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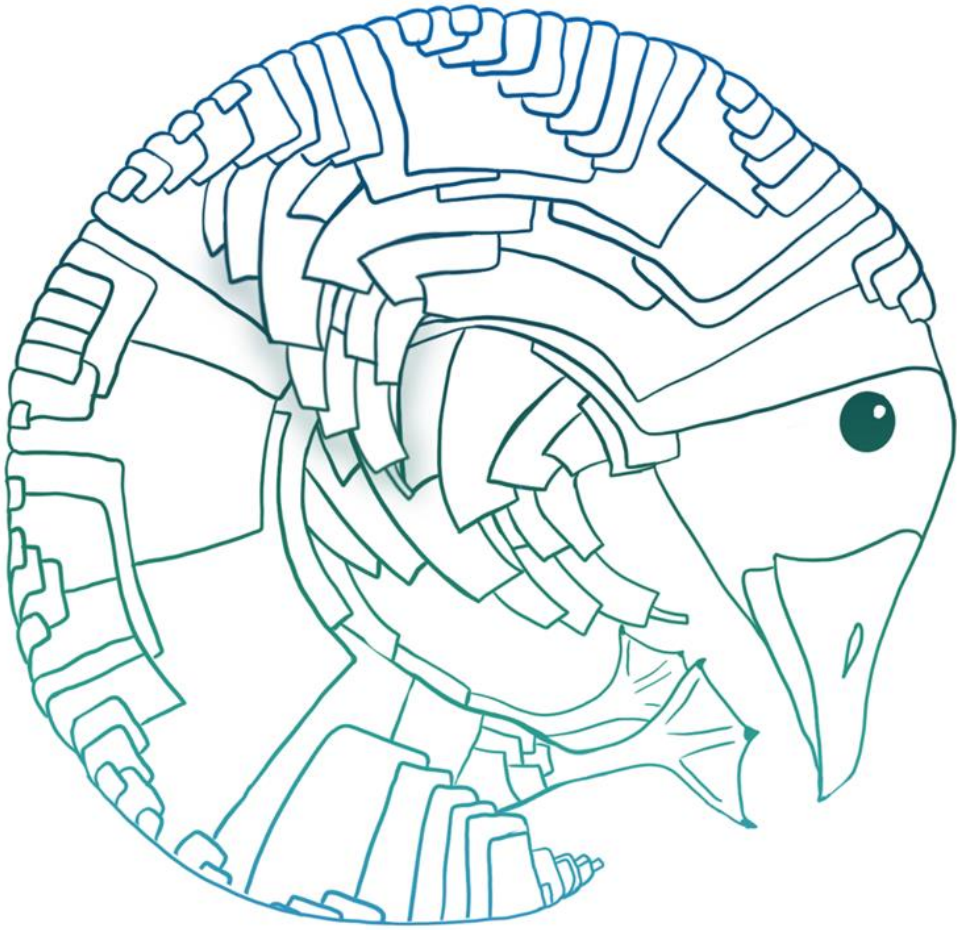
Surveillance report: Respiratory viruses in Switzerland

Season 2024–2025 (weeks 40/2024-16/2025)



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Cover image

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

Table of content

List of abbreviations

ARI	acute respiratory infection
CDC	Centers for disease control and prevention
CDV	canine distemper virus
CPE	cytopathic effect
Ct	cycle threshold
DNA	deoxyribonucleic acid
ECDC	European centre for disease prevention and control
EQAP	external quality assessment programme
FOPH	federal office of public health
GISAID	global initiative on sharing all influenza data
HA	haemagglutinin assay
HAI	haemagglutinin inhibition assay
HAdV	human adenovirus
HBoV	human bocavirus
HCoV	human coronavirus
HMPV	human metapneumovirus
HPIV	human parainfluenza
HRI	highly reduced inhibition
IAV	influenza A virus
IBV	influenza B virus
IC_{50}	half inhibitory concentration
ILI	influenza-like illness(es)
IRMA	Iterative Refinement Meta-Assembler
M	matrix
MDCK	Madin-Darby canine kidney cells
MDCK-SIAT1	sialic acid-enriched MDCK cells
MUNANA	20-(4-methylumbelliferyl)-a-D-N-acetylneuraminic acid (fluorescence assay)
NA	neuraminidase
NAI	neuraminidase inhibitor
NH	northern hemisphere
NI	normal inhibition
NRCI	national reference centre of influenza
NP	nucleoprotein
PA	acidic protein
Q25, Q75	25%, 75% quartiles
RBC	red blood cell

RI	reduced inhibition
RNA	ribonucleic acids
RV/EV	rhinoviruses/enteroviruses
RSV	respiratory syncytial virus
rRT-PCR	real-time reverse-transcription polymerase chain reaction
SARS-CoV-2	severe acute respiratory syndrome coronavirus 2
SH	southern hemisphere
SPSP	swiss pathogen surveillance platform
VADR	Viral Annotation DefineR
Vic, Yam	Victoria, Yamagata lineage
VOC	variant of concern
VOI	variant of interest
VUM	variant under monitoring
WHO	world health organization
WHO CC	WHO Collaborative Centre
WIC	worldwide influenza centre

Abstract

Summary of influenza and other respiratory virus surveillance, 2024-2025 Season

For the fifth consecutive year within the Sentinella surveillance network, nasopharyngeal swabs received at the National Influenza Reference Centre were tested not only for influenza viruses but also for SARS-CoV-2, RSV A and B, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV1-4, HBoV, HAdV, RV/EV, and HMPV. Among the 2,084 samples analysed, 1,409 tested positives for at least one respiratory virus. Influenza A and B viruses, RV/EV, and SARS-CoV-2 were the most frequently detected pathogens during the 2024-2025 season (week 40/2024 to week 16/2025).

Of the 2,084 samples tested, 585 (28 %) were positive for influenza viruses, with the first detection occurring during week 41/2024. In Switzerland, influenza activity reached levels comparable to those observed in pre-COVID-19 seasons. Both influenza A and B viruses co-circulated, with co-dominance of subtypes A(H1N1)pdm09 and A(H3N2).

The majority of A(H1N1)pdm09 viruses belonged to genetic clade 6B.1A.5a.2a, with a minority in subgroup 5a.2a.1. Antigenically characterised A(H1N1)pdm09 isolates were closely related to the 2024-2025 Northern Hemisphere vaccine strain A/Victoria/4897/2022. A(H3N2) viruses detected in Switzerland mainly belonged to subclade 2a.3a.1 of genetic group 3C.2a1b.2a and were well recognised by antisera raised against the recommended vaccine strain A/Thailand/8/2022 (clade 2a.3a.1). All influenza B viruses belonged to clade V1A.3a.2 and subclade C.5.1, C.5.7, and C.5.6, and were antigenically like the recommended vaccine strain B/Austria/1359417/2021.

The 2024-2025 influenza season was characterized by a return to high and prolonged virus circulation compared to the previous season (2023-2024). The epidemic threshold was crossed in week 50/2024, peaked in week 05/2025, and ended in week 14/2025, lasting a total of 17 weeks.

To date, despite the detection of avian A(H5N1) virus in wild birds in Switzerland, no zoonotic influenza infections have been reported.

Résumé

Résumé de la surveillance de l'activité grippale et autres virus respiratoires 2024-2025

Pour la cinquième année consécutive au sein du réseau de surveillance Sentinella, les prélèvements nasopharyngés reçus au Centre National de Référence de l'Influenza, ont non seulement été dépistés pour les virus de l'influenza mais aussi pour le SARS-CoV-2, VRS A et B, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV1-4, HBoV, HAdV, RV/EV et HMPV. Parmi les 2'084 échantillons analysés, 1'409 se sont révélés positifs pour au moins un virus respiratoire. Les virus de l'influenza A et B, du RV/EV et du SARS-CoV-2 étaient les plus fréquemment détectés durant cette saison (semaines 40/2024 à 16/2025).

La grippe a fait son apparition au sein du réseau Sentinella dès la semaine 41/2024. Sur les 2'084 échantillons dépistés, 585 (28 %) étaient positifs pour un virus grippal. En Suisse, l'activité de la grippe a atteint des niveaux comparables aux saisons précédant la pandémie COVID-19. Les virus influenza de type A et B co-circulaient, avec une co-dominance des sous-type A(H1N1)pdm09 et A(H3N2).

Les virus de sous-type A(H1N1)pdm09 appartenaient majoritairement au clade génétique 6B.1A.5a.2a et une minorité au groupe 5a.2a.1. Les isolats A(H1N1)pdm09 antigéniquement caractérisés étaient proches de la souche vaccinale recommandée pour l'hémisphère nord 2024-2025, soit A/Victoria/4897/2022. Les virus influenza A de sous-type A(H3N2) détectés en Suisse appartenaient majoritairement au sous-clade 2a.3a.1 du groupe génétique 3C.2a1b.2a. Ces isolats étaient bien reconnus par les antisera dirigés contre la souche vaccinale recommandée pour l'hémisphère nord pour 2024-2025, soit A/Thailand/8/2022 (clade 2a.3a.1). Quant aux virus de l'influenza B, tous appartenaient au clade V1A.3a.2, des sous-clades C.5.1, C.5.7, et C.5.6 et tous étaient antigéniquement proches de la souche vaccinale recommandée pour l'hémisphère nord 2024-2025, B/Austria/1359417/2021.

La saison grippale 2024-2025 a été caractérisée par un retour à une circulation virale élevée et prolongée par rapport à la saison précédente (2023-2024). Le seuil épidémique a été franchi en semaine 50/2024 et a fini en semaine 14/2025, avec un pic en semaine 05/2025, soit une durée de 17 semaines.

A ce jour, et bien que le virus aviaire A(H5N1) soit détecté en Suisse chez les oiseaux sauvages, aucune infection grippale zoonotique n'a été recensée.

Zusammenfassung

Zusammenfassung der Überwachung der Influenza- und anderer respiratorischer Viren, Saison 2024/2025

Zum fünften Mal in Folge wurden im Rahmen des Sentinella-Überwachungsnetzwerks nasopharyngeale Abstriche, die am Nationalen Referenzzentrum für Influenza eingegangen sind, nicht nur auf Influenzaviren, sondern auch auf SARS-CoV-2, RSV A und B, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV1-4, HBoV, HAdV, RV/EV und HMPV getestet. Von den 2'084 analysierten Proben waren 1'409 positiv für mindestens ein respiratorisches Virus. Am häufigsten nachgewiesen wurden Influenza A- und B-Viren, RV/EV sowie SARS-CoV-2 während der Saison 2024-2025 (Kalenderwochen 40/2024 bis 16/2025).

Influenza-Aktivität wurde erstmals in Kalenderwoche 41/2024 im Sentinella-Netzwerk festgestellt. Von den 2'084 getesteten Proben waren 585 (28 %) positiv für Influenzaviren. In der Schweiz erreichte die Influenza-Aktivität ein Niveau, das mit den Saisons vor der COVID-19-Pandemie vergleichbar ist. Influenza A- und B-Viren zirkulierten gleichzeitig, mit einer Ko-Dominanz der Subtypen A(H1N1)pdm09 und A(H3N2).

Die Mehrheit der A(H1N1)pdm09-Viren gehörte zum genetischen Kladen 6B.1A.5a.2a, eine Minderheit zum Subkladen 5a.2a.1. Antigenisch charakterisierte A(H1N1)pdm09-Isolate waren der für die Nordhalbkugel 2024-2025 empfohlenen Impfstoffstamm A/Victoria/4897/2022 ähnlich. Die in der Schweiz nachgewiesenen A(H3N2) Viren gehörten überwiegend zum Subkladen 2a.3a.1 der genetischen Gruppe 3C.2a1b.2a und wurden gut durch Antiseren gegen den empfohlenen Impfstoffstamm A/Thailand/8/2022 (Klade 2a.3a.1) erkannt. Alle Influenza-B-Viren gehörten zur Klade V1A.3a.2, insbesondere zu den Subkladen C.5.1, C.5.7 und C.5.6, und waren antigenisch dem empfohlenen Impfstoffstamm B/Austria/1359417/2021 ähnlich.

Die Influenza-Saison 2024-2025 war durch eine Rückkehr zu einer intensiven und verlängerten Viruszirkulation im Vergleich zur vorherigen Saison 2023-2024 gekennzeichnet. Sie begann in Kalenderwoche 50/2024, erreichte ihren Höhepunkt in Woche 05/2025 und endete in Woche 14/2025, mit einer Gesamtdauer von 17 Wochen.

Bis heute wurde trotz des Nachweises des aviären A(H5N1) Virus bei Wildvögeln in der Schweiz keine zoonotische Influenzainfektion gemeldet.

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) since 1986 [1]. The physicians, who voluntarily participate to the Sentinella surveillance network, report cases of patients presenting symptoms of influenza-like illness (ILI) and/or acute respiratory infection (ARI) 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), respiratory syncytial virus (RSV), human coronaviruses (HCoV namely NL63, HKU1, OC43 and 229E), human parainfluenza (HPIV) 1-4 viruses, human bocavirus (HBoV), human adenovirus (HAdV), human rhinovirus/enterovirus (RV/EV) and human metapneumovirus (HMPV).

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 characterised by a sudden onset of fever (> 38 °C) with cough and/or sore throat.

The NRCI performs additional characterisation of samples positive for either SARS-CoV-2, RSV or Influenza. 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 and SARS-CoV-2 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. The testing algorithm applied at the NRCI is depicted in Figure 1. Basic statistical analyses are performed using Microsoft Excel 365.

This report summarises the demographic, epidemiological and virological data from samples processed and analysed by the NRCI from September 28, 2024, to April 18, 2025 (week 40/2024 to week 16/2025).

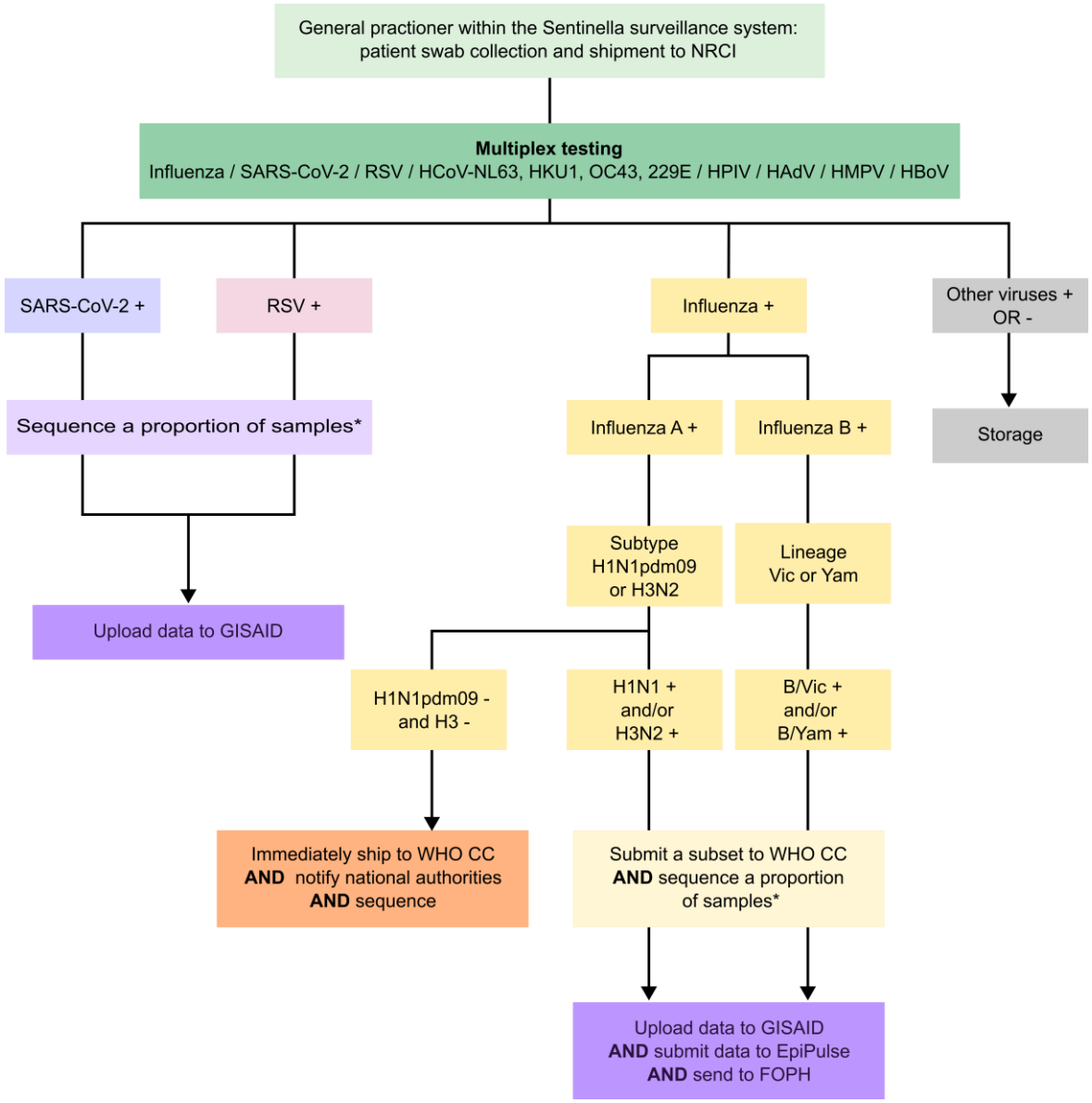


*Figure 1: Workflow applied by NRCI to samples collected through the Sentinella network. * Sequencing criteria are as follow: Ct values ≤25 for influenza and RSV or ≤28 for SARS-CoV-2 and absence of co-detection with another respiratory virus.*

B. Attributes of the study population

From week 40/2024 to week 16/2025, 2'084 nasopharyngeal samples were collected by 77 sentinel practitioners and sent for screening at the NRCI. With the swab specimen, practitioners join a form specifying the suspicion criteria (ARI and/or ILI), the gender, the age of the patient as well as their vaccination status for both influenza and SARS-CoV-2 (for details on vaccination, refer to the chapter "Vaccination").

1. Consultations for ILI and/or ARI symptoms

During the 2024-2025 season, the NRCI received 513 samples from patients with ARI symptoms, 82 samples from patients with ILI symptoms and practitioners declared both ARI and ILI symptoms for 1,384 patients. No information regarding symptomatology was available for 105 samples (Figure 2).

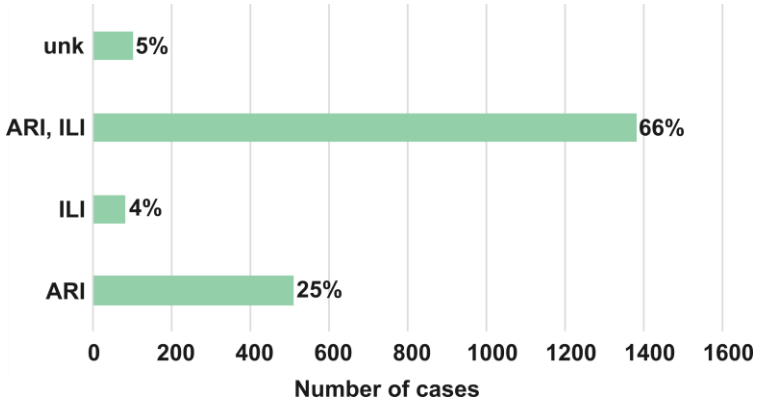


Figure 2: Distribution of the suspicion criteria among the samples tested by the NRCI between week 40/2024 and week 16/2025. ARI: acute respiratory infection; ILI: Influenza-like illness; unk: unknown.

2. Stratification by age and gender

Using the data reported by the practitioners, the Sentinella cohort was further stratified by gender (male or female) and by age in years (0 to 4, 5 to 14, 15 to 29, 30 to 64, and over 65). Data for age and gender were available for all the participants, and sampling was equally distributed between men and women (Figure 3). The overall median age was 43 ranging from 0 to 101 years (Q25: 27, Q75: 60). The median age for women was 45 years (Q25:29, Q75:61) ranging from 0 to 101 years. The median age for men was 40 years (Q25:24, Q75:58) ranging from 0 to 93 years.

Age group (in years)	Men	Women	Total
0-4	52	40	92
(%)	*5.4%*	*3.5%*	*4.4%*
5-14	64	59	123
(%)	*6.7%*	*5.2%*	*5.9%*
15-29	188	195	383
(%)	*19.7%*	*17.3%*	*18.4%*
30-64	487	599	1086
(%)	*50.9%*	*53.1%*	*52.1%*
≥65	165	235	400
(%)	*17.3%*	*20.8%*	*19.2%*
Total	**956**	**1128**	**2084**
(%)	*46%*	*54%*	*100%*

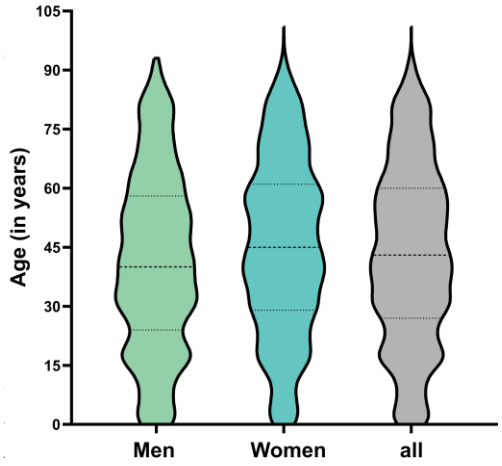


Figure 3: Age and gender distribution of the Sentinella cohort from week 40/2024 and week 16/2025. Left: table showing total number and percentage in each category. Right: pyramid representing the age distribution according to the gender. The dashed line represents the median and the dotted line the 25 % (Q25) and 75 % (Q75) quartiles.

C. Virological results

1. Circulating respiratory viruses

From week 40/2024 to week 16/2025, a total of 2'084 nasopharyngeal samples were screened for Influenza, SARS-CoV-2, RSV, HCoV NL63, HCoV HKU1, HCoV OC43, HCoV 229E, HPIV, HBoV, HAdV, RV/EV and HMPV. A total of 1'409 samples tested positive.

a. Positive samples per age group over time

The percentage of positive specimens tested within the Sentinella network was analysed weekly for each age group. Overall, the highest percentage of positive samples was observed in the 30- to 64-year-old group with a mean at 36.9 %. The lowest percentage was observed in population aged 0- to 14-year-old with a mean at 4.80 % in the 0- to 4-year-old and a mean at 4.65 % in the 5- to 14-year-old (Figure 4). Of note, the positivity rate peaked during week 1/2025 for the adult (30- to 64-year-old; mean 55 %) and young adult (15- to 29-year-old; mean 35 %) groups, whereas no tests were positive during the same period in the newborn (0- to 4-year-old) and toddler (5- to 14) groups. Of note, the total number of specimens sent to the NRCI between weeks 52 and week 1 was the lowest observed during the whole season (n = 50 with only one sample in age group 0- to 14-year-old) (Figure 5.b).

