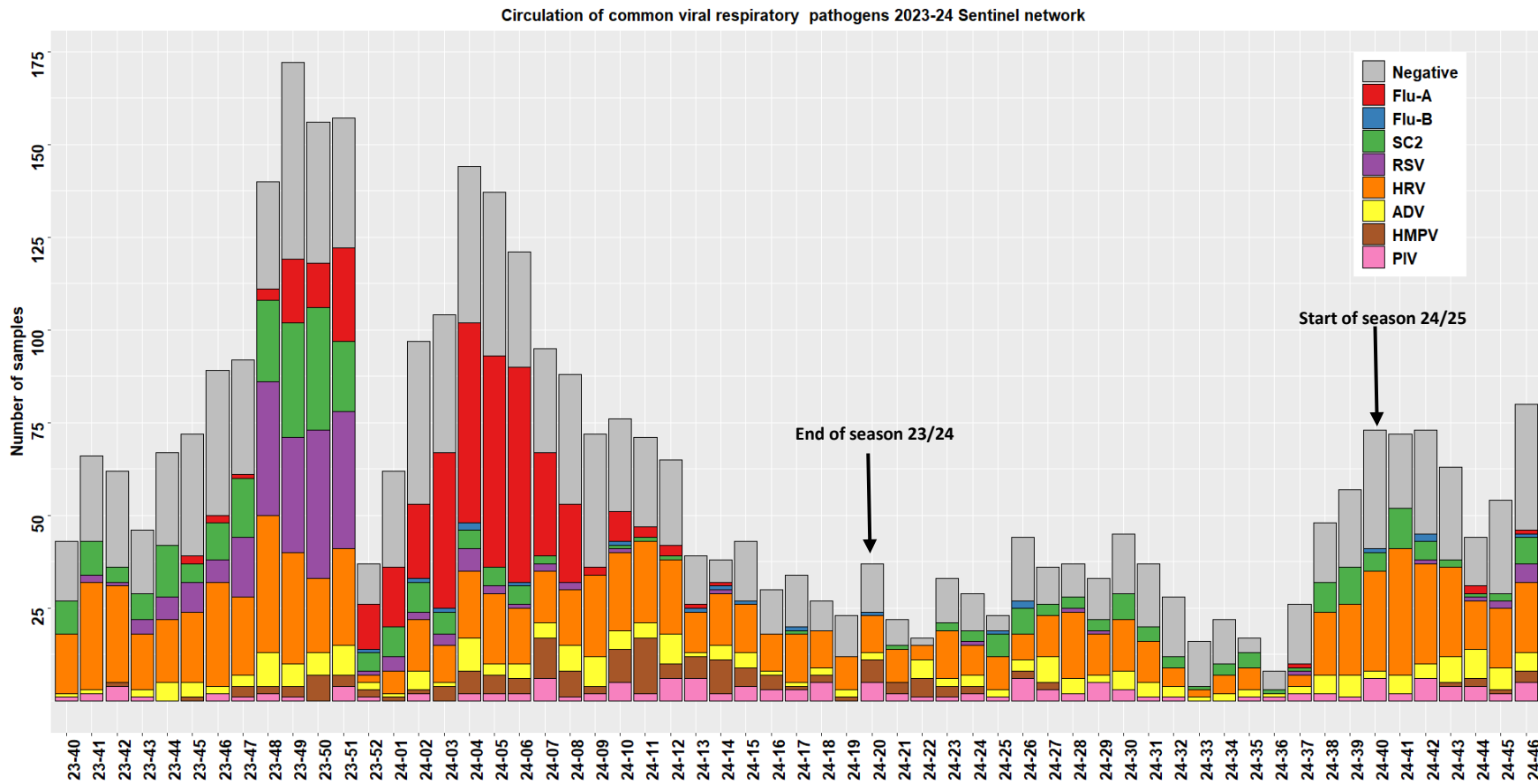


Figure 3. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not yet consolidated.  
 FLU-A: influenza A; FLU-B: influenza B; PIV: parainfluenzavirus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: human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

## SARS-CoV-2 Genomic Surveillance

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 (4.3.1, pango-data 1.30, mode UShER).

### Sequencing activity

110 samples from 793 cases (13.9%) reported in Luxembourg were sequenced with specimen dates between week 2024/41 and 2024/43. Approximately 54.6% were hospital samples and the remaining samples were community samples.

### Variant circulation

For samples sequenced between 7<sup>th</sup> and 27<sup>th</sup> of October 2024 (2024/41-2024/43), the estimated distribution was **56.4%** (95%CI: 46.6-65.8%) for **KP.3** and **35.4%** for **XEC** (95%CI: 26.6-45.2%), which is a recombinant of JN.1 sub-variants.

The sub-variants that are currently circulating show many genetic differences compared to previous circulating Omicron variants, so several sub-variants with key mutations are closely monitored.

