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Continued expansion of high pathogenicity avian influenza H5 in wildlife in South America and incursion into the Antarctic region

OFFLU *ad-hoc* group on HPAI H5 in wildlife of South America and Antarctica

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Abstract

This report summarises the spread and impact of high pathogenicity avian influenza of the subtype H5 (HPAI H5) clade 2.3.4.4b in South America, its incursion into South Georgia, and the risk for further spread in the Antarctic region and for incursion into Oceania. The focus of the report is on HPAI H5 in wildlife, and covers neither spread in poultry nor sporadic spillover to humans, as these are the subjects of other reports. We do fully support a One Health approach to HPAI H5: an integrated, unifying approach that aims to sustainably balance and optimise the health of people, animals (wild and domestic) and ecosystems.

Between the first detection of HPAI H5 virus in South America in October 2022 and November 2023, the deaths of 597,832 birds of at least 82 species and 50,785 mammals of at least 10 species have been reported, with the bulk of the reported mortality occurring in Peru and Chile. The highest numbers of reported mortalities in association with the HPAI H5 outbreak include marine mammal species, such as South American sea lions (*Otaria byronia*) (~32,000) and southern elephant seals (*Mirounga leonina*) (~17,000), and seabird species, such as cormorants (*Phalacrocoracidae*) (~262,000), Peruvian boobies (*Sula variegata*) (~242,000), Peruvian pelicans (*Pelecanus thagus*) (~62,000), Humboldt penguins (*Spheniscus humboldti*) (~4,000), various species of gulls (*Larus* spp.) (~7,000), terns (*Larosterna inca*, *Sterna hirundinacea* and *Thalasseus* spp.) (~3,500) and frigatebirds (*Fregata* spp.) (~7,000). These numbers undoubtedly represent only a fraction of the total mortality.

The first incursion of HPAI H5 virus into the Antarctic region was detected in October 2023 in South Georgia (Islas Georgia del Sur), part of the Scotia Arc. At the same time, virus incursion was detected in the Falkland Islands (Islas Malvinas), on the continental shelf of South America. The species found infected or suspected infected with HPAI H5 virus include brown skua (*Stercorarius antarcticus*), kelp gull (*Larus dominicanus*), southern fulmar (*Fulmarus glacialoides*), black-browed albatross (*Thalassarche melanophris*), grey-headed albatross (*Thalassarche chrysostoma*) and southern elephant seal, and could be involved in the next stage of spread of HPAI H5 virus in the Antarctic region. The risk of viral transmission to other islands of the Scotia Arc and the Antarctic Peninsula is considered high, and considered medium to several islands that lie in the southern parts of the Pacific, Atlantic and Indian Oceans. From these locations, HPAI H5 virus is likely to spread further in the Antarctic region; and from there, incursion into Oceania is plausible.

HPAI H5 virus is likely to spread further among Antarctic wildlife, potentially infecting the 48 species of birds and 26 species of marine mammals which inhabit this region. The negative impact of HPAI H5 on Antarctic wildlife could be immense, because their presence in dense colonies of up to thousands of pinnipeds and hundreds of thousands of birds facilitates virus transmission and may result in high mortality. As has been seen in the northern hemisphere, it is possible that HPAI H5 virus will persist in the Antarctic region in coming years and spread variably among its wildlife populations. Although little can be done to stop virus spread, there are a few options for response available. It is important to continue monitoring and surveillance of wildlife populations for HPAI H5 virus incursion and assessing spread and impact of disease, both to provide information for wildlife managers to adapt conservation plans, and to help policymakers mitigate and prevent future HPAI outbreaks. It is also important to take biosafety measures to reduce the risk of human-mediated spread of HPAI H5 virus to new areas, and to reduce the risk of human infection with HPAI H5 virus.

1. Emergence and spread of HPAI H5 from 1996 until July 2023

It has taken 27 years for the currently circulating high pathogenicity avian influenza virus of the H5 subtype (HPAI H5) to spread from east Asia to the southern tip of South America. Viruses of this so-called goose/Guangdong/1996 (Gs/GD) lineage were first detected in commercially farmed geese in China in 1996, circulated and evolved in poultry for several years, and subsequently spilled over into wild birds, causing multiple outbreaks in wild birds and poultry in Asia, Europe and Africa in subsequent years. In 2021 a HPAI H5N1 virus belonging to clade 2.3.4.4b of the Gs/GD lineage spread across the Atlantic Ocean to North America. The virus reached South America in October 2022, and rapidly spread southwards. It was first detected in Tierra del Fuego, the southern tip of South America, in April 2023. The spread of HPAI H5 in South America in this period has been described in the previous OFFLU statement and published in August 2023 (1).

2. HPAI H5 in wildlife in South America, 2022 to 2023: overall wildlife mortality and virus spread since July 2023

The overall mortality of wildlife in South America between the arrival of HPAI H5 virus in October 2022 and December 2023 includes 597,832 birds and 50,785 mammals (Annex 1), with the bulk of the mortality occurring in seabirds and marine mammals in Peru (557,140 seabirds and 10,458 marine mammals) and Chile (29,432 seabirds and 20,179 marine mammals). South American sea lions (*Otaria byronia*) and southern elephant seals (*Mirounga* leonina) were the most affected marine mammals, but smaller mortalities of South American fur seals (*Arctocephalus australis*), otters (*Lontra* spp.) and cetaceans have also been linked to HPAI H5. Among seabirds, Guanay cormorants (*Leucocarbo bougainvilliorum*), Peruvian boobies (*Sula variegata*), Peruvian pelicans (*Pelecanus thagus*), Humboldt penguins (*Spheniscus humboldti*), and various species of gulls (*Larus* spp.), terns (*Larosterna inca*, *Sterna hirundinacea* and *Thalasseus* spp.) and frigatebirds (*Fregata* spp.) appear to have been the most affected. Only a small proportion of animals found dead in the region were tested for HPAI H5 virus, hence it is possible that some mortalities were due to causes other than HPAI H5. Nevertheless, since the number of marine animals found dead in the region during this period was orders of magnitude greater than in previous years, it is reasonable to attribute the majority of these deaths to HPAI H5. It is also worth considering that the numbers of carcasses found and recorded are undoubtedly only a fraction of the total number of individuals that died, especially for those dying at sea.

Genetic studies published thus far have confirmed that all HPAI strains circulating in South America belong to the clade 2.3.4.4b, are of subtype H5N1 and are derived from strains that circulated in North America in 2021–2022 (2-10). Furthermore, these studies have revealed that the HPAI H5N1 viruses infecting marine mammals in Peru and Chile have shown mutations characteristic of adaptation to the mammalian hosts in which they were found, whilst retaining the ability to infect birds (7, 9). This implies that these viruses have the capacity for a broad and flexible host range, increasing their ability to spread and sustain year-round transmission across different wildlife populations. Furthermore, the viruses detected in mammals with adaptive mutations that may reflect enhanced replication in these hosts raises concern on the increased potential to infect humans. Fortunately, despite the extensive infection of marine mammals, the number of human infections has remained low in South America with only two cases reported thus far, associated with exposure to backyard poultry and contaminated environments, respectively (one in Ecuador in January 2023, and the other in Chile in March 2023 (11, 12)). Notably, the virus implicated in the human case in northern Chile possessed mammalian adaptations in the PB2 segment, namely the mutations D701N and Q591K, which were also present in phylogenetically clustering viruses found in sea lions and a shorebirds in Chile (9, 12).

Since the previous OFFLU statement in August 2023 (1), the following events are of significance to wildlife:

- Brazil reported mortality of >900 terns along its coast between May and July 2023. Four species were affected, including South American terns (*Sterna hirundinacea*), Cayenne terns (*Thalasseus acuflavidus eurygnathus*) and Royal terns (*Thalasseus maximus*) which are native to the region, as well as common terns (*Sterna hirundo*) which are migrants from the northern hemisphere (13). Genetic analyses revealed that the virus from a Cayenne tern was closely related to the strains that circulated among swans in Uruguay and seabirds in Chile, indicating that transmission likely occurred locally in South America (10).
- In September 2023, HPAI H5 virus was detected for the first time in the Galápagos Archipelago. The virus was detected in a small number of great frigatebirds (*Fregata minor*) at Genovesa Island and red-footed boobies (*Sula sula*) at San Cristóbal and Genovesa Islands (14). These detections were made following mortalities of these species, but no estimates of the number affected have been published thus far. The Galápagos are home to a large number of endemic seabirds and marine mammals, which would presumably be susceptible to HPAI H5 virus if it spread locally, with potentially disastrous impacts.
- In October 2023, more than 1,700 South American sea lions and South American fur seals were found dead along the coasts of Uruguay and southernmost Brazil, and the majority of these deaths were attributed to HPAI H5 (14-16). This represents a northward spread of the South American sea lion mortality previously seen in Argentina; however, the mortality in Uruguay and Brazil comprised a substantially larger proportion of South American fur seals. This suggests that the greater mortality of South American sea lions (compared to South American fur seals) seen in Argentina may have reflected regional differences in species distribution and habitat use, and not species-specific differences in susceptibility to the virus. This implies that clustered populations of fur seals may be highly vulnerable to HPAI H5, for example in the case of Antarctic fur seals (*Arctocephalus gazella*) for which 95% of their global breeding population is concentrated in South Georgia (Islas Georgia del Sur).
- In October and November 2023, a mass mortality of southern elephant seal pups was attributed to HPAI H5 in Peninsula Valdés, Chubut, Argentina. It was estimated that 97.4% of the pups died, which represents an estimated death toll of 17,400 individuals (17). There is also evidence that substantial numbers of adults may have died at sea, although the death toll could not be estimated. This is the single largest mortality of southern elephant seals on record, and may have profound and long-lasting effects on the viability of this population, which produces >5% of global pup production of this species (18).