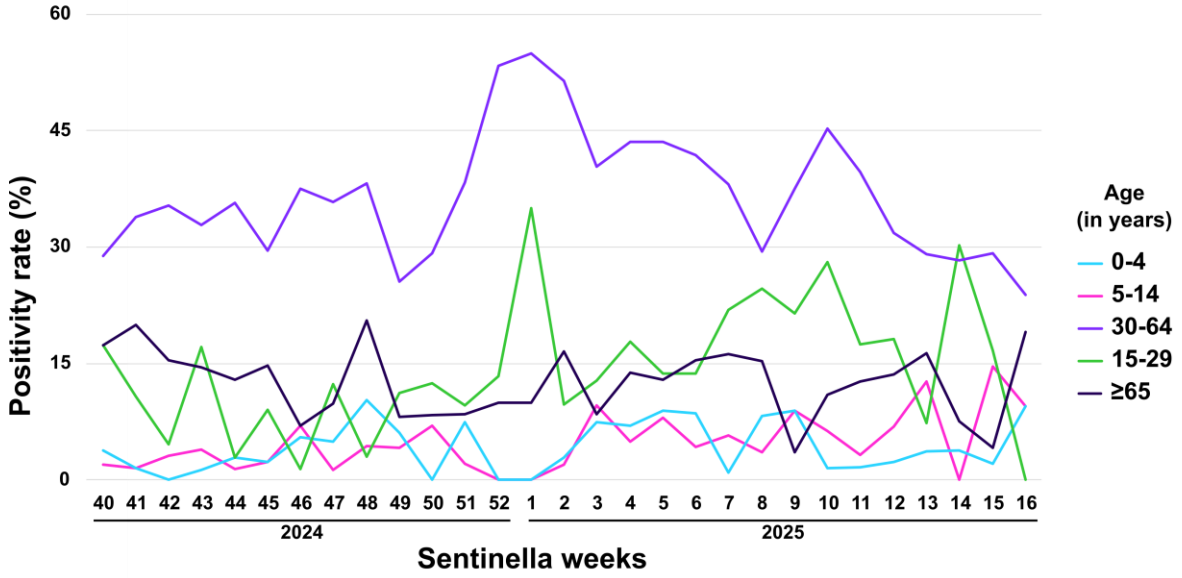


Figure 4: Percentage of respiratory viruses detected weekly in Sentinel cohort stratified by age group.

b. Positive samples and respiratory viruses' distribution over time

One thousand four hundred and nine (1'409) samples tested positive for at least one respiratory virus, corresponding to 67.6 % of the total number of samples analysed. However, since some samples contained more than one virus, a total of 1'519 viruses were identified. The distribution of viruses is shown in Figure 5.a, with the total number of positive results and their respective percentages indicated. The sum of all percentages reached 105.28 %, which is explained by the presence of multiple viruses in 102 samples (Figure 5.a) (further details provided below).

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, was calculated from epidemiological week 40/2024 to week 16/2025. The highest positivity rate was recorded during week 01/2025, reaching 90 %. Yet, due to the holidays period, the number of samples received that week was limited (n = 20), and therefore this positivity rate should be interpreted with caution. The lowest weekly positivity rate of 50 % could be observed during week 49/2024. Over the surveillance period, the median weekly positivity rate for the 2024-2025 season was 67.27 %, (Q25: 60.42, Q75: 74.40) (Figure 5.b).

At the beginning of the season, SARS-CoV-2 and RV/EV were the two dominant circulating viruses. From week /2024 onward, they were progressively replaced by influenza viruses and RSV. Influenza detection started to increase during week 48/2024, first with IAV and then for both IAV and IBV from week 02/2025. After week 52/2024, the detection of RV/EV stabilised in the 5-10 % positivity range and

started to increase again from week 12/2025 reaching a 30 % positivity rate by week 16/2025. HCoV OC43, HCoV NL63, and HAdV were regularly detected throughout the surveillance period. HPIV2/4 was regularly detected during weeks 40 to 49/2024, followed by sporadic detection until the end of the season. Even if at low numbers, HPIV1/3 was observed at the beginning and the end of the monitored period. HCoV 229E, HCoV HKU1 and HBoV were sporadically detected throughout the season.

Of note, the NRCI received an increased volume of nasopharyngeal swabs between week 04/2025 and week 07/2025. This corresponds to the peak of ARI/ILI consultations in Switzerland which was on week 06/2025 (Appendix 1).

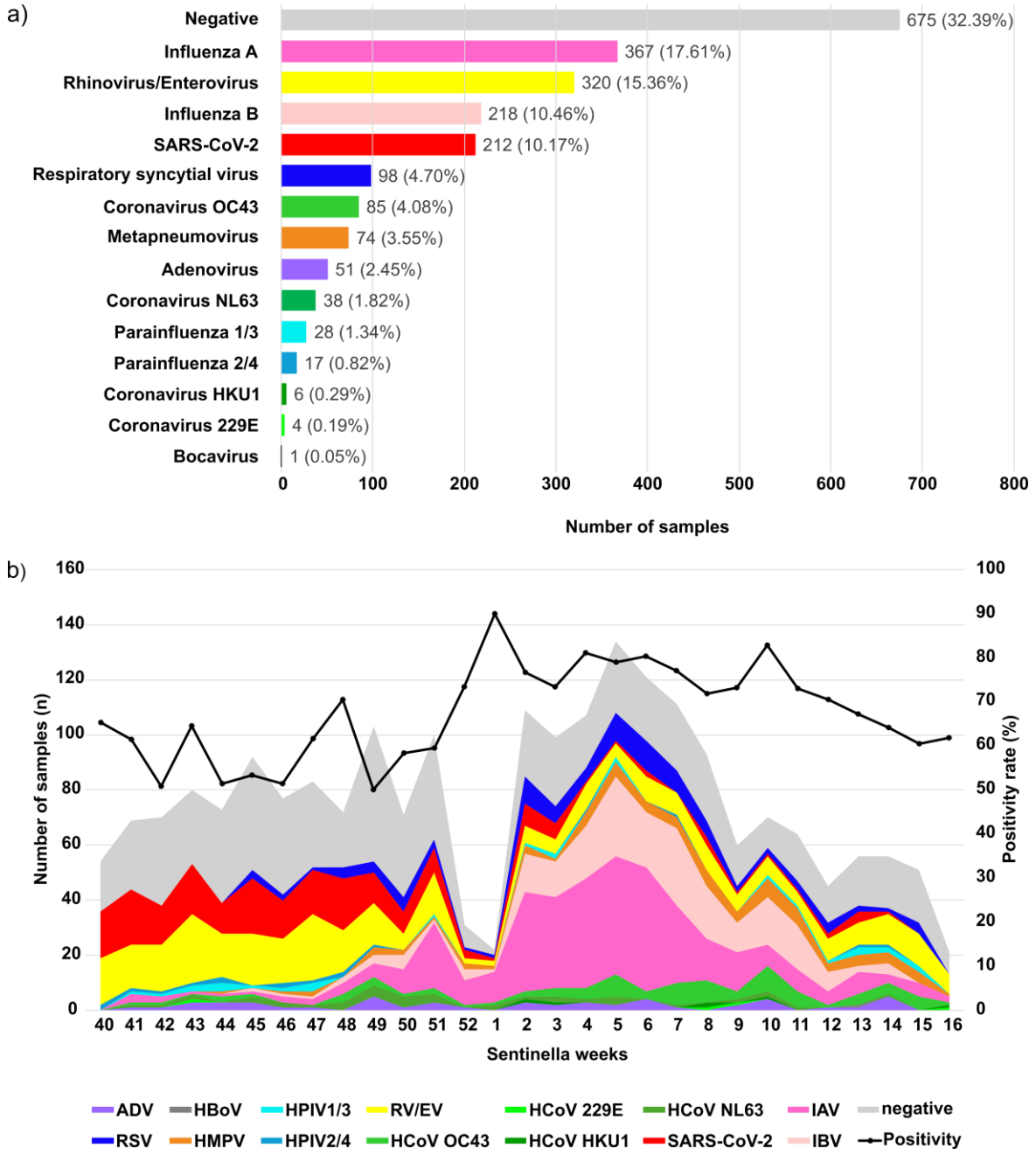


Figure 5: Circulating respiratory virus detected in the Sentinella cohort from week 40/2024 to week 16/2025. a) Graph representing the total number of positive samples and their relative percentage. b) Temporal distribution of respiratory viruses detected. The line with marks represents the positivity rate (ratio between the number of sample positive for any viruses and the total number of samples received). The stacked areas represent the total number of samples positive for a given virus.

c. Distribution of the circulating viruses per age group

Stratification of positive specimens by age group revealed that all respiratory viruses were detected across all age categories, with two exceptions: Human Bocavirus (HBoV) was identified only once in the 0–4-year-old group, and Human Coronavirus 229E (HCoV 229E) was detected three times in the 30-64-year-old group and once in individuals aged ≥65 years (Figure 6).

The distribution patterns varied depending on the virus analysed. Influenza A virus (IAV) and influenza B virus (IBV) exhibited distinct age-related trends. Both viruses showed low detection rates in the 0-4-year-old group; however, IBV demonstrated a decreasing positivity rate with increasing age, peaking at 22.8 % in the 5-14-year-old group and declining to 1 % in the ≥65-year-old group. In contrast, IAV maintained a relatively stable positivity rate of approximately 15 % across all age groups above 5 years.

SARS-CoV-2 displayed an inverse trend to IBV, with positivity rates increasing with age and reaching the highest level in the ≥65-year-old group. Respiratory syncytial virus (RSV) showed a bimodal distribution, with the highest positivity rate in the 0-4-year-old group (15.6 %) and a secondary increase in the ≥65-year-old group (7 %).

Rhinovirus/Enterovirus (RV/EV) were consistently detected across all age groups with a positivity rate of approximately 25 % in the 0-14-year-old groups and of around 15 % in individuals older than 15 years.

Human coronavirus OC43 (HCoV-OC43) was present at similar levels in all age groups. Human metapneumovirus (HMPV) and Human adenovirus (HAdV) were distributed across all ages group with peak positivity rate in the 0-4-year-old at 5.7 % and 8.2 % respectively. Human Parainfluenza viruses (HPIV1-4), although detected at low frequencies, were present in all age groups.

d. Co-detection rate

Among the 1’409 positive samples, 102 (7.2 %) tested positive for two or more viruses. The most common combination was RV/EV with SARS-CoV-2 (n = 9,9.2 % of all co-detection), followed by RV/EV with RSV (n = 7.1 %) (Figure 7). RSV and influenza were the viruses detected in most cases of co-detection (42 % of all co-detection) while SARS-CoV-2 was detected in 24.5 % of all co-detection events (Appendix 2).

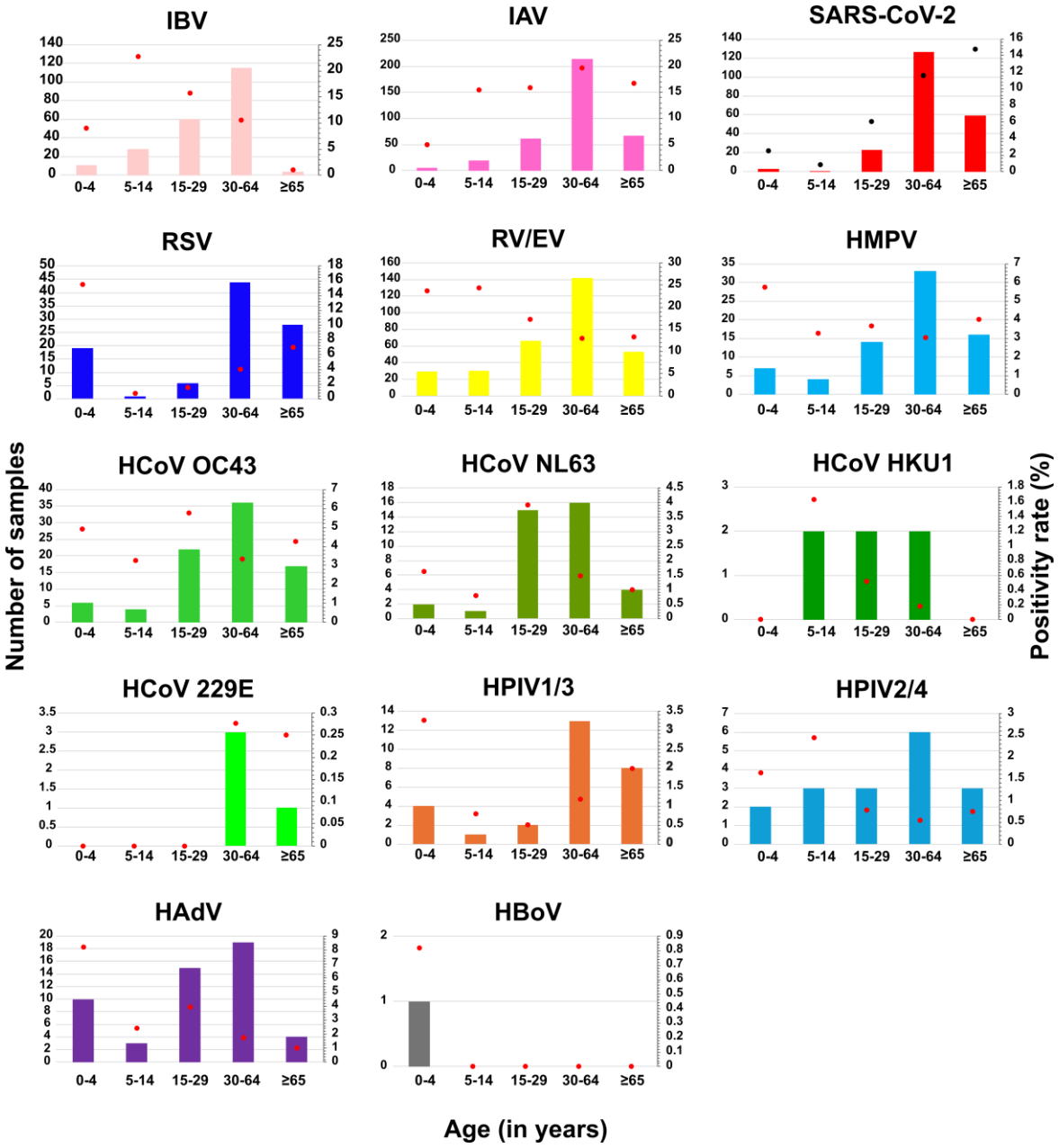


Figure 6: Prevalence of respiratory viruses by age groups. Bars represent the absolute number of detections and dots represent the positivity rate. The positivity rate is a ratio between the number of samples positive for a given virus in the indicated age group and the total number of samples received.

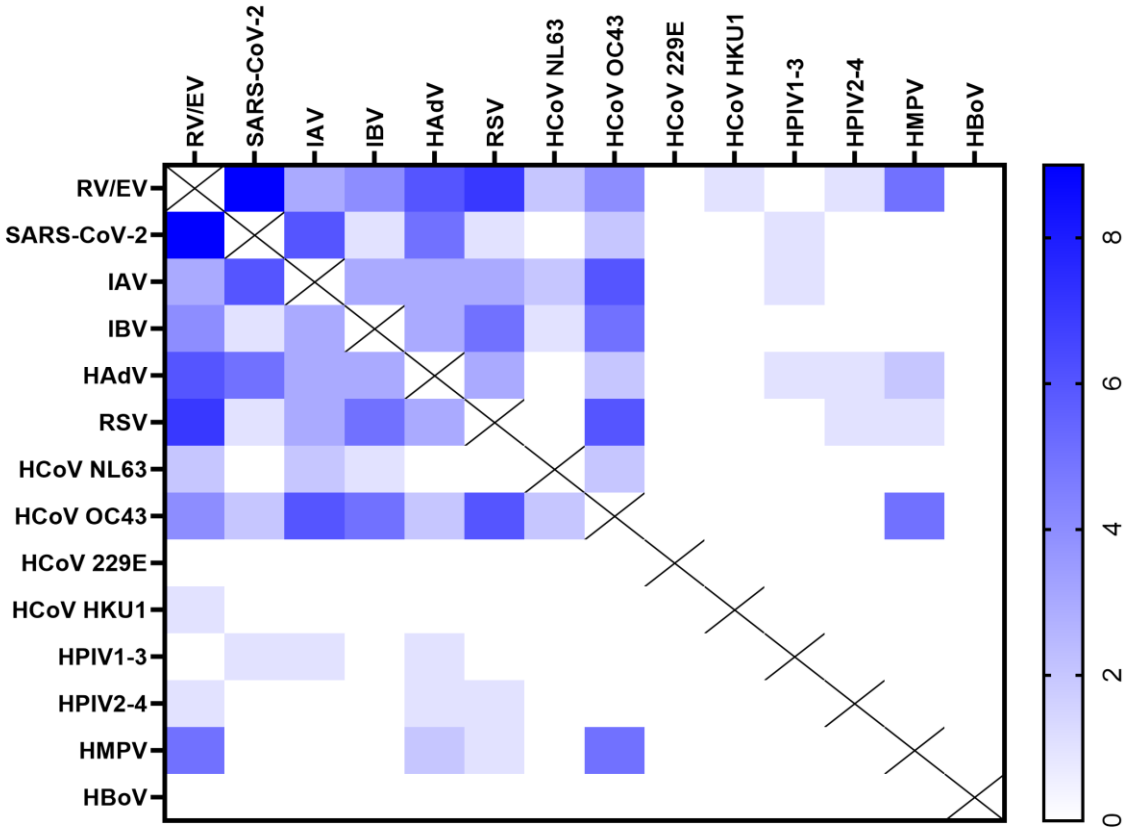


Figure 7: Frequency of co-detected viruses in absolute number.

2. Influenza viruses

a. Characterisation of subtypes and lineages

From week 40/2024 to 16/2025, a total of 585 influenza viruses were detected. This number included 367 IAV and 218 IBV (Figure 8.a). IAV were further subtyped either as A/H1N1pdm09 (n = 184; 50.1 %) or as A/H3N2 (n = 182, 49.6 %). Only one IAV and one IBV 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 could be identified.

Within the Sentinella surveillance network, influenza season started during week 50/2024 when crossing the 10 % positivity threshold defined by the European Centre for Disease Control and Prevention (ECDC) and immediately reaching a positivity rate of 19.4 % (Figure 8.b). The epidemic period lasted 17 weeks until week 14/2025 (positivity rate 15.09 %). The first IAV and IBV cases were detected in week 41/2024 and 45/2024, respectively. The median influenza positivity rate was 19.44 % (Q25: 4.62, Q75: 44.64) with a range from 0 % to 60 %. A peak of 73 laboratory-confirmed cases was recorded during epidemiological week 05/2025. This peak also aligns with the maximum number of influenza-like illness (ILI) consultations, which occurred in week 06/2025 (Appendix 1). Co-dominance of influenza A/H1N1pdm09, A/H3N2 and influenza B viruses was observed along the surveillance period. It should be noted that during epidemiological week 01/2025, the number of samples collected for analysis was low due to the holiday period. As a result, the corresponding positivity rate should be interpreted with caution.

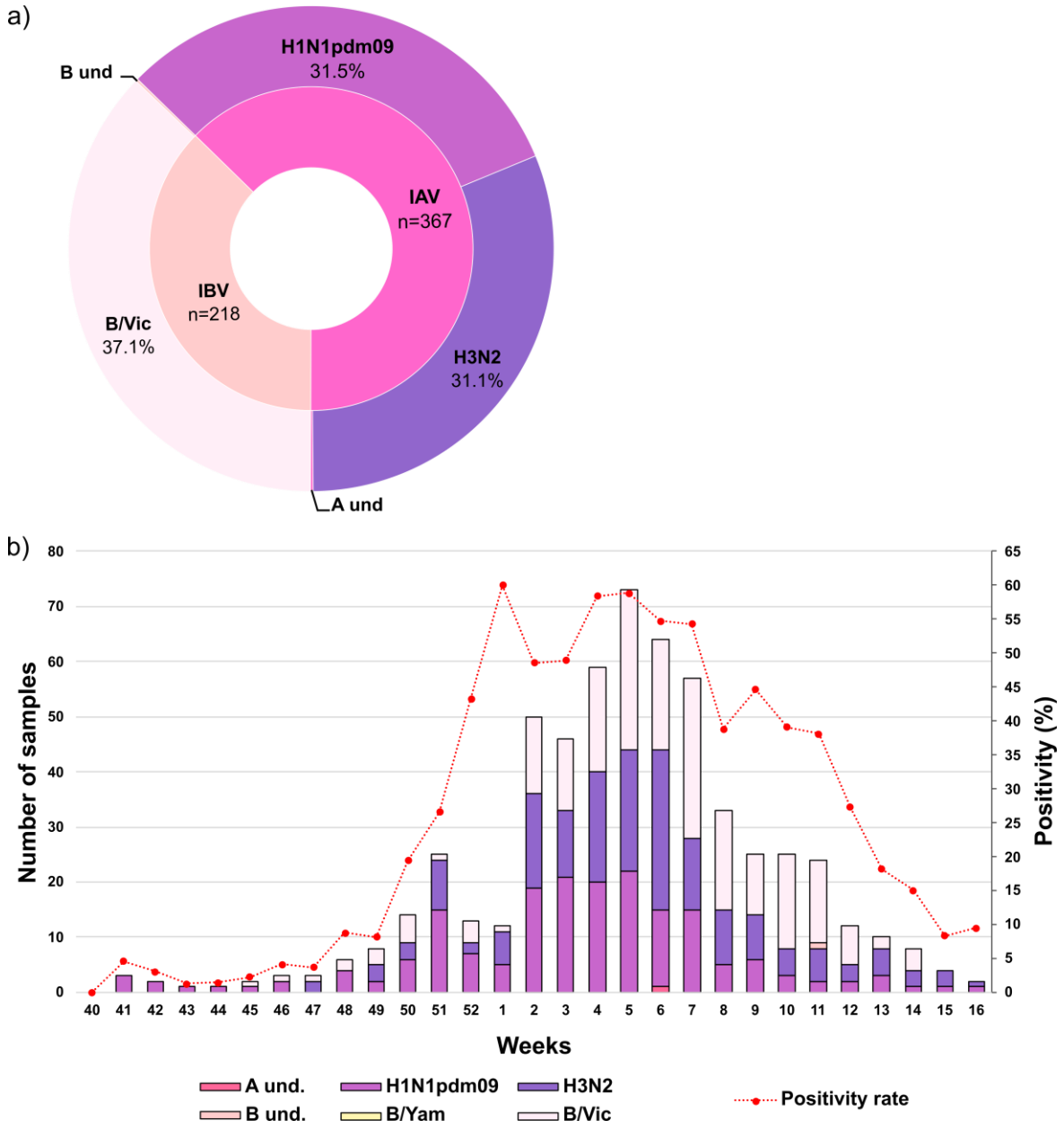


Figure 8: Proportion and temporal distribution of Influenza subtypes and lineages detected from week 40/2024 to 16/2025. a) Doughnut chart representing the number of IAV and IBV detected and the relative percentage of the different subtypes and lineage. b) Graph representing the number of samples tested positive for influenza and 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) at the Genome Centre, 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].

