



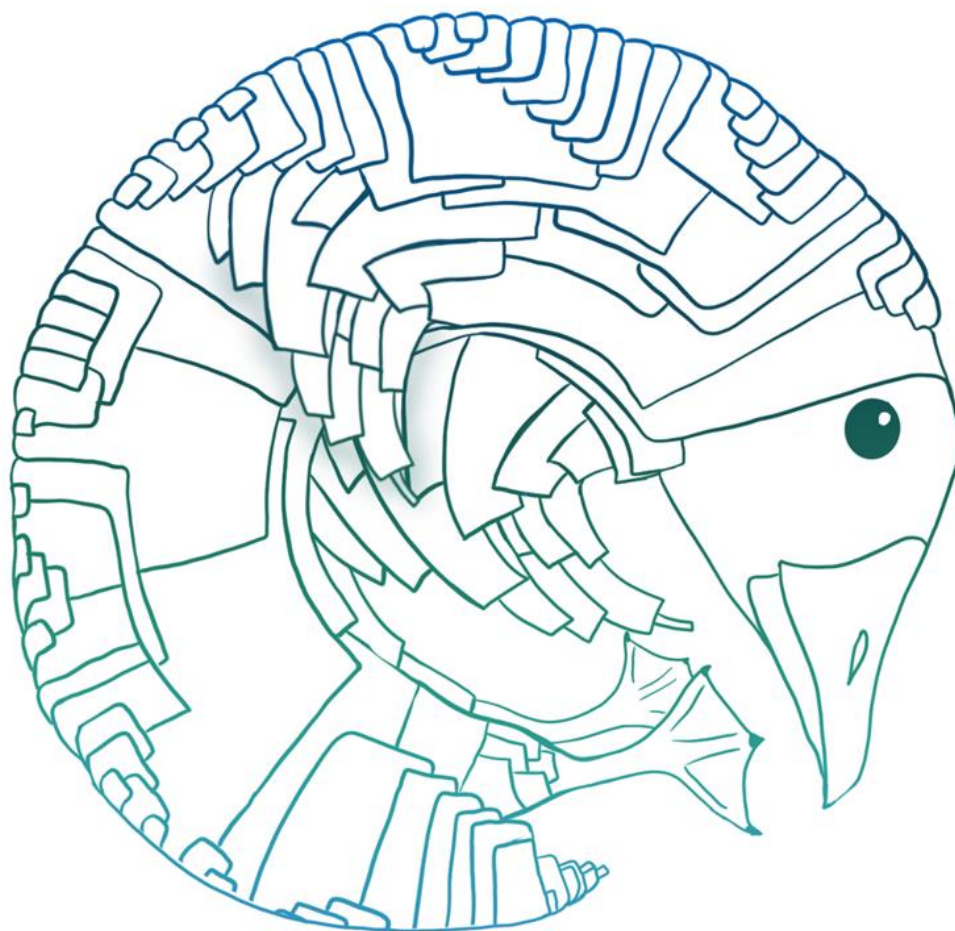
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Surveillance report: Respiratory viruses in Switzerland

Season 2025–2026 (weeks 40/2025-20/2026)



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Cover image

Phylogenetic tree representing a wild goose. Digital illustration created using Procreate® by Lisa Spedaliero

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Abstract

Summary of influenza and other respiratory viruses' surveillance, 2025-2026 Season

As part of the Sentinella surveillance network, the National Reference Centre of Influenza (NRCI) receives nasopharyngeal swabs collected nationwide and test them for the presence of influenza viruses, SARS-CoV-2, and respiratory syncytial virus (RSV). During the period from week 40/2025 to week 20/2026, 1514 samples were analysed of which 645 (42.6%) tested positive for at least one respiratory virus. SARS-CoV-2 was detected in 152 samples (10 %), circulating predominantly during autumn before declining to low levels. RSV was detected in 103 samples (6.8 %) with only a modest increase observed in early spring (around week 09/2026). Influenza viruses were detected in 427 samples (28.2%), with the first cases identified in epidemiological week 42/2025. This influenza season was characterised by an early onset, high intensity, and prolonged circulation compared with the previous season. The epidemic threshold was crossed in week 45/2025, influenza activity peaked in week 01/2026, and transmission returned below threshold levels in week 12/2026, resulting in a season duration of 19 weeks.

Influenza A viruses predominated, with subtype A(H3N2) circulating more frequently than A(H1N1)pdm09. In contrast, influenza B virus circulation was negligible both in Switzerland and Europe. Most A(H1N1)pdm09 viruses belonged to genetic clade 6B.1A.5a.2a.1, subclade D.3.1.1. Antigenic characterisation indicated that these viruses remained moderately related to the 2025-2026 Northern Hemisphere vaccine strain A/Victoria/4897/2022 and showed a closer relationship to the more recent A/Missouri/11/2025-like strain. The majority of A(H3N2) viruses belonged to genetic group 2a.3a.1, with an overrepresentation of subclade K. These viruses were poorly recognised by antisera raised against the recommended NH 2025-2026 vaccine strain A/Croatia/10136RV/2023 (subclade J.2).

Résumé de la surveillance de l'activité grippale et autres virus respiratoires 2025-2026

Dans le cadre du réseau de surveillance Sentinella, le Centre national de référence pour l'Influenza (CNRI) reçoit des prélèvements nasopharyngés collectés dans tout le pays et les analyse afin de détecter la présence de virus influenza, du SARS-CoV-2 et du virus respiratoire syncytial (VRS). Au cours de la période allant de la semaine 40/2025 à la semaine 20/2026, 1 514 échantillons ont été analysés, dont 645 (42,6 %) se sont révélés positifs pour au moins un virus respiratoire. Le SARS-CoV-2 a été détecté dans 152 échantillons (10 %), il a circulé principalement à l'automne avant de reculer à des niveaux faibles. Le VRS a été détecté dans 103 échantillons (6,8 %), avec une augmentation modérée observée au début du printemps (autour de la semaine 09/2026). Les virus de l'influenza ont été détectés dans 427 échantillons (28,2 %), les premiers cas ayant été identifiés au cours de la semaine épidémiologique 42/2025. Cette saison grippale s'est caractérisée par un début précoce, une forte intensité et une circulation prolongée par rapport à la saison précédente. Le seuil épidémique a été franchi au cours de la semaine 45/2025, l'activité grippale a atteint son pic au cours de la semaine 01/2026 et la transmission est repassée sous le seuil épidémique au cours de la semaine 12/2026, ce qui a donné lieu à une saison d'une durée de 19 semaines.

Les virus de la grippe A ont prédominé, le sous-type A(H3N2) circulant plus fréquemment que le sous-type A(H1N1)pdm09. En revanche, la circulation du virus de la grippe B a été négligeable tant en Suisse qu'en Europe. La plupart des virus A(H1N1)pdm09 appartenaient au clade 6B.1A.5a.2a.1, sous-clade D.3.1.1. La caractérisation antigénique a montré que ces virus restaient modérément apparentés à la souche vaccinale de l'hémisphère nord pour la saison 2025-2026, A/Victoria/4897/2022, et présentaient une plus grande proximité avec la souche plus récente de type A/Missouri/11/2025. La majorité des virus A(H3N2) appartenaient au groupe génétique 2a.3a.1, avec une surreprésentation du sous-clade K. Ces virus étaient faiblement reconnus par les antisérums produits contre la souche vaccinale recommandée pour l'hémisphère nord 2025-2026, A/Croatia/10136RV/2023 (sous-clade J.2).

Zusammenfassung der Überwachung von Influenza- und anderer respiratorischer Viren, Saison 2025-2026

Als Teil des Sentinella-Überwachungsnetzwerks erhält das Nationale Referenzzentrum für Influenza (NRCI) landesweit entnommene Nasen-Rachen-Abstriche und untersucht diese auf das Vorhandensein von Influenzaviren, SARS-CoV-2 und dem Respiratorischen Synzytial-Virus (RSV). Im Zeitraum von Woche 40/2025 bis Woche 20/2026 wurden 1.514 Proben analysiert, von denen 645 (42,6 %) positiv auf mindestens ein Atemwegsvirus waren. SARS-CoV-2 wurde in 152 Proben (10 %) nachgewiesen und zirkulierte vorwiegend im Herbst, bevor die Fallzahlen auf ein niedriges Niveau zurückgingen. RSV wurde in 103 Proben (6,8 %) nachgewiesen, wobei im frühen Frühjahr (um Woche 09/2026) nur ein moderater Anstieg zu beobachten war. Influenzaviren wurden in 427 Proben (28,2 %) nachgewiesen, wobei die ersten Fälle in der epidemiologischen Woche 42/2025 identifiziert wurden. Diese Grippezeit war im Vergleich zur vorangegangenen Saison durch einen frühen Beginn, eine hohe Intensität und eine längere Zirkulationsdauerperiode gekennzeichnet. Die Epidemieschwelle wurde in Woche 45/2025 überschritten, die Grippeaktivität erreichte ihren Höhepunkt in Woche 01/2026, und die Übertragung sank in Woche 12/2026 wieder unter die Schwellenwerte, was zu einer Saisonlänge von 19 Wochen führte.

Es dominierten Influenza-A-Viren, wobei der Subtyp A(H3N2) häufiger zirkulierte als A(H1N1)pdm09. Im Gegensatz dazu war die Zirkulation von Influenza-B-Viren sowohl in der Schweiz als auch in Europa vernachlässigbar. Die meisten A(H1N1)pdm09-Viren gehörten zur genetischen Klade 6B.1A.5a.2a.1, Subklade D.3.1.1. Die antigene Charakterisierung ergab, dass diese Viren weiterhin mäßig verwandt mit dem Impfstamm A/Victoria/4897/2022 für die Saison 2025–2026 auf der Nordhalbkugel waren und eine engere Verwandtschaft zum neueren A/Missouri/11/2025-ähnlichen Stamm aufwiesen. Die Mehrheit der A(H3N2)-Viren gehörte zur genetischen Gruppe 2a.3a.1, wobei die Untergruppe K überrepräsentiert war. Diese Viren wurden von Antisera, die gegen den empfohlenen Impfstamm A/Croatia/10136RV/2023 (Untergruppe J.2) für die nördliche Hemisphäre 2025–2026 gebildet worden waren, nur schlecht erkannt.

A. The Sentinella surveillance system for respiratory viruses

The Sentinella surveillance system is a community-based network of about 150 to 250 primary care physicians (general practitioners, paediatricians and internists) founded in 1986 [1]. The physicians, who voluntarily participate to the Sentinella surveillance network, report cases of patients presenting symptoms of acute respiratory infection (ARI) with or without influenza-like illness (ILI) to the Federal Office of Public Health (FOPH). A subgroup of sentinel practitioners collects nasopharyngeal swabs, which are sent to the National Reference Centre of Influenza (NRCI) for respiratory viruses' screening.

Samples are tested using multiplex RT-PCR to detect the following viruses: influenza A and B viruses (IAV and IBV), severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and respiratory syncytial virus (RSV).

The NRCI performs additional characterisation of samples positive for either virus. Eligible samples are submitted to genetic characterisation using whole genome sequencing. The genetic information obtained are used to track phylogenetic evolution of viruses and relevant mutations having an impact on viral resistance to treatment. For influenza viruses, we can identify mutations conferring resistance to neuraminidase and/or polymerase inhibitor while in the case of RSV, we can identify mutations that may confer resistance to existing monoclonal antibody prophylaxis or treatments. All influenza positive samples undergo further characterisations to define their subtype and lineage (i.e: Influenza A/H1N1pdm09 or A/H3N2 or B/Victoria or B/Yamagata). A subset of these samples is cultured and subjected to a haemagglutination inhibition assay to determine their antigenic proximity with vaccine and/or reference strains.

This report summarises the demographic, epidemiological and virological data from samples processed and analysed by the NRCI from September 29, 2025, to May 17, 2026 (week 40/2025 to week 20/2026).

ARI is defined as the acute onset of illness with cough, sore throat, shortness of breath or rhinitis and of infectious origin, as judged by a physician.

ILI is a specific form of ARI characterised by the sudden onset of a high fever (>38 °C), a cough or a sore throat.

B. Characteristics of the study population

From week 40/2025 to week 20/2026, 1514 nasopharyngeal swabs were collected by 85 sentinel practitioners and submitted to the NRCI for screening. Each specimen was accompanied by a standardised reporting form documenting the clinical suspicion criteria (ARI – inclusion criteria - with or without ILI), as well as patient demographics (sex and age) and vaccination status for both influenza and SARS-CoV-2.

During the 2025-2026 season, analysed samples were obtained from patients presenting with ARI symptoms, of whom 65.9 % also presented with ILI. Based on practitioner-reported data, the Sentinella cohort was stratified by sex and by age groups (0 to 4, 5 to 14, 15 to 29, 30 to 64, and over 65 years). Data for age and gender were available for all the participants. Women accounted for 52.4 % of the population. The overall median age was 44 years-old (range: 0-99; Q1: 25, Q3: 62). The median age was 48 years in women (range: 0-99; Q1: 29, Q3: 62) and 40 years in men (range: 0-92; Q1: 21, Q3:61) (Figure 1).

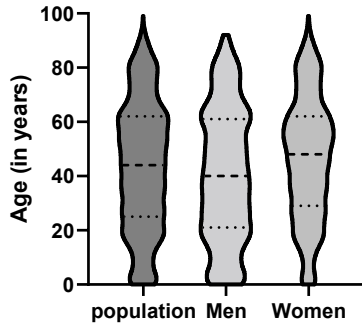


Figure 1: Violin plot representing the age distribution according to the gender. The dashed line represents the median and the dotted line the 25 % (Q1) and 75 % (Q3) quartiles.

C. Virological results

From week 40/2025 to week 20/2026, a total of 1514 nasopharyngeal samples were received at the NRCI and screened for Influenza, SARS-CoV-2 and RSV. The complete workflow of analysis is summarised in Figure 2.

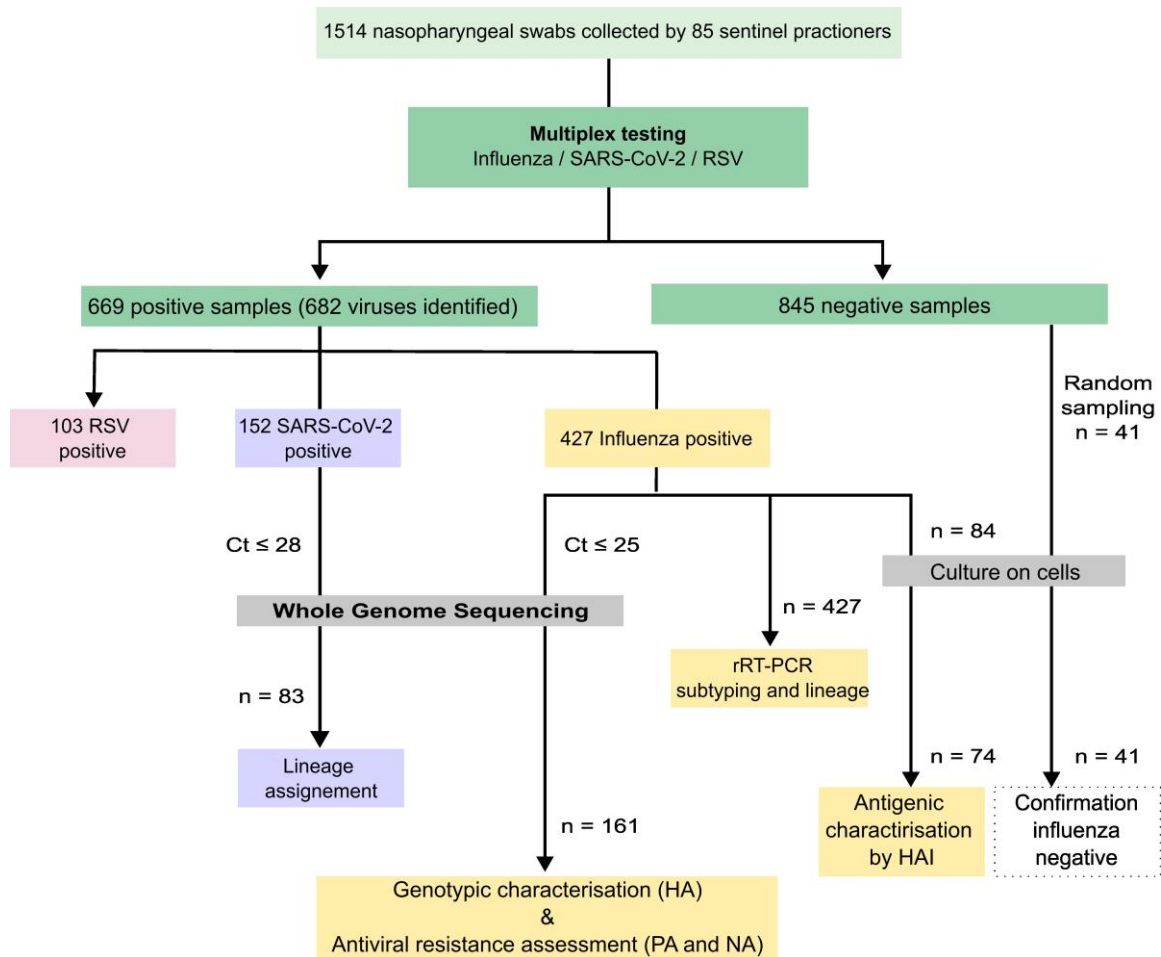


Figure 2: Representation of Sentinel samples collection and processing.

