

Respiratory Viruses in Luxembourg (ReViLux)

Report – Sentinel Week 50 and Sequencing Update

Summary

In week **2025/50**, consultations for acute respiratory infections (**ARI**) remained above **10%**, while influenza-like illness activity (**ILI**) remained within ECDC-defined baseline levels (**4.6%**).

During week 2025/50, 78 sentinel samples were analysed, with respiratory viruses detected in 70.5% of cases; **RSV (28.6%)** was the most prevalent, followed by **human rhinovirus (24.7%)** and **influenza A (17.9%)**. RSV activity increased significantly compared to previous weeks, and since the start of the season 64 RSV cases have been confirmed, predominantly **RSV-A (63.6%)**. Influenza A has remained above 15% for two weeks, mainly driven by **A(H3)**, accounting for **75%** of the subtyped cases this season.

Recent SARS-CoV-2 genomic surveillance in Luxembourg indicates ongoing diversification of circulating lineages. **XFG** remained predominant, accounting for 57.6% of sequences in weeks 2025/42-45 and **40.6% in weeks 2025/46-49**, with its sub-lineage **XFG.3** representing 28.0% and **23.9%** in the same periods. During weeks 2025/46-49, **NB.1.8.1** increased from 13.1% to **23.9%**, while **BA.3.2.2** emerged to **6.5%**, highlighting the importance of ongoing monitoring.

Variants under monitoring (BA.3.2)

The World health organisation recently classified BA.3.2 as a variant under monitoring due to its genetic difference and potential implication for immune escape. BA.3.2 differs from BA.3 in the Spike protein by 53 mutation and has further diversified into two sub-lineages (BA.3.2.1 and BA.3.2.2).

BA.3.2 was firstly detected in end of November 2024, initially occurring sporadically. More recently, the proportion of BA.3.2.2 appears to increase globally. In Luxembourg, BA.3.2.2 was first identified in the beginning of November 2025, primarily in community samples and patients below 50 years. Although BA.3.2 exhibits antigenic deviation from previous variants and the current vaccine strain, there is currently no evidence to suggest that BA.3.2 infections are associated with increased disease severity or reduced vaccine effectiveness. Ongoing monitoring is essential to assess its impact.

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

During weeks 2025/47-50, consultations for acute respiratory infections (ARI) remained above 10%. In contrast, influenza-like illness (ILI) remained below 5% and within baseline levels according to ECDC and the Moving Epidemic Method, although detections of influenza A continued to increase.

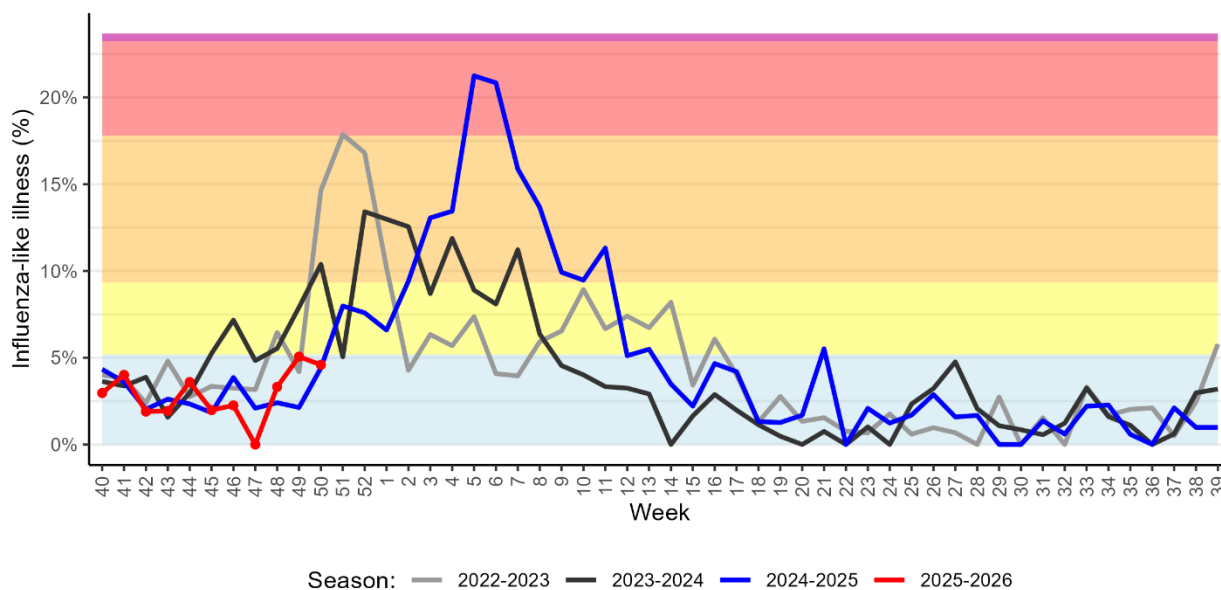
Similar patterns have been observed in previous seasons. Historical trends in ILI consultations are presented in figure 2, and a detailed summary of the ARI and ILI case counts for the past four weeks is provided in table 1.

