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Influenza Virological and Epidemiological season report prepared for the WHO Consultation on the Composition of Influenza Virus Vaccines for the Southern Hemisphere 2027

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Spotlight: The epidemic came early where the A(H3N2) "K" drift variant got a head start

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. Designated subclade K, this new strain was associated with unusually early outbreaks in several countries, including Norway where it constituted nearly all H3N2 viruses after September. The emerging K variant's role as a driver of the early outbreak is supported by the observation that influenza did not peak early in parts of the country where subtype H1N1 and not H3N2 predominated in the early weeks. This is exemplified by Vestland county in Figure 1.

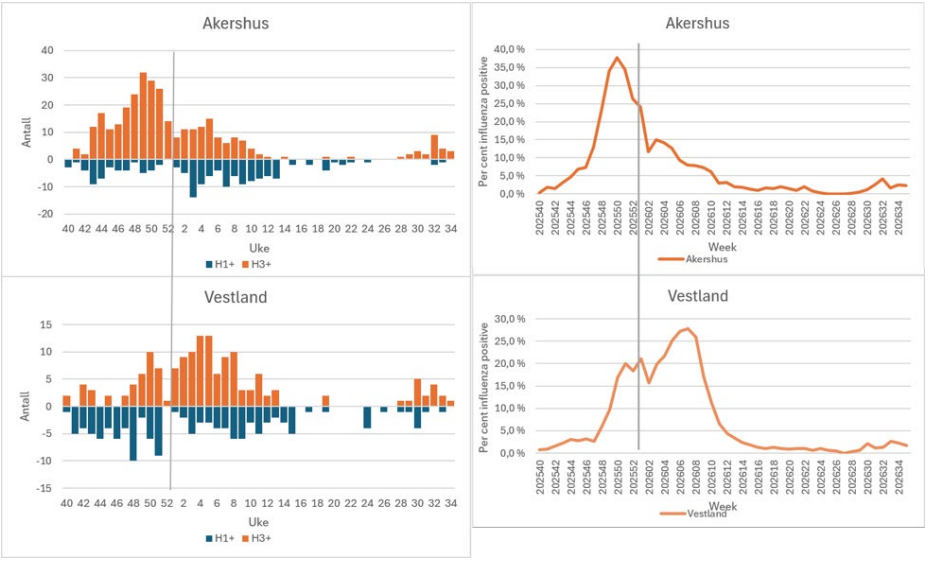

Figure 1. Left panel: Weekly numbers of influenza A subtype results for the counties Akershus and Vestland, from positive specimens received in the NIC. The numbers for H1 are plotted downward and are meant to be read as positive values. Right panel: weekly influenza positivity rates by all laboratories, on samples from the same counties. This graph is part of Figure 5 within this report.

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The 2025-2026 influenza season, Norway by week 34/2026

Summary

- Since week 35/2025, 28,918 infections with influenza A and a mere 768 with influenza B have been detected by Norwegian laboratories, out of nearly 340,000 patients tested. 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 predominated, particularly in the counties where influenza peaked early. Influenza positivity rate subsequently declined, stabilised at an intermediate level in January-February, and then fell to baseline levels by mid-April which is quite early. In late summer there has been a slight increase in type A detections, mostly H3N2.
- 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 67% of the influenza cases, followed by A(H1N1) at 30% and less than 3% 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 is relatively similar to previous seasons but with a less pronounced top in school-age children.
- In the 2025/26 season, 34% (916/2738) of influenza-positive samples received for surveillance were whole-genome sequenced. In addition, 110 viruses representing the genetic diversity observed during the season were shared with the WHO Collaborating Centre for further characterization. All A(H1N1) viruses belonged to clade 5a.2a.1. The predominant subclade shifted from D.3.1 before the season to D.3.1.1 during the season, and by the end of the season 85% of A(H1N1) viruses belonged to D.3.1.1. All A(H3N2) viruses belonged to clade 2a.3a.1, of which 93% were classified as subclade K, with only sporadic detections of J.2, J.2.2, J.2.3 and J.2.4. All B/Victoria viruses belonged to clade V1A.3a.2, with C.5.6 (33%) and C.5.1 (32%) being the most frequently detected subclades.
- 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 rise, peak and decline of influenza-like illness incidence was in good agreement with the virological influenza surveillance. Although consultations in primary care did not exceed moderate levels, several indicators suggest that this was one of the most severe influenza seasons in recent years, particularly for the oldest age groups. The season was characterized by a high number of reported outbreaks in healthcare institutions, substantial numbers of hospital and intensive care (ICU) admissions, and a high number of influenza-associated deaths, mainly among older adults.

- The vaccine coverage for the age group 65 years and older was 69% this season, 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. 170 000 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 circulate in wild birds in Norway, with one outbreak in commercial poultry in 2025. HPAIV H5N1 and H5N5 were both detected, with sporadic detections in wild mammals, including in the High Arctic. No human cases have been detected, and the general risk of human infection is assessed as very low.

Influensasesongen 2025-2026 i Norge (Norwegian summary)

Hovedbudskap

- Siden uke 35/2025 er det i Norge påvist 28 918 laboratoriebekreftede tilfeller av influensavirus A-infeksjon og 768 tilfeller med influensavirus B, blant nesten 340 000 testede pasienter. Laboratoriepåvist influensa begynte å øke tidlig, passerte utbruddsgrensen (10% positive av testede) i uke 48. Allerede i uke 50-52 ble utbruddstoppen passert i størsteparten av landet, med en toppnotering på 30 % influensapositive. 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. Forekomsten av influensapåvisninger gikk deretter ned til et middels nivå i januar-februar og falt deretter til basalnivå allerede i april. På sensommeren har det vært en svak oppgang i påvisninger, for det meste A(H3N2).
- 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 67 % av influensatilfellene, fulgt av A(H1N1) med 30 % og B/Victoria-linje med under 3 %.
- 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. I likhet med forrige sesong ser vi også nå at eldre er mindre overrepresentert i A(H3N2)-påvisning enn vi er vant til fra tidligere. Småbarn var også sterkere representert. For influensa B var aldersprofilen nokså lik tidligere sesonger, men toppen hos barn i skolealder var litt mindre uttalt.
- I løpet av sesongen har 34% (916/2 738) av mottatte influensapositive prøver blitt fullgenomsekvensert, og 110 virus som representerer alle påviste sekvensvarianter har blitt delt med WHO internasjonalt referanselaboratorium.
  Alle sekvenserte A(H1N1)-virus tilhørte klade 5a.2a.1. Mens subklade D.3.1 var vanligst i forkant av sesongen, ble subklade D.3.1.1 klart vanligst når sesongen kom i gang. For hele sesongen utgjør D.3.1.1 85 % av sekvenserte H1N1-virus.
  Alle A(H3N2)-virus var i klade 2a.3a.1. De aller fleste (93 %) har tilhørt den nye K-subkladen, med kun et fåtall virus subkladene J.2, J.2.2, J.2.3 og J.2.4. Alle sekvenserte influensa B-virus tilhørte B/Victoria-klade V1A.3a.2, de vanligste subkladene var C.5.6 (33 %) og C.5.1 (32 %).

- 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.
- Forekomsten av influensalignende sykdom (ILS) i primærhelsetjenesten utviklet seg i godt samsvar med den virologiske overvåkingen. Selv om andelen ILS-konsultasjoner aldri kom over moderat nivå, tilsier flere andre overvåkingsindikatorer at dette var en av de alvorligste influensasesongene i senere år, særlig hos eldre. Det var høyere antall varslede utbrudd i institusjoner, mange sykehus- og intensivinnleggelser, og relativt mange influensarelaterte dødsfall – hovedsakelig blant eldre.
- Vaksinasjonsdekningen blant personer over 65 år var 69 % denne sesongen. Det har blitt distribuert omtrent 1,7 millioner doser vaksiner totalt. Dette er noe mer enn forrige sesong (ca. 170 000 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 sirkulere hos ville fugler i Norge, med ett utbrudd i kommersielt fjørfehold i 2025. Både HPAI H5N1 og H5N5 ble påvist, med sporadiske funn i ville pattedyr, inkludert i Arktis. 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 2024/2025 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 A(H5N5) in a poultry backyard flock in November 2024. No human cases were detected.

The 2025/2026 season, weeks 35/2025 through 34/2026

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

Virological surveillance data

Laboratory confirmed influenza: Virological surveillance

Altogether, nearly 340,000 patients in Norway have been tested for influenza during weeks 35/2025 – 34/2026, resulting in 29,203 recorded detections of influenza A virus (97 % of the influenza detections) and a mere 799 influenza B virus (3 % of influenza detections) (Figure 2, Table 1).

From these patients, 2,505 influenza A and 233 influenza B positive specimens have been referred by testing laboratories to the NIC for further identification and characterisation. Among these, 2,455 type A viruses have so far been subtyped; 937 H1(38 %) and 1,518 H3 (62 %). Of the remaining 50 type A-positive specimens received that have not been subtyped, 1 was confirmed as influenza A virus but too weak for successful subtyping, 16 could not be confirmed as influenza A in the NIC (four were SARS-CoV-2 positive and probably erroneously declared) and the remainder were not yet tested for subtype.
Out of the 233 referred specimens with an initial influenza B positive result, 221 were confirmed as belonging to the B/Victoria/2/1987 lineage. Five initially influenza B positive specimens could not be verified in the NIC, four were confirmed as influenza B but too weak for successful lineage typing, and three had not yet been tested by the time of the data snapshot.

In addition to this, primary testing laboratories have identified 1,587 type A viruses as H1 and 172 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% 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 stabilised at a level around 16-17 % positivity rate in weeks 2 – 8. After this, there was a relatively rapid decline that came down to baseline levels already around week 16, which is earlier than usual.
Looking aside 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; that outbreak, driven by the significantly drifted A/Fujian/411/2002(H3N2) strain, peaked in week 49/2003.

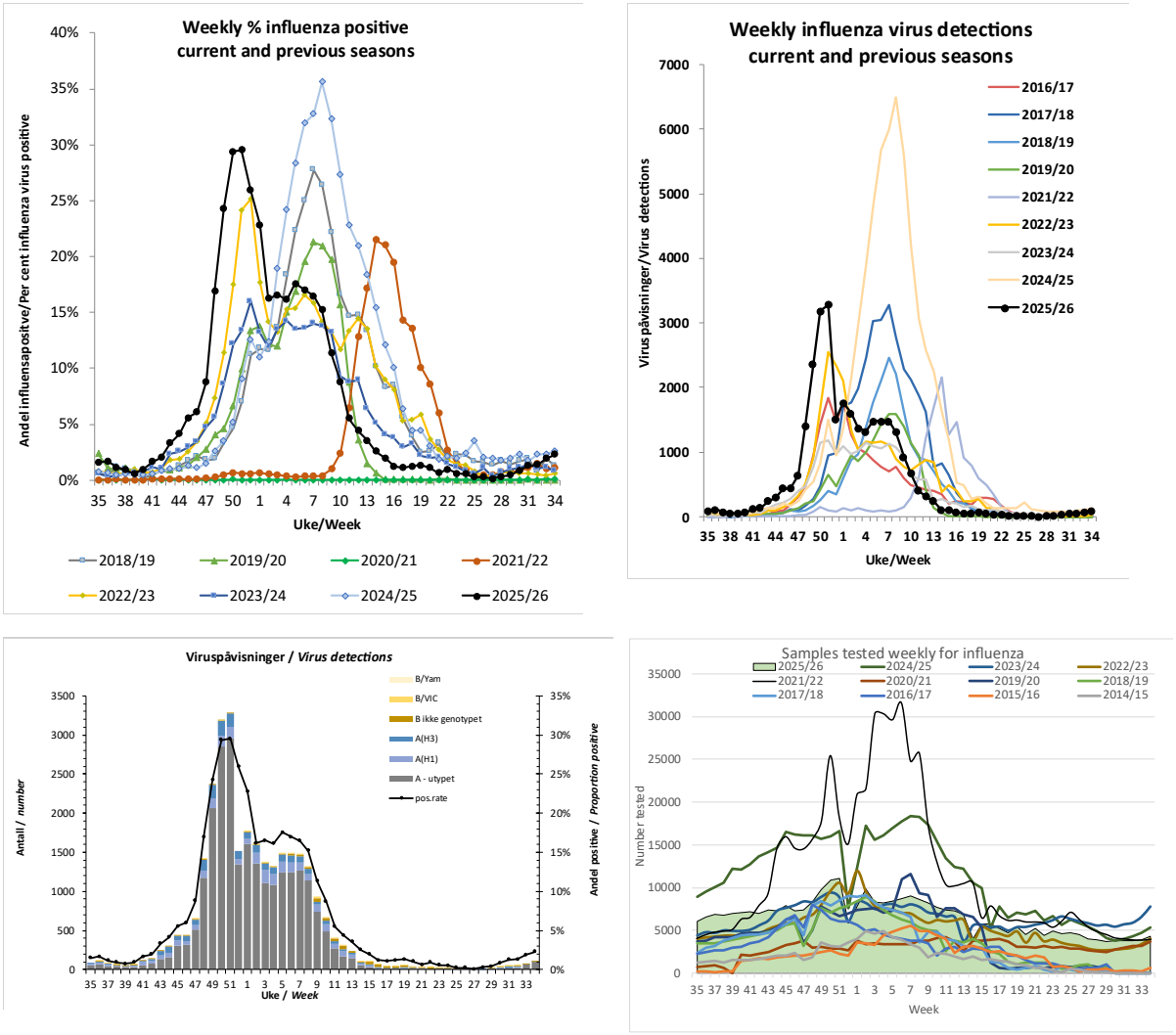

Figure 2. Laboratory detections, Norway 2025-2026. Upper left-hand panel: Weekly proportion of influenza virus positive tested patients, with previous season proportions shown for comparison. Upper right-hand panel: Weekly number of influenza virus detections, with previous season numbers shown for comparison. 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 3, Figure 5). 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 when more than 80% was H3N2, the proportion of H3N2 declined and among the few type A viruses circulating in spring and until midsummer, H1N1 was in majority. When sporadic cased started to increase again in late summer, H3N2 viruses again have been the most common (Figure 3). In Western Norway, where the proportion of A(H3N2) viruses was initially lower, there was no pronounced pre-New Year peak (Figure *6*). 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 5). 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.

