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Swiss national RSV, SARS-CoV-2 and Influenza genomic surveillance program: October 2025

1. Summary:

This report covers the fifth and final sequencing batch of the 2024–2025 national genomic surveillance program, dedicated exclusively to SARS-CoV-2.
Samples were collected between April 1 and September 15, 2025, and sequenced using the Illumina COVIDSeq (ARTIC v4) assay.

A total of 250 isolates were received by the Health 2030 Genome Center, with 235 (94%) successfully submitted to GISAID following quality control by the Swiss Pathogen Surveillance Platform (SPSP).

Among sequences passing QC, lineage XFG accounted for approximately 71.5% (168/235), in line with trends observed through national wastewater surveillance. Other detected lineages included residual LP.8.x and KP.3.x sublineages at low frequency.

No high-level resistance mutations to antiviral agents such as nirmatrelvir/ritonavir (Paxlovid®) were identified.

2. Sequencing overview

Site	Received by GC	Sequenced	Submitted to SPSP	Received by SPSP	Successfully submitted to GISAID	Success rate
HUG (routine/Sentinella)	96 (70/26)	96	96	96	93 (69/24)	97%
Bern (IFIK)	20	20	20	20	20	100%
Basel (USB)	30	30	30	30	29	97%
Zurich (IMV)	43	43	43	43	33	77%
Lausanne (CHUV)*	30	30	30	30	29	97%
Sion (ICH)	31	31	31	31	31	100%
Total	250	250	250	250	235	94%

*CHUV directly submitted to SPSP for GISAID deposition.

Sentinella positive specimens (from 22.05.2025 to October 4)

	SARS-CoV-2
Total number of positive specimens	51
Meeting sequencing criteria*	35
Included**	26

**Reasons for Sentinella specimen meeting sequencing criteria not to be sent to sequencing: missing tube, not enough volume, other reason

3. Lineage Distribution and Mutations analysis

Analysis through Nextclade identified a strong predominance of lineage XFG (71.5%), consistent with the national wastewater data.
A limited number of residual LP.8.1 and KP.3.x sublineages were also observed, none associated with increased immune escape or antiviral resistance.
Mutation screening based on the Stanford 3CLpro inhibitor resistance database revealed no variants harboring mutations known to reduce Paxlovid® efficacy.

4. Technical Notes

While all samples were expected to be processed using the Illumina COVIDSeq (ARTIC v4) assay, metadata from some entries listed *"Illumina Respiratory Virus Enrichment kit."*
This discrepancy likely reflects a metadata input error; confirmation is ongoing.
All sequences underwent centralized analysis and quality control through SPSP before deposition to GISAID.

5. Methods

Samples originated from six tertiary hospital laboratories across Switzerland.
Sequencing was performed at the Health 2030 Genome Center using the Illumina COVIDSeq (ARTIC v4) assay according to manufacturer's instructions.
Data were analyzed and validated by SPSP using Nextclade and the Stanford 3CLpro mutation reference.

6. Conclusion

This fifth and final batch concludes the 2024–2025 national genomic surveillance season.
SARS-CoV-2 circulation during early autumn 2025 was dominated by lineage XFG, with no evidence of new variants of concern or resistance-associated mutations.

The program achieved a high overall sequencing success rate and provided a coherent genomic overview aligned with wastewater surveillance data.

7. Acknowledgements

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