nature portfolio

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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 *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	Zen 2.3 Microscopy Software
Data analysis	Imaris versions 8 to10 (Bitplane - OXFORD Instruments); ImageJ (Fiji), version 2.14.0/1.54f (National Institutes of Health); GraphPad Prism 10 (Dotmatics); Adobe Photoshop version 25.4 (Adobe); Adobe Illustrator version 28(Adobe);Python Programming Language (Python Software Foundation). The code for the scRNAsequencing analysis is available on: DOI:10.5281/zenodo.16914738 https://doi.org/10.5281/zenodo.16914738.

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

All the data generated in this study are provided in the main text or the Supplementary Information/Source Data file. Source Data are provided with this paper. The raw data is stored in The Johns Hopkins Research Data Repository https://doi.org/10.7281/T1K3HJNO.

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

Life sciences study design

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

Sample size	No predetermination of sample size was calculated. We defined a minimum of n=3 and a maximum of n=10 animals to be sufficient based on our previous analysis of similar experiments and on the internal controls and degree of variability between samples in the different experiments.
Data exclusions	No data were excluded from the imaging analysis.
Replication	At least 3 individual animals were analyzed per genotype or experimental condition to ensure data reproducibility. The reported results were replicated in all attempts.
Randomization	Sample collection was randomized to avoid any bias in the analyzes.
Blinding	The investigators were blinded to group allocation during imaging data collection 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

n/a	Involved in the study
☐	☒ Antibodies
☐	☒ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used

anti-CTIP2 (1:1000, rat monoclonal, ab18465 Abcam, clone 25B6, current lot: GR322373-4)
anti-CUX1 (1:1000, rabbit polyclonal, 11733-1-AP Proteintech, current lot: 00050220)
anti-BRN2 (1:1000, rabbit monoclonal, 12137 Cell Signaling, clone D2C1L)
anti-Ki67 (1:500, rabbit polyclonal, ab15580 Abcam, current lot: GR3285096-1)
anti-Ki67 (1:500, rat monoclonal, 14-5698-82 Thermo Fisher Scientific, clone SolA15, current lot: 2496198)
anti-Pax6 (1:250, mouse monoclonal, MA1-109 Thermo Fisher Scientific, clone 13B10-1A10, current lot: XD341788)
anti-Pax6 (1:500, rabbit polyclonal, 901301 Biolegend, clone Poly19013, current lot: B343290)
anti-TBR2 (1:500, rat monoclonal, 14-4875-82 Thermo Fisher Scientific, clone Dan11mag, current lot: 2488481)
anti-TBR2 (1:500, rabbit polyclonal, ab183991 Abcam, clone EPR19012, current lot: GR3237130-1)
anti-SOX9 (1:1000, rabbit monoclonal, ab185966 Abcam, clone EPR14335-78 current lot: GR3194558-4)
anti-PH3 (1:1000, rat monoclonal, ab10543 Abcam, clone HTA28, current lot: 1052214-1)
anti-g-TUBULIN (1:500, goat polyclonal, A. Holland gift, Levine, M. S. et al. Centrosome Amplification Is Sufficient to Promote Spontaneous Tumorigenesis in Mammals. Dev Cell 40, 313-322.e5 (2017))
anti-Centrin (1:500, rabbit polyclonal, A. Holland gift, Moyer, T. C. & Holland, A. J. PLK4 promotes centriole duplication by phosphorylating STIL to link the procentriole cartwheel to the microtubule wall. Elife 8, e46054 (2019)).

Validation

Anti-CTIP2 (validated by IHC in mouse brain sections at different ages in the manufacturer's website);
Anti-CUX1 (validated by IHC in adult mouse brain sections in the manufacturer's website);
Anti-BRN2 (validated by IHC in mouse and rat brain sections in the manufacturer's website; validated in Barao et al. Nat Commun 15, 8043 (2024)
Anti-Ki67 (validated by IHC in mouse brain sections in the manufacturer's websites);
Anti-Pax6 (validated by IHC in mouse brain sections in the manufacturer's websites)
Anti-TBR2 (validated by IHC in mouse brain sections at different ages in the manufacturer's websites);
Anti-SOX9 (validated by IHC in mouse brain tissue in the manufacturer's website);
Anti-PH3 (manufacturer's referred references);
Anti-g-TUBULIN (validated by A. Holland's group: Levine, M. S. et al. Centrosome Amplification Is Sufficient to Promote Spontaneous Tumorigenesis in Mammals. Dev Cell 40, 313-322.e5 (2017));
Anti-Centrin (validated by A. Holland's group: Moyer, T. C. & Holland, A. J. PLK4 promotes centriole duplication by phosphorylating STIL to link the procentriole cartwheel to the microtubule wall. Elife 8, e46054 (2019)).

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)

State the source of each cell line used and the sex of all primary cell lines and cells derived from human participants or vertebrate models.

Authentication

Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.

Mycoplasma contamination

Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.

Commonly misidentified lines
(See ICLAC register)

Name any commonly misidentified cell lines used in the study and provide a rationale for their use.

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	Syngap1+/- heterozygous knockout mice, Syngap1 GAP mutants (+/GAP*, GAP*/GAP*), and WT (Control) littermates were maintained on a mixed background of C57/B6J and 129/SvEv background and were crossed at adult age to obtain mutant mice and control littermates at the different ages reported in this study (Embryonic ages 14.5 and 18.5 (E14.5 and E18.5) and postnatal ages 0 and 13 (P0 and P13)). Emx1-Cre [B6.129S2-Emx1tm1(cre)Krj], Brn2 conditional knockout [Brn-2fl/fl] and Brn1 conditional knockout [Brn-1fl/fl - generated in this study] mice were crossed at adult age to obtain Emx1-Cre;Brn1fl/fl;Brn2fl/fl mice and control littermates at embryonic ages 14.5 (E14.5).
Wild animals	This study did not involve wild animals.
Reporting on sex	Sex was not determined for embryonic or postnatal day 0 samples. For P13 analysis, since no differences have been reported between males and females for the analyzed markers in our previous studies we have included both sexes in these analysis - Fig. 3c and 3d: control = 3 males and 1 female; Syngap1+/- = 2 males and 2 females.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	All animal experiments adhered to the guidelines of the National Institute of Health and were approved by the Institutional Animal Care and Use Committee at Johns Hopkins University School of Medicine.

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, mosiacism, off-target gene editing) were examined.*