

Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 24 and Sequencing Update

Summary

At the end of week 2024/24, the sentinel network detected a baseline epidemic activity, based on none of the consultations being associated with influenza-like illness. Among the specimens collected by the sentinel network over the last two weeks, the percentage of positive tests for Human rhinovirus was 39.2% followed by 9.8% for Adenovirus and 9.8% for Metapneumovirus. SARS-CoV-2 circulation increased from 2.9% in weeks 21/22 to 9.8 % in weeks 23/24. Low circulation of RSV was detected over the last two weeks.

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 week 2024/20, several sub-variants of JN.1 have been circulating in Luxembourg.

The estimated distribution for JN.1 was 34.2% (95%CI: 23.7-44.6%), KP.2 was 30.4% (95%CI: 20.5-41.8%), and 29.1% (95%CI: 19.4-40.4%) for KP.3 during the weeks 2024/21-2024/23.

Currently circulating variants under monitoring

KP.2 and **KP.3** are descendants of SARS-CoV-2 Omicron variant JN.1 with particular mutations in the spike protein- in this case positions 346 and 456. Both variant (especially KP.3) proportions have increased over the past few weeks rapidly. The estimated proportion of KP.3 increased from 9.3% to nearly 30% over the last three weeks in Luxembourg. **JN.1.18** and **JN.1.7** are also assigned as variants under monitoring. In Luxembourg only low proportions have been detected.

Currently, there are no indications that these sub-variants would be more likely to cause severe illness compared to previous sub-variants.

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 (2024/24), no consultation was 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. 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.

Laboratory results

Over the last two weeks, the most frequently detected viruses (according to positivity rates) were Human rhinovirus (39.2%), followed by Adenovirus (9.8%) and Metapneumovirus (9.8%). This season positivity rates of Influenza A peaked in week 2024/06 (52.7%). Since week 2024/14 and 2024/20, no new cases of Influenza A and B have been detected, respectively.

Over the past few weeks, low circulation of RSV were detected. Overall, this season/ inter-season, the highest impact of RSV was seen among the 1-4 years age group (Figure3). To date, 153 RSV detections were further subtyped as either RSV A (N=132, 85.7%) or RSV B (N=22, 14.3%).

SARS-CoV-2 positivity has decreased since the start of 2024, from 14.1% in week 2024/01 to 2.4% in week 2024/07. Over the last two weeks, SARS-CoV-2 positivity increased from 2.9% (weeks 21/22) to 9.3% (weeks 23/24) within the sentinel network.

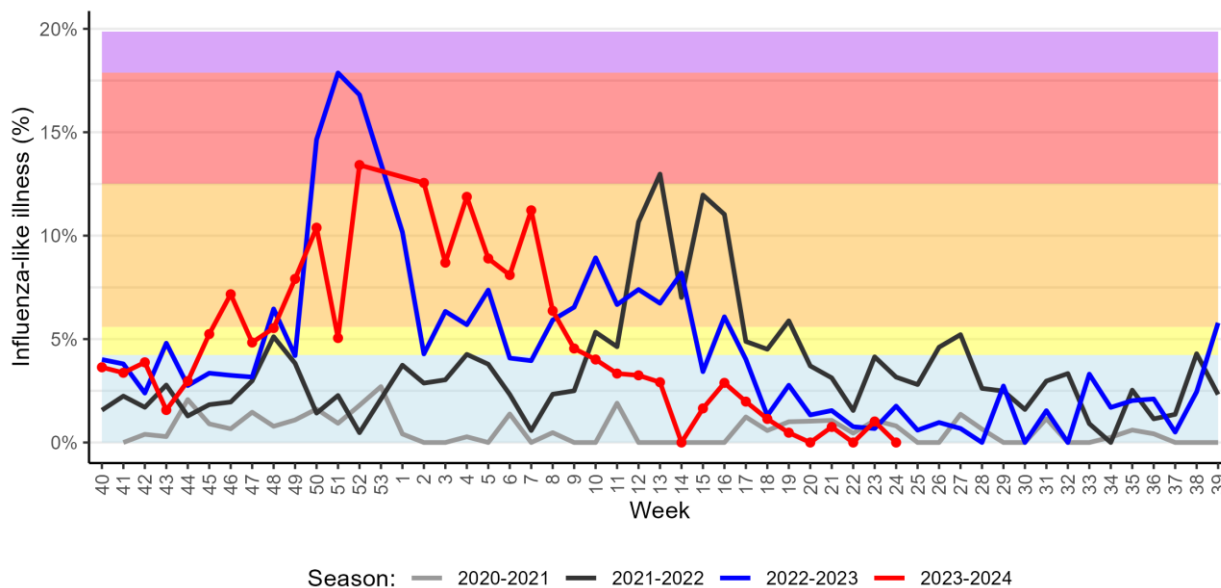


Figure 1. Percentage of patients with influenza-like illness over the last three seasons
Background colours according to intensity of circulation: baseline, low, medium, high, very high. Data from 2024/01 not presented as low return