1. Circulating respiratory viruses

a. Test positivity

During the 2025-2026 season, a total of 669 samples tested positive representing a cumulative overall test positivity rate of 44.2 %. The weekly positivity rate, defined by the ratio between the number of samples with at least one virus detected and the total number of samples received in the same week, was calculated from epidemiological week 40/2025 to week 20/2026 (Figure 3). The highest positivity rate was recorded during week 01/2026, reaching 75 %. Yet, due to the holidays period, the number of samples received that week was limited (n = 32), and therefore this positivity rate should be interpreted with caution. Over the surveillance period, the median weekly positivity rate was 29.8 % (Q1: 18.6 %, Q75: 50 %).

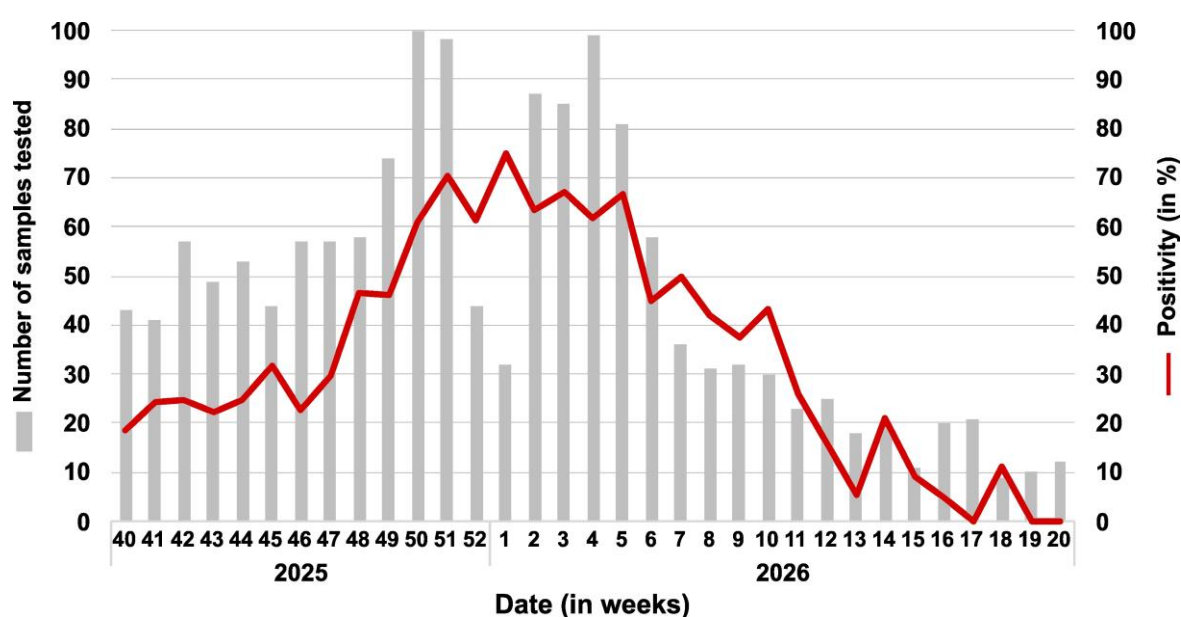


Figure 3: Overall positivity rate (ratio between the number of sample positive for any viruses and the total number of samples received) and total number of samples tested weekly from week 40/2025 to week 20/2026.

A total of 682 viruses were identified. The distribution of viruses is shown in Figure 4.a, with the total number of positive results and their respective percentages indicated. The sum of all percentages reached 100.9 %, which is explained by co-detections in 13 samples (further details provided below).

Figure 4.b shows weekly positivity rate stratified by viruses. At the beginning of the season, SARS-CoV-2 was the dominant circulating virus. From week 44/2025 onward, it was progressively replaced by influenza viruses. Influenza detection rate increased rapidly to cross the 10 % positivity threshold a first time in week 45/2025 and a second time in week 48/2025 after a deep just below 10 % in week 47/2025. The Influenza epidemics lasted for 14 weeks. RSV was detected at a low level from week 47/2025 onward and we observed a small wave of RSV between week 04/2026 and week 12/2026. Between week 14/2026 and week 20/2026, the circulation of all three respiratory viruses tested was very low. Notably, IBV circulation was negligible throughout the season with only three samples testing positive.

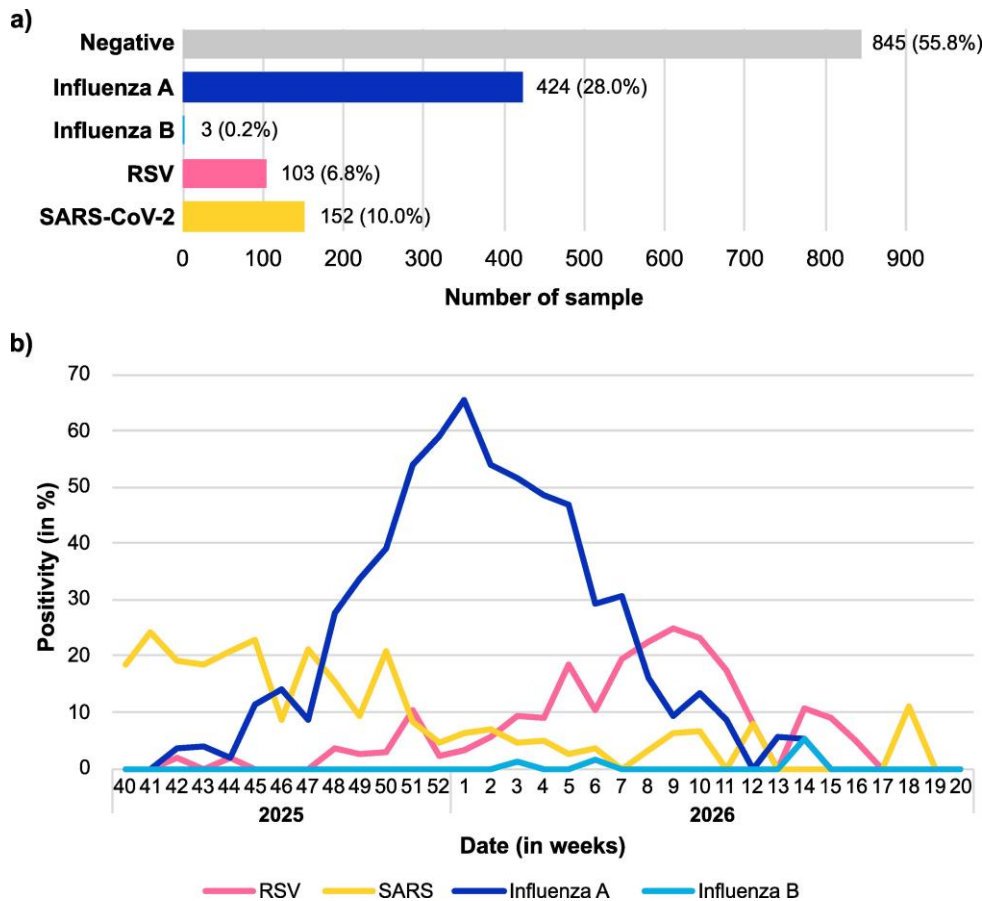


Figure 4: Pathogen-specific test positivity. **a)** Graph representing the total number of samples and the relative percentage in each category. **b)** Temporal distribution of respiratory viruses. The line represents the positivity rate (ratio between the number of sample positive for a given viruses and the total number of samples received).

b. Positive samples per age group over time

Stratification of positive specimens by age group revealed that all respiratory viruses were detected across all age categories. However, age distribution patterns varied by virus (Figure 5). For RSV, the highest prevalence (15 %) was observed in the 0-4-year-old group, with a median patient age of 50 years (Q1: 22; Q3: 63). For SARS-CoV-2, prevalence increased with age, with a median patient age of 50 years (Q1: 28; Q3: 62), but remained relatively low during the surveillance period reaching only 10 % in the patients >30 years. For Influenza A, we observed a pic in prevalence (50 %) in the 5-14-year-old group while in the patient above 30-year-old it was just below 30 %. Influenza A positive samples were more likely to test positive for A /H3N2, and this pattern was particularly pronounced among patients aged 5-29 years. The median age of patients infected with A/H3N2 was 37 years (Q1: 20.25; Q3: 60), compared with 51 years for those infected with A/H1N1 (Q1: 30.25; Q3: 62). Due to the very low number of samples, this analysis could not be performed for Influenza B viruses.

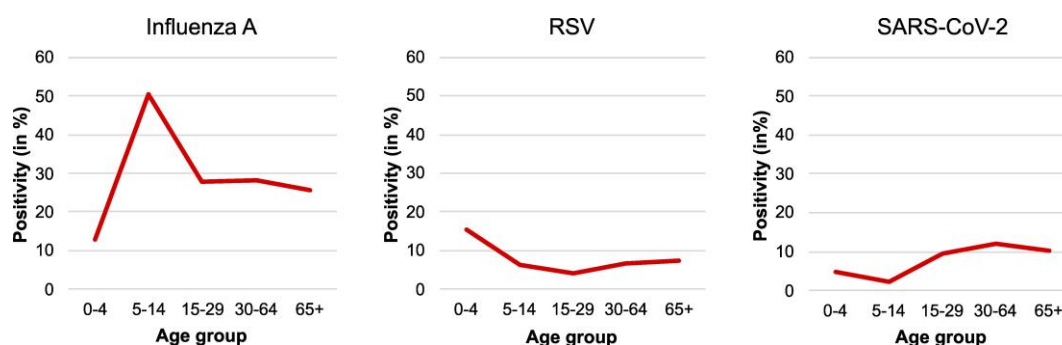


Figure 5: Prevalence of respiratory viruses by age groups. The positivity rate is a ratio between the number of samples positive for a given virus in the indicated age group and the total number of samples received in that age group.

c. Co-detection rate

Among the 669 positive samples, 13 (1.9 %) were positive for two respiratory viruses. Influenza A and SARS-CoV-2 represented the most common co-detection ($n = 7$, 53.8 %), followed by Influenza A and RSV ($n = 3$, 23.1 %). The overall low frequency of co-detection is likely attributable to the limited co-circulation of these viruses during the surveillance period. While influenza activity peaked, RSV and SARS-CoV-2 circulation remained low. Furthermore, the RSV peak occurred near the end of the influenza season, at a time when SARS-CoV-2 activity was still minimal. This temporal separation likely reduced the probability of concurrent infections (Figure 4.b).

2. Influenza viruses

a. Characterisation of subtypes and lineages

From week 40/2025 to 20/2026, a total of 427 influenza viruses were detected. This number included 424 IAV and 3 IBV. IAV were further subtyped either as A/H1N1pdm09 ($n = 165$; 38.9 %) or as A/H3N2 ($n = 228$, 53.8 %). 31 IAV (7.3 %) could not be subtyped due to low viral load. All IBV detected belonged to the B/Victoria lineage. No IBV from the B/Yamagata lineage were identified.

Within the Sentinella surveillance network, influenza season started during week 45, 2025 when crossing the 10 % positivity threshold defined by the European Centre for Disease Control and Prevention (ECDC). However, we observed a deep below the 10 % threshold during week 47, followed by a rebound with positivity rate during week 48/2025 reaching 28 %. The peak reached a positivity rate of almost 66 % during week 01/2026. Then started decreasing to drop below the 10 % threshold on week 09/2026. The influenza season lasted for 19 weeks and was dominated by the circulation of A/H3N2 while Influenza B were only sporadically detected (Figure 6).

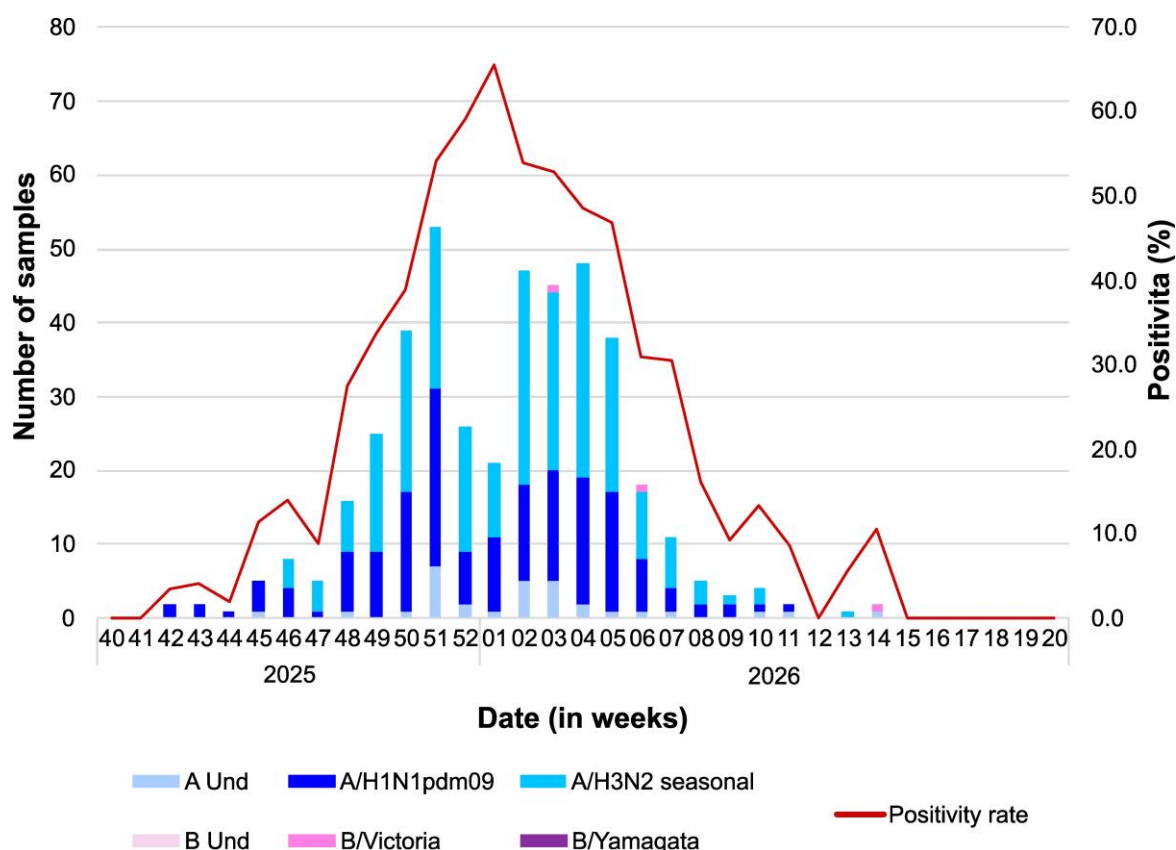


Figure 6: Proportion and temporal distribution of Influenza subtypes and lineages detected from week 40/2025 to 20/2026. Bars represent the number of samples tested positive for influenza and the line represent the positivity rate. A und. and B und.: influenza A and B viruses that could not be further subtyped (undefined).

b. Genetic and antigenic characterisation

A subset of IAV and IBV were sent for whole genome sequencing (WGS) to Microsynth AG, followed by data analysis performed by the Swiss Pathogen Surveillance Platform (SPSP). SPSP then uploaded sequences on GISAID (Global Initiative on Sharing All Influenza Data) [2]. A small subset of samples (n = 17) was sequenced by the World Influenza Centre in London and their sequences were also uploaded on GISAID.

From October 2025 to April 2026, a total of 60 A/H1N1pdm09, 96 A/H3N2, and 1 B/Vic isolates were successfully sequenced (Table 1) (Appendix 1, Appendix 2, Appendix 3). The sequencing of the haemagglutinin (HA) gene enables precise phylogenetic classification of each viral strain into its respective clade and subclade. Additionally, sequence data from the neuraminidase (NA) and polymerase acidic (PA) gene segments are used to assess potential resistance to antivirals.

Table 1: Summary of the number of samples sent for WGS and recovery rate.

	# samples sent	# samples recovered	# sequenced recovered (%)		
			HA	NA	PA
A/H1N1	62	60	60 (96.8)	56 (90.3)	59 (5.1)
A/H3N2	97	96	96 (98.9)	96 (98.9)	96 (98.9)
B/Vic	1	1	1 (100)	1 (100)	1 (100)
Total	160	157	157	153	156

Among the IAV and IBV positive samples, 80 were selected for virus isolation via cell culture. Of these, 71 (88.8 %) exhibited a cytopathic effect (CPE) and were subsequently subjected to haemagglutination (HA) assay. A total of 35 A/H1N1pdm09, 35 A/H3N2, 3 B\Victoria) isolates demonstrated HA titres ≥ 8 and were further analysed using the haemagglutination inhibition (HAI) assay.

During the surveillance period, the NRCI send data to the ECDC (European Centre for Disease prevention and Control) via the EpiPulse platform. Data include genetic and antigenic characteristics, as well as phenotypic and genotypic assessment that are used to fill the *Inflantivir* form.

Influenza A/H1N1

HA(H1) sequences from the Sentinella network were aligned with the reference HA(H1) sequences from ECDC (Appendix 7), clade and subclades were obtained using Nextclade v3.21.2 [3].

HA sequence analysis showed that circulating viruses belonged predominantly to clades 6B.1A.5a.2a (5a.2a) and 6B.1A.5a.2a.1 (5a.2a.1). From week 40/2025 to week 20/2026, clade 5a.2a.1 was overwhelmingly dominant, particularly subclade D.3.1.1 (Figure 7).

