

Federal Office of Public Health FOPH
Public Health Directorate Communicable
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**Swiss national RSV, SARS-CoV-2 and Influenza genomic
surveillance program: November 2024 – Preliminary report**

Geneva Centre for
Emerging Viral Diseases

Division of Infectious
Diseases

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1. Preliminary report:

This report covers the samples collected between 24 September and 28 November, corresponding to the first sequencing batch of the new integrated RSV, SARS-CoV-2 and influenza genomic surveillance program.

To enable simultaneous sequencing of various respiratory viruses, the Illumina Respiratory Virus Oligo Panel assay is used. This capture-based assay replaces the traditional amplicon-based approach. Analyses are performed by the 2030 Health Genome Center and the Swiss Pathogen Surveillance platform (SPSP).

Origin of the samples is the Sentinella program in priority, complemented by a random selection of samples originating from 6 hospital laboratories to reach 200 specimens (Table 1, Table 2 and Table 3).

Sequencing data has been delayed for this report due to manual cross-checking with the SPSP platform as a quality control, and other issues that arose with the first use of this multi-viral panel. A follow-up report will be issued in January 2025 that will include data and insight gleaned from the sequence data.

For the first batch of this respiratory virus sequencing program, 200 samples of respiratory pathogens were obtained from the Sentinella program, the Institut für Medizinische Virologie (IMV) in Zurich, the Centre hospitalier universitaire Vaudois (CHUV) in Lausanne, the Hôpitaux universitaires de Genève (HUG) in Geneva, Universitätsspital Basel (USB), the Institut Central des Hôpitaux (ICH) in Sion, and the Institut für Infektionskrankheiten (IFIK) in Bern.

Note that all Sentinella specimens are processed at the Geneva University Hospitals laboratory of virology.

Of the 200 samples tested for respiratory infections, 155 were positive for SARS-CoV-2, (see table 1). 27 for influenza (18 Influenza A, 5 Influenza B, and 4 unspecified Influenza), and 18 for RSV.

Table 1: Origin of the samples

	SARS-CoV-2	Influenza	RSV
Sentinella	80	9 (7A, 2B)	2
Laboratory network	75	18 (11 A, 3B, 4 NA)	16
Total	155	27	18

Table 2: Sentinella positive specimens (from Septembre 27 to November 26, 2024)

	SARS-CoV-2	Influenza	RSV
Meeting sequencing criteria*	113	9 (7A, 2B)	2
Included**	80	9 (7A, 2B)	2

Table 3: Detailed origin of samples by originating lab.

Site	SARS-CoV-2	Influenza	RSV
CHUV	8	6 (5A, 1B)	6
HUG	0	2(1A, 1B)	3
ICH	8	5 (4A, 1B)	7
IFIK	11	4	0
IMV	14	1 (A)	0
USB	34	0	0
Total	75	18 (11 A, 3B, 4 NA)	16

**Sequencing criteria

- Influenza and RSV : Ct values < 25; SARS-CoV-2: Ct value < 32
- AND absence of co-infection with another respiratory virus

** reason for non-inclusion: missing tube, not enough volume, other reason

Acknowledgements:

<https://bsse.ethz.ch/cevo/research/sars-cov-2/swiss-sars-cov-2-sequencing-consortium.html>

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