- In October and November 2023, HPAI H5 was confirmed in several species of terns at numerous sites along the coast of Patagonia, Argentina. This included South American terns, Cayenne terns and Royal terns. At Punta Leon breeding colony, all three species of terns, plus imperial cormorants (*Leucocarbo atriceps*) and kelp gulls (*Larus dominicanus*) were confirmed positive. Of these, terns were the species displaying the most severe neurological signs followed by death, and suffered acute high mortality over 2–3 weeks, affecting over 60% of the colony (>2,000 birds found dead). Interestingly, kelp gulls appeared to experience much lower morbidity and mortality, in spite of this species being frequently seen scavenging on South American sea lions, southern elephant seals and seabirds that had died from HPAI H5 in the region. The clinical signs observed in symptomatic kelp gulls also seemed milder (ruffled feathers, conjunctivitis and lethargy) than those seen in tern species (severe neurological and respiratory signs), suggesting that kelp gulls may be more resilient to the infection.
- In October and November 2023, HPAI H5 was detected for the first time in the Falkland Islands (Islas Malvinas). The detections were made from two southern fulmars (*Fulmarus glacialoides*) and two black-browed albatrosses (*Thalassarche melanophris*) found dead at different sites (19). The positive detection in one of the black-browed albatrosses, at Steeple Jason Island, was associated with mortality of approximately 30 black-browed albatrosses (19). This is concerning because Steeple Jason Island is home to ~200,000 breeding pairs of black-browed albatrosses, representing nearly half of the species' population at the Falkland Islands (Islas Malvinas) which in turn concentrates 70% of the species' global population (20). Furthermore, the archipelago is a critically important breeding habitat for numerous seabird species such as penguins, petrels and shearwaters.
- In November 2023, the mortality of 1,000 great frigatebirds and 6,000 magnificent frigatebirds (*Fregata magnificens*) on the coast of Ecuador was attributed to HPAI H5 (14). Although HPAI H5 virus infection had been previously detected in frigatebirds, this was the first large-scale mortality event attributed to HPAI H5. This highlights that other populations of frigatebirds may also be at risk, which is concerning for critically endangered species such as the Atlantic lesser frigatebird (*Fregata trinitatis*) and the Christmas frigatebird (*Fregata andrewsi*).
- In November 2023, mortalities of puna (James's) flamingos (*Phoenicoparrus jamesi*) were recorded in Catamarca (220 individuals) and La Rioja (17 individuals), in northwest Argentina (21, 22). HPAI H5 virus infection was confirmed as the cause of death of individuals in Catamarca (23). This is the first mass mortality of flamingos attributed to HPAI H5, which raises concern for the populations of puna flamingos (which has IUCN assessment 'Near threatened', stable) and Andean flamingos (*Phoenicoparrus andinus*) (IUCN 'vulnerable', declining), both of which are endemic to the Andes highlands.
- A number of HPAI H5 virus detections have been made in migratory seabirds and shorebirds found dead in non-breeding areas along the coast of South America, such as: waved albatross (*Phoebastria irrorata*) in Peru, elegant tern (*Thalasseus elegans*), sanderling (*Calidris alba*), sooty shearwater (*Ardenna grisea*), southern giant petrel (*Macronectes giganteus*) and black-browed albatross in northern Chile, common tern, Manx shearwater (*Puffinus puffinus*), white-chinned petrel (*Procellaria aequinoctialis*) and Antarctic prion (*Pachyptila desolata*) in Brazil (14). These

detections demonstrate that seabirds are being exposed to the virus during their migration, raising concern of their potential role in transporting it to breeding colonies upon returning for the nesting season. Furthermore, considering that many of these species are pelagic, these detections suggest at-sea transmission among seabirds may be occurring.

3. Incursion of HPAI H5 into South Georgia (Islas Georgia del Sur)

The first incursion of HPAI H5 virus into the Antarctic region was detected in a brown skua (*Stercorarius antarcticus*) found dead on 8 October 2023 on Bird Island, South Georgia (Islas Georgia del Sur) (3). South Georgia (Islas Georgia del Sur) is part of the Antarctic region based on its location south of the Antarctic polar front (Figure 1). However, it is not located within the area south of 60º South Latitude to which the Antarctic Treaty applies.

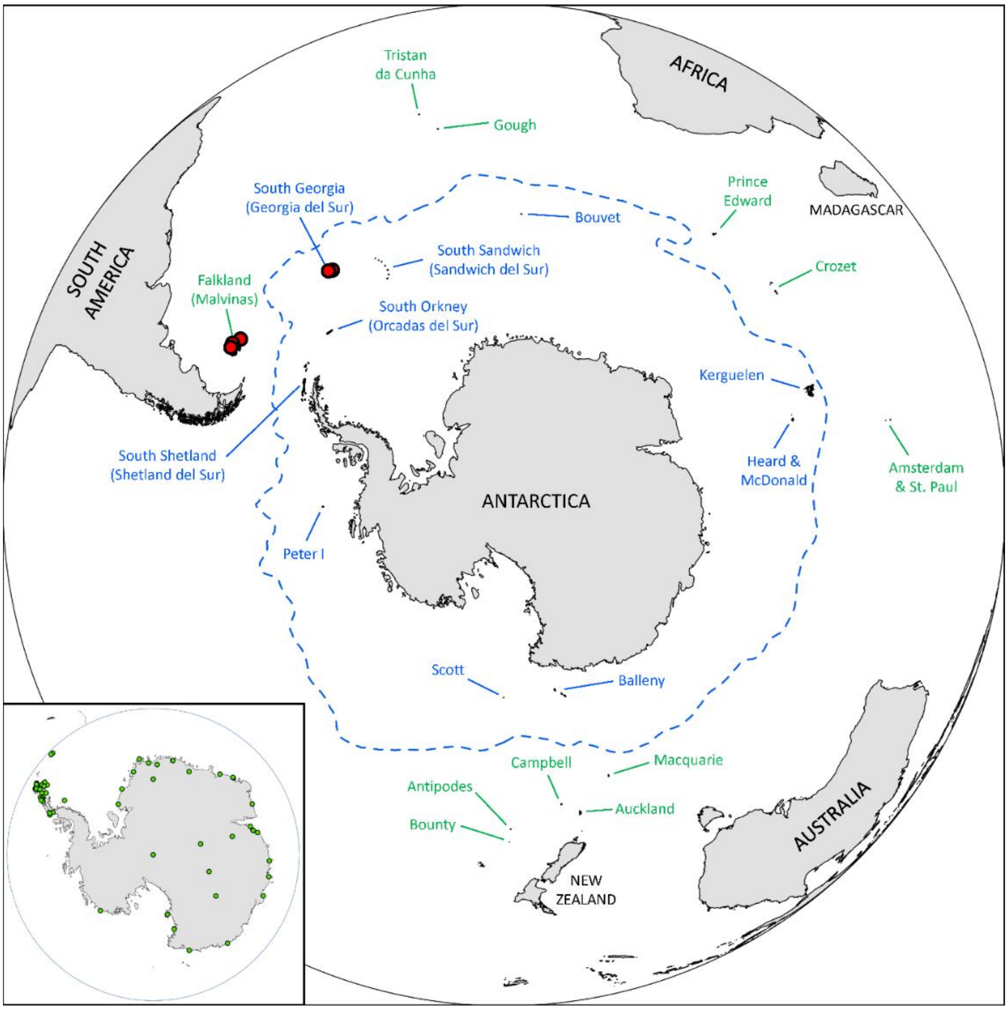

Fig. 1 *Map of Antarctica, showing the approximate position of the Antarctic Polar Front (dashed blue line, drawn from (24)) and the location of the island groups in the Antarctic (blue) and Subantarctic (green) island groups. Red dots represent confirmed HPAI H5N1 cases as of 15 December 2023.* ***Inset.*** *Map of Antarctica with research stations indicated by green dots. Locations of research stations were derived from the Council of Managers of National Antarctic Programs (25). Blue line here shows the 60º South Latitude.*

The first indication of HPAI H5 virus incursion in South Georgia (Islas Georgia del Sur) was on 17 September 2023, when a southern giant petrel with neurological signs consistent with HPAI was observed on Bird Island. It died and its carcass was scavenged by brown skuas and other southern giant petrels. On 8 October, brown skuas with neurological signs were observed at the same location, and by 17 November 57 brown skuas had been found dead there. By virological analysis, all 15 brown skuas and 6 of 18 kelp gulls found dead and sampled on Bird Island and four other locations on South Georgia (Islas Georgia del Sur) between 8 October and 3 November were found to be infected with HPAI H5N1 virus. By genetic analysis, the HPAI H5N1 virus from Bird Island clustered with those from Uruguay, Peru and Chile collected between December 2022 and April 2023. However, genetic analysis also indicated that there were insufficient virus sequences available in the public database to characterise the evolutionary ancestry of the virus more accurately (3).