This distribution was consistent with patterns observed elsewhere in Europe. Among the Swiss isolates analysed, 58 were classified as clade 5a.2a.1 and only two as clade 5a.2a. In contrast, during the 2024/2025 season, 5a.2a viruses predominated, whereas 5a.2a.1 viruses emerged mainly towards the end of the season.

Within clade 5a.2a.1, two distinct subclades were identified, each defined specific amino acid mutations in the HA1 gene: subclade D.3.1 (reference strain A/Missouri/11/2025) with clusters defined by amino acid T120A, I372V, I460T and V520A (n = 5); subclade D.3.1.1 with substitutions R113K, A139D, E283K, K302E (n = 53). Two sequences were assigned to the clade 5a.2a and subclade C.1.9.3 (reference strain A/Hungary/286/2024) with amino acid S83P and I183T (Figure 7).

For antigenic characterisation of A/H1N1pdm09 viruses, HAI were performed using antisera against: A/Guangdong-Maonan/SWL1536/2019 strain (Clade 5a.1 (B)), A/Victoria/4897/2022 (Clade 5a.2a.1 (D)), strain present in the egg-based vaccine for NH season 24-25) and A/Bahrain/25220003050/2025 (Clade 5a.2a.1 (D.3.1)) (Table 2). HAI results showed that ferret antisera raised against the NH vaccine strain A/Victoria/4897/2022 recognised viruses from clade 5a.2a and 5a.2a.1 rather well. Ferret antisera raised against A/Missouri/11/2025-like (A/Bahrain/25220003050/2025 was used at the NRCI) recognized recently circulating viruses from both 5a.2a and 5a.2a.1 clades well. Two isolates were antigenically different from the three antisera tested.

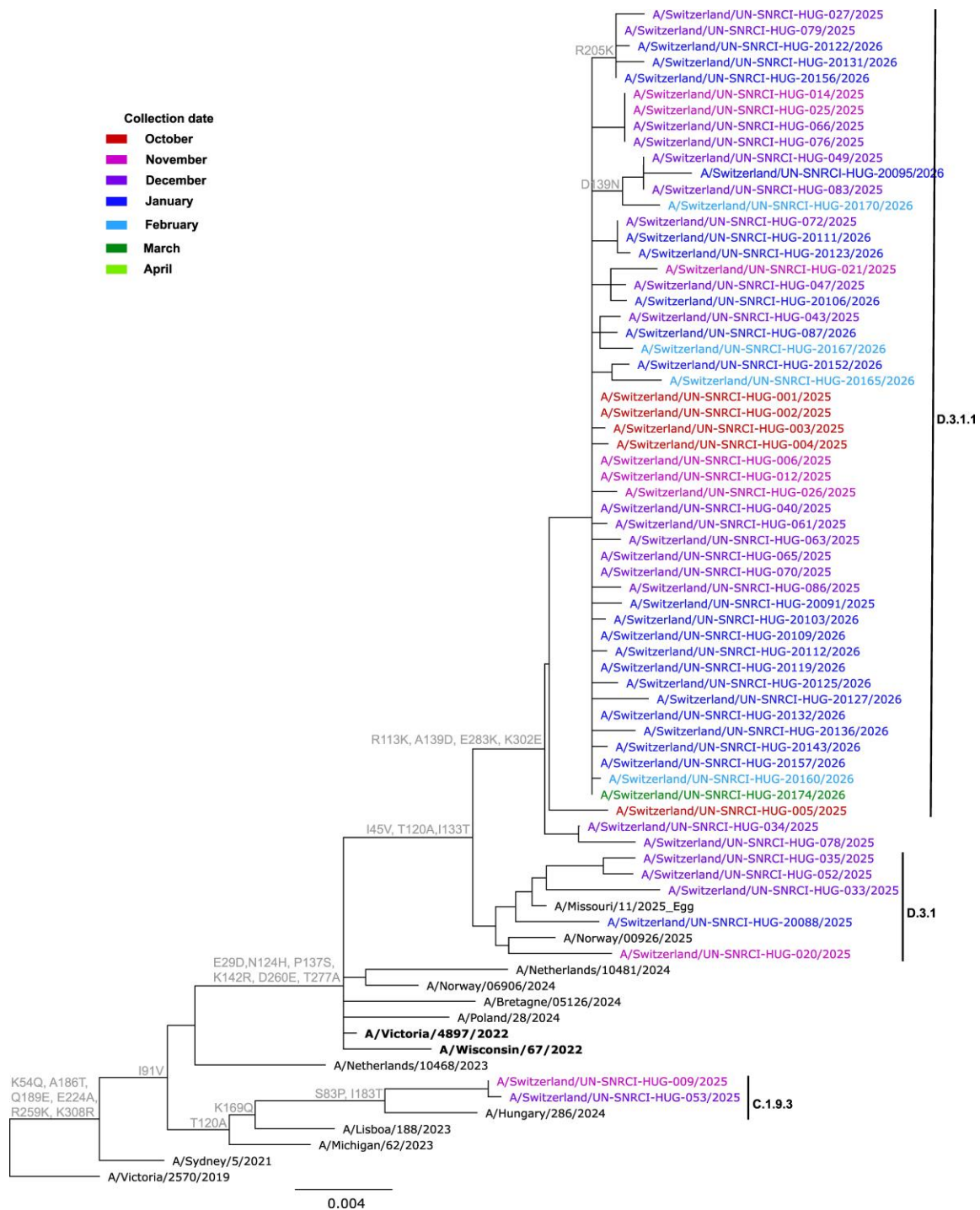


Table 2: Antigenic analysis of influenza A/H1N1pdm09 viruses. Test viruses were sequenced except for those indicated with an asterisk (*) and viruses sequenced by the WIC are indicated with a circumflex (^).

			Post-infection ferret antiserum		
			A/Guangdong-Maonan/SWL153 6/19	A/Victoria/4897/ 22	A/Bahrain/25220 003050/2025
Viruses	Genetic group	Collection Date			
REFERENCE VIRUSES					
A/Guangdong-Maonan/SWL1536/2019	B		1024	16	16
A/Victoria/4897/2022	D		16	512	512
A/Bahrain/25220003050/2025	D.3.1		16	2048	1024
TEST VIRUSES					
A/Switzerland/UN-SNRCI-HUG-001/2025^	D.3.1.1	2025-10-16	64	256	x
A/Switzerland/UN-SNRCI-HUG-002/2025^	D.3.1.1	2025-10-17	16	2048	x
A/Switzerland/UN-SNRCI-HUG-003/2025^	D.3.1.1	2025-10-20	<16	1024	x
A/Switzerland/UN-SNRCI-HUG-005/2025^	D.3.1.1	2025-10-30	<16	1024	x
A/Switzerland/UN-SNRCI-HUG-006/2025^	D.3.1.1	2025-11-03	16	512	x
A/Switzerland/UN-SNRCI-HUG-009/2025^	C.1.9.3	2025-11-05	128	1024	512
A/Switzerland/UN-SNRCI-HUG-012/2025^	D.3.1.1	2025-11-17	<16	1024	512
A/Switzerland/UN-SNRCI-HUG/014/2025^	D.3.1.1	2025-11-14	64	4096	2048
A/Switzerland/UN-SNRCI-HUG/ns0101/2025*		2025-11-25	16	128	128
A/Switzerland/UN-SNRCI-HUG/ns0102/2025*		2025-11-25	64	4096	2048
A/Switzerland/UN-SNRCI-HUG-021/2025^	D.3.1.1	2025-11-26	16	1024	1024
A/Switzerland/UN-SNRCI-HUG/ns0103/2025*		2025-12-18	64	8192	4096
A/Switzerland/UN-SNRCI-HUG-070/2025	D.3.1.1	2025-12-17	<16	2048	1024
A/Switzerland/UN-SNRCI-HUG/ns0104/2025*		2025-12-29	16	2048	1024
A/Switzerland/UN-SNRCI-HUG.083/2025	D.3.1.1	2025-12-29	<16	2048	512
A/Switzerland/UN-SNRCI-HUG-20103/2026	D.3.1.1	2026-01-07	<16	2048	1024
A/Switzerland/UN-SNRCI-HUG-20111/2026	D.3.1.1	2026-01-12	16	4096	2048
A/Switzerland/UN-SNRCI-HUG-20112/2026	D.3.1.1	2026-01-13	16	4096	2048
A/Switzerland/UN-SNRCI-HUG/ns0105/2026*		2026-01-12	<16	2048	1024
A/Switzerland/UN-SNRCI-HUG-20119/2026	D.3.1.1	2026-01-16	16	4096	1024
A/Switzerland/UN-SNRCI-HUG-20125/2026	D.3.1.1	2026-01-19	<16	4096	1024
A/Switzerland/UN-SNRCI-HUG-20143/2026	D.3.1.1	2026-01-23	64	64	64
A/Switzerland/UN-SNRCI-HUG/ns0106/2026*		2026-01-26	128	128	128
A/Switzerland/UN-SNRCI-HUG-20160/2026	D.3.1.1	2026-02-01	16	128	128
A/Switzerland/UN-SNRCI-HUG/ns0107/2026*		2026-02-05	32	16	32
A/Switzerland/UN-SNRCI-HUG/ns0108/2026*		2026-02-06	16	4096	2048
A/Switzerland/UN-SNRCI-HUG-20167/2026	D.3.1.1	2026-02-09	16	4096	1024
A/Switzerland/UN-SNRCI-HUG/ns0109/2026*		2026-02-13	<16	<16	<16
A/Switzerland/UN-SNRCI-HUG/ns0110/2026*		2026-02-17	<16	4096	1024
A/Switzerland/UN-SNRCI-HUG/ns0111/2026*		2026-02-20	16	1024	512
A/Switzerland/UN-SNRCI-HUG-20170/2026	D.3.1.1	2026-02-23	16	4096	2058
A/Switzerland/UN-SNRCI-HUG/ns0112/2026*		2026-02-24	16	2048	1024
A/Switzerland/UN-SNRCI-HUG/ns0113/2026*		2026-03-24	16	128	128
A/Switzerland/UN-SNRCI-HUG/ns0114/2026*		2026-03-11	16	4096	2048

<4-fold
 4-fold
 8-fold
 >8-fold

Influenza A/H3N2

HA(H3) sequences from the Sentinella cohort were aligned with the reference HA(H3) sequences from ECDC (Appendix 8), clade and subclades were obtained using Nextclade v3.21.2 [3].

K189R; and K characterised by K2N, S144N [a potential addition of an N-glycosylation site], N158D, I160K, Q173R, T328A and S378N) (Figure 8). Subclade K was reported to be overrepresented across Europe. For more information on subclade K refer to paragraphe D.1.

Table 3: Antigenic analysis of influenza A/H3N2 viruses. Test viruses were sequenced except for those indicated with an asterisk (*) and viruses sequenced by the WIC are indicated with a circumflex (^).

			Post-infection ferret antiserum			
Viruses	Genetic group	Collection Date	A/Darwin/9/2021	A/Thailand/8/2022	A/Croatia/10136RV/2023	A/Valladolid/1187/2025
REFERENCE VIRUSES						
A/Darwin/9/2021	G.1		256	32	128	32
A/Thailand/8/2022	J		128	128	256	64
A/Croatia/10136RV/2023	J.2		256	256	1024	64
A/Valladolid/1187/2025	J.2.4		32	16	64	1024
TEST VIRUSES						
A/Switzerland/UN-SNRCI-HUG/010/2025	K	2025-11-10	<16	16	16	128
A/Switzerland/UN-SNRCI-HUG/011/2025	K	2025-11-10	<16	16	<16	256
A/Switzerland/UN-SNRCI-HUG/ns0301/2025*		2025-11-14	16	16	16	512
A/Switzerland/UN-SNRCI-HUG/013/2025^	K	2025-11-14	<16	16	16	256
A/Switzerland/UN-SNRCI-HUG/016/2025	K	2025-11-17	16	32	32	512
A/Switzerland/UN-SNRCI-HUG/017/2025	K	2025-11-18	<16	16	16	256
A/Switzerland/UN-SNRCI-HUG/019/2025	K	2025-11-24	<16	16	32	256
A/Switzerland/UN-SNRCI-HUG/071/2025	K	2025-12-18	<16	16	32	512
A/Switzerland/UN-SNRCI-HUG/ns0302/2025*		2025-12-17	<16	16	16	128
A/Switzerland/UN-SNRCI-HUG/082/2025	K	2025-12-29	16	16	64	512
A/Switzerland/UN-SNRCI-HUG/ns0303/2026*		2026-01-06	16	32	64	1024
A/Switzerland/UN-SNRCI-HUG/ns0304/2026*		2026-01-06	32	32	128	1024
A/Switzerland/UN-SNRCI-HUG/ns0305/2026*		2026-01-06	<16	16	32	256
A/Switzerland/UN-SNRCI-HUG/ns0306/2026*		2026-01-05	<16	16	32	1024
A/Switzerland/UN-SNRCI-HUG/ns0307/2026*		2026-01-06	32	64	64	256
A/Switzerland/UN-SNRCI-HUG-20113/2026	K	2026-01-13	16	32	32	32
A/Switzerland/UN-SNRCI-HUG-20120/2026	K	2026-01-16	<16	16	16	256
A/Switzerland/UN-SNRCI-HUG-20121/2026	K	2026-01-14	<16	<16	<16	128
A/Switzerland/UN-SNRCI-HUG-20142/2026	K	2026-01-22	32	32	32	64
A/Switzerland/UN-SNRCI-HUG/ns0308/2026*		2026-01-26	32	32	64	64
A/Switzerland/UN-SNRCI-HUG-20144/2026	K	2026-01-22	32	32	32	32
A/Switzerland/UN-SNRCI-HUG-20145/2026	K	2026-01-22	32	32	32	32
A/Switzerland/UN-SNRCI-HUG/ns0309/2026*		2026-01-27	128	128	128	128
A/Switzerland/UN-SNRCI-HUG-20147/2026	K	2026-01-26	64	64	64	128
A/Switzerland/UN-SNRCI-HUG-20148/2026	K	2026-01-27	32	32	64	128
A/Switzerland/UN-SNRCI-HUG/ns0310/2026*		2026-02-09	32	16	<16	32
A/Switzerland/UN-SNRCI-HUG-20166/2026	K	2026-02-09	<16	16	32	32
A/Switzerland/UN-SNRCI-HUG-20168/2026	K	2026-02-13	<16	<16	<16	32
A/Switzerland/UN-SNRCI-HUG/ns0311/2026*		2026-02-13	16	32	32	32
A/Switzerland/UN-SNRCI-HUG/ns0312/2026*		2026-02-20	16	16	32	32
A/Switzerland/UN-SNRCI-HUG-20169/2026	K	2026-02-20	32	63	<16	16
A/Switzerland/UN-SNRCI-HUG/ns0313/2026*		2026-02-26	32	32	32	32
A/Switzerland/UN-SNRCI-HUG/ns0314/2026*		2026-03-02	<16	16	16	16
A/Switzerland/UN-SNRCI-HUG-20172/2026	K	2026-03-02	32	32	64	128
A/Switzerland/UN-SNRCI-HUG/ns0315/2026*		2026-03-05	32	32	128	256



For antigenic characterisation of A/H3N2 viruses, HAI were performed using antisera against: A/Darwin/9/2021 (clade 2a (G.1)), A/Thailand/08/2022 (clade 2a.3a.1 (J)), A/Croatia/10136RV/2023 (clade 2a.3a.1 (J.2)), and A/Valladolid/1187/2025 (clade 2a.3a.1 (J.2.4)) (Table 3).

Post-infection ferret antisera raised against egg-propagated A/Croatia/10136RV/2023-like (clade 2a.3a.1, subclade J.2) viruses, representing the A(H3N2) component for the NH 2025-2026 influenza vaccines, showed poor recognition with circulating subclade K viruses. Post-infection ferret antisera raised against egg-propagated A/Singapore/GP20238/2024-like J.2.4 viruses (A/Valladolid/1187/2025 was used at the NRCI) showed good recognition of viruses from the subclade K early in the season.

However, this was lost mid-season. Indeed, circulating viruses were then poorly recognised by the antisera. This observation could be explained by the presence of additional mutations that have not yet been assigned (Table 3).

Influenza B

HA(B/Vic) sequences from the Sentinella cohort were aligned with the reference HA(B) sequences from ECDC (Appendix 9), clade and subclades were obtained using Nextclade v3.21.2 [3].

During season 2025-2026, the NRCI received only 3 samples that tested positive for Influenza B and only one of them fulfilled the criteria for sequencing. This sequence belonged to the B/Victoria lineage within the clade V1A.3a.2 (C.5.7).

For antigenic characterisation of B/Victoria viruses, HAI were performed using antisera against: B/Washington/02/2019 (clade V1A.3), B/Austria/1359417/2021 (clade V1A.3a.2 (C)), and B/Stockholm/3/2022 (clade V1A.3a.2 (C.5)) (Table 4). Circulating viruses appeared to be well recognised by ferret antisera raised against recent strains. However, the limited number of samples tested does not allow firm conclusions to be drawn.

Table 4: Antigenic analysis of influenza B(Vic). Test viruses were also sequenced except for those indicated with an asterisk (*).

