Global Ecology and Biogeography

WILEY

Global Ecology and Biogeography A Journal of Macroecology

DATA ARTICLE OPEN ACCESS

Introducing FAMM: An Open-Access Database of Fossil Arctic Marine Mammals

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Received: 25 March 2025 | **Revised:** 19 August 2025 | **Accepted:** 28 August 2025

Handling Editor: Catalina Pimiento Hernandez

Funding: This work was supported by Villum Fonden (YIP 13151) and the Australian Research Council (DP240102019).

Keywords: ancient DNA | Arctic | database | fossil | mammal | marine | radiocarbon | stable isotope

ABSTRACT

Motivation: The Arctic is currently experiencing the strongest effects of climate change on Earth. These effects, including sea ice loss, are already modifying the ecologies of the 11 species of marine mammals found in the Arctic year-round. Data from contemporary individuals are often applied to understand how these species may respond to future climate change. The inclusion of fossil data can provide greater insight into species histories. Conservation approaches are increasingly enhanced by including ancient biomolecular data such as radiocarbon age, stable isotopes, and ancient DNA. However, analytical quality is challenged by data degradation over time, lack of cross-linkage between different ancient biomolecular data, and widely varying metadata standards across fields. Here, we compile and present an open-access database of Fossil Arctic Marine Mammals (FAMM) containing nearly 3400 specimens with harmonised primary and molecular biodiversity data, providing a crucial resource to Arctic biodiversity and environmental research.

Types of Variables Collected: FAMM contains records and metadata of Arctic marine mammal macrofossils, including: taxonomy; geographic provenance; radiocarbon age; stable isotopes; and ancient DNA. FAMM aligns with Darwin Core standards for reproducibility.

Spatial Location and Grain: Arctic and sub-Arctic.

Time Period and Grain: Last Interglacial (130,000 years BP) to ~1500 CE.

Major Taxa and Level of Measurement: All 11 extant endemic Arctic marine mammal species: bowhead whale (*Balaena mysticetus*); narwhal (*Monodon monoceros*); beluga whale (*Delphinapterus leucas*); polar bear (*Ursus maritimus*); walrus (*Odobenus rosmarus*); ringed seal (*Pusa hispida*); bearded seal (*Erignathus barbatus*); hooded seal (*Cystophora cristata*); harp seal (*Pagophilus groenlandicus*); spotted seal (*Phoca largha*); and ribbon seal (*Histriophoca fasciata*). We also include the historically extinct Steller's sea cow (*Hydrodamalis gigas*).

Global Ecology and Biogeography, 2025; 34:e70120
https://doi.org/10.1111/geb.70120

Software Format: Data are provided as three csv files on Dryad: (1) A key describing columns in the FAMM database; and (2) the FAMM database; (3) a key explaining museum acronyms used in FAMM.

1 | Introduction

The Arctic is facing ongoing rapid warming and significant sea ice declines (Rantanen et al. 2022). Conservation of Arctic ecosystems, particularly their endemic marine megafauna which rely on sea ice, is of utmost importance. Contemporary and recent historical (< 500 years) biodiversity data is often applied to understand species demographic changes over decadal scales to help understand the ongoing and future response of species to climate change. However, contemporary data lack a long-term understanding of species demographic histories (Fordham et al. 2020; Smith 2021). Broader temporal perspectives are needed to understand species' long-term responses to climate change.

The fossil record provides evidence of species presence spatiotemporally. Fossil chronologies of individual species provide crucial data on their distributions and responses to change (Fordham et al. 2022). Utilising this information can greatly assist in guiding conservation initiatives for species under threat (Fordham et al. 2020).

Conservation-paleoecological efforts can be enhanced by interdisciplinary approaches beyond simple presence/absence of a species (Smith 2021). Biomolecular data, including stable isotopes and ancient DNA retrieved from fossils, provide additional layers of information on past individuals and populations, supplementing existing radiocarbon data (Borge et al. 2007; Dyke et al. 1996; Szpak et al. 2019). These paleoarchives yield further insights into ecological and evolutionary processes both across and within species and populations. Harmonising this data enables a more holistic understanding of outstanding questions in ecology and evolutionary biology (Skovrind et al. 2024; Smith et al. 2022; Szpak et al. 2019; Westbury et al. 2024).