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2024/21	14	10.53	1	0.75	133
2024/22	29	15.10	0	0.00	192
2024/23	29	14.72	2	1.02	197
2024/24	34	17.99	0	0.00	189

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

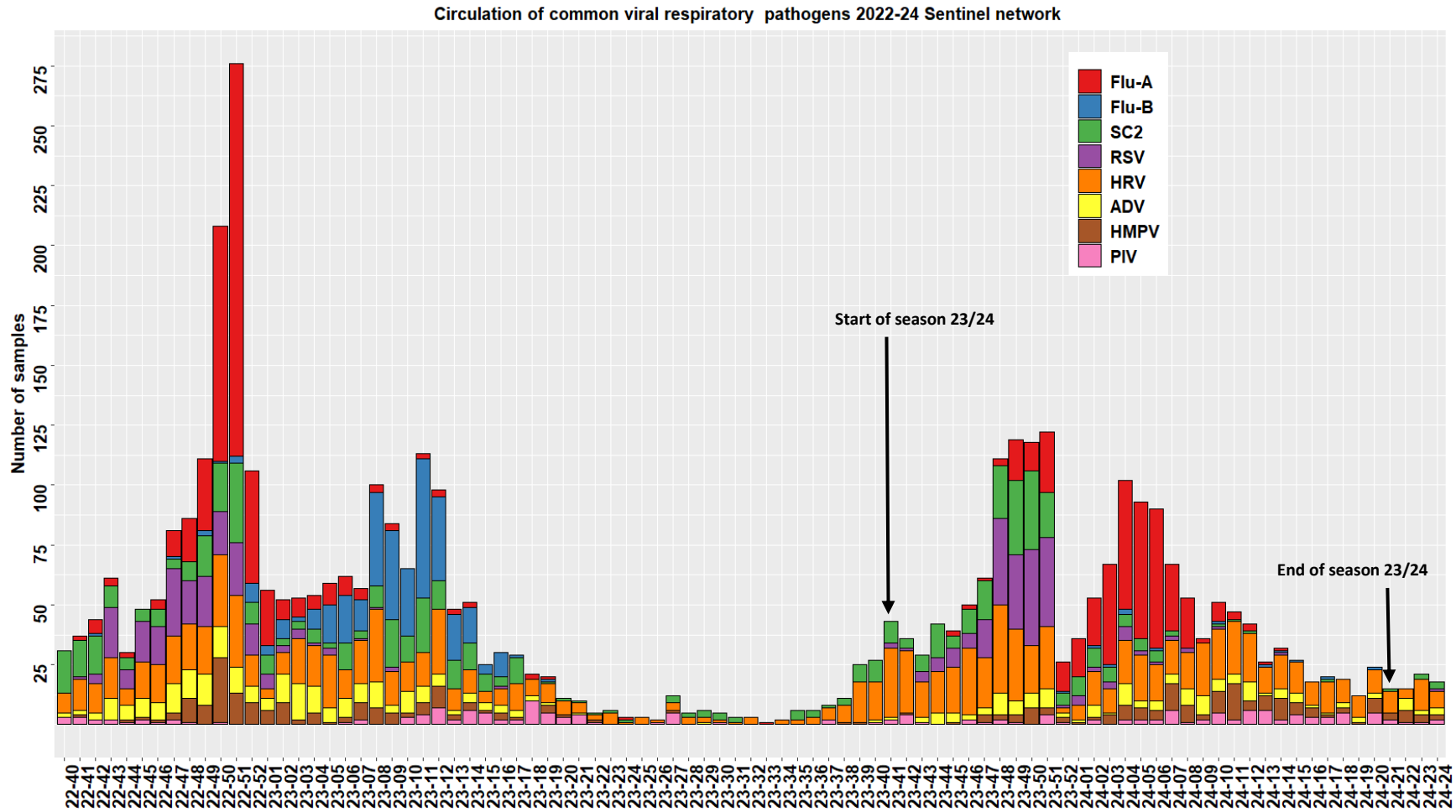


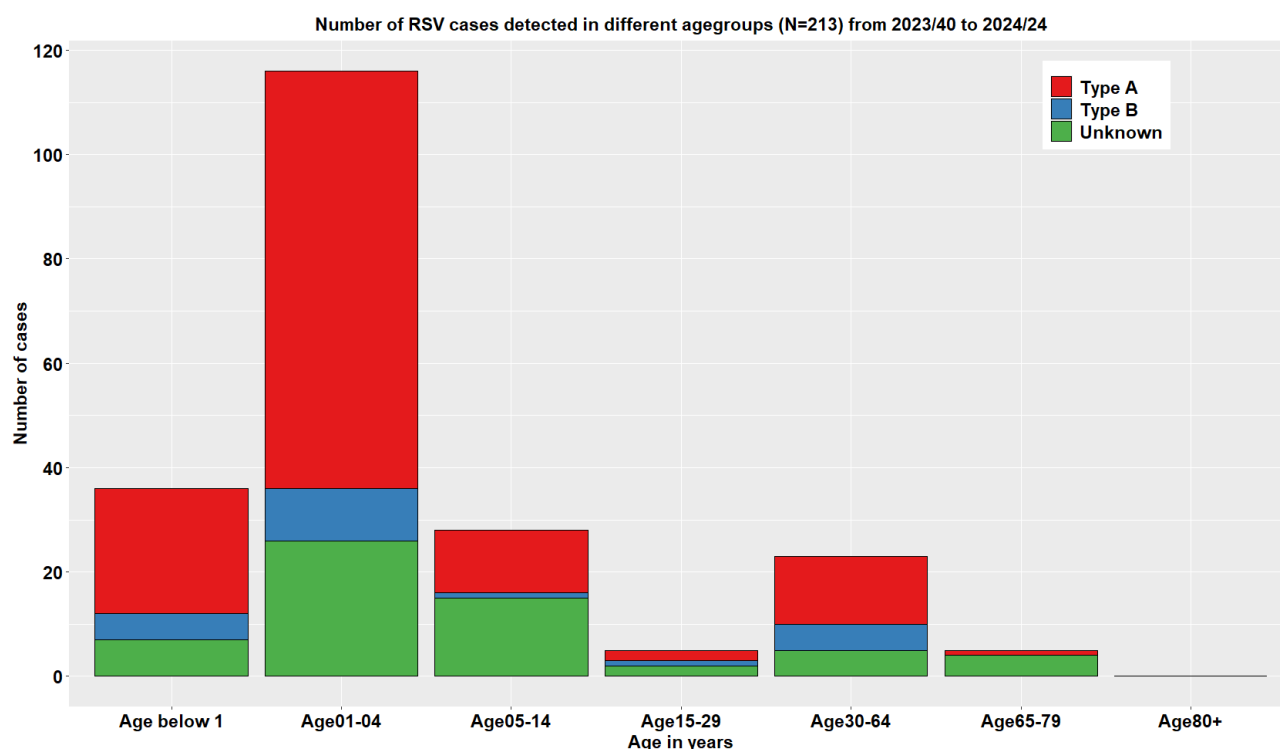
Figure 2. Distribution of respiratory viruses detected within the Sentinel Network, by calendar week. Results from last weeks are not yet consolidated.
 FLU-A: influenza A; FLU-B: influenza B; PIV: parainfluenzavirus; RSV: respiratory syncytial virus; ADV: adenovirus; MPV: metapneumovirus; HRV: human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

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

Virus	Season 2023/24		Season 2022/23
	Positivity Rate in %		
	w21/22	w23/24	w23/24
Human rhinovirus	38.2	39.2	25.0
Adenovirus	14.7	9.8	0.0
Metapneumovirus	23.5	9.8	0.0
SARS-CoV-2	2.9	9.3	7.4
Parainfluenzavirus	8.8	5.9	0.0
Respiratory syncytial virus	0.0	2.0	0.0
Influenzavirus B	0.0	0.0	0.0
Influenzavirus A	0.0	0.0	3.7

*Co-detection counted once for each virus detected.

Figure 3. Displays RSV cases according to different age groups with highest impact among the 1-4 years old.



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 and Nanopore 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 1.27, mode USHER). In order to allow easier visualisation, WHO and Nextstrain categorisations are also used.

