

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
<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 ImageJ v2.0, PISA v0.7, QuantStudio Real-Time PCR Software v1.3, STAR v2.7.2b, metaX v2.0.0

Data analysis AlphaFold2 v2.1.0, ChimeraX v1.0, ClusPro v2.0, ClusterProfiler v4.0.0, Cutadapt v1.9, DESeq2 v1.32.0, GSEA v4.1.0, HawkDock v2, HISAT2 v2.2.1, InterProScan v4.8, Monocle3 v1.0.0, PISA v0.7, Prism Graphpad v9.0, SAW v1.0, SciBet v1.0, Seurat v4.0.0, SignalP v6.0, SingleR v1.8.0, UMAP v0.5.6

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 sequencing data generated in this study have been deposited in the NCBI Sequence Read Archive (SRA) database under accession code SAMN48269365 [<https://dataview.ncbi.nlm.nih.gov/object/SAMN48269365>]. The processed sequencing data are provided in the Supplementary Information (Supplementary data

1-7) [https://doi.org/10.6084/m9.figshare.29134847]. The nucleotide sequences of T. canis genes daf-9, daf-12 and pebp1 have been deposited in the NCBI GenBank under accession codes PV590097 [https://www.ncbi.nlm.nih.gov/nucleotide/PV590097], PV590098 [https://www.ncbi.nlm.nih.gov/nucleotide/PV590098] and PV590067 [https://www.ncbi.nlm.nih.gov/nucleotide/PV590067] (cf. U29761), respectively. Source data are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

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 if 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.

Reporting on race, ethnicity, or other socially relevant groupings

Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status). Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.) Please provide details about how you controlled for confounding variables in your analyses.

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](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

Molecular assays (qRT-PCR, Western blot, ELISA): Three to six independent biological replicates (samples) per group were used. This sample size is standard for these well-established, highly quantitative techniques, where technical replication within samples provides robust measurement, and prior literature demonstrates consistent detection of significant effects at this level. A power analysis was performed to determine the minimum sample size required for the behavioural assays. Mouse experiments: twelve mice per experimental group were included. This sample size provides sufficient statistical power to detect biologically relevant effects with acceptable variance, based on power analysis of similar experiments in published literature and our pilot data. Rat (Predator scent): A single anesthetized rat was used solely as the source of predator scent for the light/dark box assay. Rat and cat were not part of the experimental groups being statistically compared; its scent stimulus was applied uniformly to the testing environment for mice in the behavioral test.

Data exclusions

No data were excluded from any analyses in this study.

Replication

Measurements within each biological replicate were also conducted in technical replicates (e.g., triplicates) to ensure precision. The results in this study are replicable.

Randomization

BALB/c mice from a single source batch (Qizhen Laboratory Animal Technology) were randomly allocated to experimental groups using a random number generator. For larval experiments, a homogeneous suspension from a single culture flask was prepared, and larvae were randomly distributed into treatment wells with equal numbers per replicate. Group allocation and subsequent culture conditions were identical for all subjects/cultures.

Blinding

Personnel performing experimental investigations (RT-qPCR, Western blotting, and animal experiments) were blinded to sample group identities and expected outcomes. Only sample group numbers were provided during data acquisition and analysis.

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		Methods	
n/a	Involved in the study	n/a	Involved in the study
☐	☒ Antibodies	☒	☐ ChIP-seq
☒	☐ Eukaryotic cell lines	☒	☐ Flow cytometry
☒	☐ Palaeontology and archaeology	☒	☐ MRI-based neuroimaging
☐	☒ Animals and other organisms		
☒	☐ Clinical data		
☒	☐ Dual use research of concern		
☒	☐ Plants		

Antibodies

Antibodies used	Bioss Antibodies (1. GAPDH Mouse mAb, Catalog number: bsm-33033M, Clonality: Monoclonal(4F8)); Custom-generated antibodies (1. Mouse anti-rTc-DAF-9, polyclonal; 2. Mouse anti-rTc-DAF-12, polyclonal; 3. Mouse anti-rTc-Beta-actin, polyclonal).
Validation	Custom polyclonal antibodies (anti-rTc-DAF-9, -DAF-12, Beta-actin) were generated in mice against recombinant proteins and affinity-purified. Specificity was demonstrated by antigen-blocking assays, pre-immune serum controls, and detection of expected molecular weights (63, 88, and 48 kDa).

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	Mouse, Mus musculus, BALB/c, 6-8 week old; Rat, Rattus norvegicus, SD, 10 week old
Wild animals	This study did not involve wild animals.
Reporting on sex	Sex of mouse was not considered in the experimental design.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	All experiments involving mice and rat followed the regulations of the Guide for the Care and Use of Laboratory Animals and were approved by the Laboratory Animal Welfare Ethics Committee at Zhejiang University, Hangzhou, China (permit no. ZJU20250029). All mice were maintained under a 12-hour light/12-hour dark cycle, at 22 ± 2 °C ambient temperature and 50 ± 5% relative humidity, with ad libitum access to food and water.

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

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.