REPORT

2026

NORWAY:

Interim Influenza Virological and Epidemiological season report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Northern Hemisphere 2026/2027

February 2026

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Norwegian Institute of Public Health

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Division of Infection Control

Department of Virology; Section for Influenza and other respiratory viruses, and

Department of Infection Control and Vaccines; Section for Respiratory, Blood-borne and Sexually transmitted infections

Spotlight: Early emergence of A(H3N2) “K” drift variant

A newly emerged A(H3N2) genetic group, with several key HA substitutions, evolved from the J.2.4 group and spread globally in the second half of 2025. In the autumn of 2025, this new strain caused unusually early outbreaks in several countries, including Norway. The sudden expansion of this genetic group here already in August, as evident in Figure 1, provided a clear early signal about its significant epidemic potential and initiated rapid follow-up immunity investigations in Norway with results suggesting that the H3N2 K subclade did not display increased immune evasion compared to the J.2 H3 subclade.

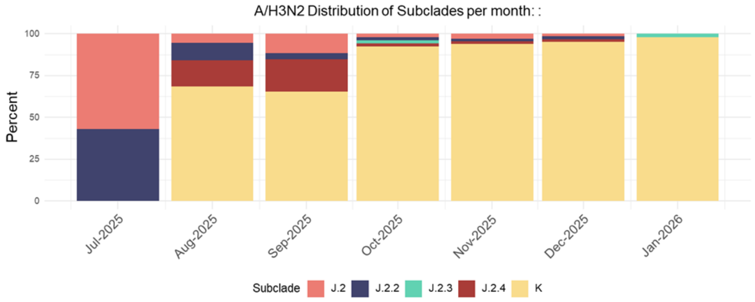

Figure 1 NextStrain subclade (Lower) distribution of A(H3N2) viruses in Norway, July 2025 – January 2026. This graph is part of Figure 13 within this report.

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The 2025-2026 influenza season, Norway by week 4/2026

Summary

- Laboratory confirmed influenza started to rise early, exceeded the 10% outbreak threshold in week 48 and in large parts of Norway peaked already in weeks 50-52, with positivity rate at 31%. This is the earliest seasonal influenza peak since 2003. Some counties in the south and west had a later start and did not have a pronounced early peak. Influenza A(H3N2) viruses have been predominant, particularly in the counties where influenza peaked early. Influenza positivity rate subsequently declined to 17% in week 2/2026 and has stabilised at 16 – 17% in following weeks. Since week 35/2025, 20,798 infections with influenza A and a mere 125 with influenza B have been detected by Norwegian laboratories, out of > 170,000 patients tested.
- Based on the weekly total numbers of detected influenza A and B, and the weekly proportions of subtypes and lineages, we estimate that A(H3N2) constituted approximately 70% of the influenza cases, followed by A(H1N1) at 28% and less than 1% B/Victoria-lineage.
- In age profile analysis of detected cases, the 0–4-year-olds and elderly over 65 years were the groups most likely to be diagnosed with A(H1N1). Infants were slightly less elevated than in some prior seasons, and the elevated likelihood in the 65-79 years group is a novel development. For A(H3N2) detections, the trend observed last year, with less elevated likelihood for the elderly than before, persisted while there was a more elevated incidence in infants. For influenza B, the pattern seems to differ from previous seasons in that there no longer is elevated incidence in school-age children and that the elderly are no longer strongly under-represented.
- This far, 34% (525/1542) of all influenza positive samples received for surveillance have been whole genome sequenced. 75 viruses, representing the spectrum of genetic variants we have observed, have been shared with WHO-CC. Among the A(H1N1) viruses, we have seen a shift in subclades from the D.3.1 dominated pre-season to a D.3.1.1 dominated season. As of week 4, D.3.1.1 is making up 86% of all H1N1. All A(H3N2) this season belonged to the 2a.3a.1 clade, of which most (98%) have been subclade K with only sporadic detections of J.2 (2%), J.2.2 (1%), J.2.3(1%) and J.2.4 (1%). All five sequenced influenza B viruses belonged to the B/Victoria V1A.3a.2 clade, of those 2 (40%) belonged to subclade C.5.6 (40%) two (40%) to C.5.6.1 and one (10%) to C.5.1.
- Interestingly, a few cases of both H1N1 and H3N2 influenza viruses this season have a mutation profile indicating restored susceptibility to adamantanes. Influenza A viruses have generally been highly resistant to antiviral adamantanes for many years.
- Seroepidemiological analysis of protective antibody responses against all influenza subtypes indicate that immunity was at a relatively high level in late summer 2025. The H3N2 K subclade did not display increased immune evasion compared to the J.2 subclade, although we cannot exclude that immune evasive properties not assessed in our analysis have contributed to a fitness advantage for the K subclade. Protective antibodies against clades 5a.2a.1 of A(H1N1) and 3A.2 of B/Victoria increased for all age groups collected in 2025, compared to sera collected in 2024.
- The proportion of influenza-like illness (ILI) began to rise gradually from week 46/2025 and the epidemic threshold was crossed in week 48/2025, the same week that the outbreak threshold was crossed for per cent test positives in the general and sentinel virological surveillance. Influenza activity peaked in week 1 when 2,4 % of the

consultations were due to influenza-like illness, which indicates a medium intensity level according to the MEM-thresholds. The ILI indicator resided at medium level for three weeks.

- Between week 35/2025 and week 04/2026, 5,168 (92,4 per 100,000 inhabitants) new hospital admissions with influenza were reported, with the highest incidence among those aged 80+, followed by 65-79 years and children under 5 years. Influenza A virus dominated. Between week 40/2025 and week 05/2026, 194 (3.5 per 100,000 inhabitants) intensive care admissions with influenza were reported. Between week 35/2025 and week 04/2026, 270 influenza associated deaths were registered. The cumulative number of influenza-associated hospitalisations, ICU admissions and deaths reported so far in 2025-26, compared to previous seasons, suggest that this will be one of the more severe seasons in Norway over the last years.
- The vaccine coverage for the age group 65 years and older was 69% per week 6/2026, and the total number of distributed doses in Norway so far this season is 1.7 million. This is somewhat more than last season (approx. 150 000 more doses). 87 percent of the doses were administered before week 48 when the epidemic threshold was reached.
- Highly pathogenic avian influenza viruses (HPAIV) belonging to H5 HA clade 2.3.4.4b continued to be detected in wild birds in Norway, with one associated poultry outbreak in the autumn of 2025. No human cases have been detected, and the general risk for human infection is assessed as very low.

Influensasesongen 2025-2026 i Norge (Norwegian summary)

Hovedbudskap

- Laboratoriepåvist influensa begynte å øke allerede i uke 43, og i størsteparten av landet ble en topp nådd i uke 50-52. Dette er den tidligste sesonginfluensatoppen siden 2003. Tre fylker, Vestland, Rogaland og Agder hadde en senere utbruddstart og hadde ikke den samme influensatoppen før nyttår som ellers i landet. Influensavirus A(H3N2) har dominert, særlig i delene av landet med tidlig start på utbruddet. Andelen influensapositive har etter toppen på rundt 31 % positive falt ned til 17 % i uke 2, og har holdt seg rundt 16 – 17 % i uke 2 – 4. I perioden fra uke 35/2025 er det, blant mer enn 170 000 testede, registrert 20 798 laboratorieverifiserte influensa A-infeksjoner mens det kun er påvist 125 tilfeller med influensa B.
- Basert på de ukentlige antallene influensa A- og B-påvisninger og ukentlige andeler av influensa A-subtyper og B-linjer, estimerer vi at influensa A(H3N2) hittil har utgjort omtrent 71 % av influensatilfellene, fulgt av A(H1N1) med 28 % og B/Victoria-linje med under 1 %.
- Aldersprofilanalyse viser at 0-4-åringer og eldre over 65 år har høyest sannsynlighet for å teste positivt for influensa A(H1N1). Småbarn har ikke ligget like mye høyere som i tidligere sesonger, og den forhøyede insidensen i gruppen 65-79 er ny denne sesongen. O likhet med forrige sesong ser vi også nå at eldre under er mindre overrepresentert i H3N2-påvisning enn vi er vant til fra tidligere. For influensa B skiller aldersprofilen seg fra tidligere sesonger ved at barn i skolealder og ikke er like overrepresentert, og at eldre ikke er like underrepresentert blant påvisningene. Tallene for influensa B er imidlertid meget lave.

- Så langt har 34% (525/1 542) av mottatte influensapositive prøver blitt fullgenomsekvensert, og 75 virus som representerer alle påviste sekvensvarianter har blitt delt med WHO internasjonalt referanselaboratorium.
  Blant A(H1N1)-virus har vi sett en endring fra subklade D.3.1 som vanligste virus i forkant av sesongen, til subklade D.3.1.1 når sesongen kom i gang. Pr. uke 4/2026 utgjør D.3.1.1 86 % av sekvenserte H1N1-virus denne sesongen.
  Blant A(H3N2)-virus har alle vært i klade 2a.3a.1, De aller fleste (98 %) har tilhørt den nye K-subkladen, med kun subklade J.2. De fem sekvenserte influensa B-virusene har alle tilhørt B/Victoria-klade V1A.3a.2, med to i subklade C.5.6, to i subklade C.5.6.1 og en i C.5.1.
- I nesten 20 år har omtrent alle influensa A-virus hos mennesker vært resistente mot adamantaner. Denne sesongen har vi observert noen få H1N1- og H3N2-virus som ikke lenger bærer slik resistensmutasjon.
- Serologisk analyse av beskyttende antistoffer viser at immuniteten i befolkningen var forholdsvis høy mot alle influensasubtypene sensommeren 2025. Nivå av beskyttende antistoffer mot H3N2 K-subkladen var sammenlignbar med beskyttende antistoffer mot J.2 subkladen, og viste dermed ingen økt grad av immununnvikelse. Vi kan likevel ikke utelukke at K-subkladen har immununnvikende egenskaper som ikke er fanget opp i våre analyser. Beskyttende nivå av antistoffer mot kladene 5a.2a.1 fra A(H1N1) og 3A.2 fra B/Victoria økte i serumprøver innsamlet i august 2025 for alle aldersgrupper, sammenlignet med prøver innsamlet i 2024.
- Andelen influensalignende sykdom (ILS) steg gradvis fra uke 46/2025 og utbruddsterskelen ble passert i uke 48/2025, samtidig som terskelen for prosentvis testpositivitet i fyrtårn- og laboratoriebasert system. Toppen ble nådd i uke 1/2026 da 2,4 % av konsultasjonene i primærhelsetjenesten skyldtes influensalignende sykdom. Dette tilsvarte et middels intensitetsnivå i henhold til ILI MEM-tersklene. ILI-indikatoren holdt seg på middels nivå i tre uker.
- Mellom uke 35/2025 og uke 4/2026 ble det rapportert 5,168 (92,4 per 100,000 innbyggere) sykehusinnleggelser med influensa. Høyest forekomst ble rapportert for aldersgruppen 80+, etterfulgt av aldersgruppene 65-79 og barn under 5 år. Influensa A-virus dominerte. Mellom uke 40/2025 og uke 5/2026 ble det rapportert 194 (3,5 per 100 000 innbyggere) intensivinnleggelser med influensa. Mellom uke 35/2025 og uke 4/2026 ble det rapportert om 270 influensaassosierte dødsfall. Det kumulative antallet innleggelser i sykehus og intensivavdeling samt influensa-relaterte dødsfall så langt, tyder på at denne sesongen kan bli stående som en av de mer alvorlige de siste årene.
- Vaksinasjonsdekningen blant personer over 65 år var 69 % per uke 6. Det har blitt distribuert omtrent 1,7 millioner doser vaksiner totalt. Dette er noe mer enn forrige sesong (ca. 150 000 flere doser). 87 prosent av dosene ble satt innen utløpet av uke 48 da utbruddsterskelen ble passert.
- Høypatogene fugleinfluensavirus (HPAIV) tilhørende H5 HA-klade 2.3.4.4b fortsatte å bli påvist hos ville fugler i Norge, samt ett utbrudd i kommersielt fjørfehold høsten 2025. Ingen tilfeller av smitte til mennesker har blitt funnet, og risikonivået for mennesker generelt i Norge vurderes som svært lavt.

A look back at the preceding 2023/2024 season

During the preceding 2024-25 season, laboratory confirmed influenza started to rise from baseline in late November 2024, crossed the virological outbreak threshold in week 52, and peaked around week 8 with a positivity rate of 35.5 % which is on par with the peak of the 2017-2018 season. 44,930 infections with influenza A and 15,514 with influenza B were detected by Norwegian laboratories, out of > 520,000 patients tested. The very high number of tested was driven by outbreaks of pertussis and *Mycoplasma pneumoniae* in 2024.

We estimate that A(H1N1) constituted approximately 46 % of the influenza cases, followed by B/Victoria-lineage with 28 % and A(H3N2) with 27 %.

The proportion of primary care influenza-like illness (ILI) cases began to rise gradually from week 50/2024 and the epidemic threshold was crossed in week 02/2025, two weeks later than crossing the outbreak threshold for per cent test positives. Influenza activity peaked in week 9 when 2,8 % of the consultations were due to influenza-like illness, which indicates a medium intensity level according to the MEM-thresholds. The ILI indicator resided at medium level for four weeks.

Altogether 10,657 (190.5 per 100,000 inhabitants) samples positive for influenza virus were reported among hospitalized patients, with the highest incidence among those aged 65-79 and 80+, followed by children under 5 years. 278 (5.0 per 100,000 inhabitants) intensive care admissions with influenza were reported, and 375 influenza associated deaths were registered. These numbers were greater than the last few previous seasons indicating that the 2024-2025 influenza season was relatively severe.

In age profile analysis of detected cases, the 0–4-year-olds were more than twice more likely to be diagnosed with A(H1N1) than other ages, similar to profiles in previous seasons. Surprisingly, for A(H3N2) detections, the elderly were not over-represented as they have been in previous years. For influenza B/Victoria, younger age groups, particularly 5–14-year-olds, were much more likely to be diagnosed than those who are older; elderly were particularly under-represented.

Whole genome sequencing was done for 14,5 % (742/5,115) of all influenza positive samples received for surveillance. 101 viruses, representing the spectrum of genetic variants we have observed, were shared with WHO. Among the A(H1N1) viruses, the initially dominant 5a.2a clade was replaced by the 5a.2a.1 viruses from March 2025 onwards. Among the 5a.2a.1 viruses the D.3 subclade was the most common (27%) followed by D.3.1 (26%).
A(H3N2) viruses predominantly (99 %) belonged to the 2a.3a.1 clade, of which most (58%) were subclade J.2, followed by J.2.2 (34%). In August, subclade J.2.4 viruses with some additional mutations appeared. All sequenced influenza B viruses belonged to the B/Victoria V1A.3a.2 clade, with 56% being subclade C.5.1, 20% C.5.7, 15% C.5.6, 7% C.3, and 2% C.5.

The vaccine coverage for the age group 65 years and older was 66%, and the total number of distributed doses in Norway was 1.56 million. This was at the same level as preceding season. 99 percent of the doses were administered before the epidemic threshold was reached.

Highly pathogenic avian influenza viruses (HPAIV) belonging to H5 HA clade 2.3.4.4b continued to be detected in wild birds in Norway, with sporadic spillover to mammalian carnivores. Detections were fewer and more scattered compared to the summer of 2023. There was one outbreak of HPAIV AH5N5 in a poultry backyard flock in November 2024. No human cases were detected.

The 2025/2026 season, weeks 35/2025 through 4/2026

The components of the surveillance system are briefly described in Appendices.

Virological surveillance data

Laboratory confirmed influenza: Virological surveillance

Altogether, more than 170,000 patients in Norway have been tested for influenza during weeks 35/2025 – 4/2026, resulting in 20,798 recorded detections of influenza A virus (99.4 % of the influenza detections) and a mere 125 influenza B virus (0.6 % of influenza detections) (Figure 2, Table 1).

From these patients, 1,363 influenza A and 19 influenza B positive specimens have so far been referred by testing laboratories to the NIC for further identification and characterisation. Among these, 1,318 type A viruses have so far been subtyped; 439 H1(33 %) and 879 H3 (67 %). Of the remaining 45 type A-positive specimens received that have not been subtyped, a few (3) specimens were confirmed as influenza A virus but too weak for successful subtyping, 7 could not be confirmed as influenza A in the NIC (several of these specimens had also other respiratory viruses detected in the submitting laboratory) and the remainder were not yet tested for subtype.
Out of the 19 referred specimens with an initial influenza B positive result, 14 were confirmed as belonging to the B/Victoria/2/1987 lineage. Two initially influenza B positive specimens could not be verified in the NIC and three had not yet been tested by the time of the data snapshot (but have subsequently been verified as B/Victoria).

In addition to this, primary testing laboratories have identified 1,152 type A viruses as H1 and 150 as H3, of which many have been forwarded to the NIC and also subtyped there. This subtype testing is highly biased since several laboratories are testing for H1pdm09 but not H3. In order to avoid this bias, subtyped viruses that have not been tested for both circulating HA subtypes are not reported by subtype internationally and not used for subtype proportion calculations.

The number of detections started to rise in mid-October, and grew quite rapidly until a peak in positivity rate of 30.6 % was reached in mid-December (week 51) (Figure 2, Table 1). The outbreak threshold at 10 % positivity rate for the virological surveillance was surpassed in week 48. After week 51, detections declined and has stabilised at al level around 16-17 % positivity rate in weeks 2 – 4. Apart from the 2009 pandemic when detections peaked in week 43, we have to go back to the 2003/2004 season to find a similarly early peak; the outbreak, driven by the significantly drifted A/Fujian/411/2002(H3N2) strain, peaked in week 49/2003.

