

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☐ ☒ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection

The sequencing data was generated by us, life history data was extracted from the literature. No software was used to collect the data.

Data analysis

All software and versions used for data pre-processing and downstream analyses are mentioned in the methods section and the supplementary material. Proprietary code is deposited on github and the respective links are provided in the text.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All data generated for this study are archived under bioproject PRJEB37019 in NCBI's sequencing read archive (SRA). See table S6 for detailed information on accession numbers by sample.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Estimation of genetic variation and its relationship to species abundance, life history parameters, and conservation status as described in detail in the methods section.
Research sample	Tissue samples from individuals of pinniped species from across the globe. All samples were available previously and no additional field work was done for the purpose of this study.
Sampling strategy	We aimed for a minimum of 10 chromosomes to obtain a reliable estimate of genetic variation in the population for 17 different species (as e.g. used for simulations in Carling & Brumfield (2007)). Where possible, several populations were included to test for robustness of 'species' genetic variation estimates. 1. M. D. Carling, R. T. Brumfield, Gene Sampling Strategies for Multi-Locus Population Estimates of Genetic Diversity (θ). PLoS ONE. 2, e160 (2007).
Data collection	From each sample, we extracted DNA and generated ddRAD data as made available in the SRA archive of NCBI. Published and unpublished genomes were acquired from identified sources.
Timing and spatial scale	As specified above, the samples have been obtained as part as individual studies from a large group of researchers. They were obtained in different batches and ddRAD data was generated accordingly. Batch effects have been explicitly considered. Once our goal of >15 species was reached we started analyzing the genetic data altogether.
Data exclusions	Data were excluded according to data quality as specified in detail in the methods section.
Reproducibility	We explicitly included several populations for each species to test for reproducibility of estimates among populations with shallow differentiation. As a precursor study for this manuscript, we (i.e. Shafer et al.) ran a series of tests to assess robustness for population genetic estimates from ddRAD data. 1. A. B. A. Shafer et al., Bioinformatic processing of RAD-seq data dramatically impacts downstream population genetic inference. Methods Ecol Evol. 8, 907–917 (2017).
Randomization	All statistical analyses were also performed controlling for phylogenetic relationships. Demographic analyses were subjected to bootstrapping.
Blinding	Library preparation were done by lab staff who had no insight into the study setup. For the analyses standardized bioinformatic pipelines have been used on all samples excluding human bias.
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Samples were obtained as part of independent research programs unrelated to this study. This being a global collection of samples conditions varied across species.
Location	see Table S6.
Access and import/export	Sampling and sample import was conducted in accordance with local legal requirements.
Disturbance	Disturbance includes stress to the animals during capture and biometric measurements, and possible pain during tissue sampling. Restraining was reduced to a time minimum, and tissue samples were reduced in size allowing for sufficient DNA extraction to reduce pain to a minimum.

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involvement in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	n.a.
Wild animals	see Supplementary Table 6.
Field-collected samples	Tissue samples were cryopreserved prior to extraction of DNA.
Ethics oversight	Ethical approval only relates to local sampling which was conducted prior to this study. Sampling permissions are specified in Supplementary Table 2.

Note that full information on the approval of the study protocol must also be provided in the manuscript.