Sequencing activity

79 samples from 154 cases (51.3%) reported in Luxembourg were sequenced with specimen dates between week 2024/21 and 2024/23. Approximately 17.7% were hospital samples and the remaining samples were community samples. Sequencing data probably does not fully represent virus circulation within the population.

Variant circulation

For samples sequenced between 13th May and 9th of June 2024 (2024/21-2024/23), the estimated distribution was 34.2% (95%CI: 23.7-44.6%) for JN.1, 30.4% for KP.2 (95%CI: 20.5-41.8%) and 29.1% for KP.3 (95%CI: 19.4-40.4%). Since week 2024/17 the proportions of KP.2 and KP.3 have increased steadily.

An overview of the variants and lineages circulating over the past 20 weeks 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 2024/18 to 2024/23. Previously reported cases might be updated by retrospective analysis.

Lineage	weeks 18-20		weeks 21-23	
	%	CI %	%	CI %
JN.1*	50.0	36.7 – 63.3	34.2	23.7 - 44.6
KP.2	27.8	16.5 – 41.6	30.4	20.5 – 41.8
KP.3	9.3	3.1 – 20.3	29.1	19.4 – 40.4
JN.1.18	1.9	0.0 – 9.9	3.8	0.7 – 10.7
JN.1.7	3.7	0.0 – 12.8	2.5	0.3 – 8.9
Other	7.4	2.1 - 17.9	0	0.0 - 0.0

*JN.1 excludes sub-lineages listed in table

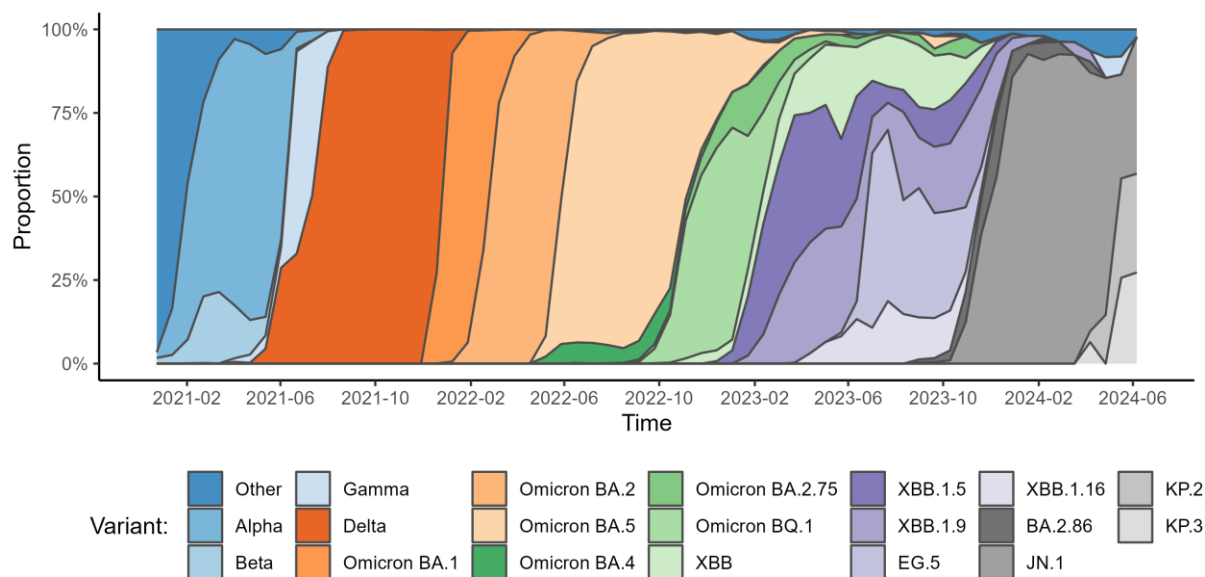


Figure 4. Proportion of each variant circulating in Luxembourg since January 2021.

All displayed variants include descendant lineages, except those specified on the legend. For example, XBB does not include XBB.1.5, XBB.1.16, EG.5 and XBB.1.9

Clinical and epidemiological factors

Over the past 4 weeks (2024/20-2024/23), 17 (16.3%) samples from hospital laboratories and 87 (83.7%) samples from private laboratories/ sentinel practitioners were sequenced. Table 4 compares sampling setting of JN.1 and KP.2/KP.3.

Table 4. Comparison of lineage distribution by sampling setting.