From October 2024 to April 2025, a total of 84 A/H1N1pdm09, 86 A/H3N2, and 112 B/Vic isolates were sequenced (Table 1). A total of 81 complete genome were recovered for A/H3N2 viruses and of 105 for B/Vic viruses. However, only 5 complete genomes were recovered for A/H1N1pdm09 viruses with the nucleoprotein (NP) segment most often missing. All obtained sequences were submitted to Global Initiative on Sharing All Influenza Data (GISAID) (Appendix 3, Appendix 4, Appendix 5). 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	**# samples in GISAID**	**# sequenced recovered (%)**			**Total sequences recovered**
			HA	NA	PA	
A/H1N1	84	83	80 (95.2)	83 (98.8)	82 (97.6)	245
A/H3N2	86	83	82 (95.3)	82 (95.3)	82 (95.3)	246
B/Vic	112	110	108 (96.4)	110 (98.2)	108 (96.4)	326
Total	282	276	270 (95.7)	275 (97.5)	272 (96.5)	817

Among the IAV and IBV positive samples, 115 were selected for virus isolation via cell culture. Of these, 81 (70.4 %) exhibited a cytopathic effect (CPE) and were subsequently subjected to haemagglutination (HA) assay. A total of 77 influenza (24 A/H1N1pdm09, 26 A/H3N2, 27 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 Sentinalla cohort were aligned with the reference HA(H1) sequences from ECDC (Appendix 8), clade and subclades were obtained using Nextclade v3.8.1 [3].

Among the sequenced A/H1N1pdm09 viruses, HA sequence analysis revealed that they belonged to clades 5a.2a and 5a.2a.1. Between week 40/2024 and week 16/2025, most HA sequenced belong to clade 5a.2a with an overrepresentation of the subclade C.1.9.3 (reference strain A/Hungary/286/2024). From December onward, viruses within subclade 5a.2a. began to appear, nearly all of which were assigned to subclade D.3 (reference strain A/Norway/00926/2025), except for one (Figure 9 and Figure 10).

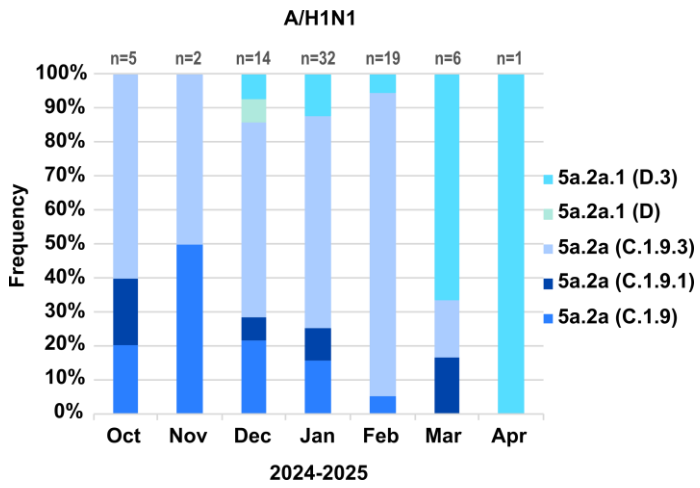


Figure 9: Time-dependent variation in frequencies of HA(H1) genetic clades and subclades (in brackets) in Sentinella population. Clade and subclade were obtained using Nextclade v3.8.1.

In line with what was observed across Europe, most isolates identified in Switzerland (n = 67) belonged to the clade 6B.1A.5a.2a (5a.2a) and a smaller proportion (n = 13) to the clade 6B.1A.5a.2a.1(5a.2a.1). Within the clade 5a.2a (C.1), three distinct subclades were identified, each defined by specific amino acid mutations in the HA1 gene: subclade C.1.9 (reference strain A/Lisboa/188/2023) with clusters defined by amino acid K54Q, A186T, Q189E, E224A, R259K, K308R (n = 11); subclade C.1.9.1 with specific amino acid P137S (n = 6); subclade C.1.9.3 (reference strain A/Hungary/286/2024) with amino acid S83P (n = 50) (Figure 10).

As for the 5a.2a.1 viruses (n = 13), they were split into two subgroups. The majority belonged to the subgroup D.3 (n = 12), defined by HA1 amino acid substitutions T216A and T120A (reference strain A/Norway/00926/2025). One isolate was identified in the subgroup D represented by A/Victoria/4897/2022 virus, with T216A substitution (Figure 10).

For antigenic characterisation of A/H1N1pdm09 viruses, HAI were performed using antisera against: A/Victoria/4897/2022 (Clade 5a.2a.1 (D)) and A/Guangdong-Maonan/SWL1536/2019 strain (Clade 5a.1 (B)) (Table 2). HAI titres show that NH 2024-2025 and SH 2025 vaccine strain A/Victoria/4897/2022 generally recognised both 5a.2a and 5a.2a.1 clade viruses well. Most viruses circulating in Switzerland during the season 2024-2025 were poorly recognised by the antiserum raised against A/Guangdong-Maonan/SWL1536/2019 strain. One isolate was antigenically distinct from both antisera tested.

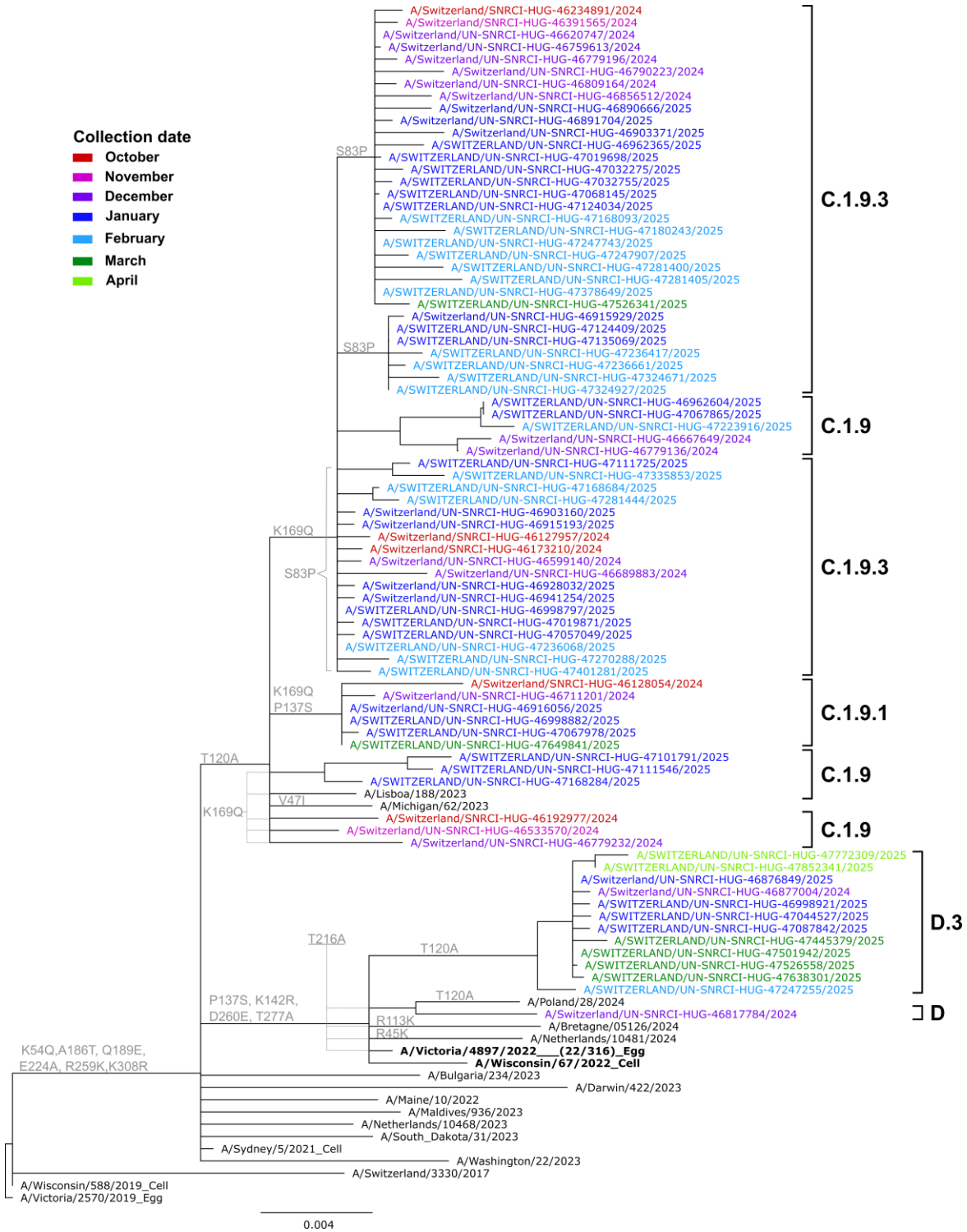


Figure 10: Maximum likelihood phylogenetic trees inferred using Geneious Prime® from HA(H1) sequence data. Annotation of amino acids substitutions was performed with Nextclade and TESSy. Reference strains are in black and vaccine strains are in bold. Colours indicate collection date of the nasopharyngeal swab.

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

	Post-infection ferret antiserum	
Viruses	A/Guangdong-Maonan/SWL1536/19	A/Victoria/4897/2022
A/Guangdong-Maonan/SWL1536/19	**1024**	16
A/Victoria/4897/2022	<16	**512**
A/Switzerland/SNRCI-HUG-46127957/2024	32	128
A/Switzerland/UN-SNRCI-HUG-46534666/2024*	128	2048
A/Switzerland/UN-SNRCI-HUG-46689883/2024	128	2048
A/Switzerland/UN-SNRCI-HUG-46667649/2024 ^	16	1024
A/Switzerland/SNRCI-HUG-46391565/2024	64	1024
A/Switzerland/SNRCI-HUG-46192977/2024	1024	4096
A/Switzerland/UN-SNRCI-HUG-46779136/2024	64	1024
A/Switzerland/UN-SNRCI-HUG-46928032/2025	256	4096
A/Switzerland/UN-SNRCI-HUG-45706081/2025	64	2048
A/Switzerland/SNRCI-HUG-46128054/2024	64	2048
A/Switzerland/UN-SNRCI-HUG-47572077/2025*	64	2048
A/Switzerland/UN-SNRCI-HUG-47168324/2025*	<16	256
A/Switzerland/UN-SNRCI-HUG-46876403/2025*	128	4096
A/Switzerland/UN-SNRCI-HUG-46779232/2024	128	4096
A/Switzerland/UN-SNRCI-HUG-46941235/2025*	64	2048
A/Switzerland/UN-SNRCI-HUG-46877004/2024	32	2048
A/Switzerland/UN-SNRCI-HUG-46876343/2025*	64	8192
A/Switzerland/UN-SNRCI-HUG-46856512/2024	64	512
A/Switzerland/UN-SNRCI-HUG-47111725/2025	64	2048
A/Switzerland/UN-SNRCI-HUG-47223916/2025	128	1024
A/Switzerland/UN-SNRCI-HUG-46962365/2025	256	4096
A/Switzerland/UN-SNRCI-HUG-47168284/2025	128	2048
A/Switzerland/UN-SNRCI-HUG-47649841/2025	64	4096
A/Switzerland/UN-SNRCI-HUG-47044527/2025	32	1024

Influenza A/H3N2

HA(H3) sequences from the Sentinella cohort were aligned with the reference HA(H3) sequences from ECDC (Appendix 9), clade and subclades were obtained using Nextclade v3.8.1 [3].

HA sequences of A/H3N2 virus belonged to both clades 2a.3a.1 and 2a.3a with the majority into the clade 2a.3a.1. Since November 2024, subclade J.2 (reference strains A/District of Columbia/27/2023, and A/Croatia/10136RV/2023) became the most frequent (Figure 11).

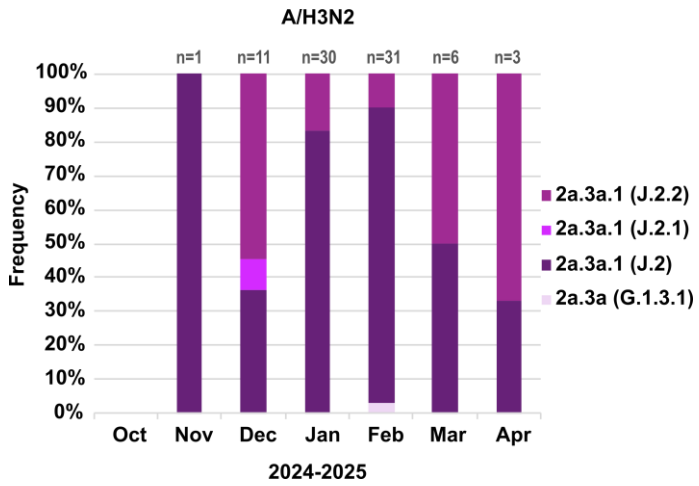


Figure 11: Time-dependent variation in frequencies of HA(H3) genetic clades and subclades (in brackets) in Sentinella population. Clade and subclade were obtained using Nextclade v3.8.1.

Eighty-one A/H3N2 isolates sequenced belonged to clade 2a.3a.1 and only one belonged to the subclade 2a.3a. In line with observation in Europe, the A/H3N2 strains detected in Switzerland have further diversified into subgroups, all except one have been characterised by amino acid substitutions I140K, and I223V (reference and vaccine 2024/2025 strain A/Thailand/8/2022, clade 2a.3a.1). The isolates were further assigned to three different subgroups within clade 2a.3a.1: subclade J.2 (reference and recommended vaccine NH-SH virus A/Croatia/10136RV/2023) constituted of additional amino acid substitutions N122D and K276E (n = 61); subclade J.2.2 (reference strain A/Lisboa/216/2023) characterised by specific amino acid substitutions S124N. The remaining sample was attributed to the subclade J.2.1 (reference A/WestVirginia/51/2024 virus) characterised by additional amino acid substitution P239S. One A/H3N2 was attributed to the subclade 2a.3a (G.1.3.1) (reference strain A/Finland/402/2023), characterised by amino acid substitution E50K, D53N, N96S, and I192F (Figure 12).

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)), and A/Croatia/10136RV/2023 (clade 2a.3a.1 (J.2)) (Table 3).

HAI titres show that most isolates circulating in Switzerland during the 2024-2025 season were well recognised by the SH 2024 and NH 2024-25 vaccine strains, egg-based A/Thailand/08/2022 (2a.3a.1 (J)). One isolate was antigenically distinct from the three antisera tested (Table 3).

Figure 12: Maximum likelihood phylogenetic trees inferred using Geneious Prime® from HA(H3) sequence data. Annotation of amino acids substitutions was performed with Nextclade and TESSy. Reference strains are in black and vaccine strains are in bold. Colours indicate collection date of the nasopharyngeal swab.

Table 3: Antigenic analysis of influenza A/H3N2. Reference viruses are in grey and test viruses are in black. 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	A/Darwin /9/2021	A/Thailand /8/2022	A/Croatia /10136RV/2023
A/Darwin/9/2021	**128**	64	16
A/Thailand/8/2022	512	**256**	256
A/Croatia/10136RV/2023	128	256	**256**
A/Switzerland/UN-SNRCI-HUG-46600365/2024	32	32	32
A/Switzerland/UN-SNRCI-HUG-46723057/2024	32	32	32
A/Switzerland/UN-SNRCI-HUG-47303107/2025*	32	32	16
A/Switzerland/UN-SNRCI-HUG-47468433/2025*	<16	16	16
A/Switzerland/5735/2024 ^	256	512	128
A/Switzerland/UN-SNRCI-HUG-47302844/2025*	256	512	256
A/Switzerland/UN-SNRCI-HUG-47582365/2025	128	256	256
A/Switzerland/UN-SNRCI-HUG-47661090/2025	1024	2048	512
A/Switzerland/UN-SNRCI-HUG-47582171/2025*	1024	1024	512
A/Switzerland/UN-SNRCI-HUG-47526372/2025	128	512	256
A/Switzerland/UN-SNRCI-HUG-47572010/2025	512	1024	512
A/Switzerland/UN-SNRCI-HUG-47223969/2025	512	512	512
A/Switzerland/5158/2024 ^	256	1024	256
A/Switzerland/UN-SNRCI-HUG-46927701/2025	512	1024	512
A/Switzerland/UN-SNRCI-HUG-46916246/2025	256	512	256
A/Switzerland/UN-SNRCI-HUG-46737106/2025*	256	512	512
A/Switzerland/UN-SNRCI-HUG-46747581/2024	128	128	64
A/Switzerland/UN-SNRCI-HUG-46856433/2024	256	512	256
A/Switzerland/UN-SNRCI-HUG-47088280/2025	512	1024	512
A/Switzerland/UN-SNRCI-HUG-47795894/2025	256	256	256
A/Switzerland/UN-SNRCI-HUG-47044215/2025	128	256	128
A/Switzerland/UN-SNRCI-HUG-47223528/2025	128	256	128
A/Switzerland/UN-SNRCI-HUG-47168213/2025	256	256	128
A/Switzerland/UN-SNRCI-HUG-47112364/2025*	2048	2048	1024
A/Switzerland/UN-SNRCI-HUG-47894198/2025	512	1024	512
A/Switzerland/UN-SNRCI-HUG-47783582/2025	1024	1024	1024

Influenza B

HA(B/Vic) sequences from the Sentinella cohort were aligned with the reference HA(B) sequences from ECDC (Appendix 10), clade and subclades were obtained using Nextclade v3.8.1 [3].

All the HA sequences (n = 108) collected since October 2024 belonged to the clade V1A.3a.2 (C) divided in three main subclades: C.5.7 (reference strain B/Guangxi-Beiliu/2298/2023), C.5.6 (reference strain B/Switzerland/329/2024), and C.5.1 (reference strain B/Catalonia/2279261NS/2023) (Figure 13).

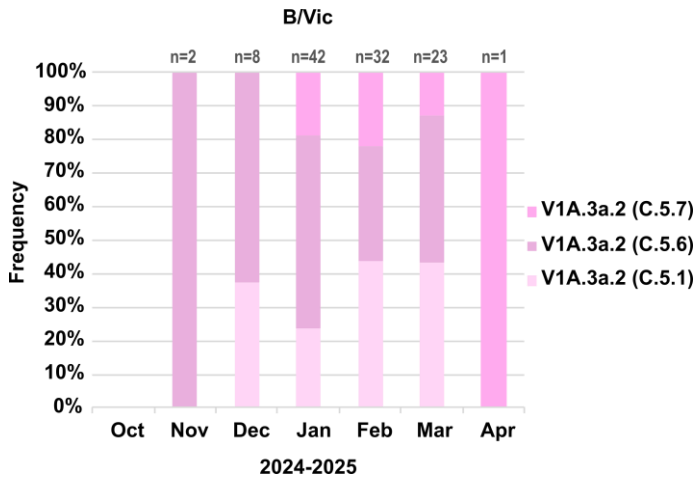


Figure 13: Time-dependent variation in frequencies of HA(B/Vic) genetic clades and subclades (in brackets) in Sentinella population. Clade and subclade were obtained using Nextclade v3.8.1.

Influenza B/Victoria lineage in the clade V1A.3a.2 (C) are characterised by the amino acid residues A127T, P144L, and K203R (vaccine strain B/Austria/1359417/2021) (Figure 14). Within the V1A.3a.2 clade, the isolates were separated into three subclades. Fifty-two viruses belonged to the subclade C.5.6 and characterised by amino acid substitution D197E and D129N. Thirty-seven isolates were attributed to the subclade C.5.1 with additional amino acid changes E183K. Nineteen viruses belonged to the C.5.7 subclade characterized by amino acid substitutions E183K and additional E128G (Figure 14).

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).

All V1A.3a.2 (C) isolates tested were well recognised by the antiserum raised against the B/Austria/1359417/2021 vaccine strain (Table 4).

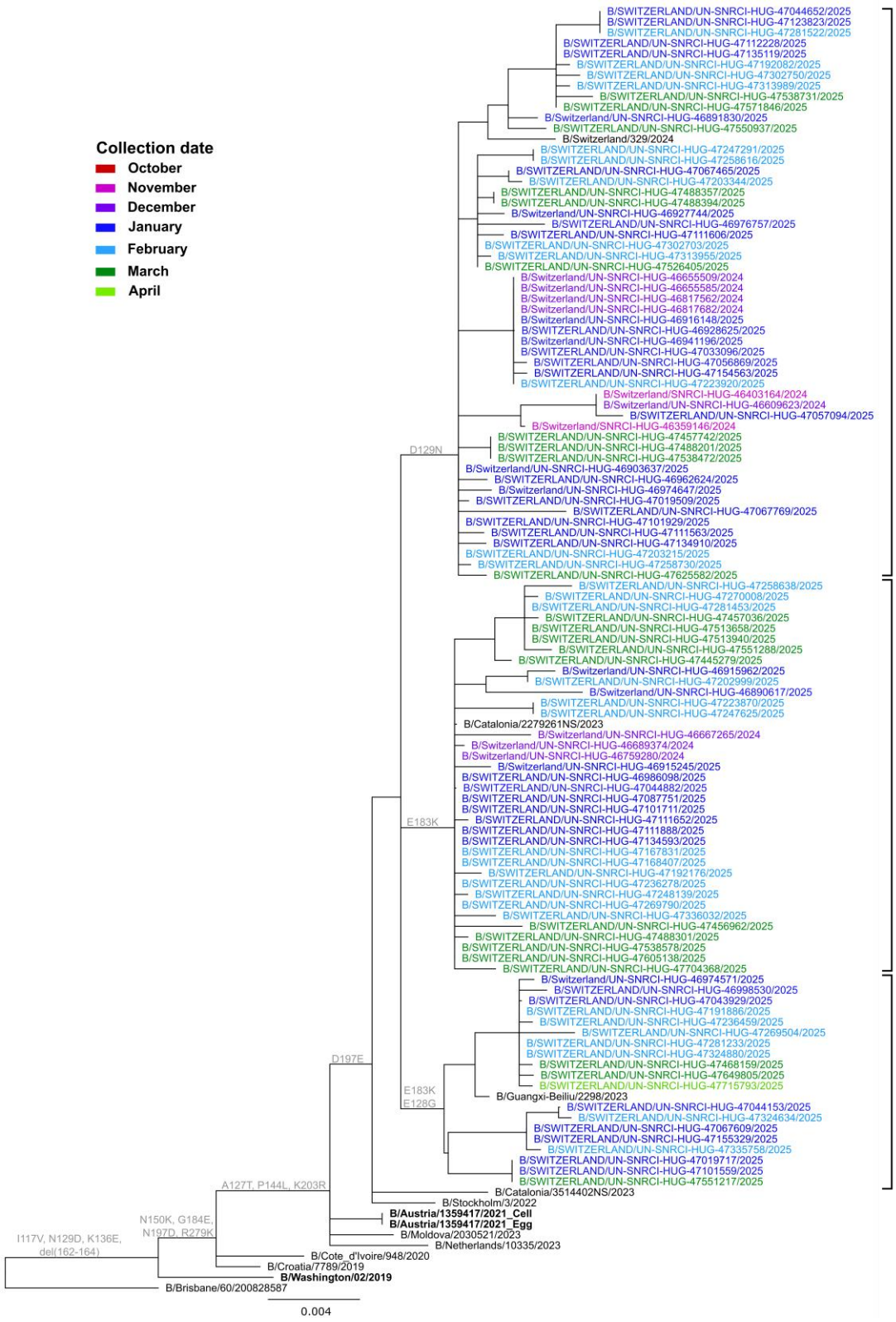


Figure 14: Maximum likelihood phylogenetic trees inferred using Geneious Prime® from HA(B/Vic) sequence data. Annotation of amino acids substitutions was performed with NextClade and TESSy. Reference strains are in black and vaccine strains are in bold. Colours indicates collection date of the nasopharyngeal swab.