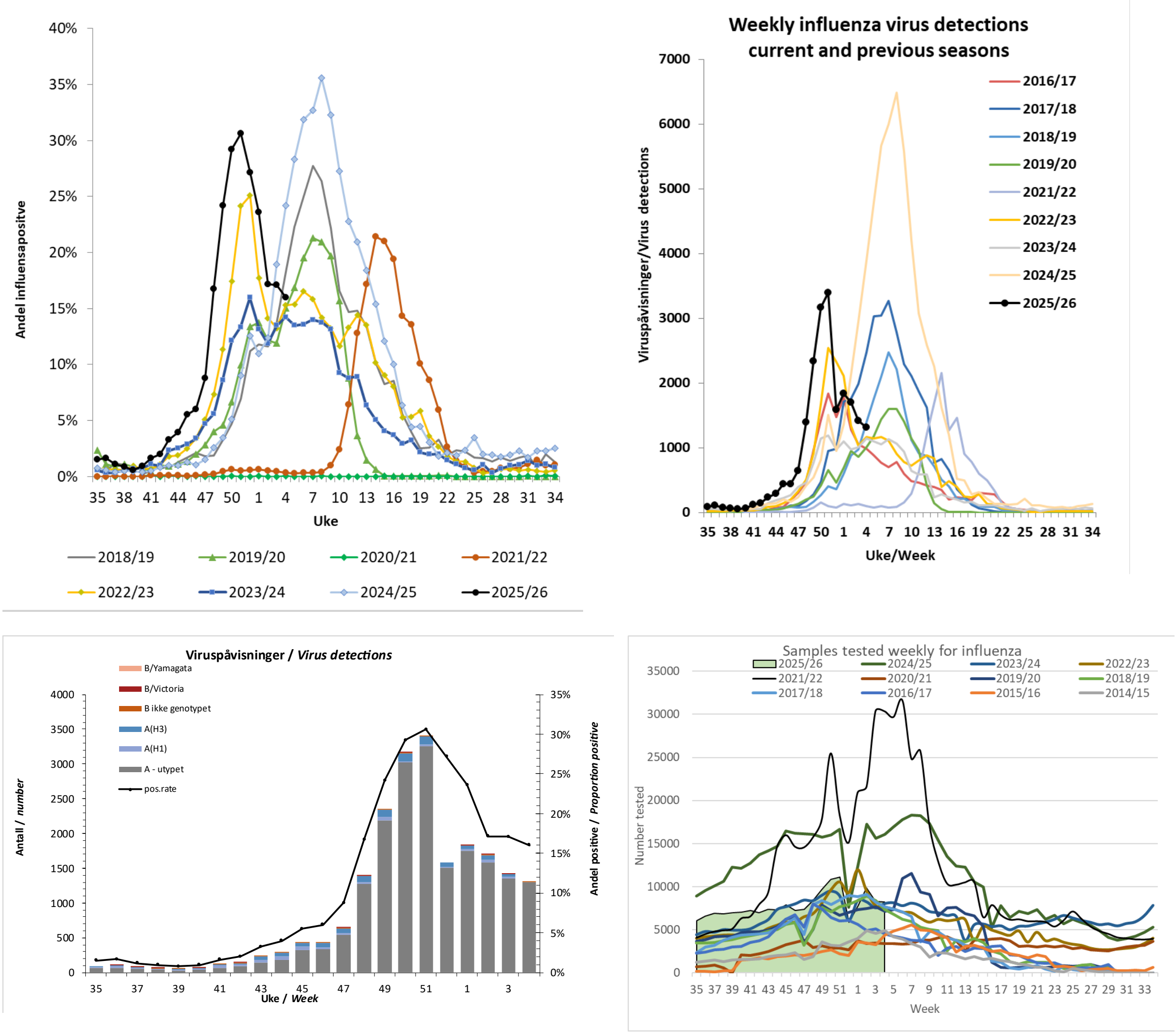


Figure 2. Laboratory detections, Norway 2025-2026. Upper left-hand panel: Weekly proportion of influenza virus positive tested patients, with previous season proportions shown for comparison. Upper right-hand panel: Weekly number of influenza virus detections, with previous season numbers shown for comparison. Lower left-hand panel: Weekly number of the different influenza viruses, displayed as stacked bars. Lower right-hand panel: weekly number of patients tested for influenza, compared to other seasons.

Type A viruses have been in very strong majority over type B throughout the period and in all parts of the country. (Figure 4). Among the type A viruses influenza A(H1N1) viruses were in majority in early autumn, but A(H3N2) took over when activity started to increase from mid-October and onwards. Since the peak in week 51/2025, the proportion of H3N2 has declined from around 80 % to around 60% in week 4/2026. (Figure 3). In Western Norway, where the proportion of A(H3N2) viruses was initially lower, there was no pronounced pre-New Year peak. Influenza B viruses have been exclusively B/Victoria/2/87-lineage. The initial majority of the H1 subtype persisted longer in Western and Northern Norway (Figure 4). The subtype analysis is limited to viruses that have been tested for both H1 and H3, since many laboratories test only for H1 and not H3, thus producing a strong subtype bias.

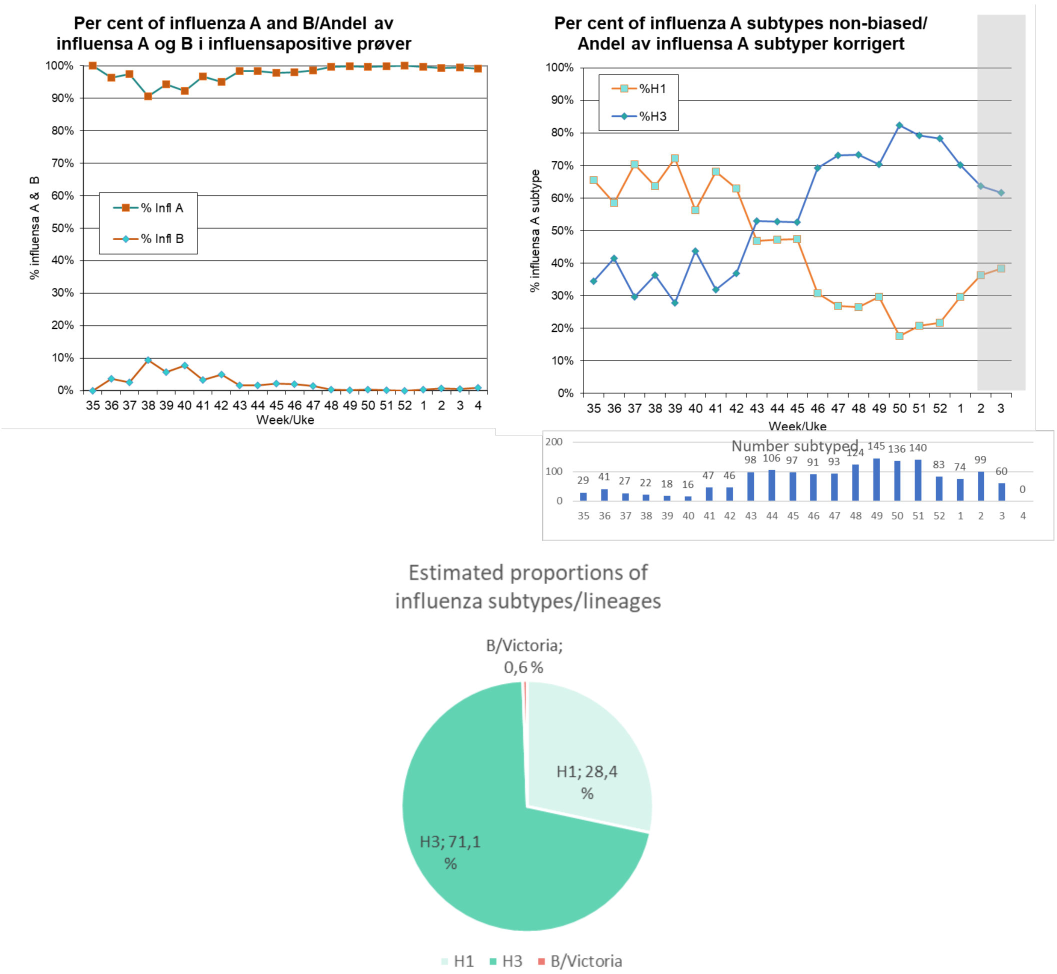
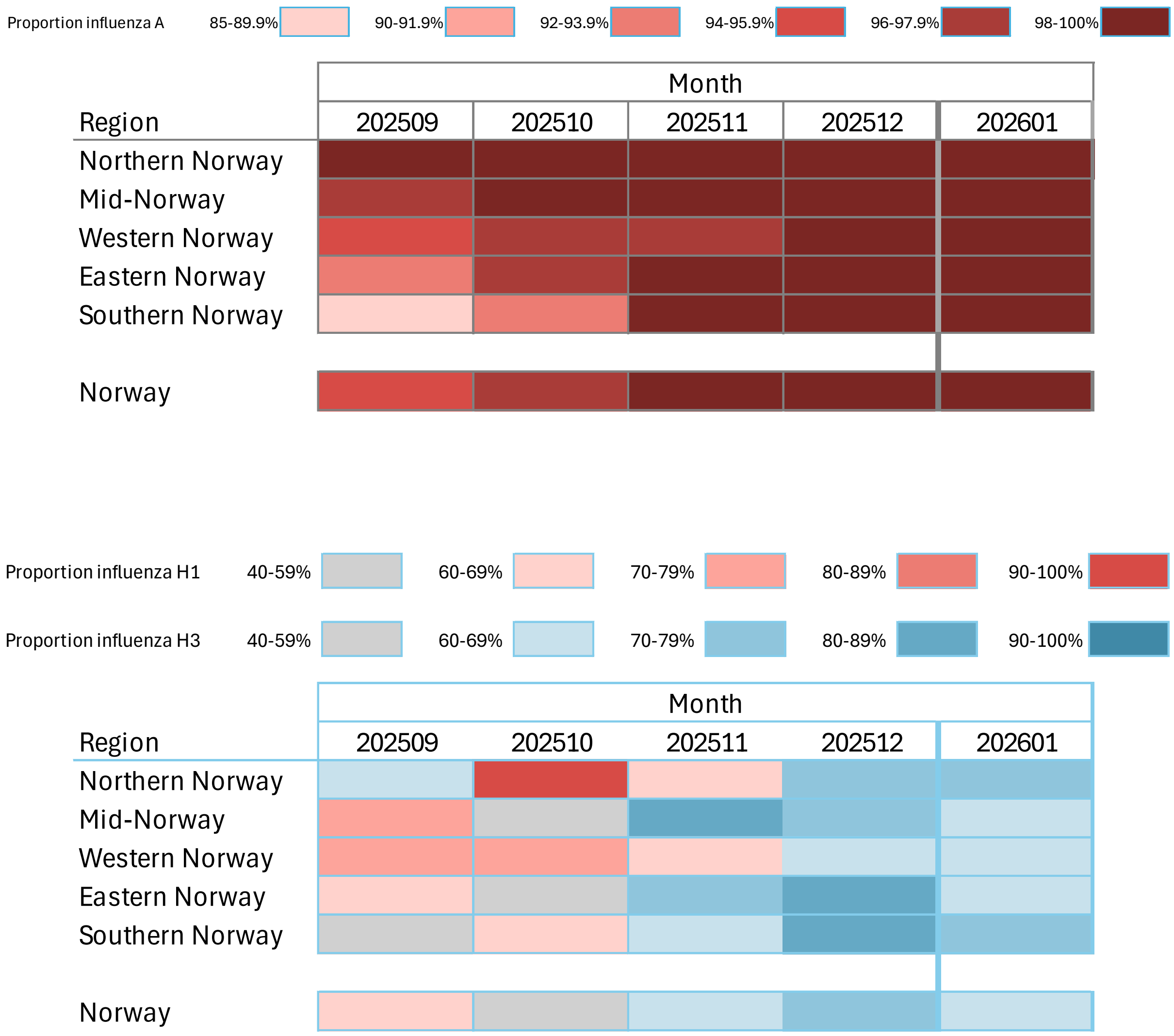


Figure 3. Influenza virus detections since week 35/2025, proportions per type A and B (upper left panel) and influenza A subtypes H1 and H3 (upper right panel). Only viruses tested for both subtypes are counted in the subtype analysis. Bars below show weekly number of subtyped samples.
The lower pie chart displays estimated proportions of the three circulating influenza viruses, produced by projection of the weekly A subtype and B lineage proportions onto the weekly numbers of influenza A and B detections, respectively.



Proportion influenza A: 85-89.9% · 90-91.9% · 92-93.9% · 94-95.9% · 96-97.9% · 98-100%

Region	202509	202510	202511	202512	202601
Northern Norway	98-100%	98-100%	98-100%	98-100%	98-100%
Mid-Norway	96-97.9%	98-100%	98-100%	98-100%	98-100%
Western Norway	94-95.9%	96-97.9%	96-97.9%	98-100%	98-100%
Eastern Norway	92-93.9%	96-97.9%	98-100%	98-100%	98-100%
Southern Norway	85-89.9%	92-93.9%	98-100%	98-100%	98-100%
Norway	94-95.9%	96-97.9%	98-100%	98-100%	98-100%

Proportion influenza H1: 40-59% · 60-69% · 70-79% · 80-89% · 90-100%

Proportion influenza H3: 40-59% · 60-69% · 70-79% · 80-89% · 90-100%

Region	202509	202510	202511	202512	202601
Northern Norway	H3 60-69%	H1 90-100%	H1 60-69%	H3 70-79%	H3 70-79%
Mid-Norway	H1 70-79%	40-59%	H3 80-89%	H3 70-79%	H3 60-69%
Western Norway	H1 70-79%	H1 70-79%	H1 60-69%	H3 60-69%	H3 60-69%
Eastern Norway	H1 60-69%	40-59%	H3 70-79%	H3 80-89%	H3 60-69%
Southern Norway	40-59%	H1 60-69%	H3 60-69%	H3 80-89%	H3 70-79%
Norway	H1 60-69%	40-59%	H3 60-69%	H3 70-79%	H3 60-69%

Figure 4. Monthly proportions of influenza virus detections since September 2025, type (top panel) and subtype (bottom panel) proportions per geographic region. Only viruses tested for both subtypes are counted in the subtype analysis.

Age distribution of A(H1N1), A(H3N2), and B/Victoria detections

As in previous seasons, the age profile, in this analysis displayed as normalised incidence of laboratory verified cases, differs between the circulating influenza viruses. This season's profiles for A(H1N1), A(H3N2) and B viruses are plotted in Figure 5.

For A(H1N1), the youngest children and elderly above 65 years were the most likely to get a positive H1 result, whereas the 5 – 29-year-olds were least likely. The elevated likelihood for the elderly under 80 years is a relatively novel development, and the incidence in infants is less elevated than in the seasons 2017 - 2020.

For A(H3N2), the youngest age group and elderly 80 years and older have been more than twice as likely to test positive as all ages seen together, with the 5-29-year-olds being slightly above the all-ages average, and 30-64-year-olds being slightly below. The elevated incidences for those 80 years and older were noticeably higher in the three earliest seasons analysed. For elderly between 65 and 79 years, on the other hand, the incidences are no longer elevated.

For influenza B (all lineage-tested have been B/Victoria-lineage), the number of detections is very low so far. The pattern may seem to differ from previous seasons. School-age children have typically been the most likely to be influenza B (i.e., B/Victoria-lineage) positive, but this does not appear to be the case this season. Conversely, small children and elderly past 80 years appear to have a higher normalised incidence than before. The change for the 5-14-year-olds may be related to the noticeable increase in pre-season seropositivity in this age group in August 2025.

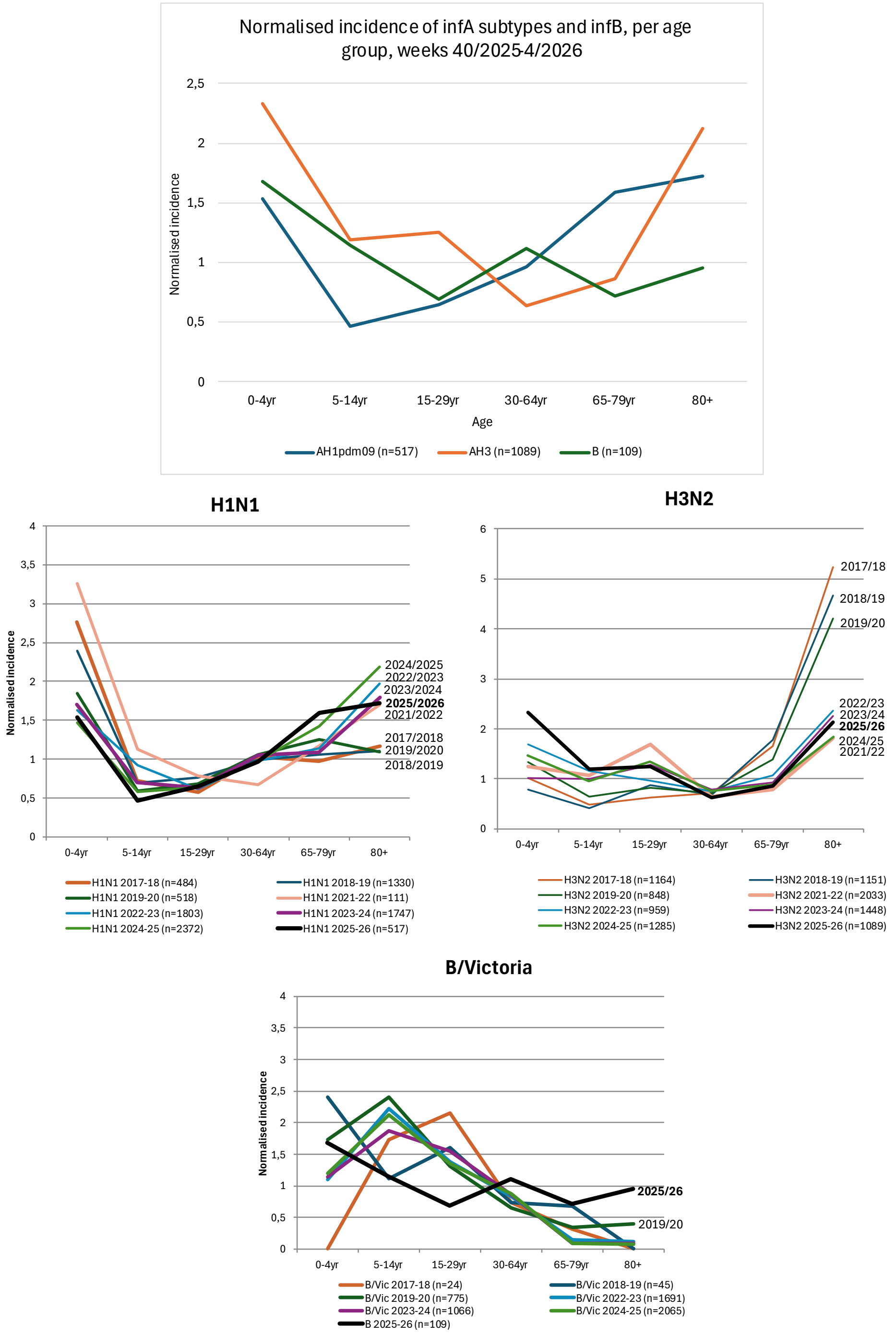


Figure 5. Age profiles of influenza viruses in the 2025/2026 influenza season up to week 4/2026. The score for each age group is the frequency of detections per age group population size, normalised against the combined frequency for all ages (=1). An age group with a score of 2 means that members of that group are twice as likely to get this diagnosis, compared to all ages. The bottom graphs show comparisons to corresponding profiles in earlier seasons.

