



The surveillance programme for avian influenza (AI) in Norwegian wildlife 2025

REPORT 35/2026

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Suggested citation

Ytrehus, Bjørnar, Granstad, Silje, Gjerset, Britt, Tønnessen, Ragnhild, Åkerstedt, Johan. The surveillance programme for avian influenza (AI) in Norwegian wildlife 2025. Surveillance programme report. Veterinærinstituttet 2026. © Norwegian Veterinary Institute, copy permitted with citation.

Quality controlled by

Merete Hofshagen, Surveillance Programme Coordinator, Norwegian Veterinary Institute

Commissioned by

Norwegian Food Safety Authority



Published

2026 on www.vetinst.no
ISSN 1890-3290 (electronic edition)
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Colophon

Cover photo: Colourbox
www.vetinst.no

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Summary

The current surveillance report is part of Norway's contribution to the European Union's Surveillance Programme for avian influenza in poultry and wild birds and reports the surveillance of wild birds and mammals. This mandatory surveillance program is complemented by surveillance performed in the project One Health for Surveillance, which also is reported here to provide a full picture. Influenza A virus was detected in 161 of 880 wild birds examined for avian influenza in Norway in 2025. Among all wild birds sampled through active or passive surveillance, HPAI H5 subtype virus was detected in samples from 77 birds. Sixty-five of the confirmed HPAI-positive wild birds in 2025 were identified through passive surveillance, i.e. sampling of birds that were found dead or diseased and euthanised. Among these HPAI detections, forty-six were H5N1, ten were H5N5, and nine were classified as H5Nx virus. Of the 88 wild mammals tested as part of passive surveillance, five arctic foxes and one red fox tested positive for HPAI H5N5. Active surveillance detected influenza A virus in 82 wild birds, of which 18 were characterised as avian influenza H5, and twelve of these were confirmed as HPAI. HPAI cases were reported in 18 wild bird species.

Introduction

Norway has implemented a surveillance programme for avian influenza (AI) in wild birds and mammals. The surveillance is part of the European Union's Surveillance Programme for avian influenza in poultry and wild birds and performed in accordance with Commission Delegated Regulation (EU) 2020/689 (1). The Norwegian Food Safety Authority (NFSA) is responsible for the surveillance programme and contributes with collection of samples from the field, while the Norwegian Veterinary Institute (NVI) manages the planning, laboratory analyses, and reporting components. The programme is based on virological investigations of samples from live or hunted wild birds of target species (active surveillance) and dead or moribund wild birds and mammals (passive surveillance). Active surveillance of AI in wild birds has been running in the years 2005-2007, 2009-2010, and from 2016 and onwards. Passive surveillance in wild birds has been ongoing without interruption since 2005 (see [previous surveillance reports](#)). Results of avian influenza virus (AIV) testing in wild mammals are also included in this report.

In addition to the above-mentioned surveillance programme, NVI participates in the project "Setting up a coordinated surveillance under the One Health approach ([OH4Surveillance](#))" funded by the European Union (Grant Agreement No. 101131473) under the EU4Health Programme. The aim of this project is to protect public health through early detection of emerging and re-emerging zoonotic pathogens in animals and the environment. OH4Surveillance is a consortium of eleven participating countries and is led by Statens Serum Institut (SSI) in Denmark. In Norway, the Norwegian Institute of Public Health (NIPH, Folkehelseinstituttet) is the beneficiary institution and leads the work, while NVI is an affiliated institution and performs the surveillance activities, including laboratory analyses. The project period is from 2024 to 2026. In Norway, a substantial part of OH4Surveillance focus on strengthening the passive surveillance of HPAI. This has been pursued by implementing a range of measures to increase engagement and facilitate participation among scientific and amateur ornithologists, rangers from the Norwegian Nature Inspectorate (SNO), personnel from the Norwegian Institute for Nature Research (NINA) and the Norwegian Polar Institute (NPI), taxidermists, and others who through their occupations or hobbies visit remote areas and/or are in frequent contact with wild birds. In other parts of the project, NVI has initiated collaborations to enhance active surveillance (included in this report) and serological surveys (reported elsewhere).