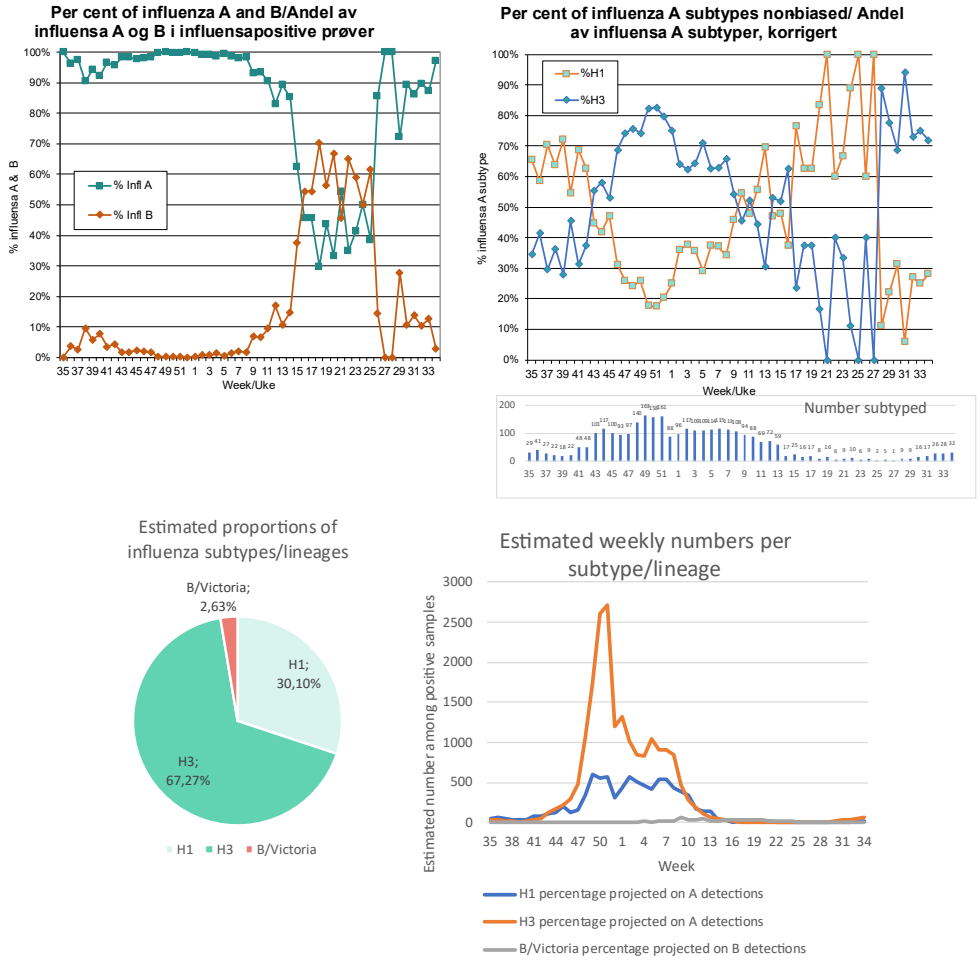

Figure 3. Influenza virus detections since week 35/2025, proportions per type A and B (upper left panel) and influenza A subtypes H1 and H3 (upper right panel). Only viruses tested for both subtypes are counted in the subtype analysis. Bars below show weekly number of subtyped samples.
The lower left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

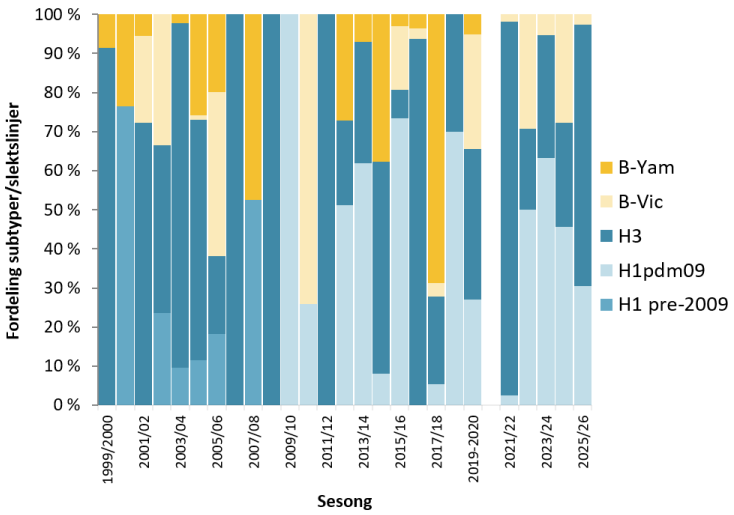

Figure 4. Historical influenza A subtype and B lineage proportions, 1999-2026

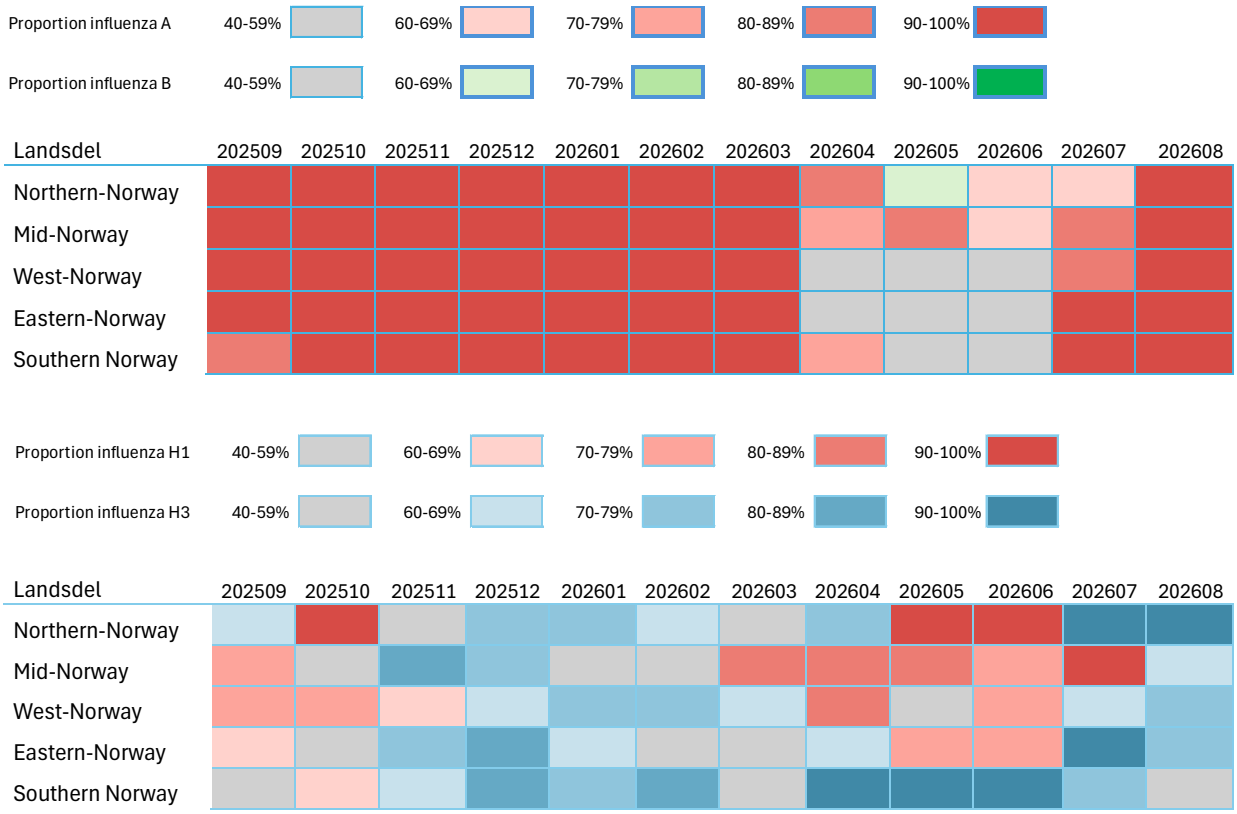

Figure 5. Monthly proportions of influenza virus detections since September 2025, type (top panel) and subtype (bottom panel) proportions per geographic region. Only viruses tested for both subtypes are counted in the subtype analysis.

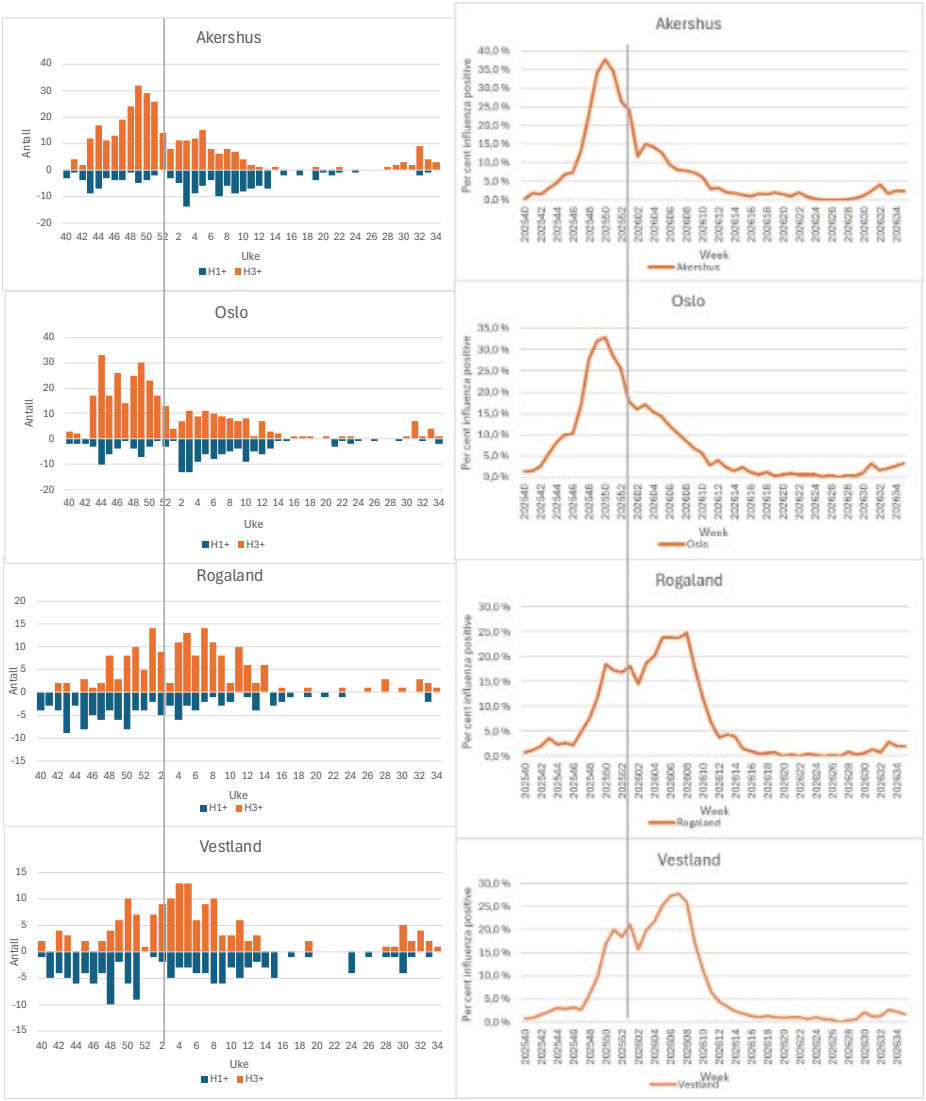

Figure 6. Left panel: Weekly numbers of influenza A subtype results for selected Norwegian counties, from positive specimens received in the NIC. The numbers for H1 are plotted downward and are meant to be read as positive values. Right panel: weekly influenza positivity rates by all laboratories, on samples from the same counties.

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 7.

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, including those under 80 years, is a relatively novel development, and the incidence in infants is less elevated than in the seasons 2017 – 2020 and in 2022.

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 30-64-year-olds being slightly below the all-ages average. 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 has been low this season. The age pattern may seem to differ slightly from previous seasons. School-age children are still the most likely to be influenza B/Victoria-lineage positive, but the over-representation is now less pronounced. The elderly have been strongly under-represented the last few seasons.

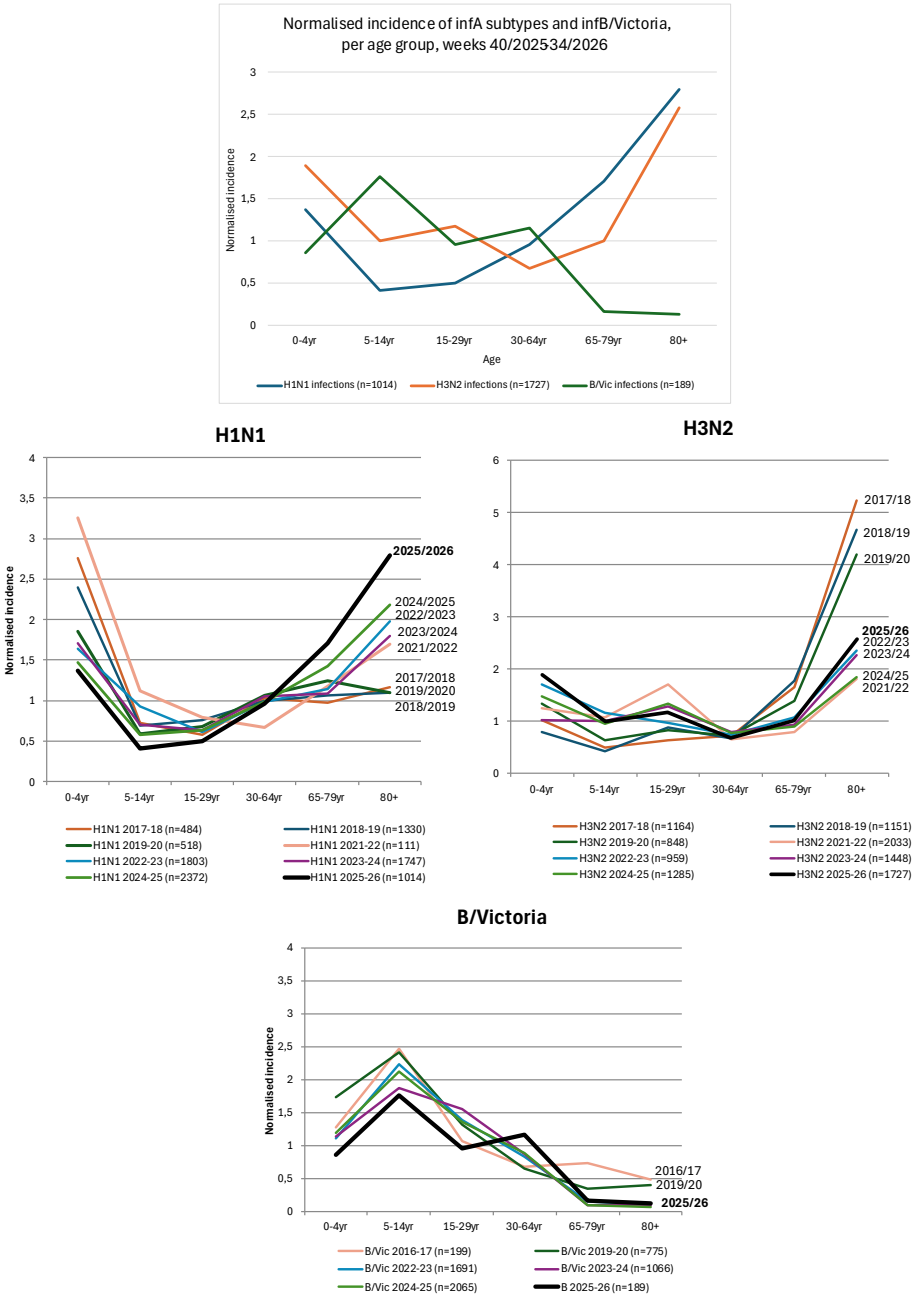

Figure 7. Age profiles of influenza viruses in the 2025/2026 influenza season up to week 34/2026. The score for each age group is the frequency of detections per age group population size, normalised against the combined frequency for all ages (=1). An age group with a score of 2 means that members of 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 35/2025through week 34/2026 (sentinel and non-sentinel data combined). Numbers provided here for A(H1) and A(H3) are limited to viruses tested for both subtypes.