Table 1 Weekly total number of specimens tested for influenza, proportion of specimens positive for influenza virus, and influenza virus detections per type/subtype/lineage, in Norway from week 40/2024 through week 34/2025 (sentinel and non-sentinel data combined). Numbers provided here for A(H1) and A(H3) are not comparable since several laboratories test for H1pdm09 but not for H3.

	Viruspåvisninger/*Virus detections*							
UKE/ *week*	Prøver/ *Specimens*	% positive	A(utypet) *not subtyped*	A(H1)	A(H3)	B ikke genotypet *not lineage typed*	B/ Victoria lineage	B/ Yamagata lineage
35	6077	1,5 %	55	28	9	0	0	0
36	6582	1,7 %	61	29	15	3	1	0
37	6909	1,1 %	43	26	8	1	1	0
38	6813	0,9 %	41	11	5	4	2	0
39	6944	0,7 %	31	13	5	3	0	0
40	7046	0,9 %	34	16	10	4	1	0
41	7219	1,6 %	56	43	15	4	0	0
42	7002	2,0 %	73	41	19	6	1	0
43	7388	3,3 %	137	47	53	4	0	0
44	7308	4,0 %	157	60	67	5	0	0
45	7913	5,5 %	306	64	56	10	0	0
46	7265	6,0 %	319	46	64	9	0	0
47	7370	8,8 %	512	51	74	9	1	0
48	8339	16,8 %	1173	95	126	3	1	0
49	9679	24,2 %	2064	119	156	2	0	0
50	10828	29,2 %	2857	121	177	7	2	0
51	11110	30,6 %	3077	157	162	4	0	0
52	5852	27,2 %	1426	69	95	0	0	0
1	7758	23,6 %	1684	69	74	5	1	0
2	9890	17,1 %	1453	147	85	9	2	0
3	8298	17,1 %	1185	172	54	5	3	0
4	8200	16,0 %	1183	110	8	12	0	0
Total	171790	12 %	17927	1534	1337	109	16	0
UKE/ *week*	Prøver/ *Specimens*	% positive	A(utypet) *not subtyped*	A(H1)	A(H3)	B ikke genotypet *not lineage typed*	B/ Victoria lineage	B/ Yamagata lineage
		Type A: 20798		Type B: 125				

Sentinel-based virological surveillance, primary care

From week 35/2025 through week 4/2026, 822 sentinel specimens have been tested, with 179 detections of influenza virus A (33 subtype H1, 122 subtype H3, and 24 not yet subtyped), and 5 influenza virus B (of which 2 are Victoria-lineage and 3 are not yet lineage identified, with none being Yamagata-lineage). In addition, 41 SARS-CoV-2, 23 RSV, 69 rhinovirus, 3 human metapneumovirus (hMPV), 26 parainfluenza virus and 13 other human coronaviruses were detected (Figure 7, Table 2).

In the sentinel testing, influenza detections surpassed the 10% outbreak threshold in week 48 and passed a positivity rate peak at 57% in week 51. Thus, both the outbreak start and peak weeks coincided with the surveillance based on results from all laboratories and the clinical ILI surveillance.

Among the detected influenza viruses, A(H3N2) have so far constituted 66%, followed by A(H1N1) at 18%. Influenza A viruses that have not yet been subtyped constitute 13%. Influenza B viruses constitute 3% (Figure 6). Compared to the frequencies estimated for all laboratory detections (Figure 3), the pattern is similar but the frequency of influenza B is larger in the primary care sentinel surveillance than in the comprehensive surveillance that represents a mixture of primary care and hospitalised cases.

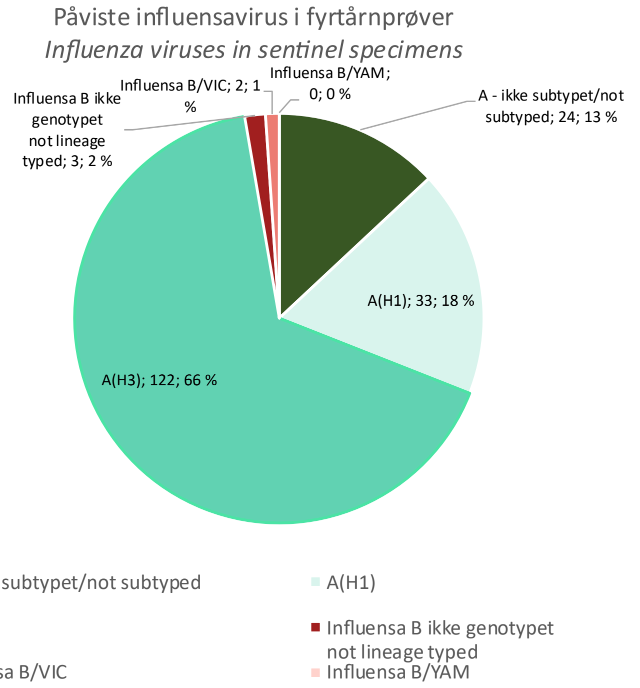
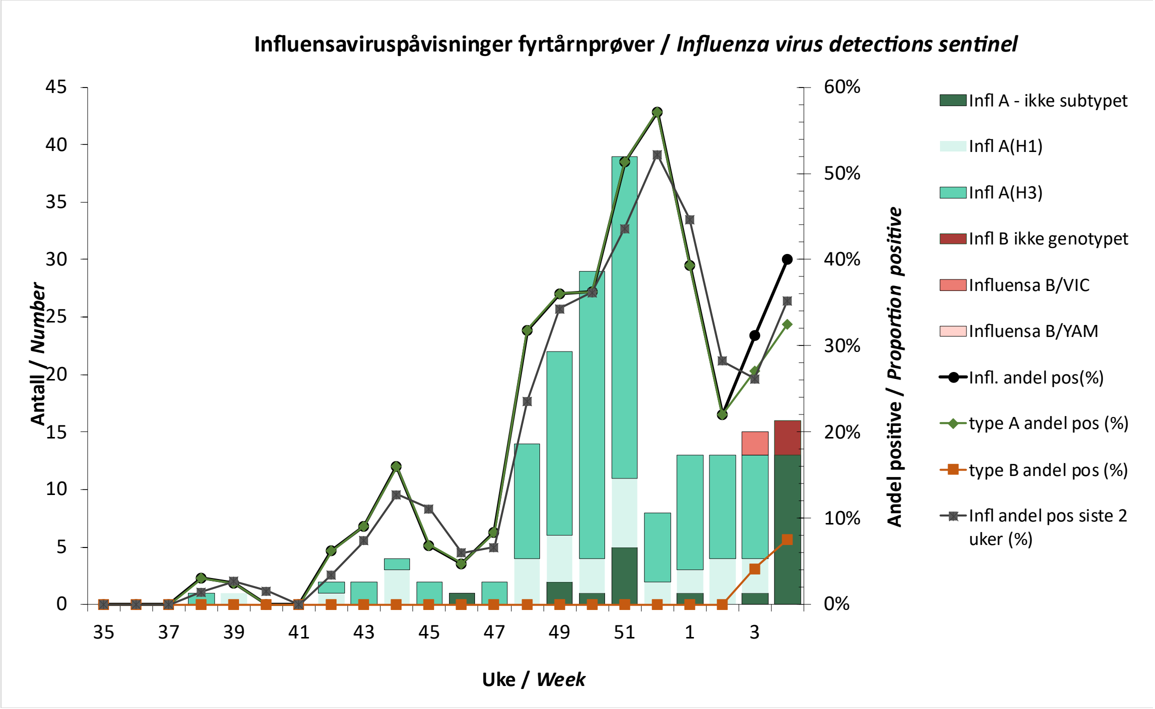


Figure 6. Proportions of influenza virus subtypes and lineages detected in sentinel specimens in the 2025/2026 season, by week 34/2025.

Almost half of all sentinel surveillance samples are taken from the age group 30-64 (49%). The second-largest group in this dataset is the 15–29-year-olds (20%), followed by 65–79-year-olds (14%) and 5–14-year-olds (8%) and. The two least represented age groups were the youngest, 0-4 years (4 %), and the oldest, 80 years and older (4%). Compared to the comprehensive surveillance that captures the testing in all laboratories, the sentinel surveillance has a lower proportion of the youngest and the oldest, and a higher proportion of persons 5-64 years old.



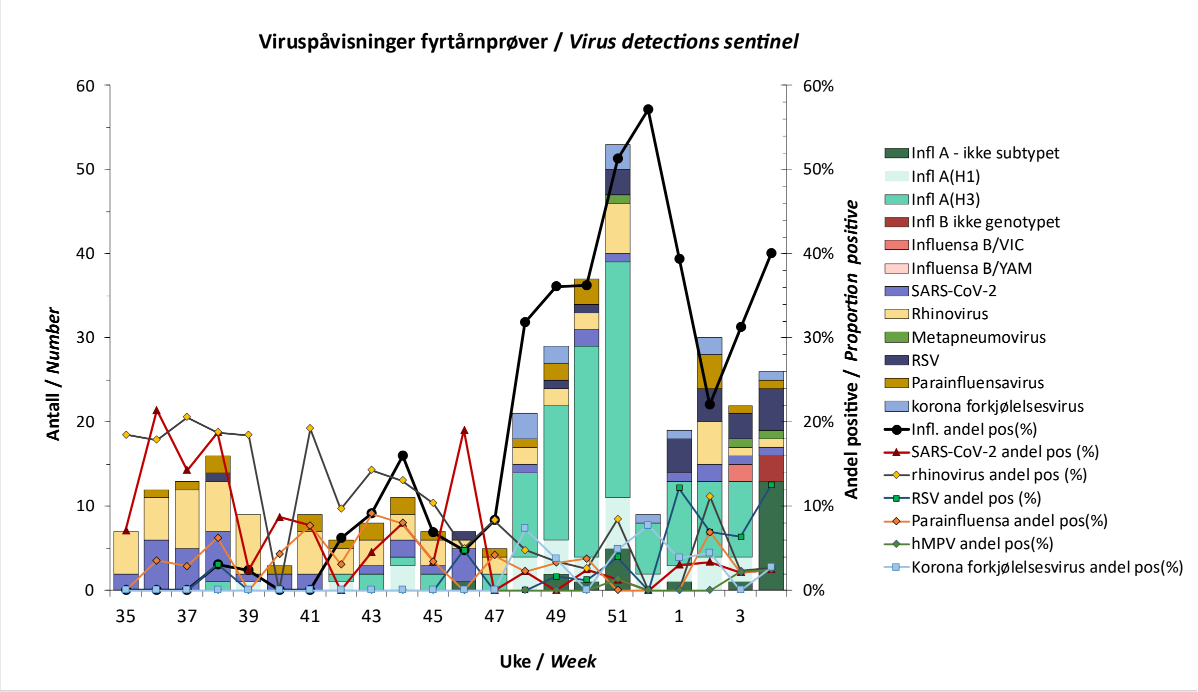


Figure 7. Weekly numbers of detections and per cent positives of influenza viruses (upper panel) and all surveyed respiratory viruses (lower panel) in the respiratory sentinel surveillance.

Apart from the early start of the influenza outbreak and the low number of SARS-CoV-2 detections, the pattern of respiratory virus detections did not differ from previous seasons (Figure 8).

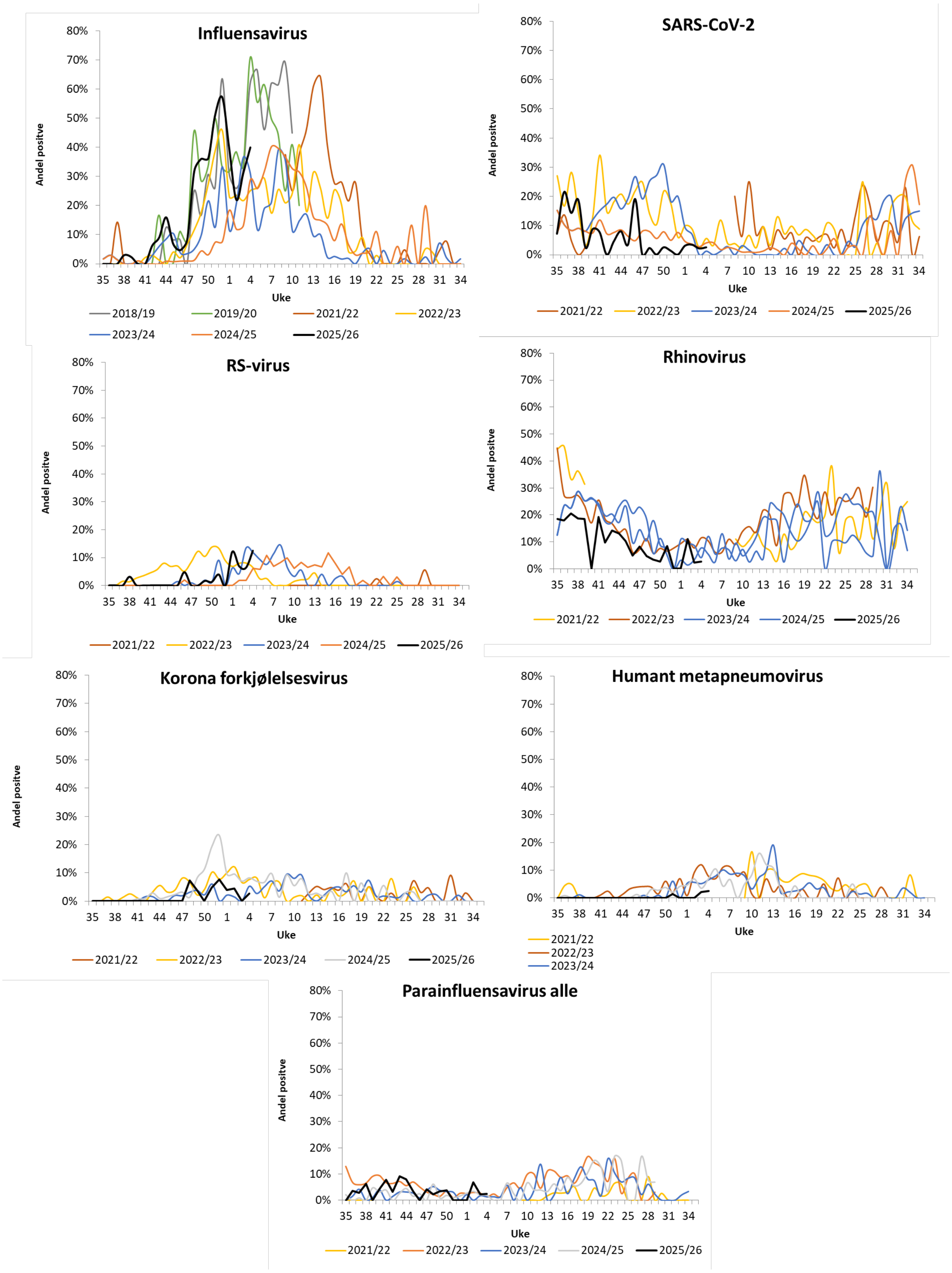


Figure 8. Proportion positive sentinel specimens in the current season (week 35/2025 and onward, black line), compared to six preceding seasons, for influenza viruses, SARS-CoV-2, RSV, rhinovirus, common cold coronaviruses, human metapneumovirus and parainfluenza viruses. Data for the most recent week is incomplete.