Fully leveraging primary and molecular biodiversity data from fossil archives for scientific inquiry requires standardised data collection, which is challenged by varying reporting standards across different scientific disciplines. Data reporting standards are frequently updated (e.g., radiocarbon), which risks data becoming obsolete over time (Escribano et al. 2016; Herrando-Pérez 2021). Metadata reporting in original manuscripts is typically poor even for simple data structures (Kelly et al. 2022). Data leakage and erosion of valuable metadata over time (e.g., locality descriptions, radiocarbon metadata) further render many specimens as unfit for use in conservation initiatives (Mesibov 2018; Peterson et al. 2018). Finally, data from different biomolecular analyses on the same specimen have rarely been linked to each other and may be presented in multiple independent studies published decades apart without knowledge of other data users (Feng et al. 2022). Simply put, many data do not meet FAIR (Findable, Accessible, Interoperable, and Reproducible) principles (Wilkinson et al. 2016), and significant person-hours are needed to expand the utility of this data.

To meet these challenges for Arctic marine ecosystems, we compile and present FAMM (version 1.1): an open-access database of Fossil Arctic Marine Mammals. FAMM is a synthesis of available Arctic marine mammal fossil material and contains primary biodiversity information (taxonomic identity, geographic provenance) and ancient biomolecular information (radiocarbon age, stable isotopes, ancient DNA) that have been harmonised together. FAMM enables stronger interdisciplinary marine mammal research and conservation initiatives across the Arctic.

2 | Data Collection

2.1 | General Data Collection

Over a 10-month period (May 2021–March 2022), we accessed specimen records and any associated biomolecular data from available repositories. More detailed data collection information is provided as Supporting Information.

2.2 | Databases

We accessed databases of relevant fossil information including: Neotoma (Williams et al. 2018); Paleobiology Database; Canadian Archaeological Radiocarbon Database (Morlan 1999); VertNet; Arctos; and the Global Biodiversity Information Facility. We additionally accessed datasets compiled by Arctic paleoecological experts (Harington 2003)—and sourced all relevant papers within. We verified the accuracy and precision of database records by checking with the primary sources. This rescued much data that had become obsolete/unusable due to metadata leakage (sensu Escribano et al. 2016; Peterson et al. 2018).

2.3 | Literature Search

We searched the primary literature using detailed search strings for each species via Scopus and Web of Science. Our search strings are available as Table S1.

2.4 | Additional Literature Records

After collecting our literature (including references from databases), we identified additional relevant manuscripts by searching through citation networks using ResearchRabbit software (Chandra et al. 2021). We accepted published papers, masters/PhD theses, and grey literature sources, including many non-English language publications. ResearchRabbit netted far more papers than the search strings, as many zooarchaeological publications that contain fossil material do not make it explicit in their abstracts. In September 2024, we used ResearchRabbit again to find additional papers that had been published after our initial searches.

2.5 | Merging Data Sources and Deduplication

After compiling all datasets, we manually combined specimens that had been doubly counted, using all available IDs (e.g., radiocarbon, museum, Bordon site, etc.). We started with the oldest publications and updated FAMM records as new papers were published. Many specimens simultaneously exist in multiple publications/databases (with widely varying metadata-reporting quality) as many genetic/isotopic analyses are performed on specimens long after they had been radiocarbon dated (e.g., Westbury et al. 2024).

2.6 | Future Additions to FAMM

The FAMM database will be continuously updated as new specimens are discovered, and different biomolecular analyses are performed on existing specimens. Researchers wishing to contribute data to FAMM should email the corresponding authors.