There also was evidence of HPAI-associated mortality of southern elephant seals on South Georgia (Islas Georgia del Sur). This is of concern because of the catastrophic mortality HPAI H5 already has shown to cause at Península Valdés (17), and because more 50% of the global pup production of this species takes place at South Georgia (26). The first indication was on 31 October 2023, when southern elephant seals in Moltke Harbour were observed with respiratory signs or were found dead (3). By 20 November, high mortality of southern elephant seal pups had been observed at three sites around South Georgia (Islas Georgia del Sur) (27), and by 26 November, southern elephant seals suspected of HPAI had been observed at ten different sites around South Georgia (Islas Georgia del Sur) (28, 29). However, nasal and rectal swabs of three southern elephant seals found dead on 31 October were negative for HPAI virus by virological analysis, consisting of real-time reverse transcription polymerase chain reaction (3). A possible reason for these negative results may be due to tropism of HPAI H5 virus for the central nervous system of seals, which requires sampling of the brain but was not performed in this case for biosafety reasons (30). Further sample collection from southern elephant seals on South Georgia (Islas Georgia del Sur) is being undertaken to confirm the presence of HPAI H5 virus. Between 4 and 26 November, further suspected cases in brown skuas, kelp gulls, southern giant petrels and Antarctic terns (*Sterna vittata*) have been reported along the east coast of South Georgia (Islas Georgia del Sur) (28, 29) .

4. Risk for spread of HPAI H5 to other parts of the Antarctic region

Antarctica can be defined in different ways. The provisions of the Antarctic Treaty apply to the area south of 60 degrees Southern Latitude, including all ice shelves (31). However, biogeographically (i.e. based on the distribution of species and ecosystems in space and time), the Antarctic region extends north of this line and includes the waters and islands up to the Antarctic polar front, the boundary where southern, colder and nutrient-rich waters meet warmer waters. The Antarctic convergence is also the northern limit of the area of the Convention for the Conservation of Antarctic Marine Living Resources (32). For the purpose of this report, we will consider the Antarctic region from the biogeographical perspective.

Information on the HPAI H5 virus incursions into the Falkland Islands (Islas Malvinas) and South Georgia (Islas Georgia del Sur)—in particular, the avian and mammalian species affected or suspected, and when and where they were found—helps to understand how the virus reached these islands. This information also helps to assess what the next stage may be in the spread of HPAI H5 virus into the Antarctic region.

The Patagonian Shelf may have an important role in the recent epidemiology of HPAI H5 (33). The Patagonian Shelf adjoins the coasts of Uruguay, Argentina and the Falkland Islands (Islas Malvinas), extending from 35 degrees Southern Latitude south to the tip of Tierra del Fuego, and from the coast to approximately the 1000 m isobath. The Patagonian Shelf in the Southwest Atlantic Ocean is an important foraging ground for a large number of top predators, including albatrosses, petrels, penguins, sea lions, and elephant seals. More than 60 species of resident and visiting seabirds forage there (34, 35). Since there was high HPAI-associated mortality of seabirds and southern elephant seals in October and November 2023 on the coast of Argentina, and of South American sea lions and South American fur seals since August 2023 on the coast of Argentina, Uruguay and southern Brazil (see above), all adjoining the Patagonian Shelf, it is probable that the seabirds foraging on the Patagonian Shelf in recent months were exposed to HPAI H5 virus.

Of the avian species confirmed or suspected for HPAI H5 virus infection in the Falkland Islands (Islas Malvinas) and South Georgia (Islas Georgia del Sur), the majority are species that use the Patagonian Shelf as a staging area during the austral winter, which is the period outside the breeding season for many species. From there, they return between September and November, the dates when HPAI virus detections or suspicions occurred, to their breeding sites, which —except for the southern fulmar— include the Falkland Islands (Islas Malvinas) and South Georgia (Islas Georgia del Sur) (36). Another suspected avian species regarding virus transmission, the southern giant petrel, is present year-round on South Georgia (Islas Georgia del Sur), but has a large home range and also disperses widely over the Southern Ocean including the Patagonian Shelf during the non-breeding period (37). Therefore, it is possible that these avian species became infected with HPAI H5 virus on the Patagonian Shelf and introduced it onto Falkland Islands (Islas Malvinas) and South Georgia (Islas Georgia del Sur), although an alternative or additional possibility for some species (southern giant petrel, brown skua) is local infection by scavenging on contaminated carcasses. The latter route of infection also is most likely for the kelp gull, found positive for HPAI H5 virus on South Georgia (Islas Georgia del Sur), because it is largely resident there.

Assuming that these avian species (brown skua, southern fulmar, black-browed albatross, grey-headed albatross, Antarctic prion) did become infected on the Patagonian Shelf, to which locations could they introduce HPAI H5 virus?

Brown skuas that spend the austral winter on the Patagonian shelf breed on other islands of the Scotia Arc and on the northern part of the Antarctic Peninsula. Alternatively, they may fly to breeding sites on Subantarctic islands in the southern Atlantic Ocean (Tristan da Cunha, Gough and Bouvet Islands) and may come in contact with brown skuas that have been wintering around Africa and breed on Subantarctic Islands in the southern Indian Ocean (Prince Edward, Crozet, and Kerguelen Islands) (38).

For southern fulmars, the closest breeding sites from the Falkland Islands (Islas Malvinas) are the South Sandwich Islands (Islas Sándwich del Sur), the South Orkney Islands (Islas Orcadas del Sur), the Antarctic Peninsula and Peter I Island (39).

Black-browed albatrosses—besides breeding on the Falkland Islands (Islas Malvinas) and South Georgia—also breed on other (sub-)Antarctic islands including Crozet, Kerguelen, and Heard & McDonald Islands. Later in the breeding season, birds from South Georgia (Islas Georgias del Sur) may also travel up to c. 3000 km from their breeding sites, especially to the Antarctic Peninsula and South Orkney Islands (Islas Orcadas del Sur), but birds from the Falkland Islands (Islas Malvinas) remain close to their colonies during the whole breeding period. Post-breeding, the majority of Falkland Islands (Islas Malvinas) birds remain on the Patagonian Shelf throughout the year, while birds from South Georgia (Islas Georgias del Sur) migrate primarily northeast across the South Atlantic to the coastal shelf of South Africa and the Benguela Current area, with small proportions wintering on the Patagonian Shelf or around Australia (40).

Grey-headed albatrosses—besides breeding on South Georgia (Islas Georgia del Sur)—also breed at other Subantarctic islands including Prince Edward, Crozet, Kerguelen, and Macquarie. This species has a circumpolar distribution over cold Subantarctic and Antarctic waters (41). Movements of non-breeding grey-headed albatrosses have only been reported for birds breeding on South Georgia (Islas Georgia del Sur). They showed one of three migratory movements, (i) residence in the southwest Atlantic and adjacent areas (including the Patagonian Shelf); (ii) return migrations to winter in habitats known to be used by other albatrosses in the Indian Ocean; and (iii) one or more global circumnavigations—always in eastward direction—with foraging in areas and habitats used in options (i) and (ii) and also in additional staging areas in the Indian and Pacific Oceans (42).

Antarctic prions are the most southerly breeding of all prion species. Individuals that spend the austral winter on the Patagonian shelf may nest in large numbers on all islands of the Scotia Arc. Large numbers of subspecies of Antarctic Prion breed on subantarctic islands in the Indian Ocean, near New Zealand, and probably near the Antarctic continent on Scott Island. This species breeds in large colonies in self-excavated burrows in areas with moss vegetation, or in rock crevices. They congregate in large rafts at sea just before dusk and attend the colonies in huge flocks just after dark. After the breeding season, Antarctic Prions disperse in a wide geographical range between the Antarctic pack-ice in the South and about 35 degrees south. They are commonly found on the Patagonian Shelf and in the Humboldt Current off South America during the austral winter. One infected Antarctic Prion was found in Brazil (Annex 1). This bird probably originates from the breeding colonies in the South Atlantic (based on (43)), although Antarctic Prions from South Georgia can also disperse into the Pacific (44).

Besides avian species, information on suspected HPAI H5 virus infection in southern elephant seals in South Georgia (Islas Georgia del Sur) also helps both to understand how the virus reached these islands and to assess what the next stage may be in the spread of HPAI virus into the Antarctic region. It is possible that southern elephant seals at South Georgia (Islas Georgia del Sur) initially acquired the infection locally, by contact with infected birds (e.g. brown skua, southern giant petrel, kelp gull) or haul-out sites contaminated with their faeces. Alternatively, infected southern elephant seals from the Patagonian Shelf and adjoining coasts—e.g. Península Valdés where there was a large die-off of this species—may have introduced the virus to South Georgia (Islas Georgia del Sur). It fits specifically with the immigration of southern elephant seals from Peninsula Valdes to South Georgia (Islas Georgia del Sur) during the post-breeding moulting season, and emigration of individuals to the South Shetland Islands (Islas Shetland del Sur) (45). From South Georgia (Islas Georgia del Sur), it is possible that infected southern elephant seals transport the virus to the remainder of the Scotia Arc—South Shetland Islands (Islas Shetland del Sur), South Orkney Islands (Islas Orcadas del Sur), and South Sandwich Islands (Islas Sándwich del Sur)—and to the Antarctic Peninsula. This fits with the general migration patterns of southern elephant seals, which leave their breeding sites after breeding or moulting and migrate south to Antarctica to feed on squid and fish at the edge of the sea-ice (reference).