Table 2. Weekly virus detections in the virological sentinel system (fyrtårnsystemet)

Week	Specimens tested	Influenza A - not subtyped	A(H1)	A(H3)	Influenza B untyped	B/Victoria	B/Yamagata	Influenza % positive	Influenza A % positive	Influenza B % positive	SARS-CoV-2 antall	% positive	RSV	% positive	Rhinovirus	% positive	Parainfluensa 1	Parainfluensa 2/4	Parainfluensa 3	All parainfl. % positive	Metapneumovirus	% positive	Common cold coronavirus	% positive
35	28	0	0	0	0	0	0	0 %	0 %	0 %	2	7 %	0	0 %	5	19 %	0	0	0	0 %	0	0 %	0	0 %
36	28	0	0	0	0	0	0	0 %	0 %	0 %	6	21 %	0	0 %	5	18 %	0	0	0	4 %	0	0 %	0	0 %
37	35	0	0	0	0	0	0	0 %	0 %	0 %	5	14 %	0	0 %	7	21 %	1	0	0	3 %	0	0 %	0	0 %
38	33	0	0	1	0	0	0	3 %	3 %	0 %	6	19 %	1	3 %	6	19 %	0	0	1	6 %	0	0 %	0	0 %
39	41	0	1	0	0	0	0	2 %	2 %	0 %	1	2 %	0	0 %	7	18 %	0	0	0	0 %	0	0 %	0	0 %
40	23	0	0	0	0	0	0	0 %	0 %	0 %	2	9 %	0	0 %	0	0 %	0	0	1	4 %	0	0 %	0	0 %
41	26	0	0	0	0	0	0	0 %	0 %	0 %	2	8 %	0	0 %	5	19 %	0	0	1	8 %	0	0 %	0	0 %
42	32	0	1	1	0	0	0	6 %	6 %	0 %	0	0 %	0	0 %	3	10 %	0	0	1	3 %	0	0 %	0	0 %
43	22	0	0	2	0	0	0	9 %	9 %	0 %	1	5 %	0	0 %	3	14 %	0	0	2	9 %	0	0 %	0	0 %
44	25	0	3	1	0	0	0	16 %	16 %	0 %	2	8 %	0	0 %	3	13 %	0	0	1	8 %	0	0 %	0	0 %
45	29	0	0	2	0	0	0	7 %	7 %	0 %	1	3 %	0	0 %	3	10 %	0	0	1	3 %	0	0 %	0	0 %
46	21	1	0	0	0	0	0	5 %	5 %	0 %	4	19 %	1	5 %	1	5 %	0	0	0	0 %	0	0 %	0	0 %
47	24	0	0	2	0	0	0	8 %	8 %	0 %	0	0 %	0	0 %	2	8 %	0	0	0	4 %	0	0 %	0	0 %
48	44	0	4	10	0	0	0	32 %	32 %	0 %	1	2 %	0	0 %	2	5 %	1	0	0	2 %	0	0 %	3	7 %
49	61	2	4	16	0	0	0	36 %	36 %	0 %	0	0 %	1	2 %	2	3 %	0	0	0	3 %	0	0 %	2	3 %
50	80	1	3	25	0	0	0	36 %	36 %	0 %	2	3 %	1	1 %	2	3 %	2	0	1	4 %	0	0 %	0	0 %
51	76	5	6	28	0	0	0	51 %	51 %	0 %	1	1 %	3	4 %	6	8 %	0	0	0	0 %	1	1 %	3	4 %
52	14	0	2	6	0	0	0	57 %	57 %	0 %	0	0 %	0	0 %	0	0 %	0	0	0	0 %	0	0 %	1	7 %
1	33	1	2	10	0	0	0	39 %	39 %	0 %	1	3 %	4	12 %	0	0 %	0	0	0	0 %	0	0 %	1	3 %
2	59	0	4	9	0	0	0	22 %	22 %	0 %	2	3 %	4	7 %	5	11 %	1	0	1	7 %	0	0 %	2	3 %
3	48	1	3	9	0	2	0	31 %	27 %	4 %	1	2 %	3	6 %	1	2 %	1	0	0	2 %	1	2 %	0	0 %
4	40	13	0	0	3	0	0	40 %	33 %	8 %	1	3 %	5	13 %	1	3 %	0	0	1	3 %	1	3 %	1	3 %
Sum	822	24	33	122	3	2	0				41		23		69		6	0	11		3		13	

Genetic characterization of influenza viruses in Norway

During the current influenza season (week 35-2025 and onwards), the Norwegian Institute of Public Health (NIPH) has received 1,542 influenza virus specimens for analysis. Of these, 34% (525 viruses) have undergone whole-genome sequencing (Table 3). Additionally, 70 viruses have been shared with the WHO Collaborating Centre in the UK (Worldwide Influenza Centre, Francis Crick Institute), according to a sequencing-first selection to ensure phenotypic characterisation of as many genetic variants as possible. All 525 haemagglutinin (HA) gene sequences have been submitted to the GISAID EpiFlu database, along all other genes that meet the quality criteria for submission.

Of those 525 samples 100 came from the Sentinel surveillance program and 425 from the general surveillance program. Furthermore 100 samples were taken from hospitalised patients and 318 samples came from outpatients. For 107 cases we lack information to correctly attribute them.

Most of our sequenced samples came from patients age 25-59 (n= 192) followed by the oldest age group 60+ (n=138) The younger age groups were represented with 88 samples from the 15–24-year-olds, 62 samples for the 5-14 age group and 46 samples from the youngest (0-4).

We have here used the term “clade” for the WHO HA clade nomenclature, and “subclade” for the more detailed NextStrain nomenclature.

H1N1 viruses

During the 2024/25 influenza season, we only detected H1N1 viruses belonging to the *6B.1A.5a.2a.1* clade; the most recent *5a.2a* virus was detected in July 2025. All *5a.2a.1* viruses are further defined as *genAH1/Missouri/11/2025-like* according to the WHO/ECDC characterisation guidelines. However, we have seen a shift in subclades within the *5a.2a.1* clade from the **D.3.1** dominated pre-season to the **D.3.1.1** dominated season. In summer 2025 we saw an increase in **D.3.1** viruses with the additional haemagglutinin substitutions **R113K; A139D; E283K; K302E** which was later classified as **D.3.1.1**. Over autumn until the start of the season these viruses increased in prevalence and reached 95% (20/21) in January 2026. Overall, this season we sequenced 148 **H1N1** and 125 (86%) of those belong to the **D.3.1.1** subclade (Figure 9, Table 3).

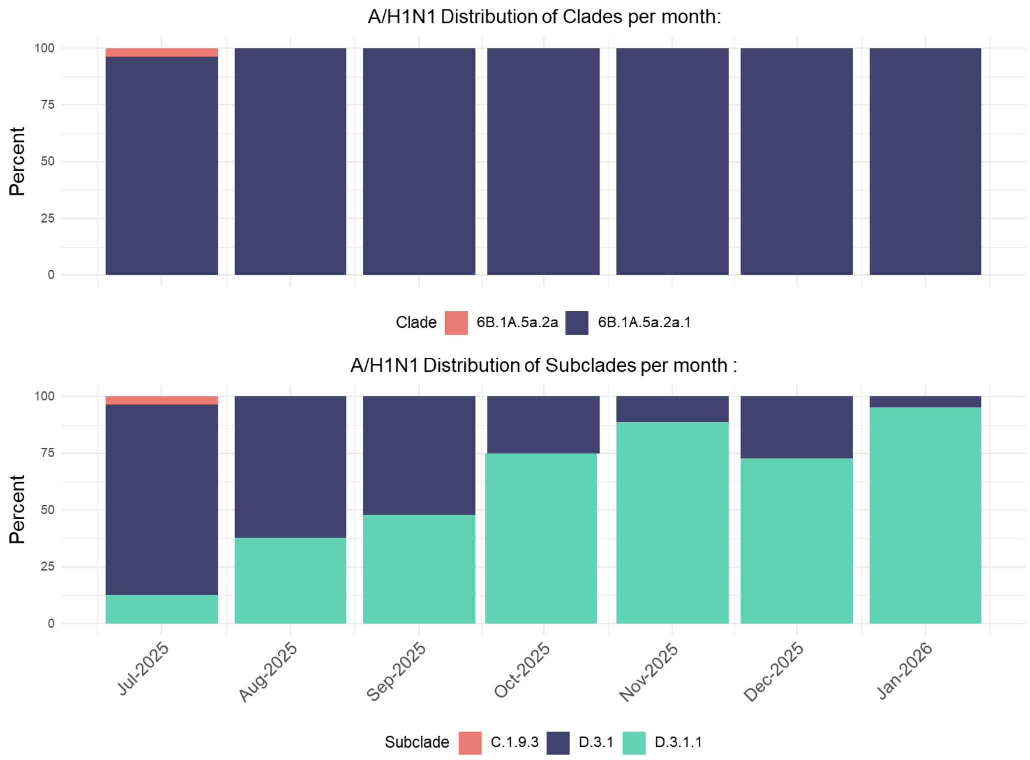


Figure 9. Clade (Upper) and subclade (Lower) distribution of H1N1 viruses in Norway for Season 2025/2026

Cluster analysis:

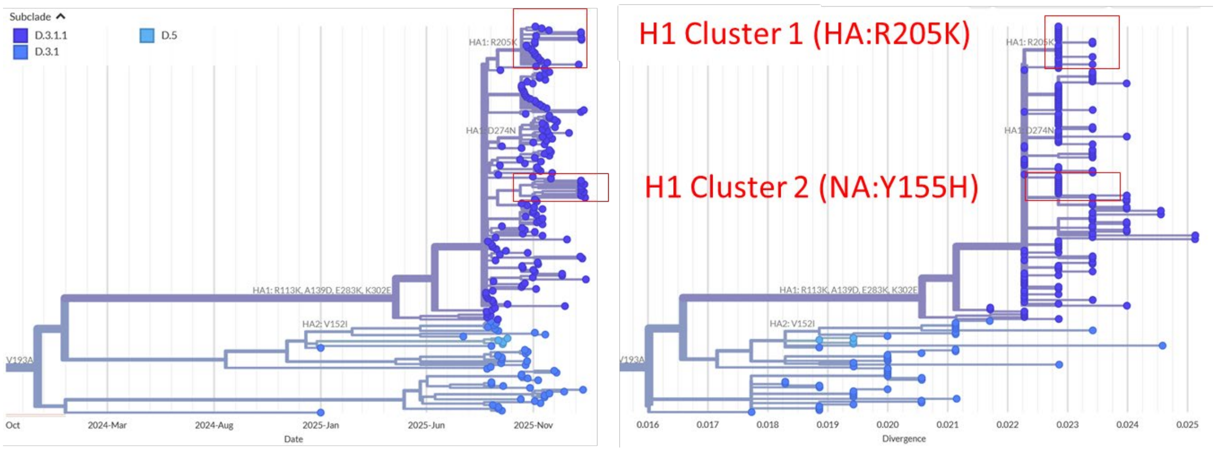


Figure 10 Clade 6B.1A.5a.2a.1, NextStrain phylogenetic tree of the haemagglutinin of the H1N1 viruses from Norway from week 35 2025 until week 4 2026, compared to the reference sequences for season 2025/26 provided by the ECDC/WHO Influenza characterization guidelines. Colours represent subclades; branches are labelled with amino acid substitutions. Left: On a time axis. Right: On a divergence axis. The full NextStrain tree is available here.

The **D.3.1.1** were dominant this season although we had sporadic detection of **D.3.1s** as well (Figure 9). Most **D.3.1** were genetically very similar with the exception of a cluster with an additional HA:**R113Q** that was sporadically picked up (6/148). However, the **D.3.1.1** have recently been expanding their genetic repertoire with two clusters of note.

The first cluster has an additional HA:**R205K** and is significant as this represents an epitope mutation (Figure 11). These viruses came from all over Norway and were first detected in October 2025.

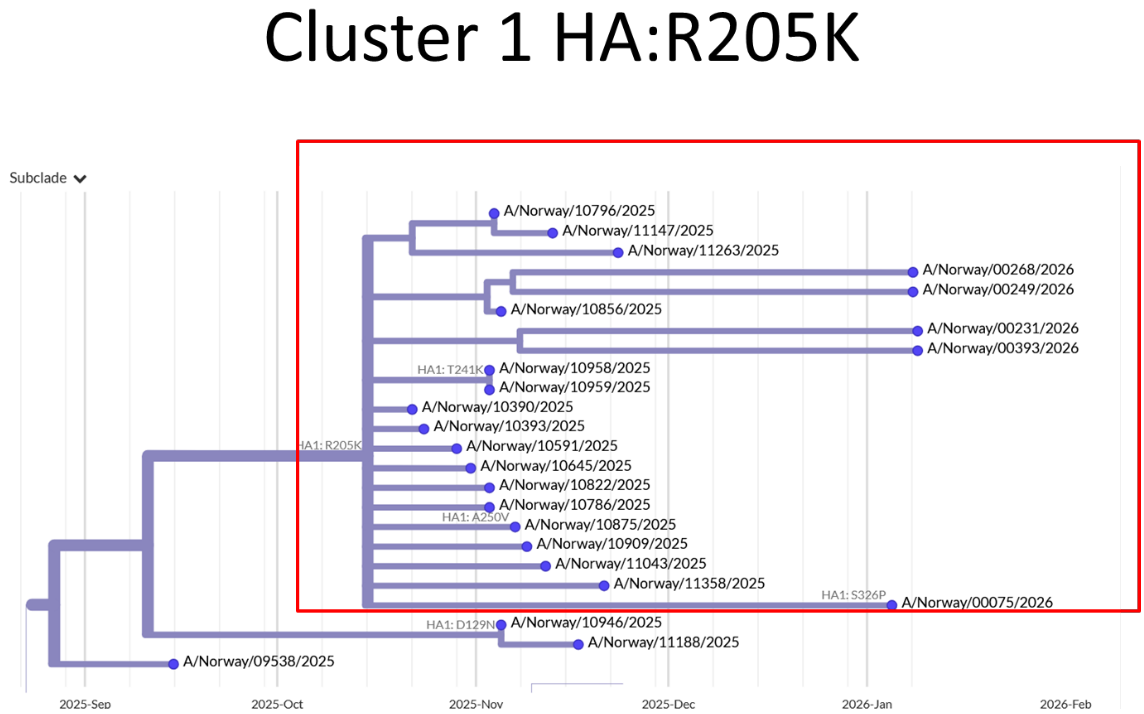

Cluster 1 HA:R205K

Figure 11 Clade 6B.1A.5a.2a.1, Subclade D.3.1.1 H1 Cluster 1 NextStrain phylogenetic focus tree of the haemagglutinin of the H1N1 viruses from Norway from week 35 2025 until week 4 2026, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions tip labels refer to virus names. The full NextStrain tree is available here.

The second cluster of note belongs also to the **D.3.1.1** subclade with no additional haemagglutinin substitutions but carries a unique substitution in the Neuraminidase gene a NA:**Y155H** (Figure 12**)** that could influence drug susceptibility, depending on the genetic context. We are in the process to follow up with phenotypic testing to ascertain the effect in current pdm09 viruses. These viruses have not been detected before January 2026 and made up 10 of 21 (48%) H1N1 sequences in January, they were detected in multiple counties in Norway with no obvious connection or treatment history in our data.

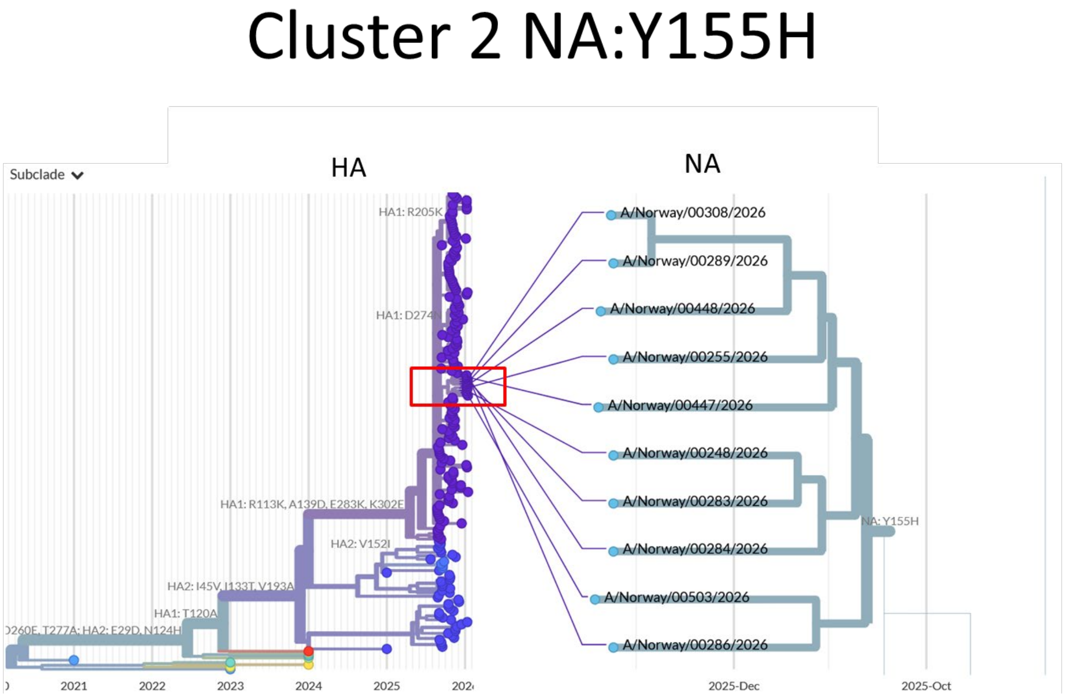


Figure 12 Clade 6B.1A.5a.2a.1, Subclade D.3.1.1 H1 Cluster 2 NextStrain phylogenetic focus tree of the haemagglutinin of the H1N1 viruses from Norway from week 40 2025 until week 4 2026, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions tip labels refer to virus names. The full NextStrain tree is available here.

H3N2 viruses

During the 2025/26 influenza season in Norway, all sequenced **H3N2** viruses belonged to the 2a.3a.1 clade (Figure , Table 3).

Within this_clade, the main group of viruses detected belonged to the **K** (269/284, 95%) subclade, with sporadic detections of **J.2** (6/284, 2%), **J.2.2** (3/284, 1%), **J.2.3**(2/284, 1%) and **J.2.4** (4/284, 1%) (Figure , Figure 14, Table 3).