Table 4: Antigenic analysis of influenza B(Vic). Reference viruses are in grey and test viruses are in black. Test viruses were also sequenced except for those indicated with an asterisk (*) and viruses sequenced by the WIC are indicated with a circumflex (^).

	Post-infection ferret antiserum		
Viruses	B/Washington /02/19	B/Austria /1359417/2021	B/Stockholm /3/2022
B/Washington/02/2019	**256**	<16	<16
B/Austria/1359417/2021	<16	**1024**	128
B/Stockholm/3/2022	32	256	**256**
B/Switzerland/8393/2024 ^	64	512	1024
B/Switzerland/4213/2024 ^	64	512	1024
B/Switzerland/UN-SNRCI-HUG-46759280/2024	64	1024	2048
B/Switzerland/UN-SNRCI-HUG-46916148/2025	64	1024	2048
B/Switzerland/UN-SNRCI-HUG-46962624/2025	32	256	512
B/Switzerland/UN-SNRCI-HUG-47043929/2025	64	512	2048
B/Switzerland/UN-SNRCI-HUG-46890617/2025	16	256	256
B/Switzerland/UN-SNRCI-HUG-47649805/2025	64	512	512
B/Switzerland/UN-SNRCI-HUG-47302750/2025	32	256	512
B/Switzerland/UN-SNRCI-HUG-47367142/2025*	32	512	512
B/Switzerland/UN-SNRCI-HUG-47468159/2025	32	256	512
B/Switzerland/UN-SNRCI-HUG-47302703/2025	32	256	512
B/Switzerland/UN-SNRCI-HUG-47488357/2025	32	256	512
B/Switzerland/UN-SNRCI-HUG-47033096/2025	128	128	256
B/Switzerland/UN-SNRCI-HUG-47354327/2025*	128	256	256
B/Switzerland/UN-SNRCI-HUG-47571846/2025	64	512	1024
B/Switzerland/UN-SNRCI-HUG-47111888/2025	64	512	1024
B/Switzerland/UN-SNRCI-HUG-47456962/2025	128	1024	2048
B/Switzerland/UN-SNRCI-HUG-47354303/2025*	128	512	2048
B/Switzerland/UN-SNRCI-HUG-47526405/2025	64	512	1024
B/Switzerland/UN-SNRCI-HUG-47354436/2025*	32	256	256
B/Switzerland/UN-SNRCI-HUG-47715793/2025	64	512	1024
B/Switzerland/UN-SNRCI-HUG-47223870/2025	64	512	1024
B/Switzerland/UN-SNRCI-HUG-47044153/2025	64	1024	4096
B/Switzerland/UN-SNRCI-HUG-47123823/2025	128	1024	2048
B/Switzerland/UN-SNRCI-HUG-47168407/2025	32	512	1024
B/Switzerland/UN-SNRCI-HUG-47223920/2025	16	1024	512

c. Antiviral susceptibility

For all viruses with successfully sequenced PA gene, no genetic markers associated with reduced inhibition by baloxavir marboxil were identified [4] [5]. We identified the L28P mutation in sample A/Switzerland/UN-SNRCI-HUG-47572010/2025 which was shown to result in 0.4-2.6 EC_{50} fold change. As of July 2025, only a fold-change value > 3-fold is considered as reduced susceptibility to baloxavir marboxil.

All viruses with successfully sequenced NA genes were screened for genetic markers associated with reduced susceptibility to neuraminidase inhibitors (NAIs) [4]. Additionally, NA inhibition assays (MUNANA) were conducted on three samples to assess their phenotypic susceptibility (Table 5 and Figure 15):

- Six samples had genotypic markers that alone are not associated with reduced susceptibility to NAIs but that can be led to reduced inhibition (RI) or highly reduced inhibition (HRI) when associated with other mutation.
    - The S247N mutation was found in four samples: A/Switzerland/UN-SNRCI-HUG-46759613/2024, A/Switzerland/UN-SNRCI-HUG-46809164/2024, A/SWITZERLAND/UN-SNRCI-HUG-47044527/2025, A/Switzerland/UN-SNRCI-HUG-47638301/2025. Phenotypic analysis was not performed for these mutations.
    - The phenotypic impact of the mutations identified in samples A/SWITZERLAND/UN-SNRCI-HUG-47236417/2025 (I117M) and B/SWITZERLAND/UN-SNRCI-HUG-47281233/2025 (T106I) when present alone are unknown. When tested by MUNANA, substitution I117M was associated with normal inhibition (NI) for both inhibitors tested. However, the IBV harbouring the T106I substitution displayed normal inhibition (NI) to Zanamivir but RI to Oseltamivir. The fold change in IC_{50} was just above the threshold.
- One sample, A/Switzerland/UN-SNRCI-HUG-46876849/2024, displayed the I223T mutation which is associated with either NI or RI for oseltamivir in A/H1N1pdm09 viruses. Phenotypic analysis was not performed for this mutation.
- One sample, A/SWITZERLAND/UN-SNRCI-HUG-47067935/2025, displayed the H275Y substitution, which is associated with highly reduced susceptibility to oseltamivir in A/H1N1pdm09 viruses. Phenotypic testing confirmed highly reduced inhibition (HRI) by Oseltamivir and NI by Zanamivir.

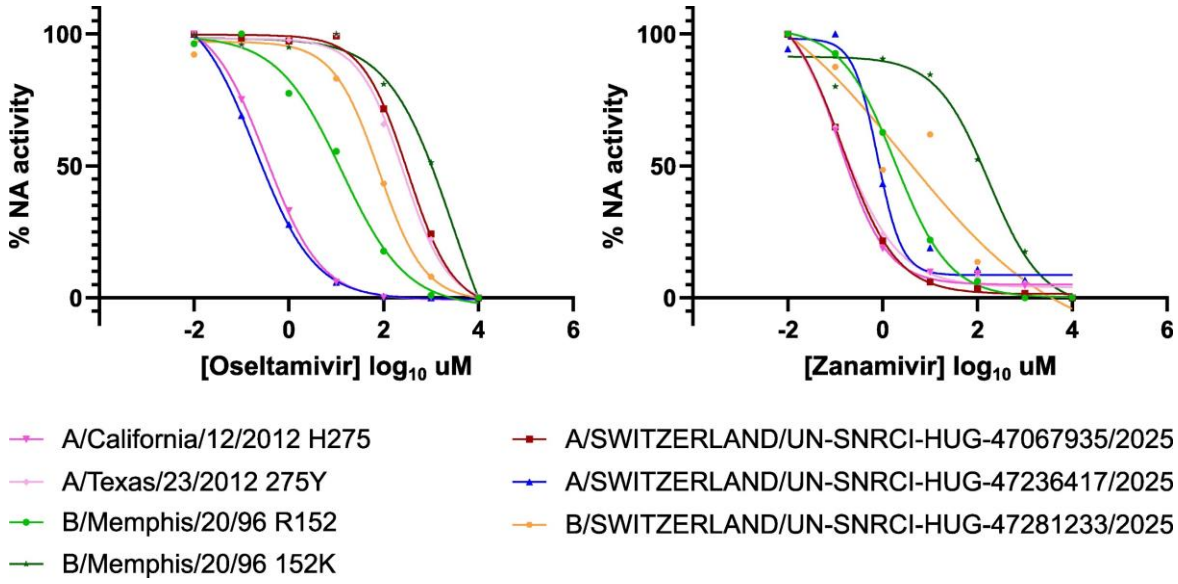


Figure 15: Dose-response inhibition curve of neuraminidase activity by oseltamivir and zanamivir.

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

Strains		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	A/California/12/2012	none	NI	NI	NI (1)	NI (1)
	A/Texas/23/2012	H275Y	**HRI**	NI	**HRI** (785)	NI (0.9)
	B/Memphis/20/1996	none	NI	NI	NI (1)	NI (1)
		R150K	**HRI**	**HRI**	**HRI** (232)	**HRI** (94)
	A/Switzerland/UN-SNRCI-HUG-47067935/2025 (H1N1)pdm09	H275Y	**HRI**	NI	**HRI** (978)	NI (1.1)
	A/Switzerland/UN-SNRCI-HUG-47236417/2025 (H1N1)pdm09	I117M	unk	unk	NI (0.6)	NI (6.2)
	B/Switzerland/UN-SNRCI-HUG-47281233/2025 (B(Vic))	T106I	unk	unk	**RI** (6.1)	NI (1.5)

[a] Numbering based on the neuraminidase subtype N1 for type A viruses and the neuraminidase of type B viruses.

[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 IC_{50} (half maximal inhibitory concentration) relative to wild-type virus. For type A viruses: <10-fold - NI; 10-100-fold - RI; >100-fold - HRI. For type B viruses: <5-fold - NI; 5-50-fold - RI; >50-fold - HRI

d. Suspicion of zoonotic influenza

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, samples 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. The latter are analysed using a rRT-PCR with the capacity to distinguish IAV of human and animal origin, both avian and porcine. Positive samples are further characterised by sequencing.

From week 40/2024 to week 16/2025, three nasal swabs from Swiss farmers with ILI symptoms were sent to the NRCI for swine influenza suspicions. They all turned out negative.

Furthermore, the NRCI received one suspicion for influenza HxNy in January 2025. The patient was hospitalized and tested positive for IAV A/HxN2 and IBV with Ct values at the limit of detection of our H3 and N2 subtyping PCR. The remaining sample (very low volume) was sent to the WIC for further characterization, but the virus could neither be isolated or sequenced.

3. Genetic characterisation of SARS-CoV-2

A total of 126 SARS-CoV-2 genomes were sent for whole genome sequencing (WGS) at the Genome Centre, followed by data analysis performed by the Swiss Pathogen Surveillance Platform (SPSP). SPSP then upload 118 sequences on GISAID (Appendix 6). Clades were assigned using Nextclade v3.8.1 [3], with a clade definition from Nextstrain and Pango-lineage [6, 7].

From October 2024 to January 2025, we observed the circulation of mainly two Variant Under Monitoring (VUM): lineage KP.3.1.1 and lineage XEC. Since January 2025, the emergence of new lineages classified as VUM, including recombinant forms, LP.8.1, LF.7, and XFG has been observed, although their detection rates remained very low (Figure 16).

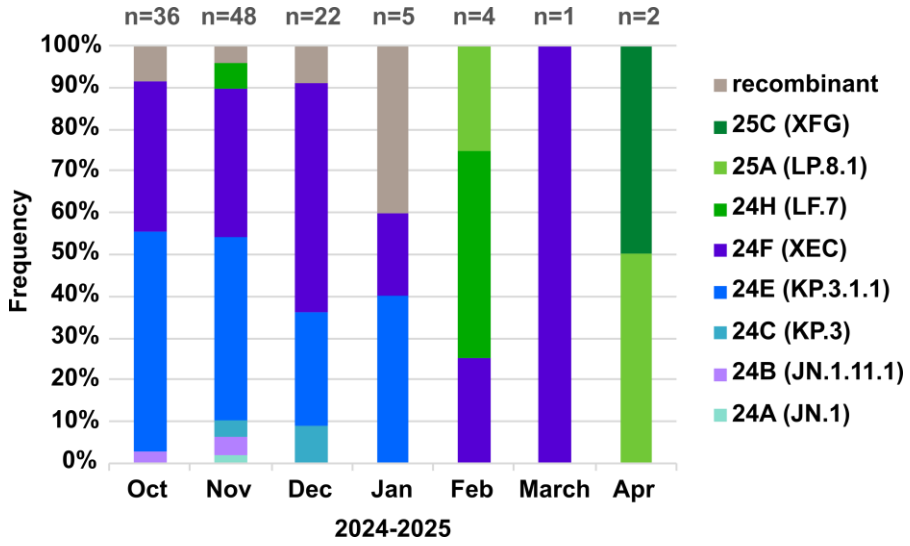


Figure 16: Time-dependent variation in frequencies of SARS-CoV-2 variants in Sentinella population.

4. Genetic characterisation of RSV

A total of 40 RSV isolates were sent for whole genome sequencing (WGS) at the Genome Centre, followed by data analysis performed by the Swiss Pathogen Surveillance Platform (SPSP). SPSP then upload 36 sequences on GISAID (Appendix 7). Lineage were assigned using Nextclade v3.8.1 [3], according to the clade definition by Goya *et al.* and the RSV Genotyping Consensus Consortium [8].

Both serotype A and B circulated in Switzerland between week 40/2024 and week 16/2025 (Figure 17). Sequences were screened for the presence of genetic markers associated with reduced susceptibility to the newly approved monoclonal antibody nirsevimab. No such mutations were identified in the isolates sequenced [9-11].

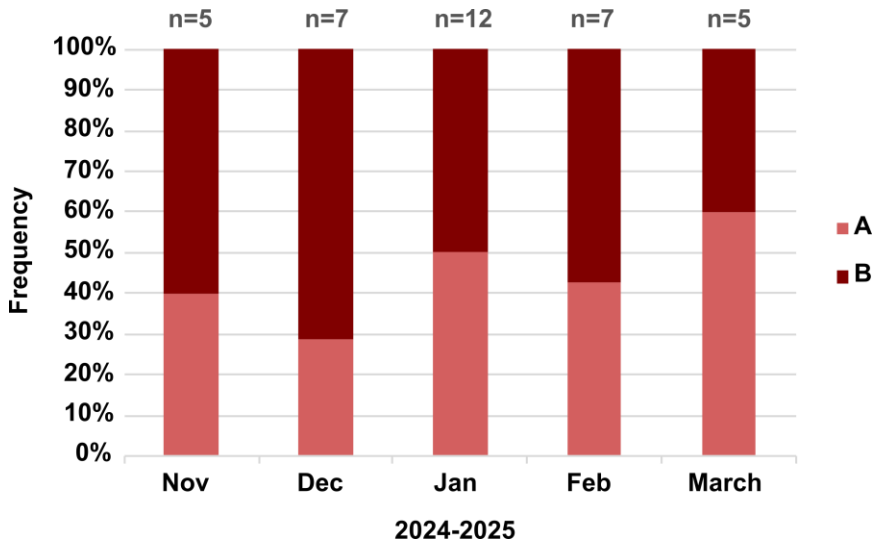


Figure 17: Time-dependent variation in frequencies of RSV subtypes in Sentinella population.

D. Vaccination

1. Vaccination status of the study population and impact on infection

In Switzerland, different vaccines are available to protect against infection with influenza and SARS-Cov-2 viruses. All available influenza vaccines in Switzerland are quadrivalent and patients have a choice of egg-based or cell-based production [12]. Influenza strains present in the vaccine composition are based according to the WHO recommendation [13] and are summarised in Table 6. Available SARS-CoV-2 vaccines in Switzerland are based on the mRNA technology [14]. Practitioners participating in the Sentinella cohort have been asked to fill the vaccination status.

Table 6: Vaccine strains recommended by the WHO and present in the influenza vaccine available in Switzerland for the season 2024/2025.

	Egg-based vaccine	Cell-based vaccine
A(H1N1)	A/Victoria/4897/2022 (H1N1)pdm09-like	A/Wisconsin/67/2022 (H1N1)pdm09-like
A(H3N2)	A/Thailand/8/2022 (H3N2)-like	A/Massachusetts/18/2022 (H3N2)-like
B/Victoria	B/Austria/1359417/2021-like	
B/Yamagata	B/Phuket/3073/2013-like	

For influenza, the vaccination information concerned the current season. Patients were classified in three categories: 'vaccinated', if they received an influenza vaccine for the 2024-2025 season; 'not vaccinated', if they have never received an influenza vaccine or haven't received the 2024-2025 vaccine; and 'unknown', if the patient does not know its vaccine status. For the period from week 40/2024 to week 16/2025, 6 % of samples were obtained from patients who did not know their vaccine status, 12 % who had received the vaccine and a large majority (82 %) of samples were collected from patients who were not vaccinated. When looking at the proportion of the different vaccine status per age group (Figure 18.a), it is noticeable that in patient aged 65 and over, 35 % were vaccinated. The lowest vaccination rate was observed in the 15-29 years-old (3 %) while in the other age groups the vaccination rate was around 7 %. The detection or absence of detection of influenza viruses was further analysed depending on the influenza vaccination status (Figure 18.b). A proportion comparison test was used to assess statistical differences between the groups. Only the difference between the vaccinated group

and non-vaccinated group for the detection of influenza B/Victoria was statistically significant (p-value < 0.01), indicating that the detection on B/Vic is more frequent in the non-vaccinated group.

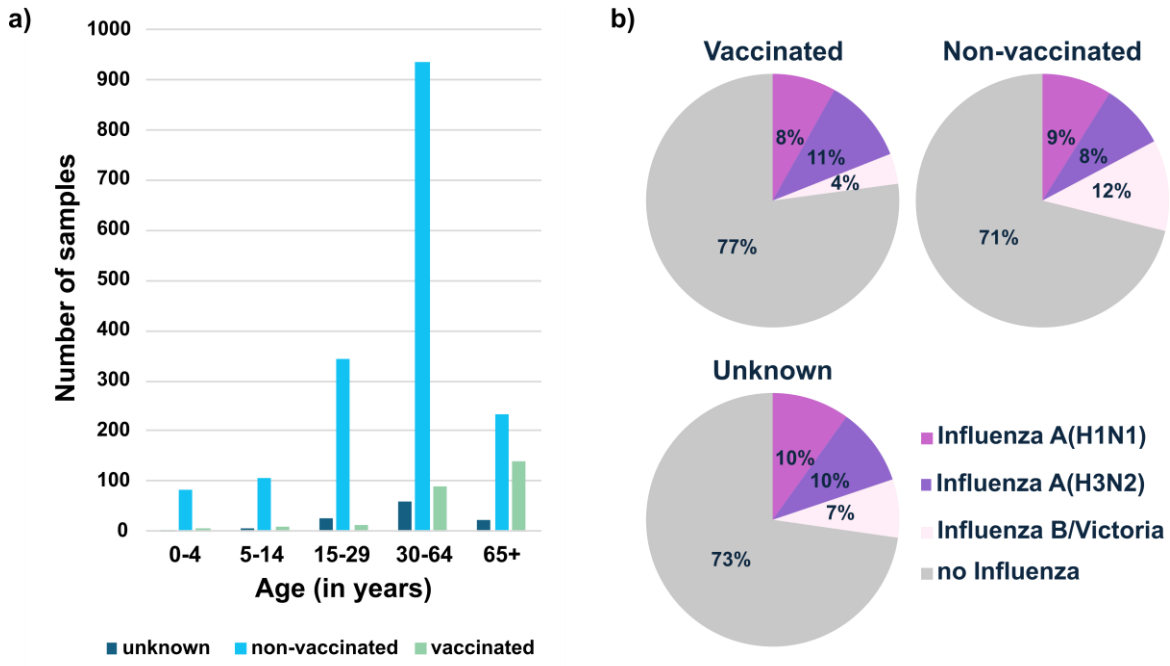


Figure 18: Influenza vaccine status of the Sentinella cohort and its impact on influenza infection. a) Graph representing the number of samples collected according to the patient age and influenza vaccination status. b) Pie chart representing the occurrence or absence of detection of influenza viruses depending on the vaccination status of the patient.

For SARS-CoV-2, patients were asked if they had received a dose of vaccine within the last 6 months and were divided into three groups depending on their answer: 'vaccinated' if they received a dose no later than 6 months before the sample date; 'not-vaccinated' if their vaccination was older than 6 months; 'unknown' if the patient did not know its vaccine status. For the period from week 40/2024 to week 16/2025, 8 % of samples were from patients who did not know their vaccine status, 4 % had received the vaccine no later than 6 months earlier and a large majority (88 %) of samples were collected from patients who were not vaccinated. When looking at the proportion of the different vaccine status per age group (Figure 19.a), it is noticeable that in all age groups, except ≥ 65, the vaccination rate was below 2.5 % with an unknown vaccination status around 8 %. In the population aged 65 and older, the vaccination rate reached 15 %. The proportion of samples that were either positive or negative for SARS-CoV-2 was further analysed: between 8 and 10 % of samples tested positive for SARS-CoV-2 independently of the vaccination status on the patient (Figure 19.b).

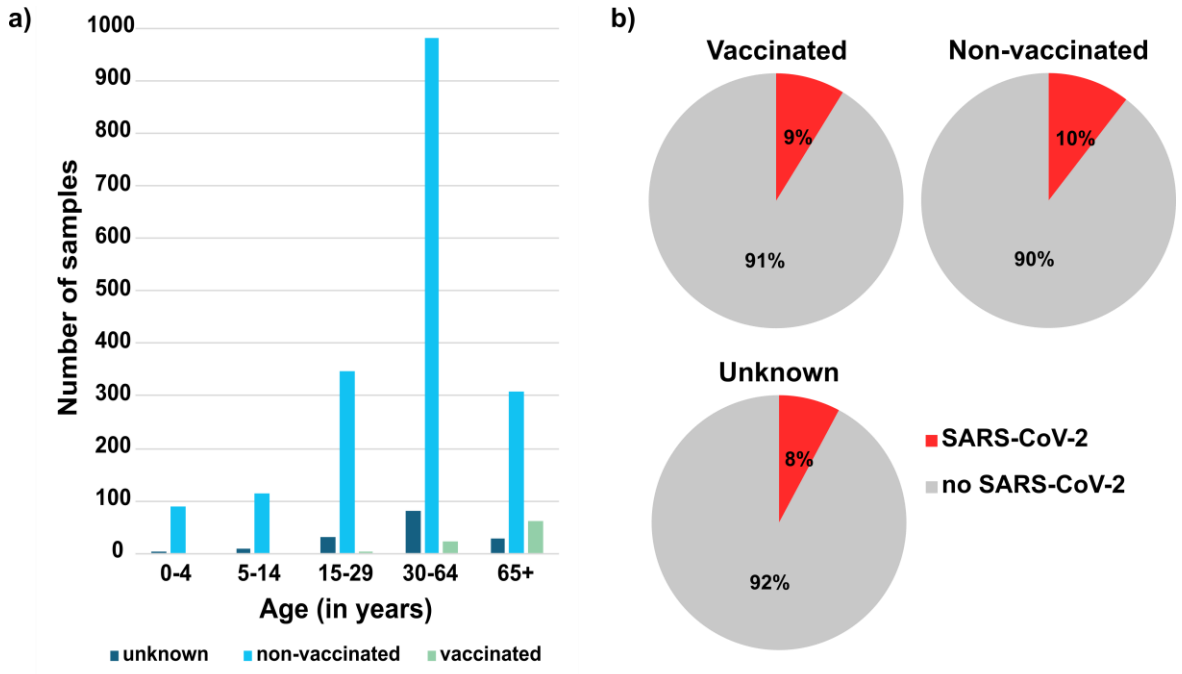


Figure 19: SARS-CoV-2 vaccine status of the Sentinella cohort and its impact on SARS-CoV-2 infection. a) Graph representing the number of samples collected according to the patient age and SARS-CoV-2 vaccination status. b) Pie chart representing the occurrence or absence of detection of SARS-CoV-2 viruses depending on the vaccination status of the patient.

