nature portfolio

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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 *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	Software was only used for data analyses.
Data analysis	All softwares we used in this study have been listed in the Methods section.All software used in this study included: SOApec v2, wtdbg2 v2.4.1,NextPolish v1.0, 3D-DNA v180114, BUSCO v 4.1.2, Fastp v0.20, SPAdes, TransDecoder v5.5.0, RepeatModeler v1.0.11, RepeatMasker v4.0.7, Tandem Repeats Finder v4.07, Augustus v3.2.1, BLAT v. 35, GeneWise v2.4.1, Evidence Modeler v1.1.1, InterProScan v5, BWA v0.7.12-r1039, SAMtools v1.4, FreeBayes v0.9.10-3-g47a713e, PLINK v1.90b6.6, PHYLIP v3.697, Admixture v1.3.0, PSMC, NOVOPlasty v4.3.1, MUSCLE v3.8.425, RAxML-8.2.12, MCMCtree v4.9j, Last v956, Multiz v1, BLAST v2.9.0, MAFFT v7.471, AlphaFold2, UCSF Chimera, Hisat2 v 2.1.0, StringTie v1.3.6.

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

The sequence data and genome assembly files of the hadal snailfish have been deposited in the NCBI BioProject database with accession numbers PRJNA852951 (genome data) and PRJNA855356 (transcriptome data). The custom scripts have deposited in GitHub (https://github.com/wenjie-xu-nwpu/hadal_snailfish).

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design whether sex and/or gender was determined based on self-reporting or assigned and methods used. Provide in the source data disaggregated sex and gender data where this information has been collected, and consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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	Analyses consisted of standard bioinformatic pipelines. Detailed methods, and parameters and softwares used are described in the manuscript. When possible replicates were used to increase statistical power, and all data was confirmed to be of high quality before analyses.
Research sample	Four hadal snailfish collected from the Marianas Trench, along with four Tanaka's snailfish collected from the southern Yellow Sea. The specific sampling locations are detailed in supplementary table 1.
Sampling strategy	Sampling procedures and sample sizes for individual experiments are provided in the Methods section. Genomic DNA was extracted from the muscle of four hadal snailfish collected from the Mariana Trench, and four Tanaka's snailfish collected from the southern Yellow Sea. Data quality was assessed and determined to be of high quality before and after analyses as described in the manuscript.
Data collection	All data were collected in the author's laboratory or downloaded from NCBI Genbank and the literature described in the manuscript. See the method section for details.
Timing and spatial scale	N/A
Data exclusions	No data collected were excluded from analyses.
Reproducibility	The genomes of hadal snailfish and Tanaka's snailfish were sequenced and combined to the chromosome level. In transcriptome sequencing, more than one biological replicate was analyzed for each sample. More details are provided in the methods and

	supplementary table.
Randomization	No randomization is required since the samples are collected randomly by the deep-sea landers.
Blinding	No blinding was required.

Did the study involve field work? ☐ Yes ☒ No

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

Methods

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

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	N/A
Wild animals	Animal sampling was carried out in accordance with the animal experimentation guidelines and regulations of the Institute of Deep-sea Science and Engineering. The Mariana hadal snailfish specimens were captured in the field (142°16.7761'E, 11°01.0362'N) in the Mariana Trench at a depth of 7254 m on December 14, 2019 by a trapping-cage mounted on the deep-sea landers carried by the research ship "Tan Suo Yi Hao". Tanaka's snailfish specimens were collected by trawling during on 14 December 2018 in the south-central Yellow Sea.
Reporting on sex	The results of the current study apply to all sexes of hadal snailfish. Due to difficulties in sample collection, information on sex was not collected in this study.
Field-collected samples	N/A
Ethics oversight	No ethical approval was required.

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