			Post-infection ferret antiserum		
			B/Washington/02/2029	B/Austria/1359417/2021	B/Stockholm/3/2022
Viruses	Genetic group	Collection Date			
REFERENCE VIRUSES					
B/Washington/02/2029	A.3.2		256	<16	<16
B/Austria/1359417/2021	C		<16	1024	128
B/Stockholm/3/2022	C.5		32	256	256
TEST VIRUSES					
B/Switzerland/UN-SNRCI-HUG/118/2026	C.5.7	2026-01-14	16	512	512
B/Switzerland/UN-SNRCI-HUG/ns01/2026*		2016-02-02	32	1024	1024
B/Switzerland/UN-SNRCI-HUG/ns02/2026*		2026-04-02	32	32	32

<4-fold
 4-fold
 8-fold
 >8-fold

c. Antiviral susceptibility

Of 152 PA gene sequences (56 A/H1N1pdm09 and 60 A/H3N2) screened for genetic markers associated with reduced susceptibility to the endonuclease inhibitor baloxavir marboxil, only one showed evidence of possible reduced inhibition (virus strain: A/Switzerland/UN-SNRCI-HUG-20091/2025 (H1N1)). The detected mutation, E199G, was reported with an EC₅₀ fold change comprise between 0.5 to 3.7 depending on the publication [4-6]. As of July 2025, only a fold-change value >3-fold is considered as reduced susceptibility to baloxavir marboxil.

Of 152 NA gene sequences (56 A/H1N1pdm09 and 96 A/H3N2) screened for genetic markers associated with reduced susceptibility to neuraminidase inhibitors (NAIs), two (1.3 %) had I223V and S247N substitutions (strain: A/Switzerland/UN-SNRCI-HUG-043/2025 (H1N1) and A/Switzerland/UN-SNRCI-HUG-087/2026 (H1N1)). Of note, 36 (23 %) A/H1N1 NA sequences presented the S247N substitution which, alone, doesn't confer reduced inhibition but represent genetic predisposition to acquire resistance.

A small subset of A/H1N1pdm09 viruses were subjected to NA inhibition assays (MUNANA) to access their phenotypic susceptibility to oseltamivir and zanamivir. Those strains were selected based on their genetic profile: two viruses had I223V and S247N substitutions and showed reduced inhibition to oseltamivir in the assay; three viruses had S247N substitution and showed normal inhibition to both oseltamivir and zanamivir; one virus had no substitutions and showed no resistance (Table 5).

Table 5: Neuraminidase amino acid substitutions assessed for their effects on inhibition by neuraminidase inhibitors.

	Amino acid substitution ^a	Expected susceptibility based on genotype		Assessed susceptibility by NA inhibition assay ^b (IC ₅₀ fold change) ^c	
		Oseltamivir	Zanamivir	Oseltamivir	Zanamivir
REFERENCE VIRUSES					
A/California/12/2012	none	NI	NI	NI (1)	NI (1)
A/Texas/23/2012	H275Y	HRI	NI	HRI (840)	NI (1.49)
TEST VIRUSES					
A/Switzerland/UN-SNRCI-HUG-027/2025	S247N	NI	NI	NI (3.64)	NI (4.21)
A/Switzerland/UN-SNRCI-HUG-043/2025	I223V + S247N	RI	NI	RI (13.52)	NI (3.72)
A/Switzerland/UN-SNRCI-HUG-047/2025	S247N	NI	NI	NI (3.54)	NI (1.52)
A/Switzerland/UN-SNRCI-HUG-066/2025	none	NI	NI	NI (1.15)	NI (1.40)
A/Switzerland/UN-SNRCI-HUG-072/2025	S247N	NI	NI	NI (3.27)	NI (3.45)
A/Switzerland/UN-SNRCI-HUG-087/2026	I223V + S247N	RI	NI	RI (15.03)	NI (2,45)

^a Numbering based on the neuraminidase subtype N1 for type A

^b Assessed by NA inhibition fluorescent assay (MUNANA). NAI phenotype is shown according to the referenced studies: NI, normal inhibition; RI, reduced inhibition; HRI, highly reduced inhibition

^c Fold-changes in IC₅₀ (half maximal inhibitory concentration) relative to wild-type virus. For type A viruses: <10-fold - NI; 10-100-fold - RI; >100-fold - HRI.

3. Genetic characterisation of SARS-CoV-2

A total of 87 SARS-CoV-2 samples were sent for whole genome sequencing (WGS) to Microsynth AG, followed by data analysis performed by the Swiss Pathogen Surveillance Platform (SPSP). SPSP then upload 83 sequences on GISAID (Appendix 4). Clades were assigned using Nextclade v3.8.1 [3], with a clade definition from Nextstrain and Pango-lineage [7, 8].

Between October 2025 and May 2026, SARS-CoV-2 genetic surveillance in Switzerland identified the circulation of two Variants Under Monitoring (VUMs), with XFG/XFG.* predominating (66 % of sequenced samples) and NB.1.8.1 detected at a lower frequency (2 %). No Variants of Interest (VOIs) were observed during the study period (Figure 9). Multiple additional lineages circulated at low frequencies, with variants belonging to the PQ.* lineage accounting for 11 % of all sequenced samples and with sub-lineage PQ.16.1.1 classified as VUM in July 2026 [9].

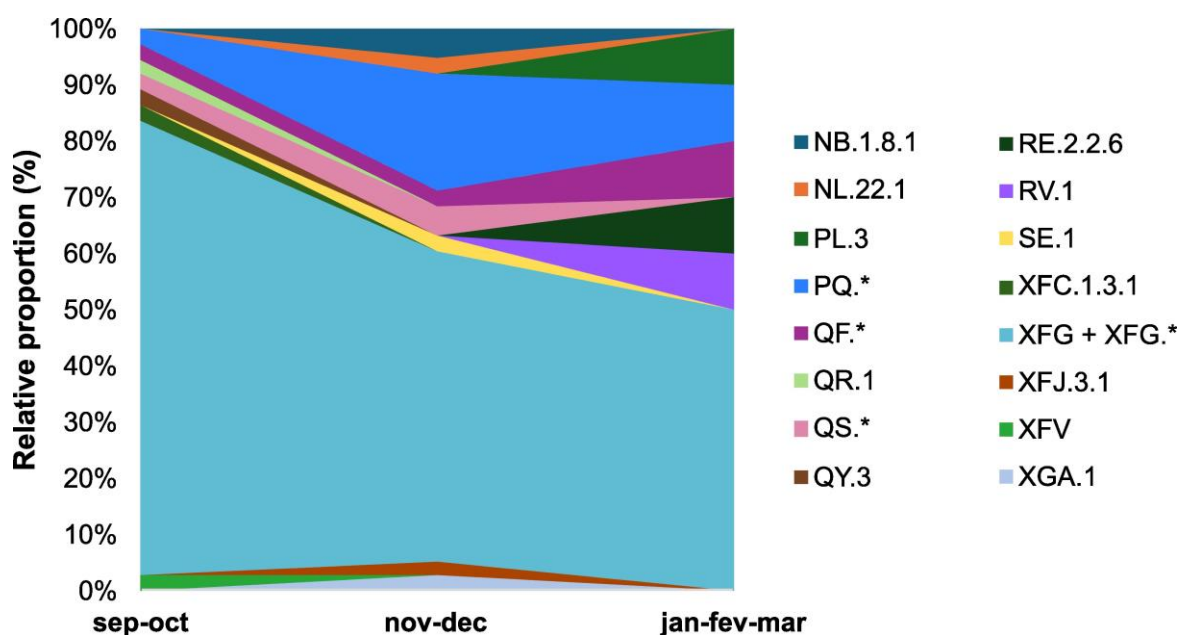


Figure 9: Time-dependent variation in frequencies of SARS-CoV-2 variants in Sentinella population.

4. Genetic characterisation of RSV

A total of 48 RSV isolates were submitted to the Genome Centre for whole-genome sequencing (WGS), with subsequent data analysis performed by the Swiss Pathogen Surveillance Platform (SPSP). However, due to technical difficulties encountered during the library preparation and sequencing steps, SPSP was unable to generate genome assemblies of sufficient quality for further analysis.

D. Epidemiological summary: comparison of national and international data

1. Influenza viruses

In Europe, the 2025-2026 respiratory virus season (week 40/2025 to week 20/2026) was characterised by an intense influenza season with positivity above the 10 % threshold starting in week 44 and lasting for 19 weeks. The percentage of positive samples showed a steady rise, plateaued at about 43 % from week 50/2025 to week 01/2026 and decreased until week 10/2026 crossing below the threshold of 10 %.

In all surveillance systems, influenza A viruses predominated during the 2025-2026 season, with A/H3N2 viruses circulating more frequently than A/H1N1pdm09. Influenza B virus circulation was very limited but increased slightly in the Americas and Asia towards the end of the season [10, 11]. All the Influenza B sequenced worldwide belonged to the B/Victoria lineage (clade V1A.3a.2), with co-circulation of subclades C.3.1 (vaccine reference B/Kanagawa/AC2414/2025), C.5.6 (vaccine reference B/Switzerland/329/2024), and C.5.7 (reference B/Greece/5509/2024). (Figure 11 and Figure 12). More than >99 % of A/H1N1 viruses sequenced globally belonged to clade 5a.2a.1 subclade D (vaccine reference A/Victoria/4897/2022), with over 93 % assigned to subclade D.3.1. The reference strain A/Missouri/11/2025 was selected for the vaccine for the NH season 2026-2027 vaccine composition (Figure 11). All A/H3N2 viruses sequenced in the WHO European region belong to clade J (reference strain A/Thailand/8/2022) which is further divided in 5 subclades: subclade J.2 (reference strain A/Croatia/10136RV/2023) accounted for approximately 22 % of sequences, whereas subclade K (formerly J.2.4.1) represented more than 70 % of total sequences (Figure 11 and Figure 12).

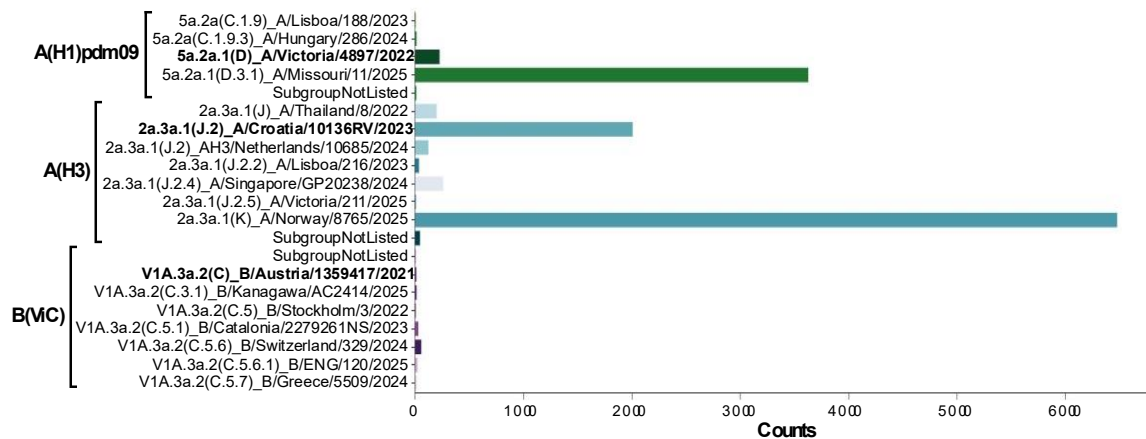


Figure 10: Cumulative influenza virus detections by genetic clade from week 40/2025 to week 20/2026 in Europe. Vaccine clade(subclade)_strain in the NH 2025-2026 season are shown in bold. Adapted from <https://erviss.org/>. Country selection: WHO/EURO region. © World Health Organization 2026.

Subclade K emerged and expanded rapidly during the Southern Hemisphere winter of 2025, becoming the predominant A(H3N2) lineage worldwide during the 2025-2026 season. Genetic analyses identified several additional haemagglutinin (HA) amino acid substitutions, including K2N, S144N, N158D, I160K, Q173R, T328A and S378N, relative to subclade J.2.4, with several of these changes located within key antigenic sites involved in antibody recognition [12-14]. These mutations were associated with antigenic drift and are thought to have contributed to the successful global spread of subclade K viruses. Post-infection ferret antisera raised against the A(H3N2) vaccine strain included in the 2025-2026 Northern Hemisphere vaccine showed substantially reduced reactivity against subclade K viruses, indicating marked antigenic differences from previously circulating strains [15]. However, interim influenza vaccine effectiveness estimates against A(H3N2) infection ranged from approximately 25 % to 45 % across age groups. Although vaccine effectiveness was moderate and within the lower range typically observed for A(H3N2) viruses, the level of protection observed in the population was greater than anticipated based solely on genetic and ferret antisera antigenic characterisation data [16-18].

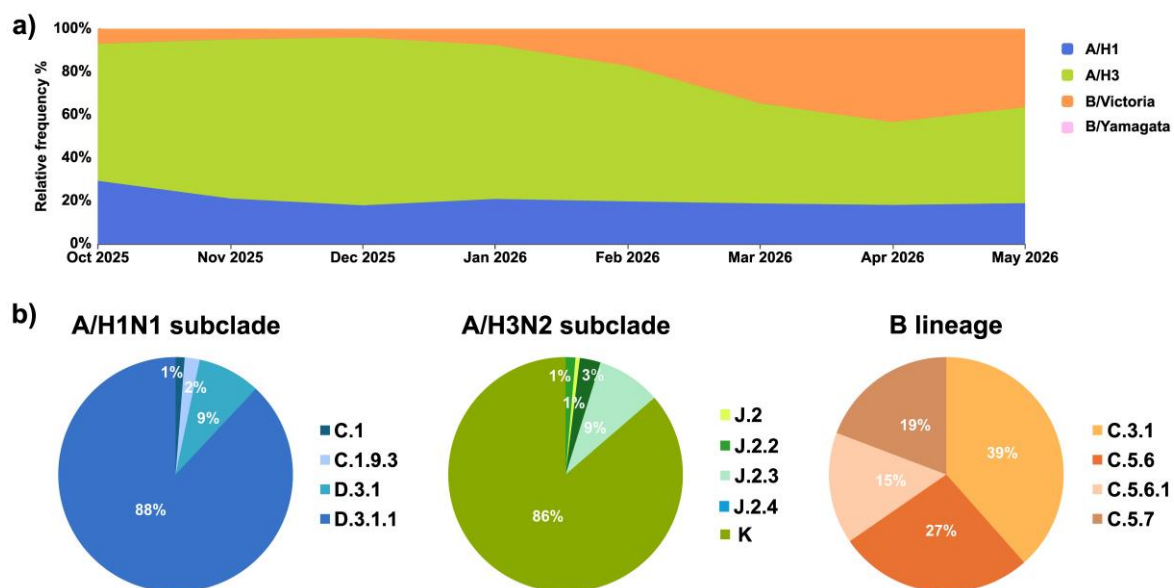


Figure 11: Worldwide distribution of Influenza viruses. **a)** relative frequencies over time as displayed on GISAID; **b)** representation of genetic subclades, obtained with full HA sequences as deposited in GISAID and classified using Nextclade. GISAID criteria were as follow: 1) Basic filters: type = A or B, H = 1 or 3, N = 1 or 2, host = human, location = all), 2) additional filters: Collection date from 29.09.2025 to 17.05.2026, submission date until 01.07.2026, submitting laboratory = GISRS submission*, required segments = HA (only complete), sampling strategy = Sentinel surveillance (ILI, ARI, SARI and other). This resulted in a total of 242 A/H1N1, 655 A/H3N2 and 26 B sequences analysed. *not specified for IBV.

2. SARS-CoV-2

Between 2020 and 2025, SARS-CoV-2 transitioned from a pandemic-level threat to an endemic respiratory virus, with recurrent waves of infection driven by emerging variants. Surveillance strategies rapidly switched from widespread diagnostic testing to targeted sentinel surveillance, wastewater-based monitoring, and hospital-based reporting systems, enabling continued tracking of the virus's genetic evolution and epidemiological dynamics. [19, 20].

From October 2025 to May 2026, global SARS-CoV-2 circulation remained dominated by descendants of the Omicron JN.1 lineage, with continued diversification into numerous sublineages. The recombinant lineage XFG and its sublineages (XFG.*) became the predominant variants in many regions, while NB.1.8.1, designated by the WHO as a Variant Under Monitoring (VUM), circulated at lower but notable levels. NB.1.8.1 was associated with increased transmission and partial immune escape compared with earlier lineages; however, available evidence did not indicate increased disease severity or a substantial reduction in vaccine effectiveness against severe outcomes [9, 21]. No Variants of Concern (VOCs) were identified globally during this period, and the global SARS-CoV-2 landscape remained dominated by Omicron-derived lineages. Genetic diversity remained high, with numerous low-frequency lineages co-circulating worldwide. Variants belonging to the PQ.* lineage were detected at low prevalence during the study period; notably, the descendant lineage PQ.16.1.1 was subsequently designated by the WHO as a VUM in July 2026 following an increase in its global proportion. Despite ongoing viral evolution and lineage turnover, available evidence did not indicate increased disease severity compared with other circulating variants, underscoring the importance of continued genomic surveillance (Figure 13) [22, 23].

