

Reporting Summary

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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

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Data analysis

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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

All data presented in the paper are available from the authors upon reasonable request.

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](https://www.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	Animal procedures were approved by the Government of Upper Bavaria. Sample sizes were chosen based on guidance from the literature. Investigators were not blinded to the identity of groups. For all animal studies, animals of the same gender, age, and genetic background were randomized for grouping. Statistical analyses were performed using SPSS 18.0 (IBM, Chicago, IL, USA). Inter-group differences were assessed for significance using the paired t test. Mean values and error bars are presented as mean \pm SD and differences were considered significant if *** $p < 0.001$.
Data exclusions	Animal procedures were approved by the Government of Upper Bavaria. Sample sizes were chosen based on guidance from the literature. Investigators were not blinded to the identity of groups. For all animal studies, animals of the same gender, age, and genetic background were randomized for grouping. Statistical analyses were performed using SPSS 18.0 (IBM, Chicago, IL, USA). Inter-group differences were assessed for significance using the paired t test. Mean values and error bars are presented as mean \pm SD and differences were considered significant if *** $p < 0.001$.
Replication	Animal procedures were approved by the Government of Upper Bavaria. Sample sizes were chosen based on guidance from the literature. Investigators were not blinded to the identity of groups. For all animal studies, animals of the same gender, age, and genetic background were randomized for grouping. Statistical analyses were performed using SPSS 18.0 (IBM, Chicago, IL, USA). Inter-group differences were assessed for significance using the paired t test. Mean values and error bars are presented as mean \pm SD and differences were considered significant if *** $p < 0.001$.
Randomization	Animal procedures were approved by the Government of Upper Bavaria. Sample sizes were chosen based on guidance from the literature. Investigators were not blinded to the identity of groups. For all animal studies, animals of the same gender, age, and genetic background were randomized for grouping. Statistical analyses were performed using SPSS 18.0 (IBM, Chicago, IL, USA). Inter-group differences were assessed for significance using the paired t test. Mean values and error bars are presented as mean \pm SD and differences were considered significant if *** $p < 0.001$.
Blinding	Animal procedures were approved by the Government of Upper Bavaria. Sample sizes were chosen based on guidance from the literature. Investigators were not blinded to the identity of groups. For all animal studies, animals of the same gender, age, and genetic background were randomized for grouping. Statistical analyses were performed using SPSS 18.0 (IBM, Chicago, IL, USA). Inter-group differences were assessed for significance using the paired t test. Mean values and error bars are presented as mean \pm SD and differences were considered significant if *** $p < 0.001$.

Reporting for specific materials, systems and methods

Materials & experimental systems

n/a	Involved in the study
<input type="checkbox"/>	<input checked="" type="checkbox"/> Unique biological materials
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input type="checkbox"/>	<input checked="" type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

Unique biological materials

Policy information about [availability of materials](#)

Obtaining unique materials

Antibodies

Antibodies used calcein AM/EthD-1, Thermo Scientific

Validation Not applicable (NA)

Eukaryotic cell lines

Policy information about [cell lines](#)

Cell line source(s) ATCC, Manassas, VA, USA

Authentication --

Mycoplasma contamination --

Commonly misidentified lines
(See [ICLAC](#) register)

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Animals and other organisms

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

Laboratory animals Female athymic Fox-N-1 nude mice 6 weeks old and female C57BL/6 mice

Wild animals NA

Field-collected samples NA