	Viruspåvisninger/*Virus detections*							
UKE/ *week*	Prøver/ *Specimens*	% positive	A *not subtyped*	A(H1)	A(H3)	B *not lineage typed*	B/ Victoria lineage	B/ Yamagata lineage
35	6077	1,5 %	63	19	10	0	0	0
36	6582	1,7 %	64	24	17	3	1	0
37	6909	1,1 %	50	19	8	1	1	0
38	6813	0,9 %	35	14	8	4	2	0
39	6944	0,7 %	31	13	5	3	0	0
40	7047	0,9 %	38	12	10	4	1	0
41	7219	1,6 %	66	33	15	4	0	0
42	7003	2,0 %	85	30	18	6	0	0
43	7391	3,3 %	139	45	56	4	0	0
44	7323	4,1 %	179	49	68	5	0	0
45	7915	5,5 %	328	47	53	10	0	0
46	7267	6,0 %	336	29	64	9	0	0
47	7370	8,8 %	542	25	72	9	1	0
48	8356	16,9 %	1267	34	106	3	1	0
49	9711	24,3 %	2194	42	121	2	0	0
50	10862	29,4 %	3021	28	130	7	2	0
51	11123	29,6 %	3127	28	133	4	0	0
52	5837	25,9 %	1425	18	70	0	0	0
1	7752	22,9 %	1670	24	72	5	1	0
2	9900	16,2 %	1475	42	75	9	2	0
3	8294	16,5 %	1253	41	68	5	5	0
4	8227	16,1 %	1200	39	70	10	8	0
5	8444	17,6 %	1359	33	81	5	4	0
6	8728	17,0 %	1346	43	72	16	6	0
7	8990	16,5 %	1336	42	71	23	7	0
8	8633	15,2 %	1183	37	71	17	4	0
9	8237	11,3 %	773	43	51	44	19	0
10	7666	8,8 %	538	48	40	33	12	0
11	7363	5,5 %	296	33	36	28	10	0
12	7258	4,4 %	194	40	32	39	15	0
13	6891	3,5 %	158	41	18	26	0	0
14	3995	2,6 %	70	8	9	14	1	0
15	5735	1,9 %	43	12	13	30	11	0
16	5748	1,2 %	15	6	10	30	7	0
17	5267	1,1 %	9	13	4	22	9	0
18	4752	1,2 %	9	5	3	27	13	0
19	5461	1,3 %	15	10	6	27	13	0
20	4563	1,1 %	10	5	1	21	11	0
21	5275	0,7 %	10	9	0	13	3	0
22	4404	0,9 %	4	6	4	13	13	0
23	4886	0,7 %	8	4	2	13	7	0
24	4644	0,6 %	6	8	1	8	7	0
25	4693	0,3 %	3	2	0	7	1	0
26	4522	0,3 %	7	3	2	2	0	0
27	4028	0,10 %	3	1	0	0	0	0
28	3889	0,3 %	4	1	8	0	0	0
29	3736	0,5 %	4	2	7	4	1	0
30	3762	1,0 %	18	5	11	3	1	0
31	3819	1,3 %	27	1	16	6	1	0
32	3839	1,5 %	26	7	19	5	1	0
33	3915	2,2 %	48	7	21	8	3	0
34	4364	2,5 %	73	9	23	3	0	0
Total	339429		26183	1139	1881	594	205	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: 29203			Type B: 799			

Sentinel-based virological surveillance, primary care

From week 35/2025 through week 34/2026, 1589 sentinel specimens were tested, with 338 detections of influenza virus A (77 subtype H1, 243 subtype H3, and 18 not yet subtyped), and 10 influenza virus B (of which all were Victoria-lineage). In addition, 57 SARS-CoV-2, 89 RSV, 159 rhinovirus, 33 human metapneumovirus (hMPV), 57 parainfluenza virus and 42 common cold coronaviruses were detected (Figure 9, 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. A secondary peak around week 5 was mainly driven by positive specimens from western Norway that had a later influenza peak than most of the country.

Among the detected influenza viruses, A(H3N2) constituted 70%, followed by A(H1N1) at 22%. Influenza A viruses that have not yet been subtyped constitute 5%. Influenza B viruses constituted 3% (Figure 7). Compared to the frequencies estimated for all laboratory detections (Figure 3), the pattern in the primary care sentinel surveillance was similar to the comprehensive surveillance that represents a mixture of primary care and hospitalised cases.

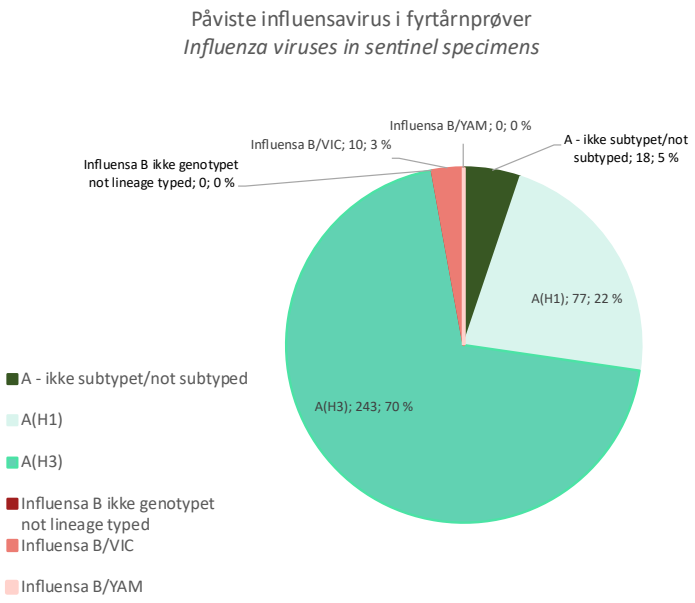

Figure 8. Proportions of influenza virus subtypes and lineages detected in sentinel specimens in the 2025/2026 season, by week 34/2026.

Almost half of all sentinel surveillance samples are taken from the age group 30-64 (47%). The second-largest group in this dataset is the 15–29-year-olds (22%), followed by 65–79-year-olds (14%) and 5–14-year-olds (7%) and. The two least represented age groups were the youngest, 0-4 years (5 %), and the oldest, 80 years and older (5%). Compared to the comprehensive surveillance that captures the testing in all laboratories, the sentinel surveillance has a lower proportion of the youngest and the elderly, and a higher proportion of persons 5-64 years old.

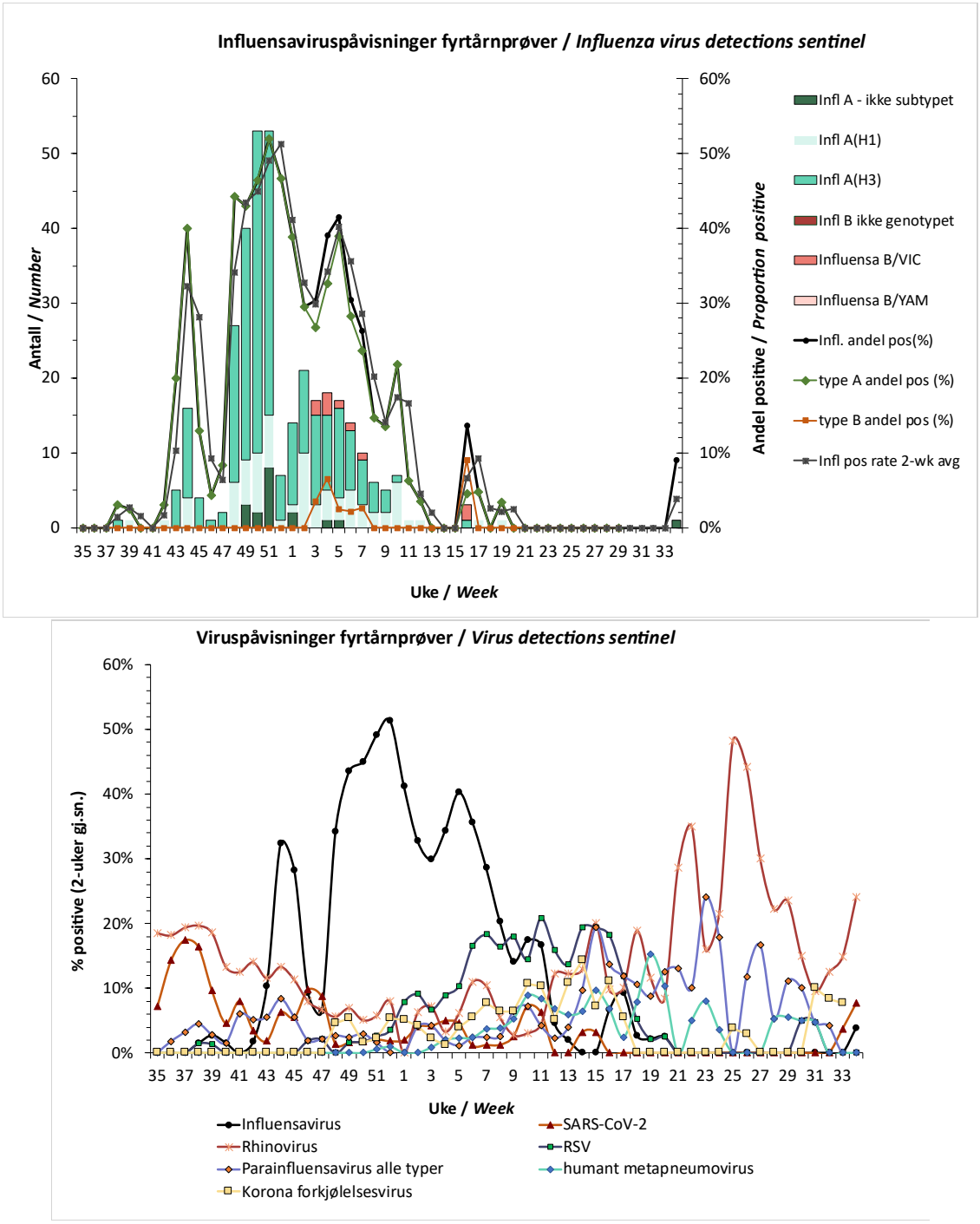

Figure 9. Weekly numbers of detections and per cent positives of influenza viruses (upper panel) and per cent positives (2-week averages) for all surveyed respiratory viruses (lower panel) in the respiratory sentinel surveillance.

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 9).

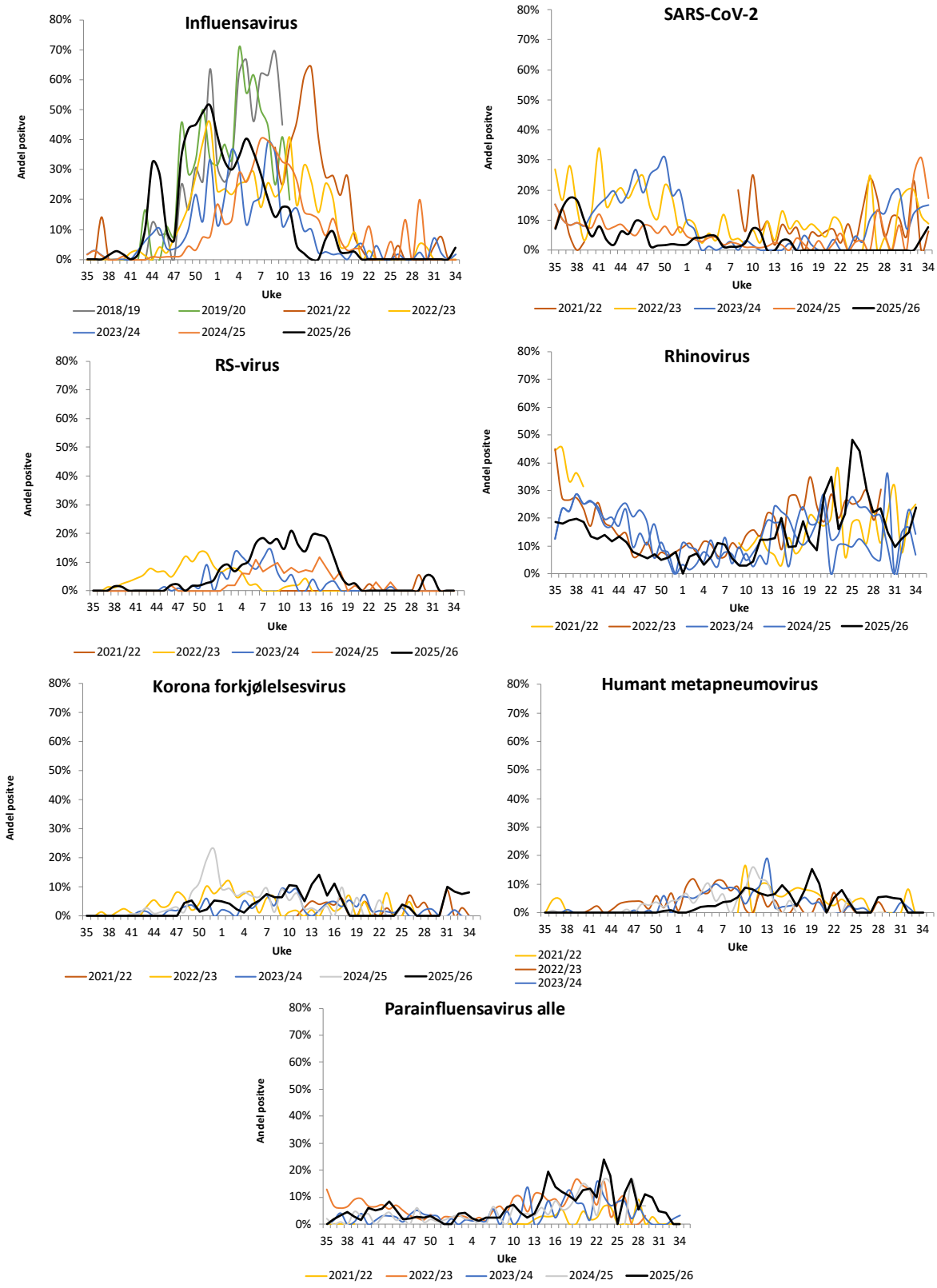

Figure 10. Proportion positive sentinel specimens in the current season (2-week moving averages, week 35/2025 and onward, black line), compared to six preceding seasons, for influenza viruses, SARS-CoV-2, RSV, rhinovirus, common cold coronaviruses, human metapneumovirus and parainfluenza viruses. Data for the most recent week is incomplete.