The **K** subvariant was first detected in Norway in August 2025, there it made up more than 65% of all H3N2 sequences. From there it reached dominance quickly and makes up 98% of all H3N2 sequences in January 2026. Within the **K** subclade sporadic amino acid substitutions occurred however the host of the H3N2 **K** subclade remain genetically identical on an amino acid level

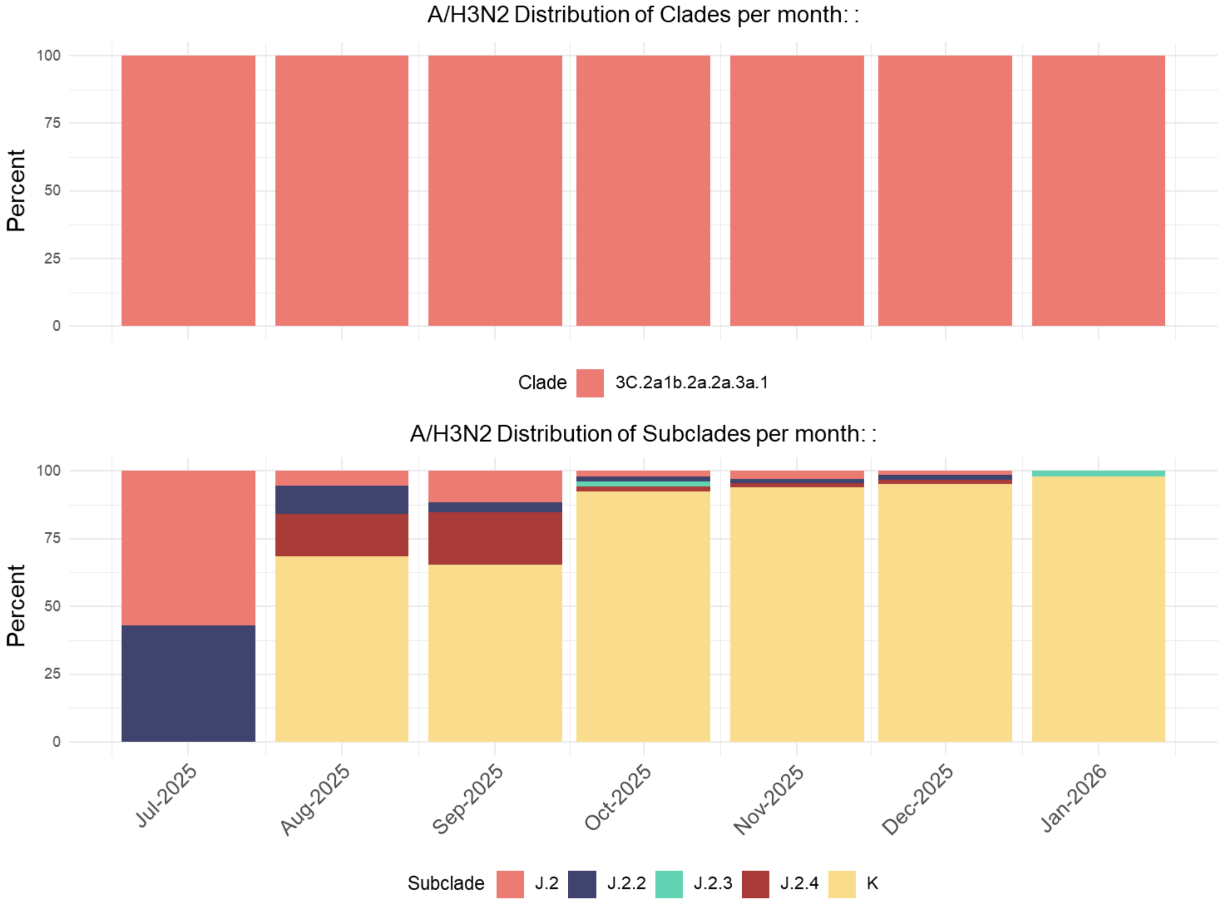


Figure 13 Clade (Upper) and subclade (Lower) distribution of H3N2 viruses in Norway for Season 2025/2026

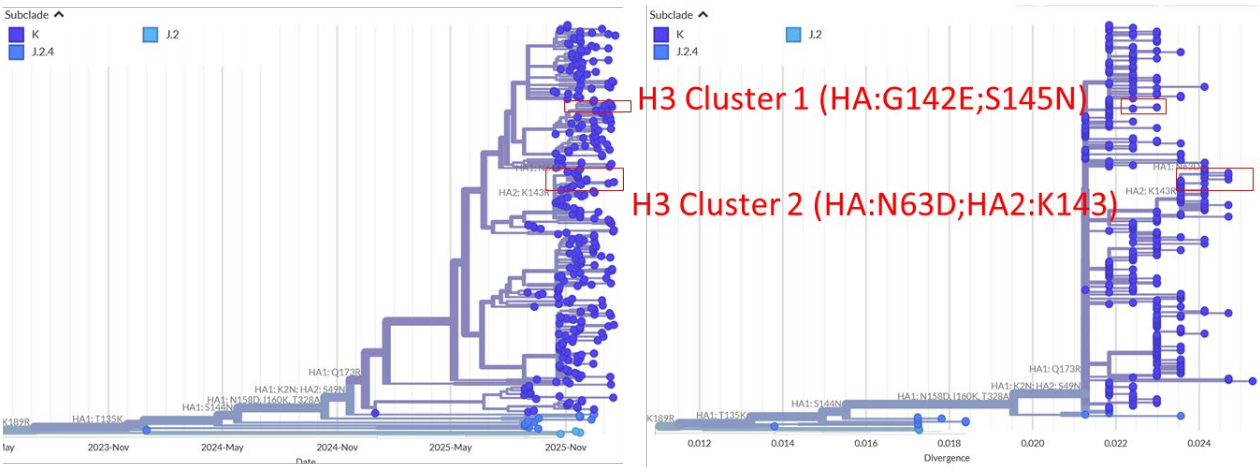


Figure 14 Clade 2a.3a.1, NextStrain phylogenetic tree of the haemagglutinin of the H3N2 viruses from Norway from week 35 2025 until week 4 2026, compared to the reference sequences for season 2025/26 provided by the ECDC/WHO influenza characterization guidelines. Colours represent subclades; branches are labelled with amino acid substitutions. Left: On a time axis. Right: On a divergence axis. The full NextStrain tree is available here.

Cluster 1 HA:N63D;K143R

Figure 15 Clade 2a.3a.1, Subclade K H3 Cluster 1 NextStrain phylogenetic focus tree of the haemagglutinin of the H3N2 viruses from Norway from week 35 2025 until week 4 2026, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions tip labels refer to virus names. The full NextStrain tree is available here.

Cluster analysis: Two clusters of notes have recently been detected, the first (H3 Cluster 1) carries additional HA substitutions **G142E** and **E145N**. Only three viruses so far have been detected as recently as January 2026, in one state of Norway. However, these substitutions are close the receptor binding site and epitope A substitutions making them of particular interest (Figure 15).

The second cluster (H3 Cluster2) carries an additional HA: **N63D** and a HA2:**K143R** which leads to the loss of a glycosylation site (NCT -> DCT) at position 63. These viruses were last detected in December 2026 and were spread over 4 states in Norway (Figure).

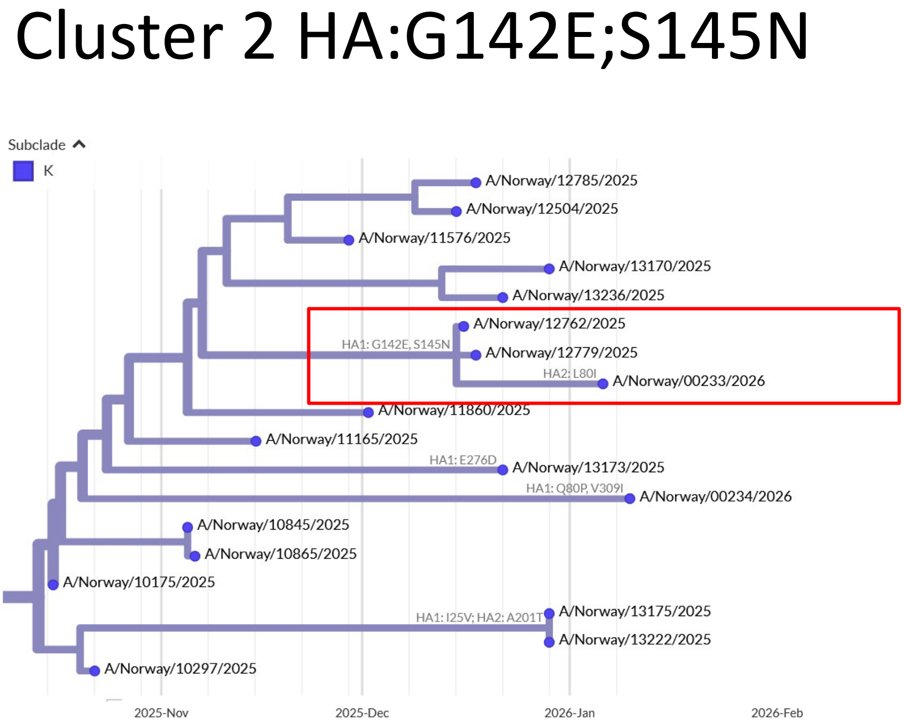


Figure 16 Clade 2a.3a.1, Subclade K H3 Cluster 2 NextStrain phylogenetic focus tree of the haemagglutinin of the H3N2 viruses from Norway from week 35 2025 until week 4 2026, on a time axis. Colours represent subclades; branches are labelled with amino acid substitutions tip labels refer to virus names. The full NextStrain tree is available here.

B/Victoria-lineage viruses

During the 2025/26 influenza season, only five **B/Victoria-lineage** viruses were sequenced in Norway. Of those, all belong to the V1A.3a.2 clade (5/5, 100%)(Figure 17, Table 3.).

Further Characterisation of these viruses show that four of those are classified as *genBVicB/Switzerland/329/2024 like* viruses and belong so subclade **C.5.6** (2/5, 40%) **C.5.6.1** (2/5, 40%). One virus is a *genBVicB/Catalonia/2279261NS/2023 like* virus belonging to subclade **C.5.1** and carries additional substitutions **HA:N126S, E128K, A202V** and **HA2:R151K.**

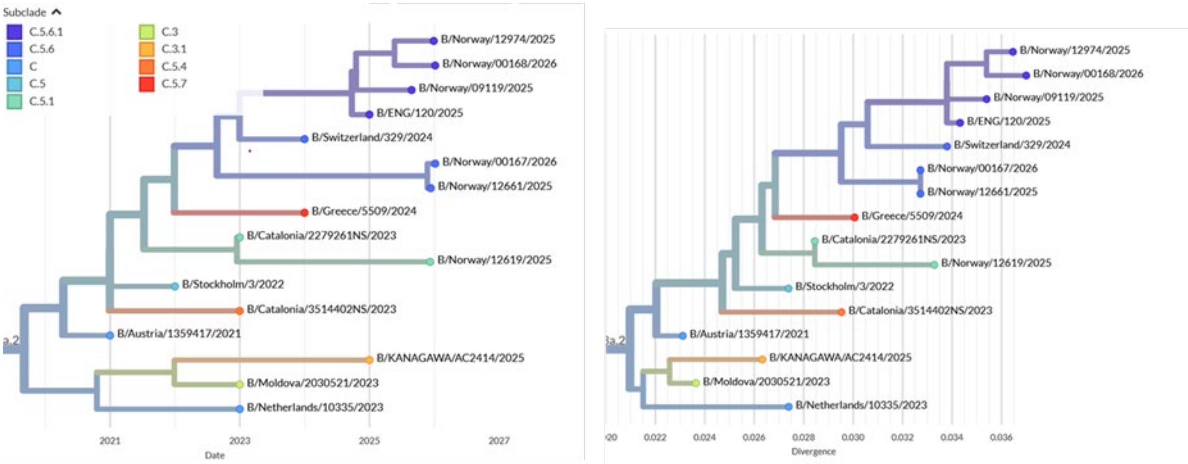


Figure 17 NextStrain phylogenetic tree of the haemagglutinin of the B-Victoria viruses from Norway from week 35 2025 until week 4 2026, compared to the reference sequences for season 2025/26 provided by the ECDC/WHO Influenza characterization guidelines. Colours represent subclades; branches are labelled with amino acid substitutions. Left: On a time axis. Right: On a divergence axis. The full NextStrain tree is available here

Table 3 Genetic classification of Influenza viruses 2025/26 Season in Norway

WHO/ECDC kategori	Clade	Subclade	aug.25	sep.25	okt.25	nov.25	des.25	jan.26	Total
A/H1N1	**-**	**-**	**10**	**45**	**44**	**72**	**11**	**21**	**203**
genAH1/Missouri/11/2025	6B.1A.5a.2a.1	D.3.1	2 (20%)	23 (51.1%)	11 (25%)	8 (11.1%)	3 (27.3%)	1 (4.8%)	48
genAH1/Missouri/11/2025	6B.1A.5a.2a.1	D.3.1.1	8 (80%)	22 (48.9%)	33 (75%)	64 (88.9%)	8 (72.7%)	20 (95.2%)	155
A/H3N2	**-**	**-**	**7**	**26**	**52**	**134**	**52**	**46**	**317**
genAH3/Croatia/10136RV/2023	3C.2a1b.2a.2a.3a.1	J.2	0 (0%)	3 (11.5%)	1 (1.9%)	4 (3%)	1 (1.9%)	0 (0%)	9
genAH3/Lisboa/216/2023	3C.2a1b.2a.2a.3a.1	J.2.2	0 (0%)	1 (3.8%)	1 (1.9%)	2 (1.5%)	0 (0%)	0 (0%)	4
genAH3/Netherlands/10685/2024	3C.2a1b.2a.2a.3a.1	J.2.3	0 (0%)	0 (0%)	1 (1.9%)	0 (0%)	0 (0%)	1 (2.2%)	2
genAH3/Singapore/GP20238/2024	3C.2a1b.2a.2a.3a.1	J.2.4	4 (57.1%)	5 (19.2%)	1 (1.9%)	2 (1.5%)	1 (1.9%)	0 (0%)	13
genAH3/Norway/8765/2025	3C.2a1b.2a.2a.3a.1	K	3 (42.9%)	17 (65.4%)	48 (92.3%)	126 (94%)	50 (96.2%)	45 (97.8%)	289
B/Victoria	**-**	**-**	**1**	**0**	**0**	**0**	**2**	**2**	**5**
genBVicB/Catalonia/2279261NS/2023	V1A.3a.2	C.5.1	0 (0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (50%)	0 (0%)	1
genBVicB/Switzerland/329/2024	V1A.3a.2	C.5.6.1	1 (100%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0%)	1 (50%)	2
genBVicB/Switzerland/329/2024	V1A.3a.2	C.5.6	0 (0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (50%)	1 (50%)	2

Surveillance of antiviral resistance in Influenza viruses

So far this season, 470 influenza viruses have been genetically analyzed for resistance mutations. One influenza A(H1N1) virus carried a genetic marker for resistance to oseltamivir and zanamivir with an I223R mutation in the neuraminidase gene. The sample was taken in week 38, 2025, and the patient's antiviral use is unknown. No viruses were resistant to baloxavir.

Nearly half of the H1N1 viruses in the latest sequencing batch showed the presence of the NA Y155H mutation, which, in pre-pandemic 2009 H1N1 influenza viruses, induced resistance to oseltamivir (Tamiflu®) and zanamivir. However, studies done on the H1N1pdm09 lineage in early years after the 2009 pandemic indicated that this mutation did not have the same effect on these viruses. Phenotypic resistance analyses are currently underway at the Norwegian Institute of Public Health (NIPH) to determine the clinical relevance of this mutation.

All circulating seasonal influenza A viruses have been resistant to adamantanes for many years. However, three H3N2 and one H1N1 have been found this season with no genetic markers of adamantane resistance. The H3N2s are all from the same doctor's office with sample dates in week 47/48 2025, suggesting a limited transmission chain with no recent detections. They are classified as J.2 with an additional HA: S145N. The H1N1 has a sample date of week 2 2026 and belongs to subclade D.3.1.1 with no additional HA substitutions.

Seroepidemiology:
Population immunity against recent influenza viruses, August 2025

In August each year, the National Influenza Seroepidemiology Programme solicits approximately 2000 anonymised residual sera from clinical/microbiological laboratories across Norway. The sera, aimed to be representative of the Norwegian population geographically and by age composition, are tested by the haemagglutination-inhibition assay (HAI) to determine the antibody immunity against relevant circulating influenza viruses. Analyses of a subset of 922 sera collected in August 2025 are presented here. The main findings are shown in Figure 18 in comparison to data from 2023 and 2024, in Table 4 for the last 5 years, and summarised as follows:

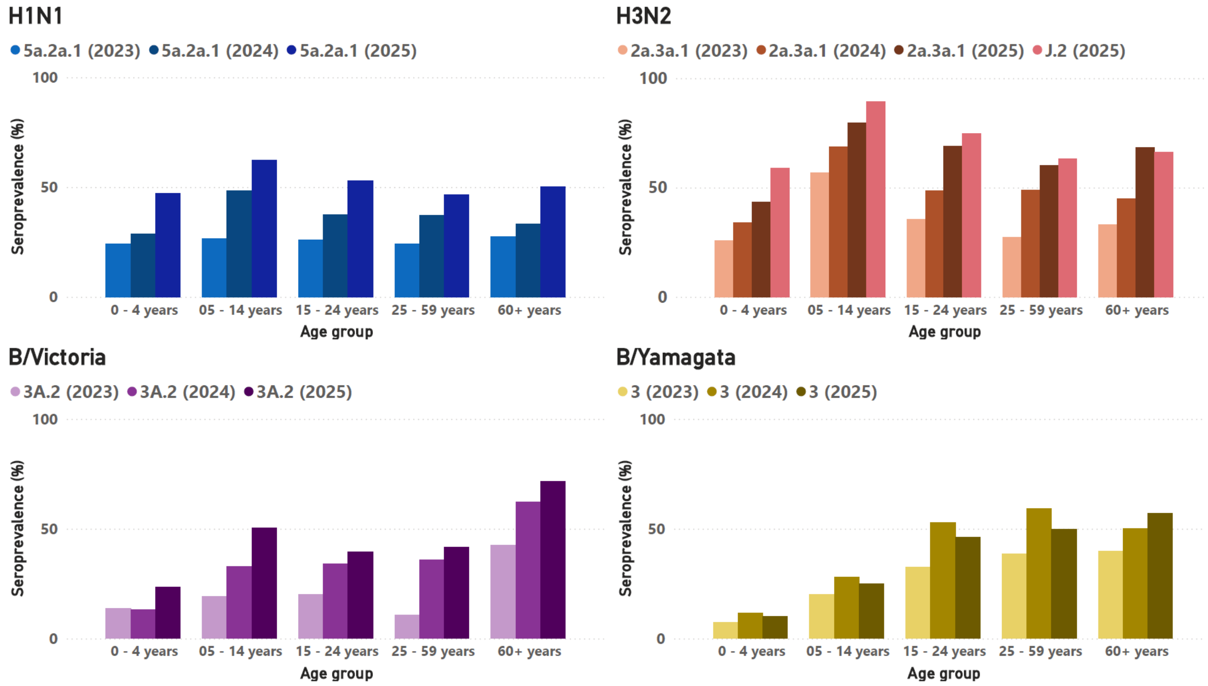


Figure 18. Seroprevalence in August 2023, 2024, and 2025 against current influenza A and B strains in various age groups. HAI was performed against A/Norway/31694/2022 (H1N1, clade 6B.1A.5a.2a.1), A/Thailand/8/2022 (H3N2, 3C.2a1b.2a.2a.3a.1), A/Croatia/10136RV/2023 (H3N2, 3C.2a1b.2a.2a.3a.1 (J.2 subclade)) B/Austria/1359417/2021 (Victoria lineage, V1A.3a.2) and B/Phuket/3073/2013 (Yamagata lineage). The year the sera was analysed is indicated in parenthesis behind the clade name. Protective HAI titres were defined as ≥40 for influenza A and ≥80 for ether treated influenza B.