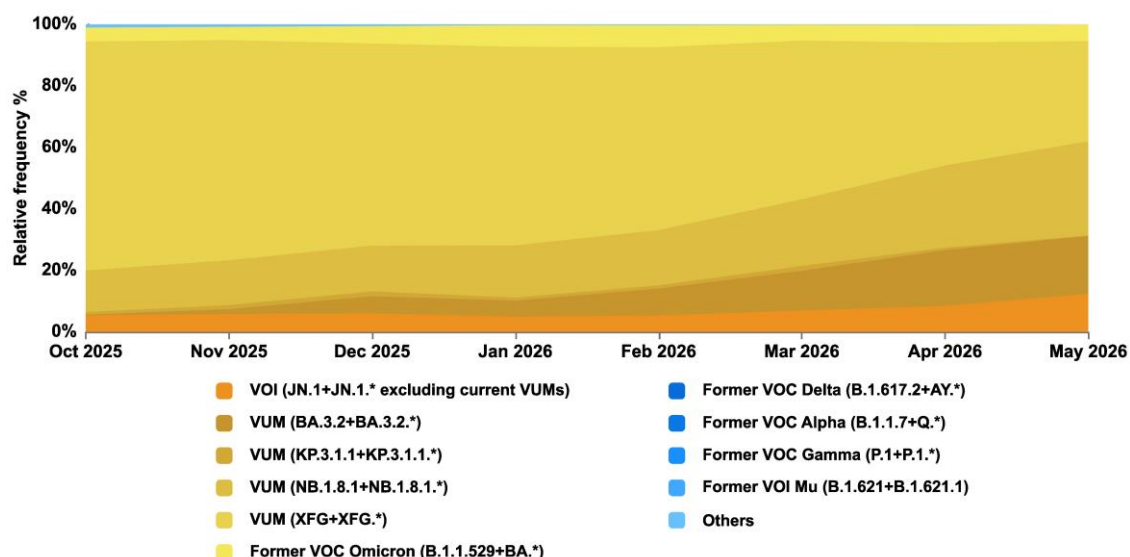


Figure 12: Relative frequency of SARS-CoV-2 VOC/VOI/VUM from October 2025 to May 2026 worldwide. Adapted from GISAID.

3. RSV

In temperate regions, RSV epidemics typically emerge during the winter months, often co-circulating with influenza and other respiratory viruses [24, 25].

However, the onset of the COVID-19 pandemic in 2020 and the widespread implementation of non-pharmaceutical interventions significantly disrupted the usual epidemiological patterns of RSV worldwide [26]. In Switzerland, RSV activity during the 2020-2021 season was notably delayed, with cases emerging during an atypical inter-seasonal period in June and July 2021. Comparable trends were reported in Germany and the Netherlands. By October 2022, RSV cases in Switzerland had risen sharply, preceding the seasonal influenza wave and persisting until March 2023. This extended period of viral activity marked a deviation from the norm [27].

During the surveillance periods from October 2023 to April 2025, RSV circulation patterns largely reverted to their pre-pandemic seasonal rhythm, although activity remained at relatively low levels [10]. Since the end of 2024, the widespread implementation of nirsevimab - a long-acting monoclonal antibody for RSV prevention in infants - has been associated with a measurable reduction in RSV transmission and hospitalisation rates, particularly in regions with high immunisation coverage. Epidemiological data suggest that nirsevimab prevented approximately 40 % to 50 % of RSV cases among neonates and young children [28-30].

During season 2025-2026, similar to that observed during recent post-pandemic seasons, RSV activity started later than historical averages in several regions, with epidemic waves extending into the spring months. Both RSV-A and RSV-B co-circulated across Europe, with no clear predominance of either subtype (Figure 14). Although no sequencing data were available for Switzerland, this pattern is likely to have been similar, as RSV circulation trends in Switzerland generally mirror those observed in neighbouring countries.

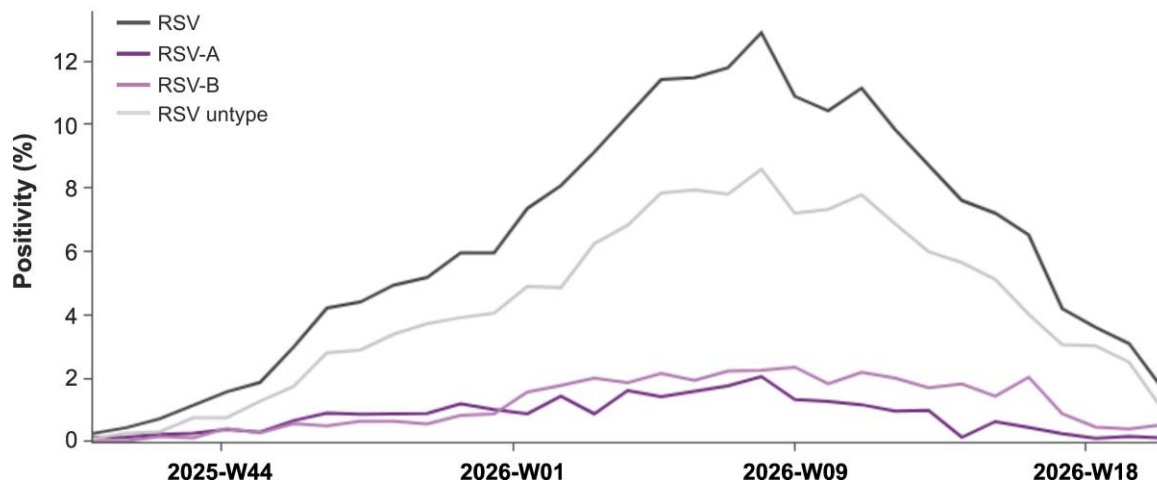


Figure 13: Aggregate weekly test positivity of RSV from week 40/2025 to week 20/2026 in Europe. Taken from <https://erviss.org/>. Country selection: WHO/EURO region. © World Health Organization 2026.

E. Suspicion of zoonotic transmission

In 2001, the Federal Food Safety and Veterinary Office initiated a collaborative project with the Federal Office of Public Health, the Institute of Virology of the Vetsuisse Faculty of the University of Zurich, the Pig Health Service (SSP) of SUISAG, and the NRCI, which aimed at monitoring the swine influenza circulation in Switzerland. The project is named “Surveillance of swine influenza in pigs and humans”. In this context, specimens from farm pigs with respiratory symptoms are sent to, and analysed by, the National Veterinarian Institute (Vetvir, Zurich). In parallel, nasal swabs from pig breeders (or their employees), who have been in contact with influenza-infected animals and present with ILI symptoms, are sent to the NRCI. Samples are screened using the commercially available BioFire® Respiratory Panel 2.1 *plus*. As well as a rRT-PCR adapted from the 2009 USA Centers for Disease Prevention and Control (CDC) protocol, detecting both animal and human matrix gene sequences of Influenza A and an in-house RT-PCR used for subtyping Influenza A viruses and specific for human H1N1pdm09 and H3N2.

From week 40/2025 to week 20/2026, the NRCI received 3 non-sentinel samples originating from Swiss farmers having contact with sick pigs:

- Sample 1 tested negative for Influenza A and Influenza B but positive for Rhinoviruses in the BioFire®.
- Sample 2 tested negative for Influenza A and Influenza B but positive for Rhinoviruses and Parainfluenza virus 1 in the BioFire®.
- Sample 3 tested positive for Influenza A both with the BioFire® and our in-house RT-PCR targeting the matrix gene. However, the in-house PCR for seasonal human Influenza A subtyping was negative suggesting a zoonotic transmission. The sample was submitted to in-house next generation sequencing using MinION (LSK114, Oxford Nanopore Technologies). A blast analysis confirmed that the sequenced segments (3/8) matched to swine viruses circulating in Europe with the best matched strain being A/swine/Spain/28000-1/2021(H1N1). This sample was sent to the WIC in London for further analysis.

F. Method development within the NRCI

1. Primer update for Influenza subtyping

During the summer 2025, a new variant of seasonal influenza A/H3N2 subclade JK appeared. This variant accumulated mutations in the HA gene resulting in a poor recognition by the primers used for Influenza A/H3 subtyping. These primers are included in a quadriplex RT-PCR which allows simultaneous detection of H1, N1, H3 and N2.

Primer update

The current primers and probe were aligned on sequences published on GISAID for viruses from recent subclade J.2.4, K and from virus circulating in Switzerland during the 2024-25 season (Appendix 5). It appeared that both primers had mismatch at their 3' end compared to the recent subclade J.2.4 and K which probably resulted in the lack of detection of those H3 subtypes. Thus, sequences for both the forward and reverse primer were slightly modified to match the current circulating strains (Table 6). The sequence of the probe was kept identical since no mutations were detected in that region.

*Table 6: Sequences of the current primers and the tested primers. Nucleotides in red were removed. Nucleotides in orange were modified. Nucleotides in green were added. *based on CDC Realtime RTPCR (rRTPCR) Protocol for Detection and Characterization of Influenza, Revised April 4, 2006.*

Name	Sequence 5' → 3'	
AH3cdcFor	AAGCATTCCYAATGACAAACCM	Current primers*
AH3cdcRev	ATTGCRCCRAATATGCCTCTAGTM	
A.H3 2025 For	AGCATTCCYAATGACAAACCG	Tested primers
A.H3 2025 Rev	GCTATTGCRCCRAATATGCCTC	

Tested parameters and results

To evaluate the performance of the new primer set, we tested different parameters: specificity (ability to exclusively amplify the target sequence); correlation (agreement between measured and expected values); reproducibility (consistency of results across repeated experiments); and exactitude (closeness of measurements to the true value).

To test for sensitivity, we used clinical samples that were tested negative for SARS-CoV-2, RSV and Influenza A/B using the diagnostic method in place at the HUG, as well as external quality controls received previously. Those external controls were known to be positive for hCoV-OC43, RSV, SARS-CoV-2, Influenza B (Victoria and Yamagata) and Influenza A (H9, H5, H3v of porcine origine). The tested primers exhibit good specificity; they do not produce false positives for HA subtypes such as H5 and H9 or for Influenza B strains, nor do they detect other viruses (RSV, SARS-CoV-2 or HCoV-OC43). In certain cases, even if the primers are design to detect seasonal H3, they may detect H3 subtypes of animal origin. This is the case here with the one H3v tested, which is an H3 subtype of porcine origin.

To test for correlation, we used clinical samples positive for Influenza A/H3 dating from before 2023 and from November 2025. For samples taken before 2023, the two PCR tests perform equally well. However, for samples from November 2025, only the tested primers detect H3. The old ones do not detect them.

To test reproducibility, we made five independent RT-PCR on the same positive sample. The coefficient of variation for the tested primers was like the one of the current primers and below 3 %.

To test for exactitude, we used external quality controls positive for Influenza A/H3. The tested primers detected 100 % of the samples with identical performance to the current primers.

Conclusion

The evaluated primer set showed comparable performance to the current primers when tested on A/H3-negative samples and A/H3-positive samples collected before 2023. However, overall performance was superior, as the new primers successfully detected both historical A/H3 viruses and the variants that emerged in autumn 2025, thereby providing broader detection coverage.

2. In-house sequencing of early season H3N2

At the beginning of the 2025-2026 season, A/H3N2 influenza viruses appeared antigenically different from those circulating during the previous season. This led expert and the media to question whether Switzerland was also experiencing an early wave of infection caused by A/H3N2 subclade K. Using the sequencing facility at HUG and its in-house expertise with MinION (Oxford Nanopore technologies), the NRCI was able to rapidly sequence the first A/H3N2 samples received at the start of the season. Out of 10 samples processed, one failed sequencing. Analysis of the nine successful sequenced showed that eight viruses belonged to the A/H3N2 subclade K, while one belonged to the ancestor A/H3N2 subclade J.2.4.

The same samples were subsequently submitted to the WHO Collaborative Centre in London for sequencing using the Illumina platform. This provided an opportunity to compare the in-house performances with that of the World Influenza Centre in London. Due to a technical issue at the WIC, only four A/H3N2 genomes were available for comparison.

Table 7: Summary of similarity in percent (%) between nucleotide sequences obtained in-house compared to nucleotide sequences obtained at the WHO CC in London.

Virus strain	Segment							
	PB2	PB1	PA	HA	NP	NA	MP	NS
A/Switzerland/UN-SNRCI-HUG/013/2025	100	no seq ^a	100	100	100	100	100	100
A/Switzerland/UN-SNRCI-HUG/022/2025	100	no seq ^a	100	99.9	100	100	100	100
A/Switzerland/UN-SNRCI-HUG/023/2025	100	N ^b	100	100	100	100	100	100
A/Switzerland/UN-SNRCI-HUG/024/2025	100	N ^b	100	100	99.9	100	100	100

^a no sequence was obtained at the WIC

^b two nucleotides were not sequence at the end of the WIC sequence

Conclusion:

The encouraging results obtained in this study support the development of an in-house Nanopore sequencing workflow for Sentinella samples. This approach would facilitate rapid sequence generation, thereby enhancing the timeliness and epidemiological relevance of the data.

G. Collaborative projects

Between October 2025 and May 2026, the NRCI provided materials to the following institutions for various research and diagnostic purposes, as detailed below:

- With the Centre for emerging infectious diseases (CMVE)

In October 2025, the NRCI shared around 200 ul of nasopharyngeal swabs positive for human coronavirus (hCoV) NL63, OC43, 229E and/or HKU1 collected since 2020 by the NRCI with Pr Isabella Eckerle. The project is to investigate if the co-circulation of SARS-CoV-2 has exerted any evolutionary pressure on the other coronaviruses found in humans in terms of changes in their genomic sequence

by sequencing the positive hCoV samples from Sentinella. For this project, the NRCI shared 61 hCoV-E229, 30 hCoV-HKU1, 91 hCoV-NL63 and 150 hCoV-OC43.

- With the laboratory of Spiez – Biology division (Federal Office for Civil Protection)

The NRCI shared an aliquot of nasopharyngeal swabs received via the Sentinella surveillance system with Dr Laura Laloli. 20 swabs were positive for Influenza A, 3 for Influenza B, 3 for SARS-CoV-2, 3 for RSV and 3 were negative. The samples will be used at the NGS facility of the Virology Group at the Spiez Laboratory to validate a next-generation sequencing (NGS) method for subtyping influenza A viruses (IAV).

- With the University of Lausanne and University Hospital of Lausanne

The NRCI shared four nasopharyngeal swabs received via the Sentinella surveillance system that tested positive for Influenza A(H3N2) virus with Dr Valeria Cagno (Laboratory of Antiviral Research). The project is to identify which residues in the hemagglutinin are important to mediate the inhibitory activity of macromolecules presenting sialylated glycans.

H. Evaluation of testing accuracy (External quality control)

To assess our internal performances, the NRCI participates yearly in the external quality control programme for the detection of influenza viruses and SARS-CoV-2 by RT-PCR organised by the WHO. The results received by the NRCI for Panel 24 (2025) are summarised below:

- The NRCI received the panel on 08.09.2025 and reported the results on 03.10.2025 for a turnaround time of 25 days.
- The NRCI attained a full score for (see certificate in Appendix 6):
 - Detection of influenza viruses by RT-PCR (Table 8)
 - Antiviral susceptibility testing of influenza viruses (Table 9)
 - Detection of SARS-CoV-2 by RT-PCR (Table 8)
- The NRCI successfully reported result for the optional sequencing panel of HA gene clade (Table 9).

Table 8: EQA panel 24 (2025) for detection of influenza viruses and SARS-CoV-2 by RT-PCR

Sample	Intended result	Submitted result	Remark ^d
V01-2025	Negative [^]	RSV	
V02-2025	Influenza A(H9)	Influenza A(H9)	
V03-2025	Influenza A(H5)	Influenza A(H5N1)	
V04-2025	SARS-CoV-2	SARS-CoV-2	
V05-2025	Influenza A(H1)pdm09	Influenza A(H1N1)pdm09	
V06-2025	Influenza A(H5)	Influenza A(H5N1)	
V07-2025	SARS-CoV-2	SARS-CoV-2	
V08-2025	Negative [^]	RSV	
V09-2025	Influenza A(H3)	Influenza A(H3N2)	
V10-2025	Influenza A(H5)	Influenza A(H5N1)	
V11-2025	SARS-CoV-2	SARS-CoV-2	
V12-2025	Influenza B	Influenza B (Victoria lineage)	
V13-2025	Swine influenza A(H3)	Influenza A(H3)v	N.A.
V14-2025	Influenza B	Influenza B (Yamagata lineage)	
V15-2025	Negative	Negative	

[^] Positive for respiratory syncytial virus: Result will only be scored if tested

Table 9: EQA panel 24 (2025): optional antiviral susceptibility testing panel and sequencing panel.

OPTIONAL: Antiviral susceptibility testing panel / Sequencing panel

Sample No.	Results	Amino acid substitution associated with reduced susceptibility	Phenotypic antiviral susceptibility results		HA gene clade (subclade) ^c	Remark ^d
			Oseltamivir	Zanamivir		
<u>A(H1N1)pdm09</u> NAI01P-2025 NAI01G-2025	Intended	Mixed PA-38I/T ^a	NI	NI	6B.1A.1	
	Submitted	PA-I38T	NI	NI	6B.1A.1	
<u>A(H1N1)pdm09</u> NAI02P-2025 NAI02G-2025	Intended	NA-I223V, NA-S247N ^b	NI / RI	NI	N.A.	
	Submitted	223V, 247N	RI	NI		
<u>A(H3N2)</u> NAI03P-2025 NAI03G-2025	Intended	NA-E119V ^b	RI / HRI	NI	N.A.	
	Submitted	119V	HRI	NI		
<u>B(Victoria)</u> NAI04P-2025 NAI04G-2025	Intended	None	NI	NI	V1A.3a.2	
	Submitted	None	NI	NI	V1A.3a.2 (C.5.7)	

NI: Normal inhibition; RI: Reduced inhibition; HRI: Highly reduced inhibition; N.A.: Not applicable

^a For educational purpose

^b Neuraminidase numbering based on residue position in N1

^c For samples of sequencing panel (NAI01G-2025 and NAI04G-2025) only

^d Annotation for incorrect results

RT-PCR: (I) Incorrect typing/subtyping/lineage; (II) Incorrect virus; (III) >1 target detected; (IV) False negative; (V) False positive

Antiviral: (i) Genotypic results; (ii) Phenotypic results

I. Materials and methods used by the NRCI

1. Identification of cases

A network of primary care practitioners voluntarily participates, on a yearly basis, in the national epidemiological and virological surveillance of influenza. Each week, they are requested to report ILI and ARI cases. According to ECDC and WHO criteria [31], ILI definition is declared as an acute

respiratory infection with a fever measured to $\geq 38^{\circ}\text{C}$ and cough. Since October 2022, acute respiratory infection (ARI) is defined as an acute onset of illness with cough, sore throat, shortness of breath or rhinitis and of infectious origin, as judged by a physician.