Table 1. Syndromic surveillance over the last 4 weeks

Week	ARI		ILI		Total consultations
	N	%	N	%	
2025/47	18	16.51	0	0.00	109
2025/48	43	15.87	9	3.32	271
2025/49	41	17.30	12	5.06	237
2025/50	42	13.77	14	4.59	305

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

Figure 1. Percentage of patients with Influenza-like illness over the last three seasons and 2025-2026 (red); Background colours according to intensity of circulation: baseline, low, medium, high, very high.



Laboratory results

During calendar week 2025/50, the LNS received 78 samples. Of these, 39.7% (N=31) were from adults aged 18 to 64 years, followed closely by 38.5% (N=30) from children under 5 years. Children aged 5 to 17 years accounted for 21.8% (N=17), while no samples were received from patients aged ≥ 65 years. Overall, 38.5% (N=30) were female and 61.5% (N=48) were male patients.

Respiratory viruses were detected in 55 (70.5%) of the 78 sentinel samples. The predominant pathogen was **RSV (28.6%)**, followed by **human rhinovirus (24.7%)** and **influenza A (17.9%)**. Compared to the previous two weeks, influenza A activity increased slightly from 16.9% to 17.9%, whereas RSV activity increased markedly from 18.1% to 28.6%, surpassing human rhinovirus as the dominant pathogen for the first time this season.

Since the beginning of the season, 64 cases of RSV have been confirmed. Subtyping identified 35 RSV-A (63.6%) and 20 (36.4%) RSV- B cases. Approximately 38% of RSV infections occurred in children under 2 years of age, 23% in children aged 2 to 4 years, and 19% in adults aged 18 to 64 years.

Influenza A activity has remained above 15% for two consecutive weeks, driven primarily by A(H3). Among 43 detected cases this season, 75% (N=27) were subtyped as A(H3) and 25% (N=9) as A(H1)pdm09; subtyping is still pending for 7 cases. Slightly less than 50% of influenza A cases occurred in adults aged 18 to 64 years, followed by 37% in children aged 5 to 17 years.

