

Life Sciences Reporting Summary

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For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

For genotype detection from the re-sequencing data we based sample size and coverage on published simulation data. For the cohort modeling, all individuals collected during the dedicated MSS (Marine Scotland Science) deep-water bottom trawl survey of the continental slope west of Scotland between the years 1998-2015 were included in the analysis (120 hauls yielding a total of 176,733 fish).

2. Data exclusions

Describe any data exclusions.

For the cohort modeling, in order to assess cohort-specific depth change over the first 12 years of life, cohorts of fish spawned between years 1996 and 2003 were selected (age 12 and below), corresponding to 33,741 fish. For the analysis of alternative ontogenetic strategies, in order to achieve model convergence, only data for which the estimated density of fish was greater than 299 individuals per km² were kept, corresponding to 81,549 fish.

3. Replication

Describe whether the experimental findings were reliably reproduced.

There were no experimental findings to be replicated.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

No randomization was applied

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Investigators were not blinded to allocation for outcome assessment for the genetic analyses. While no randomization or blinding was applied to the survey data, the modelling method used for the analysis of alternative ontogenetic strategies (latent class model) allows the assignment of fish to two strategies without investigator intervention and, by using non-informative priors, without use of prior knowledge.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☒ ☐ A statement indicating how many times each experiment was replicated
- ☐ ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☐ ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☐ ☒ The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

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

7. Software

Describe the software used to analyze the data in this study.

For the genetic analyses a diversity of published software packages were applied and these are described in detail in the methods and supplementary texts. For the cohort modelling all models were developed in R 3.2.3 using the package rjags (Plummer et al. 2016)

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

Materials are available on a collaborative basis.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

N/A

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

N/A

b. Describe the method of cell line authentication used.

N/A

c. Report whether the cell lines were tested for mycoplasma contamination.

N/A

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

N/A

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

For genetic analyses samples were derived from materials collected during this study and earlier studies by deep water trawls, and details are provided in the supplementary methods. For the cohort analyses, data used in this analysis correspond to a re-utilisation of survey data collected from a total of 176,733 roundnose grenadier (*Coryphaenoides rupestris*) fish with pre-anal fin length ranging from 0.5 to 29.5cm over a period from 1998 to 2015. All fish were brought dead on board of the research vessel.

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

N/A