2. WHO vaccine recommendation for influenza season 2025-2026

The WHO's recommendation for influenza vaccine composition is based on a predictive assessment of the most probable circulating strain for the upcoming season. This prediction integrates genetic and antigenic characterisation of the currently circulating strain, human serology data, virus fitness forecast, antiviral resistance profiles, vaccine effectiveness evaluations, and the availability of candidate vaccine viruses.

The recommendation for the 2025-2026 season was based on data collected between September 2024 and January 2025 within the Global Influenza Surveillance Response System network (GISRS) [15]. The NRCI actively participates in this selection by submitting genetic data to the EpiPulse platform (sequences for 70 viruses) and sending 30 representative influenza samples to the Worldwide Influenza Centre (WIC) in London. During that period, the HA genes of A/H1N1pdm09 viruses circulating globally belonged to the clade 5a.2a and 5a.2a.1 which are well recognised by antisera raised against the vaccine strains (cell culture-propagated A/Wisconsin/67/2022 and egg-propagated A/Victoria/4897/2022). The HA genes of A/H3N2 viruses belonged to the 2a.3a.1 subclade J.2 and antisera raised against A/District of Columbia/27/2023 and A/Croatia/10136RV/2023 showed improved recognition compared to antisera raised against the previous vaccine strains (cell culture-propagated A/Massachusetts/18/2022 and egg-propagated A/Thailand/8/2022). All circulating influenza B viruses were of the B/Victoria lineage. Notably, there have been no confirmed naturally occurring virus detection for the B/Yamagata lineage since March 2020 prompting the WHO to advised manufacturers to exclude the B/Yamagata lineage from vaccines. The vaccine strains recommended by the WHO are listed in Table 6 and when a quadrivalent vaccines are still used the B/Yamagata component can be added.

Table 6: WHO recommendation on vaccine composition in the Northern hemisphere for season 2025-2026.

	Egg-based vaccine	Cell-based vacine
A(H1N1)	A/Victoria/4897/2022 (H1N1)pdm09-like	A/Wisconsin/67/2022 (H1N1)pdm09-like
A(H3N2)	A/Croatia/10136RV/2023 (H3N2)-like	A/District of Columbia/27/2023 (H3N2)-like
B/Victoria	B/Austria/1359417/2021 (B/Victoria lineage)-like	
B/Yamagata*	B/Phuket/3073/2013 (B/Yamagata lineage)-like	

* only in quadrivalent vaccines

E. Annual comparison over the period from October 2020 to April 2025

Analysis of surveillance data collected by the NRCI offers valuable insights into the epidemiological dynamics of RSV, SARS-CoV-2, and influenza infections across the past five seasons (Figure 20). During the winter of 2020-2021, only SARS-CoV-2 was detected, and at relatively low levels, while RSV and influenza viruses were absent from circulation. This absence is most likely attributable to the widespread implementation of social distancing measures and the use of face coverings. In Switzerland, these protective measures were lifted on 17 February 2022. In the subsequent 2021–2022 winter season, RSV re-emerged towards the end of 2021, and influenza activity peaked in April 2022, with circulation increasing shortly after the lifting of restrictions. SARS-CoV-2 continued to circulate throughout the year. From the 2022–2023 season onwards, a gradual re-establishment of pre-pandemic seasonal patterns was observed, with RSV predominantly circulating during autumn and winter, and influenza activity mainly occurring from late December to the end of March. Since early 2024, SARS-CoV-2 circulation has remained low, with a moderate increase noted during the autumn months.

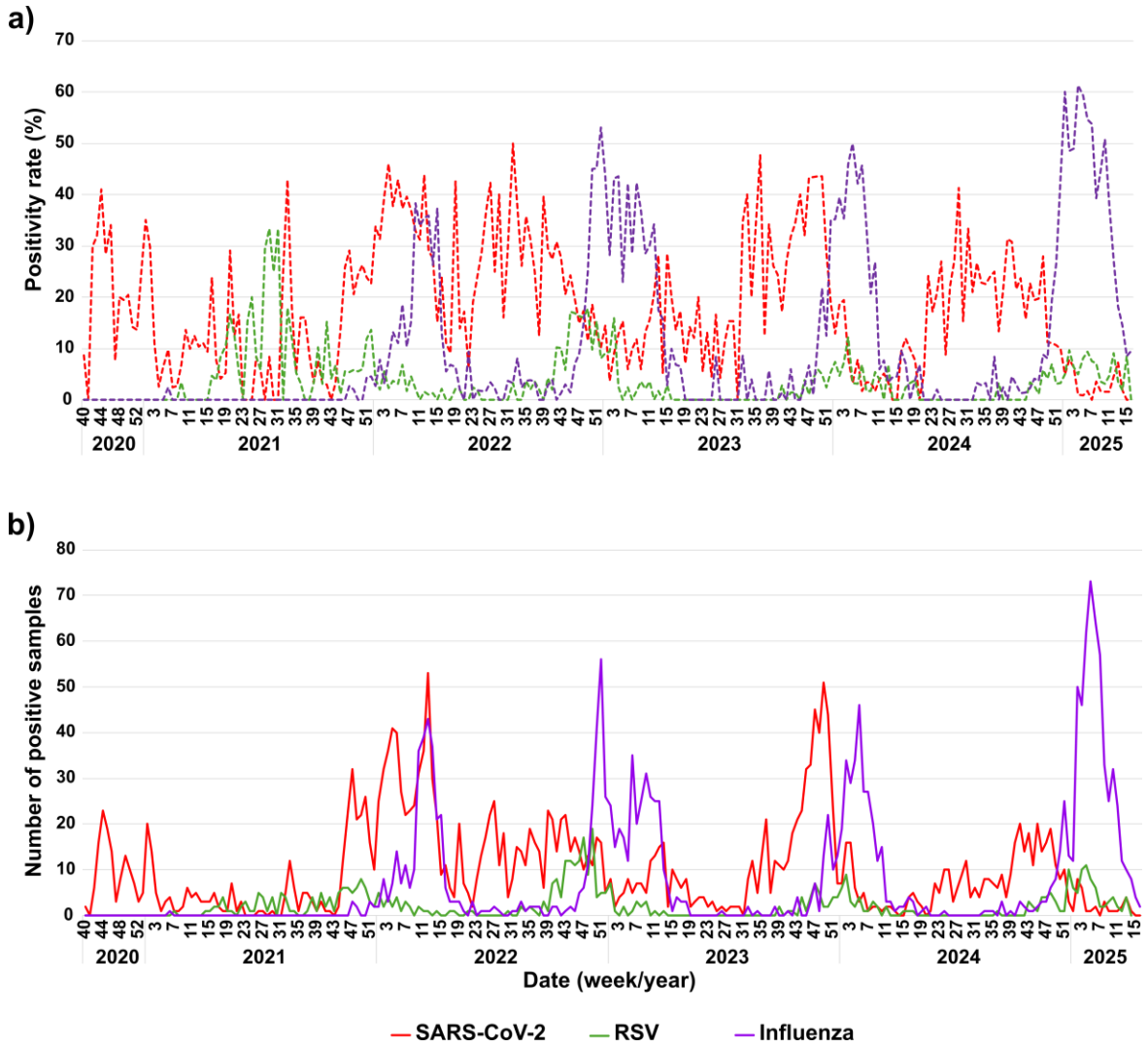


Figure 20: Aggregate weekly test positivity (a) and weekly detections (b) from week 40/2020 to week 16/2025 for SARS-CoV-2, RSV and Influenza viruses.

F. Epidemiological summary: comparison of national and international data

1. Influenza viruses

In Europe, the 2024-2025 respiratory virus season (week 40 to week 16) was characterised by an intense influenza season with positivity above the 10 % threshold starting in week 50 and lasting for 17 weeks. A return to pattern observed before the COVID-19 pandemic was observed during the 2023-2024 season [16] and was confirmed with the 2024-2025 season [17]. The percentage of positive samples showed a steady rise, plateaued at about 48 % from week 04/2025 to week 06/2025 and decreased until week 16/2025 crossing below the threshold of 10 %. In all surveillance systems, influenza A viruses predominated during this season with a slight dominance of influenza A/H1N1pdm09 over A/H3N2. Influenza B viruses prevalence started to increase in week 02/2025. Except for few countries, including Croatia, Portugal and Slovakia, where the season started with a high prevalence of influenza B [18].

The majority (>80 %) of A/H1N1 viruses sequenced globally belong to clade 5a.2a subclade C.1.9 which was further split in four subclades. Subclade C.1.9.3 represented about 60 % of all sequenced and was

predominant in Europe (Figure 21). Fewer A/H1N1 were assigned to clade 5a.2a.1 major subclade D (vaccine reference A/Victoria/4897/2022) which was further split in 5 subclades. Subclade D.3 was detected in Europe, but it represents a minority of sequences. The recently emerged subclade D.5 circulated mainly in Brazil (Figure 22) [19].

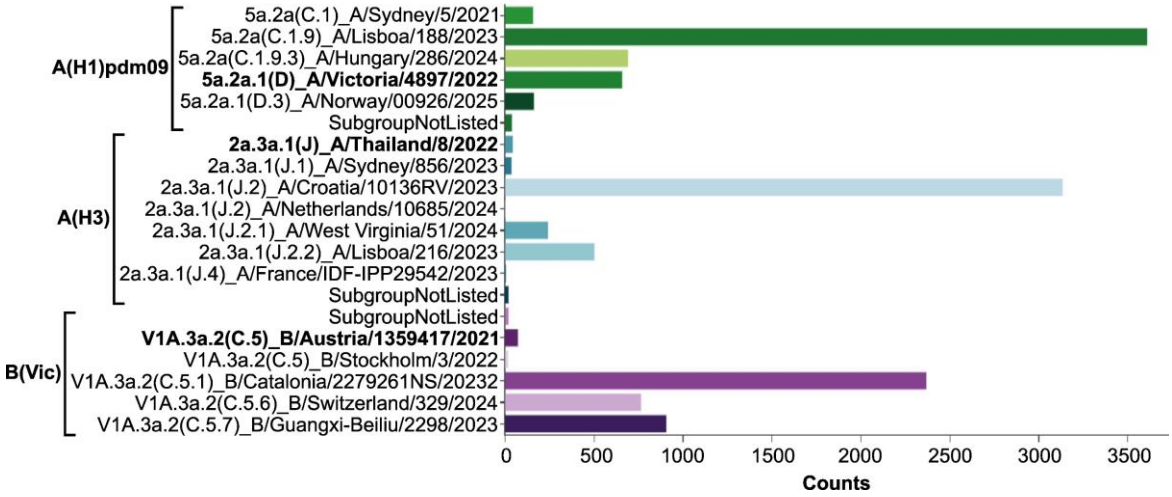


Figure 21: Cumulative influenza virus detections by genetic clade from week 40/2024 to week 16/2025. Vaccine clade(subclade)_strain are shown in bold. Country selection: Austria, Belgium, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Liechtenstein, Lithuania, Luxembourg, Malta, Netherland, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden. © 2025 European Centre for Disease Prevention and Control, available under a CC BY 4.0 licence.

During the reporting period, most A/H3N2 viruses belonged to the clade 2a.3a.1 subclade J. This subclade was further divided into 4 subclades, of these the clade J.2 (vaccine reference A/Croatia/10136RV/2023) became prevalent in the southern hemisphere winter season 2024 and was predominantly circulating worldwide during the season 2024-2025 (Figure 22). This trend was also present in Europe and in Switzerland.

All the B/Victoria strains circulating worldwide are from clade V1A.3a.2, with co-circulation of subclades C.5.1 (vaccine reference B/Catalonia/2279261NS/2023), C.5.6 (vaccine reference B/Switzerland/329/2024), and C.5.7 (reference B/Guangxi-Beiliu/2298/2023 strain). Of note, no B/Yamagata lineage viruses have been detected since March 2020.

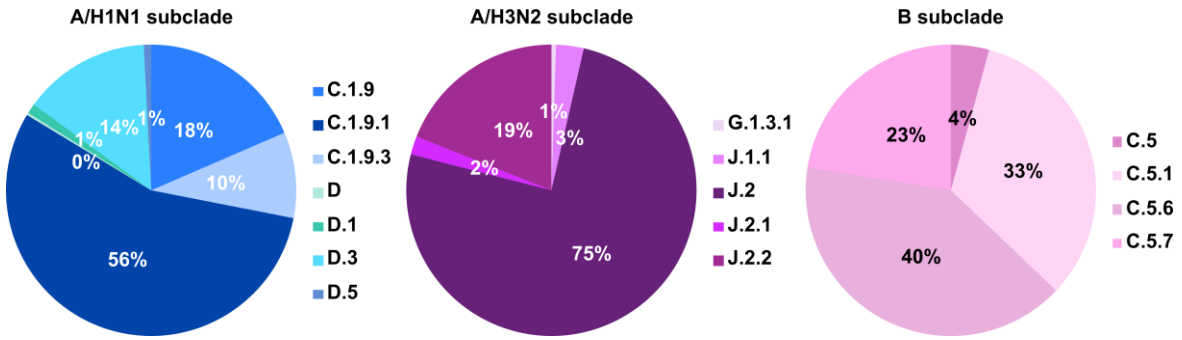


Figure 22: Worldwide representation of genetic subclades, obtained with full HA sequences as deposited in GISAID and classified using Nextclade. GISAID criteria were as follow: 1) Basic filters: type = A or B, H = 1 or 3, N = 1 or 2, host = human, location = all), 2) additional filters: Collection date from 30.09.2024 to 20.04.2025, submission date until 12.06.2025, submitting laboratory = GISRS submission, required segments = HA, sampling strategy = Sentinel surveillance (ILI, ARI and SARI). This resulted in a total of 369 A/H1N1, 195 A/H3N2 and 328 B sequences analysed.

2. SARS-CoV-2

Between 2020 and 2025, SARS-CoV-2 transitioned from a pandemic-level threat to an endemic respiratory virus, with recurent 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. [20, 21].

In both the southern hemisphere and northern hemisphere, SARS-CoV-2 activity has decreased over the past months [18, 22, 23]. In early 2025, the global positivity rate ranged from 5 % to 7 % [24]. Global epidemiological data indicating reduced detection rates of SARS-CoV-2, combined with the lack of genetic evidence of increased transmissibility, support the hypothesis that the virus may have entered an endemic phase characterised by a defined seasonality.

Since its first emergence, SARS-CoV-2 has undergone continuous evolution, with multiple waves driven by variants of concern (VOCs) such as Alpha, Delta, and Omicron (and its sublineages). Since 2023, Omicron sub-lineages have dominated, with JN.1 becoming a Variant of Interest (VOI) in late 2023. By 2025, new variants under monitoring (VUMs) such as LP.8.1, XEC, and NB.1.8.1 emerged (Figure 23). NB.1.8.1, emerged in Asia at the beginning of March and has rapidly spread across the world. It appeared in Europe toward the end of April, after our surveillance period but has now also reach Switzerland (as of mid-June 2025) [20, 25].

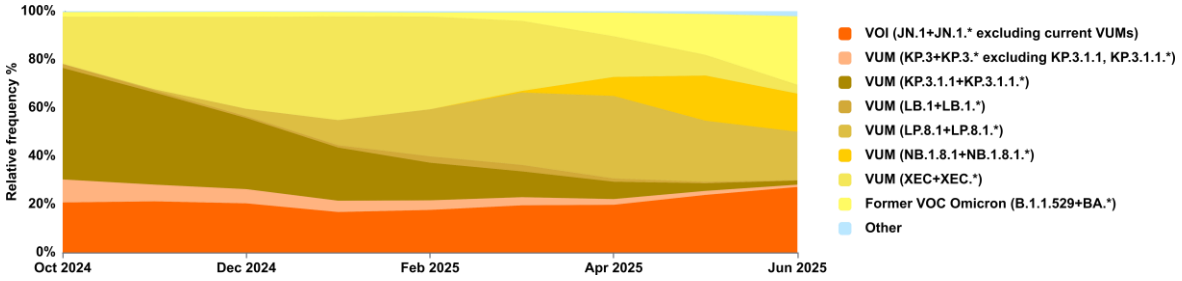


Figure 23: Relative frequency of SARS-CoV-2 VOC/VOI/VUM from October 2024 to June 2025 worldwide. Adapted from GISAID.

3. RSV

In temperate regions, RSV epidemics typically emerge during the winter months, often co-circulating with influenza and other respiratory viruses [26, 27].

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 [28]. 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 (Figure 20). Comparable trends were reported in Germany and the Netherlands. Across much of European countries, RSV circulation was minimal in 2020 but resurged during the summer months of 2021 and 2022. These outbreaks were marked by a high number of detections, captured through both primary care and hospital-based surveillance systems. 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 (Figure 20). Nevertheless, a gradual return to the typical winter seasonality was noted across Europe thereafter (Figure 24). During the surveillance periods from October 2023 to April 2025, RSV circulation patterns largely reverted to their pre-pandemic seasonal rhythm, though at low levels [18]. During the season 2024-2025, 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 [29-31]. In some regions, a delayed and slightly lower peak was observed in Sentinel networks for the RSV season 2024-25, possibly reflecting a potential broader effect of the implementation. However, this trend must be interpreted with caution, as interannual variability and potential biases in surveillance systems may also influence observed patterns.

During a seasonal epidemic, RSV-A and -B co-circulate [32], although RSV-A in some epidemiological studies seems to predominate over RSV-B [33, 34]. During the season from week 40/2024 to week 16/2025, RSV-A and RSV-B appears to co-circulate without a real dominance of one serotype over the other. This was observed in Europe (Figure 24) and in Switzerland.

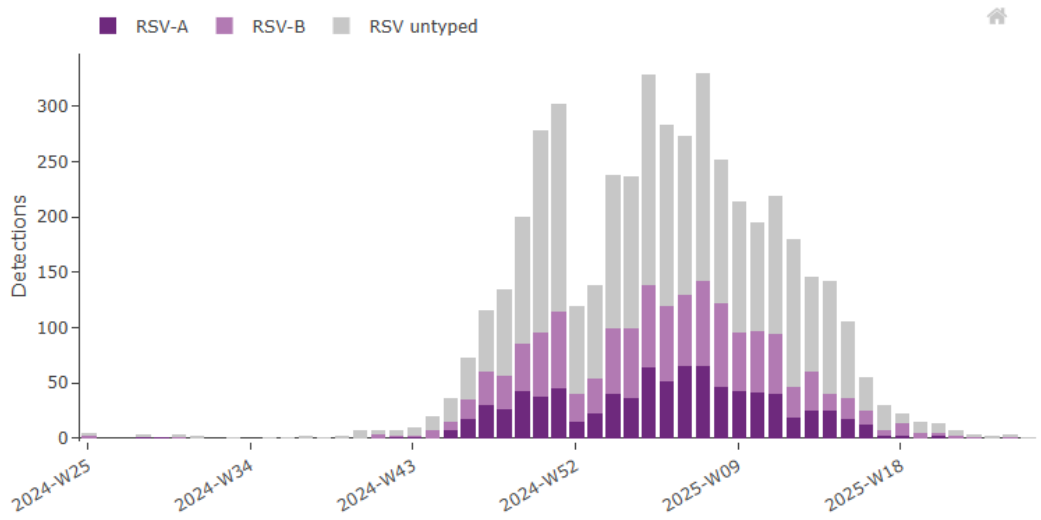


Figure 24: Aggregate weekly detection of RSV. Country selection: Austria, Belgium, Bulgaria, Croatia, Cyprus, Czechia, Denmark, Estonia, Finland, France, Germany, Greece, Hungary, Iceland, Ireland, Italy, Latvia, Liechtenstein, Lithuania, Luxembourg, Malta, Netherland, Norway, Poland, Portugal, Romania, Slovakia, Slovenia, Spain, Sweden. © 2025 European Centre for Disease Prevention and Control, available under a CC BY 4.0 licence.

G. Method development within the NRCI

In the context of the recent H5N1 outbreak in dairy cattle in the USA, we obtained material from Richard Webby (Saint Jude Children's Research Hospital) to verify whether our PCR detects the strain A/Bovine/Ohio/B24OSU-439/2024(H5N1). We received total RNA from the virus and a plasmid coding solely for the HA segment. Using the plasmid, we could test the two PCR available at the NRCI to detect H5 (H5 IVAD and H5 Viet) while using the total RNA, we could test the two H5 specific PCRs and the M specific PCR (AB CDC). The M specific PCR was only positive when using the total RNA while the two H5 specific PCRs were positive when using both the RNA and the plasmid as template (Figure 25). The NRCI also tested the PCR used for the typisation of the seasonal influenza. This quadriplex PCR assay enable the detection of H1, H3, N1 and N2 subtypes. When tested with total RNA from H5N1, the assay yielded a positive result for N1 only (data not shown).

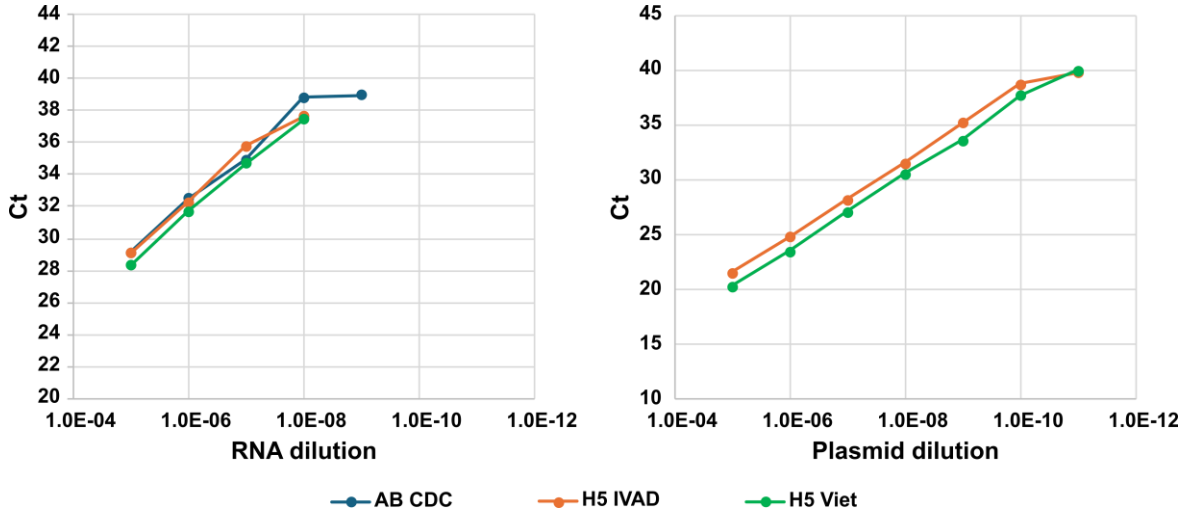


Figure 25: Graphic representation of Ct values obtained using total RNA (left) or plasmid coding for the HA segment (right) of the strain A/dairy cow/Ohio/B24OSU-439/2024(H5N1). M specific PCR (AB CDC), and HA specific PCRs (H5 IVAD and H5 Viet) were performed using a QuantStudio 5.

H. Collaborative projects and publications

1. Report on the surveillance of IAV in pigs and human

The Swiss national program for the surveillance of influenza A viruses in pigs and humans: genetic variability and zoonotic transmissions from 2010 – 2022 | medRxiv (preprint) [35]

This study presents the results of the Swiss national program for the surveillance of influenza viruses in pigs and humans from 2010 – 2022. It is a collaborative project between the Federal Food Safety and Veterinary Office, 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.