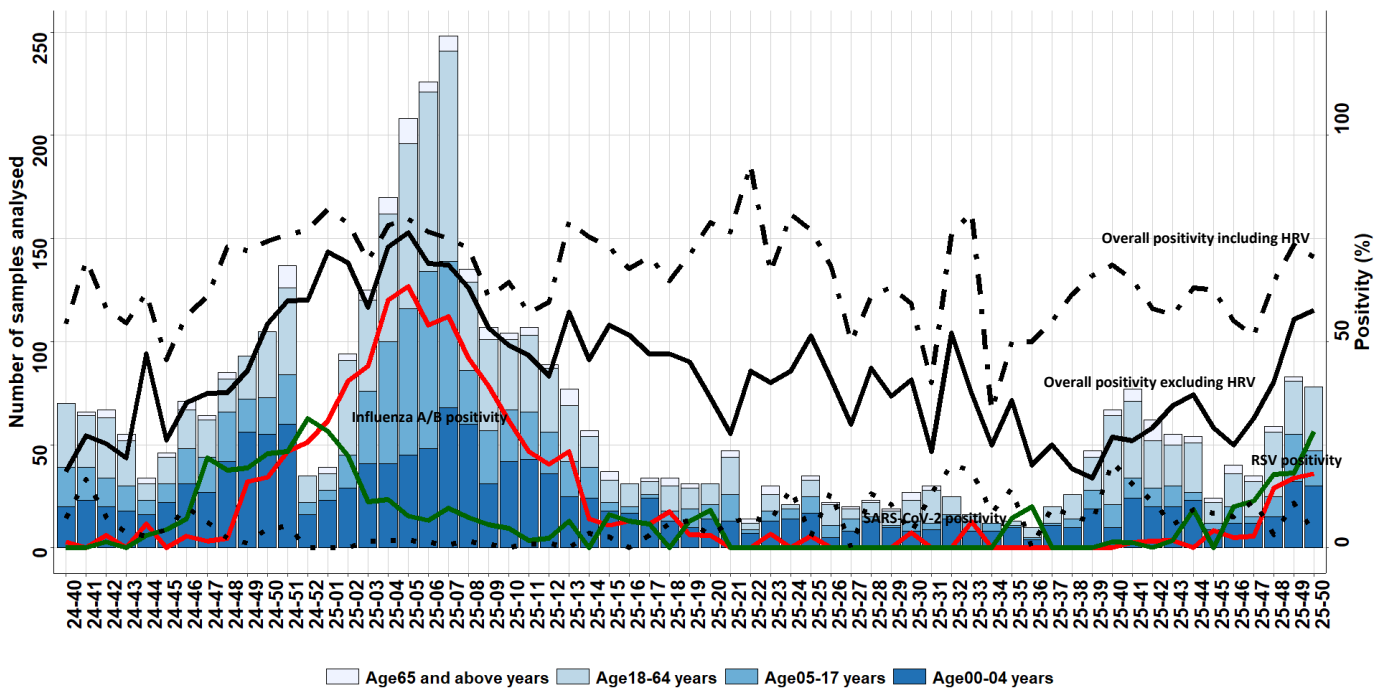
An overview of the circulating viral pathogens in the sentinel network in Luxembourg during the current and previous (inter)- season is presented in figure 2, 3 and table 2.

Table 2. Distribution of respiratory viruses detected within the Sentinel Network over the past 4 weeks compared to previous season; Results from last weeks are not all yet consolidated.

Virus	Season 2025/26					Season 2024/25		
	Positivity Rate in %							
	W47	W48	W49	W50	Total N (%)	W49	W50	Total N (%)
Respiratory syncytial virus	11.4	17.7	18.1	28.6	64 (10.1)	19.4	22.9	287 (9.9)
Human rhinovirus	20.0	33.9	30.1	24.7	217(34.2)	41.9	37.1	720 (24.8)
Influenzavirus A	2.9	14.5	16.9	17.9	43 (6.8)	15.1	14.3	502 (17.2)
Adenovirus	2.9	3.2	4.8	7.8	37 (5.8)	7.5	7.6	203 (7.0)
Metapneumovirus	2.9	3.2	4.8	3.9	14 (2.2)	0.0	1.9	157 (5.4)
SARS-CoV-2	11.4	3.2	10.8	3.8	64 (10.0)	1.1	4.8	80 (2.7)
Parainfluenzavirus	0.0	1.6	4.8	2.6	36 (5.7)	2.2	5.7	99 (3.4)
Influenzavirus B	0.0	0.0	0.0	0.0	0 (0.0)	1.1	2.9	404 (13.9)

*Co-detection is counted once for each virus detected.

Figure 2. Presents number of sentinel samples received per week by age-group (weeks 2024/40 to 2025/50) including overall sample positivity- including human rhinovirus (HRV, dot-dash line), excluding HRV (black line), SARS-CoV-2 (dotted line), influenza **combined** (red) and RSV (green); Secondary axis corresponds to positivity; Results from last weeks are not all yet consolidated.