3 | Data Structure

3.1 | Data Composition and General Structure

The FAMM (version 1.1) database covers a temporal range from the Eemian (~130,000 years BP) to historical times (~1500 CE). FAMM contains fossil occurrence and associated biomolecular data for all 11 extant species of marine mammals found in the Arctic year-round across Cetacea, Ursidae, and Pinnipedia: bowhead whale; narwhal; beluga; polar bear; walrus; ringed seal; bearded seal; hooded seal; harp seal; spotted seal; ribbon seal; and the historically extinct Steller's sea cow.

FAMM aligns with existing Darwin Core standards (Wieczorek et al. 2012) and contains information for over 100 variables spanning five broad types of paleo-archives: general metadata (including any specimen IDs), primary biodiversity metrics (taxonomic identity and geographic provenance), radiocarbon dating, stable isotopes, and ancient DNA. FAMM includes detailed metadata and comments to provide necessary context for utilising these valuable paleo-archives.

3.2 | Metadata and Specimen ID

Many specimens exist as independent records with separate identifiers in different databases and repositories (i.e., occurrence, radiometric, stable isotopic, ancient DNA), but these linkages are not commonly reported and are rarely linked across sub-disciplines (Feng et al. 2022). We included any relevant ID information attributable to a specimen, noting that many specimens in FAMM still lack museum labels.

3.3 | Primary Biodiversity Data

We recorded primary biodiversity data on all FAMM specimens (Peterson et al. 2018). We geolocated coordinates based on site descriptions, adding spatial uncertainty metrics (e.g., coordinateUncertaintyInMeters, which we specify in km) (Wieczorek et al. 2004).

3.4 | Radiocarbon Dating

Where available, we recorded radiocarbon information from directly dated specimens, and from specimens with good stratigraphic association with other radiocarbon-dated material. Where reported, we noted when radiocarbon dates were generated via 'standard' beta-counting techniques or from AMS dating, and which dates had been normalised for isotopic fractionation to −25‰ for $\delta^{13}C$ (i.e., conventional dates). We quantified the robustness of radiocarbon dates following an established protocol (Barnosky and Lindsey 2010).

We note site-specific ΔR values necessary for marine reservoir corrections, but note that the latest marine radiocarbon calibration curve is inappropriate for polar regions (Heaton, Bard, et al. 2023; Heaton, Butzin, et al. 2023; Heaton et al. 2020). For Arctic specimens where ΔR values are complex, radiocarbon-dating co-stratigraphic terrestrial material in assemblages is often preferable, though see (Dyke et al. 2019) for commentary. In the Supporting Information, we provide pros and cons of different approaches to calibrating Arctic marine radiocarbon dates, as doing so is highly challenging and not straightforward, particularly for Pleistocene dates (Table S2). However, we caution that there is not a one-size-fits-all method for calibrating Arctic marine radiocarbon dates.

3.5 | Stable Isotopes

We recorded stable isotope data and analytical precision metrics ($\delta^{13}C$, $\delta^{15}N$, C/N ratio, skeletal element, tissue analysed) following best practices of existing databases such as IsoBank (Pauli et al. 2015, 2017) and IsoArcH (Salesse et al. 2018). We also report uncertainty metrics, though we caution that many of the reported uncertainties lack reference data to be substantiated (Szpak et al. 2017). Most stable isotope analyses were performed on bulk bone collagen, but we noted if alternative tissues (e.g., dentine) were analysed. We further noted if non-traditional isotopic data (e.g., sulphur or zinc) were available (McCormack et al. 2021; Szpak and Buckley 2020).

3.6 | Ancient DNA

We reported information from specimens that had been analysed for ancient DNA, including whether genetic material was successfully recovered. Where available, we included GenBank IDs for any specimen with successfully extracted genetic material.