2. Technique Sharing: the HAI assay

Influenza A(H1N1)pdm09 virus resistance to baloxavir, oseltamivir and sialic acid mimetics in single and dual therapies: Insights from human airway epithelia and murine models.

The NRCI was contacted by the group of Prof Caroline Tapparel (University of Geneva, CH) to further investigate the impact of substitutions in the HA on viral receptor binding and drug susceptibility. They performed HA assay and HAI assay under the supervision of the NRCI. In this publication, they evaluate the potential use of HA-targeting drug as antiviral for influenza infection [36].

3. Data Sharing

Epidemiological trends of SARS-CoV-2, Influenza virus and respiratory syncytial virus infections in the canton of Geneva, Switzerland, winter season 2024-2025: an integrated surveillance study (submitted to Rapid Communication à *Eurosurveillance*).

This study describes the epidemiology of SARS-CoV-2, Influenza and RSV infection in the district of Geneva as reported in three different systems: Sentinella, wastewater and HUG.

4. Material sharing

Between October 2024 and April 2025, the NCRI provided materials to the following institutions for various research and diagnostic purposes, as detailed below:

- With the Centre for emerging infectious diseases (CMVE)

In January 2025, the NRCI shared five SARS-CoV-2 positive nasopharyngeal swabs (listed below) with Pr. Isabella Eckerle and Dr. Olha Puhach from the CMVE in Geneva (CH). Their project is the production of viral isolates from specific SARS-CoV-2 variants to share with the WHO Biohub in Spiez.

In July 2025, the NRCI shared five RSV/A and five RSV/B isolates from NRCI clinical samples (listed below) with Dr. Manel Essaidi-Laziosi from the CMVE in Geneva (CH). The project is to produce viral stocks to assess the immune escape capacity of RSV A and B strains using sera from vaccinated individuals or the nirsevimab antibody using neutralisation assay. Furthermore, these would be used to study the virus-host interaction between RSV and child human airway epithelia (HAE) model.

- With the University of Geneva

In April 2025, the NRCI shared two Influenza B positive culture originating from a nasopharyngeal swab with Pr Mirco Schmolke from the department of Microbiolgy and Molecular Medicine in the University of Geneva (CH). The project is to determine the host response to Influenza B infection in human cell line and tissues.

- With Spiez laboratory and the Institute of medical virology

In May 2025, the NRCI shared two plasmids from 1/100 and 1/1000 dilutions of DNA designed from the cleavage site modified HA of A/Bovine/Ohio/B24OSU-439/2024 (H5N1) with Dr. Christian Beuret from Spiez Laboratory in Bern (CH) and with Drs. Irene Völlmy and Jon Juder at the institute of Medical Virology in the University of Zurich (CH). The project aims to assess the performance of laboratory developed tests for the detection of recent H5N1 (2024) strains of bovine origin.

I. Materials and methods used by the NRCI

1. Identification of cases

A network (Sentinella) 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 [37], ILI definition is declared as an acute respiratory infection with a fever measured to ≥38 °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 [38].

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 [a]

All nasopharyngeal swabs received at the NRCI are submitted to rRT-PCR screening for influenza, SARS-Co-2, RSV, HCoVs NL63/HKU1/OC43/229E, HPIV, HBoV, HAdV, RV/EV and HMPV.

1) SARS-CoV-2 viruses were screened using the Cobas® SARS-CoV-2 reagents on a Cobas® 6800 instrument according to manufacturer's instructions.

2) Other respiratory viruses were screened using a combination of eight custom rRT-PCR mixes produced by Eurogentec. Mixes' targets are grouped as follows:

- RSV/canine distemper virus (CDV, internal control for RNA/DNA extraction efficiency and PCR inhibitor)
- HCoV NL63/OC43
- HCoV 229E/HKU1
- HBoV/HPIV2/4 (does not distinguish between HPIV 2 and 4)
- HMPV/HPIV1/3 (does not distinguish between HPIV 1 and 3)
- RV/EV
- HAdV/CDV
- FluA/B

Briefly, 800 µl of the initial respiratory specimens are extracted using the QiaSymphony magnetic-particle system (Qiagen, Basel, Switzerland) and viral RNA/DNA is recovered in 100 µl of elution buffer. rRT-PCR reactions were performed using 5 µl of extracted RNA/DNA and 15 µl of reaction mix and run on QuantStudio 5 thermocycler. Samples were considered positive, if they yielded a Ct value ≤ 37 and if an increase in fluorescent signal was observed in both the amplification and multicomponent plot.

3) Influenza A and B screening rRT-PCR is adapted from 2007 and 2009 USA CDC protocols and from Franshawe *et al.* [39]. The duplex rRT-PCR targets are the matrix (M) protein and the non-structural (NS) protein genes for influenza A and B viruses, respectively. 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 discriminate between influenza A/H1N1pdm09 and A/H3N2 strains. H1 and N2 primers-probe combinations were designed in-house. H3 CDC primers-probe combination was part of 2007 CDC protocol and N1 primers-probe combination was adapted from Henritzi *et al.* [40]. The quadruplex assay exhibits a detection limit similar to the diagnostic rRT-PCR. The N1 combination can detect H1N1v[b], swH1N1[c] and H5N1[d] isolates tested during the assay validation process. The H3 and N2 rRT-PCR combinations are also able to detect the A/Wisconsin/12/2010 H3N2 triple reassortant (H3N2tr) [41], although the latter virus is not known to circulate in Switzerland. Nevertheless, if needed,

[a] The evaluation of the proficiency of the Laboratory of Virology at Geneva University Hospitals in performing molecular detection of influenza viruses is accessed through the World Health Organization (WHO) External Quality Assessment Programme (EQAP) for the Detection of Influenza Viruses by RT-PCR and was initiated in 2007 by the WHO (https://www.who.int/influenza/gisrs_laboratory/external_quality_assessment_project/en/).

[b] H1N1v: A/Switzerland/***2244/2011 and A/Berne/****6552/2017, variants isolated from Swiss pig breeders

[c] swH1N1 35 (2008): virus isolated from a Swiss pig

[d] H5N1: A/Hong Kong/6841/2010 (EQAP panel 16) and A/goose/Qinghai/1A/05*A/PR8/34(INT)

additional tests are available at the NRCI to discriminate seasonal H3N2 from H3N2tr viruses. Influenza B/Yamagata/16/88-like (Yam) and B/Victoria/2/87-like (Vic) lineages are distinguished using a duplex rRT-PCR adapted from Schweiger *et al.* [42, 43]. rRT-PCR reactions were performed using 5 µl of extracted RNA and 20 µl of SuperScript™ III Platinum™ One-Step qRT-PCR Kit w/ROX (Invitrogen™) reaction mix and run on Quantstudio 5 thermocyclers. Samples were considered positive, if they yielded a Ct value ≤ 40 and if an increase in fluorescent signal was observed in both the amplification and multicomponent plot.

3. Antigenic and genetic characterization 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 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 segment HA. 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.

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 D^3 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, then, 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 7) and are thereby, adjusted yearly. Since the serum is initially diluted 1/8, the titres provided in Table 7 should be multiplied by 8 to obtain the final titres.

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 7: Antigenic tables for the 2024-25 influenza season. These tables correspond to the HI titres of reference influenza antigens incubated with ferret reference antisera provided by the WHO.

	A/Guangdong-Maonan/SWL1536/19 06.05.2024 F11/20	A/Victoria/4897/22 19.09.2024 F06/23
A/Guangdong-Maonan/SWL1536/2019	1024	16
A/Victoria/4897/2022	<16	512

	A/Darwin/9/2021 19.09.2023 F14/22	A/Thailand/8/2022 06 05.2024 F34/23	A/Croatia/10136RV/2023 09.12.2024 F16/24
A/Darwin/9/2021	128	64	16
A/Thailand/8/2022	512	256	256
A/Croatia/10136RV/2023	128	256	256

	B/Washington/02/19 06.05.2024 F42/19	B/Austria/1359417/2021 06.05.2024 F44/21	B/Stockholm/3/2022 09.12.2024 F28/22	B/Phuket/3073/13 11.2021
B/Washington/02/2019	256	<16	<16	<16
B/Austria/1359417/2021	<16	1024	128	<16
B/Stockholm/3/2022	32	256	256	<16
B/Phuket/3073/2013	<16	<16	<16	512

c. Whole Genome sequencing

As part of the genomic surveillance program for respiratory viruses, including seasonal influenza, SARS-CoV-2, and RSV, the NRCI collaborated with the Health 2030 Genome Centre's DNA Sequencing and Data Analytics and Interpretation Platforms. Sample processing was conducted using the Illumina Respiratory Virus Oligo Panel (Illumina), following the manufacturer's protocol. For sequencing, only samples that tested positive for Influenza A/B and RSV A/B with cycle threshold (Ct) values below 25, and for SARS-CoV-2 with Ct values below 28, were selected. Samples exhibiting co-detection of multiple pathogens were excluded. 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 a custom pipeline developed by the Swiss Institute of Bioinformatics (SIB). For SARS-CoV-2 genome, sequence assembly was conducted using the V-pipe workflow, with 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 national and international databases, including the Swiss Pathogen Surveillance Platform (SPSP), the European Nucleotide Archive (ENA), GenBank, and Global Initiative on Sharing All Influenza Data (GISAID) (Appendixes 3-7).

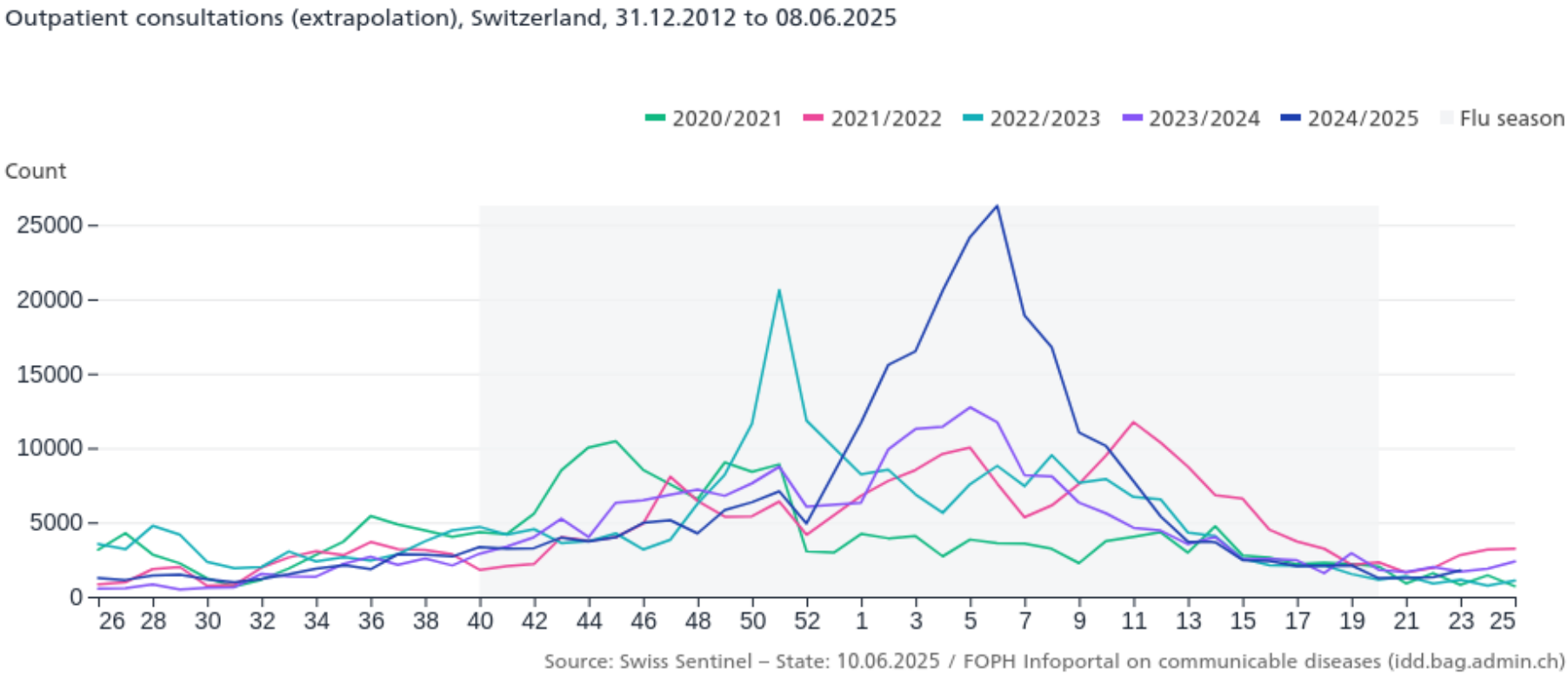
d. Data availability

Sequence data used to generate the following figures Figure 22are available on GISAID (https://gisaid.org/) via GISAID identifiers:

- Figure 9 and Figure 10: EPI_SET_250814ec
- Figure 11 and Figure 12: EPI_SET_250814us
- Figure 13 and Figure 14: EPI_SET_250814sm
- Figure 22: EPI_SET_250813et (for A/H1N1), EPI_SET_250813mt (for A/H3N2) and EPI_SET_250813bz (for B/Vic).

J. Appendixes

Appendix 1: Seasonal comparison of consultations due to an influenza-like illness, https://www.idd.bag.admin.ch/diseases/influenza/statistic



Appendix 2: Description of the co-detection.

Weeks	Co-detections											total positive samples	% co-detections
40	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2									2	34	5.88
41	HPIV2-4/ RV-EV	RV-EV/HCoVOC43	RV-EV/SARS-CoV2								3	40	7.50
42	IA/HCoVNL63	RV-EV/SARS-CoV2									2	33	6.06
43	RV-EV/SARS-CoV2	RV-EV/HAdV									3	49	6.12
44	HCoVOC43/HAdV	SARS-CoV2/ HAdV	SARS-CoV2/ HAdV								3	36	8.33
45	RV-EV/HCoVNL63	SARS-CoV2/ HAdV	HPIV1-3/SARS-CoV2	VRS/RV-EV							4	47	8.51
46	IB/VRS/SARS-CoV2	HPIV2-4/ HAdV	VRS/RV-EV	HMPV/RV-EV							4	37	10.81
47	HMPV/RV-EV	SARS-CoV2/ HAdV									2	50	4.00
48	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2	RV-EV/SARS-CoV2	RV-EV/HCoVOC43							4	48	8.33
49	IB/HAdV	RV-EV/HAdV	HAdV /VRS/RV-EV	HCoVOC43/SARS-CoV2							4	49	8.16
50	IA/HCoVOC43										1	42	2.38
51	RV-EV/IA	IA/SARS-CoV2	RV-EV/HCoVOC43	HMPV/HAdV	RV-EV/HCoVNL63	RV-EV/IA	RV-EV/HAdV				7	56	12.50
52	VRS/RV-EV										1	22	4.55
1	IB/HCoVOC43/VRS										1	18	5.56
2	HMPV/HCoVOC43	IA/SARS-CoV2	IA/HCoVNL63	SARS-CoV2/ HAdV	IA/VRS	IB/HAdV					6	79	7.59
3	IA/SARS-CoV2	HAdV /VRS	RV-EV/IB	VRS/RV-EV	IA/SARS-CoV2						5	69	7.25
4	HMPV/RV-EV	IA/HAdV	RV-EV/HAdV	HMPV/HCoVOC43	IA/HCoVOC43	IA/SARS-CoV2					6	82	7.32
5	HPIV1-3/IA	IB/IA	IB/HCoVNL63	IA/HCoVOC43	RV-EV/IB	RV-EV/HAdV	IB/IA	HCoVOC43/VRS	HCoVOC43/VRS/IB	HAdV /VRS	10	98	10.20
6	IA/SARS-CoV2	RV-EV/IA	RV-EV/IB	IB/HAdV							4	94	4.26
7	IB/IA	HPIV2-4/ VRS	HCoVOC43/HCoVNL63/IB	HCoVOC43/VRS/IB	RV-EV/IB						5	81	6.17
8	HMPV/HCoVOC43	IA/HCoVOC43	RV-EV/HCoVHKU1	VRS/RV-EV	IA/HCoVOC43	IB/HCoVOC43	HCoVOC43/VRS				7	61	11.48
9	HMPV/RV-EV	IA/VRS	VRS/IB	IA/HAdV							4	41	9.76
10	IA/HAdV	HMPV/RV-EV	HMPV/HCoVOC43	HCoVOC43/HCoVNL63	IA/HCoVOC43						5	53	9.43
11	HMPV/VRS										1	46	2.17
12	IA/VRS										1	31	3.23
13	RV-EV/SARS-CoV2	HCoVOC43/SARS-CoV2									2	37	5.41
14	HPIV1-3/HAdV	RV-EV/HCoVOC43	HMPV/HCoVOC43/HAdV								3	34	8.82
15	VRS/RV-EV	HCoVOC43/VRS									2	29	6.90
16											0	13	0.00
Total											102		

Appendix 3: Table of Sentinella Influenza A/H1N1pdm09 sequences submitted to GISAID (40/2024-16/2025)

Isolate name	Collection Date	GISAID_ID	Subtype
A/Switzerland/SNRCI-HUG-46127957/2024	11.10.2024	EPI_ISL_19632801	A/H1N1pdm09
A/Switzerland/SNRCI-HUG-46128054/2024	10.10.2024	EPI_ISL_19651500	A/H1N1pdm09
A/Switzerland/SNRCI-HUG-46173210/2024	17.10.2024	EPI_ISL_19651501	A/H1N1pdm09
A/Switzerland/SNRCI-HUG-46192977/2024	18.10.2024	EPI_ISL_19651504	A/H1N1pdm09
A/Switzerland/SNRCI-HUG-46234891/2024	23.10.2024	EPI_ISL_19651499	A/H1N1pdm09
A/Switzerland/SNRCI-HUG-46391565/2024	11.11.2024	EPI_ISL_19651503	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46533570/2024	26.11.2024	EPI_ISL_19698105	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46599140/2024	02.12.2024	EPI_ISL_19698119	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46620747/2024	05.12.2024	EPI_ISL_19698201	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46667649/2024	09.12.2024	EPI_ISL_19698187	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46689883/2024	11.12.2024	EPI_ISL_19698112	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46710901/2024	13.12.2024	EPI_ISL_19698179	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46711201/2024	16.12.2024	EPI_ISL_19698109	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46759613/2024	20.12.2024	EPI_ISL_19698124	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46779136/2024	20.12.2024	EPI_ISL_19698136	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46779196/2024	20.12.2024	EPI_ISL_19698140	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46779232/2024	20.12.2024	EPI_ISL_19698150	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46790223/2024	23.12.2024	EPI_ISL_19698192	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46809164/2024	23.12.2024	EPI_ISL_19698191	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46817784/2024	27.12.2024	EPI_ISL_19698106	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46856512/2024	30.12.2024	EPI_ISL_19698115	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46876849/2025	02.01.2025	EPI_ISL_19698194	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46877004/2024	31.12.2024	EPI_ISL_19698700	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46890666/2025	06.01.2025	EPI_ISL_19698107	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46891704/2025	07.01.2025	EPI_ISL_19698180	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46903160/2025	06.01.2025	EPI_ISL_19698118	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46903371/2025	07.01.2025	EPI_ISL_19698123	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46915193/2025	08.01.2025	EPI_ISL_19698210	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46915929/2025	08.01.2025	EPI_ISL_19698128	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46916056/2025	07.01.2025	EPI_ISL_19698212	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46928032/2025	09.01.2025	EPI_ISL_19698184	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46941254/2025	10.01.2025	EPI_ISL_19698198	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46962365/2025	13.01.2025	EPI_ISL_19805797	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46962604/2025	13.01.2025	EPI_ISL_19805781	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46998797/2025	14.01.2025	EPI_ISL_19805771	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46998882/2025	16.01.2025	EPI_ISL_19805886	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-46998921/2025	15.01.2025	EPI_ISL_19805783	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47019698/2025	17.01.2025	EPI_ISL_19805878	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47019871/2025	17.01.2025	EPI_ISL_19805882	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47032275/2025	20.01.2025	EPI_ISL_19805908	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47032755/2025	20.01.2025	EPI_ISL_19805889	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47043996/2025	20.01.2025	EPI_ISL_19805805	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47044527/2025	20.01.2025	EPI_ISL_19805832	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47057049/2025	22.01.2025	EPI_ISL_19805849	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47067865/2025	23.01.2025	EPI_ISL_19805859	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47067935/2025	22.01.2025	EPI_ISL_19805784	A/H1N1pdm09

A/Switzerland/UN-SNRCI-HUG-47067978/2025	22.01.2025	EPI_ISL_19805897	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47068145/2025	23.01.2025	EPI_ISL_19805861	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47087842/2025	23.01.2025	EPI_ISL_19805855	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47101791/2025	27.01.2025	EPI_ISL_19805893	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47111546/2025	28.01.2025	EPI_ISL_19805895	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47111725/2025	28.01.2025	EPI_ISL_19805824	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47124034/2025	28.01.2025	EPI_ISL_19805785	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47124409/2025	29.01.2025	EPI_ISL_19805773	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47135069/2025	30.01.2025	EPI_ISL_19805902	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47168093/2025	03.02.2025	EPI_ISL_19805843	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47168284/2025	31.01.2025	EPI_ISL_19805808	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47168684/2025	03.02.2025	EPI_ISL_19805801	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47180243/2025	04.02.2025	EPI_ISL_19805789	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47223916/2025	07.02.2025	EPI_ISL_19805879	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47236068/2025	10.02.2025	EPI_ISL_19805892	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47236417/2025	10.02.2025	EPI_ISL_19805802	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47236661/2025	07.02.2025	EPI_ISL_19805905	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47247255/2025	08.02.2025	EPI_ISL_19805822	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47247743/2025	11.02.2025	EPI_ISL_19805876	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47247907/2025	11.02.2025	EPI_ISL_19805852	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47270288/2025	12.02.2025	EPI_ISL_19805810	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47281400/2025	14.02.2025	EPI_ISL_19805820	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47281405/2025	14.02.2025	EPI_ISL_19805898	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47281444/2025	14.02.2025	EPI_ISL_19805817	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47324671/2025	19.02.2025	EPI_ISL_19906881	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47324927/2025	19.02.2025	EPI_ISL_19906840	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47335853/2025	20.02.2025	EPI_ISL_19805798	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47378649/2025	25.02.2025	EPI_ISL_19805791	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47401281/2025	26.02.2025	EPI_ISL_19805815	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47445379/2025	04.03.2025	EPI_ISL_19906851	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47501942/2025	07.03.2025	EPI_ISL_19906865	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47526341/2025	12.03.2025	EPI_ISL_19906855	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47526558/2025	12.03.2025	EPI_ISL_19906886	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47638301/2025	24.03.2025	EPI_ISL_19906857	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47649841/2025	25.03.2025	EPI_ISL_19906849	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47772309/2025	07.04.2025	EPI_ISL_19906885	A/H1N1pdm09
A/Switzerland/UN-SNRCI-HUG-47852341/2025	14.04.2025	EPI_ISL_19906878	A/H1N1pdm09

Appendix 4: Table of Sentinella Influenza A/H3N2 sequences submitted to GISAID (40/2024-16/2025)