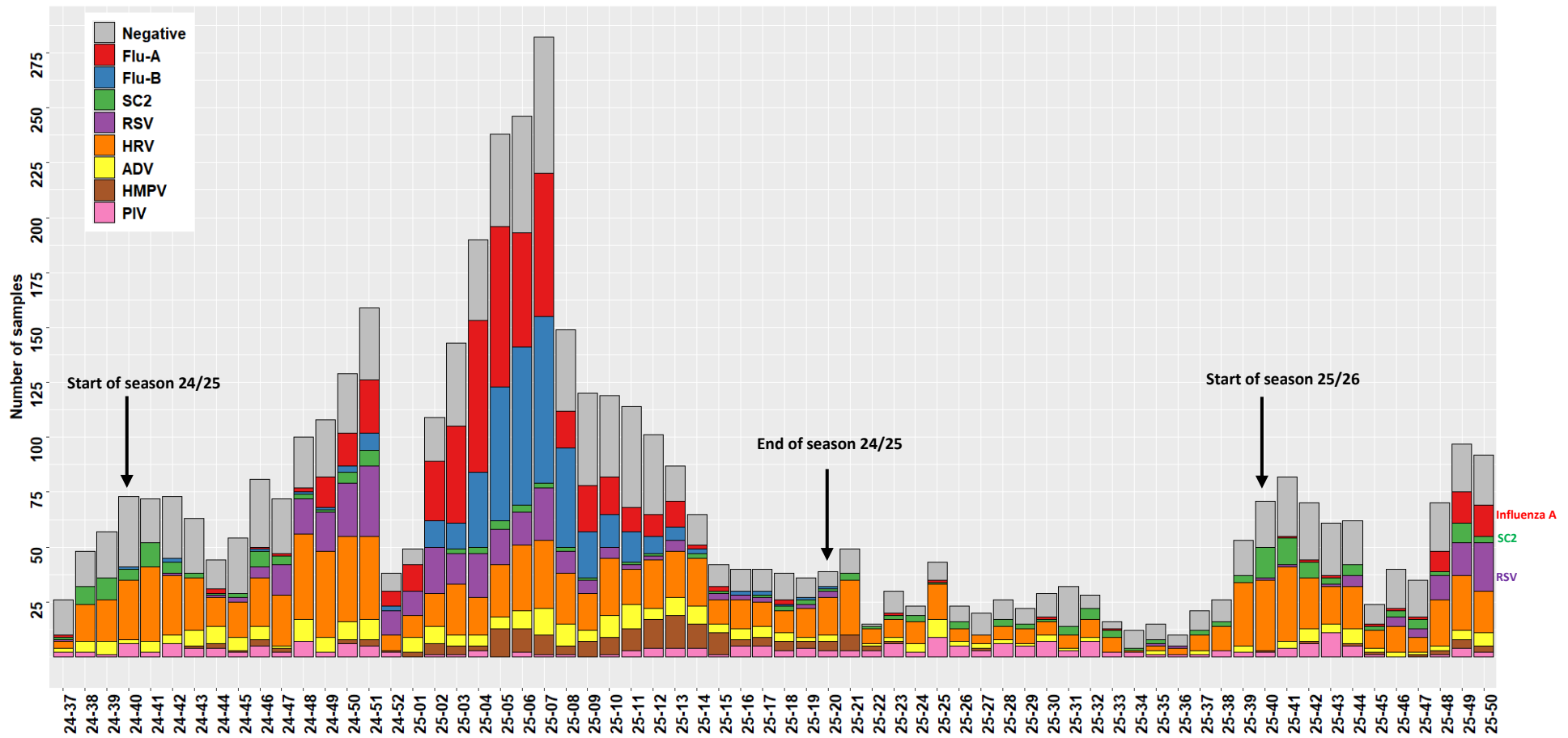


Figure 3. Circulation of respiratory viruses detected within the Sentinel Network by calendar week (seasons 24/25 and 25/26). FLU-A: influenza A; FLU-B: influenza B; PIV: parainfluenza virus; RSV: respiratory syncytial virus; ADV: adenovirus; HMPV: metapneumovirus; HRV: human rhinovirus; SC2: SARS-CoV-2; Results from last weeks are not all yet consolidated.

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: 4.3.4; 1.36 mode UShER).

Sequencing activity

Of the 273 reported cases in Luxembourg, 138 samples (50.5%) were successfully sequenced. Specimen collection dates ranged from calendar weeks 46 to 49 of 2025. Among these, 24.6% (N=34) were obtained from hospital settings, while 75.4% (N=104) originated from the community. Sequencing efforts prioritized the most recent specimens and those from hospitalized patients. Any low coverage will be addressed in subsequent sequencing runs.

