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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.

Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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
☐	☒	An indication of 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 statistics 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
☐	☒	Clearly defined error bars *State explicitly what error bars represent (e.g. SD, SE, CI)*

Our web collection on statistics for biologists may be useful.

Software and code

Policy information about availability of computer code

Data collection	All data collection used in this study are described in method section and supplementary table 6 of the manuscript.
Data analysis	All open or commercial software and parameters used in this study are described in the supplementary files and method section of the manuscript. No custom scripts are used in this study.

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 upon request. 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

The Antarctic blackfin icefish (C. aceratus) genome and transcriptome data has been deposited in NCBI database as BioProject PRJNA420419. RAD-tag sequences of all mapped individuals are available online at the NCBI Sequence Read Archive (accession number SRP118539).

Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

Life sciences study design

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

Sample size	Samples were were collected by opportunity. An individual specimen was used for genome sequencing. One of each male and female specimens were used for linkage analysis and a male individual was used for miRNA analysis.
Data exclusions	No data were excluded.
Replication	In this study, replication is not used. To verify the genome assembly completeness, BUSCO analysis was used and a number statistical methods were applied to verify the results such as likelihood Ratio tests for positively selected genes and Fisher's exact test for gene enrichment test. Detailed information is described in method section.
Randomization	As this study is about de novo genome assembly, randomization is not relevant to this work.
Blinding	As this study is about de novo genome assembly, blinding is not relevant to this work.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
☒	☐ Unique biological materials
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☐	☒ Animals and other organisms
☒	☐ Human research participants

Methods

n/a	Involved 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	This study didn't used any of the laboratory animals.
Wild animals	A female individual specimen used for genome sequencing was captured by hook and line fishing method and female and male specimens used for miRNA and linkage analysis were captured by bottom trawling. Before dissect tissues, specimens were anesthetized by MS-222 (200 mg/L tricaine methanesulfonate, Sigma Aldrich, Inc. St. Louis, MO, USA). Detailed protocol is fully described in method section from line 279 to line 363.
Field-collected samples	Field-collected specimens were directly transported alive to laboratory and maintained in seawater aquaria at –1 °C to 0 °C before experiments.