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

Week	Specimens tested	A - not subtyped	A(H1)	A(H3)	B untyped	B/Victoria	B/Yamagata	Influenza % positive	A % positive	B % positive	SARS-CoV-2 antall	% positive	RSV	% positive	Rhinovirus	% positive	Parainfluensa 1	Parainfluensa 2/4	Parainfluensa 3	All parainfl. % positive	Metapneumovirus	% positive	Andre 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	24	0	0	0	0	0	0	0 %	0 %	0 %	2	8 %	0	0 %	1	5 %	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	33	0	1	0	0	0	0	3 %	3 %	0 %	0	0 %	0	0 %	3	10 %	0	0	1	3 %	0	0 %	0	0 %
43	25	0	0	5	0	0	0	20 %	20 %	0 %	1	5 %	0	0 %	3	14 %	0	0	2	9 %	0	0 %	0	0 %
44	40	0	4	12	0	0	0	40 %	40 %	0 %	2	8 %	0	0 %	3	13 %	0	0	1	8 %	0	0 %	0	0 %
45	31	0	0	4	0	0	0	13 %	13 %	0 %	1	3 %	0	0 %	3	10 %	0	0	1	3 %	0	0 %	0	0 %
46	23	0	0	1	0	0	0	4 %	4 %	0 %	4	18 %	1	4 %	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	61	0	6	21	0	0	0	44 %	44 %	0 %	1	2 %	0	0 %	2	4 %	1	0	0	2 %	0	0 %	3	5 %
49	93	3	6	31	0	0	0	43 %	43 %	0 %	1	1 %	2	3 %	6	9 %	0	0	0	3 %	0	0 %	2	2 %
50	114	2	8	43	0	0	0	46 %	46 %	0 %	2	2 %	1	1 %	2	2 %	2	0	1	3 %	0	0 %	0	0 %
51	102	8	7	38	0	0	0	52 %	52 %	0 %	2	2 %	4	4 %	8	9 %	0	0	0	0 %	1	1 %	3	3 %
52	15	0	1	6	0	0	0	47 %	47 %	0 %	0	0 %	0	0 %	0	0 %	0	0	0	0 %	0	0 %	1	7 %
1	36	2	1	11	0	0	0	39 %	39 %	0 %	1	3 %	4	11 %	0	0 %	0	0	0	0 %	0	0 %	1	3 %
2	71	0	10	11	0	0	0	30 %	30 %	0 %	3	5 %	5	8 %	5	10 %	1	0	1	6 %	0	0 %	2	3 %
3	56	0	3	12	0	2	0	30 %	27 %	4 %	2	4 %	3	5 %	2	4 %	1	0	0	2 %	1	2 %	0	0 %
4	46	1	4	10	0	3	0	39 %	33 %	7 %	3	7 %	6	13 %	1	2 %	0	0	1	2 %	1	2 %	1	2 %
5	41	1	3	12	0	1	0	41 %	39 %	2 %	1	2 %	3	7 %	4	10 %	0	0	0	0 %	1	2 %	2	5 %
6	46	0	5	8	0	1	0	30 %	28 %	2 %	0	0 %	11	25 %	5	12 %	1	0	1	5 %	1	2 %	2	4 %
7	38	0	3	6	0	1	0	26 %	24 %	3 %	1	3 %	4	11 %	3	8 %	0	0	0	0 %	2	5 %	3	8 %
8	41	0	2	4	0	0	0	15 %	15 %	0 %	0	0 %	9	22 %	1	3 %	0	0	2	5 %	1	3 %	1	2 %
9	37	0	2	3	0	0	0	14 %	14 %	0 %	2	5 %	5	14 %	1	3 %	1	0	2	8 %	3	8 %	3	8 %
10	32	0	6	1	0	0	0	22 %	22 %	0 %	3	9 %	5	16 %	1	3 %	0	0	1	6 %	3	9 %	3	9 %
11	16	0	1	0	0	0	0	6 %	6 %	0 %	0	0 %	5	31 %	1	7 %	0	0	0	0 %	1	6 %	1	6 %
12	28	0	1	0	0	0	0	4 %	4 %	0 %	0	0 %	2	7 %	4	15 %	1	0	0	4 %	2	7 %	1	4 %
13	23	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	5	22 %	2	9 %	1	0	0	4 %	1	4 %	4	17 %
14	8	0	0	0	0	0	0	0 %	0 %	0 %	1	13 %	1	13 %	2	25 %	1	0	0	25 %	1	13 %	0	0 %
15	23	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	5	22 %	4	18 %	0	0	4	17 %	2	9 %	2	9 %
16	22	0	0	1	0	2	0	14 %	5 %	9 %	0	0 %	3	14 %	0	0 %	0	0	2	10 %	1	5 %	2	9 %
17	21	0	1	0	0	0	0	5 %	5 %	0 %	0	0 %	2	10 %	4	19 %	0	0	3	14 %	0	0 %	0	0 %
18	17	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	3	19 %	1	0	0	6 %	3	18 %	0	0 %
19	29	0	1	0	0	0	0	3 %	3 %	0 %	0	0 %	1	3 %	2	7 %	0	0	2	10 %	4	14 %	0	0 %
20	11	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	1	11 %	1	0	1	18 %	0	0 %	0	0 %
21	12	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	5	42 %	0	0	1	8 %	0	0 %	0	0 %
22	8	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	2	25 %	0	0	1	13 %	1	13 %	0	0 %
23	17	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	2	12 %	0	0	5	29 %	1	6 %	0	0 %
24	11	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	4	36 %	0	0	0	0 %	0	0 %	0	0 %
25	16	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	9	56 %	0	0	0	0 %	0	0 %	1	6 %
26	18	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	6	33 %	1	0	3	22 %	0	0 %	0	0 %
27	12	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	3	25 %	1	0	0	8 %	0	0 %	0	0 %
28	7	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	1	17 %	0	0	0	0 %	1	14 %	0	0 %
29	11	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	3	27 %	0	0	2	18 %	0	0 %	0	0 %
30	9	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	1	11 %	0	0 %	0	0	0	0 %	1	11 %	0	0 %
31	12	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	2	17 %	0	0	1	8 %	0	0 %	2	17 %
32	12	0	0	0	0	0	0	0 %	0 %	0 %	0	0 %	0	0 %	1	8 %	0	0	0	0 %	0	0 %	0	0 %
33	15	0	0	0	0	0	0	0 %	0 %	0 %	1	7 %	0	0 %	3	20 %	0	0	0	0 %	0	0 %	2	13 %
34	11	1	0	0	0	0	0	9 %	9 %	0 %	1	9 %	0	0 %	3	30 %	0	0	0	0 %	0	0 %	0	0 %
Sum	1589	18	77	243	0	10	0				57		89		159		15	0	42		33		42	

Genetic characterization of influenza viruses in Norway

During the current influenza season (week 35-2026 and onwards), the Norwegian Institute of Public Health (NIPH) has received 2,738 non-sentinel influenza virus positive specimens for analysis. In addition, there were 348 influenza virus positive sentinel specimens. Overall, 29% (916 viruses) have undergone whole-genome sequencing (Table 3), 150/348 (43%) of those from sentinel surveillance and 766/2,738(28%) of those from general surveillance. Furthermore, 208/916 (23%) samples were taken from hospitalised patients, and 673/916 (73%) samples came from outpatients. For 35 cases we lack information to correctly attribute them.

Most of our sequenced samples came from patients age 25-59 (n= 362/40%) followed by the oldest age group 60+ (n=256/28%) The younger age groups were represented with 134 (15%) samples from the 15–24-year-olds, 90 (1%) samples for the 5-14 age group and 74 (1%) samples from the youngest (0-4).

Additionally, 110 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 897 haemagglutinin (HA) gene sequences have been submitted to the GISAID EpiFlu database, along all other genes that meet the quality criteria for submission.

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

For a full overview of the data presented here you can visit our statistic site (https://statistikk.fhi.no/ngs/) for the tables or our nextclade site (https://nextstrain.org/groups/niph) for the phylogenetic analysis.

A(H1N1) viruses

During the 2025/26 influenza season, we only detected A(H1N1) viruses belonging to the *6B.1A.5a.2a.1* clade. 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. Since then, only two **D.3.1** have been detected in Norway. Overall, this season we sequenced 357 A(H1N1) and 306 (86%) of those belong to the **D.3.1.1** subclade (Figure 9, Table 3).

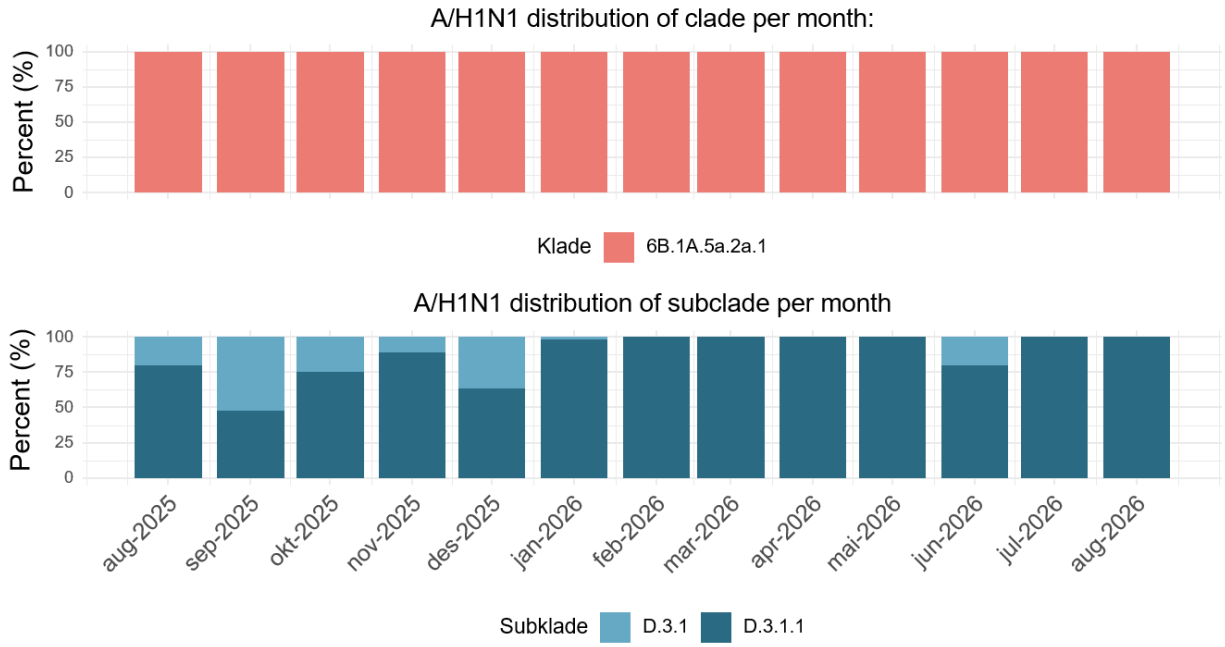

Figure 11. Clade (Upper) and subclade (Lower) distribution of H1N1 viruses in Norway for Season 2025/2026

Cluster analysis:

The **D.3.1.1** viruses were dominant this season although we had sporadic detection of **D.3.1s** as well (Figure 11). Most of the season the **D.3.1** were genetically very similar. However, the **D.3.1.1** viruses have recently been expanding their genetic repertoire.

The cluster of interest has an additional substitution in the HA1:**D139N** (Figure 13) and has been expanding up until August 2026. The first detection of this cluster has been January 2026, and the proportion of detections have steadily increased over the summer months (although submissions and sequencing numbers were particularly low in these months).