Variant circulation

Recent SARS-CoV-2 genomic surveillance in Luxembourg indicates continued phylogenetic divergence among circulating lineages. The **XFG** lineage, first detected in March 2025, remains predominant, accounting for **57.6%** of sequences in weeks **2025/42-45** and **40.6%** in weeks **2025/46-49**. Its sub-lineage **XFG.3** continues to represent a significant proportion (**28.0%** and **23.9%**, respectively). **NB.1.8.1**, another JN.1 derived recombinant variant, is showing a resurgent increasing trend from **13.1% to 23.9% over the same period**, likely driven by growing genetic diversity and competitive fitness. Notably, **BA.3.2.2**, first detected in November 2025, emerged from undetectable levels to **6.5%** in weeks 2025/46-49, suggesting a potential growth advantage and warranting close monitoring.

A summary of all circulating variants identified in the selected sample, along with those under WHO variants under monitoring, is provided in table 4 and figure 6.

Among hospital patients (N=34), nearly half (47.1%) of the sequenced samples were from individuals > 75 years. In contrast, above 90% of community cases were ≤ 75 years. Overall, in this selected cohort (N=138), females predominate in the community setting (67.3%), whereas males predominate in the hospital setting (64.7%).

Table 3 compares sampling setting and variant prevalence over the past four weeks. **NB.1.8.1** was primarily detected in the community (27%) compared to the hospital (11.8%). Overall the detection of **BA.3.2.2** was below 10% with most cases (88%) identified in community samples from patients aged < 50 years.

Table 3. Comparison of sub-variants by sampling setting

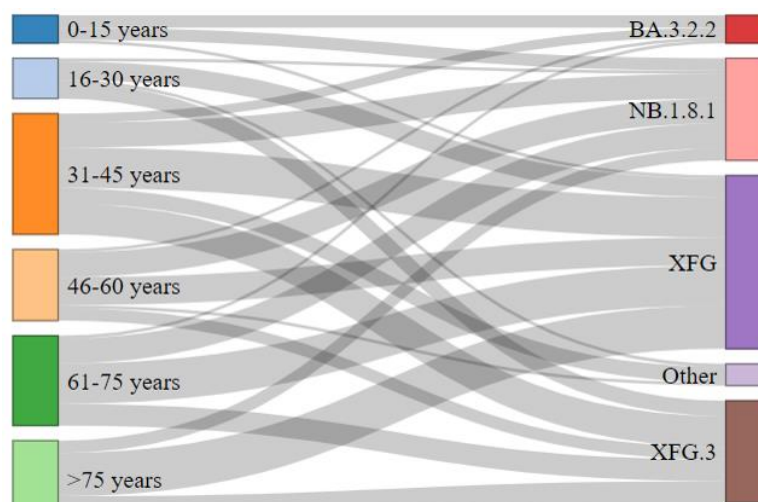
Comparison of variant detection during weeks 2025/46-49		
Lineage	Community (N=104)	Hospital (N=34)
XFG	62 (59.6%)	27 (79.4%)
NB.1.8.1	28 (26.9%)	4 (11.8%)
BA.3.2.2	8 (7.7%)	1 (2.9%)
Other	6 (5.8%)	2 (6.3%)

Table 4. Distribution of SARS-CoV-2 lineages detected during weeks 2025/42 to 2025/49; Previously reported cases might be updated by retrospective analysis;

JN.1 and XFG excludes sub-variants listed in table.

Lineage	First detection in Luxembourg	Under WHO monitoring	weeks 42-45 (N=229)		weeks 46-49 (N=138)	
			%	CI %	%	CI %
XFG*	13.03.2025	yes	57.6	51.0 – 64.1	40.6	32.3 – 49.3
XFG.3	22.04.2025	under XFG	28.0	22.2 – 34.2	23.9	17.1 – 31.9
NB.1.8.1	07.04.2025	yes	13.1	9.0 – 18.2	23.9	17.1 – 31.9
BA.3.2.2	11.11.2025	yes	0.0		6.5	3.0 – 12.0
Other	not applicable	no	0.9	0.1 – 3.1	2.9	0.8 – 7.3
LP.8.1	05.11.2024	yes	0.4	0.01 – 2.4	1.5	0.2 – 5.1
JN.1*	25.08.2023	yes	0.0	0.09 – 2.6	0.7	0.2 – 4.0
KP.3	03.04.2024	yes	0.0		0.0	

Figure 5. Distribution of XFG, XFG.3, NB.1.8.1 and Other detected during weeks 2025/46 to 2025/49 (N=138) by age groups