An overview of the variants and lineages circulating is displayed in Figure 5, and further details are shown in Table 3. The history of the circulation of each variant since January 2021 is displayed in Figure 4.

*Table 3. Distribution of SARS-CoV-2 lineages detected during weeks 2024/38 to 2024/43. Previously reported cases might be updated by retrospective analysis.*

Lineage	weeks 38-40		weeks 41-43	
	%	CI %	%	CI %
<b>KP.3</b>	<b>59.8</b>	<b>50.1 – 69.0</b>	<b>56.4</b>	<b>46.6 – 65.8</b>
XEC	28.6	20.4 – 37.8	35.4	26.6 – 45.2
JN.1	1.8	0.2 – 6.3	5.5	2.0 – 11.5
KP.2	3.6	0.9 – 8.9	1.8	0.2 – 6.4
LB.1	4.5	1.5 – 10.1	0.9	0.9 – 5.0
Other	1.8	0.2 – 6.3	0.0	

\*JN.1 excludes sub-lineages listed in table

During weeks 2024/41 to 2024/44, 54 (45.0%) samples from hospital laboratories and 66 (55.0%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting and variants.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	Total	Women	Men	Total
KP.3	63.3%	66.7%	<b>65.0%</b>	56.5%	55.6%	<b>56.0%</b>
XEC	36.7%	33.3%	<b>35.0%</b>	43.5%	44.4%	<b>44.0%</b>
<b>Total</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>	<b>100.0%</b>

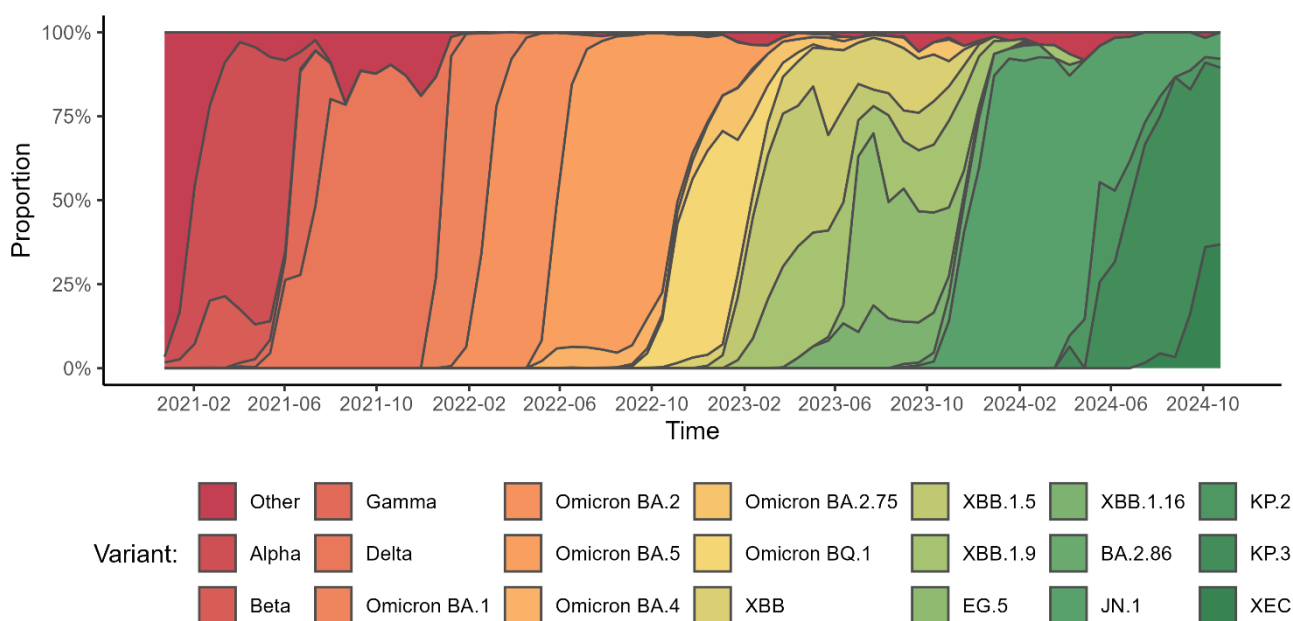


Figure 4. Proportion of each variant circulating in Luxembourg since January 2021. All displayed variants include descendant lineages, except those specified on the legend