Since 2023 there has been a gradual increase in protective HAI titres (here referred to as seroprevalence) against the H1N1 5a.2a.1 clade (A/Norway/31694/2022), likely reflecting extensive circulation of the clade during the 2023/24 and 2024/25 seasons. In August 2025, the seroprevalence in the 5 – 14 years age group was 62% against A/Norway/31694/2022, while the 0-4 years and the 25 – 59 years age groups had the lowest seroprevalence with 47%. For the other age groups (15-24 year and 60+ years), the seroprevalence was approx. 50%. The A/Victoria/4897/2022 strain (clade 5a.2a.1) was a part of the seasonal influenza vaccine for the Northern Hemisphere in 2023/2024 and may have contributed to the increased seroprevalence seen in the serum samples collected in August 2024 and 2025.

The seroprevalence against the H3N2 clade 2a.3a.1 (A/Thailand/8/2022) increased in all age groups from 2023 to 2024 and increased again from 2024 to 2025. In sera from 2025 the seroprevalence ranged from 44% in the 0-4 years age group, to 80% in the 5-14 years age group. Seroprevalence against the drifted J.2 subclade of 2a.3a.1 (represented by the A/Croatia/10136RV/2023 strain) was comparable to the seroprevalence against A/Thailand/872022 in the older age groups and even higher in the younger age groups. The A/Croatia/10136RV/2023 strain was first included in the egg-based influenza vaccine for the 2025/2026 influenza season.

With the emergence of the H3N2 K subclade in September 2025, additional analyses were performed to assess immunity in comparison to the ancestral J.2 subclade. Due to technical challenges with the K subclade in HAI assays, microneutralization assays (MNA) were performed on cell-grown A/Norway/8765/2025 (K subclade) in comparison to cell-grown A/District of Columbia/27/2023 (J.2 subclade). A subset of serum samples from different age groups was analysed. While the antibody titres were generally lower for cell-grown H3N2 strains compared to egg-grown strains in HAI, the level of neutralizing antibodies was largely similar between the K subclade and the J.2 subclade (Figure 19). The results indicate that the K subclade did not display a clear advantage in terms of immune evasion in any of the analysed age groups.

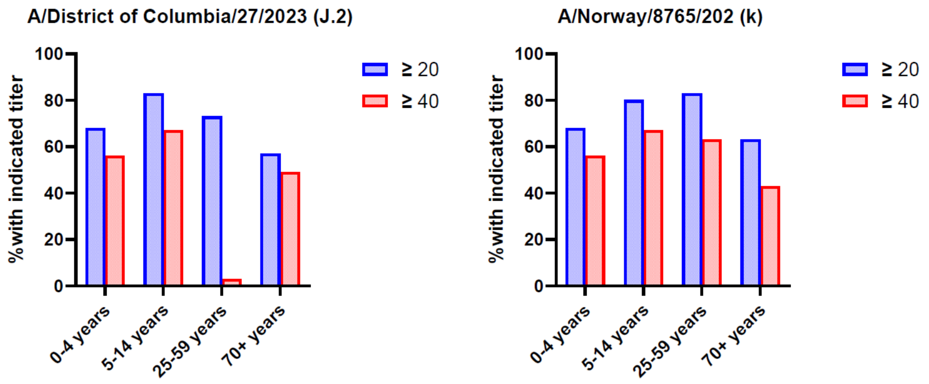


Figure 19. Neutralising antibodies against J.2 and K subclades in residual sera. A subset of residual serum samples from the age groups 0-4 years (25 samples), 5-14 years (30 samples), 25-59 years (30 samples) and 70+ years (35 samples) were analysed by microneutralisation assays against A/District of Columbia/27/2023 and A/Norway/8765/2025. The percentage of samples within each age group with end point titres equal to or above 20 or 40 is indicated in the graph.

The seroprevalence against contemporary B/Austria/1359417/2021 (Victoria lineage, clade 3a.2) increased in all age group from 2024 to 2025. The increase was most marked in the 5-14 years group, which typically has had the highest frequency of detections in the in-season surveillance. In the age groups 5-14, 15-24 and 25-59, seroprevalence in 2025 was 42 - 50%. The oldest age group had the highest seroprevalence of 72%, while the 0-4 years age group had the lowest seroprevalence of 24%. The seroprevalence likely reflects a combination of infection and that the B/Austria/1359417/2021 strain has been included in the seasonal influenza vaccine since the 2022/2023 season.

For the B/Phuket/3073/2013 strain (Yamagata lineage clade 3), the August 2025 seroprevalence was 46 – 57% in the age groups 15 – 24, 25 – 59 and 60+ years. In the youngest age groups, the seroprevalence was 10% (0-4 years) and 25% (5-14 years). The B/Yamagata lineage has not circulated in the population since 2020, although the B/Phuket/3073/2013 strain has been part of the tetravalent influenza vaccine since the 2015/16 season and until the 2024/25 season.

Table 4. Influenza seroepidemiology results in August 2025 – Seroprevalence* in age groups.

For comparison data from studies performed for the preceding years 2021-2024 are also included. Due to the covid-19 pandemic, no HAI assays were performed in 2020.

Influenza strains (Year$^{\$}$)	**Age groups**						
	0-4	**5-14**	**15-24**	**0-24**	**25-59**	**60+**	**All ages**
H1 Victoria/2570/19 (2021)	8	37	47	36	22	20	27
H1 Victoria/2570/19 (2022)	4	34	42	32	36	42	35
H1 Victoria/2570/19 (2023)	16	62	60	52	49	53	51
H1 Norway/31694/22 (2023)**	24	27	26	26	24	27	26
H1 Norway/31694/22 (2024)**	29	48	38	40	37	33	38
H1 Norway/31694/22 (2025)*	***47***	***62***	***53***	***56***	***47***	***50***	***51***
H3 Cambodia/e0826360/20 (2021)	13	61	61	52	51	32	48
H3 Darwin/9/21 (2021)	20	39	18	28	18	20	23
H3 Darwin/9/21 (2022)	18	35	29	30	16	17	22
H3 Darwin/9/21 (2023)	27	59	36	45	25	32	35
H3 Thailand/8/22 (2023)	26	57	36	43	27	33	35
H3 Thailand/8/22 (2024)	34	69	49	53	49	45	50
H3 Thailand/8/22 (2025)	***44***	***80***	***69***	***68***	***60***	***68***	***65***
H3 Croatia/10136RV/23 (2025)*	***59***	***89***	***75***	***77***	***63***	***66***	***70***
B/Wash/02/19 (Vic-Δ3B) (2021)	6	4	5	5	12	13	10
B/Cote d'Ivoire/948/20 (Vic-Δ3B) (2021)	8	3	7	6	8	23	10
B/Austria/1359417/21 (Vic-Δ3B) (2022)**	0	2	10	5	7	26	10
B/Austria/1359417/21 (Vic-Δ3B) (2023)**	14	19	20	19	11	42	20
B/Austria/1359417/21 (Vic-Δ3B) (2024)**	13	33	34	29	36	62	38
B/Austria/1359417/21 (Vic-Δ3B) (2025)*	***24***	***50***	***39***	***41***	***42***	***72***	***47***
B/Yam Phuket/3073/13 (2021)**	0	20	27	19	28	18	22
B/Yam Phuket/3073/13 (2022)**	0	23	42	27	35	31	31
B/Yam Phuket/3073/13 (2023)**	7	20	32	22	39	40	32
B/Yam Phuket/3073/13 (2024)**	12	28	53	33	59	50	46
B/Yam Phuket/3073/13 (2025)*	***10***	***25***	***46***	***28***	***50***	***57***	***41***
Sera analysed (n): 2021 Aug	48	107	114	269	250	137	656
Sera analysed (n): 2022 Aug	90	210	204	504	455	238	1197
Sera analysed (n): 2023 Aug	108	225	213	546	462	252	1260
Sera analysed (n): 2024 Aug	114	205	189	508	412	226	1146
Sera analysed (n): 2025 Aug	***85***	***167***	***155***	***407***	***329***	***186***	***922***

$^{\$}$Year of serum collection and HI analysis.

*All entries are per cent of sera having HI titres ≥ 40 for the A strains and ≥ 80 for the ether-treated B strains.

**(Corresponding to) components of the Northern hemisphere influenza vaccine (trivalent/quadrivalent) for the season 2025-2026.

B/Yam: B/Yamagata/16/1988 lineage; **B/Vic**: B/Victoria/2/1987 lineage

Selected epidemiological surveillance data

Influenza-like illness (ILI) in primary health care

The proportion of ILI consultations began to rise gradually from week 46/2025, a few weeks earlier than in the preceding seasons. This season's epidemic threshold, defined by the Moving Epidemic Method (MEM), was crossed in week 48/2025 (Figure 23, Figure 24). Influenza activity peaked in week 1 when 2,4 % of the consultations were due to influenza-like illness, which indicates a medium intensity level according to the MEM-thresholds. The ILI indicator resided at this level for three weeks (Figure 24). After the peak, the proportion of ILI consultations had a sharp decrease, and at present this decrease continues. In week 4 1,2 % of the consultations were due to influenza like illness. This corresponds to low intensity level according to the ILI MEM-thresholds. Compared to previous seasons, the age group 0-4 had an earlier and higher intensity than usual, with a peak in week 51 when 3,8 % of the consultations in this age group were due to ILI.

When comparing the ILI proportion to proportion positive laboratory tests with influenza virus, this season's ILI crossed the outbreak threshold the same week as the crossing of the virological outbreak threshold (week 48 when proportion positive tests increase above 10 %).

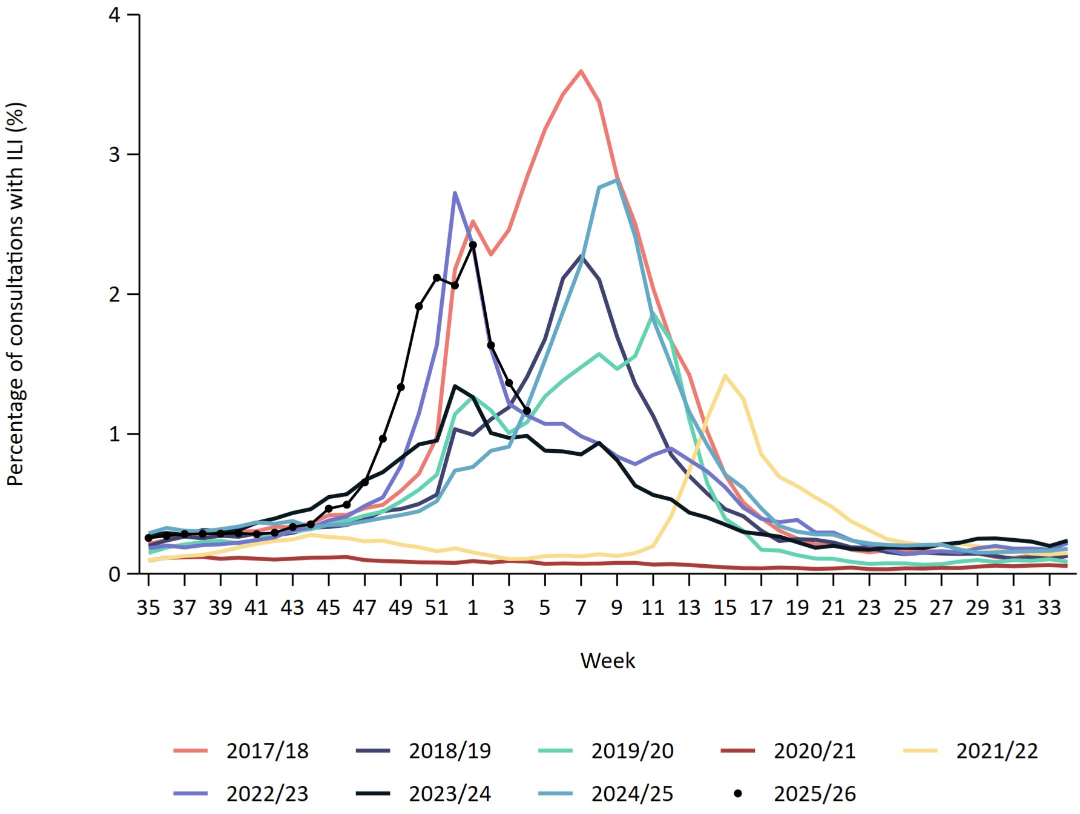


Figure 20. Weekly proportion of consultations for ILI, Norway 2025-2026 season (black dotted line). The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week, including the seven previous seasons for comparison. Source: NorSyss with data from KUHR, NIPH.

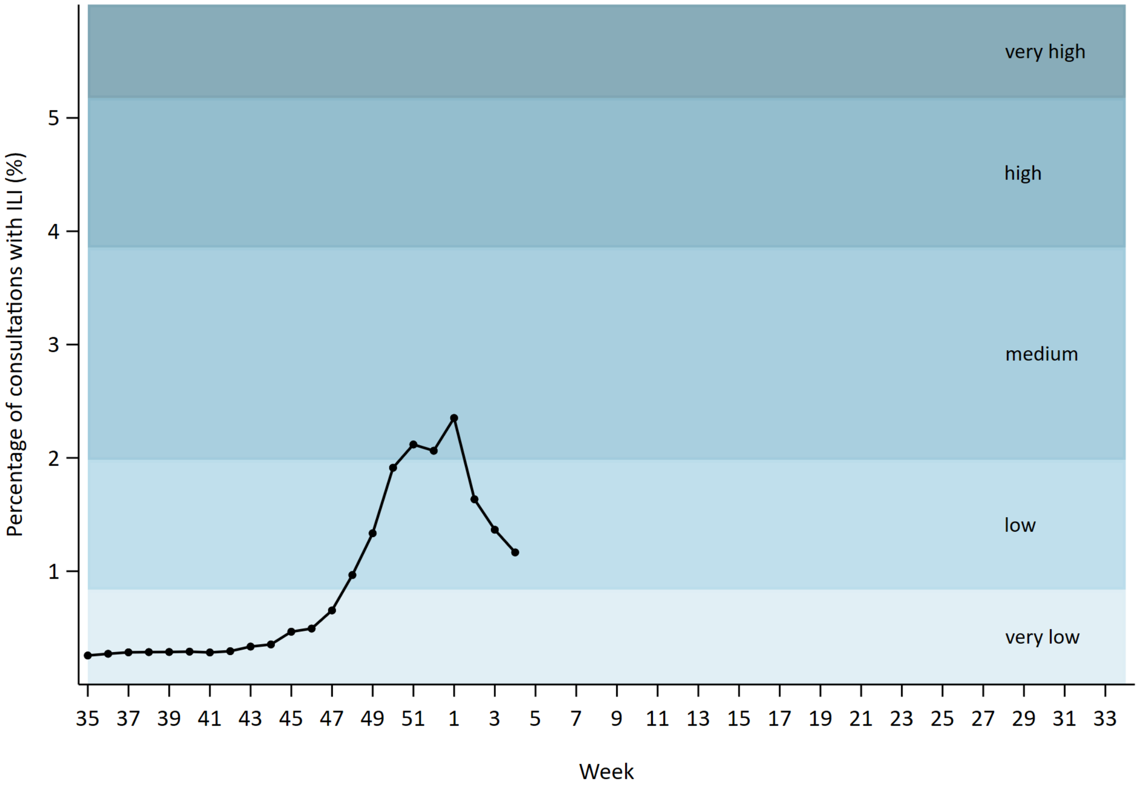
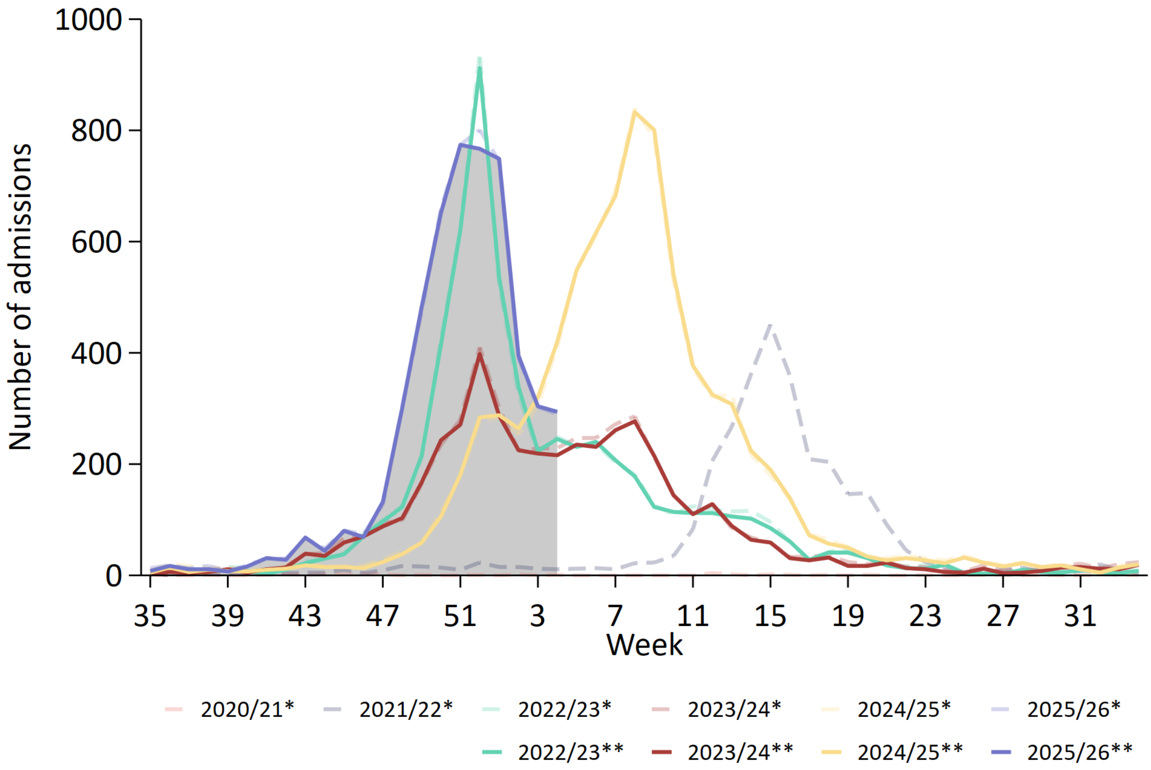


Figure 21. MEM intensity levels, Norway 2025-2026 season. The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week. Source: NorSySS with data from KUHR, NIPH.