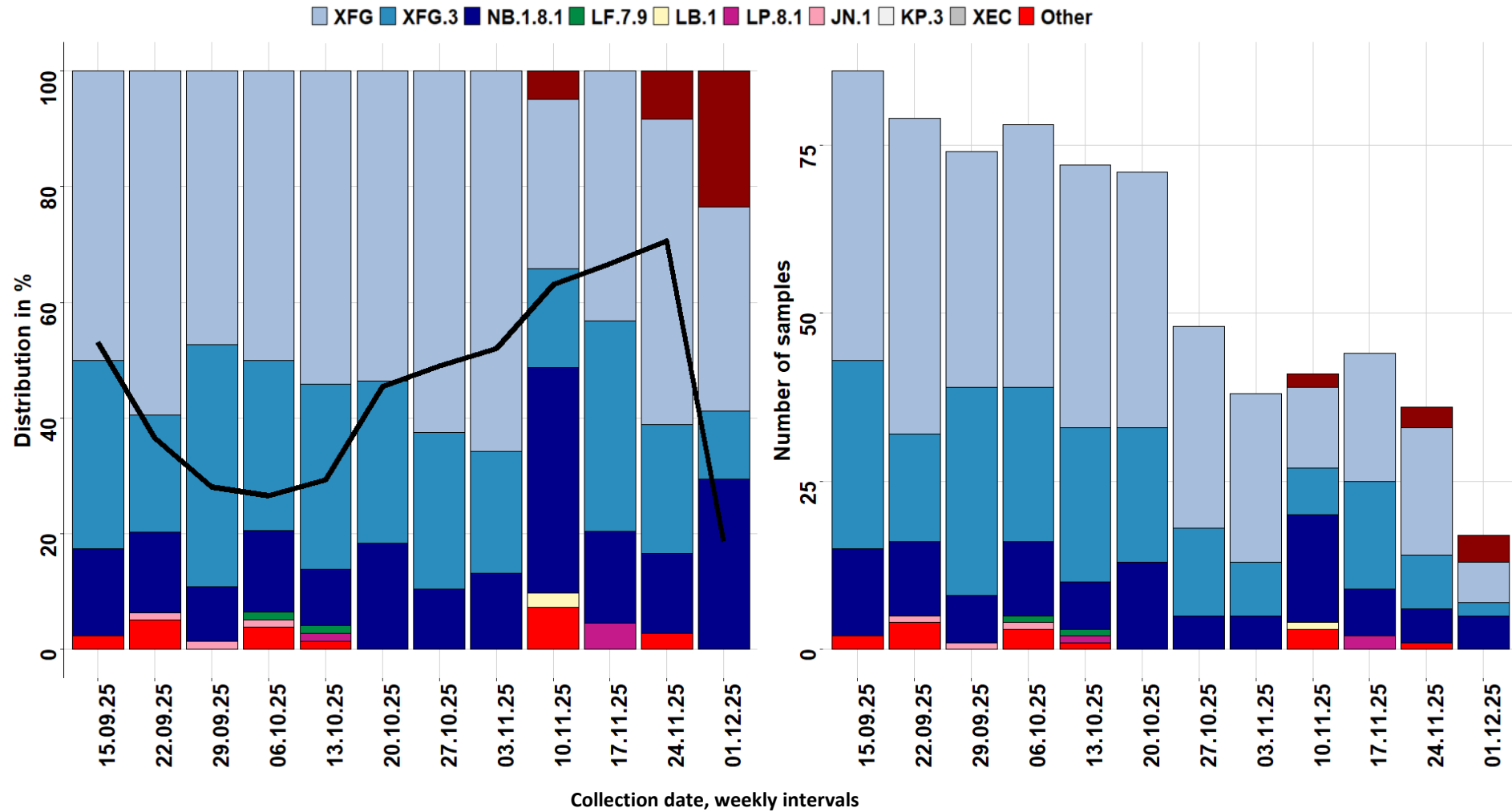


Figure 6. Lineage distribution and sequencing coverage from week 2025/38 (15.09.2025) to week 2025/49 (01.12.2025) in weekly intervals; All displayed variants include descendant lineages- except those specified on the legend. Other: recent cases-recombinant XFC, and XFG; during this period no further KP.3 or XEC cases have been detected

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