A subgroup of these sentinel practitioners collects nasopharyngeal swabs from patients fitting the ILI and ARI case definitions for respiratory viruses screening. The practitioners are required to complete a brief case report form. The following data are collected: age, sex, sample date, suspicion ILI and/or ARI, and vaccination status (for the current season for influenza and a dose not older than 6 months for COVID-19).

2. Molecular screening

All nasopharyngeal swabs received at the NRCI are screened by rRT-PCR for Influenza A, Influenza B, SARS-CoV-2 and RSV using the cobas[®] Respiratory Flex kit on the cobas[®] 6800 automated system according to manufacturer's instructions.

RNA from influenza-positive nasopharyngeal swabs is then extracted using the QiaSymphony magnetic-particle system (Qiagen, Basel, Switzerland) and recovered in elution buffer. The extracted RNA is subsequently used for IAV subtyping and IBV lineage determination. For these assays, rRT-PCR reactions are performed using 5 μl of extracted RNA and 20 μl of SuperScript[™] III Platinum[™] One-Step qRT-PCR Kit w/ROX (Invitrogen[™]) and run on Quantstudio 5 thermocyclers. Samples are considered positive if they yield a Ct value ≤ 40 and show an increase in fluorescent in both the amplification and multicomponent plots.

IAV positive samples are further subtyped using an in-house quadruplex rRT-PCR targeting the HA (H1 and H3) and the NA (N1 and N2) genes to distinguish between influenza A/H1N1pdm09 and A/H3N2 viruses. The H1 and N2 primers-probe sets were designed in-house. The H3 primers-probe set was adapted from the CDC protocol and updated this season [32]. The N1 primers-probe set was adapted from Henritzi *et al.* [33]. Additional molecular assays are available at the NRCI, when required, to differentiate seasonal influenza viruses from zoonotic influenza viruses. IBV lineage determination is performed using a duplex rRT-PCR adapted from Schweiger *et al.* [34, 35], allowing discrimination between the B/Yamagata/16/88-like (Yam) and B/Victoria/2/87-like (Vic) lineages.

3. Antigenic characterisation of influenza virus

A selection of influenza viruses is submitted to phenotypic and genotypic analysis. In general, five RT-PCR positive samples with Ct values <30 are chosen per week for further characterisation and are submitted to a haemagglutination inhibition (HAI) assay. This latter allows assessment of the antigenic similarity between reference and circulating influenza strains.

a. Cell culture

Both influenza positive and negative samples are cultured on Madin-Darby canine kidney (MDCK) and sialic acid-enriched MDCK (MDCK-SIAT1) cells. This ensures that a low positivity rate for influenza is not due to a rRT-PCR detection defect. For example, this could be the case in the presence of viruses carrying mutations in the genomic regions targeted by rRT-PCR screening.

Briefly, 400 μl of transport medium containing nasopharyngeal swabs are incubated at 33°C on MDCK cells and 37°C on MDCK-SIAT1. The presence of a cytopathic effect (CPE) is monitored for a period of up to 7 days. If CPE is present, samples are submitted to an haemagglutination and haemagglutination inhibition (HAI) assays. If CPE is absent or low after 7 days, the cells are screened for influenza viruses by immunofluorescence using fluoresceinated monoclonal influenza A and B antibodies combined with mouse fluorescein isothiocyanate-conjugate (QuidelOrtho IF D³ Ultra DFA Respiratory Virus Screening & Identification kit, San Diego, USA).

b. Haemagglutination inhibition (HAI) assay

A two-fold serial dilution is performed using 50 µl of viral suspension buffer in SALK solution (5 %) and 25 µl of glutaraldehyde-fixed guinea pig red blood cells (RBC) (1.5 %) are added for 1 h incubation at 4 °C. The HA titre is defined as the last dilution in which the complete haemagglutination is still observed. For samples where the HA titre is >8, HAI assay is performed as follows: 25 µl of reference antisera are added in the first two wells of a 96-well plate. Two-fold dilutions are prepared by adding 25 µl of SALK solution (5 %) in the second well. 25 µl are then collected from the same well and the procedure is repeated to the end of each line. 25 µl of viral suspension containing 4 HA units are added to the antisera dilution and incubated for 1 h at room temperature. 25 µl of guinea pig RBC are then added to each well. The plates are incubated for 1 h at 4 °C. The HAI titre corresponds to the last antiserum dilution for which HA is still inhibited. This titre is compared to the homologous titre obtained with reference strains submitted to their corresponding antigenic antisera (antigenic table). The antigenic tables are influenza strain-specific (Table 10) and are thereby, adjusted yearly.

Reference antisera and corresponding viral strains are kindly provided by the World Health Organisation (WHO) Collaborating Centre Reference Laboratory at the Francis Crick Worldwide Influenza Centre (WIC, London, UK). HAIs are performed with glutaraldehyde fixed guinea pig Red Blood Cells (RBC) (Charles River, Lyon, France).

Table 10: Antigenic tables for the 2025-26 influenza season. These tables correspond to the HAI titres of reference influenza antigens incubated with ferret reference antisera provided by the WHO.

H1N1				
Strains	Ferret antisera	A/Guangdong-Maonan/SWL1536/19 03.12.2025 F09/20	A/Victoria/4897/22 03.12.2025 F05/23	A/Bahrain /25220003050/2025 03.12.2025 F 32/25
A/Guangdong-Maonan/SWL1536/19		1024	<16	<16
A/Victoria/4897/22		<16	512	512
A/Bahrain /25220003050/2025		<16	2048	1024

H3N2					
Strains	Ferret antisera	A/Darwin/9 /2021 03.12.2025 F14/22	A/Thailand/8 /2022 03.12.2025 F38/23	A/Croatia/1013 6RV/2023 03.12.2025 F45/24	A/Valladolid/11 87/2025 03.12.2025 F09/25
A/Darwin/9/2021		256	32	128	32
A/Thailand/8/2022		128	128	256	64
A/Croatia/10136RV/20 23		256	256	1024	64
A/Valladolid/1187/202 5		32	16	64	1024

B/Victoria-like			
Ferret Antisera	B/Washington/02/2019	B/Austria/1359417/2021	B/Stockholm/3/2022
Strains	03.12.2025 F37/19	03.12.2025 F45/21	03.12.2025 F 28/22
B/Washington/02/2019	256	16	<16
B/Austria/1359417/2021	<16	1024	128
B/Stockholm/3/2022	32	256	256

4. Genetic characterisation of influenza virus by whole genome sequencing

A subset of influenza positive samples with Ct values <25 and with no co-detection is also submitted for whole genome sequencing to assess the phylogeny of the circulating viruses and to determine genetic proximity to reference vaccine strains based on the HA gene. Sequencing also allows for the detection of key mutations previously described as conferring resistance to NA inhibitors (NAIs) or baloxavir marboxil treatments, while M and NS genes sequencing allows to check the adequacy of rRT-PCR primers and probes used for influenza A and B screening.

As part of the genomic surveillance programme for respiratory viruses, including seasonal influenza viruses, SARS-CoV-2, and RSV, the NRCI submits selected samples to Microsynth AG (Balgach, Switzerland) for whole-genome sequencing on an Illumina NovaSeq platform. For influenza viruses, whole genomes are amplified using established RT-PCR protocols for influenza A [36] and influenza B [37]. Sequencing libraries are subsequently prepared from the resulting amplicons using the Illumina® DNA Prep (M) Tagmentation kit (Art. No. 20018705) and sequenced according to the manufacturer's instructions. RSV whole-genome sequencing follows a similar amplicon-based approach to that used for influenza viruses and consists of a one-step RT-PCR amplification followed by tagmentation-based library preparation. The primer scheme used for RSV amplification has been described previously by *Dong et al.* [38]. SARS-CoV-2 genomes are amplified using the ARTIC SARS-CoV-2 Amplicon Panel from IDT prior to library preparation and sequencing.

Sequence assembly for influenza viruses and RSV was performed using the Iterative Refinement Meta-Assembler (IRMA). The resulting viral sequences underwent quality control using both the Viral Annotation Definer (VADR) system and custom internal checks developed by the Swiss Institute of Bioinformatics (SIB). For SARS-CoV-2 genome, sequence assembly and quality control was conducted using the V-pipe workflow, with additional in-house quality checks applied to the generated sequences. Clade assignments were determined using Nextclade and Pangolin softwares. Additionally, antiviral resistance-associated mutations in influenza viruses were assessed using FluR, an in-house analysis pipeline. The resulting consensus sequences were submitted to the Global Initiative on Sharing All Influenza Data (GISAID), to the ENA repository and shared directly with the FOPH (Appendix 1, Appendix 2, Appendix 3, Appendix 4).

5. Data availability

Sequence data used to generate the following figures are available on GISAID (<https://gisaid.org/>) via GISAID identifiers:

- Figure 7: EPI_SET_260721qr
- Figure 8: EPI_SET_260721pw
- Figure 12: EPI_SET_260724o (for A/H1N1), EPI_SET_260724ou (for A/H3N2) and EPI_SET_260818tp (for B/Vic).

6. Raw material storage

The NRCI stores all positive samples with a remaining volume greater than 200 μL . In addition, a subset of negative samples is also stored each season.

J. Appendixes

Appendix 1: Table of Sentinella Influenza A/H1N1 sequences submitted to GISAID (40/2025-20/2026)

Isolate name	Collection Date	Subtype or lineage	GISAID_ID
A/Switzerland/UN-SNRCI-HUG/001/2025	2025-10-16	A/H1N1	EPI_ISL_20298144
A/Switzerland/UN-SNRCI-HUG/002/2025	2025-10-17	A/H1N1	EPI_ISL_20298142
A/Switzerland/UN-SNRCI-HUG/003/2025	2025-10-20	A/H1N1	EPI_ISL_20298140
A/Switzerland/UN-SNRCI-HUG/004/2025	2025-10-22	A/H1N1	EPI_ISL_20298138
A/Switzerland/UN-SNRCI-HUG/005/2025	2025-10-30	A/H1N1	EPI_ISL_20298137
A/Switzerland/UN-SNRCI-HUG/006/2025	2025-11-03	A/H1N1	EPI_ISL_20298135
A/Switzerland/UN-SNRCI-HUG/009/2025	2025-11-10	A/H1N1	EPI_ISL_20298133
A/Switzerland/UN-SNRCI-HUG/012/2025	2025-11-17	A/H1N1	EPI_ISL_20298129
A/Switzerland/UN-SNRCI-HUG/014/2025	2025-11-14	A/H1N1	EPI_ISL_20298131
A/Switzerland/UN-SNRCI-HUG/020/2025	2025-11-25	A/H1N1	EPI_ISL_20298128
A/Switzerland/UN-SNRCI-HUG/021/2025	2025-11-26	A/H1N1	EPI_ISL_20298126
A/Switzerland/UN-SNRCI-HUG/025/2025	2025-11-27	A/H1N1	EPI_ISL_20298124
A/Switzerland/UN-SNRCI-HUG/026/2025	2025-11-28	A/H1N1	EPI_ISL_20298123
A/Switzerland/UN-SNRCI-HUG/027/2025	2025-12-01	A/H1N1	EPI_ISL_20335758
A/Switzerland/UN-SNRCI-HUG/033/2025	2025-12-04	A/H1N1	EPI_ISL_20335694
A/Switzerland/UN-SNRCI-HUG/034/2025	2025-12-03	A/H1N1	EPI_ISL_20335689
A/Switzerland/UN-SNRCI-HUG/035/2025	2025-12-04	A/H1N1	EPI_ISL_20335761
A/Switzerland/UN-SNRCI-HUG/040/2025	2025-12-08	A/H1N1	EPI_ISL_20335697
A/Switzerland/UN-SNRCI-HUG/043/2025	2025-12-11	A/H1N1	EPI_ISL_20335752
A/Switzerland/UN-SNRCI-HUG/047/2025	2025-12-11	A/H1N1	EPI_ISL_20335738
A/Switzerland/UN-SNRCI-HUG/049/2025	2025-12-11	A/H1N1	EPI_ISL_20335756
A/Switzerland/UN-SNRCI-HUG/053/2025	2025-12-15	A/H1N1	EPI_ISL_20335767
A/Switzerland/UN-SNRCI-HUG/061/2025	2025-12-17	A/H1N1	EPI_ISL_20335754
A/Switzerland/UN-SNRCI-HUG/063/2025	2025-12-16	A/H1N1	EPI_ISL_20335755
A/Switzerland/UN-SNRCI-HUG/065/2025	2025-12-17	A/H1N1	EPI_ISL_20335728
A/Switzerland/UN-SNRCI-HUG/066/2025	2025-12-16	A/H1N1	EPI_ISL_20335722
A/Switzerland/UN-SNRCI-HUG/068/2025	2025-12-18	A/H1N1	EPI_ISL_20335735
A/Switzerland/UN-SNRCI-HUG/070/2025	2025-12-17	A/H1N1	EPI_ISL_20335751
A/Switzerland/UN-SNRCI-HUG/072/2025	2025-12-18	A/H1N1	EPI_ISL_20335733
A/Switzerland/UN-SNRCI-HUG/074/2025	2025-12-19	A/H1N1	EPI_ISL_20335695
A/Switzerland/UN-SNRCI-HUG/076/2025	2025-12-19	A/H1N1	EPI_ISL_20335743
A/Switzerland/UN-SNRCI-HUG/078/2025	2025-12-22	A/H1N1	EPI_ISL_20335734
A/Switzerland/UN-SNRCI-HUG/079/2025	2025-12-23	A/H1N1	EPI_ISL_20335753
A/Switzerland/UN-SNRCI-HUG/083/2025	2025-12-29	A/H1N1	EPI_ISL_20335725
A/Switzerland/UN-SNRCI-HUG/086/2025	2025-12-29	A/H1N1	EPI_ISL_20335691
A/Switzerland/UN-SNRCI-HUG/087/2026	2026-01-02	A/H1N1	EPI_ISL_20335693
A/Switzerland/UN-SNRCI-HUG-20088/2025	2025-12-29	A/H1N1	EPI_ISL_20480804
A/Switzerland/UN-SNRCI-HUG-20091/2025	2025-12-31	A/H1N1	EPI_ISL_20480867
A/Switzerland/UN-SNRCI-HUG-20095/2026	2026-01-05	A/H1N1	EPI_ISL_20480795
A/Switzerland/UN-SNRCI-HUG-20103/2026	2026-01-07	A/H1N1	EPI_ISL_20480828

A/Switzerland/UN-SNRCI-HUG-20106/2026	2026-01-09	A/H1N1	EPI_ISL_20480812
A/Switzerland/UN-SNRCI-HUG-20109/2026	2026-01-13	A/H1N1	EPI_ISL_20480866
A/Switzerland/UN-SNRCI-HUG-20111/2026	2026-01-12	A/H1N1	EPI_ISL_20480809
A/Switzerland/UN-SNRCI-HUG-20112/2026	2026-01-13	A/H1N1	EPI_ISL_20480802
A/Switzerland/UN-SNRCI-HUG-20117/2026	2026-01-14	A/H1N1	EPI_ISL_20480836
A/Switzerland/UN-SNRCI-HUG-20119/2026	2026-01-16	A/H1N1	EPI_ISL_20480790
A/Switzerland/UN-SNRCI-HUG-20122/2026	2026-01-15	A/H1N1	EPI_ISL_20480798
A/Switzerland/UN-SNRCI-HUG-20123/2026	2026-01-17	A/H1N1	EPI_ISL_20480832
A/Switzerland/UN-SNRCI-HUG-20125/2026	2026-01-19	A/H1N1	EPI_ISL_20480794
A/Switzerland/UN-SNRCI-HUG-20127/2026	2026-01-20	A/H1N1	EPI_ISL_20480825
A/Switzerland/UN-SNRCI-HUG-20131/2026	2026-01-20	A/H1N1	EPI_ISL_20480848
A/Switzerland/UN-SNRCI-HUG-20133/2026	2026-01-23	A/H1N1	EPI_ISL_20480839
A/Switzerland/UN-SNRCI-HUG-20143/2026	2026-01-26	A/H1N1	EPI_ISL_20480829
A/Switzerland/UN-SNRCI-HUG-20147/2026	2026-01-28	A/H1N1	EPI_ISL_20480799
A/Switzerland/UN-SNRCI-HUG-20148/2026	2026-01-30	A/H1N1	EPI_ISL_20480816
A/Switzerland/UN-SNRCI-HUG-20151/2026	2026-02-01	A/H1N1	EPI_ISL_20480793
A/Switzerland/UN-SNRCI-HUG-20156/2026	2026-02-05	A/H1N1	EPI_ISL_20480831
A/Switzerland/UN-SNRCI-HUG-20158/2026	2026-02-09	A/H1N1	EPI_ISL_20480863
A/Switzerland/UN-SNRCI-HUG-20161/2026	2026-02-23	A/H1N1	EPI_ISL_20480856
A/Switzerland/UN-SNRCI-HUG-20164/2026	2026-03-11	A/H1N1	EPI_ISL_20480813
A/Switzerland/UN-SNRCI-HUG-20165/2026	2026-01-20	A/H1N1	EPI_ISL_20480853
A/Switzerland/UN-SNRCI-HUG-20169/2026	2026-01-22	A/H1N1	EPI_ISL_20480855

