nature portfolio

Corresponding author(s): Lily Fogg, Walter Salzburger, Dorota Skowronska-Krawczyk

Last updated by author(s): Oct 28, 2025

# Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies 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<br>*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<br>*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 | No custom software/code was used for data collection. Data were acquired on the following instruments using their standard manufacturer control software/firmware: Illumina NovaSeq6000 (sequencing), Agilent TapeStation (RNA/DNA quality assessment), Leica DM4 (brightfield microscopy), Zeiss LSM900 with Airyscan 2 (confocal microscopy), Keyence BZ-X700 (RNAscope imaging), Varian Cary 50 Scan UV–Vis spectrophotometer (rhodopsin absorption), SpectralLED light source coupled to an integrating sphere and PhotoResearch PR-655 SpectraScan spectroradiometer (corneal transmittance), and Thermo Fisher Q Exactive mass spectrometer with Vanquish LC system (lipidomics). |
| Data analysis | Open-source and commercial software/code were used for genomic, transcriptomic, and phylogenetic analyses.<br>Sequence data processing and assembly: fastp (v.0.23.4), ABySS (v.2.3.1), BUSCO (v.5.4.5)<br>Phylogenetic analyses: MUSCLE (v.5.1), trimAl (v.1.4.1), IQ-TREE (v.2.0), ASTRAL (v.5.7.8), iTOL (v.6.9.1)<br>Genome annotation and gene mining: TBLASTN (v.2.11.0), EXONERATE (v.2.4.0), BRAKER (v.3), AGAT (v.1.4.1), HISAT2 (v.2.2.1), STAR (v.2.7.10b), HTSeq (v.2.0.2), Geneious Prime (v.2022.2.2)<br>Selection analyses: PAML (v.4.10), HyPhy (v.2.5.63) implementing RELAX and aBSREL models<br>Visualization and statistics: GraphPad Prism (v.7), R (v.4.4.0) |

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio 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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Newly identified coding sequences (PV442159-PV442194; https://www.ncbi.nlm.nih.gov/nuccore/?term=PV442159:PV442194[accn]) as well as raw genomic and transcriptomic reads and genome assembly are available through GenBank (PRJNA1246101; https://www.ncbi.nlm.nih.gov/bioproject/PRJNA1246101) and the NCBI Sequencing Read Archive (see Table S2 for accession numbers). All other data are available via Figshare (https://figshare.com/s/9d86a7c9eccced4c6505) or are provided in the main manuscript or Supplementary Information.

## Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

| | |
|---|---|
| Reporting on sex and gender | Human samples were obtained from a 50 year old female. |
| Reporting on race, ethnicity, or other socially relevant groupings | Korean. |
| Population characteristics | No specific characteristics available. |
| Recruitment | No specific recruitment was applied. |
| Ethics oversight | Human donor eyes were obtained and managed in compliance with the Declaration of Helsinki. De-identified eyeballs were obtained from the Willed Body Program at the University of California, Irvine (Irvine, CA). |

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

# 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 | This study investigates the molecular and cellular mechanisms underlying the visual system of the Greenland shark (Somniosus microcephalus). The work integrates comparative genomics, transcriptomics, histology, and biochemical assays to characterize phototransduction and DNA repair pathways. Quantitative data were generated from independent biological replicates (n = 3 retinas for transcriptomic analyses; n = 3 eyes for histology; n = 6 corneas for transmittance measurements), with each replicate representing tissue from a distinct individual, except for one case (both the left and right cornea were used for transmittance measurements for one individual). Experimental units comprised individual sharks or tissue samples, and no experimental treatments or manipulations beyond sample preservation and processing were applied. Comparative analyses incorporated publicly available genomic and transcriptomic datasets from other chondrichthyan species as detailed in the Methods. |
| Research sample | The research sample consisted of Greenland sharks (Somniosus microcephalus) collected off Disko Island, Greenland (69°15'N, 53° 34'W) between 2020 and 2024 under scientific collection permits. A total of 10 individuals were used for the study, all individuals were adults (5 males, 5 females; 1.03–3.65 m total length; estimated age range: 100-134 years), and were euthanized immediately after capture to preserve tissue integrity. Retinal, corneal, and other tissues were collected for histological, molecular, and biochemical analyses. The Greenland shark was selected due to its extreme longevity and unique deep-sea ecology, providing an opportunity to study molecular adaptations to low-light environments and slow aging. The sampled individuals are representative of the adult Greenland shark population inhabiting the central West Greenland shelf. |
| Sampling strategy | The Greenland sharks used in this study were caught between 2020 and 2024 using scientific long lines off the coast of the University of Copenhagen's Arctic Station on Disko Island, Greenland (69°15'N, 53°34'W). These specimens are rare and valuable and it is not possible to predict how many specimens will be caught in advance. Thus, no statistics were used to pre-determine sample size and we simply used the number of samples that we were able to obtain from the wild. |