Based on these data, the above-named species could be involved in the next stage of HPAI H5 virus spread in the Antarctic region. The risk of infection via these species is considered high for other islands of the Scotia Arc and the Antarctic Peninsula, and considered intermediate for several islands that lie in the southern parts of the Pacific, Atlantic and Indian Oceans, from west to east: Peter I, Tristan da Cunha, Gough, Bouvet, Prince Edward, Crozet, Kerguelen Islands. The introduction of HPAI H5 virus to these locations during the breeding season, when many Antarctic bird and mammal species are aggregated at high densities, is likely to result in rapid local spread associated with high mortality in several of these species, as has been seen in continents where the virus already has become established. Details of the avian, pinniped, and cetacean species that may be affected (Annex 2) are provided in the previous OFFLU update (1, 46-48).

If HPAI H5 virus completes the above-suggested stage of spread, further virus spread in the Antarctic region is likely given the many avian and mammalian species that probably are susceptible to infection and their overlapping ranges that form a wide circumpolar band around the south pole (Figure 2). This virus spread in the Antarctic region, which consists of dense breeding colonies or other aggregations of susceptible avian or mammalian hosts at variable distances of tens to hundreds of kilometres from each other, can be compared to a relay race, with the virus as baton, infected migrating hosts as runners, and common foraging/stopover/breeding sites, as relay stations. How far the virus is able to spread in the Antarctic region depends on the length of the relays (which is determined by the distance that infected migrating hosts travel during the period of infection, which is about 4 to 7 days) (49-51), and the success of virus transfer to new migrating hosts at the relay stations (which is increased by local virus amplification, and determined in part by the number and density of susceptible hosts at the relay station).

On the Antarctic continent several scenarios are plausible. For example, if HPAI virus enters one of the emperor penguin (*Aptenodytes forsteri*) breeding colonies, that are located on the sea ice along the edge of the whole Antarctic continent (52), it could potentially spread to adjacent emperor penguin colonies via scavenging birds including southern giant petrels and south polar skuas (*Catharacta maccormicki*). In this way, circumpolar spread of HPAI virus could occur to the whole emperor penguin population.

If HPAI virus infects either Weddell seals (*Leptonychotes weddellii*) or crabeater seals (*Lobodon carcinophaga*), which are distributed all around the Antarctic continent (53, 54), the virus could spread to other seals of this species, especially when they haul out in small multi-species groups on ice floes along the coast. In this way, HPAI virus could spread throughout the whole crabeater and Weddell seal populations. Birds scavenging on seal carcasses could play a role in transmission. Such scavenging birds include southern giant petrels, south polar skuas and snowy sheathbills (*Chionis albus*) for carcasses on land (55-

58), and southern fulmars, Cape petrels (*Daption capense*) and Wilson's storm-petrels (*Oceanites oceanicus*) for carcasses in the water (59).

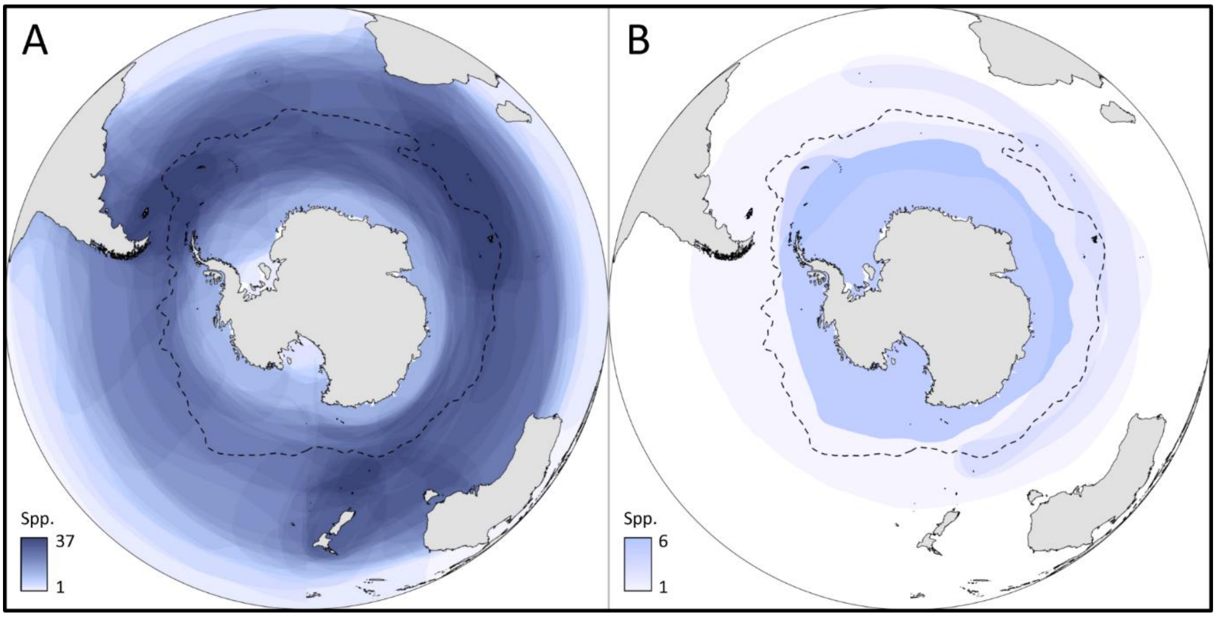

Fig 2. *Geographic distribution of seabird diversity (A), and pinniped diversity (B). These maps show the number of avian and pinniped species occurring per location, as a measure of the potential for HPAI H5 virus to spread. Avian and pinniped diversity are drawn using the same colour gradient and were derived from publicly-available species distribution maps (BirdLife International and Handbook of the Birds of the World, 2019; International Union for Conservation of Nature and Natural Resources, 2019).*

If HPAI virus infects any of the above-named scavenging avian species, they not only can spread the virus further along the continent of Antarctic, but also transport the virus to any of the Antarctic islands like Bouvet Island, where they have breeding sites. Once present on an Antarctic island, the virus could spread to other avian species with breeding colonies on that island. Please see the previous OFFLU update for more details of avian, pinniped and cetacean populations at risk of HPAI in the Antarctic region.

5. Risk of spread of HPAI H5 to Oceania

Oceania is the only geographical region where the Gs/GD lineage of HPAI H5 virus has not been detected (as of December 2023). The term Oceania is used here to denote the geographical region which includes most of the island countries and territories in the Pacific Ocean, as well as Australia**.** Current risk assessments focus on potential incursion from Asia and North America, through two main scenarios (60): First, incursion via migratory shorebirds and seabirds. Oceania comprises the key non-breeding area for shorebirds utilising the East-Asian Australasian flyway. Millions of shorebirds breeding in North America and Asia arrive in Oceania between September and November each year, following stopover sites in China, southeast Asia and Indonesia (61). Similarly, millions of seabirds arrive to breed in Australia, such as the short-tailed shearwater (*Puffinus tenuirostris*), which spends the non-breeding season in the north Pacific. (62) Presently, the likelihood of this scenario is considered moderate. Second, incursion via local movements of ducks within the Australo-Papuan Zone (east of the Wallace Line). Presently, the likelihood of this scenario is considered moderate given no evidence of Gs/GD HPAI H5 virus east of the Wallace line, however this clade was reported on the island of Borneo in 2022 which is adjacent to the Wallace line (63, 64). While these scenarios comprise the most likely routes of incursion to Oceania, a third scenario is also plausible: incursion via the Antarctic region. Due to limited available data on avian population structures or fine-scale tracking data, there is high uncertainty around this third scenario.

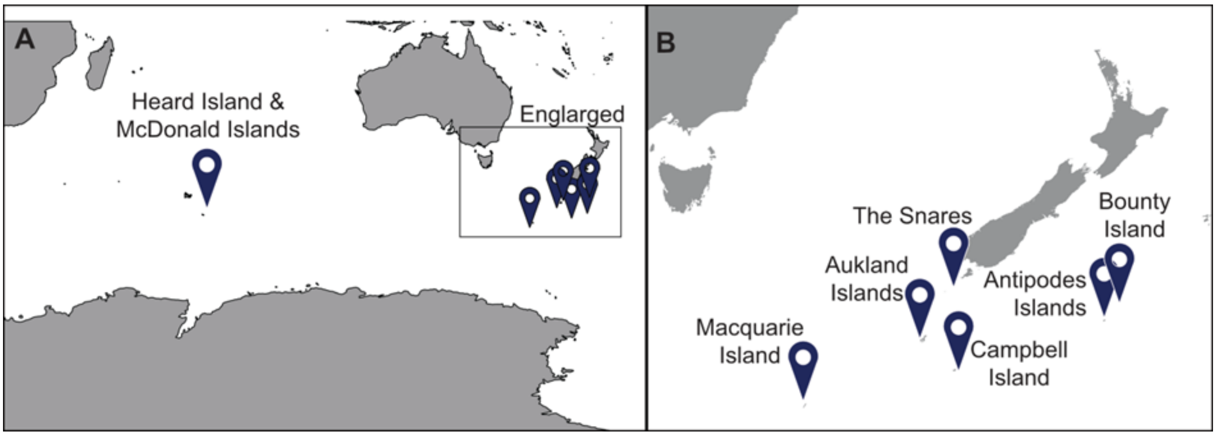

Fig 3: *Subantarctic islands at the interface between the Antarctic region below and Oceania above, with the Heard & McDonald Islands furthest west (A). Subantarctic islands located around New Zealand (B).*