4 | Patterns in the Data

FAMM contains data for 3392 fossil specimens, which is more than four times larger than sample sizes of Arctic marine mammal material in existing radiocarbon databases (e.g., a 2021 download of CARD) (Morlan 1999). Bowhead whales are the most abundant taxon ($n=1087$, 32% of all specimens), followed by walrus ($n=645$), ringed seal ($n=526$), and polar bear ($n=433$). For polar bears, this reflects a > 6-fold increase in total specimens relative to the most recently compiled fossil polar bear dataset ($n=70$) (Seppä et al. 2023), speaking to the thorough coverage overall in FAMM. FAMM contains extralimital records well outside contemporary geographic distributions for all extant species except ribbon seal ($n=7$), spotted seal ($n=15$), and hooded seal ($n=24$), which all had the fewest records of any species (Figures S1–S12).

FAMM contains fossil data from 18 different countries across the Arctic and sub-Arctic. Nearly half of the specimens ($n=1598$, 47%) are from Canada, largely owing to archaeological records from the Canadian Arctic Archipelago and bowhead whale strandings (Figure 1; Figures S1–S12). Fennoscandia and the United States contain an additional ~15% each of all records, largely due to coastal archaeological sites.

Most records are from coastal sites or from areas near paleocoastlines that have since been uplifted due to isostatic rebound. The few offshore records in FAMM were found opportunistically via dredging. Despite covering roughly 1/3 of the Arctic basin, relatively few records ($n=217$; 6.4%) exist from the Russian Arctic. This primarily results from the region's remoteness and preservation biases. We conferred with Russian palaeontology and archaeology experts on Arctic marine mammal subfossil material, who have attested that FAMM comprehensively represents the current knowledge of this material (Baryshnikov 2022; Shpak 2025).

The vast majority of FAMM specimens (> 86%) had robust radiocarbon chronology (Figure 2). Pinniped specimens tended to be indirectly dated based on associations with archaeological material, whereas non-pinnipeds were more likely to be directly dated as they were often isolated strandings. Stable isotope coverage was generally low (~23% of all specimens), but proportionally higher for pinnipeds (~78% of pinniped specimens). Ancient DNA coverage was lower (~8% of all specimens), owing to the more recent rise of the paleogenetics field.

The majority of records in FAMM (~65%) are of Late Holocene age (4.3 kyrs BP—500 years BP; Figure 1). This is largely a result of many specimens (mostly pinnipeds) being identified from archaeological deposits associated with the peopling of the North American Arctic. About 5% of specimens are Late Pleistocene-aged. Only 39 specimens (~0.1%) lacked age information.