Appendix 2: Table of Sentinella Influenza A/H3N2 sequences submitted to GISAID (40/2025-20/2026)

Isolate name	Collection Date	Subtype	ISAID_ID
A/Switzerland/UN-SNRCI-HUG/008/2025	2025-11-05	A/H3N2	EPI_ISL_20298154
A/Switzerland/UN-SNRCI-HUG/013/2025	2025-11-14	A/H3N2	EPI_ISL_20298152
A/Switzerland/UN-SNRCI-HUG/022/2025	2025-11-27	A/H3N2	EPI_ISL_20298146
A/Switzerland/UN-SNRCI-HUG/023/2025	2025-11-25	A/H3N2	EPI_ISL_20298150
A/Switzerland/UN-SNRCI-HUG/024/2025	2025-11-26	A/H3N2	EPI_ISL_20298148
A/Switzerland/UN-SNRCI-HUG/029/2025	2025-12-02	A/H3N2	EPI_ISL_20335769
A/Switzerland/UN-SNRCI-HUG/030/2025	2025-12-02	A/H3N2	EPI_ISL_20335759
A/Switzerland/UN-SNRCI-HUG/031/2025	2025-12-03	A/H3N2	EPI_ISL_20335739
A/Switzerland/UN-SNRCI-HUG/032/2025	2025-12-03	A/H3N2	EPI_ISL_20335742
A/Switzerland/UN-SNRCI-HUG/036/2025	2025-12-05	A/H3N2	EPI_ISL_20335736
A/Switzerland/UN-SNRCI-HUG/037/2025	2025-12-08	A/H3N2	EPI_ISL_20335698
A/Switzerland/UN-SNRCI-HUG/038/2025	2025-12-08	A/H3N2	EPI_ISL_20335727
A/Switzerland/UN-SNRCI-HUG/039/2025	2025-12-08	A/H3N2	EPI_ISL_20335750
A/Switzerland/UN-SNRCI-HUG/041/2025	2025-12-08	A/H3N2	EPI_ISL_20335765
A/Switzerland/UN-SNRCI-HUG/042/2025	2025-12-10	A/H3N2	EPI_ISL_20335745
A/Switzerland/UN-SNRCI-HUG/044/2025	2025-12-10	A/H3N2	EPI_ISL_20335731
A/Switzerland/UN-SNRCI-HUG/045/2025	2025-12-09	A/H3N2	EPI_ISL_20335724
A/Switzerland/UN-SNRCI-HUG/046/2025	2025-12-09	A/H3N2	EPI_ISL_20335764
A/Switzerland/UN-SNRCI-HUG/048/2025	2025-12-10	A/H3N2	EPI_ISL_20335741

A/Switzerland/UN-SNRCI-HUG/050/2025	2025-12-10	A/H3N2	EPI_ISL_20335723
A/Switzerland/UN-SNRCI-HUG/051/2025	2025-12-16	A/H3N2	EPI_ISL_20335696
A/Switzerland/UN-SNRCI-HUG/052/2025	2025-12-15	A/H3N2	EPI_ISL_20335740
A/Switzerland/UN-SNRCI-HUG/054/2025	2025-12-10	A/H3N2	EPI_ISL_20335726
A/Switzerland/UN-SNRCI-HUG/055/2025	2025-12-15	A/H3N2	EPI_ISL_20335748
A/Switzerland/UN-SNRCI-HUG/056/2025	2025-12-16	A/H3N2	EPI_ISL_20335692
A/Switzerland/UN-SNRCI-HUG/057/2025	2025-12-16	A/H3N2	EPI_ISL_20335766
A/Switzerland/UN-SNRCI-HUG/058/2025	2025-12-16	A/H3N2	EPI_ISL_20335730
A/Switzerland/UN-SNRCI-HUG/059/2025	2025-12-17	A/H3N2	EPI_ISL_20335746
A/Switzerland/UN-SNRCI-HUG/060/2025	2025-12-17	A/H3N2	EPI_ISL_20335757
A/Switzerland/UN-SNRCI-HUG/062/2025	2025-12-17	A/H3N2	EPI_ISL_20335762
A/Switzerland/UN-SNRCI-HUG/064/2025	2025-12-16	A/H3N2	EPI_ISL_20335747
A/Switzerland/UN-SNRCI-HUG/067/2025	2025-12-16	A/H3N2	EPI_ISL_20335699
A/Switzerland/UN-SNRCI-HUG/069/2025	2025-12-18	A/H3N2	EPI_ISL_20335690
A/Switzerland/UN-SNRCI-HUG/071/2025	2025-12-18	A/H3N2	EPI_ISL_20335729
A/Switzerland/UN-SNRCI-HUG/073/2025	2025-12-17	A/H3N2	EPI_ISL_20335768
A/Switzerland/UN-SNRCI-HUG/075/2025	2025-12-22	A/H3N2	EPI_ISL_20335732
A/Switzerland/UN-SNRCI-HUG/077/2025	2025-12-22	A/H3N2	EPI_ISL_20335721
A/Switzerland/UN-SNRCI-HUG/080/2025	2025-12-23	A/H3N2	EPI_ISL_20335763
A/Switzerland/UN-SNRCI-HUG/081/2025	2025-12-22	A/H3N2	EPI_ISL_20335749
A/Switzerland/UN-SNRCI-HUG/082/2025	2025-12-29	A/H3N2	EPI_ISL_20335744
A/Switzerland/UN-SNRCI-HUG/084/2025	2025-12-29	A/H3N2	EPI_ISL_20335737
A/Switzerland/UN-SNRCI-HUG/085/2025	2025-12-23	A/H3N2	EPI_ISL_20335760
A/Switzerland/UN-SNRCI-HUG-20089/2025	2025-12-30	A/H3N2	EPI_ISL_20480854
A/Switzerland/UN-SNRCI-HUG-20090/2025	2025-12-31	A/H3N2	EPI_ISL_20480805
A/Switzerland/UN-SNRCI-HUG-20092/2025	2025-12-31	A/H3N2	EPI_ISL_20480861
A/Switzerland/UN-SNRCI-HUG-20093/2026	2026-01-06	A/H3N2	EPI_ISL_20480837
A/Switzerland/UN-SNRCI-HUG-20096/2026	2026-01-06	A/H3N2	EPI_ISL_20480817
A/Switzerland/UN-SNRCI-HUG-20097/2026	2026-01-05	A/H3N2	EPI_ISL_20480826
A/Switzerland/UN-SNRCI-HUG-20098/2026	2026-01-06	A/H3N2	EPI_ISL_20480792
A/Switzerland/UN-SNRCI-HUG-20099/2026	2026-01-06	A/H3N2	EPI_ISL_20480815
A/Switzerland/UN-SNRCI-HUG-20100/2026	2026-01-06	A/H3N2	EPI_ISL_20480823
A/Switzerland/UN-SNRCI-HUG-20102/2026	2026-01-06	A/H3N2	EPI_ISL_20480864
A/Switzerland/UN-SNRCI-HUG-20104/2026	2026-01-07	A/H3N2	EPI_ISL_20480791
A/Switzerland/UN-SNRCI-HUG-20105/2026	2026-01-06	A/H3N2	EPI_ISL_20480841
A/Switzerland/UN-SNRCI-HUG-20108/2026	2026-01-09	A/H3N2	EPI_ISL_20480838
A/Switzerland/UN-SNRCI-HUG-20110/2026	2026-01-13	A/H3N2	EPI_ISL_20480834
A/Switzerland/UN-SNRCI-HUG-20113/2026	2026-01-13	A/H3N2	EPI_ISL_20480796
A/Switzerland/UN-SNRCI-HUG-20114/2026	2026-01-13	A/H3N2	EPI_ISL_20480807
A/Switzerland/UN-SNRCI-HUG-20120/2026	2026-01-16	A/H3N2	EPI_ISL_20480801
A/Switzerland/UN-SNRCI-HUG-20121/2026	2026-01-14	A/H3N2	EPI_ISL_20480868
A/Switzerland/UN-SNRCI-HUG-20124/2026	2026-01-16	A/H3N2	EPI_ISL_20480830
A/Switzerland/UN-SNRCI-HUG-20126/2026	2026-01-19	A/H3N2	EPI_ISL_20480803
A/Switzerland/UN-SNRCI-HUG-20128/2026	2026-01-21	A/H3N2	EPI_ISL_20480851
A/Switzerland/UN-SNRCI-HUG-20129/2026	2026-01-21	A/H3N2	EPI_ISL_20480850

A/Switzerland/UN-SNRCI-HUG-20130/2026	2026-01-20	A/H3N2	EPI_ISL_20480821
A/Switzerland/UN-SNRCI-HUG-20132/2026	2026-01-22	A/H3N2	EPI_ISL_20480808
A/Switzerland/UN-SNRCI-HUG-20134/2026	2026-01-22	A/H3N2	EPI_ISL_20480860
A/Switzerland/UN-SNRCI-HUG-20135/2026	2026-01-22	A/H3N2	EPI_ISL_20480847
A/Switzerland/UN-SNRCI-HUG-20136/2026	2026-01-22	A/H3N2	EPI_ISL_20480862
A/Switzerland/UN-SNRCI-HUG-20137/2026	2026-01-26	A/H3N2	EPI_ISL_20480827
A/Switzerland/UN-SNRCI-HUG-20138/2026	2026-01-27	A/H3N2	EPI_ISL_20480859
A/Switzerland/UN-SNRCI-HUG-20140/2026	2026-01-27	A/H3N2	EPI_ISL_20480833
A/Switzerland/UN-SNRCI-HUG-20141/2026	2026-01-29	A/H3N2	EPI_ISL_20480843
A/Switzerland/UN-SNRCI-HUG-20142/2026	2026-01-29	A/H3N2	EPI_ISL_20480814
A/Switzerland/UN-SNRCI-HUG-20144/2026	2026-01-29	A/H3N2	EPI_ISL_20480824
A/Switzerland/UN-SNRCI-HUG-20145/2026	2026-01-29	A/H3N2	EPI_ISL_20480797
A/Switzerland/UN-SNRCI-HUG-20146/2026	2026-01-28	A/H3N2	EPI_ISL_20480857
A/Switzerland/UN-SNRCI-HUG-20149/2026	2026-01-30	A/H3N2	EPI_ISL_20480865
A/Switzerland/UN-SNRCI-HUG-20152/2026	2026-02-03	A/H3N2	EPI_ISL_20480822
A/Switzerland/UN-SNRCI-HUG-20153/2026	2026-02-02	A/H3N2	EPI_ISL_20480845
A/Switzerland/UN-SNRCI-HUG-20154/2026	2026-02-03	A/H3N2	EPI_ISL_20480835
A/Switzerland/UN-SNRCI-HUG-20155/2026	2026-02-05	A/H3N2	EPI_ISL_20480806
A/Switzerland/UN-SNRCI-HUG-20157/2026	2026-02-09	A/H3N2	EPI_ISL_20480852
A/Switzerland/UN-SNRCI-HUG-20159/2026	2026-02-13	A/H3N2	EPI_ISL_20480819
A/Switzerland/UN-SNRCI-HUG-20160/2026	2026-02-20	A/H3N2	EPI_ISL_20480810
A/Switzerland/UN-SNRCI-HUG-20162/2026	2026-03-02	A/H3N2	EPI_ISL_20480842
A/Switzerland/UN-SNRCI-HUG-20163/2026	2026-03-05	A/H3N2	EPI_ISL_20480800
A/Switzerland/UN-SNRCI-HUG-20166/2026	2026-01-21	A/H3N2	EPI_ISL_20480846
A/Switzerland/UN-SNRCI-HUG-20167/2026	2026-01-22	A/H3N2	EPI_ISL_20480849
A/Switzerland/UN-SNRCI-HUG-20168/2026	2026-01-21	A/H3N2	EPI_ISL_20480818
A/Switzerland/UN-SNRCI-HUG-20170/2026	2026-01-21	A/H3N2	EPI_ISL_20480858
A/Switzerland/UN-SNRCI-HUG-20172/2026	2026-01-21	A/H3N2	EPI_ISL_20480811
A/Switzerland/UN-SNRCI-HUG-20173/2026	2026-01-21	A/H3N2	EPI_ISL_20480840
A/Switzerland/UN-SNRCI-HUG-20174/2026	2026-01-23	A/H3N2	EPI_ISL_20480820

Appendix 3: Table of Sentinella Influenza B/Vic sequences submitted to GISAID (40/2024-16/2025)

Isolate name	Collection Date	Lineage	GISAID_ID
B/Switzerland/UN-SNRCI-HUG-20118/2026	2026-01-14	B/Victoria	EPI_ISL_20480844

Appendix 4: Table of Sentinella SARS-CoV-2 isolates submitted to GISAID (40/2024-16/2025)

Isolate name	Pangolin clade	clade_display	Collection Date	GISAID_ID
hCoV-19/Switzerland/UN-SNRCI-22001/2025	XFG.16	25C	2025-09-29	EPI_ISL_20511591
hCoV-19/Switzerland/UN-SNRCI-22002/2025	XFG.3.1.9	25C	2025-09-30	EPI_ISL_20511705
hCoV-19/Switzerland/UN-SNRCI-22003/2025	XFG.5.1	25C	2025-09-30	EPI_ISL_20511594
hCoV-19/Switzerland/UN-SNRCI-22004/2025	XFG.3	25C	2025-10-01	EPI_ISL_20511611
hCoV-19/Switzerland/UN-SNRCI-22005/2025	XFG.9	25C	2025-10-01	EPI_ISL_20511614
hCoV-19/Switzerland/UN-SNRCI-22006/2025	PQ.2.7	25B	2025-10-06	EPI_ISL_20511746
hCoV-19/Switzerland/UN-SNRCI-22007/2025	XFG.9.5	25C	2025-10-07	EPI_ISL_20511639