There are a number of Subantarctic islands at the interface between the Antarctic region and Oceania, which include Macquarie (54.6208° S, 158.8556° E), Auckland (50.7447° S, 166.0564° E), Campbell (52.5372° S, 169.1445° E), Snares (48.0352° S, 166.5480° E), Antipodes (49.684°S, 178.781°E) and Bounty Islands (47.7333° S, 179.0500° E) (Figure 3). These Subantarctic islands are largely occupied by members of the Charadriiformes (n=31 species recorded), Sphenisciformes (n=12 species recorded), Procellariiformes (n=50 species recorded), and Pelecaniiformes (n=11 species recorded). The islands are also occupied by a number of Anseriformes (n=13 species recorded), including Pacific black duck (*Anas supercilliosa*) and mallards (*Anas platyrhynchos*), which are also found in Australia and New Zealand, although genetic studies indicate movement of these ducks to be localised. Numerous passerine species are also present, although many are introduced species including blackbirds (*Turdus merula*), chaffinches (*Fringilla coelebs*) and starlings (*Sturnus vulgaris*). These islands are also important areas for Subantarctic fur seals (*Arctocephalus tropicalis*), Antarctic fur seals (*Arctocephalus gazella)*, New Zealand fur seals (*Arctocephalus forsteri)* and southern elephant seals. The more distant Antarctic Heard and McDonald Islands (53.0818° S,73.5042° E) are occupied mostly by Procellariiformes (n=32 species recorded) and Sphenisciformes (n=7 species recorded). They are also breeding sites for Subantarctic fur seals, Antarctic fur seals, southern elephant seals, but are also used year-round by non-breeding and juvenile leopard seals (*Hydrurga leptonyx*), and both Weddell and crabeater seals are occasional visitors.

Could Gs/GD HPAI H5 virus arrive with the long-distance movements of seabirds directly from the Antarctic region adjacent to South America? Numerous seabird species have circumpolar distributions that include South Georgia and the Subantarctic Islands of Oceania, such as brown skua and northern giant petrel (*Macronectes halli*). Limited available tracking data, largely from breeding individuals, demonstrate regionally restricted movements (65). However, kernel density analysis of non-breeding brown skuas tagged on Crozet and Kerguelen Islands indicate that birds connect Southern Africa with Australia, demonstrating potentially vast long-distance movements in this species, which has been shown to be infected with HPAI H5 (38). Northern giant petrels, which visit Australia, New Zealand and associated islands have long-distance movement whereby young birds tend to disperse great distances from the breeding colonies, often with an eastward movement likely due to prevailing westerly winds such that birds from the Oceania Subantarctic islands (e.g. Macquarie Island) may disperse to South America, including one confirmed detection of a bird banded on Macquarie Island found on South Georgia (66-69). Unfortunately, there is no available tracking data from kelp gulls and southern fulmars from Oceania's Subantarctic islands, as these species similarly have large circumpolar distributions, are a "scavenger species", and have been found infected with H5 HPAI on South Georgia and the Falkland Islands. Given the almost 10,000 km between the Subantarctic islands around South America and Oceania, this scenario would require (a) birds be capable of long-distance flight while infected, and (b) this distance be covered in a short period of time (*i.e.* no longer than the duration of infection). Studies of albatross flight indicate a maximum speed of ~20 m/sec (~70 km/hr) (70), such that a wandering albatross (*Diomedea exulans*) could theoretically take a minimum of 5.7 days to fly from Tierra del Fuego to New Zealand, which is within the expected range of duration of infection.

An additional scenario becomes plausible only when HPAI H5 virus infections occur in the area of Antarctic directly south of Oceania (i.e Wilkes Land, Victoria Land and the Ross Sea). Numerous seabird species utilizing the Subantarctic islands adjacent to Oceania, New Zealand and Australia for breeding rely on the polar front as a key foraging area. For example, tracking studies of short-tailed shearwaters breeding in South Australia, Victoria and Tasmania, demonstrated that the polar front is a key foraging area (71-74). Similarly, foraging locations for Macquarie Island king penguins (*Aptenodytes patagonicus*) for 23 individuals tracked during late incubation (late December 1998–January 1999) showed that animals forage south and east of Macquarie Island, extending as far south as the polar front (75). Key scavenging and predatory species, including giant petrels (*Micronectes* spp), southern Fulmar, and brown skuas also are also likely to connect the Subantarctic islands with the polar front. Southern elephant seals and leopard seals also connect the Subantarctic islands and Oceania with both species considered vagrant species to the southern coasts of Australia including Tasmania, Victoria, and South Australia (76 2016). In New Zealand, leopard seals have been reclassified as 'resident' (77). Both species also visit the New Zealand coast.

The potential role of the Antarctic Heard and McDonald Islands is less clear. The avian populations of these islands comprise mostly penguins and pelagic seabirds such that it is plausible that HPAI H5 could arrive at these islands through birds foraging at the polar front. However, whether HPAI H5 would be carried the >4000 km from the Heard and McDonald Islands to Australia and New Zealand is governed by the same constraints as outlined above: birds need to be able to move a great distance within the infectious period of HPAI.

Given movement data demonstrating connectivity between the polar front to both the Antarctic and Subantarctic islands of Oceania, and Oceania itself, it is plausible that if HPAI H5 were present in the Antarctic region directly south of Oceania, it could be introduced to Oceania.

6. Response options

There are several options for response by people in the Antarctic region, including those working at the many Antarctic research stations (Figure 1). A number of responses are summarised below, with a focus on responses that aim to prevent or reduce the impact of HPAI H5 on wildlife populations as much as possible. Please see the previous OFFLU report for more details on these response options (1).

6.1 Surveillance of wildlife populations for incursion and assessing disease impact upon incursion

The surveillance of HPAI H5 viruses in wildlife in the Antarctic region, including timely sharing of disease diagnosis and of viral genome sequences, will enable observation of virus evolution and prompt detection of new virus introductions, reassortant viruses and genetic mutations, all of which are relevant for animal and public health (78).

As is the case with all World Organisation for Animal Health (WOAH) -listed diseases, only validated reports are accepted for inclusion in the World Animal Health Information System (WAHIS). WAHIS provides public and transparent access to the world animal health situation. A key element of WAHIS is an early warning system for the immediate management of alert notices for WOAH-listed diseases and emerging diseases, including HPAI. Reports of WOAH-listed diseases such as HPAI, are made by the country Delegate or Focal point (from Member countries), and usually requires diagnostic confirmation from a designated country reference laboratory. Notwithstanding, suspect events (i.e., unconfirmed or suspect mortalities) are covered under Article 1.1.5 which encourages member countries to provide WOAH with other important animal health information beyond confirmed listed or emerging diseases (WOAH Terrestrial Code, chapters 1.1.3 and 1.1.5 (79)). In the case of outbreaks in the Antarctic region or Subantarctic islands, there could be a delay of several weeks before the HPAI diagnosis can be confirmed at a reference laboratory. To partially compensate for this, the Antarctic Wildlife Health Network of the Scientific Committee on Antarctic Research have established a central repository to record and monitor all suspected and confirmed HPAI outbreaks in the region, to assist with monitoring the movement of HPAI throughout the Subantarctic and Antarctic regions but to also increase our understanding of its impacts on wildlife populations (29). All reports of unusual behaviour and mortality of wildlife are recorded in the database. Information about existing reports is provided to the public including date and location of detection, species affected and status (confirmed, suspected, or under investigation).

It is likely that collection, shipment and testing of samples in many parts of the Antarctic region will be complicated by challenges including transport and site access; lack of trained and permitted staff and limited access to adequate personal protective equipment (PPE) to collect samples; lack of trained staff and appropriate laboratory facilities to test samples; and permit requirements to import/export samples from gateway cities for testing in appropriate and certified laboratories, especially for scientists traveling on tourist vessels.

Well-documented descriptions of HPAI H5 outbreaks in wildlife are important to evaluate the impact of this disease on wildlife populations. This information can help wildlife managers to adapt conservation plans, and can help policymakers with planning to mitigate and prevent future HPAI outbreaks, not only in poultry and humans, but also in wildlife (80).

It is possible that HPAI H5 virus will remain present in the Antarctic region in coming years and spread among populations and species of wild birds and mammals unevenly and erratically, based on its epidemiology in other parts of the world. In Europe, for example, the virus has remained present in wild bird populations since 2020, with notable HPAI-associated die-offs of barnacle geese (*Branta leucopsis*) and great skuas (*Stercorarius skua*) in 2020-2021, of northern gannets (*Morus bassanus*) and Sandwich terns (*Thalasseus sandvicensis*) in 2021-2022, of black-headed gulls (*Chroicocephalus ridibundus*) in 2022-2023, and of common cranes (*Grus grus*) in autumn 2023-2024 (81, 82 2023, 83, 84). Monitoring the dynamics of HPAI virus infection in wildlife populations and assessing the population impact of HPAI is therefore not only a response option for the coming months, but for the coming years. There are several methods to do so.