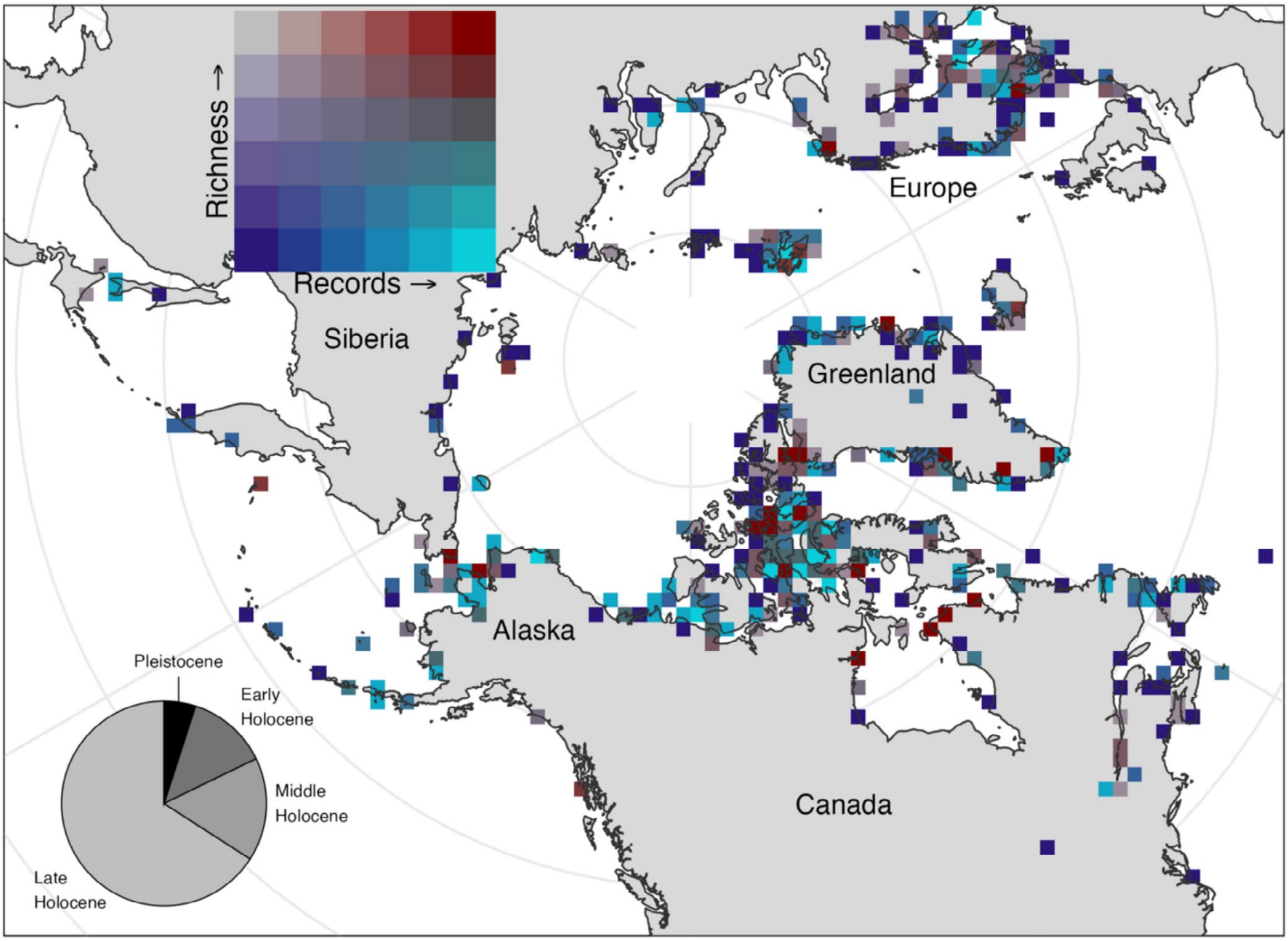

FIGURE 1 | Data coverage in the Fossil Arctic Marine Mammal (FAMM) database. Bivariate choropleth map of species richness and number of records shown in 150 km × 150 km grid cells. Pie chart of the temporal coverage of specimens in FAMM: Pleistocene 129–11.7 kyr BP; Early Holocene 11.7–8.2 kyr BP; Middle Holocene 8.2–4.2 kyr BP; Late Holocene 4.2 kyr BP-1500 CE.

