

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

No software was used to collect the data in the study.

Data analysis

A large number of software applications were used in this study. All software used (custom and commercial/publicly available) are listed in the Methods. All custom scripts are available on request from the corresponding authors.

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

Sequence data have been deposited in the European Nucleotide Archive (ENA). Assemblies and annotation are available at WormBase and WormBase-ParaSite. All have been submitted to GenBank under BioProjects listed in Supplementary Table 1.

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	Sample size was determined by the availability of parasite material. All samples were surplus material from other ongoing research projects, and due to the difficulties involved with obtaining parasite material, sample size was determined primarily by sample availability, rather than a predetermined number.
Data exclusions	Some samples provided for this study were of poor quality, and thus the resulting data was of insufficient quality to warrant inclusion in the data set. Exclusion criteria were not predetermined.
Replication	Experimental findings were not reproduced due to the scale of the study, in terms of time and cost, combined with the issue associated with obtaining parasite material.
Randomization	Allocation of samples into experimental groups was done so based on taxonomic classification.
Blinding	Blinding was not relevant to this study as analysis were explicitly comparative.

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

Unique biological materials

Policy information about [availability of materials](#)

Obtaining unique materials	Not all unique materials used in this study are available due to a number of them being from wild or livestock animals, rather than laboratory maintained animals. They are either unique samples that could not easily be obtained again, or all the available sample has been used up in this experiment. In some cases, material from laboratory maintained populations may be available on request where feasible.
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Animals and other organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research

Laboratory animals	Samples obtained were parasite materials that were surplus to other existing ongoing projects, either from wild animals, laboratory animals or already dead animals (e.g. from an abattoir). Further details on the samples are given in Supplementary Table 1.
Wild animals	Samples obtained were parasite materials that were surplus to other existing ongoing projects, either from wild animals, laboratory animals or already dead animals (e.g. from an abattoir). Further details on the samples are given in Supplementary Table 1.
Field-collected samples	Samples obtained were parasite materials that were surplus to other existing ongoing projects, either from wild animals,

Field-collected samples

laboratory animals or already dead animals (e.g. from an abattoir). Further details on the samples are given in Supplementary Table 1.