Avian influenza viruses (AIVs) are influenza A viruses that evolve rapidly by genetic drift and reassortment. Wild waterfowl, such as ducks, geese, swans, waders and gulls, are natural reservoir hosts for low pathogenic avian influenza viruses (LPAIVs). These birds rarely develop clinical disease when infected with LPAIVs but shed large amounts of virus in their faeces (2). Some LPAIVs can infect poultry, typically causing only mild disease. However, LPAIVs of the H5 and H7 subtypes can mutate into highly pathogenic avian influenza viruses (HPAIVs) when

introduced into poultry flocks (3). HPAI is a severe infectious disease, causing high mortality in poultry. Migratory birds play a major role in the global spread of HPAI viruses (4, 5). Since 2021, HPAI H5Nx viruses belonging to the H5 clade 2.3.4.4b have established in wild birds (6), and this has also led to an increase in number of cases in wild mammals (7).

Highly pathogenic avian influenza was confirmed for the first time in Norway in 2020, when HPAIV H5N8 was detected in wild and captive birds (8). Since 2021, H5N1 has been the predominating HPAI subtype in Europe, including Norway, causing sporadic cases of severe illness and occasionally outbreaks with high mortality in birds and sporadic, but sometime fatal disease in mammals. In 2022, HPAI H5N1 was diagnosed in red foxes (*Vulpes vulpes*), marking the first detections of this disease in terrestrial mammals in Norway (9). Subtype H5N5 has also circulated in birds in Northern Norway with sporadic detections in other parts of northern Europe. H5N5 has also caused infections in lynx (*Lynx lynx*), otter (*Lutra lutra*) and red foxes in the same locations and periods as the virus has been detected in birds.

Aims

The aim of the national surveillance programme is to monitor the prevalence of AIVs in wildlife, emphasising the H5 and H7 subtypes. The surveillance is conducted in accordance with Commission Delegated Regulation (EU) 2020/689 (1).

Materials and methods

Sampling

Cloacal/rectal and tracheal/oropharyngeal swabs for virological testing were collected from live or hunted wild birds (active surveillance), and moribund or dead wild birds and mammals (passive surveillance). Tissue samples, particularly from brain and lungs, were occasionally collected from mammals when available.

For regular active surveillance, sampling equipment was sent to designated ornithologists and hunters. The recruitment of samplers was based on their geographical location and estimated access to hunted or live birds within *Anseriformes* and *Laridae*, respectively. Geographical regions were mainly targeted for active surveillance by a risk-based approach considering the relative density of poultry farms in each area and their overlap with the flyways and resting areas of many species of waterfowl (10,11). Active surveillance was ongoing year-round, for example during ringing of birds, but with a focus primarily in the autumn during hunting season.

For the active surveillance conducted under the OH4Surveillance project, bird populations considered to have a high likelihood of HPAIV presence were selected either due to recent outbreaks affecting these populations or because their migration patterns may facilitate the introduction of new HPAIV strains. In this work, NVI cooperates with, or receives samples from, field personnel at NINA and the NPI.

Passive surveillance was conducted by collecting swabs from dead or moribund wild birds and mammals across the entire country. Inspectors from the NFSA were responsible for the regular passive surveillance sampling. The wild bird species sampled were generally in accordance with, but not limited to, the EFSA list of target wild bird species for passive surveillance activities (12). Samples, mainly swabs, were taken from wild mammals in cases where HPAI was suspected based on clinical signs or when found dead in areas where it was plausible that HPAI circulated among birds. Passive surveillance continued throughout the year. The passive surveillance carried out under the OH4Surveillance project enabled field ornithologists at NINA and NPI, rangers from SNO, and other contributors to submit samples from birds found dead or moribund and subsequently euthanised, without relying on the availability of local NFSA inspectors. Sample kits with pre-paid postage were distributed free of charge and could be ordered through a [dedicated webpage](#).

Staff involved in sampling activities received written instructions on sampling procedure and were requested to fill in registration forms for individual cases. Swabs were placed in transport medium immediately after sampling and shipped directly to the NVI. Upon arrival, samples were registered and processed immediately or stored for a few days at 4°C until testing.