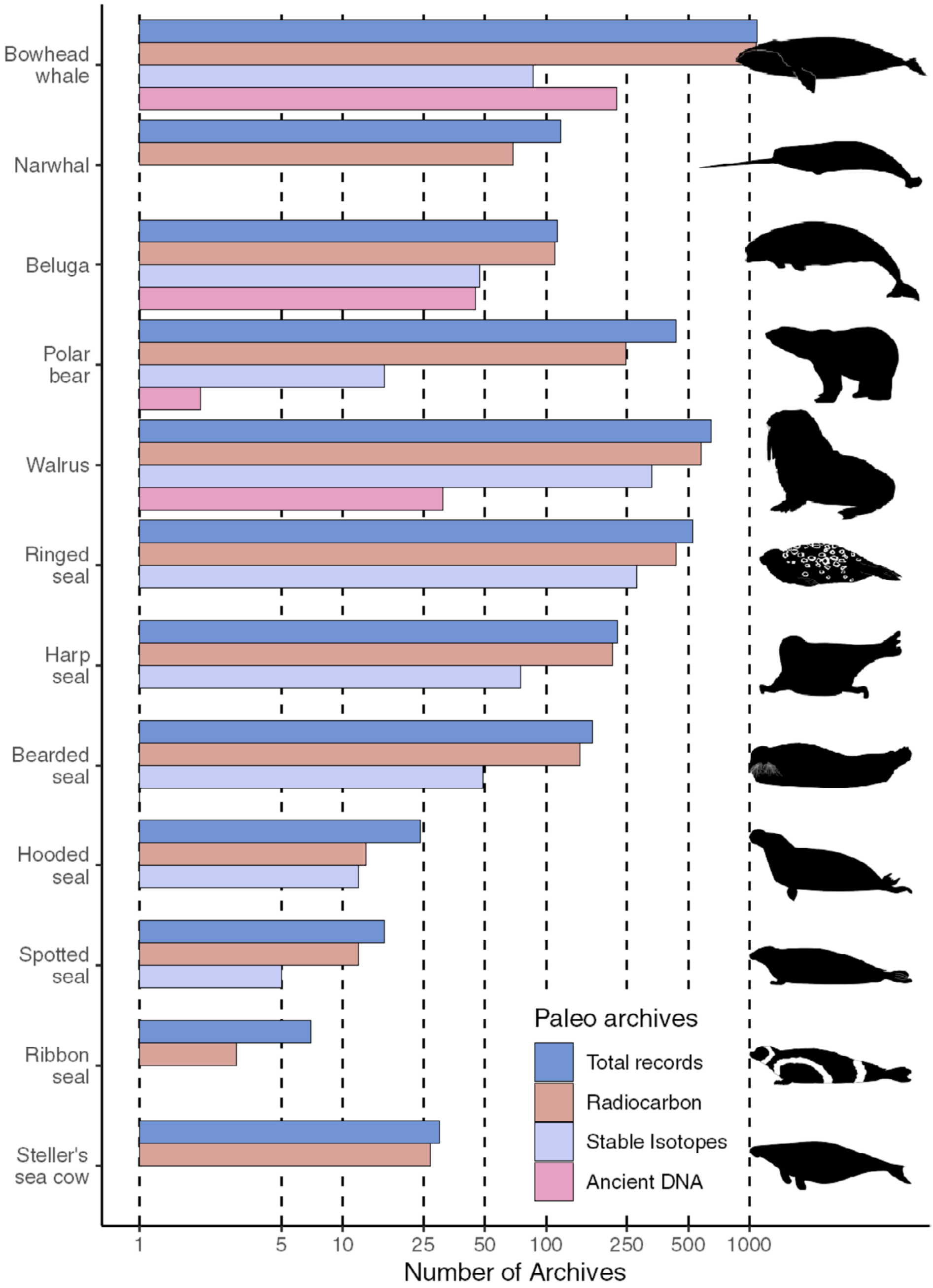

FIGURE 2 | Species-level data coverage in FAMM. Log-transformed histograms of sample size for each type of paleo archive (total records, radiocarbon [including both directly- and indirectly- dated material, stable isotopes, and ancient DNA]) by species. Taxa are ordered by taxonomic group (Cetaceans = bowhead whale, narwhal, beluga; Carnivorans = polar bear; Pinnipeds = walrus, seals; Steller's sea cow). Outlines of bowhead whale, narwhal, beluga, polar bear, walrus, harp seal, spotted seal, and Steller's sea cow are sourced from PhyloPic.

5 | Data Applications

Paleoecological databases with a regional focus are well established in terrestrial systems for questions specific to those areas (Peters et al. 2019). We have extended this approach to the marine realm, which can feed directly into conservation initiatives. In addition to the broad spatio-temporal coverage within FAMM, the inclusion of associated biomolecular data enables outstanding interdisciplinary questions to be addressed, such as those utilised in analyses of community structure changes (Smith et al. 2016), species ecological flexibility through time and across their ranges (Skovrind et al. 2024), and ecological modelling initiatives (Canteri et al. 2022; Fordham et al. 2022; Pilowsky et al. 2023).