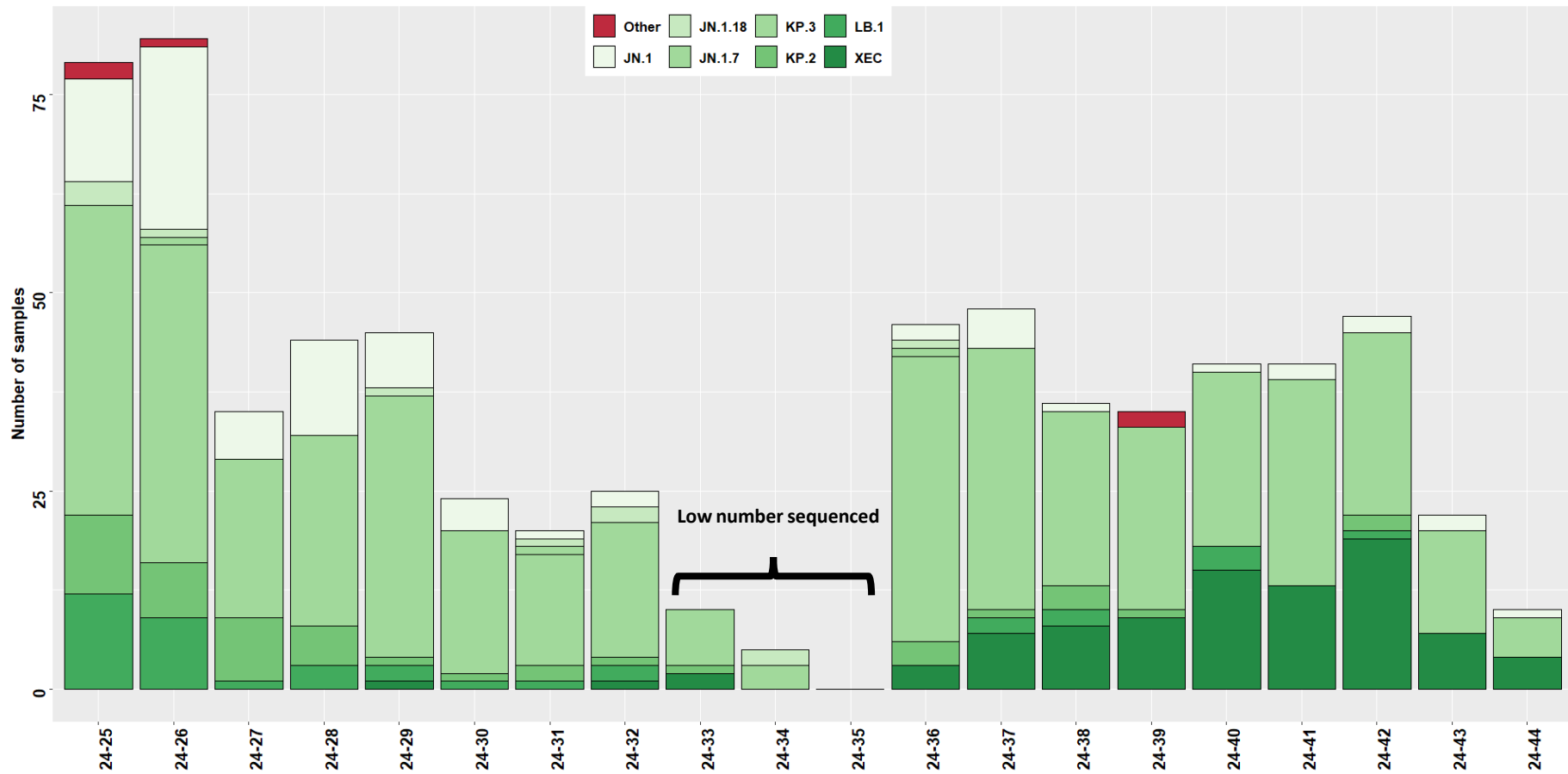


Figure 5. Distribution of lineages since 2024/25 (last 20 weeks).

\* All displayed variants include descendant lineages, except those specified on the legend. Other in week “2024-39”: recombinant lineage of LB.1 and KP.3

## References

European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 18 November 2024, from <https://www.ecdc.europa.eu/en/covid-19/variants-concern>

European Centre for Disease Prevention and Control. Communicable Disease Threats Report Week  
<https://www.ecdc.europa.eu/en/publications-data/communicable-disease-threats-report-9-15-november-2024-week-46>

GISAID. EpiCoV – Pandemic coronavirus causing COVID-19. Retrieved 18 October 2024, from <https://www.gisaid.org>

GitHub - cov-lineages/pangolin: Software package for assigning SARS-CoV-2 genome sequences to global lineages. (2024). Retrieved 18 November 2024, from <https://github.com/cov-lineages/pangolin>

Hadfield J., Megill C., Bell S., Huddleston J., Potter B., Callender C. et al. (2018). Nextstrain: real-time tracking of pathogen evolution. *Bioinformatics*, 34(23), 4121-4123. doi: 10.1093/bioinformatics/bty407

Rambaut A., Holmes E., O’Toole Á., Hill V., McCrone J., Ruis C. et al. (2020). A dynamic nomenclature proposal for SARS-CoV-2 lineages to assist genomic epidemiology. *Nature Microbiology*, 5(11), 1403-1407. doi: 10.1038/s41564-020-0770-5

World Health Organization. Tracking sars-COV-2 variants Retrieved 18 November 2024, from <https://www.who.int/activities/tracking-SARS-CoV-2-variants>