Mammals suspected of being infected with HPAIV were in most cases submitted as whole carcasses and sampled and necropsied under biosecurity level 3 conditions. In mammals, swabs from the brain, trachea and rectum were taken, often supplemented by tissue samples taken during necropsy. On some occasions, swabs from the brain were taken through foramen magnum in the field and submitted together with tracheal and rectal swabs for examination for HPAIV.

Analyses

Samples were tested for AIVs using a real-time reverse transcriptase polymerase chain reaction (rRT-PCR). The rRT-PCR used was an influenza A virus matrix (M) gene method recommended by the European Union Reference Laboratory (EURL) for Avian Influenza (12). The M gene rRT-PCR can detect all influenza A viruses but cannot be used to determine the haemagglutinin (HA) or neuraminidase (NA) subtypes. Therefore, the influenza A virus positive samples were further analysed using H5- and H7-specific PCRs (13). If samples were H5- or H7-positive, the HA cleavage site was sequenced to determine pathogenicity and confirm HPAI or LPAI virus infection. From June 2022, pathotyping by sequencing was replaced by a more rapid HPAI H5-detection rRT-PCR assay for 2.3.4.4b viruses recommended by the EURL (14). Additional NA subtyping rRT-PCR was performed on positive samples by methods recommended by EURL (15). Representative AIV-positive samples from the surveillance programme underwent whole-genome sequencing; however, only the HA and NA subtypes and the pathotype results are presented in this report.

Results and discussion

In total, samples from 880 wild birds were analysed for the presence of influenza A virus (Table 1). Most of the samples (701) were collected and analysed within the surveillance programme NFSA is responsible for, i.e. to fulfil Commission Delegated Regulation (EU) 2020/689. Active sampling of hunted birds and live birds during ringing accounted for 451 samples, while 250 samples were analysed as part of the passive surveillance. In addition, OH4Surveillance-activities provided 179 samples that were relevant for this report: 95 collected by active sampling and 84 as a part of passive surveillance. Most of the samples were collected from late summer to late autumn. A total of 161 wild birds (18.3%) tested positive for influenza A virus. Of these, none were H7-positive, while 90 (10.2%) were H5-positive. HPAIV was detected in 77 wild birds (8.8%) in 2025.

Active surveillance in 2025 detected influenza A virus in 82 (15.0%) out of 546 wild birds sampled (Table 2). Influenza A virus was detected in 61.7% (50/82) of Common Teals (*Anas crecca*), 45.5% (5/11) of Eurasian wigeons (*Mareca penelope*), 25.0% (5/20) of Lesser Black-backed Gulls (*Larus fuscus*), 22.5% (18/80) of Mallards (*Anas platyrhynchos*), 12.0% (3/25) of Common gulls (*Larus canus*), and 2.6% (1/38) of European Herring Gulls (*Larus argentatus*). All influenza A positive samples were further analysed for the presence of subtype H5 or, if negative, for H7. Eighteen of the 82 influenza A-positive samples were H5-positive, while none was H7-positive. Pathotyping and NA subtyping revealed three Eurasian wigeons and three Common Teals positive for HPAI H5N1. The remaining six Teals were diagnosed as H5Nx, since NA subtyping and pathotyping was not successful due to low viral load.

Active surveillance under OH4Surveillance in 2025 focused on sampling black-legged kittiwakes (*Rissa tridactyla*) from a breeding colony at Ekkerøy in Finnmark affected by a large HPAI outbreak in 2023 (16), as well as birds from the bird colony at Svarthammaren in Queen Maud Land in Antarctica. None of the 40 kittiwakes from Ekkerøy, nor 19 Antarctic Petrels (*Thalassoica antarctica*), 9 Snow Petrels (*Pagodroma nivea*) or 23 South Polar Skuas (*Stercorarius maccormicki*) from Queen Maud Land, tested positive for influenza A virus.

Table 1. Number of wild birds sampled in the surveillance programme for avian influenza in Norway in 2025.