FAMM can also be linked with the rapidly expanding field of environmental/sedimentary ancient DNA to alleviate some of the biases present in the marine mammal fossil record, notably for the reduced coverage of Pleistocene-aged and lack of offshore material. Marine sediment cores exist from many regions across the Arctic and sub-Arctic. These cores can infill gaps in the fossil record, providing robust data for species presence/absence across the seascape (Schreiber et al. 2025; Seersholm et al. 2016; Zimmermann et al. 2023). However, DNA extracted from these cores cannot provide insights at the individual- and population scale that biomolecular data retrieved from macrofossils (such as those in FAMM) provide, as macrofossils are what the sedimentary ancient DNA researchers ultimately use to ground their analyses.

The Arctic has warmed at four times the rate of the global average and has lost 70% of summer sea ice extent in recent decades (Rantanen et al. 2022). Conservation of Arctic endemics must be data-driven and led by standardised biodiversity data, an example of which is provided in FAMM. Ultimately, we believe FAMM will be widely applicable towards guiding conservation strategies that have been benchmarked on long-term data. In an era of marked climate change, the past represents an indispensable key to understanding the present and predicting the future.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data are available at the following reference on Dryad ('Introducing FAMM: an open-access database of Fossil Arctic Marine Mammals—Reviewer Link', 2025). No code is applicable.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section. **Data S1:** geb70120-sup-0001-supinfo.docx. **Table S1:** Search strings used. **Table S2:** Pros and cons of methods to calculate marine reservoir age (MRA) values and ΔR values, particularly for high-latitude samples. **Figure S1:** The spatio-temporal distribution of bowhead whales (*Balaena mysticetus*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current bowhead whale IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S2:**. The spatio-temporal distribution of beluga whales (*Delphinapterus leucas*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current beluga whale IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S3:** The spatio-temporal distribution of narwhal (*Monodon monoceros*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current narwhal IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S4:**. The spatio-temporal distribution of polar bears (*Ursus maritimus*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current polar bear IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S5:** The spatio-temporal distribution of walrus (*Odobenus rosmarus*) in the FAMM database. Three additional Pleistocene records (not shown) are from British Columbia, California, and Virginia. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current walrus IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S6:** The spatio-temporal distribution of bearded seals (*Erignathus barbatus*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current bearded seal IUCN range polygon. **Figure S7:** The spatio-temporal distribution of hooded seals (*Cystophora cristata*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current hooded seal IUCN range polygon. **Figure S8:** The spatio-temporal distribution of ribbon seals (*Histriophoca fasciata*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current ribbon seal IUCN range polygon. **Figure S9:** The spatio-temporal distribution of harp seals (*Pagophilus groenlandicus*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current harp seal IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S10:** The spatio-temporal distribution of spotted seals (*Phoca largha*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current spotted seal IUCN range polygon. Silhouette sourced from PhyloPic. **Figure S11:** The spatio-temporal distribution of ringed seals (*Pusa hispida*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. The blue shaded area denotes the current ringed seal IUCN range polygon. **Figure S12:** The spatio-temporal distribution of the historically extinct Steller's sea cow (*Hydrodamalis gigas*) in the FAMM database. Dark red dots denote Pleistocene-age records. Dark orange dots denote Early Holocene-age records. Light orange dots denote Middle Holocene-age records. Light dots denote Late Holocene-age records. We use contemporary sea level, but note that sea level changes in the Arctic vary considerably depending on eustatic sea level rise and proximity to past ice sheets. Silhouette sourced from PhyloPic. **Figure S13:**. High-resolution time series for abundant species in FAMM. Log-transformed sample sizes in 500-year time bins for eight of the most abundant ($n > 30$; see Figure 2) species in FAMM. (a) bowhead whale; (b) narwhal; (c) beluga; (d) polar bear; (e) walrus; (f) ringed seal; (g) harp seal; (h) bearded seal. Dates included are any uncalibrated date of a specimen, whether raw versus normalised, direct versus indirect, and are all without any marine reservoir correction.