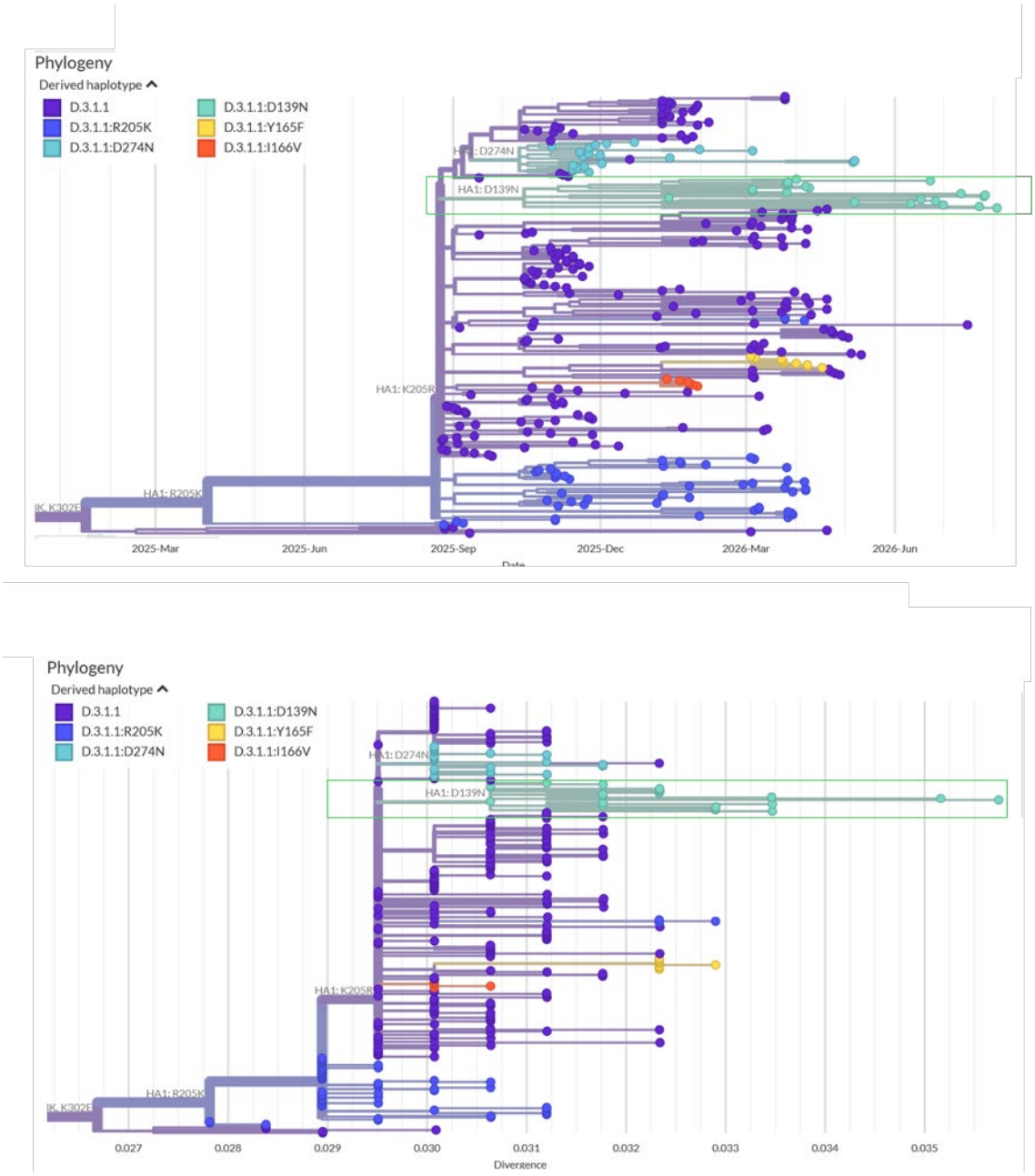

Figure 12 Clade 6B.1A.5a.2a.1, Subclade D.3.1.1 NextStrain phylogenetic focus tree of the haemagglutinin of the H1N1 viruses from Norway from week 35 2025 until week 34 2026, on a time axis (top) and divergence axis (bottom). Colours represent derived haplotype; branches are labelled with amino acid substitutions tip labels refer to virus names.

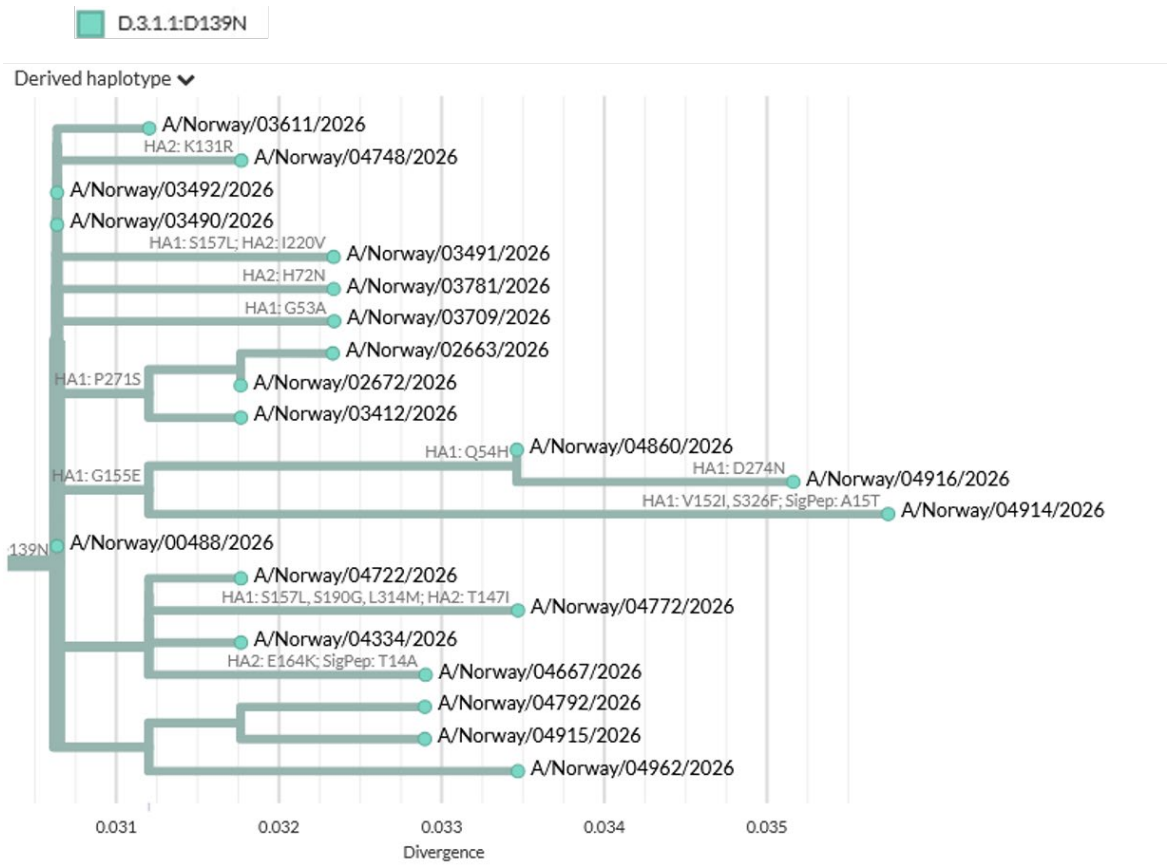

Figure 13 **Clade 6B.1A.5a.2a.1, Subclade D.3.1.1 + D139N NextStrain phylogenetic focus tree of the haemagglutinin of the H1N1 viruses from Norway from week 35 2025 until week 34 2026, on divergence axis. Colours represent derived haplotype; branches are labelled with amino acid substitutions tip labels refer to virus names.**

Within the **D.3.1.1 +HA1:D139N** cluster (Figure 13) of viruses a subcluster with an additional **HA1:G155E** has emerged that represents an additional epitope substitution. Interestingly one of those viruses (*A/Norway/04916/2026*) in the cluster also carries a **HA1:D274N** substitution that was also found in **D.3.1.1** viruses earlier in the season that were subsequently not detected over summer. This co-evolution in such a short time span could point towards a site of importance.

A(H3N2) viruses

During the 2025/26 influenza season in Norway, all sequenced A(H3N2) viruses belonged to the 2a.3a.1 clade (Figure 17, Table 3).

Within this clade, the main group of viruses detected belonged to the **K** (449/482, 93%) subclade, with sporadic detections of **J.2** (9/482, 2%), **J.2.2** (5/482, 1%), **J.2.3**(3/482, 1%) and **J.2.4** (14/482, 3%) (Figure 17, 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 93% of all H3N2 sequences in the 2025/26 season.

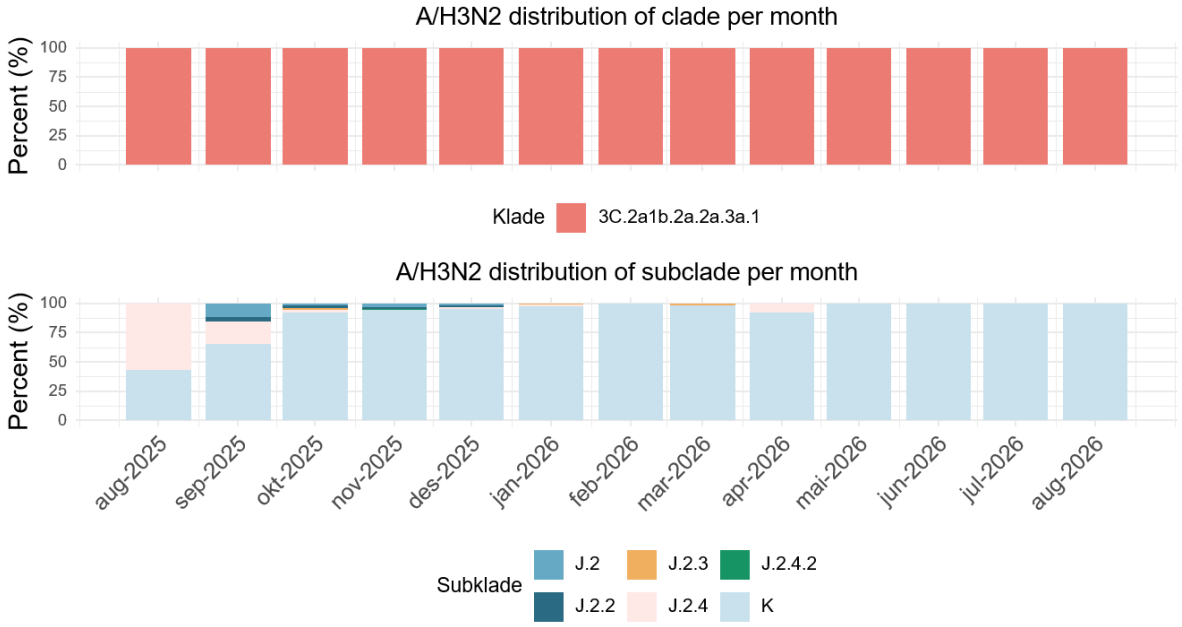

Figure 14 Clade (Upper) and subclade (Lower) distribution of H3N2 viruses in Norway for Season 2025/2026

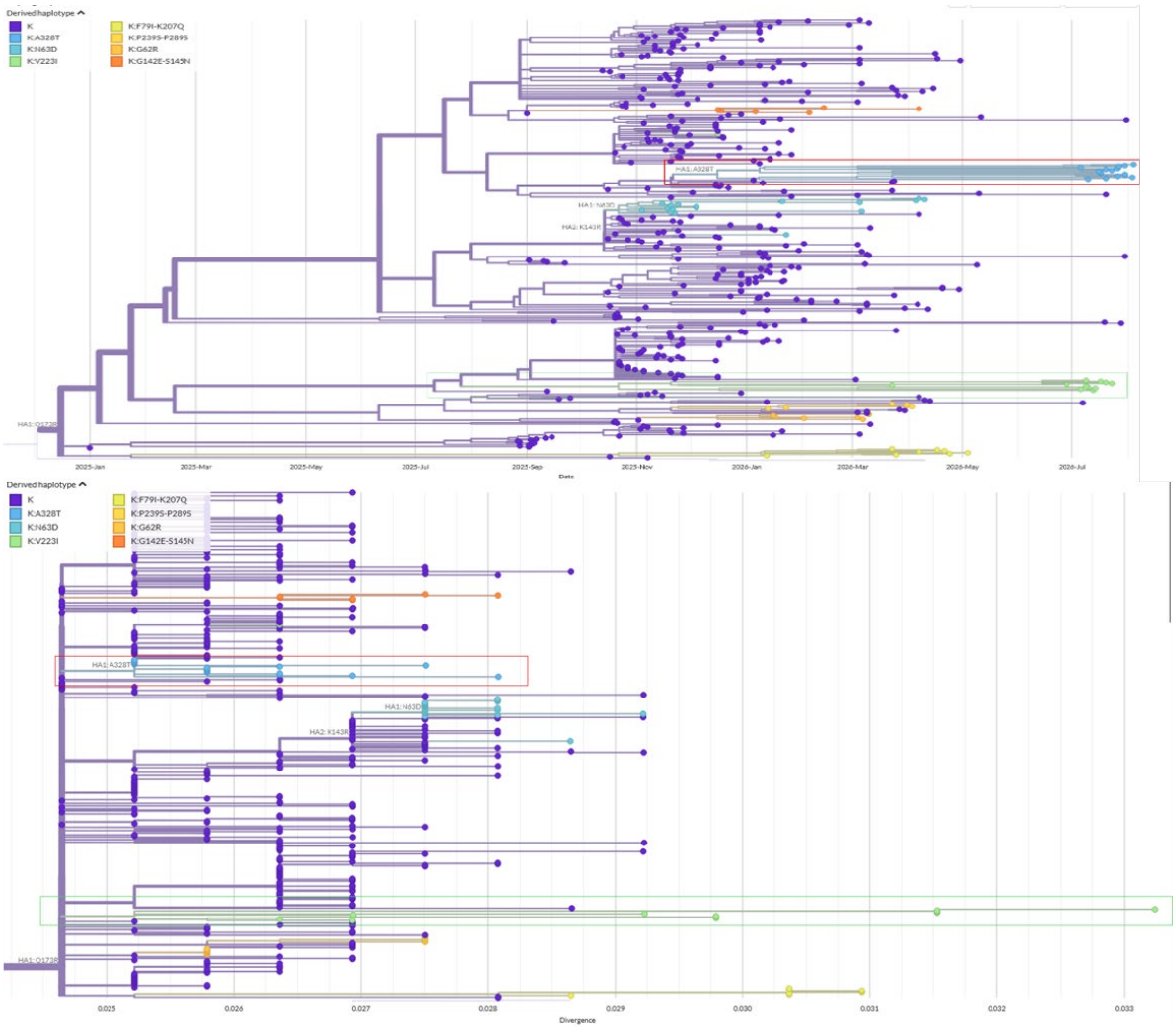

Figure 15. Clade 2a.3a.1, NextStrain phylogenetic tree of the haemagglutinin of the H3N2 viruses from Norway from week 35 2025 until week 34 2026, compared to the reference sequences for season 2025/26 provided by the ECDC/WHO influenza characterization guidelines. Colours represent derived haplotype; branches are labelled with amino acid substitutions. Top: On a time axis. Bottom: On a divergence axis.

Cluster analysis: Two clusters of notes have recently been detected, the first one is a cluster in subclade **K** cluster with an additional **HA1: A328T** substitution (red box Figure 19). This cluster was first detected in July and made up 14/29 (48%) of all detected H3N2 of that month (Figure 15, Figure 16); while in August it represents 2/2 detections. These viruses were isolated from all over Norway with no discernible pattern.