	Total 2025	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec
Active surveillance													
HPAI H5N1	6										6		
HPAI H5Nx	6										6		
H5Nx	6										6		
Other influenza A*	64									37	24	3	
Influenza A negative	464	21	52	7	8	3	50	28	38	169	75	13	
Total	546	21	52	7	8	3	50	28	38	206	117	16	0
Passive surveillance													
HPAI H5N1	46		1	2					24	5	1	3	10
HPAI H5N5	10						2	2	1	5			
HPAI H5Nx	9						1	1	4	1	1	1	
H5N1	3								1				2
H5Nx	4								3				1
Other influenza A*	7	1								3	2		1
Influenza A negative	255	11	7	12	20	18	25	37	40	30	27	7	21
Total	334	12	8	14	20	18	28	40	73	44	31	11	35
Active and passive surveillance													
Total	880	33	60	21	28	21	78	68	111	250	148	27	35

* Other influenza A: H5/H7-negative

Passive surveillance in 2025 detected influenza A virus in 79 (23.7%) of 334 dead or moribund wild birds sampled. Among these, HPAIVs were detected in 65 birds. Forty-six of the HPAI detections were H5N1, ten were H5N5 and nine were classified as H5Nx virus, i.e. NA subtyping was not successful due to low viral load in the samples. The number of wild birds sampled from each county or territory are shown in Figure 1.

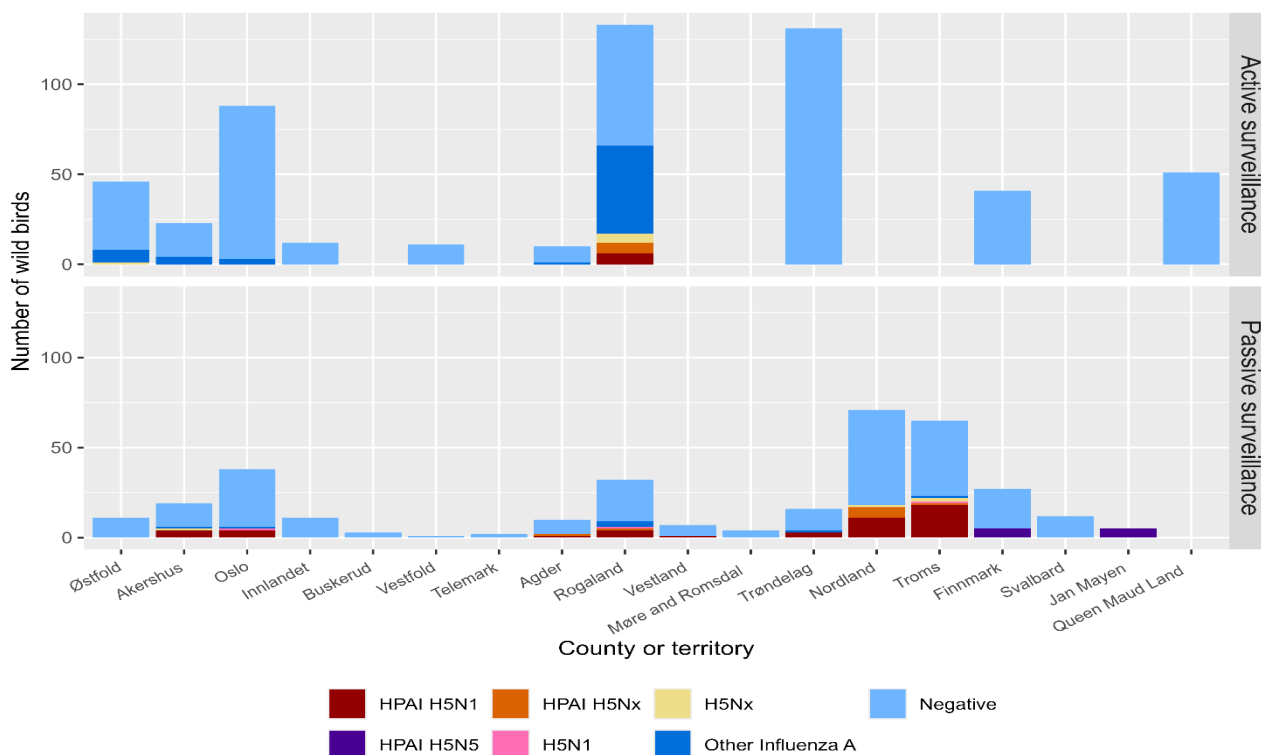


Figure 1. The number of wild birds from counties and territories included in the active and passive surveillance programmes for avian influenza in Norway in 2025.