Isolate name	Collection Date	GISAID_ID	Subtype
A/Switzerland/SNRCI-HUG-46478886/2024	20.11.2024	EPI_ISL_19651498	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46600365/2024	03.12.2024	EPI_ISL_19698122	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46655118/2024	09.12.2024	EPI_ISL_19698193	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46723057/2024	13.12.2024	EPI_ISL_19698197	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46747581/2024	18.12.2024	EPI_ISL_19698113	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46747776/2024	17.12.2024	EPI_ISL_19698132	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46747884/2024	17.12.2024	EPI_ISL_19698114	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46759771/2024	18.12.2024	EPI_ISL_19698143	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46779898/2024	19.12.2024	EPI_ISL_19698195	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46817703/2024	24.12.2024	EPI_ISL_19698698	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46817828/2024	23.12.2024	EPI_ISL_19698710	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46856433/2024	31.12.2024	EPI_ISL_19698173	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46877773/2025	03.01.2025	EPI_ISL_19698709	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46890800/2025	07.01.2025	EPI_ISL_19698200	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46891800/2025	06.01.2025	EPI_ISL_19698196	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46903127/2025	07.01.2025	EPI_ISL_19698189	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46916246/2025	08.01.2025	EPI_ISL_19698186	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46927701/2025	09.01.2025	EPI_ISL_19698167	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46928701/2025	09.01.2025	EPI_ISL_19805853	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46949402/2025	10.01.2025	EPI_ISL_19698174	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46962670/2025	13.01.2025	EPI_ISL_19805865	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46977041/2025	13.01.2025	EPI_ISL_19805828	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46986050/2025	14.01.2025	EPI_ISL_19805770	A/H3N2
A/Switzerland/UN-SNRCI-HUG-46986310/2025	15.01.2025	EPI_ISL_19805839	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47032867/2025	16.01.2025	EPI_ISL_19805856	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47044215/2025	21.01.2025	EPI_ISL_19805867	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47044410/2025	21.01.2025	EPI_ISL_19805890	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47044444/2025	21.01.2025	EPI_ISL_19805858	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47044470/2025	20.01.2025	EPI_ISL_19805827	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47044733/2025	21.01.2025	EPI_ISL_19805788	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47044809/2025	21.01.2025	EPI_ISL_19805794	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47056662/2025	23.01.2025	EPI_ISL_19805881	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47056688/2025	21.01.2025	EPI_ISL_19805903	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47068015/2025	23.01.2025	EPI_ISL_19805862	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47088280/2025	27.01.2025	EPI_ISL_19805874	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47101673/2025	28.01.2025	EPI_ISL_19805790	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47101995/2025	27.01.2025	EPI_ISL_19805782	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47123932/2025	29.01.2025	EPI_ISL_19805780	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47134679/2025	29.01.2025	EPI_ISL_19805868	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47134693/2025	31.01.2025	EPI_ISL_19805826	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47134953/2025	29.01.2025	EPI_ISL_19805823	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47134971/2025	30.01.2025	EPI_ISL_19805814	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47167982/2025	03.02.2025	EPI_ISL_19805819	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47168213/2025	03.02.2025	EPI_ISL_19805803	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47179763/2025	03.02.2025	EPI_ISL_19805775	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47179807/2025	03.02.2025	EPI_ISL_19805763	A/H3N2

A/Switzerland/UN-SNRCI-HUG-47191747/2025	04.02.2025	EPI_ISL_19805807	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47191782/2025	04.02.2025	EPI_ISL_19805884	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47191816/2025	04.02.2025	EPI_ISL_19805873	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47191933/2025	04.02.2025	EPI_ISL_19805821	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47191975/2025	05.02.2025	EPI_ISL_19805806	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47191987/2025	05.02.2025	EPI_ISL_19805835	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47203193/2025	06.02.2025	EPI_ISL_19805804	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47203235/2025	06.02.2025	EPI_ISL_19805779	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47203408/2025	05.02.2025	EPI_ISL_19805887	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47203478/2025	06.02.2025	EPI_ISL_19805914	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47223528/2025	07.02.2025	EPI_ISL_19805813	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47223969/2025	07.02.2025	EPI_ISL_19805913	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47224179/2025	07.02.2025	EPI_ISL_19805796	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47224331/2025	07.02.2025	EPI_ISL_19805767	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47224433/2025	07.02.2025	EPI_ISL_19805765	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47247408/2025	11.02.2025	EPI_ISL_19805787	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47247518/2025	11.02.2025	EPI_ISL_19805907	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47247586/2025	10.02.2025	EPI_ISL_19805848	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47247863/2025	11.02.2025	EPI_ISL_19805846	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47303055/2025	14.02.2025	EPI_ISL_19805869	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47335112/2025	20.02.2025	EPI_ISL_19805778	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47367107/2025	24.02.2025	EPI_ISL_19805800	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47378908/2025	25.02.2025	EPI_ISL_19805825	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47420197/2025	26.02.2025	EPI_ISL_19805841	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47420381/2025	28.02.2025	EPI_ISL_19805816	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47433403/2025	28.02.2025	EPI_ISL_19805900	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47487920/2025	28.02.2025	EPI_ISL_19906863	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47502473/2025	11.03.2025	EPI_ISL_19906843	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47526372/2025	10.03.2025	EPI_ISL_19906846	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47551343/2025	14.03.2025	EPI_ISL_19906854	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47572010/2025	17.03.2025	EPI_ISL_19906841	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47582365/2025	18.03.2025	EPI_ISL_19906887	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47661090/2025	25.03.2025	EPI_ISL_19906862	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47783582/2025	08.04.2025	EPI_ISL_19906892	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47795894/2025	08.04.2025	EPI_ISL_19906858	A/H3N2
A/Switzerland/UN-SNRCI-HUG-47894198/2025	17.04.2025	EPI_ISL_19906866	A/H3N2
A/Switzerland/UN-SNRCI-HUG-48085405/2025	09.05.2025	EPI_ISL_19906875	A/H3N2

Appendix 5: Table of Sentinella Influenza B/Vic sequences submitted to GISAID (40/2024-16/2025)

Isolate name	Collection Date	GISAID_ID	Lineage
B/Switzerland/SNRCI-HUG-46359146/2024	07.11.2024	EPI_ISL_19651505	B/Vic
B/Switzerland/SNRCI-HUG-46403164/2024	11.11.2024	EPI_ISL_19632802	B/Vic
B/Switzerland/UN-SNRCI-HUG-46609623/2024	03.12.2024	EPI_ISL_19698206	B/Vic
B/Switzerland/UN-SNRCI-HUG-46655509/2024	09.12.2024	EPI_ISL_19698199	B/Vic
B/Switzerland/UN-SNRCI-HUG-46655585/2024	09.12.2024	EPI_ISL_19698209	B/Vic
B/Switzerland/UN-SNRCI-HUG-46667265/2024	09.12.2024	EPI_ISL_19698203	B/Vic
B/Switzerland/UN-SNRCI-HUG-46689374/2024	12.12.2024	EPI_ISL_19698188	B/Vic
B/Switzerland/UN-SNRCI-HUG-46759280/2024	19.12.2024	EPI_ISL_19698185	B/Vic
B/Switzerland/UN-SNRCI-HUG-46817562/2024	23.12.2024	EPI_ISL_19698213	B/Vic
B/Switzerland/UN-SNRCI-HUG-46817682/2024	23.12.2024	EPI_ISL_19698155	B/Vic
B/Switzerland/UN-SNRCI-HUG-46890617/2025	06.01.2025	EPI_ISL_19698125	B/Vic
B/Switzerland/UN-SNRCI-HUG-46891830/2025	06.01.2025	EPI_ISL_19698177	B/Vic
B/Switzerland/UN-SNRCI-HUG-46903637/2025	07.01.2025	EPI_ISL_19698108	B/Vic
B/Switzerland/UN-SNRCI-HUG-46915245/2025	06.01.2025	EPI_ISL_19698126	B/Vic
B/Switzerland/UN-SNRCI-HUG-46915962/2025	08.01.2025	EPI_ISL_19698211	B/Vic
B/Switzerland/UN-SNRCI-HUG-46916148/2025	08.01.2025	EPI_ISL_19698702	B/Vic
B/Switzerland/UN-SNRCI-HUG-46927744/2025	08.01.2025	EPI_ISL_19698175	B/Vic
B/Switzerland/UN-SNRCI-HUG-46928625/2025	08.01.2025	EPI_ISL_19805872	B/Vic
B/Switzerland/UN-SNRCI-HUG-46941196/2025	10.01.2025	EPI_ISL_19698164	B/Vic
B/Switzerland/UN-SNRCI-HUG-46962624/2025	13.01.2025	EPI_ISL_19805768	B/Vic
B/Switzerland/UN-SNRCI-HUG-46974571/2025	14.01.2025	EPI_ISL_19698182	B/Vic
B/Switzerland/UN-SNRCI-HUG-46974647/2025	13.01.2025	EPI_ISL_19698208	B/Vic
B/Switzerland/UN-SNRCI-HUG-46976757/2025	14.01.2025	EPI_ISL_19805764	B/Vic
B/Switzerland/UN-SNRCI-HUG-46986098/2025	15.01.2025	EPI_ISL_19805774	B/Vic
B/Switzerland/UN-SNRCI-HUG-46998530/2025	16.01.2025	EPI_ISL_19805883	B/Vic
B/Switzerland/UN-SNRCI-HUG-47019509/2025	17.01.2025	EPI_ISL_19805812	B/Vic
B/Switzerland/UN-SNRCI-HUG-47019717/2025	17.01.2025	EPI_ISL_19805888	B/Vic
B/Switzerland/UN-SNRCI-HUG-47033096/2025	20.01.2025	EPI_ISL_19805866	B/Vic
B/Switzerland/UN-SNRCI-HUG-47043929/2025	20.01.2025	EPI_ISL_19805776	B/Vic
B/Switzerland/UN-SNRCI-HUG-47044153/2025	21.01.2025	EPI_ISL_19805811	B/Vic
B/Switzerland/UN-SNRCI-HUG-47044652/2025	21.01.2025	EPI_ISL_19805844	B/Vic
B/Switzerland/UN-SNRCI-HUG-47044882/2025	21.01.2025	EPI_ISL_19805880	B/Vic
B/Switzerland/UN-SNRCI-HUG-47056869/2025	21.01.2025	EPI_ISL_19805845	B/Vic
B/Switzerland/UN-SNRCI-HUG-47057094/2025	22.01.2025	EPI_ISL_19805842	B/Vic
B/Switzerland/UN-SNRCI-HUG-47067465/2025	22.01.2025	EPI_ISL_19805772	B/Vic
B/Switzerland/UN-SNRCI-HUG-47067609/2025	21.01.2025	EPI_ISL_19805857	B/Vic
B/Switzerland/UN-SNRCI-HUG-47067769/2025	22.01.2025	EPI_ISL_19805786	B/Vic
B/Switzerland/UN-SNRCI-HUG-47087751/2025	24.01.2025	EPI_ISL_19805850	B/Vic
B/Switzerland/UN-SNRCI-HUG-47101559/2025	27.01.2025	EPI_ISL_19805912	B/Vic
B/Switzerland/UN-SNRCI-HUG-47101711/2025	27.01.2025	EPI_ISL_19805834	B/Vic
B/Switzerland/UN-SNRCI-HUG-47101929/2025	27.01.2025	EPI_ISL_19805818	B/Vic
B/Switzerland/UN-SNRCI-HUG-47111563/2025	28.01.2025	EPI_ISL_19805885	B/Vic
B/Switzerland/UN-SNRCI-HUG-47111606/2025	28.01.2025	EPI_ISL_19805906	B/Vic
B/Switzerland/UN-SNRCI-HUG-47111652/2025	27.01.2025	EPI_ISL_19805836	B/Vic
B/Switzerland/UN-SNRCI-HUG-47111888/2025	28.01.2025	EPI_ISL_19805799	B/Vic
B/Switzerland/UN-SNRCI-HUG-47112228/2025	29.01.2025	EPI_ISL_19805871	B/Vic

B/Switzerland/UN-SNRCI-HUG-47123823/2025	30.01.2025	EPI_ISL_19805830	B/Vic
B/Switzerland/UN-SNRCI-HUG-47134593/2025	29.01.2025	EPI_ISL_19805777	B/Vic
B/Switzerland/UN-SNRCI-HUG-47134910/2025	29.01.2025	EPI_ISL_19805766	B/Vic
B/Switzerland/UN-SNRCI-HUG-47135119/2025	29.01.2025	EPI_ISL_19805833	B/Vic
B/Switzerland/UN-SNRCI-HUG-47154563/2025	31.01.2025	EPI_ISL_19805911	B/Vic
B/Switzerland/UN-SNRCI-HUG-47155329/2025	31.01.2025	EPI_ISL_19805792	B/Vic
B/Switzerland/UN-SNRCI-HUG-47167831/2025	04.02.2025	EPI_ISL_19805896	B/Vic
B/Switzerland/UN-SNRCI-HUG-47168407/2025	03.02.2025	EPI_ISL_19805831	B/Vic
B/Switzerland/UN-SNRCI-HUG-47191886/2025	04.02.2025	EPI_ISL_19805838	B/Vic
B/Switzerland/UN-SNRCI-HUG-47192082/2025	05.02.2025	EPI_ISL_19805863	B/Vic
B/Switzerland/UN-SNRCI-HUG-47192176/2025	05.02.2025	EPI_ISL_19805875	B/Vic
B/Switzerland/UN-SNRCI-HUG-47202999/2025	04.02.2025	EPI_ISL_19805847	B/Vic
B/Switzerland/UN-SNRCI-HUG-47203215/2025	06.02.2025	EPI_ISL_19805899	B/Vic
B/Switzerland/UN-SNRCI-HUG-47203344/2025	06.02.2025	EPI_ISL_19805909	B/Vic
B/Switzerland/UN-SNRCI-HUG-47223870/2025	07.02.2025	EPI_ISL_19805795	B/Vic
B/Switzerland/UN-SNRCI-HUG-47223920/2025	07.02.2025	EPI_ISL_19805840	B/Vic
B/Switzerland/UN-SNRCI-HUG-47236278/2025	10.02.2025	EPI_ISL_19805864	B/Vic
B/Switzerland/UN-SNRCI-HUG-47236459/2025	10.02.2025	EPI_ISL_19805910	B/Vic
B/Switzerland/UN-SNRCI-HUG-47247291/2025	10.02.2025	EPI_ISL_19805901	B/Vic
B/Switzerland/UN-SNRCI-HUG-47247625/2025	11.02.2025	EPI_ISL_19805769	B/Vic
B/Switzerland/UN-SNRCI-HUG-47248139/2025	12.02.2025	EPI_ISL_19805877	B/Vic
B/Switzerland/UN-SNRCI-HUG-47258616/2025	11.02.2025	EPI_ISL_19805829	B/Vic
B/Switzerland/UN-SNRCI-HUG-47258638/2025	11.02.2025	EPI_ISL_19805793	B/Vic
B/Switzerland/UN-SNRCI-HUG-47258730/2025	11.02.2025	EPI_ISL_19805854	B/Vic
B/Switzerland/UN-SNRCI-HUG-47269504/2025	10.02.2025	EPI_ISL_19805870	B/Vic
B/Switzerland/UN-SNRCI-HUG-47269790/2025	13.02.2025	EPI_ISL_19805851	B/Vic
B/Switzerland/UN-SNRCI-HUG-47270008/2025	10.02.2025	EPI_ISL_19805891	B/Vic
B/Switzerland/UN-SNRCI-HUG-47281233/2025	15.02.2025	EPI_ISL_19805860	B/Vic
B/Switzerland/UN-SNRCI-HUG-47281453/2025	14.02.2025	EPI_ISL_19805904	B/Vic
B/Switzerland/UN-SNRCI-HUG-47281522/2025	13.02.2025	EPI_ISL_19805809	B/Vic
B/Switzerland/UN-SNRCI-HUG-47302703/2025	17.02.2025	EPI_ISL_19805894	B/Vic
B/Switzerland/UN-SNRCI-HUG-47302750/2025	17.02.2025	EPI_ISL_19805837	B/Vic
B/Switzerland/UN-SNRCI-HUG-47313955/2025	18.02.2025	EPI_ISL_19906874	B/Vic
B/Switzerland/UN-SNRCI-HUG-47313989/2025	17.02.2025	EPI_ISL_19906871	B/Vic
B/Switzerland/UN-SNRCI-HUG-47324634/2025	19.02.2025	EPI_ISL_19906856	B/Vic
B/Switzerland/UN-SNRCI-HUG-47324880/2025	18.02.2025	EPI_ISL_19906867	B/Vic
B/Switzerland/UN-SNRCI-HUG-47335758/2025	20.02.2025	EPI_ISL_19906880	B/Vic
B/Switzerland/UN-SNRCI-HUG-47336032/2025	19.02.2025	EPI_ISL_19906838	B/Vic
B/Switzerland/UN-SNRCI-HUG-47445233/2025	03.03.2025	EPI_ISL_19906876	B/Vic
B/Switzerland/UN-SNRCI-HUG-47445279/2025	05.03.2025	EPI_ISL_19906872	B/Vic
B/Switzerland/UN-SNRCI-HUG-47456962/2025	04.03.2025	EPI_ISL_19906877	B/Vic
B/Switzerland/UN-SNRCI-HUG-47457036/2025	03.03.2025	EPI_ISL_19906842	B/Vic
B/Switzerland/UN-SNRCI-HUG-47457742/2025	06.03.2025	EPI_ISL_19906852	B/Vic
B/Switzerland/UN-SNRCI-HUG-47468159/2025	06.03.2025	EPI_ISL_19906845	B/Vic
B/Switzerland/UN-SNRCI-HUG-47487888/2025	06.03.2025	EPI_ISL_19906850	B/Vic
B/Switzerland/UN-SNRCI-HUG-47488201/2025	07.03.2025	EPI_ISL_19906894	B/Vic
B/Switzerland/UN-SNRCI-HUG-47488301/2025	06.03.2025	EPI_ISL_19906864	B/Vic
B/Switzerland/UN-SNRCI-HUG-47488357/2025	10.03.2025	EPI_ISL_19906853	B/Vic
B/Switzerland/UN-SNRCI-HUG-47488394/2025	07.03.2025	EPI_ISL_19906859	B/Vic

B/Switzerland/UN-SNRCI-HUG-47513658/2025	11.03.2025	EPI_ISL_19906847	B/Vic
B/Switzerland/UN-SNRCI-HUG-47513940/2025	11.03.2025	EPI_ISL_19906893	B/Vic
B/Switzerland/UN-SNRCI-HUG-47526405/2025	12.03.2025	EPI_ISL_19906860	B/Vic
B/Switzerland/UN-SNRCI-HUG-47538472/2025	14.03.2025	EPI_ISL_19906848	B/Vic
B/Switzerland/UN-SNRCI-HUG-47538578/2025	13.03.2025	EPI_ISL_19906839	B/Vic
B/Switzerland/UN-SNRCI-HUG-47538731/2025	13.03.2025	EPI_ISL_19906891	B/Vic
B/Switzerland/UN-SNRCI-HUG-47550937/2025	14.03.2025	EPI_ISL_19906884	B/Vic
B/Switzerland/UN-SNRCI-HUG-47551217/2025	13.03.2025	EPI_ISL_19906882	B/Vic
B/Switzerland/UN-SNRCI-HUG-47551288/2025	14.03.2025	EPI_ISL_19906890	B/Vic
B/Switzerland/UN-SNRCI-HUG-47571846/2025	17.03.2025	EPI_ISL_19906883	B/Vic
B/Switzerland/UN-SNRCI-HUG-47605138/2025	20.03.2025	EPI_ISL_19906844	B/Vic
B/Switzerland/UN-SNRCI-HUG-47649805/2025	24.03.2025	EPI_ISL_19906879	B/Vic
B/Switzerland/UN-SNRCI-HUG-47625582/2025	21.03.2025	EPI_ISL_19906889	B/Vic
B/Switzerland/UN-SNRCI-HUG-47704368/2025	31.03.2025	EPI_ISL_19906869	B/Vic
B/Switzerland/UN-SNRCI-HUG-47715793/2025	01.04.2025	EPI_ISL_19906873	B/Vic