hCoV-19/Switzerland/UN-SNRCI-22008/2025	XFG.17.2.1	25C	2025-10-07	EPI_ISL_20511731
hCoV-19/Switzerland/UN-SNRCI-22009/2025	XFG.30	25C	2025-10-07	EPI_ISL_20511647
hCoV-19/Switzerland/UN-SNRCI-22010/2025	XFG.3.9	25C	2025-10-09	EPI_ISL_20511671
hCoV-19/Switzerland/UN-SNRCI-22011/2025	XFG.6.2.2	25C	2025-10-10	EPI_ISL_20511739
hCoV-19/Switzerland/UN-SNRCI-22012/2025	XFG	25C	2025-10-10	EPI_ISL_20511619
hCoV-19/Switzerland/UN-SNRCI-22013/2025	XFV	recombinant	2025-10-14	EPI_ISL_20511602
hCoV-19/Switzerland/UN-SNRCI-22014/2025	XFG	25C	2025-10-13	EPI_ISL_20511593
hCoV-19/Switzerland/UN-SNRCI-22015/2025	XFG.7	25C	2025-10-13	EPI_ISL_20511649
hCoV-19/Switzerland/UN-SNRCI-22016/2025	XFG.2.13.1	25C	2025-10-14	EPI_ISL_20511605
hCoV-19/Switzerland/UN-SNRCI-22017/2025	XFG	25C	2025-10-15	EPI_ISL_20511627
hCoV-19/Switzerland/UN-SNRCI-22018/2025	QS.3	25C	2025-10-13	EPI_ISL_20511616
hCoV-19/Switzerland/UN-SNRCI-22019/2025	XFG.3.17	25C	2025-10-16	EPI_ISL_20511604
hCoV-19/Switzerland/UN-SNRCI-22020/2025	QF.3	25C	2025-10-17	EPI_ISL_20511631
hCoV-19/Switzerland/UN-SNRCI-22021/2025	XFG.9.1	25C	2025-10-17	EPI_ISL_20511613
hCoV-19/Switzerland/UN-SNRCI-22022/2025	XFG.2	25C	2025-10-20	EPI_ISL_20511654
hCoV-19/Switzerland/UN-SNRCI-22023/2025	XFG.3.24	25C	2025-10-20	EPI_ISL_20511707
hCoV-19/Switzerland/UN-SNRCI-22024/2025	XFG.14	25C	2025-10-21	EPI_ISL_20511692
hCoV-19/Switzerland/UN-SNRCI-22025/2025	XFG.22.1	25C	2025-10-22	EPI_ISL_20511688
hCoV-19/Switzerland/UN-SNRCI-22026/2025	XFG.2.13.1	25C	2025-10-21	EPI_ISL_20511690
hCoV-19/Switzerland/UN-SNRCI-22027/2025	XFG.3	25C	2025-10-22	EPI_ISL_20511624
hCoV-19/Switzerland/UN-SNRCI-22028/2025	XFC.1.3.1	25G	2025-10-24	EPI_ISL_20511608
hCoV-19/Switzerland/UN-SNRCI-22029/2025	QY.3	25C	2025-10-24	EPI_ISL_20511741
hCoV-19/Switzerland/UN-SNRCI-22030/2025	XFG.36	25C	2025-10-28	EPI_ISL_20511697
hCoV-19/Switzerland/UN-SNRCI-22031/2025	XFG.17.2.1	25C	2025-10-28	EPI_ISL_20511727
hCoV-19/Switzerland/UN-SNRCI-22032/2025	XFG.17.2.1	25C	2025-10-29	EPI_ISL_20511643
hCoV-19/Switzerland/UN-SNRCI-22033/2025	XFG.8	25C	2025-10-29	EPI_ISL_20511603
hCoV-19/Switzerland/UN-SNRCI-22034/2025	XFG.2	25C	2025-10-31	EPI_ISL_20511712
hCoV-19/Switzerland/UN-SNRCI-22035/2025	XFG.5.4	25C	2025-10-31	EPI_ISL_20511634
hCoV-19/Switzerland/UN-SNRCI-22036/2025	PQ.17.1	25B	2025-11-03	EPI_ISL_20511618
hCoV-19/Switzerland/UN-SNRCI-22037/2025	PQ.4.7	25B	2025-11-03	EPI_ISL_20511673
hCoV-19/Switzerland/UN-SNRCI-22038/2025	QR.1	24H	2025-10-31	EPI_ISL_20511748
hCoV-19/Switzerland/UN-SNRCI-22039/2025	XFG.3.1	25C	2025-10-31	EPI_ISL_20511596
hCoV-19/Switzerland/UN-SNRCI-22040/2025	XFG.3.4.2	25C	2025-11-04	EPI_ISL_20511678
hCoV-19/Switzerland/UN-SNRCI-22041/2025	PQ.17	25B	2025-11-05	EPI_ISL_20511636
hCoV-19/Switzerland/UN-SNRCI-22042/2025	XFG.17.2.1	25C	2025-11-05	EPI_ISL_20511652
hCoV-19/Switzerland/UN-SNRCI-22043/2025	XFG.4	25C	2025-11-12	EPI_ISL_20511685
hCoV-19/Switzerland/UN-SNRCI-22044/2025	XFG.3.4.1	25C	2025-11-17	EPI_ISL_20511661
hCoV-19/Switzerland/UN-SNRCI-22045/2025	XFG.3.4.3	25C	2025-11-19	EPI_ISL_20511592
hCoV-19/Switzerland/UN-SNRCI-22046/2025	XFG.17.2.1	25C	2025-11-17	EPI_ISL_20511659
hCoV-19/Switzerland/UN-SNRCI-22047/2025	XGA.1	recombinant	2025-11-25	EPI_ISL_20511710
hCoV-19/Switzerland/UN-SNRCI-22048/2025	PQ.10.1.2	25B	2025-11-25	EPI_ISL_20511664
hCoV-19/Switzerland/UN-SNRCI-22049/2025	XFG.6.12	25C	2025-11-26	EPI_ISL_20511615
hCoV-19/Switzerland/UN-SNRCI-22050/2025	PQ.32	25B	2025-11-27	EPI_ISL_20511669

hCoV-19/Switzerland/UN-SNRCI-22052/2025	SE.1	25C	2025-12-01	EPI_ISL_20511724
hCoV-19/Switzerland/UN-SNRCI-22053/2025	XGA.1	recombinant	2025-12-04	EPI_ISL_20511617
hCoV-19/Switzerland/UN-SNRCI-22055/2025	PQ.10.1	25B	2025-12-05	EPI_ISL_20511597
hCoV-19/Switzerland/UN-SNRCI-22056/2025	XFG.3	25C	2025-12-01	EPI_ISL_20511681
hCoV-19/Switzerland/UN-SNRCI-22057/2025	PQ.17.2	25B	2025-12-08	EPI_ISL_20511683
hCoV-19/Switzerland/UN-SNRCI-22058/2025	PQ.4.1	25B	2025-12-09	EPI_ISL_20511666
hCoV-19/Switzerland/UN-SNRCI-22059/2025	XFG.3.1.12	25C	2025-12-09	EPI_ISL_20511702
hCoV-19/Switzerland/UN-SNRCI-22060/2025	XFG.17.2.1	25C	2025-12-10	EPI_ISL_20511612
hCoV-19/Switzerland/UN-SNRCI-22061/2025	XFG.17.2.1	25C	2025-12-10	EPI_ISL_20511622
hCoV-19/Switzerland/UN-SNRCI-22062/2025	XFG.14	25C	2025-12-08	EPI_ISL_20511601
hCoV-19/Switzerland/UN-SNRCI-22063/2025	XFG.17.2.1	25C	2025-12-10	EPI_ISL_20511695
hCoV-19/Switzerland/UN-SNRCI-22064/2025	XFG.3.10.1	25C	2025-12-11	EPI_ISL_20511607
hCoV-19/Switzerland/UN-SNRCI-22065/2025	XFG.17.2.1	25C	2025-12-11	EPI_ISL_20511751
hCoV-19/Switzerland/UN-SNRCI-22066/2025	XFG.17.2.1	25C	2025-12-11	EPI_ISL_20511714
hCoV-19/Switzerland/UN-SNRCI-22067/2025	XFG.36	25C	2025-12-11	EPI_ISL_20511610
hCoV-19/Switzerland/UN-SNRCI-22068/2025	QS.2	25C	2025-12-12	EPI_ISL_20511609
hCoV-19/Switzerland/UN-SNRCI-22069/2025	XFI.3.1	25H	2025-12-11	EPI_ISL_20511729
hCoV-19/Switzerland/UN-SNRCI-22070/2025	QS.2	25C	2025-12-11	EPI_ISL_20511656
hCoV-19/Switzerland/UN-SNRCI-22071/2025	XFG.3.1.3	25C	2025-12-11	EPI_ISL_20511629
hCoV-19/Switzerland/UN-SNRCI-22073/2025	PQ.11	25B	2025-12-15	EPI_ISL_20511734
hCoV-19/Switzerland/UN-SNRCI-22074/2025	NB.1.8.1	25B	2025-12-16	EPI_ISL_20511700
hCoV-19/Switzerland/UN-SNRCI-22075/2025	NL.22.1	24A	2025-12-17	EPI_ISL_20511722
hCoV-19/Switzerland/UN-SNRCI-22076/2025	XFG.2	25C	2025-12-16	EPI_ISL_20511620
hCoV-19/Switzerland/UN-SNRCI-22077/2025	QF.2.1	25C	2025-12-17	EPI_ISL_20511595
hCoV-19/Switzerland/UN-SNRCI-22078/2025	XFG.21	25C	2025-12-22	EPI_ISL_20511600
hCoV-19/Switzerland/UN-SNRCI-22080/2026	XFG.3.4.1	25C	2026-01-14	EPI_ISL_20511599
hCoV-19/Switzerland/UN-SNRCI-22081/2026	XFG.26.2.1	25C	2026-01-16	EPI_ISL_20511676
hCoV-19/Switzerland/UN-SNRCI-22082/2026	RV.1	25C	2026-01-19	EPI_ISL_20511743
hCoV-19/Switzerland/UN-SNRCI-22083/2026	PQ.39.1	25B	2026-01-19	EPI_ISL_20511736
hCoV-19/Switzerland/UN-SNRCI-22084/2026	PL.3	24H	2026-01-27	EPI_ISL_20511598
hCoV-19/Switzerland/UN-SNRCI-22085/2026	QF.5	25C	2026-02-03	EPI_ISL_20511719
hCoV-19/Switzerland/UN-SNRCI-22087/2026	XFG.23.1.5	25C	2026-02-06	EPI_ISL_20511606
hCoV-19/Switzerland/UN-SNRCI-22088/2026	XFG.6.3	25C	2026-02-26	EPI_ISL_20511641
hCoV-19/Switzerland/UN-SNRCI-22089/2026	XFG.3	25C	2026-03-17	EPI_ISL_20511717

Appendix 5: List of sequences used to align the current primers and probe for Influenza H3 subtyping.

	Nom de souche	Clade
1	A/Cardiff/4147/2025	K
2	A/England/01841968/2025	K
3	A/England/01841988/202	J.2.4
4	A/England/01845723/2025	J.2.4
5	A/England/01850184/202	J.2.4
6	A/England/01854885/2025	K
7	A/England/01854918/2025	K
8	A/England/01854927/202	J.2.4
9	A/LlanfairPG/6459/2025	K
10	A/Norway/24873/2021	K
11	A/SWITZERLAND/UN-SNRCI-HUG-47502473/2025	J.2.2
12	A/SWITZERLAND/UN-SNRCI-HUG-47526372/2025	J.2
13	A/SWITZERLAND/UN-SNRCI-HUG-47551343/2025	J.2
14	A/SWITZERLAND/UN-SNRCI-HUG-47572010/2025	J.2
15	A/SWITZERLAND/UN-SNRCI-HUG-47582365/2025	J.2.2
16	A/SWITZERLAND/UN-SNRCI-HUG-47661090/2025	J.2.2
17	A/SWITZERLAND/UN-SNRCI-HUG-47783582/2025	J.2.2
18	A/SWITZERLAND/UN-SNRCI-HUG-47795894/2025	J.2
19	A/SWITZERLAND/UN-SNRCI-HUG-47894198/2025	J.2.2



Centre for Health Protection
Department of Health
The Government of the Hong Kong Special Administrative Region

CERTIFICATE OF COMPLETION

This certificate is awarded to

National Reference Centre of Influenza, Geneva University Hospitals, Switzerland

In recognition of the completion of

EXTERNAL QUALITY ASSESSMENT PROGRAMME for

Detection of Influenza Viruses by RT-PCR*

Antiviral Susceptibility Testing of Influenza Viruses*

Detection of Severe Acute Respiratory Syndrome Coronavirus 2 by RT-PCR*

of the World Health Organization Global Influenza Surveillance and Response System

Panel 24 (2025) with attainment of full score in *

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Dr. Jaicee Lo, CHP, DH, HKSAR Government

24 April 2026

Date

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Appendix 7: Table of reference Influenza HA(H1)pdm09 sequences used in phylogenetic analyses. Amino acid substitutions are described against the root virus sequence.

Virus	Clade	Clade signature amino acids (HA1)	Nextclade subclade	Subclade substitutions	GISAIID Isolate Accession number
A/Victoria/2570/2019_Egg ¹	5a.2 (root)		C		EPI_ISL_417210
A/Sydney/5/2021_Egg ²	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1	D94N, T216A	EPI_ISL_12109635
A/Netherlands/10468/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1+I418V	I418V (HA2)	EPI_ISL_18044584
A/Michigan/62/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.8	I418V (HA2), T120A, V47I	EPI_ISL_19175842
A/Lisboa/188/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.9	I418V (HA2), T120A, K169Q	EPI_ISL_19334296
A/Hungary/286/2024	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.9.3	I418V (HA2), T120A, K169Q, S83P	EPI_ISL_19685707
A/Wisconsin/67/2022_Cell ³	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	C.1.1		EPI_ISL_15928563
A/Victoria/4897/2022_Egg ³	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D	T216A	EPI_ISL_17072386
A/Netherlands/10481/2024	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.1	T216A, R45K	EPI_ISL_19252612
A/Bretagne/05126/2024	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.2	T216A, R113K	EPI_ISL_19406762
A/Norway/00926/2025	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.3	T216A, T120A, I372V	EPI_ISL_19731580
A/Missouri/11/2025_Cell ⁴	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.3.1	T216A, T120A, I372V, I460T, V520A	EPI_ISL_19759016
A/Missouri/11/2025_Egg ⁴	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.3.1	T216A, T120A, I372V, I460T, V520A	EPI_ISL_20066835
A/Poland/28/2024	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.4	T216A, T120A	EPI_ISL_19204767
A/Norway/06906/2024	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.5	T216A, R45K	EPI_ISL_19497280

¹ WHO recommended vaccine virus from the 2021 southern hemisphere to the 2022-2023 northern hemisphere influenza seasons

² WHO recommended vaccine virus for the 2023 southern hemisphere influenza season

³ WHO recommended vaccine virus from the 2023-2024 northern hemisphere to the 2025-2026 northern hemisphere influenza seasons

⁴ WHO recommended vaccine virus for the 2026 southern hemisphere influenza season

Appendix 8: Table of reference Influenza HA(H3) sequences used in phylogenetic analyses. Amino acid substitutions are described against the root virus sequence.

Virus	Clade	Clade signature amino acids (HA1)	Nextclade subclade	Subclade substitutions	GISAIID Isolate Accession number
A/Darwin/9/2021_Egg ¹	2a (root)		G.1		EPI_ISL_3801278
A/Darwin/6/2021_Cell ¹	2a		G.1		EPI_ISL_3534319
A/Thailand/8/2022_Egg ²	2a.3a.1	2a.3a + I140K, I223V	J		EPI_ISL_16014504
A/Massachusetts/18/2022_Cell ²	2a.3a.1	2a.3a + I140K, I223V	J		EPI_ISL_16998756
A/Sydney/856/2023	2a.3a.1	2a.3a + I140K, I223V	J.1	I25V, V347M	EPI_ISL_19085832
A/Canberra/331/2023	2a.3a.1	2a.3a + I140K, I223V	J.1.1	J.1 + S145N	EPI_ISL_19030763
A/Croatia/10136RV/2023 ³	2a.3a.1	2a.3a + I140K, I223V	J.2	N122D(-CHO), K276E	EPI_ISL_19085873
A/District Of Columbia/27/2023 ³	2a.3a.1	2a.3a + I140K, I223V	J.2	N122D(-CHO), K276E	EPI_ISL_19175844
A/West Virginia/51/2024	2a.3a.1	2a.3a + I140K, I223V	J.2.1	J.2 + P239S	EPI_ISL_19376866
A/Lisboa/216/2023	2a.3a.1	2a.3a + I140K, I223V	J.2.2	J.2 + S124N	EPI_ISL_19313759
A/Netherlands/10685/2024	2a.3a.1	2a.3a + I140K, I223V	J.2.3	J.2 + N158K, K189R	EPI_ISL_19767813
A/Singapore/GP20238/2024 ⁴	2a.3a.1	2a.3a + I140K, I223V	J.2.4	J.2 + T135K(-CHO), K189R	EPI_ISL_19871656
A/Sydney/1359/2024 ⁴	2a.3a.1	2a.3a + I140K, I223V	J.2.4	J.2 + T135K(-CHO), K189R	EPI_ISL_19711425
A/Norway/8765/2025	2a.3a.1	2a.3a + I140K, I223V	K (former J.2.4.1)	J.2.4 + K2N, S144N(+CHO), N158D, I160K, Q173R, T328A, S378N	EPI_ISL_20205997
A/Victoria/211/2025	2a.3a.1	2a.3a + I140K, I223V	J.2.5	J.2 + S124N	EPI_ISL_19940075
A/France/IDF-IPP29542/2023	2a.3a.1	2a.3a + I140K, I223V	J.4	Q173R, K276E	EPI_ISL_18949967

¹ WHO recommended vaccine virus from the 2022 southern hemisphere to the 2023-2024 northern hemisphere influenza seasons

² WHO recommended vaccine virus from the 2024 southern hemisphere to the 2024-2025 northern hemisphere influenza seasons

³ WHO recommended vaccine virus from the 2025 southern hemisphere to the 2025-2026 northern hemisphere influenza seasons

⁴ WHO recommended vaccine virus for the 2026 southern hemisphere influenza season

Appendix 9: Table of reference Influenza HA(B/Vic) sequences used in phylogenetic analyses. Amino acid substitutions are described against the root virus sequence.

Virus	Clade	Clade signature amino acids (HA1)	Nextclade subclade	Subclade substitutions	GISAID Isolate Accession number
B/Brisbane/60/2008	V1A (root)		A		EPI_ISL_28587
B/Washington/02/2019_Egg ¹	V1A.3	I117V, N129D, K136E, del(162-164)	A.3.2		EPI_ISL_362540
B/Austria/1359417/2021_Cell ²	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C		EPI_ISL_983345
B/Austria/1359417/2021_Egg ²	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C		EPI_ISL_10265907
B/Netherlands/10335/2023 Egg	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.2	T182A, D197E, T221A	EPI_ISL_18109005
B/Moldova/2030521/2023	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.3	E128K, A154E, S208P	EPI_ISL_18037429
B/Kanagawa/AC2414/2025	V1A.3a.3	V1A.3a + A127T, P144L, K203R	C.3.1	D197N(+CHO)	EPI_ISL_20046941
B/Stockholm/3/2022	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5	D197E	EPI_ISL_13983278
B/Catalonia/2279261NS/2023	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5.1	D197E, E183K	EPI_ISL_18109004
B/Catalonia/3514402NS/2023	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5.4	D197E, V117I, E128K, A154T, K326R	EPI_ISL_18109028
B/Switzerland/329/2024	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5.6	D197E, D129N	EPI_ISL_19298051
B/ENG/120/2025	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5.6.1	T37I, E128D, T199A	EPI_ISL_20133956
B/Greece/5509/2024	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5.7	D197E, E183K, E128G	EPI_ISL_19298050

¹ WHO recommended vaccine virus from the 2020-2021 to the 2021-2022 northern hemisphere influenza seasons

² WHO recommended vaccine virus from the 2022 to the 2026 southern hemisphere influenza seasons

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