Table 2. Number of wild birds sampled in the active surveillance programme for avian influenza in Norway in 2025.

Species (Eng.)	Species (Nor.)	Species (Lat.)	No. sampled	Positive				
				Inf. A	H5	H5Nx	HPAI H5N1	HPAI H5Nx
Mute Swan	Knoppsvane	<i>Cygnus olor</i>	3					
Antarctic Petrel	Antarktispetrell	<i>Thalassoica antarctica</i>	19					
Barnacle Goose	Hvitkinngås	<i>Branta leucopsis</i>	2					
Black-headed Gull	Hettemåke	<i>Chroicocephalus ridibundus</i>	18					
Black-legged Kittiwake	Krykkje	<i>Rissa tridactyla</i>	40					
Canada Goose	Kanadagås	<i>Branta canadensis</i>	18					
Common Goldeneye	Kvinand	<i>Bucephala clangula</i>	3					
Common Gull	Fiskemåke	<i>Larus canus</i>	25	3				
Common Murre	Lomvi	<i>Uria aalge</i>	6					
Eurasian Goshawk	Hønsenhawk	<i>Astur gentilis</i>	1					
Eurasian Wigeon	Brunnakke	<i>Mareca penelope</i>	11	5	3		3	
European Herring Gull	Gråmåke	<i>Larus argentatus</i>	38	1				
Glaucous Gull	Polarmåke	<i>Larus hyperboreus</i>	1					
Great Black-backed Gull	Svartbak	<i>Larus marinus</i>	7					
Common Teal	Krikkand	<i>Anas crecca</i>	81	50	12	3	3	6
Greylag Goose	Grågås	<i>Anser anser</i>	66					
Lesser Black-backed Gull	Sildemåke	<i>Larus fuscus</i>	20	5				
Mallard	Stokkand	<i>Anas platyrhynchos</i>	80	18	3	3		
Northern Pintail	Stjertand	<i>Anas acuta</i>	1					
Pink-footed Goose	Kortnebbgås	<i>Anser brachyrhynchus</i>	71					
Red-breasted Merganser	Siland	<i>Mergus serrator</i>	3					
Snow Petrel	Snøpetrell	<i>Pagodroma nivea</i>	9					
South Polar Skua	Sørjo	<i>Stercorarius macormicki</i>	23					
Total			546	82	18	6	6	6

Among all wild birds sampled through active or passive surveillance, HPAIV H5 was detected in samples from 77 birds. Sixty-five of the confirmed HPAI-positive wild birds in 2025 were identified through passive surveillance, and most of these birds were found dead. HPAIV was reported in 18 wild bird species in 2025 (Table 3). The geographical distribution of HPAI-detections is shown in Figure 2. The detected subtypes and the affected species, primarily raptors, colony-breeding seabirds and waterfowl, are consistent with detections reported across Europe in 2025.