Influenza hospitalisations

Between week 35/2025 and week 04/2026, 5,168 (92.4 per 100,000 inhabitants) new hospital admissions with influenza were reported, based on diagnosis code for acute respiratory infection and positive influenza test. The number of admissions peaked in week 2025-51, with 758 new admissions (Figure 22). The highest incidence was in the age groups 80+ years followed by 65-79 years and children <1 year (Table 5). The median age of patients was 62 years. The dominance of influenza A viruses was reflected in the admissions; with few patients testing positive for influenza B (Table 5). Information on typing was available for 98,4 % of the influenza positive hospital admitted patients.

This season, there was an early increase in admissions with influenza, reflecting the early start of the outbreak. (Figure 22). The cumulative number of admissions with influenza so far this season suggests that the current influenza epidemic may result in a larger burden of severe disease than the 2022-23 and 2023-24 seasons, but likely smaller than the 2024-25 season Figure 23.



*Dashed line: admissons with a diagnostic code for influenza in the Norwegian Patient Registry
**Solid line: admissions with laboratory-confirmed influenza and diagnostic code for acute respiratory infection

Figure 22. Number of hospital admissions with influenza by week and season, Norway, 24.08.2020 - 25.01.2026 Source: The Norwegian Surveillance System for Communicable Diseases laboratory database and the Norwegian Patient Registry via Stat19.

Table 5. Number of hospital admissions with influenza and influenza A and B viruses during the 2025 -2026 season by age group, Norway, 25.08.2025 – 25.01.2026. Source: The Norwegian Surveillance System form Communicable Diseases laboratory database via Stat19

	2025-W35 – 2026-W04					
	Total		Influenza A virus		Influenza B virus	
Age group	**Number of samples**	**Samples per 100000**	**Number of samples**	**Samples per 100000**	**Number of samples**	**Samples per 100000**
0 years	112	206.8	112	206.8	0	0.0
1-4 years	219	99.2	219	99.2	0	0.0
5-14 years	187	29.8	186	29.6	1-4	-
15-29 years	282	27.0	276	26.4	1-4	-
30-64 years	1031	39.8	1013	39.1	1-4	-
65-79 years	1860	235.5	1815	229.8	1-4	-
80+ years	1477	546.0	1454	537.4	1-4	-
Total	5168	92.4	5075	90.7	8	0.1

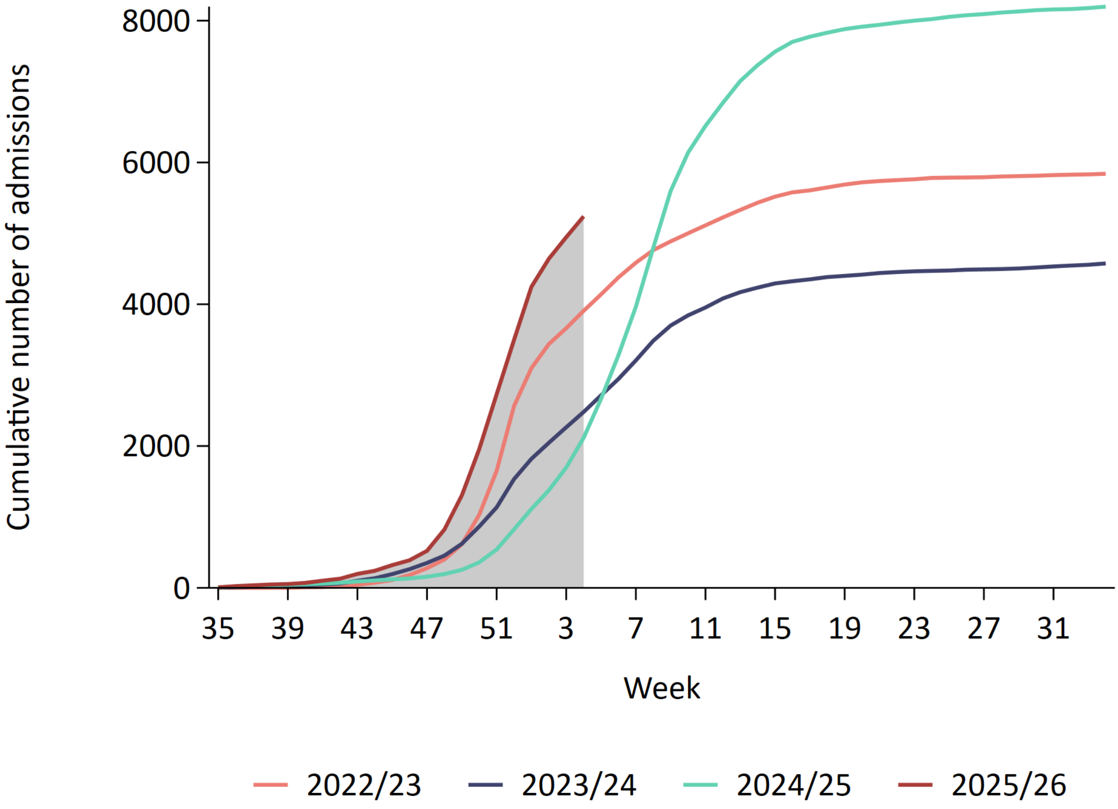
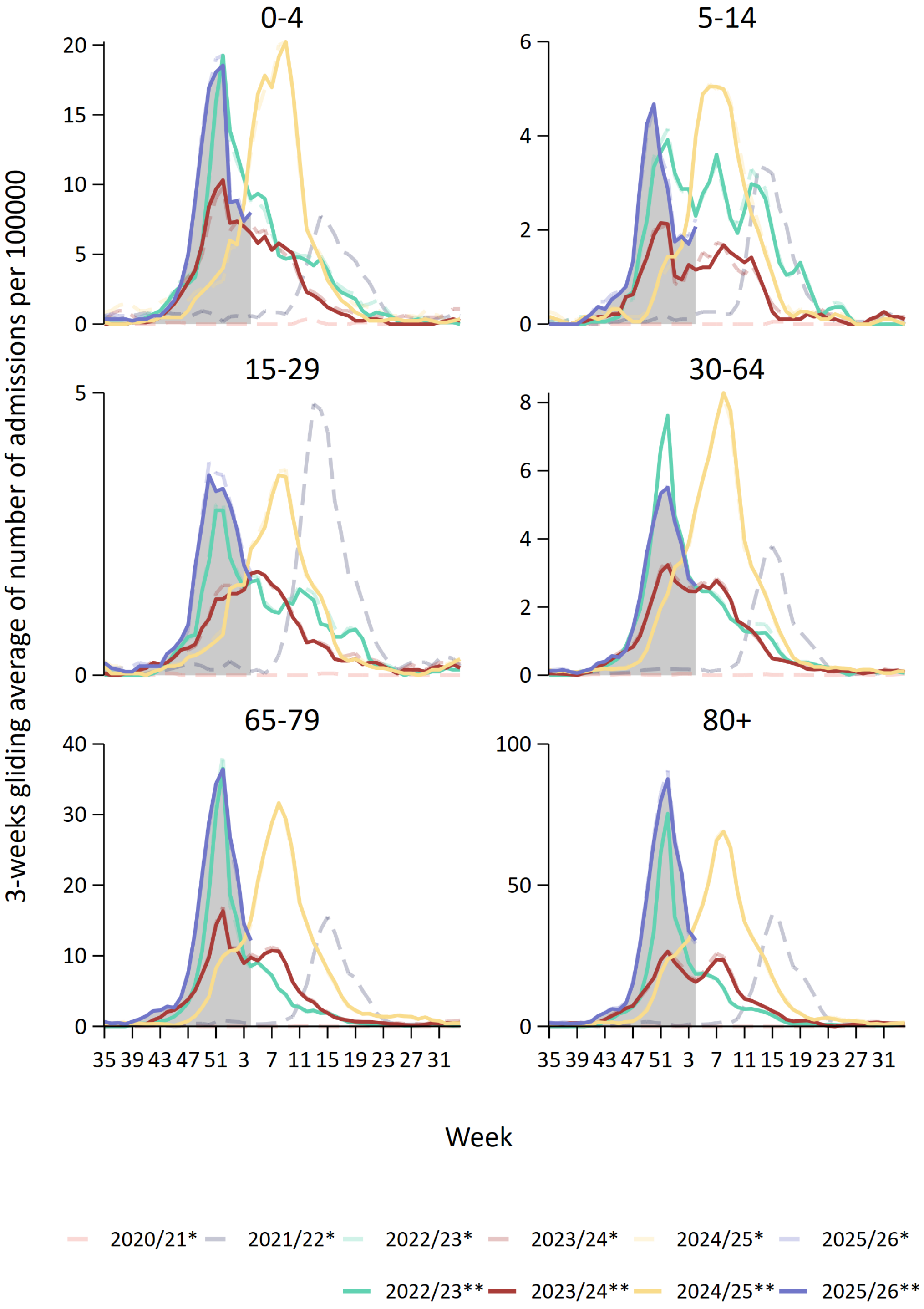


Figure 23. Cumulative number of hospital admissions with influenza per week and season, 24.8.2020 - 25.1.2026. Source: The Norwegian Surveillance System for Communicable Diseases laboratory database and the Norwegian Patient Registry via Stat19.



NB! The y-axis is different for each age group
*Dashed line: admissons with a diagnostic code for influenza in the Norwegian Patient Registry
**Solid line: admissions with laboratory-confirmed influenza
and diagnostic code for acute respiratory infection

Figure 24. Number of new hospital admissions with influenza by week and season, Norway, 24.08.2020 - 25.01.2026. Source: The Norwegian Surveillance System for Communicable Diseases laboratory database and the Norwegian Patient Registry via Stat19

Influenza patients in intensive care units (ICUs)

Between week 40/2025 and week 05/2026, a total of 194 ICU admissions (3.5 per 100,000 inhabitants) with influenza were reported. The median age of the patients was 69 (lower – upper quartile 55–78) years. The median length of stay was 3 days (lower – upper quartile 2–5 days). Fifty-nine percent of the patients received ventilatory support, and 9% died.

In comparison, 101, 127, 145, <5, 59 and 103 ICU admissions with influenza were reported in Norway during the same time period in the 2024-25, 2023-24, 2022-23, 2021-22, 2019-20 and 2018-19 seasons, respectively. On the other hand, 266, 205, 138, 63, 116 and 210 ICU admissions with influenza were reported in Norway from week 40 and up to six weeks after the peak of the influenza epidemic in the 2024-25, 2023-24, 2022-23, 2021-22, 2019-20 and 2018-19 seasons, respectively. This suggests that the current influenza epidemic appears to be one in the more severe spectrum of the past six seasons (the 2020-21 season omitted as there was no outbreak that season).

Influenza-associated deaths

Influenza-associated deaths were counted as any death with ICD-10 diagnosis codes J09-J11 stated as one of the causes of death on the death certificate. The total number of deaths caused by influenza is most likely underestimated by these estimates, since the influenza-specific ICD-codes are generally used when concurrent laboratory test results are also available, while testing for influenza in e.g. nursing homes is not comprehensive. On the other hand, testing and coding practices might have changed since the COVID-19 pandemic potentially resulting in increasing numbers for the most recent seasons.

Between week 35/2025 and 04/2026 there were 270 recorded influenza-associated deaths in Norway, compared to 80 (2024-25), 105 (2023-24), 176 (2022-23), 7 (2021-22), 41 (2019-20), 36 (2018-19), 120 (2017-18) and 178 (2016-17) for the same period in the preceding seasons (Figure 23, Figure 24). On the other hand, 308, 123, 189, 94, 116, 161, 371 and 194 influenza-associated deaths were reported from week 35 and up to 5 weeks after the peak of the influenza epidemic in seasons 2024-25, 2023-24, 2022-23, 2021-22, 2019-20, 2018-19, 2017-18 and 2016-17, respectively. The cumulative number of influenza-associated deaths reported so far in 2025-26 compared to previous seasons suggests that this will be one of the more severe seasons in Norway over the last decade.

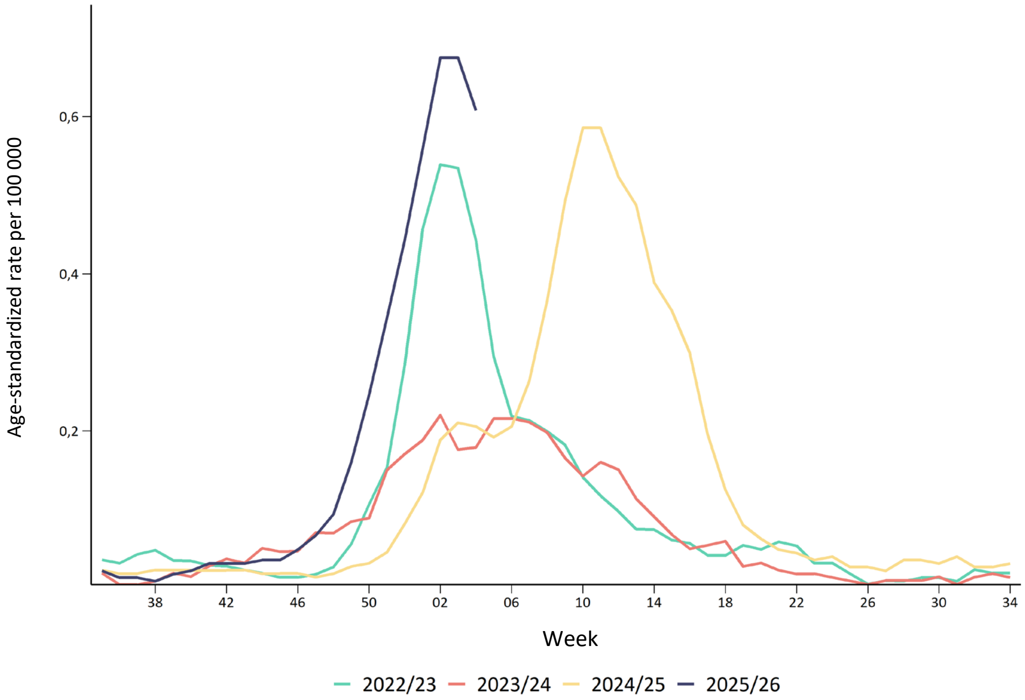


Figure 25. Age-standardized rate of influenza-associated deaths per 100 000 by week and season, Norway, 24.08.2020 - 25.01.2026. Source: The Norwegian Cause of Death Registry and the National Population Registry via Stat19.

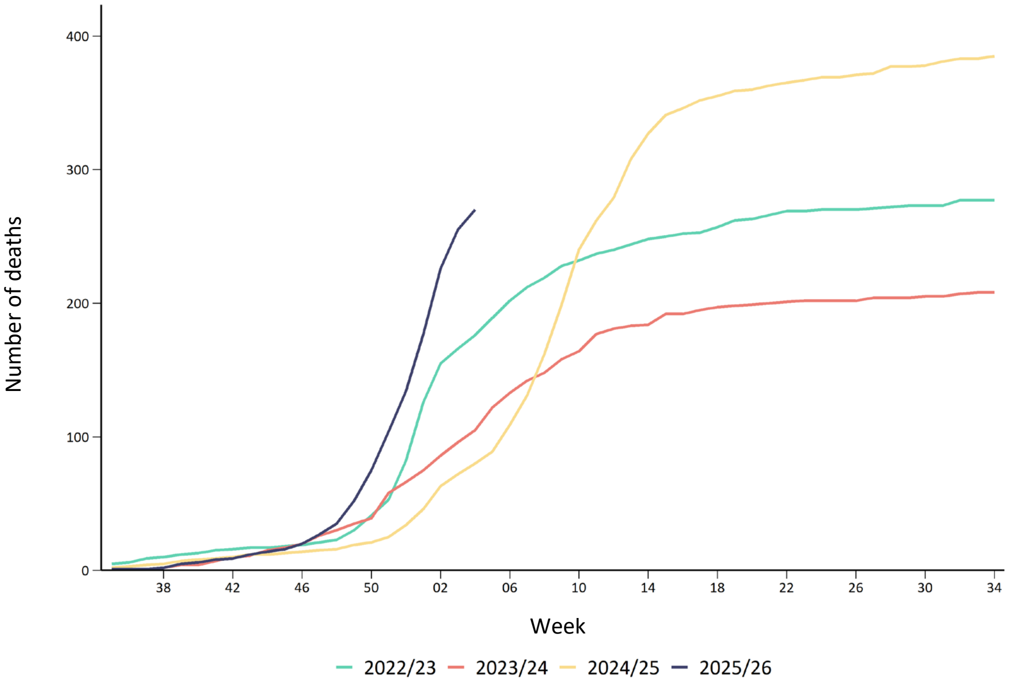


Figure 26. Cumulative number of influenza-associated deaths by week, Norway, 25.08.2025 - 25.01.2026. Source: The Norwegian Cause of Death Registry and the National Population Registry via Stat19.