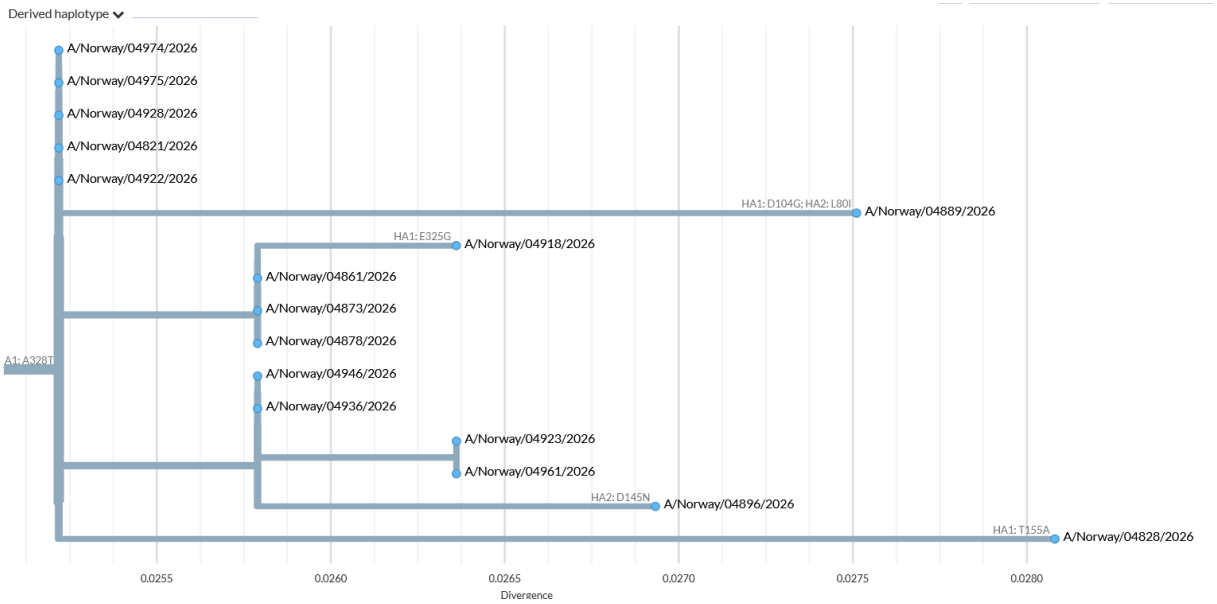

Figure 16 Clade 2a.3a.1, Subclade K H3+ A328T NextStrain phylogenetic focus tree of the haemagglutinin of the H3N2 viruses from Norway from week 35 2025 until week 34 2026, on a time axis. Colours derived haplotype; branches are labelled with amino acid substitutions tip labels refer to virus names.

The **K +HA1:V223I** cluster (green box, Figure 15) shows more genetic divergence but has been detected to a lesser degree over summer. It was first detected in June (1/1) and made up 9/45 (31%) in Juli. Due to the low sequencing numbers, it is hard to draw any conclusion based on this data alone however it seems that these viruses are geographically widespread at the moment with multiple genetic subclusters. One of these with additional substitutions HA1: S95G, S145N, S149G, I223V; SigPep: F15S is also limited to a single county so could be a localized outbreak.

B/Victoria-lineage viruses

B/Victoria-lineage viruses

During the 2025/26 influenza season, 76 B/Victoria-lineage viruses were sequenced in Norway. All viruses belonged to the V1A.3a.2 clade (76/76, 100%) (Figure 17, Table 3).

Further characterisation of these viruses showed that 25 viruses were classified as genBVicB/Switzerland/329/2024-like viruses and belonged to subclade **C.5.6** (25/76, 32.9%), while 15 viruses were classified as genBVicB/ENG/120/2025-like viruses belonging to subclade **C.5.6.1** (15/76, 19.7%). *24* were classified as genBVicB/Catalonia/2279261NS/2023-like viruses belonging to subclade **C.5.1** (24/76, 31.6%).

Of the remaining viruses, six were classified as genBVicB/Austria/1359417/2021-like viruses belonging to subclade **C.3** (6/76, 7.9%), and two belonged to subclade **C.3.3** within the same genetic group (2/76, 2.6%). Two viruses were classified as genBVicB/Greece/5509/2024-like viruses belonging to subclade **C.5.7** (2/76, 2.6%), while two viruses were classified as genBVicB/Kanagawa/AC2414/2025-like viruses belonging to subclade **C.3.1** (2/76, 2.6%) (**Figure** 17,*Table 3*).

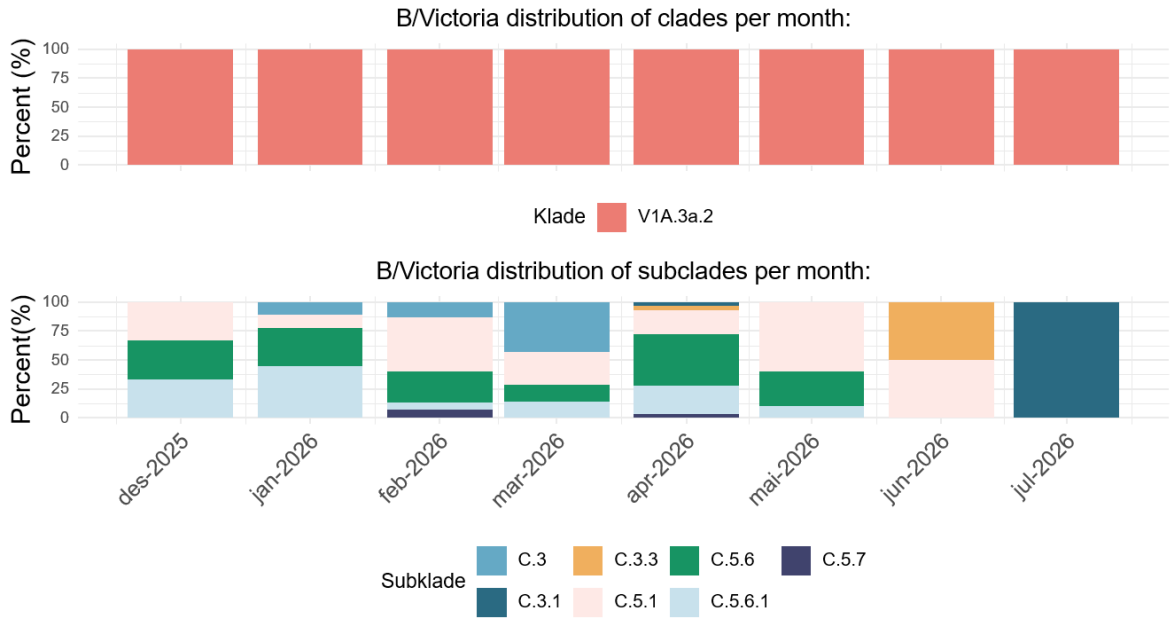

Figure 17 Clade (Upper) and subclade (Lower) distribution of B/Victoria viruses in Norway for Season 2025/2026

Cluster Analysis

The latest viruses were from **C.5.6**. and the **C.5.1** subclades (Figure 18). In the **C.5.6** subclade a cluster with an additional **HA1: E183K** was identified that formed in May and had additional detections in June 2026 and were isolates in two different counties from Norway (For example: *B/Norway/04089/2026 and B/Norway/04035/2026*).

The C.5.1 subclade cluster is marked by an additional **HA1: A276V** and has been detected in multiple counties in Norway (For example: *B/Norway/04760/2026, B/Norway/04417/2026, B/Norway/04321/2026, B/Norway/04202/2026*)

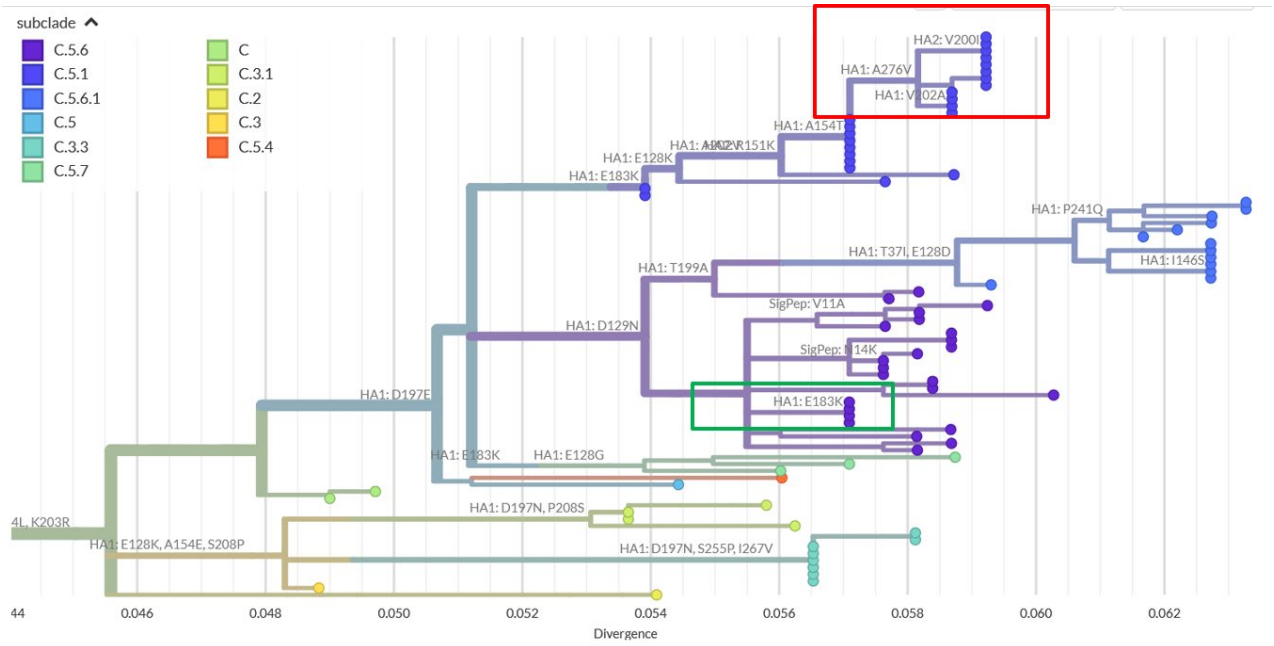

Figure 18. NextStrain phylogenetic tree of the haemagglutinin of the B-Victoria viruses from Norway from week 35 2025 until week 34 2026, compared to the reference sequences for season 2025/26 provided by the ECDC/WHO Influenza characterization guidelines. Colours represent subclades; branches are labelled with amino acid substitutions, on a divergence axis.

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

WHO/ECDC category	Clade	Sub-clade	aug-2025	sep-2025	okt-2025	nov-2025	dec-2025	jan-2026	feb-2026	mar-2026	apr-2026	may-2026	jun-2026	jul-2026	aug-2026	Total
A/H1N1	-	-	10	46	44	72	11	51	7	67	31	6	5	6	1	357
genAH1/Missouri/11/2025	6B.1A.5a.2a.1	D.3.1.1	8 (80%)	22 (47.8%)	33 (75%)	64 (88.9%)	7 (63.6%)	50 (98%)	7 (100%)	67 (100%)	31 (100%)	6 (100%)	4 (80%)	6 (100%)	1 (100%)	306
genAH1/Missouri/11/2025	6B.1A.5a.2a.1	D.3.1	2 (20%)	24 (52.2%)	11 (25%)	8 (11.1%)	4 (36.4%)	1 (2%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (20%)	0 (0%)	0 (0%)	51
A/H3N2	-	-	7	26	52	134	64	78	13	47	25	4	1	29	2	482
genAH3/Croatia/10136RV/2023	3C.2a1b.2a.2a.3a.1	J.2	0 (0%)	3 (11.5%)	1 (1.9%)	4 (3%)	1 (1.6%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	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%)	1 (1.6%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	5
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 (1.3%)	0 (0%)	1 (2.1%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	3
genAH3/Singapore/GP20238/2024	3C.2a1b.2a.2a.3a.1	J.2.4	4 (57.1%)	5 (19.2%)	1 (1.9%)	0 (0%)	1 (1.6%)	1 (1.3%)	0 (0%)	0 (0%)	2 (8%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	14
genAH3/Singapore/GP20238/2024	3C.2a1b.2a.2a.3a.1	J.2.4.2	0 (0%)	0 (0%)	0 (0%)	2 (1.5%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	2
genAH3/Norway/8765/2025	3C.2a1b.2a.2a.3a.1	K	3 (42.9%)	17 (65.4%)	48 (92.3%)	126 (94%)	61 (95.3%)	76 (97.4%)	13 (100%)	46 (97.9%)	23 (92%)	4 (100%)	1 (100%)	29 (100%)	2 (100%)	449
B/Victoria	-	-	0	0	0	0	3	9	15	7	29	10	2	1	0	76
genBVicB/Austria/1359417/2021	V1A.3a.2	C.3.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (3.4%)	0 (0%)	1 (50%)	0 (0%)	0 (0.0%)	2
genBVicB/Austria/1359417/2021	V1A.3a.2	C.3	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0%)	1 (11.1%)	2 (13.3%)	3 (42.9%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0.0%)	6
genBVicB/Catalonia/2279261NS/2023	V1A.3a.2	C.5.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (33.3%)	1 (11.1%)	7 (46.7%)	2 (28.6%)	6 (20.7%)	6 (60%)	1 (50%)	0 (0%)	0 (0.0%)	24
genBVicB/Greece/5509/2024	V1A.3a.2	C.5.7	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0%)	0 (0%)	1 (6.7%)	0 (0%)	1 (3.4%)	0 (0%)	0 (0%)	0 (0%)	0 (0.0%)	2
genBVicB/Switzerland/329/2024	V1A.3a.2	C.5.6	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (33.3%)	3 (33.3%)	4 (26.7%)	1 (14.3%)	13 (44.8%)	3 (30%)	0 (0%)	0 (0%)	0 (0.0%)	25
genBVicB/Kanagawa/AC2414/2025	V1A.3a.2	C.3.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1 (3.4%)	0 (0%)	0 (0%)	1 (100%)	0 (0.0%)	2
genBVicB/ENG/120/2025	V1A.3a.2	C.5.6.1	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	1 (33.3%)	4 (44.4%)	1 (6.7%)	1 (14.3%)	7 (24.1%)	1 (10%)	0 (0%)	0 (0%)	0 (0.0%)	15

Surveillance of antiviral resistance in Influenza viruses

During the 2025/26 season, from week 35 2025 to week 34 2026, a total of 885 influenza viruses were genetically assessed for susceptibility to the neuraminidase inhibitors oseltamivir (Tamiflu®) and zanamivir (Relenza®). Resistance-associated substitutions were detected in six influenza A(H1N1) viruses and one A(H3N2) virus. One A(H1N1) virus sampled in week 38 2025 carried the NA I223R substitution, associated with reduced susceptibility to oseltamivir and potentially to zanamivir. Four A(H1N1) viruses sampled in weeks 10, 17 (two viruses) and 18 2026 carried the NA I223V/S247N combination, associated with reduced susceptibility to oseltamivir. One additional A(H1N1) virus sampled in week 30 2026 carried H275Y, a well-established marker of highly reduced susceptibility to oseltamivir and reduced to highly reduced susceptibility to peramivir. Overall, markers associated with reduced oseltamivir susceptibility were detected in 6 of 343 (1.7%) A(H1N1) viruses.