6.1.1 Virological sampling of apparently healthy wildlife

Sampling apparently healthy wild animals for presence of virus by virological analysis of swabs from throat and cloaca (birds) or from nose and throat (mammals) allows detection of animals that are currently infected with HPAI virus without showing clinical signs. Such analysis is important to determine which wildlife species—depending on their movements—may play a role in spreading the virus over large distances (85).This is particularly relevant for species observed interacting with clinically ill animals or infected carcasses, through predation, scavenging or other behaviours (e.g., social interactions). A potential drawback is obtaining negative results if sampling occurs when animals are not actively shedding virus.

6.1.2 Serological sampling of apparently healthy wildlife

Sampling apparently healthy wild animals for presence of anti-virus antibodies by immunological analysis of blood sera allows detection of animals that have been infected with HPAI virus in the past and have survived. If an adequate and appropriately selected number of animals from the population are sampled, this provides evidence of the HPAI status of the population: whether it is still free of HPAI, whether it has been infected in the past, and to which degree it has been infected. Such analysis is particularly important to determine which wildlife populations play a role in long-term maintenance of HPAI H5 virus infection in a geographical region (86). As with virological sampling, this is particularly relevant for species observed interacting with clinically ill animals or infected carcasses. The added benefit in this case is that antibody response would be detectable beyond the usually short viremic or viral shedding period.

6.1.3 Surveillance of wildlife populations for unusual morbidity and mortality

Surveillance for a sudden increase in mortality as well as any animals showing clinical signs of central nervous system disease (e.g. twisted neck, inability to stay upright, inability to fly, uncoordinated movement, walking or swimming in circles, partial or full paralysis) often provides the first evidence that HPAI has entered a wildlife population; proof requires virus detection by virological analysis of sick or dead animals (87). Photographic, and especially video recording of such clinical signs is very important since the response to infection in many wild species is unknown. In some species clinical signs are predominantly neurological, but in others it is respiratory, or a combination of both.

The subsequent counting of dead animals and recording their demographic parameters (e.g. sex, age, etc.) during a HPAI die-off is important to provide a minimum estimate of the mortality rate in the affected wildlife population as a parameter for the impact of HPAI at the population level (88). This information is also essential to build population models, needed to estimate population recovery following outbreaks (e.g. the loss of adult or young females will have larger consequences than the loss of males).

Surveillance of wildlife populations for mortality and clinical signs suggestive of HPAI, as well as counting the number of affected animals, can be performed by dedicated observation of specific wildlife aggregation sites by researchers (89). Tourist and fisheries vessels can also be useful in assisting surveillance of monitoring wildlife populations in remote areas not frequented by scientists, government organisations or the general public. Tourist vessels have played an important role already this season in the Antarctic region by providing observational data and reporting any unusual behaviour and mortality events to the International Association of Antarctic Tour Operators and local governments immediately after sightings. These reported sightings have enabled a rapid response to suspected cases in the region. All cases for the region are then reported to the Scientific Committee on Antarctic Research's HPAI monitoring project (29), a central database for all suspected and confirmed cases in the Antarctic region. Relevant complementary data on wildlife mortality and morbidity also can be obtained from websites like eBird, observation.org, and iNaturalist, where members of the public share their nature observations (90).

6.1.4 Virological and pathological analyses of wildlife suspected of HPAI infection

Sampling carcasses of wildlife suspected of HPAI infection for presence of virus by virological analysis of swabs (see above), and—if possible—of postmortem tissue samples including brain, provides stronger evidence that a mortality event is caused by HPAI virus infection, and also can elucidate tissue tropism of HPAI H5 virus and routes of spread within populations, for example southern elephant seals. Virological analysis can be complemented by pathological analysis of the same postmortem tissues to provide evidence that the HPAI virus caused pathological damage to the tissues (91).

For above methods, appropriate biosafety measures (see below) need to be applied to minimize the chance of HPAI virus transmitting to the researchers involved, to other wild animals on site, and to wild animals at other sites. An appropriate carcass and waste disposal plan is necessary for this type of sampling.

6.2 Removal of infected carcasses from selected aggregation sites

Collecting and removing carcasses of wild animals that have died of disease can, in some cases, reduce contamination and transmission to other wild animals (92). Carcasses are an important source of virus and can remain infectious for days to weeks, depending on ambient temperature (93). Therefore, complete removal of all carcasses may be a sound management technique, especially if performed repeatedly soon after HPAI enters a site. However, although there are studies that suggest that carcass removal is effective, formal testing of its efficacy remains to be performed (94). In the Antarctic region, removal of HPAI-virus-infected carcasses rarely is possible for numerous practical and logistical reasons. However, in selected cases, e.g. a well-monitored breeding colony of a threatened wild bird species, it may be relevant.

6.3 Biosafety measures

Biosafety measures may be taken for two reasons: first, to reduce the risk of spread of HPAI virus to a new wildlife area by human movements; second, to reduce the risk of people becoming infected with HPAI virus. One set of measures to reduce the risk of virus spread to a new wildlife area consists of cleaning and disinfecting footwear, clothing, instruments and vehicles between leaving one area and entering a second one. Another set of measures consists of restricting the access of people into wildlife areas that are suspected or known to be infected, while enabling other desired measures, such as quantifying HPAI-associated wildlife mortality. Measures to reduce the risk of people becoming infected with HPAI virus include restricting activities that require contact with wildlife, training people in safely handling wildlife, and wearing personal protective gear while handling wildlife. Strictly following established guidelines for working with wildlife during outbreaks (e.g. (95) ACAP guidelines) and working with trained personnel is strongly recommended.

7. Responses to HPAI in practice at South Georgia (Islas Georgia del Sur)

In readiness for the incursion of HPAI into South Georgia (Islas Georgia del Sur), the Government of South Georgia & the South Sandwich Islands (GSGSSI) produced a handbook to safeguard South Georgia (Islas Georgia del Sur) and the South Sandwich Islands (Islas Sándwich del Sur) against the introduction and spread of invasive non-native species and pathogens, including HPAI (96). This handbook contains a separate chapter dedicated to guidance on HPAI risk and response in the Territory, which describes the tiered response in relation to risk and presence of HPAI, enhanced biosafety procedures, signs to be vigilant for and the steps that will be put in place for different groups / activities depending on the response level. When HPAI H5 virus was first suspected in a southern giant petrel with neurological signs on 17 September 2023 at Bird Island (3), the responses were put into practice. They are summarized below.

7.1 Surveillance of wildlife populations and assessing disease impact

The GSGSSI focuses on careful monitoring for morbidity/mortality and sampling carcasses for virological analysis. Researchers monitoring wildlife report any unusual behaviour or mortality to the local government (GSGSSI) and competent authorities (Department for

Environment, Food & Rural Affairs, DEFRA), and response teams subsequently investigate suspected cases, collect and test samples (throat and cloacal swabs from birds, nose and throat swabs from mammals) and monitor the movement of the virus in the region. The use of video is important to allow timely and remote assessment of unusual behaviour and mortality events by HPAI experts to ensure rapid decisions about likelihood of HPAI at a site.

Currently, all samples are shipped from South Georgia (Islas Georgia del Sur) to the WOAH reference laboratory for avian influenza at the Animal and Plant Health Agency (APHA) in the United Kingdom for PCR confirmation and whole genome sequencing.

7.2 Removal of carcasses from selected aggregation sites

GSGSSI does not recommend to collect and remove carcasses from affected colonies or other sites because it considers it to be an ineffective mitigation measure and to risk wildlife disturbance and virus spread and is logistically challenging.

7.3 Biosafety measures

GSGSSI provides detailed instructions for the donning and removal of PPE at two levels that are proportionate with risk. They are designed both to protect individuals and prevent spread between sites and species. GSGSSI also has instructions according to a tiered response in relation to the risk and presence of HPAI. These instructions consist of enhanced biosafety procedures, signs to be vigilant for, and the steps that will be put in place for different groups / activities depending on the response level. There are four response levels, ranging from 0 (no reported HPAI in Falkland Islands (Islas Malvinas) or Scotia Arc, wildlife mortality not above baseline, and no individuals showing HPAI signs) to 4 (HPAI confirmed in Falkland Islands (Islas Malvinas) or Scotia Arc, mass mortality in both birds and mammals across multiple sites). A practical aspect of this tiered response is that it does not depend on laboratory confirmation of HPAI.

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Annex 1 Number of birds and mammals reported dead from 1 November 2022 to 10th of December 2023 by countries in South America.

Asterisks indicate species-country associations where HPAI H5 virus infection was not confirmed by at least one case; Numerical comparisons among countries may be unreliable since countries differ considerably in their approach for surveillance, diagnostic methods and reporting of suspected/confirmed HPAI cases. Sources: (3, 14-17, 19, 23, 97-100). Note: FMI = Falkland Islands (Islas Malvinas).