| | |
|---|---|
| Data collection | AB, KFS, JFS, RB, and PGB collected Greenland shark specimens from the wild and recorded individual details including total length, sex, and sampling metadata. Laboratory data were collected by the respective authors performing each experiment: histological and microscopy data (LF, ET); genomic and transcriptomic sequencing data (LF); phylogenetic and gene mining analyses (LF); rhodopsin spectral measurements (ET); immunohistochemistry (WC); in situ hybridization (ET); TUNEL assays (ET); lipidomic analyses (FG); and corneal transmittance measurements (DH, AEF, CJN). All data were recorded digitally, with metadata and raw data stored in repositories and sequencing data deposited in public databases as specified in the paper. |
| Timing and spatial scale | The Greenland sharks used in this study were caught between 2020 and 2024 using scientific long lines off the coast of the University of Copenhagen's Arctic Station on Disko Island, Greenland (69°15'N, 53°34'W). The collection locations were selected because that is the natural habitat of the study species. The collection times were spread over several years as it took several field trips to collect all specimens required and field trips can only be conducted once per year (in the summer when the weather permits sampling) and when space is available on an appropriate research vessel. |
| Data exclusions | No data were excluded from the analyses. |
| Reproducibility | We endeavored to explain all methodologies in as much detail as possible to facilitate reproducibility. Furthermore, all raw and intermediate data have been made publicly available via repositories. Finally, where possible, we have retained the original tissue specimens and analyses can be re-performed from scratch if ever required. |
| Randomization | There was no group allocation. All samples were wild-caught animals and were not separated into separate groups for comparison. |
| Blinding | All researchers who performed experiments were blinded to the details of the specimens being analysed (e.g., sex, age, etc) until after data analysis was complete. This was achieved using codes assigned by researchers who collected the samples (different researchers performed animal collection and experiments). |

Did the study involve field work? ☒ Yes ☐ No

## Field work, collection and transport

| | |
|---|---|
| Field conditions | Field work was conducted off the coast of Disko Island, Greenland, between 2020 and 2024 under Arctic marine conditions. Sampling took place during the summer field seasons when sea-surface temperatures ranged from approximately 0 °C to 6 °C, with variable daylight and calm to moderate sea states typical for the region. All sampling was conducted from research vessels operated by the University of Copenhagen's Arctic Station. |
| Location | Sampling was performed in the waters surrounding the University of Copenhagen's Arctic Station on Disko Island, Greenland (69° 15'N, 53°34'W). Greenland sharks (Somniosus microcephalus) were caught using scientific longlines deployed at depths of approximately 115–300 m in coastal fjord and shelf habitats of central West Greenland. |
| Access & import/export | All fieldwork and sample collection were conducted under permits and licenses issued by the Government of Greenland in full compliance with local, national, and international regulations governing scientific collection and use of genetic resources. Shark collection and euthanasia were authorized by the Ministry of Fisheries, Hunting & Agriculture under permits 2020-26794, 2022-24744, 2023-6108, and 2024-119, and genetic resource utilization was covered by a non-exclusive licence (G24-051) issued by the Ministry of Foreign Affairs, Business and Trade. All export and transfer of samples were carried out under these authorizations and in accordance with institutional biospecimen transport guidelines. |
| Disturbance | Disturbance to wildlife and habitats was minimized by using targeted scientific longline capture methods under restricted permit quotas and short deployment durations. Only a small number of sharks were taken for scientific purposes, and individuals were euthanized immediately after capture to prevent suffering. No other wildlife or habitats were disturbed during sampling operations. |

