

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 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
<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 LC-MS data were collected using Thermo Scientific Xcalibur version 4.3.73.11 software.

Data analysis LC-MS data were converted using MSConvert (ProteoWizard v3.0.18250-994311be0), then analyzed using Metaboseek software (v0.9.7). Quantification was performed via integration in Xcalibur 4.1 QualBrowser (v4.1.31.9, Thermo Scientific). MS Excel (v2112) and Graphpad PRISM (v8.4.0) were used to plot and perform statistical analysis. NMR spectra were processed and baseline corrected using MestreLab MNOVA (v14.2.1-27684) software packages. Worm tracking data shown in Extended Data Figure 4 were generated using WormTracker (v2.0) software.

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 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 HPLC-HRMS and MS/MS data generated during this study have been deposited at MassIVE (gnps.ucsd.edu) under accession number: MSV000088750. Source data are provided with this paper.

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](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Life sciences study design

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

Sample size	Sample sizes were chosen based on previous experience for each experiment (see, for example, Wrobel, C.J.J. et al. 2021; Le, H.H. et al. 2020; Helf, M.J., Fox, B.W. et al. 2022). No statistical methods were used to predetermine sample size.
Data exclusions	No data were arbitrarily excluded.
Replication	Experiments were performed in several independent replicates (usually three or more) as indicated, at different times. All attempts at replication were successful.
Randomization	Age synchronized populations of animals were produced and assigned randomly to experimental or control groups.
Blinding	Blinding was not applicable because the acquired experimental data required manipulations of live animals that have distinct phenotypes.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

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 following C. elegans strains were used: Wild type Bristol N2, MT15434 tph-1(mg280), MT14984 tph-1(n4622), PHX3601 pah-1(syb3601), PHX3596 pah-1(syb3596); tph-1(mg280), MT7988 bas-1(ad446), CB1112 cat-2(e1112), DH10 glo-1(zu437), PS8031 cest-1.1(sy1180), PS8032 cest-1.1(sy1181), PHX3928 cest-1.2(syb3928), PS8029 cest-19(sy1178), PS8030 cest-19(sy1179), PS8008 cest-2.2(sy1170), PS8009 cest-2.2(sy1171), PHX3937 cest-3(syb3937), PS8033 cest-33 (sy1182), PS8034 cest-33 (sy1183), PS8116 cest-4(sy1192), PS8117 cest-4(sy1193), RB1804 cest-6(ok2338), PS7953 cest-8(sy1163), PS7954 cest-8(sy1164), RB2053 ges-1(ok2716), PHX3634 pah-1(syb3634)[GFP::H2B::T2A::pah-1], PHX3678 pah-1(syb3678)[GFP::H2B::T2A::pah-1];tph-1(mg280), OH17653 pah-1(syb3634)[GFP::H2B:: T2A::pah-1];nsls698 [mir-228p::NLS::RFP], OH17654 pah-1(syb3634) [GFP::H2B::T2A::pah-1];nsls698[mir-228p::NLS::RFP];tph-1[mg280], OH17655 pah-1(syb3634)[GFP::H2B::T2A::pah-1], hmnEx2123[grl-2pro::CFP + grl-18pro::YFP], PHX5218 cest-4(syb5218)[cest-4::SL2::GFP::H2B], PHX5923 bas-1(syb5923) [bas-1::SL2::GFP::H2B]. Genotypes were confirmed using PCR. Animals of all ages - egg, larval stages, and adult were used in the metabolomics and egg-laying assays.
Wild animals	No wild animals were used in this study.
Field-collected samples	No field collected samples were used in this study.
Ethics oversight	Ethics oversight is not required for work with soil nematodes.

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