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuela	Falkland
Birds													
Accipitridae													
Great black hawk	*Buteogallus urubitinga*	Least concern	500,000-4,999,999						1				
Black-chested buzzard-eagle	*Geranoaetus melanoleucus*	Least concern	unknown		13	1							
Harris's hawk	*Parabuteo unicinctus*	Least concern	unknown			2							
Anatidae													
White-cheeked pintail	*Anas bahamensis*	Least concern	unknown		1								
Yellow-billed teal	*Anas flavirostris*	Least concern	unknown			1	3						
Yellow-billed pintail	*Anas georgica*	Least concern	unknown			1							
Black-necked swan	*Cygnus melancoryphus*	Least concern	unknown			107	21		1	142			

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuela	Falkland
Black-bellied whistling-duck	*Dendrocygna autumnalis*	Least concern	200,000-2,000,000								1		
White-faced whistling-duck	*Dendrocygna viduata*	Least concern	unknown								1		
Chiloé wigeon	*Mareca sibilatrix*	Least concern	unknown			1							
Silver teal	*Spatula versicolor*	Least concern	unknown				1						
Andean goose	*Chloephaga melanoptera*	Least concern	unknown		102		2						
Coscoroba swan	*Coscoroba coscoroba*	Least concern	6,700-17,000			10							
Magellanic steamer duck	*Tachyeres pteneres*	Least concern	6,700-67,000			3							
Upland goose	*Chloephaga picta*	Least concern	unknown			5							
Ardeidae													
Great white egret	*Ardea alba*	Least concern	590,000-2,200,000			1							
Cattle egret	*Bubulcus ibis*	Least concern	unknown		1								
Snowy egret	*Egretta thula*	Least concern	unknown		1				1				
Black-crowned night-heron	*Nycticorax nycticorax*	Least concern	unknown			1							
Cathartidae													
Turkey vulture	*Cathartes aura*	Least concern	unknown			5							
American black vulture	*Coragyps atratus*	Least concern	unknown		1	2							
Andean condor	*Vultur gryphus*	Vulnerable	6,700										
Charadriidae													

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	**Peru**	**Chile**	**Argentina**	**Ecuador**	**Brazil**	**Uruguay**	**Colombia**	**Venezuela**	**Falkland**
American golden plover	*Pluvialis dominica*	Least concern	unknown						1				
Southern lapwing	*Vanellus chilensis*	Least concern	5,000,000-49,999,999			1							
Diomedeidae													
Waved albatross	*Phoebastria irrorata*	Critically endangered	unknown		3								
Black-browed albatross	*Thalassarche melanophris*	Least concern	1,400,000			1							1
Falconidae													
Crested caracara	*Caracara plancus*	Least concern	2,500,000-4,999,999		28								
Peregrine falcon	*Falco peregrinus*	Least concern	100,000-499,999		2	3							
Chimango caracara	*Phalcoboenus chimango*	Least concern	unknown			3							
Fregatidae													
Magnificent frigatebird	*Fregata magnificens*	Least concern	130,000		12			6000	1				
Great frigatebird	*Fregata minor*	Least concern	120,000					1002					
Haematopodidae													
Blackish oystercatcher	*Haematopus ater*	Least concern	20,900-87,300			50							
American oystercatcher	*Haematopus palliatus*	Least concern	unknown		2	1							
Hirundidinae													

<table>
<tr><th colspan="2" rowspan="2">Family / Common name /Species name</th><th rowspan="2">IUCN Red List assessment</th><th rowspan="2">Number of mature individuals globally (IUCN Red List)</th><th colspan="10">Number of individuals reported dead per country</th></tr>
<tr><th>Bolivia</th><th>Peru</th><th>Chile</th><th>Argentina</th><th>Ecuador</th><th>Brazil</th><th>Uruguay</th><th>Colombia</th><th>Venezuela</th><th>Falkland</th></tr>
<tr><td>Blue-and-white swallow</td><td>Pygochelidon cyanoleuca</td><td>Least concern</td><td>5,000,000-50,000,000</td><td>4</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Laridae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Inca tern</td><td>Larosterna inca</td><td>Near threatened</td><td>unknown</td><td></td><td>7987</td><td>239</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Belcher's gull</td><td>Larus belcheri</td><td>Least concern</td><td>unknown</td><td></td><td rowspan="6">1063</td><td>293</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Grey-headed gull</td><td>Larus cirrocephalus</td><td>Least concern</td><td>unknown</td><td></td><td></td><td></td><td>1</td><td>2</td><td></td><td></td><td></td><td></td></tr>
<tr><td>Kelp gull</td><td>Larus dominicanus</td><td>Least concern</td><td>unknown</td><td></td><td>4594</td><td>1</td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Brown-hooded gull</td><td>Larus maculipennis</td><td>Least concern</td><td>unknown</td><td></td><td>48</td><td></td><td></td><td>1</td><td></td><td></td><td></td><td></td></tr>
<tr><td>Grey gull</td><td>Larus modestus</td><td>Least concern</td><td>unknown</td><td></td><td>1016</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Franklin's gull</td><td>Larus pipixcan</td><td>Least concern</td><td>unknown</td><td></td><td>95</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Dolphin gull</td><td>Larus scoresbii</td><td>Least concern</td><td>6,700-19,000</td><td></td><td></td><td>2</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Black skimmer</td><td>Rynchops niger</td><td>Least concern</td><td>unknown</td><td></td><td></td><td>26</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Royal tern</td><td>Thalasseus maximus</td><td>Least concern</td><td>unknown</td><td></td><td></td><td></td><td rowspan="3">2400</td><td></td><td>60</td><td>1</td><td></td><td></td><td></td></tr>
<tr><td>Cabot's/Cayenne tern</td><td>Thalasseus acuflavidus</td><td>Least concern</td><td>325,000-430,000</td><td></td><td></td><td></td><td></td><td>858</td><td></td><td></td><td></td><td></td></tr>
<tr><td>South American tern</td><td>Sterna hirundinacea</td><td>Least concern</td><td>unknown</td><td></td><td></td><td>58</td><td></td><td></td><td>5</td><td></td><td></td><td></td></tr>
<tr><td>Elegant tern</td><td>Thalasseus elegans</td><td>Near threatened</td><td>unknown</td><td></td><td></td><td>135</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Common tern</td><td>Sterna hirundo</td><td>Least concern</td><td>unknown</td><td></td><td></td><td></td><td></td><td></td><td>15</td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Passeridae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
</table>

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuela	Falkland
House sparrow	*Passer domesticus*	Least concern	896,000,000-1,310,000,000			1							
Pelecanidae													
Brown pelican	*Pelecanus occidentalis*	Least concern	unknown								302	1	
Peruvian pelican	*Pelecanus thagus*	Near threatened	unknown		57447	4509						172	
Phalacrocoracidae													
Imperial shag	*Leucocarbo atriceps*	Least concern	unknown			7							
Guanay cormorant	*Leucocarbo bougainvilliorum*	Near threatened	unknown		254793	6380							
Neotropical cormorant	*Nannopterum brasilianus*	Least concern	unknown			726			1				
Red-legged cormorant	*Poikilocarbo gaimardi*	Near threatened	19,400-20,300			498							
Rock shag	*Leucocarbo magellanicus*	Least concern	unknown			1							
Phoenicopteridae													
Chilean flamingo	*Phoenicopterus chilensis*	Near threatened	unknown		3								
Puna (James's) flamingo	*Phoenicoparrus jamesi*	Near threatened	unknown				237						
Podicipedidae													
Great grebe	*Podiceps major*	Least concern	unknown			3							

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuela	Falkland
Procellariidae													
Sooty shearwater	*Ardenna grisea*	Near threatened	8,800,000		6	304							
Southern fulmar	*Fulmarus glacialoides*	Least concern	unknown										2
Southern giant petrel	*Macronectes giganteus*	Least concern	95,600-108,000			7							
Antarctic prion	*Pachyptila desolata*	Least concern	unknown						1				
Peruvian diving-petrel	*Pelecanoides garnotii*	Near threatened	100,000			25							
White-chinned petrel	*Procellaria aequinoctialis*	Vulnerable	3,000,000						1				
Manx shearwater	*Puffinus puffinus*	Least concern	680,000-790,000						3				
Antarctic giant petrel	*Macronectes giganteus*	Least concern	95,600-108,000			1							
Psittacidae													
slender-billed parakeet	*Enicognathus leptorhynchus*	Least concern	unknown			14							
Rallidae													
Red-gartered Coot	*Fulica armillata*	Least concern	unknown			2							
Recurvirostridae													
White-backed stilt	*Himantopus melanurus*	not classified	unknown			1							
Scolopacidae													
Ruddy turnstone	*Arenaria interpres*	Least concern	300,000-500,000		1								

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuela	Falkland
Sanderling	*Calidris alba*	Least concern	unknown		1	12							
Whimbrel	*Numenius phaeopus*	Least concern	unknown		1	2							
Lesser yellowlegs	*Tringa flavipes*	Least concern	270,000			1							
Spheniscidae													
Humboldt penguin	*Spheniscus humboldti*	Vulnerable	23,800		371*	3721							
Stercorariidae													
Brown skua	*Catharacta antarctica*	Least concern	26,000-28,000		25								
Chilean skua	*Catharacta chilensis*	Least concern	2,500-9,999			6							
Strigidae													
Tropical screech-owl	*Megascops choliba*	Least concern	500,000-4,999,999						1				
Sulidae													
Brown booby	*Sula leucogaster*	Least concern	unknown						3				
Blue-footed booby	*Sula nebouxii*	Least concern	90,000		4			3					
Red-footed booby	*Sula sula*	Least concern	1,400,000					6					
Peruvian booby	*Sula variegata*	Least concern	unknown		235643	6506							