Vaccine distribution and coverage

In the 2025/26 season as of 31st January 2026, a total of 1.71 million doses of influenza vaccine have been distributed, both from NIPH and from other wholesalers. 1.1 million of these were distributed by NIPH to the municipalities and hospitals specifically intended for persons in medical risk groups and health care workers (HCW) involved in direct patient care. The number of distributed doses has increased by 150 000 doses compared to the 2024/25 season, and the registered number of administered doses has increased by 200 000 doses (1.52 million doses) (Figure 27).

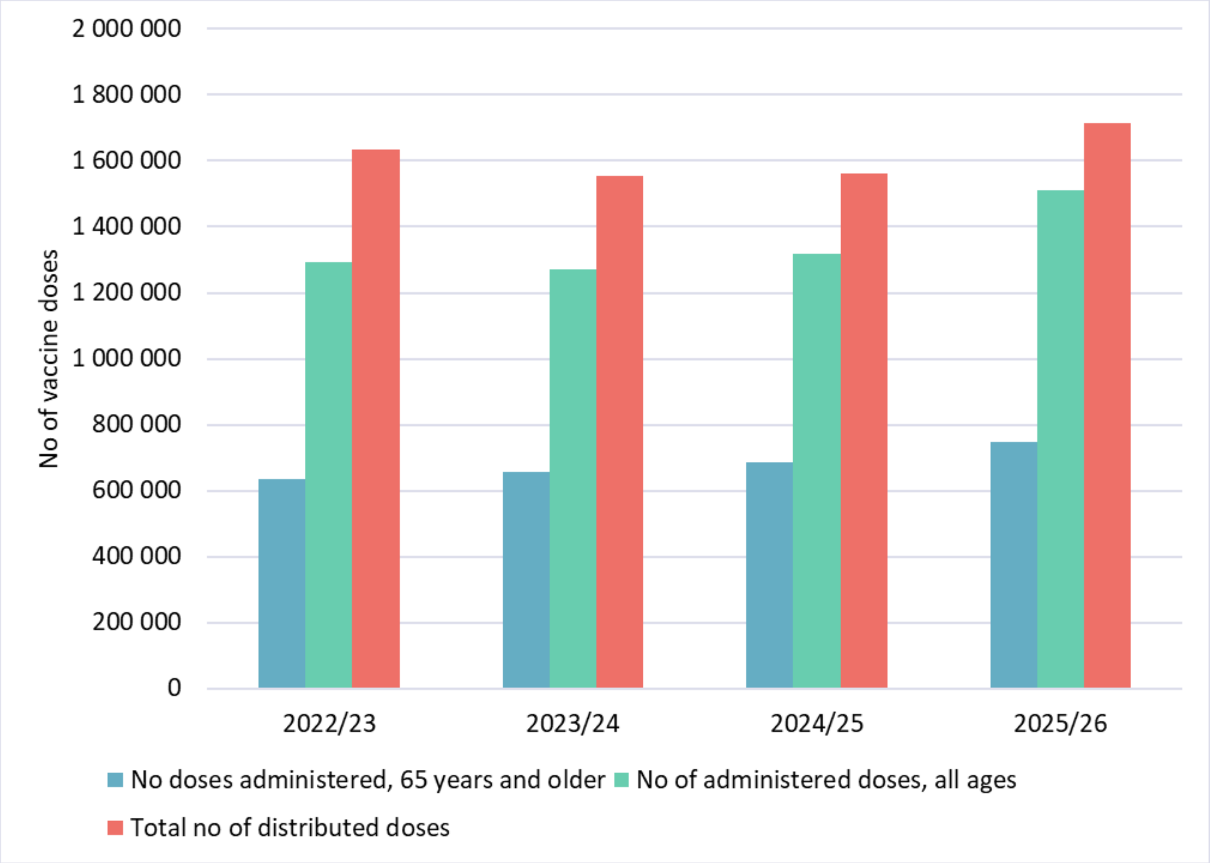


Figure 27. Influenza vaccine doses distributed in Norway and no of doses administered for all ages and for 65 years and older September 2022 through January 2026.

According to the Norwegian Immunization Registry SYSVAK (SYSVAK), at least 69 percent of the population above 65 years of age received an influenza vaccine this season (Figure 28).

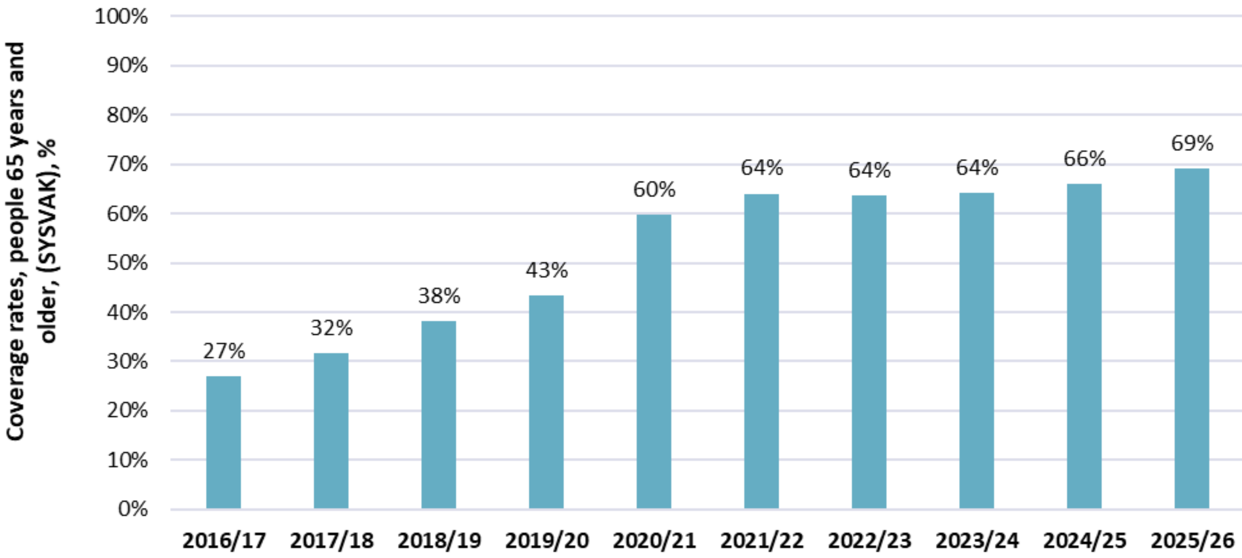


Figure 28. Vaccination coverage among the population above 65 years in Norway, 2016/17 season through to 2025/26 season as of February 2026.

Approximately 89% of the doses accounted for (distributed doses – reported discarded doses) are so far registered in SYSVAK 2025/26 season. This is probably due to a combination of underreporting and technical issues. Due to this, the vaccination coverage will also be estimated using survey data from Statistics Norway for the various risk groups and HCWs. However, these estimates will not be available until October 2026.

Vaccination timing

Vaccines for the influenza immunisation programme were sent out from week 40 to municipalities and health enterprises. Around the same time, vaccines also became available for the private market in pharmacies. Vaccination increased very rapidly to a peak of 303 000 vaccinations in week 43 and then gradually declined to a few thousand doses weekly from week 52 (Figure 29). 95% of those vaccinated received their vaccine within week 49, with expected protection within week 51, i.e. at the peak of the outbreak. 87% of the doses were administered before the epidemic threshold was passed in week 48.

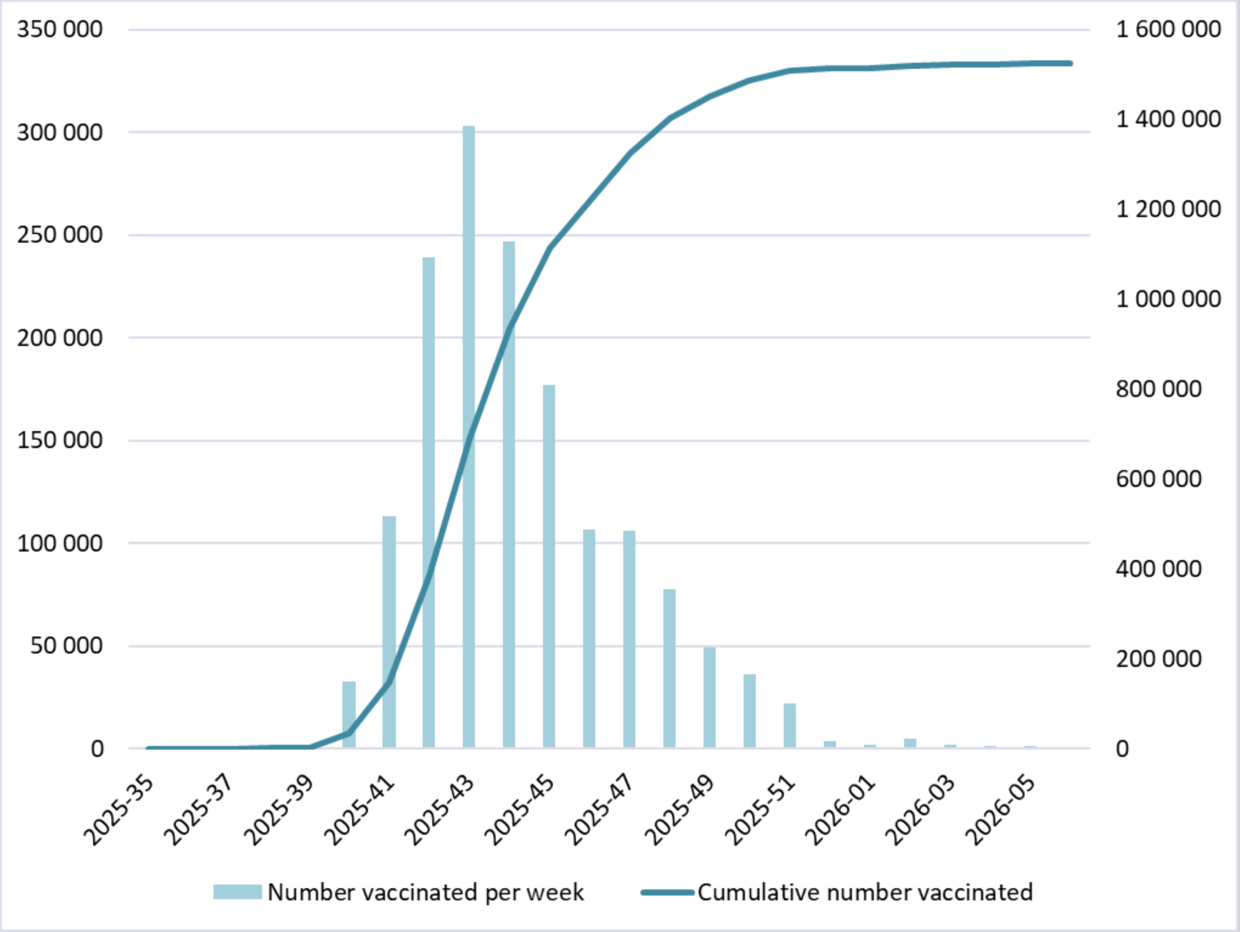


Figure 29. Number of vaccinated people per week and cumulatively in the 2025-26 season, 1. September 2025 – 8th of February 2026. Source: National Population Registry and Norwegian Immunization Registry, SYSVAK.

Animal influenza

A historically large epizootic of highly pathogenic avian influenza caused by H5Nx clade 2.3.4.4b virus is ongoing in wild and captive birds in Europe, Africa, Asia, the Americas, and the Antarctic region, with sporadic spillovers to mammals. In Norway, there have during the last year been numerous detections in wild birds but few poultry outbreaks. In the period until autumn 2025, genotype EA-2022-BB mainly circulating in marine birds in the north predominated, with one associated poultry outbreak. After this, genotype EA-2024-DI sublineage DI.2.x viruses in wild anseriform birds have caused widespread disease in southern Norway during autumn and early winter 2025/26. The Norwegian Veterinary Institute and the Norwegian Food Safety Authority are responsible for surveillance and outbreak management on the animal health side, while the NIPH contributes with public health assessments, advice and preparedness in a close OneHealth collaboration. A low number of exposed individuals subsequently developing symptoms have been tested, with no such virus detected. For more information, see status reports in Norwegian from the Norwegian Veterinary Institute (1, 2, 3), surveillance programme pages in English with annual reports: Wild birds https://www.vetinst.no/en/surveillance-programmes/avian-influenza-in-wild-birds ; Poultry https://www.vetinst.no/en/surveillance-programmes/avian-influenza-in-poultry) and joint avian influenza overview reports from EFSA, ECDC and EURL for avian influenza (4). The Veterinary Institute is routinely sharing avian influenza virus genome data in the publicly accessible GISAID EpiFlu database.

No cases of avian influenza have hitherto been detected in humans in Norway. The Norwegian Institute of Public Health has assessed the risk for human infection as very low for the general population, but increased awareness and precautionary infection control measures are recommended to prevent zoonotic infection (5).

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Previous **Norwegian reports prepared for the WHO vaccine consultation meeting:**

Available here: https://www.fhi.no/sv/influensa/influensaovervaking/who-rapporter/

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National Influenza Centre/Section of Influenza and other respiratory viruses

Section for Respiratory, Blood-borne and Sexually transmitted infections

Division for Infection Control

Norwegian Institute of Public Health,

Oslo, Norway, 15 February 2026

Appendices

Description of the surveillance and monitoring components

Influenza-like illness

Norwegian ILI surveillance data is provided by The Norwegian Syndromic Surveillance System (NorSySS), which receives data from the health finance administration (HELFO), governed by the Norwegian Directorate of Health. The data is based on ICPC-2 consultation codes for influenza on primary care physicians' reimbursement claims. NorSySS has been receiving ILI data since 2014 and is supported by retrospective data from the 2006-07 season and onwards.

Virological surveillance.

Sentinel virological surveillance: A geographically representative network of GPs contributes with clinical data and weekly samples for the integrated surveillance of respiratory viruses in Norway. The sentinel system has been reactivated after the COVID-19 pandemic and strengthened by including more GPs and engaging sentinel laboratories for some of the primary testing. At the same time, the scope of the surveillance was expanded to comprise several non-influenza respiratory viruses and the testing case definition expanded from ILI to ARI.

Comprehensive virus surveillance: In addition, medical microbiology laboratories that perform influenza diagnostics report testing data. Since 2020, all testing outcomes are reported in real-time to the national MSIS laboratory database. Surveillance statistics for laboratory confirmed influenza have been harvested from this database. These laboratories also contribute influenza positive specimens to the NIC for further characterisation. Even though most of these laboratories are affiliated to hospitals, a large proportion of specimens tested for influenza virus are from outpatients visiting general practitioners, and, during the COVID-19 pandemic, SARS-CoV-2 testing stations.

Virus characterisation: As many as possible of influenza virus positive sentinel specimens, and a selection of positive specimens from the comprehensive surveillance are subjected to whole genome sequencing (WGS) by Oxford Nanopore technology. Viruses are then selected for shipment to a WHO Collaborating Centre and/or isolated in the NIC, in order to ensure that all significant genetic variants are characterised antigenically. Viruses are also analysed with respect to antiviral resistance and other characteristics. Sequences are shared in the GISAID EpiFlu database.

All the virological surveillance data are shared internationally with ECDC and WHO Global Influenza Surveillance and Response System (GISRS).

Registry-based surveillance of influenza hospitalisations

During the autumn of 2024, the NIPH established a new data analysis platform called Stat19. In Stat19, the NIPH can link data from registries to produce relevant statistics for surveillance. Using Stat19 as the digital infrastructure, the NIPH established the SARI surveillance system, where hospital discharge codes are linked to data on PCR tests positive for influenza, which is obtained from the Norwegian Surveillance System for Communicable Diseases (MSIS) laboratory database. Case-based data on PCR-positive influenza tests is available from season 2022-2023 onward. A hospital admission with influenza is defined as SARI contacts registered as daytime treatment or admission (excluding polyclinical contacts), where the patient tested positive for influenza with a PCR test within 14 days before admission or during the hospital stay. All contacts regardless of type that occur with less than 2 days apart are defined as belonging to the same episode. The inclusion of influenza-positive patients without any diagnosis codes yet increases the timeliness of the data. The numbers presented in this report may, therefore, change as data becomes more complete.

Influenza patients in intensive care units

In the 2016-17 and 2017-18 seasons, the Norwegian Intensive Care Registry (NIR) and NIPH carried out a pilot study to see whether national surveillance of influenza patients in intensive care units is feasible. As part of the pilot, NIR asked all ICUs from week 46/2017 to report weekly numbers of patients in ICUs with laboratory-confirmed influenza, the number of patients in ICUs with clinically suspected influenza and the number of deaths among patients with confirmed or suspected influenza admitted to ICUs. Almost all ICUs in Norway reported data to NIR. Since the 2018-19 season, an electronic form has been used. Since the season 2024-25 the NIPH receives anonymized, aggregated data for surveillance purposes.

Influenza-associated deaths

Influenza-associated deaths were based on data from the Norwegian Cause of Death Registry, and were defined as deaths where J09, J10 or J11 (ICD-10) were recorded as an underlying or contributing cause of death on the death certificate.

Influenza seroepidemiology

In August each year the National Influenza Seroepidemiology Programme solicits about 2000 serum samples collected during the weeks 31-35 from clinical/microbiological laboratories covering the 15 counties of Norway. These anonymised convenience sera are aimed to be representative of the Norwegian population geographically and by age composition. Sera are tested by the haemagglutination-inhibition (HI) assays to determine the antibody immunity to relevant circulating influenza viruses. Due to capacity limitations imposed by the response to COVID-19 and subsequent austerity measures, the sera collected in 2020 were not tested for antibodies against influenza.

Vaccine distribution and coverage

Distribution data are reported by Department of Infection Control and Vaccine at NIPH and by IQVIA Solutions (distribution from other wholesalers). Vaccination coverage data are from the Norwegian immunisation registry SYSVAK. This electronic immunisation registry supplies national coverage estimates based on every individual’s vaccination status. It is mandatory to register all influenza vaccinations. However, in recent years the rate of registration has been around 84-88 of the doses distributed (adjusted for the number of discarded doses). Coverage estimates from SYSVAK are therefore considered minimum estimates.

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