The NA S247N substitution was common among A(H1N1) viruses, both alone and in combination with Y155H. A subset of these viruses was phenotypically tested against oseltamivir and zanamivir and showed normal inhibition. Similarly, phenotypically tested A(H3N2) viruses carrying S245N showed normal inhibition. These findings are important because the effect of individual substitutions can depend on the viral genetic background and cannot always be inferred from historical resistance markers alone.

One A(H3N2) virus sampled in week 28 2026 carried the NA S245N/R249E combination and was classified by the sequence-based analysis as having reduced susceptibility to oseltamivir, corresponding to 1 of 472 (0.2%) tested A(H3N2) viruses. Antiviral treatment history was unknown for all cases with resistance-associated substitutions.

No established resistance-associated substitutions to baloxavir marboxil (Xofluza®) were detected. No resistance-associated findings were detected among B/Victoria viruses.

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 19 in comparison to data from 2023 and 2024, in Table 4 for the last 5 years, and summarised as follows:

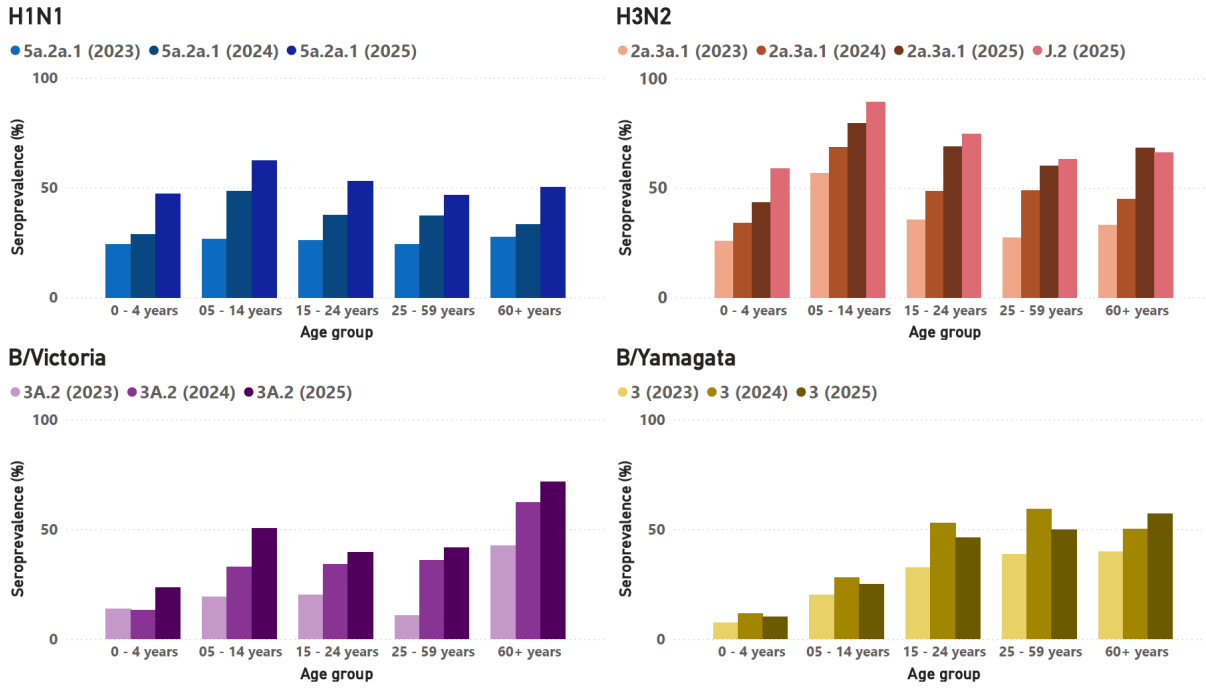

Figure 19. Seroprevalence in August 2023, 2024, and 2025 against current influenza A and B strains in various age groups. HAI was performed against A/Norway/31694/2022 (H1N1, clade 6B.1A.5a.2a.1), A/Thailand/8/2022 (H3N2, 3C.2a1b.2a.2a.3a.1), A/Croatia/10136RV/2023 (H3N2, 3C.2a1b.2a.2a.3a.1 (J.2 subclade)) 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. Our

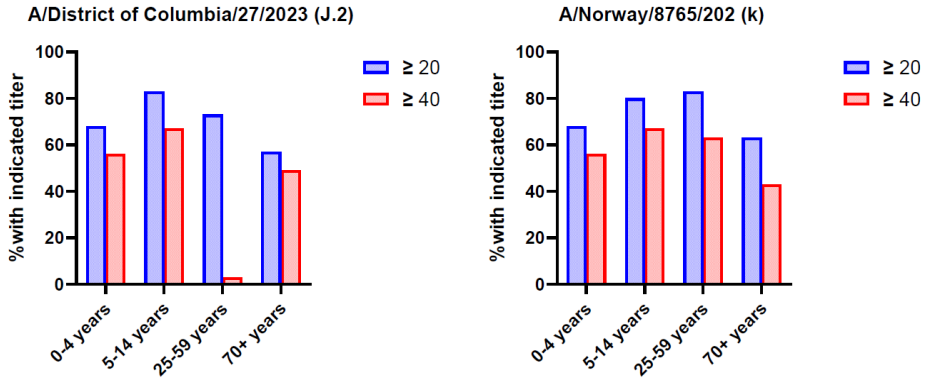

Figure 20. Neutralising antibodies against J.2 and K subclades in residual sera. A subset of residual serum samples from the age groups 0-4 years (25 samples), 5-14 years (30 samples), 25-59 years (30 samples) and 70+ years (35 samples) were analysed by microneutralisation assays against A/District of 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.

observations were published in collaboration with the World Influenza Center, The Francis Crick Institute (2).

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

Primary care consultations, outbreaks in healthcare institutions, hospital and intensive care (ICU) admissions and deaths associated with influenza in the season 2025-26 are extensively described in the End-of-season report for respiratory infections published by the NIPH on 3 September 2026. Please refer to the report for more details (1).

The 2025–26 influenza season was characterized by an early outbreak that was likely driven by the emergence of a new influenza A(H3N2) variant (Figure 26). Although consultations in primary care did not exceed moderate levels (Figure 27), several indicators suggest that this was one of the most severe influenza seasons in recent years, particularly for the oldest age groups. The season was characterized by a high number of reported outbreaks in healthcare institutions, substantial numbers of hospital and intensive care (ICU) admissions, and a high number of influenza-associated deaths, mainly among older adults. The extent to which changes in testing activity, demographic developments, and reporting practices compared with previous seasons may have influenced these findings remains uncertain.

The outbreak began several weeks earlier than usual and also peaked earlier than normal. Among the youngest children, an unusually early and rapid increase in influenza-like illness (ILI) was seen. The counties of Vestland, Rogaland, and Agder experienced a later outbreak onset and peak than the rest of the country (see End-of-season report, pages 30-34).

The highest incidence of influenza was observed among school-aged children, followed by younger children and young adults. However, children under 5 years of age and adults aged 65 years and older appear to have been more affected than in previous seasons. More influenza outbreaks were reported from healthcare institutions than ever before (see End-of-season report, page 35), likely reflecting both extensive transmission and severe disease among older adults, as well as improved outbreak reporting.

The number of hospital admissions with influenza was high and comparable to that observed in the previous season. The highest admission rates were recorded among adults aged 65 years and older and among infants. Older adults experienced the greatest burden of severe disease, with longer hospital stays, more ICU admissions, and the highest number of deaths. The number of deaths registered among those aged 65 and over was higher than during the previous seasons. Among children, hospital admissions were generally of short duration, and no influenza-associated deaths were recorded among persons under 15 years of age (see End-of-season report (1), pages 48-56).

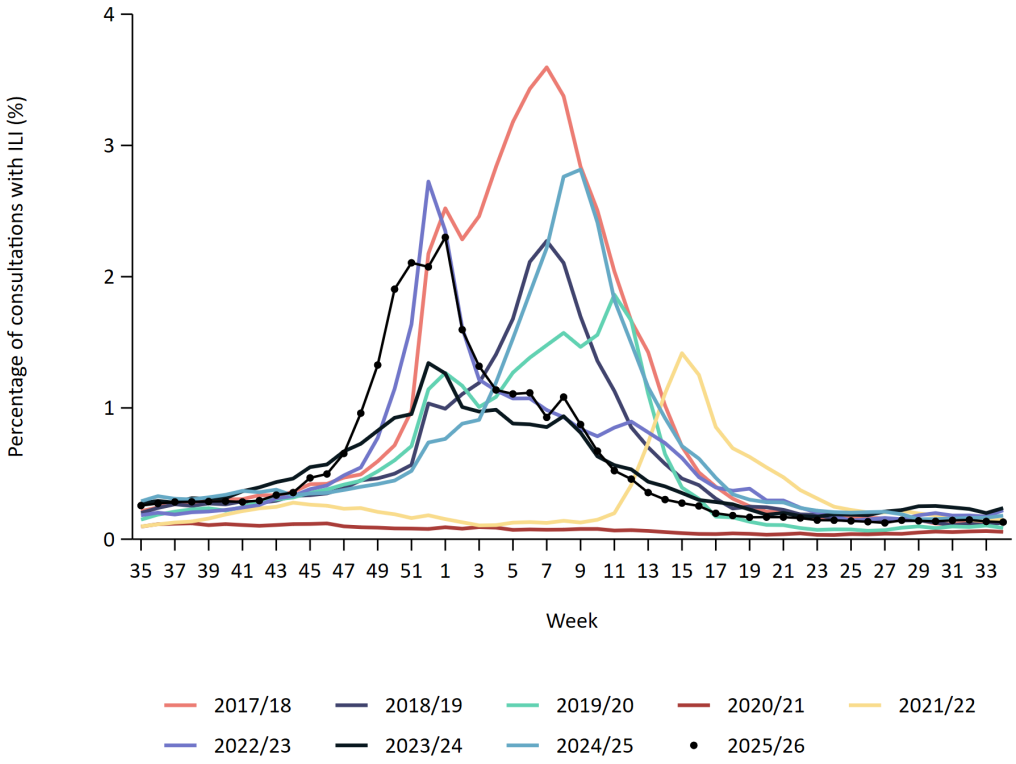

Figure 21. Weekly proportion of consultations for ILI, Norway 2025-2026 season (black dotted line). The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week, including the seven previous seasons for comparison. Source: NorSySS with data from KUHR, NIPH.

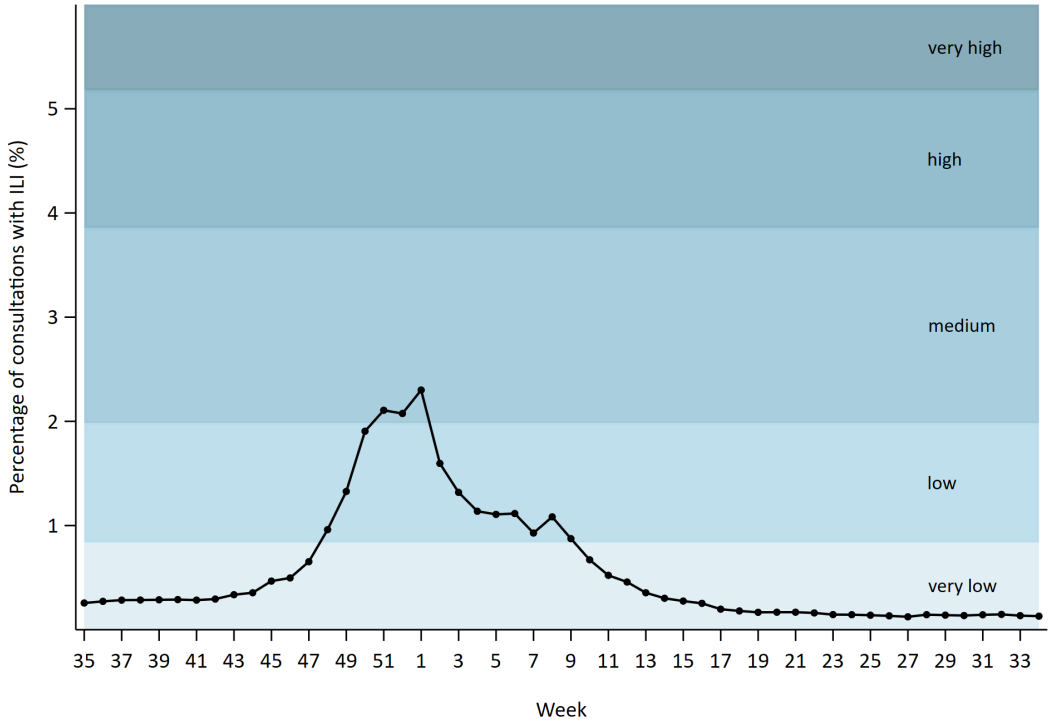

Figure 22. MEM intensity levels, Norway 2025-2026 season. The graph shows the proportion of patients in general practice and emergency clinics diagnosed with ILI, by calendar week. Source: NorSySS with data from KUHR, NIPH.

Vaccine distribution and coverage

In the 2025/26 season as of 31st May 2026, a total of 1.7 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 170 000 doses compared to the 2024/25 season, and the registered number of administered doses has increased by 200 000 doses (1.53 million doses) (Figure 27).