<table>
<tr><th colspan="2" rowspan="2">Family / Common name /Species name</th><th rowspan="2">IUCN Red List assessment</th><th rowspan="2">Number of mature individuals globally (IUCN Red List)</th><th colspan="10">Number of individuals reported dead per country</th></tr>
<tr><th>Bolivia</th><th>Peru</th><th>Chile</th><th>Argentina</th><th>Ecuador</th><th>Brazil</th><th>Uruguay</th><th>Colombia</th><th>Venezuela</th><th>Falkland</th></tr>
<tr><td colspan="2">Mammals</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Delphinidae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Chilean dolphin</td><td>Cephalorhynchus eutropia</td><td>Near threatened</td><td>unknown</td><td></td><td></td><td>1</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Short-beaked common dolphin</td><td>Delphinus delphis</td><td>Least concern</td><td>unknown</td><td></td><td>1</td><td>9*</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Dusky dolphin</td><td>Lagenorhynchus obscurus</td><td>Least concern</td><td>unknown</td><td></td><td></td><td>28</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Phocoenidae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Burmeister's porpoise</td><td>Phocoena spinipinnis</td><td>Near threatened</td><td>unknown</td><td></td><td></td><td>36</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Mustelidae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Marine otter</td><td>Lontra felina</td><td>Endangered</td><td>unknown</td><td></td><td></td><td>43</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Southern river otter</td><td>Lontra provocax</td><td>Endangered</td><td>unknown</td><td></td><td></td><td>1</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Otariidae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>South American fur seal</td><td>Arctocephalus australis</td><td>Least concern</td><td>109,500</td><td></td><td></td><td>27*</td><td>13</td><td></td><td rowspan="2">552</td><td rowspan="2">800</td><td></td><td></td><td></td></tr>
<tr><td>South American sea lion</td><td>Otaria byronia</td><td>Least concern</td><td>222,500</td><td></td><td>10457</td><td>20070</td><td>1367</td><td></td><td></td><td></td><td></td></tr>
<tr><td colspan="2">Phocidae</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>Southern elephant seal</td><td>Mirounga leonina</td><td>Least concern</td><td>325,000</td><td></td><td></td><td>16*</td><td>17400</td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
</table>

Family / Common name /Species name		IUCN Red List assessment	Number of mature individuals globally (IUCN Red List)	Number of individuals reported dead per country									
				Bolivia	Peru	Chile	Argentina	Ecuador	Brazil	Uruguay	Colombia	Venezuela	Falkland
Procyonidae													
South American coati	*Nasua nasua*	Least concern	unknown							16			

Annex 2 Antarctic and Subantarctic species list with IUCN Red List assessment and estimated number of mature individuals globally

(source: IUCN. 2023. The IUCN Red List of Threatened Species. Version 2023-1. https://www.iucnredlist.org. Accessed on December,2023)

Family	Common name	Species	IUCN Red list assessment	Number of mature individuals globally (IUCN Red List)
Birds				
Anatidae	Southern pintail	*Anas eatoni*	Vulnerable	31,200-41,400
	Yellow-billed pintail	*Anas georgica*	Least concern	unknown
Chionidae	Snowy sheathbill	*Chionis albus*	Least concern	unknown
	Black-faced sheathbill	*Chionis minor*	Least concern	8,700-13,000
Diomedeidae	Wandering albatross	*Diomedea exulans*	Vulnerable	20,100
	Sooty albatross	*Phoebetria fusca*	Endangered	21,234-28,656
	Light-mantled Albatross	*Phoebetria palpebrata*	Near threatened	58,000
	Indian yellow-nosed albatross	*Thalassarche carteri*	Endangered	82,000
Diomedeidae	Grey-headed albatross	*Thalassarche chrysostoma*	Endangered	250,000
	Black-browed albatross	*Thalassarche melanophris*	Least concern	1,400,000
Laridae	Kelp gull	*Larus dominicanus*	Least concern	unknown
	Kerguelen tern	*Sterna virgata*	Near threatened	2,300-4,300
	Antarctic tern	*Sterna vittata*	Least concern	unknown
Motacillidae	South Georgia pipit	*Anthus antarcticus*	Least concern	6,000-8,000
Oceanitidae	Black-bellied storm-petrel	*Fregetta tropica*	Least concern	unknown
	Grey-backed storm-petrel	*Garrodia nereis*	Least concern	unknown
	Wilson's storm-petrel	*Oceanites oceanicus*	Least concern	8,000,000-20,000,000
Phalacrocoracidae	Imperial shag	*Leucocarbo atriceps*	Least concern	unknown
	Kerguelen shag	*Leucocarbo verrucosus*	Least concern	unknown
Procellariidae	Kerguelen petrel	*Aphrodroma brevirostris*	Least concern	unknown
	Cape petrel	*Daption capense*	Least concern	unknown
	Southern fulmar	*Fulmarus glacialoides*	Least concern	unknown

Family	Common name	Species	IUCN Red list assessment	Number of mature individuals globally (IUCN Red List)
	Blue petrel	*Halobaena caerulea*	Least concern	unknown
Procellariidae	Southern giant petrel	*Macronectes giganteus*	Least concern	95,600-108,000
	Northern giant petrel	*Macronectes halli*	Least concern	23,600
	Slender-billed prion	*Pachyptila belcheri*	Least concern	unknown
	Fulmar prion	*Pachyptila crassirostris*	Least concern	100,000-200,000
	Antarctic prion	*Pachyptila desolata*	Least concern	unknown
	Salvin's prion	*Pachyptila salvini*	Least concern	unknown
	Fairy prion	*Pachyptila turtur*	Least concern	unknown
	Snow petrel	*Pagodroma nivea*	Least concern	unknown
	South Georgia diving petrel	*Pelecanoides georgicus*	Least concern	12,000,000
	Common diving petrel	*Pelecanoides urinatrix*	Least concern	unknown
	White-chinned petrel	*Procellaria aequinoctialis*	Vulnerable	3,000,000
	Grey petrel	*Procellaria cinerea*	Near threatened	151,500
	White-headed petrel	*Pterodroma lessonii*	Least concern	unknown
	Great-winged petrel	*Pterodroma macroptera*	Least concern	unknown
	Soft-plumaged petrel	*Pterodroma mollis*	Least concern	unknown
	Antarctic petrel	*Thalassoica antarctica*	Least concern	unknown
Spheniscidae	Emperor penguin	*Aptenodytes forsteri*	Near threatened	unknown
	King penguin	*Aptenodytes patagonicus*	Least concern	unknown
	Southern rockhopper penguin	*Eudyptes chrysocome*	Vulnerable	2,500,000
	Macaroni penguin	*Eudyptes chrysolophus*	Vulnerable	unknown
	Adelie penguin	*Pygoscelis adeliae*	Least concern	10,000,000
	Chinstrap penguin	*Pygoscelis antarcticus*	Least concern	8,000,000
	Gentoo penguin	*Pygoscelis papua*	Least concern	774,000
Stercorariidae	Brown skua	*Catharacta antarctica*	Least concern	26,000-28,000
	South polar skua	*Catharacta maccormicki*	Least concern	6,000-15,000

Family	Common name	Species	IUCN Red list assessment	Number of mature individuals globally (IUCN Red List)
Mammals				
Balaenidae	Southern right whale	*Eubalaena australis*	Least concern	unknown
Balaenopteridae	Sei whale	*Balaenoptera borealis*	Endangered	50,000
	Antarctic blue whale	*Balaenopera musculus sp. intermedia*	Critically endangered	3,000
	Common minke whale	*Balaenoptera acutorostrata*	Least concern	200,000
	Fin whale	*Balaenoptera physalus*	Vulnerable	100,000
	Humpback whale	*Megaptera novaeangliae*	Least concern	84,000
	Antarctic minke whale	*Balaenoptera bonearensis*	Near threatened	unknown
Delphinidae	Commersons's dolphin	*Cephalorhynchus commersonii*	Least concern	unknown
	Long-finned pilote whale	*Globicephala melas*	Least concern	unknown
	Hourglass dolphin	*Lagenorhynchus cruciger*	Least concern	unknown
	Southern right whale dolphin	*Lissodelphis peronii*	Least concern	unknown
	Killer whale	*Orcinus orca*	Data deficient	unknown
Neobalaenidae	Pygmy right whale	*Caperea marginata*	Least concern	unknown
Otariidae	Antarctic fur seal	*Arctocephalus gazella*	Least concern	700,000-1,000,000
	Subantarctic fur seal	*Arctocephalus tropicalis*	Least concern	200,000
	South american sea lion	*Otaria byronia*	Least concern	222,500
Phocidae	Leopard seal	*Hydrurga leptonyx*	Least concern	18,000
	Weddell seal	*Leptonychotes weddellii*	Least concern	300,000
	Crabeater seal	*Lobodon carcinophagus*	Least concern	4,000,000
	Southern elephant seal	*Mirounga leonina*	Least concern	325,000
	Ross seal	*Ommatophoca rossii*	Least concern	40,000
Phocoenidae	Spectacled porpoise	*Phocoena dioptrica*	Least concern	unknown
Physeteridae	Sperm whale	*Physeter macrocephalus*	Vulnerable	unknown
Ziphiidae	Gray's Beaked whale	*Mesoplodon grayi*	Least concern	unknown
	Southern bottlenose whale	*Hyperoodon planifrons*	Least concern	unknown
	Strap-toothed Whale	*Mesoplodon layardii*	Least concern	unknown
	Arnoux's beaked whale	*Berardius arnuxii*	Least concern	unknown