# 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 | Involved in the study |
|---|---|
| ☐ | ☒ Antibodies |
| ☐ | ☒ Eukaryotic cell lines |
| ☒ | ☐ Palaeontology and archaeology |
| ☐ | ☒ Animals and other organisms |
| ☒ | ☐ Clinical data |
| ☒ | ☐ Dual use research of concern |
| ☒ | ☐ Plants |

### Methods

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

## Antibodies

| | |
|---|---|
| Antibodies used | Anti-trimethyl histone H4 (sc-134216), anti-H3K27ac (ab-4729), anti-Rho 1D4 antibody (obtained in-house from hybridoma cells), Alexa Fluor 488-conjugated goat anti-rabbit IgG antibody (Invitrogen, A11008), and Alexa Fluor 647-conjugated goat anti-mouse IgG antibody (Invitrogen, A21235). |
| Validation | Anti-trimethyl histone H4 antibody was validated by the manufacturer for species reactivity with mouse, rat and human origin for Western Blot. Anti-H3K27ac antibody was validated by the manufacturer for species reactivity with cow, human, mouse, and rat by Western Blot, IP, IHC-P, ICC/IF, ChIP, PepArr. Validation of the 1D4 antibody is described in MacKenzie et al. "Localization of binding sites for carboxyl terminal specific anti-rhodopsin monoclonal antibodies using synthetic peptides." (Biochemistry 1984, 23(25):6544-9). The 1D4 antibody reacts with mouse, rat, human and bovine rhodopsin and is suitable for IHC, IF, co-IP and Western blot. |

## Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

| | |
|---|---|
| Cell line source(s) | HEK293S (ATCC, CRL-3022) |
| Authentication | None of the cell lines used were authenticated. |
| Mycoplasma contamination | All cell lines tested negative for Mycoplasma contamination. |
| Commonly misidentified lines (See ICLAC register) | No commonly misidentified cell lines were used in the study. |

## Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

| | |
|---|---|
| Laboratory animals | The study did not involve laboratory animals. |
| Wild animals | The wild animals used in this study consisted of Greenland sharks (Somniosus microcephalus) collected off Disko Island, Greenland (69°15'N, 53°34'W) between 2020 and 2024 under scientific collection permits. A total of 10 individuals were used for the study and all individuals were adults (5 males, 5 females; 1.03–3.65 m total length; estimated age range: 100-134 years). Animals were euthanized immediately after capture and retinal, corneal, and other tissues were collected for histological, molecular, and biochemical analyses.<br>Bovine samples were also used in this study. Bovine eyes were obtained from a commercial slaughterhouse. Each eye was dissected to remove the anterior segment, lens, and vitreous. The retina was then carefully peeled from the underlying eyecup and stored at –80°C until further processing. |
| Reporting on sex | For the focal organism (the Greenland shark), both sexes (males and females) were collected for the study. Sex was considered in the study design and both sexes were represented in the samples. Specifically, out of the 10 individuals used, 5 were male and 5 were female. |
| Field-collected samples | No laboratory work was conducted with the field-collected samples. They were euthanized immediately upon capture. |
| Ethics oversight | All sampling was carried out in accordance with laws and regulations under a permit to collect Greenland sharks for scientific purposes. The work was carried out with authorisation from the Government of Greenland under permits (2020-26794, 2022-24744, 2023-6108, 2024-119) from the Ministry of Fisheries, Hunting & Agriculture and a non-exclusive licence (G24-051) for the utilization of Greenland genetic resources issued by the Ministry of Foreign Affairs, Business and Trade. |

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

## Plants

| | |
|---|---|
| Seed stocks | n.a. |
| Novel plant genotypes | n.a. |
| Authentication | n.a. |