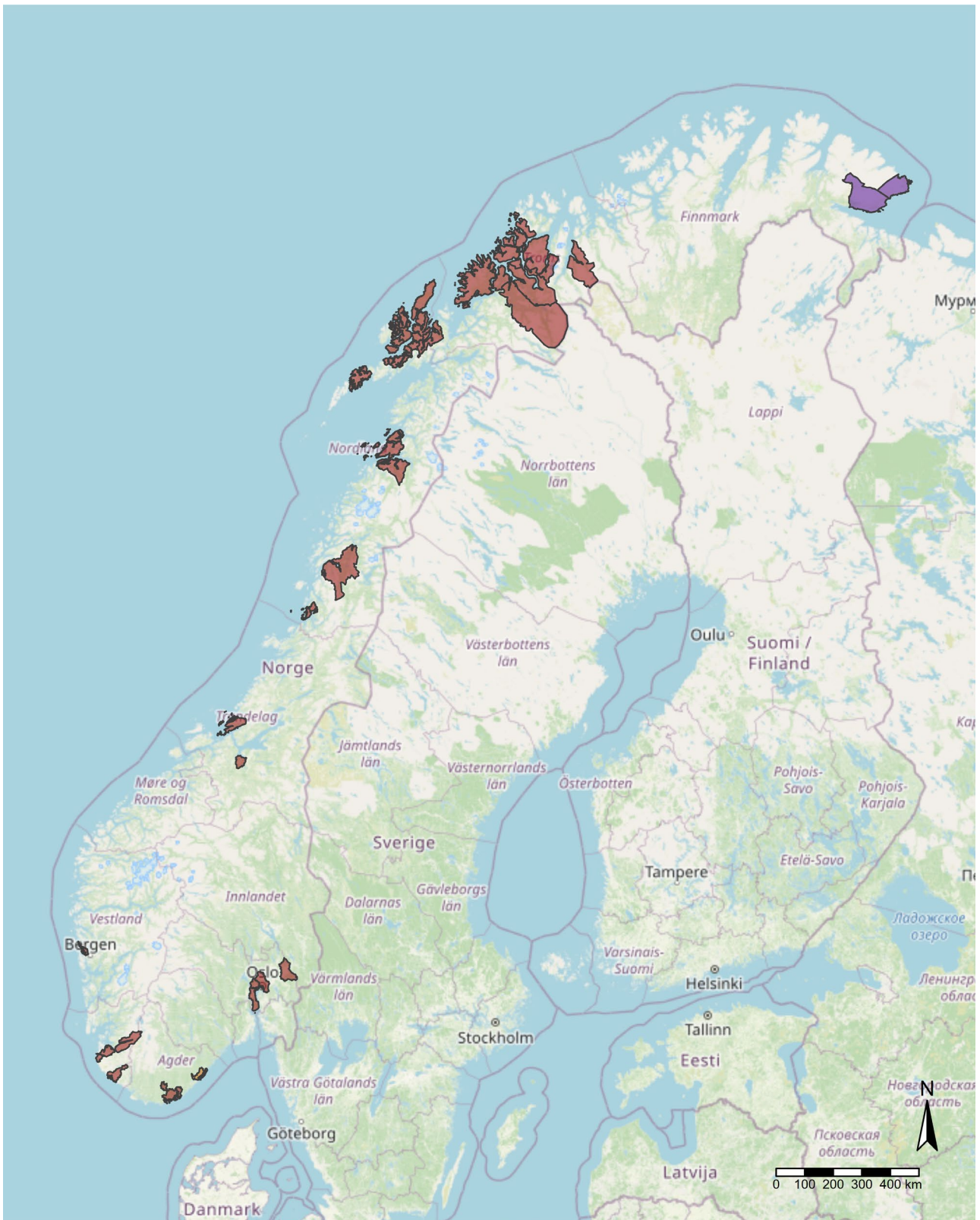


Figure 2. Geographical distribution of HPAIV detections in wild birds in Norway in 2025. Colour marks municipalities with one or more detections of HPAI-positive wild birds: HPAI H5N1 (red) and HPAI H5N5 (purple). If more than one HPAI subtype was detected in a municipality in 2025, the colour representing the most recent detected subtype at the end of the year is shown.

Table 3. Species distribution of HPAIV-positive wild birds in Norway in 2025.