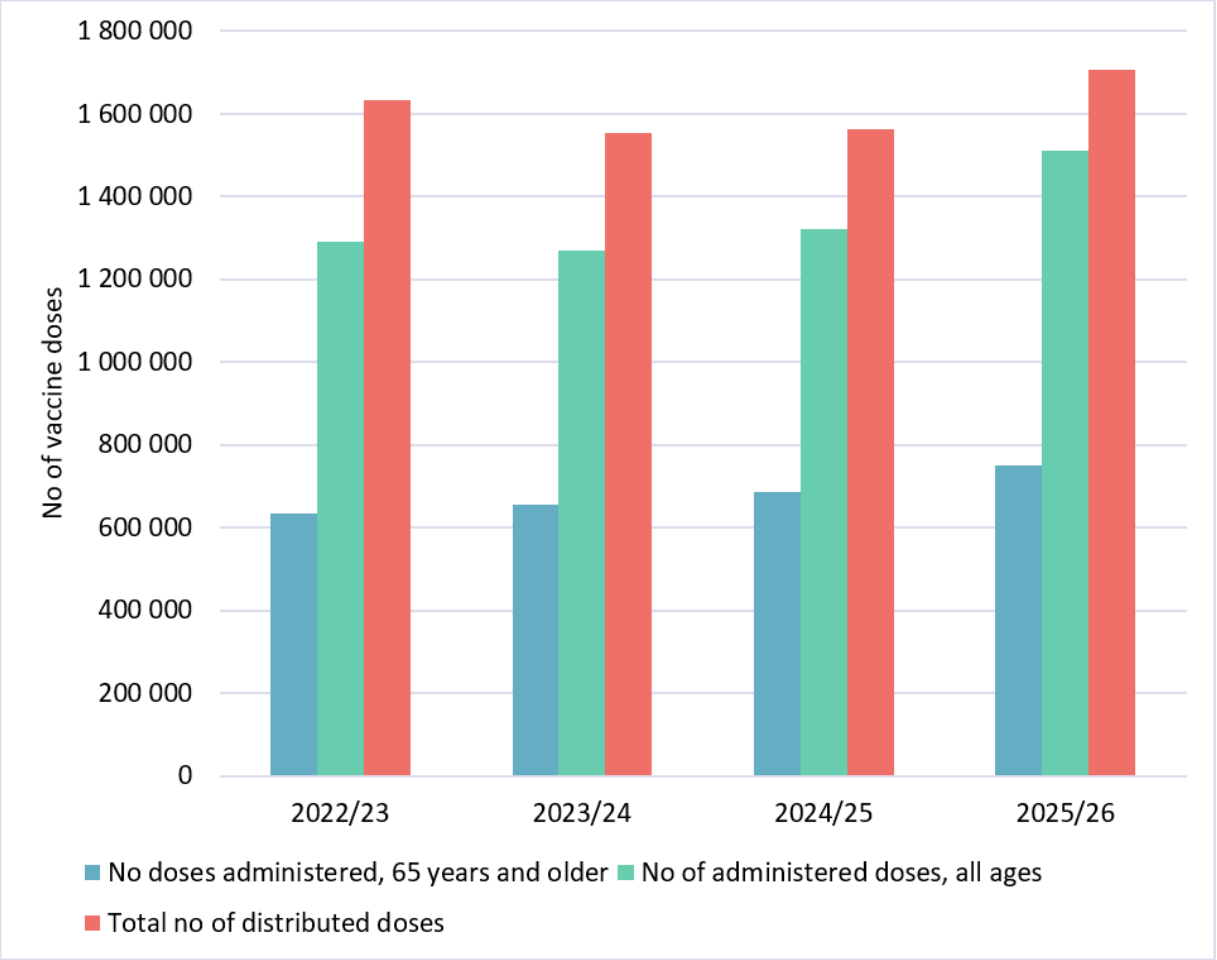

Figure 23. Influenza vaccine doses distributed in Norway and no of doses administered for all ages and for 65 years and older September 2022 through May 2026.

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).

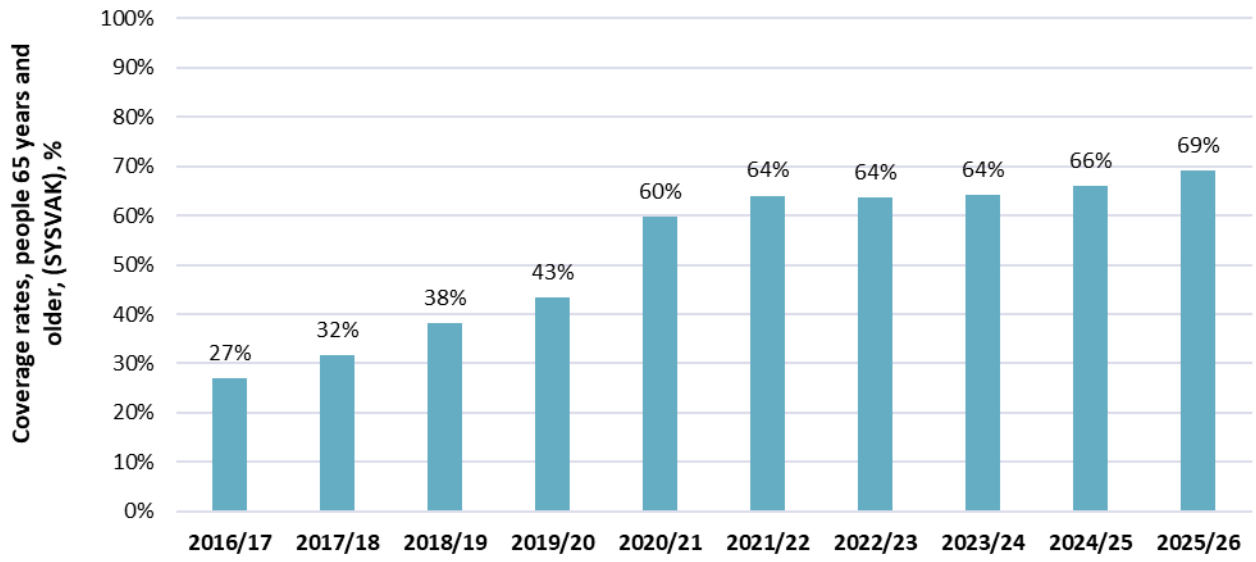

Figure 24. Vaccination coverage among the population above 65 years in Norway, 2016/17 season through to 2025/26 season as of May2026.

Approximately 94% of the doses accounted for (distributed doses – reported discarded doses) are so far registered in SYSVAK 2025/26 season. 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.

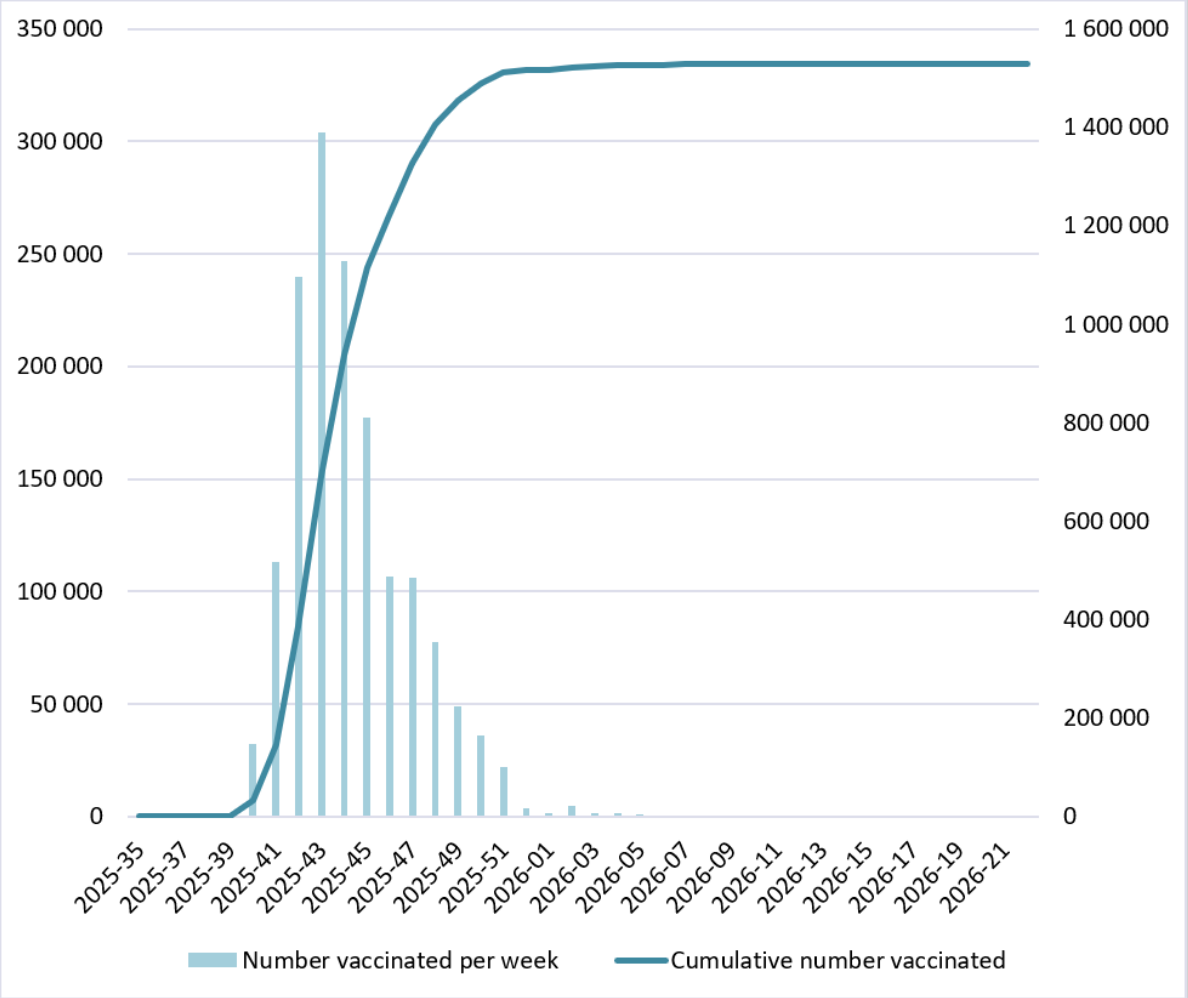

Figure 25. Number of vaccinated people per week and cumulatively in the 2025-26 season, 1. September 2025 – 31th of May 2026. Source: National Population Registry and Norwegian Immunization Registry, SYSVAK.

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 been detections of HPAIV H5N1 and H5N5 in wild birds during the last year, with sporadic detections in mammals. but only one poultry outbreak. In the period until autumn 2025, H5N1 genotype EA-2022-BB mainly circulating in marine birds in the north predominated, with one associated outbreak in commercial layers (4). This genotype has been detected sporadically in marine birds also in 2026. From autumn of 2025 onwards, genotype EA-2024-DI sublineage DI.2.x viruses have caused widespread disease in wild anseriform species in Norway, with DI.2.1 predominating. All HPAIV H5N5 detections were of genotype EA-2021-I and occurred mainly in northern and arctic areas. Recent investigations have documented multiple introductions of HPAIV into the High Arctic of Svalbard and Jan Mayen, with sporadic virus detections in wild mammals such as Arctic fox, polar bear and walrus at Svalbard. Serological surveillance in mammals in Svalbard indicates more widespread HPAIV H5 exposure in this region than is reflected by the sporadic virus detections alone. The Norwegian Food Safety Authority is responsible for surveillance and

outbreak management of avian influenza in Norway. The Norwegian Veterinary Institute supports these activities through commissioned surveillance programmes, diagnostic services, risk assessment and research. 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 (2, 3, 4), 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 (5). 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 (6).

References

1 Norwegian Institute of Public Health 2026. End-of-season report for respiratory infections. https://www.fhi.no/publ/2026/luftveisinfeksjoner-i-norge-sesongen-2025-2026/

2 Harvey R, Welsh C, Byrne AMP, Greenwood D, Stevenson-Leggett P, Galiano M, Bailey D, Chan Y-W, Boateng J, Wolmuth-Gordon H, Whitaker H, Brown KE, Jeffery-Smith A, Allen A, Amirthanlingam G, **Fossum E, Vikse EL, Rohringer A, Hungnes O, Bragstad K**, Swanton C, Williams B, Gandhi S, Gamblin S, Carr EJ, Lewis NS, Wall EC, Wu MY, Dowgier G, Hobbs A, Tan CP, Zvartau-Hind J, Miah M, Daley O, Miranda M, Bawumia P, O'Reilly N, Cheshire C, Wilson N, Ambrose K, Strange A, Kelly G, Kjær S, Rupert CL. Beale RCL, Padmasavee Papineni P, Tumena Corrah T, Richard Gilson R.
Assessment of human immunity to A/H3N2 influenza subclade K during 2025 emergence. eBioMedicine, **129**, 2026, 106332, ISSN 2352-3964, https://doi.org/10.1016/j.ebiom.2026.106332.

2 Granstad S, Ytrehus B, Helberg M, Åkerstedt J, Gjerset B, Bøe CA, Madslien K, Ånestad LM, Fosse JH, Nordstoga AB, Kampen A, Fjermestad-Eie B, Fjeldheim I, Stålcrantz J, Tønnessen R. Høypatogen aviær influensa (HPAI) i Norge, Europa og globalt. Statusrapport for perioden 21. oktober 2025 – 20. Mars 2026. Veterinærinstituttet 2026. Available from: https://www.vetinst.no/rapporter-og-publikasjoner/rapporter/2026/statusrapport-hoypatogen-aviaer-influensa-i-norge-europa-og-globalt (accessed 4 September 2026)

3 Veterinærinstituttet 2026. Fugleinfluensa hos villfugl i Norge (Avian influenza in wild birds in Norway). Available from: https://www.vetinst.no/dyr/vilt/fugleinfluensa-i-norge (accessed 4 September 2026)

4 Veterinærinstituttet 2026. Fugleinfluensa hos fjørfe i Norge (Avian influenza in poultry in Norway). Available from: https://www.vetinst.no/dyr/fjorfe/status-fugleinfluensa (accessed 4 September 2026)

5 EFSA (European Food Safety Authority), ECDC (European Centre for Disease Prevention and Control), EURL (European Union Reference Laboratory for Avian Influenza), Buczkowski, H., Ducatez, M., Fusaro, A., Gonzalez, J. L., Kuiken, T., Mirinavičiūtė, G., Ståhl, K., Staubach, S., Svartström, O., Terregino, C., Willgert, K., Alarcón, A., & Kohnle, L. (2026). Avian influenza

overview March–May 2026. EFSA Journal, 24(7), e10196, https://doi.org/10.2903/j.efsa.2026.10196

6 Folkehelseinstituttet 2025. Oppdatert folkehelserelatert risikovurdering av smittesituasjonen med høypatogen fugleinfluensa (HPAIV H5) med fokus på situasjonen i Nord-Amerika og i Norge. Available from: https://www.fhi.no/publ/2025/risikovurdering-fugleinfluensa-februar-2025/

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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Section for Respiratory, Blood-borne and Sexually transmitted infections

Division for Infection Control

Norwegian Institute of Public Health,

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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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