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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.

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	NA
Data analysis	GraphPad Prism 7, Geneious 10.0.2., MEGA7, Cytation 5

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

Data deposit code to be provided before publication

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	NA
Data exclusions	NA
Replication	For all results obtained from cell lines are repeated for three independent experiments
Randomization	NA
Blinding	NA

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

Antibodies

Antibodies used

Commercially available the primary and secondary antibodies were used in Western Blot

Anti-Niemann Pick C1 antibody
Cat#: ab108921
Host species: Rabbit
Supplier: Abcam
Dilution: 1:1,000

HRP-goat anti-mouse IgG
Cat#:405306
Host species: Goat
Supplier: BioLegend
Dilution: 1:10,000

Monoclonal anti-beta-actin antibody
Cat#:A2228
Host species: Mouse
Supplier: Sigma
Dilution: 1:10,000

Goat anti-rabbit IgG-HRP
Cat#:sc-2357
Host species: Goat
Supplier: Santa Cruz biotechnology

Dilution: 1:10,000

Validation

Describe the validation of each primary antibody for the species and application, noting any validation statements on the manufacturer's website, relevant citations, antibody profiles in online databases, or data provided in the manuscript.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	The primary bat cell lines were derived from Myotis davidii kidney (MdKi), R. leschenaultii kidney (RlKi), E. spelaea kidney (EsKi), E. spelaea lung (EsLu), and E. spelaea intestine (EsIn). Human embryonic kidney fibroblast cells (HEK293, ATCC#CRL-1573), human cervix epithelial cells (HeLa, ATCC#CCL-2), human lung epithelial cells (A549, ATCC#CCL-185), African green monkey kidney cells (Vero, clone E6, ATCC#CRL-1586), Rhesus monkey kidney epithelial cells (LLC-MK2, ATCC#CCL-7), Madin-Darby Canine kidney cells (MDCK, ATCC#CRL-2935), baby hamster kidney cells (BHK21, ATCC#CCL-10), were obtained from ATCC.
Authentication	All monkey and human cells were from ATCC with authentication. Bat cells made by ourselves were from organ. We guarantee they were from the organs described but there was no further authentication.
Mycoplasma contamination	We confirm that all cells were tested as mycoplasma negative.
Commonly misidentified lines (See ICLAC register)	None of the cell lines used are listed in the ICLAC database.