Appendix 6: 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-HUG-46011652/2024	KP.3.1.1	24E (KP.3.1.1)	20240930	EPI_ISL_19654762
hCoV-19/Switzerland/un-SNRCI-HUG-46011722/2024	XEC	24F (XEC)	20240930	EPI_ISL_19654753
hCoV-19/Switzerland/un-SNRCI-HUG-46023165/2024	KP.3	24E (KP.3.1.1)	20240930	EPI_ISL_19654694
hCoV-19/Switzerland/un-SNRCI-HUG-46023216/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20240930	EPI_ISL_19698040
hCoV-19/Switzerland/un-SNRCI-HUG-46033741/2024	XEC	24F (XEC)	20241002	EPI_ISL_19654781
hCoV-19/Switzerland/un-SNRCI-HUG-46034011/2024	XEC	24F (XEC)	20241002	EPI_ISL_19654777
hCoV-19/Switzerland/un-SNRCI-HUG-46044029/2024	KP.3.1.1	24E (KP.3.1.1)	20241002	EPI_ISL_19654763
hCoV-19/Switzerland/un-SNRCI-HUG-46044257/2024	KP.3.1.1	24E (KP.3.1.1)	20241002	EPI_ISL_19654740
hCoV-19/Switzerland/un-SNRCI-HUG-46062978/2024		24E (KP.3.1.1)	20241003	EPI_ISL_19654665
hCoV-19/Switzerland/un-SNRCI-HUG-46063273/2024	XEC	24F (XEC)	20241004	EPI_ISL_19654737
hCoV-19/Switzerland/un-SNRCI-HUG-46075544/2024	XEC	recombinant	20241007	EPI_ISL_19654754
hCoV-19/Switzerland/un-SNRCI-HUG-46075724/2024	XEC	24F (XEC)	20241007	EPI_ISL_19654772
hCoV-19/Switzerland/un-SNRCI-HUG-46086326/2024	KP.3.1.1	24E (KP.3.1.1)	20241008	EPI_ISL_19654682
hCoV-19/Switzerland/un-SNRCI-HUG-46086837/2024	XEC	24F (XEC)	20241008	EPI_ISL_19654778
hCoV-19/Switzerland/un-SNRCI-HUG-46100993/2024	KP.3.1.1	24E (KP.3.1.1)	20241009	EPI_ISL_19654743
hCoV-19/Switzerland/un-SNRCI-HUG-46101047/2024	XEC	24F (XEC)	20241007	EPI_ISL_19654768
hCoV-19/Switzerland/un-SNRCI-HUG-46101057/2024	KP.3.1.1	24E (KP.3.1.1)	20241008	EPI_ISL_19654757
hCoV-19/Switzerland/un-SNRCI-HUG-46108460/2024	KP.1.1.5	24B (JN.1.11.1)	20241010	EPI_ISL_19654726
hCoV-19/Switzerland/un-SNRCI-HUG-46108508/2024	KP.3.1.1	24E (KP.3.1.1)	20241010	EPI_ISL_19654658
hCoV-19/Switzerland/un-SNRCI-HUG-46108633/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20241009	EPI_ISL_19698041
hCoV-19/Switzerland/un-SNRCI-HUG-46109203/2024	XEC	recombinant	20241009	EPI_ISL_19654775
hCoV-19/Switzerland/un-SNRCI-HUG-46108841/2024	KP.3.1.1	24F (XEC)	20241009	EPI_ISL_19654732
hCoV-19/Switzerland/un-SNRCI-HUG-46127980/2024	KP.3.1.1	24E (KP.3.1.1)	20241010	EPI_ISL_19654761
hCoV-19/Switzerland/un-SNRCI-HUG-46140264/2024	XEC	24F (XEC)	20241011	EPI_ISL_19654780
hCoV-19/Switzerland/un-SNRCI-HUG-46140478/2024	KP.3.1	24E (KP.3.1.1)	20241014	EPI_ISL_19654710
hCoV-19/Switzerland/un-SNRCI-HUG-46151517/2024	KP.3.1.1	24E (KP.3.1.1)	20241015	EPI_ISL_19654720
hCoV-19/Switzerland/un-SNRCI-HUG-46172817/2024	KP.3.1.1	24E (KP.3.1.1)	20241017	EPI_ISL_19654769
hCoV-19/Switzerland/un-SNRCI-HUG-46172943/2024	XEC	24F (XEC)	20241016	EPI_ISL_19654676
hCoV-19/Switzerland/un-SNRCI-HUG-46204701/2024	KP.3.1.1	24E (KP.3.1.1)	20241021	EPI_ISL_19654671
hCoV-19/Switzerland/un-SNRCI-HUG-46215014/2024	XDY (consensus call)	recombinant	20241021	EPI_ISL_19698042
hCoV-19/Switzerland/un-SNRCI-HUG-46215315/2024	KP.3.1.1	24E (KP.3.1.1)	20241021	EPI_ISL_19654758
hCoV-19/Switzerland/un-SNRCI-HUG-46234561/2024	KP.3.1.1	24E (KP.3.1.1)	20241024	EPI_ISL_19654766
hCoV-19/Switzerland/un-SNRCI-HUG-46234600/2024	XEC	24F (XEC)	20241024	EPI_ISL_19654721
hCoV-19/Switzerland/un-SNRCI-HUG-46274617/2024	XEC (consensus call)	24F (XEC)	20241028	EPI_ISL_19698043
hCoV-19/Switzerland/un-SNRCI-HUG-46274662/2024	XEC	24F (XEC)	20241029	EPI_ISL_19654731
hCoV-19/Switzerland/un-SNRCI-HUG-46274782/2024	KP.3.1	24E (KP.3.1.1)	20241029	EPI_ISL_19654741
hCoV-19/Switzerland/un-SNRCI-HUG-46326247/2024	JN.1.40	24H (LF.7)	20241104	EPI_ISL_19654729
hCoV-19/Switzerland/un-SNRCI-HUG-46336599/2024	XEC	24F (XEC)	20241105	EPI_ISL_19654722
hCoV-19/Switzerland/un-SNRCI-HUG-46336855/2024	XDY (consensus call)	recombinant	20241106	EPI_ISL_19698044
hCoV-19/Switzerland/un-SNRCI-HUG-46336950/2024	XEC	24F (XEC)	20241105	EPI_ISL_19654773
hCoV-19/Switzerland/un-SNRCI-HUG-46336967/2024	JN.1.18.6	24F (XEC)	20241104	EPI_ISL_19654770
hCoV-19/Switzerland/un-SNRCI-HUG-46337063/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241106	EPI_ISL_19654736
hCoV-19/Switzerland/un-SNRCI-HUG-46348011/2024	KP.3.1.1	24E (KP.3.1.1)	20241106	EPI_ISL_19654711
hCoV-19/Switzerland/un-SNRCI-HUG-46348085/2024	KP.3.1.1	24E (KP.3.1.1)	20241106	EPI_ISL_19654648
hCoV-19/Switzerland/un-SNRCI-HUG-46348462/2024	KP.3.1.1	recombinant	20241106	EPI_ISL_19654767
hCoV-19/Switzerland/un-SNRCI-HUG-46348530/2024	XEC	24F (XEC)	20241106	EPI_ISL_19654702
hCoV-19/Switzerland/un-SNRCI-HUG-46359356/2024	KP.3.1.1	24E (KP.3.1.1)	20241107	EPI_ISL_19654730
hCoV-19/Switzerland/un-SNRCI-HUG-46359525/2024	KP.3.1.1	24E (KP.3.1.1)	20241107	EPI_ISL_19654724
hCoV-19/Switzerland/un-SNRCI-HUG-46378092/2024	XEC	24F (XEC)	20241108	EPI_ISL_19654739
hCoV-19/Switzerland/un-SNRCI-HUG-46391386/2024	KP.3.1.1	24E (KP.3.1.1)	20241111	EPI_ISL_19654669
hCoV-19/Switzerland/un-SNRCI-HUG-46391655/2024	KP.3.1.1	24E (KP.3.1.1)	20241111	EPI_ISL_19654760

hCoV-19/Switzerland/UN-SNRCI-HUG-46414030/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241113	EPI_ISL_19693064
hCoV-19/Switzerland/un-SNRCI-HUG-46414176/2024	KP.3.3	24C (KP.3)	20241112	EPI_ISL_19654725
hCoV-19/Switzerland/UN-SNRCI-HUG-46424460/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20241114	EPI_ISL_19704490
hCoV-19/Switzerland/UN-SNRCI-HUG-46424622/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241113	EPI_ISL_19704425
hCoV-19/Switzerland/UN-SNRCI-HUG-46424775/2024	JN.1.40 (consensus call)	24H (LF.7)	20241113	EPI_ISL_19704491
hCoV-19/Switzerland/un-SNRCI-HUG-46424993/2024	KP.3.1.1	24E (KP.3.1.1)	20241113	EPI_ISL_19654747
hCoV-19/Switzerland/un-SNRCI-HUG-46444504/2024	KP.3.1.1	24E (KP.3.1.1)	20241114	EPI_ISL_19654748
hCoV-19/Switzerland/un-SNRCI-HUG-46444650/2024	JN.1.40	24H (LF.7)	20241114	EPI_ISL_19654727
hCoV-19/Switzerland/un-SNRCI-HUG-46456542/2024	XEC	24F (XEC)	20241113	EPI_ISL_19654719
hCoV-19/Switzerland/un-SNRCI-HUG-46468041/2024	XEC	24F (XEC)	20241118	EPI_ISL_19654776
hCoV-19/Switzerland/un-SNRCI-HUG-46468064/2024	XEC	24F (XEC)	20241119	EPI_ISL_19654759
hCoV-19/Switzerland/un-SNRCI-HUG-46468307/2024	XEC	24F (XEC)	20241119	EPI_ISL_19654771
hCoV-19/Switzerland/un-SNRCI-HUG-46469134/2024	XEC	24F (XEC)	20241120	EPI_ISL_19654716
hCoV-19/Switzerland/un-SNRCI-HUG-46478840/2024	XEC	24F (XEC)	20241119	EPI_ISL_19654755
hCoV-19/Switzerland/un-SNRCI-HUG-46479589/2024	XEC	24F (XEC)	20241119	EPI_ISL_19654723
hCoV-19/Switzerland/UN-SNRCI-HUG-46479879/2024	XEC	24F (XEC)	20241120	EPI_ISL_19704462
hCoV-19/Switzerland/UN-SNRCI-HUG-46479907/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241119	EPI_ISL_19704424
hCoV-19/Switzerland/un-SNRCI-HUG-46508046/2024	JN.1.16	24C (KP.3)	20241122	EPI_ISL_19654687
hCoV-19/Switzerland/un-SNRCI-HUG-46508229/2024	KP.3.1.1	24E (KP.3.1.1)	20241120	EPI_ISL_19654698
hCoV-19/Switzerland/un-SNRCI-HUG-46508472/2024	XEC	24F (XEC)	20241122	EPI_ISL_19654742
hCoV-19/Switzerland/UN-SNRCI-HUG-46521435/2024	XEC	24F (XEC)	20241122	EPI_ISL_19704409
hCoV-19/Switzerland/UN-SNRCI-HUG-46521157/2024	LP.8.2 VOI GRA (JN.1+JN.1. *)	24B (JN.1.11.1)	20241125	EPI_ISL_19704460
hCoV-19/Switzerland/UN-SNRCI-HUG-46521401/2024	XEC	24E (KP.3.1.1)	20241125	EPI_ISL_19704417
hCoV-19/Switzerland/UN-SNRCI-HUG-46533526/2024	XEC	24F (XEC)	20241126	EPI_ISL_19704404
hCoV-19/Switzerland/UN-SNRCI-HUG-46533623/2024	JN.1.11 VOI GRA (JN.1+JN.1. *)	24E (KP.3.1.1)	20241126	EPI_ISL_19704493
hCoV-19/Switzerland/UN-SNRCI-HUG-46533652/2024	JN.1.11	24B (JN.1.11.1)	20241126	EPI_ISL_19704495
hCoV-19/Switzerland/UN-SNRCI-HUG-46534507/2024	XEC (consensus call)	24F (XEC)	20241126	EPI_ISL_19704395
hCoV-19/Switzerland/UN-SNRCI-HUG-46534648/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20241125	EPI_ISL_19704497
hCoV-19/Switzerland/UN-SNRCI-HUG-46544258/2024	JN.1.40 (consensus call)	24A (JN.1)	20241125	EPI_ISL_19704500
hCoV-19/Switzerland/UN-SNRCI-HUG-46544328/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241127	EPI_ISL_19704440
hCoV-19/Switzerland/UN-SNRCI-HUG-46544435/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241126	EPI_ISL_19704389
hCoV-19/Switzerland/UN-SNRCI-HUG-46555915/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241128	EPI_ISL_19704423
hCoV-19/Switzerland/UN-SNRCI-HUG-46574830/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241127	EPI_ISL_19704458
hCoV-19/Switzerland/UN-SNRCI-HUG-46587077/2024	XEC (consensus call)	24F (XEC)	20241202	EPI_ISL_19704408
hCoV-19/Switzerland/UN-SNRCI-HUG-46620799/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20241204	EPI_ISL_19704505
hCoV-19/Switzerland/UN-SNRCI-HUG-46620656/2024	XEC (consensus call)	24F (XEC)	20241204	EPI_ISL_19704504
hCoV-19/Switzerland/UN-SNRCI-HUG-46620600/2024	XEC (consensus call)	24F (XEC)	20241205	EPI_ISL_19704444
hCoV-19/Switzerland/UN-SNRCI-HUG-46609691/2024	XEC (consensus call)	24C (KP.3)	20241203	EPI_ISL_19704431
hCoV-19/Switzerland/UN-SNRCI-HUG-46609373/2024	JN.1.8 (consensus call)	24E (KP.3.1.1)	20241204	EPI_ISL_19704501
hCoV-19/Switzerland/UN-SNRCI-HUG-46609363/2024	XEC (consensus call)	24F (XEC)	20241203	EPI_ISL_19704442
hCoV-19/Switzerland/UN-SNRCI-HUG-46642029/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20241204	EPI_ISL_19704506
hCoV-19/Switzerland/UN-SNRCI-HUG-46667487/2024	XEC (consensus call)	24F (XEC)	20241210	EPI_ISL_19704421
hCoV-19/Switzerland/UN-SNRCI-HUG-46667571/2024	XEC (consensus call)	24F (XEC)	20241209	EPI_ISL_19704402
hCoV-19/Switzerland/UN-SNRCI-HUG-46667688/2024	JN.1.16 (consensus call)	24C (KP.3)	20241209	EPI_ISL_19704451
hCoV-19/Switzerland/UN-SNRCI-HUG-46710855/2024	XEC (consensus call)	recombinant	20241213	EPI_ISL_19704507
hCoV-19/Switzerland/UN-SNRCI-HUG-46736375/2024	JN.1	24E (KP.3.1.1)	20241218	EPI_ISL_19704406
hCoV-19/Switzerland/UN-SNRCI-HUG-46737049/2024	XEC (consensus call)	24F (XEC)	20241216	EPI_ISL_19704436
hCoV-19/Switzerland/UN-SNRCI-HUG-46747617/2024	XEC (consensus call)	24F (XEC)	20241218	EPI_ISL_19704509
hCoV-19/Switzerland/UN-SNRCI-HUG-46759232/2024	XEC (consensus call)	24F (XEC)	20241219	EPI_ISL_19704396
hCoV-19/Switzerland/UN-SNRCI-HUG-46779744/2024	KP.3.1.1 (consensus call)	24E (KP.3.1.1)	20241220	EPI_ISL_19704391
hCoV-19/Switzerland/UN-SNRCI-HUG-46790217/2024	XEC (consensus call)	24F (XEC)	20241220	EPI_ISL_19704413
hCoV-19/Switzerland/UN-SNRCI-HUG-46790225/2024	JN.1.11 (consensus call)	24E (KP.3.1.1)	20241223	EPI_ISL_19704511
hCoV-19/Switzerland/UN-SNRCI-HUG-46817548/2024	XEC (consensus call)	NA	20241227	EPI_ISL_19704419

hCoV-19/Switzerland/UN-SNRCI-HUG-46817824/2024	XEC (consensus call)	NA	20241223	EPI_ISL_19704446
hCoV-19/Switzerland/UN-SNRCI-HUG-46856619/2024	XEC (consensus call)	NA	20241230	EPI_ISL_19704430
hCoV-19/Switzerland/UN-SNRCI-HUG-46890908/2025	MC.1 (consensus call)	24E (KP.3.1.1)	20250106	EPI_ISL_19704449
hCoV-19/Switzerland/UN-SNRCI-HUG-46903022/2025	XEC (consensus call)	recombinant	20250107	EPI_ISL_19704428
hCoV-19/Switzerland/UN-SNRCI-HUG-46903073/2025	XEC (consensus call)	24F (XEC)	20250106	EPI_ISL_19704387
hCoV-19/Switzerland/un-SNRCI-HUG-46976880/2025	XEC (consensus call)	recombinant	20250113	EPI_ISL_19803269
hCoV-19/Switzerland/un-SNRCI-HUG-46986133/2025	MC.1 (consensus call)	24E (KP.3.1.1)	20250114	EPI_ISL_19803271
hCoV-19/Switzerland/un-SNRCI-HUG-47223826/2025	XEC (consensus call)	24F (XEC)	20250204	EPI_ISL_19803270
hCoV-19/Switzerland/un-SNRCI-HUG-47313316/2025	JN.1.16.1 (consensus call)	24H (LF.7)	20250218	EPI_ISL_19803327
hCoV-19/Switzerland/un-SNRCI-HUG-47314038/2025	NY.3 (consensus call)	25A (LP.8.1)	20250217	EPI_ISL_19803267
hCoV-19/Switzerland/un-SNRCI-HUG-47433769/2025	JN.1.16.1 (consensus call)	24H (LF.7)	20250228	EPI_ISL_19803268
hCoV-19/Switzerland/UN-SNRCI-HUG-47649989/2025	XEC.33 (Pango v.4.3.1 consensus call)	24F (XEC)	20250325	EPI_ISL_19902837
hCoV-19/Switzerland/UN-SNRCI-HUG-47739354/2025	NY.13 (Pango v.4.3.1 consensus call)	25A (LP.8.1)	20250402	EPI_ISL_19902841
hCoV-19/Switzerland/UN-SNRCI-HUG-47957090/2025	JN.1.16.1 (Pango v.4.3.1 consensus call)	25C (XFG)	20250428	EPI_ISL_19902838

Appendix 7: Table of Sentinella RSV isolates submitted to GISAID (40/2024-16/2025)

Isolate name	Subtype	Collection Date	GISAID_ID
hRSV/B/Switzerland/un-SNRCI-HUG-46326330/2024	B	2024-11-04	EPI_ISL_19632808
hRSV/B/Switzerland/un-SNRCI-HUG-46326174/2024	B	2024-11-04	EPI_ISL_19659998
hRSV/B/Switzerland/un-SNRCI-HUG-46903259/2025	B	2025-01-06	EPI_ISL_19699271
hRSV/B/Switzerland/un-SNRCI-HUG-46891850/2025	B	2025-01-06	EPI_ISL_19699272
hRSV/B/Switzerland/un-SNRCI-HUG-46748255/2024	B	2024-12-18	EPI_ISL_19699273
hRSV/B/Switzerland/un-SNRCI-HUG-46689648/2024	B	2024-12-12	EPI_ISL_19699274
hRSV/B/Switzerland/un-SNRCI-HUG-46689413/2024	B	2024-12-12	EPI_ISL_19699275
hRSV/B/Switzerland/un-SNRCI-HUG-46667750/2024	B	2024-12-10	EPI_ISL_19699276
hRSV/B/Switzerland/un-SNRCI-HUG-46599062/2024	B	2024-12-03	EPI_ISL_19699277
hRSV/B/Switzerland/un-SNRCI-HUG-46555714/2024	B	2024-11-27	EPI_ISL_19699278
hRSV/A/Switzerland/un-SNRCI-HUG-46941182/2025	A	2025-01-10	EPI_ISL_19699284
hRSV/A/Switzerland/un-SNRCI-HUG-46927800/2025	A	2025-01-09	EPI_ISL_19699285
hRSV/A/Switzerland/un-SNRCI-HUG-46736267/2024	A	2024-12-16	EPI_ISL_19699286
hRSV/A/Switzerland/un-SNRCI-HUG-46689829/2024	A	2024-12-12	EPI_ISL_19699287
hRSV/A/Switzerland/un-SNRCI-HUG-46521525/2024	A	2024-11-25	EPI_ISL_19699288
hRSV/A/Switzerland/un-SNRCI-HUG-46508338/2024	A	2024-11-21	EPI_ISL_19699289
hRSV/B/Switzerland/un-SNRCI-HUG-47168392/2025	B	2025-02-03	EPI_ISL_19808751
hRSV/A/Switzerland/un-SNRCI-HUG-47123534/2025	A	2025-01-27	EPI_ISL_19808752
hRSV/A/Switzerland/un-SNRCI-HUG-47155343/2025	A	2025-01-30	EPI_ISL_19808753
hRSV/A/Switzerland/un-SNRCI-HUG-47191914/2025	A	2025-02-04	EPI_ISL_19808754
hRSV/B/Switzerland/un-SNRCI-HUG-47057015/2025	B	2025-01-22	EPI_ISL_19808755
hRSV/B/Switzerland/un-SNRCI-HUG-47044627/2025	B	2025-01-20	EPI_ISL_19808756
hRSV/B/Switzerland/un-SNRCI-HUG-47303015/2025	B	2025-02-17	EPI_ISL_19808757
hRSV/A/Switzerland/un-SNRCI-HUG-47112101/2025	A	2025-01-28	EPI_ISL_19808758
hRSV/B/Switzerland/un-SNRCI-HUG-47236168/2025	B	2025-02-10	EPI_ISL_19808759
hRSV/B/Switzerland/un-SNRCI-HUG-47124211/2025	B	2025-01-28	EPI_ISL_19808760
hRSV/B/Switzerland/un-SNRCI-HUG-47124550/2025	B	2025-01-29	EPI_ISL_19808761
hRSV/A/Switzerland/un-SNRCI-HUG-47247325/2025	A	2025-02-11	EPI_ISL_19808762
hRSV/B/Switzerland/un-SNRCI-HUG-47223953/2025	B	2025-02-07	EPI_ISL_19808763
hRSV/A/Switzerland/un-SNRCI-HUG-47236232/2025	A	2025-02-11	EPI_ISL_19808764
hRSV/A/Switzerland/UN-SNRCI-HUG-47032938/2025	A	2025-01-20	EPI_ISL_19833314
hRSV/B/Switzerland/un-SNRCI-HUG-47625449/2025	B	2025-03-21	EPI_ISL_19906899
hRSV/A/Switzerland/un-SNRCI-HUG-47538903/2025	A	2025-03-13	EPI_ISL_19906900
hRSV/A/Switzerland/un-SNRCI-HUG-47513921/2025	A	2025-03-11	EPI_ISL_19995385
hRSV/A/Switzerland/un-SNRCI-HUG-47690717/2025	A	2025-03-28	EPI_ISL_19995386
hRSV/B/Switzerland/un-SNRCI-HUG-47572109/2025	B	2025-03-17	EPI_ISL_19995387

Appendix 8: Table of reference Influenza HA(H1)pdm09 sequences from GISAID used in phylogenetic analyses

Virus	Clade	Clade signature amino acids (HA1)	Nextclade subclade	Subclade substitutions	GISAID_ID
A/Victoria/2570/2019_Egg [1]	5a.2 (root)		C		EPI_ISL_417210
A/Wisconsin/588/2019_Cell [1]	5a.2		C		EPI_ISL_404460
A/Sydney/5/2021_Egg [2]	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1	D94N, T216A	EPI_ISL_12109635
A/Maine/10/2022	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.2	A48P	EPI_ISL_17832068
A/Washington/22/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.3	A73T, A141E, V152I, S190I, T216A	EPI_ISL_17392718
A/Maldives/936/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.4	S85P, H273Q, V321I	EPI_ISL_18110329
A/Bulgaria/234/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.5	I185V	EPI_ISL_18008533
A/South Dakota/31/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.6	L70I, K169R, K211Q	EPI_ISL_17625845
A/Darwin/422/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1.7	I533V (HA2)	EPI_ISL_18543886
A/Netherlands/10468/2023	5a.2a	K54Q, A186T, Q189E, E224A, R259K, K308R	C.1	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/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/Poland/28/2024	5a.2a.1	5a.2a + P137S, K142R, D260E, T277A	D.4	T216A, T120A	EPI_ISL_19204767

[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 southern hemisphere influenza seasons

Appendix 9: Table of reference Influenza HA(H3) sequences from GISAID used in phylogenetic analyses

Virus	Clade	Clade signature amino acids (HA1)	Nextclade subclade	Subclade substitutions	GISAID_ID
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/Stockholm/5/2021	2a		G.1		EPI_ISL_3315857
A/Norway/24873/2021	2a.3	D53N, N96S (+CHO), I192F	G.1.3		EPI_ISL_12240180
A/Finland/402/2023	2a.3a	2a.3 + E50K	G.1.3.1		EPI_ISL_18237981
A/Thailand/8/2022_Egg [2]	2a.3a.1	2a.3a + I140K, I223V	J (former H)		EPI_ISL_16014504
A/Massachusetts/18/2022_Cell [2]	2a.3a.1	2a.3a + I140K, I223V	J (former H)		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/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 for the 2025 southern hemisphere influenza season (Trivalent vaccine)

Appendix 10: Table of reference Influenza HA(B/Vic) sequences from GISAID used in phylogenetic analyses

Virus	Clade	Clade signature amino acids (HA1)	Nextclade subclade	Subclade substitutions	GISAID_ ID
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/Croatia/7789/2019	V1A.3a	V1A.3 + N150K, G184E, N197D (-CHO) and R279K	A.3.1		EPI_ISL_406236
B/Cote d'Ivoire/948/2020	V1A.3.a.1	V1A.3a + V220M, P241Q	A.3.1.1		EPI_ISL_959673
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/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/Guangxi-Beiliu/2298/2023	V1A.3a.2	V1A.3a + A127T, P144L, K203R	C.5.7	D197E, E183K, E128G	EPI_ISL_18886149

[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 2025 southern hemisphere influenza seasons

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