Species (Eng.)	Species (Nor.)	Species (Lat.)	HPAI H5N1	HPAI H5N5	HPAI H5Nx
Mute Swan	Knoppsvane	<i>Cygnus olor</i>	5		
Whooper Swan	Sangsvane	<i>Cygnus cygnus</i>	3		
Barnacle Goose	Hvitkinngås	<i>Branta leucopsis</i>	1		
Canada Goose	Kanadagås	<i>Branta canadensis</i>	1		
Common Goldeneye	Kvinand	<i>Bucephala clangula</i>	1		
Common Gull	Fiskemåke	<i>Larus canus</i>		3	1
Eurasian Eagle-Owl	Hubro	<i>Bubo bubo</i>	1		
Eurasian Goshawk	Hønsehauk	<i>Astur gentilis</i>			1
Eurasian Wigeon	Brunnakke	<i>Mareca penelope</i>	3		
European Herring Gull	Gråmåke	<i>Larus argentatus</i>	12		4
Glaucous Gull	Polarmåke	<i>Larus hyperboreus</i>		4	
Great Black-backed Gull	Svartbak	<i>Larus marinus</i>	1	2	1
Greater White-fronted Goose	Tundragås	<i>Anser albifrons</i>	1		
Common Teal	Krikkand	<i>Anas crecca</i>	3		6
Gyrfalcon	Jaktfalk	<i>Falco rusticolus</i>	1		
Little Gull	Dvergmåke	<i>Hydrocoloeus minutus</i>	1		
Mallard	Stokkand	<i>Anas platyrhynchos</i>			1
Northern Raven	Ravn	<i>Corvus corax</i>		1	
Parasitic Jaeger	Tyvjo	<i>Stercorarius parasiticus</i>	1		
Peregrine Falcon	Vandrefalk	<i>Falco peregrinus</i>	1		
Gulls, Terns, Skuas, Skimmers (species unknown)	Måkefugler (art ukjent)	<i>Lari</i> (suborder)	16		1
Total			52	10	15

In 2025, 88 wild mammals, including both marine and terrestrial species, were sampled as part of passive surveillance for AI. Five Arctic foxes (*Vulpes lagopus*) from Svalbard, and one red fox (*Vulpes vulpes*) from Troms, were positive for HPAI H5N5, whereas one Eurasian otter (*Lutra lutra*) from Troms, dead in 2024 but tested in 2025, was H5Nx, i.e. NA subtyping and pathotyping was not successful due to low viral load (Table 4). Notably, in some of the earlier carnivore cases, such as the lynx testing positive in 2024, swab samples collected from the trachea and rectum tested negative, whereas samples collected from the brain during necropsy tested positive. This has prompted a revision of the written sampling instructions, recommending routinely sampling of the brain in cases where wild mammals show clinical signs consistent with AIV infection.

Table 2. Number of wild mammals sampled for surveillance of avian influenza in Norway in 2025.

Species (Eng.)	Species (Nor.)	Species (Lat.)	No. sampled	Positive				
				Inf. A	H5	H5Nx	HPAI H5N1	HPAI H5N5
Arctic fox	Fjellrev	<i>Vulpes lagopus</i>	51	5	5			5
Eurasian otter	Oter	<i>Lutra lutra</i>	21	1	1	1		
Harbor seal	Steinkobbe	<i>Phoca vitulina</i>	4					
Harbour porpoise	Nise	<i>Phocoena phocoena</i>	2					
Least weasel	Snømus	<i>Mustela nivalis</i>	1					
Red fox	Rødrev	<i>Vulpes vulpes</i>	3	1	1			1
Reindeer	Rein	<i>Rangifer tarandus</i>	1					
Sowerby's beaked whale	Nordspisshval	<i>Mesoplodon bidens</i>	1					
Sperm whale	Spermhval	<i>Physeter macrocephalus</i>	1					
Walrus	Hvalross	<i>Odobenus rosmarus</i>	3					
Total			88	7	7	1		6

In September 2025, an outbreak of HPAI was detected in a flock with 7,500 laying hens in Hadsel municipality in Nordland County. The birds showed clinical signs consistent with HPAI and were sampled based on suspicion. PCR analysis of tracheal and cloacal swabs confirmed the presence of HPAIV subtype H5N1. In this case, spillover from wild birds was suspected.

A separate surveillance report on avian influenza in poultry (serological surveillance) is available here: [Avian influenza in poultry - Norwegian Veterinary Institute](#).

Acknowledgements

The authors would like to thank the technical staff at the Norwegian Veterinary Institute for performing the analyses with excellence. Moreover, the authors would like to thank personnel from the Norwegian Food Safety Authority, the Norwegian Institute for Nature Research, the Norwegian Polar Institute, the Norwegian Nature Inspectorate, and others for collection and submission of samples.

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