

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☐ | ☒ 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 software was used

Data analysis

R 3.6.1
 PHLAWD (no version number listed)
 AnnotationBustR 1.2
 RAxML-HPC v.8.12.2
 phytools 0.6-99
 rgbif 0.9.6
 WorldClim 2
 brms 2.10.0
 STAN 2.19.1
 ape 5.3
 FISSE (no version number listed)
 hisse 1.9.5
 dplyr 0.8.3
 Dsuite 0.3 r21
 SNPRelate 1.18.1
 ASTRAL 5.14.3
 McCortex 0.0.3-610
 IBDseq r1206
 PHLAWD 3.3a
 flexclust 1.4.0
 TreePL 1.0
 SplitsTree 4.15.1

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 and associated code is available on a Dryad digital repository at time of publication. Genome sequence data is available on the NCBI SRA at time of publication.

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	Compilation of published GenBank sequence data, data from geographic databases and the taxonomic literature, new whole genome sequencing of 100 species.
Research sample	Tissue samples from 100 Victorian cichlids from the tissue collection of OS.
Sampling strategy	One sample for each of 100 species that comprise the full range of ecological and taxonomic diversity in the radiation. Sampling was chosen on the basis of available funding in the project for genome sequencing, with a goal of maximizing ecological diversity for the given number of genomes able to be sequenced within the budget for the project.
Data collection	Whole genome sequencing, and collection via public repositories and the primary literature
Timing and spatial scale	We utilized preserved samples from the collection of OS, containing finclips from field-collected individuals from the years 1996-2014, with additional sampling performed by MM in Uganda in October 2015.
Data exclusions	No data was excluded from analyses.
Reproducibility	Citations of all data sources, and public deposition of new sequence data and curated sequence/trait/geographic data
Randomization	The work was not experimental in nature, and did not necessitate random assignment of individuals to treatment groups.
Blinding	No blinding
Did the study involve field work?	☒ Yes ☐ No

Field work, collection and transport

Field conditions	Samples from Tanzania were from previous collection work by the Seehausen lab, spanning the years 1996-2014. In conjunction with NaFIRRI, Matthew McGee performed collections in Uganda during October 2015, prior to the onset of the rainy season.
Location	Ugandan cichlids were taken from the following locations: Lake Nawampasa (1.28, 33.35), Lake Gigati (1.29, 33.53), Lake Bisina (1.66, 33.86) and Banda Island (-0.25, 32.41) using gillnets and cast nets.
Access and import/export	Permits were obtained from the Ugandan Ministry of Agriculture and Fisheries with assistance from Uganda's National Fisheries Resource Research Institute. Samples were exported from Tanzania and Uganda in accordance with national laws and international guidelines.
Disturbance	Disturbance was minimized due to sampling a small number of individuals.

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

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	The study did not involve laboratory animals.
Wild animals	MM took tissue samples and specimens from freshly killed cichlids caught by local fishermen using traditional methods overseen by NaFIRRI staff. The species, sex, and location of each individual is included in Appendix 5.
Field-collected samples	No laboratory work with live animals was performed.
Ethics oversight	All Uganda sampling was performed according to standard protocol from Uganda's National Fisheries Resource Research Institute.

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