Lineage	Community			Hospital		
	Women	Men	Total	Women	Men	Total
JN.1	32.7%	46.7%	37.8%	33.3%	50.0%	40.0%
KP.2/3	67.3%	53.3%	62.2%	66.7%	50.0%	60.0%
Total	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%

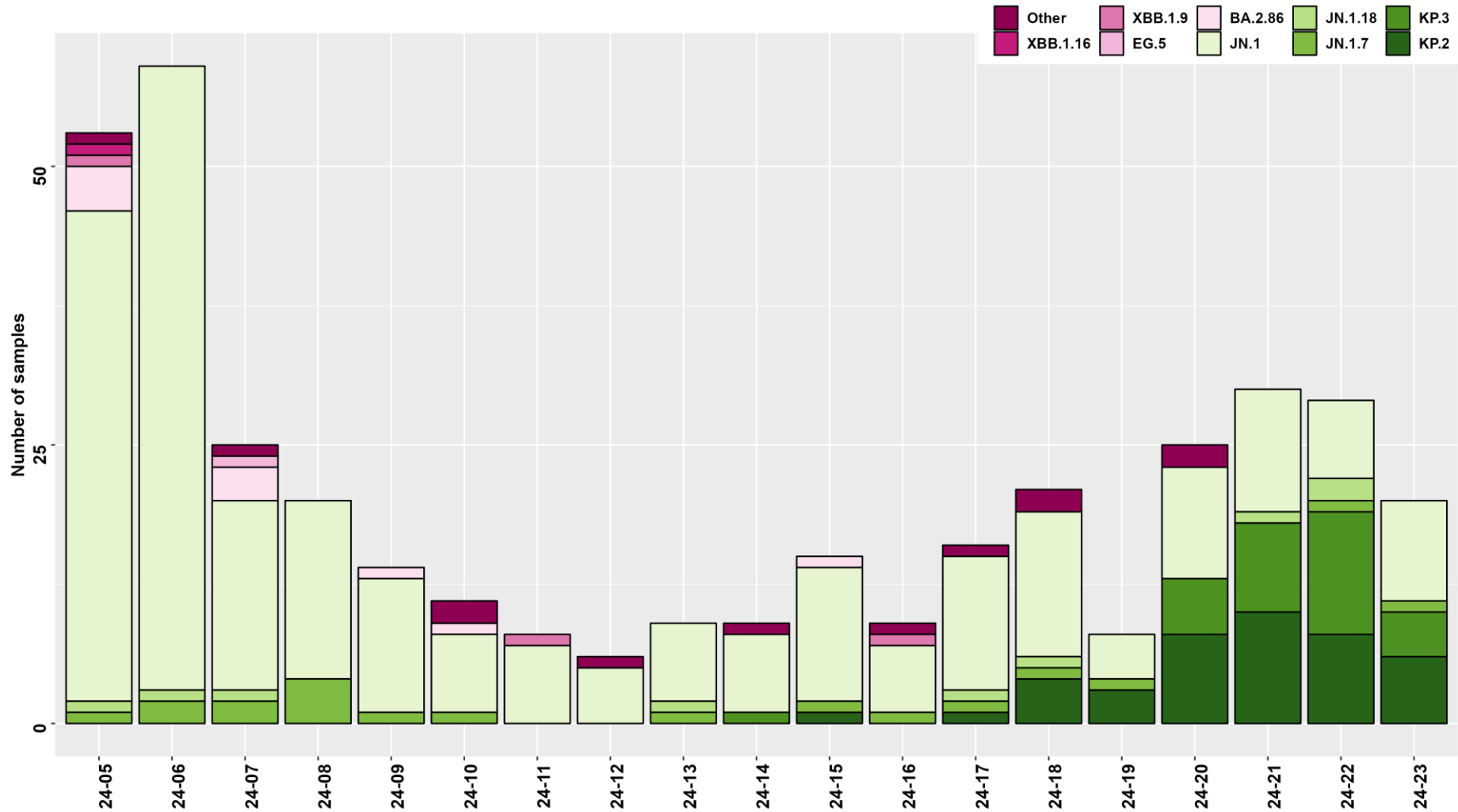


Figure 5. Distribution of lineages since 2024/05 (last 20 weeks).
 * All displayed variants include descendant lineages, except those specified on the legend.

References

European Centre for Disease Prevention and Control. SARS-CoV-2 variants of concern. Retrieved 19 June 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-8-14-june-2024-week-24>

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

GitHub - cov-lineages/pangolin: Software package for assigning SARS-CoV-2 genome sequences to global lineages. (2024). Retrieved 19 June 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 19 June 2024, from <https://www.who.int/activities/tracking-SARS-CoV-2-variants>