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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 *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 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 *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

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 for data collection
Data analysis	Cutadapt (v1.5) NGS QC Toolkit (v2.3) FastUniq Tophat2 (v2.1.0) Samtools (v0.1.18) Cufflinks (v2.2.1) Trinity (v2.1.1) CEGMA (v2.5) CD-HIT (v4.5.7) FrameDP (v2.2.1) NCBI-BLAST (v2.2.25) CPAT (v1.2) Salmon (v0.9) Metascape R(v3.0) tximport (v3.8) variancePartition (v1.12.0) DESeq2 EdgeR WGCNA (v1.63) GenAge (Build 19) STRING (v10.5) miRDeep (v2.0.0.8)

miRBase (v32)
EXUTR (v0.1.0)
miRanda (v3.3a)

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

The raw data used in this study have been deposited in the National Center for Biotechnology Information's BioProject under the accession PRJNA503704. The additional data supporting the conclusions in this paper can be available in the Supplementary Data 1-6. Other intermediate datasets generated during this study are available from the corresponding author on reasonable request.

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

Life sciences study design

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

Sample size	150 samples collected from 71 individuals in five colonies were used for transcriptome sequencing (100 RNA-Seq) and small RNA sequencing (50 miRNA-Seq). 72 qualified RNA-Seq samples, with unambiguous age (0, 1, 2, 3, 4, 5, 6) and 7+ year-old cohort, were used in the longitudinal cohort analyses. 49 pairs of RNA-Seq and corresponding miRNA-Seq samples were used in the miRNA-mRNA network analyses.
Data exclusions	12 RNA-Seq samples were excluded from data analyses due to low CEGMA scores.
Replication	The experimental findings were reliably reproduced. Adequate numbers of biological replicates were used for longitudinal transcriptome analyses.
Randomization	The samples for RNA-Seq and miRNA-Seq were collected from five different colonies during the year 2013-2016. RNA extraction and library preparation were performed with the same protocol & procedure, and Illumina sequencing was done in the same company.
Blinding	The investigators were not blinded to species, age, sex, year-of-capture and colony information during sample collection. However, clustering analyses were done with blinded information.

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	This study did not involve laboratory animals

Wild animals	100 RNA-Seq samples and 50 miRNA-Seq samples were collected from 71 female Myotis myotis bats. These individuals were caught in five colonies in Brittany during 2013-2016 (Supplementary Table 1-2). Of all individuals, 2 were caught four times in consecutive years, 2 were caught three times and 20 were caught twice, with the rest of individuals being caught only once. Bats were caught in custom harp traps as they left the roost and were initially placed in individual cloth bags. For each bat, the uropatagium was extended to expose and choose a uropatagial vein. A sterile needle (26-gauge) was used to pierce the uropatagial vein on its dorsal side, creating a drop of blood on the uropatagium surface from which a volume of 80–200 microlitre (depending on the weight of the individual) was pipetted into a cryotube (2 ml, Nalgene labware). Blood samples were flash frozen in liquid nitrogen within a maximum of a few minutes after the vein was pierced. Haemostatic gel was applied on the vein to prevent further bleeding (Bloxang, Bausch & Lomb). Water and food were offered to the bats, and they were rapidly released. Blood samples were stored at -150 °C.
Field-collected samples	Blood samples collected from the field were flash frozen in liquid nitrogen. The samples were delivered back to the lab using dry shippers within a few days. The samples were further transfered to -150°C freezers for longterm storage.
Ethics oversight	Bat capture and blood sampling were implemented in accordance with the permits and ethical guidelines issued by 'Arrêté' by the Préfet du Morbihan and the University College Dublin ethics committee.

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