nature portfolio

Corresponding author(s): Tomasz Nowakowski and Ryan Delgado

Last updated by author(s): Oct 27, 2021

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	No software used for data collection.
Data analysis	R computational language (v4.0.1) , Barcode Generator script (V2.8) , CellRanger (v3.0.2), Seurat (v3.2.0.9014, and v4.0) , Cellbender (v.0.1}, Solo (v.0.1), Monocle3 (v0.2.1.9),, BBMap (BBMap- Bushnell B. - sourceforge.net/projects/bbmap/), Bowtie (v.5.2.1), UMI-tools (v.0.5.1), pheatmap (v.1.0.12}), ImageJ (v2.3.0/1.53f).

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

scRNA-seq transcriptomic data and STICR barcode data are available at dbGAP under accession number phs002624.v1.p1. Code used in manuscript are available at https://github.com/NOW-Lab/STICR. Publicly available reference genomes hg38 and mm10 used for analysis.

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	For scRNA-seq analysis, we analyzed 6 biological samples from GW15-GW18 (3 samples assayed in vitro and 3 assayed in xenografts). For IHC analysis, 4 biological samples of GW15-GW17 were used. Sample size was determined by the number of available specimens and were chosen to be a minimum of 3. No statistical methods were used to determine sample size.
Data exclusions	No data were excluded
Replication	scRNA-seq and IHC analysis were performed using multiple samples (6 for RNA-seq and 4 for IHC as listed above) prepared on different days. All replication attempts were successful.
Randomization	Randomization was not performed in this study as we did not perform comparative analysis that required it.
Blinding	Investigators were blinded during quantification of IHC, but not not during scRNA-seq as this line of analysis does not require human quantification, but rather software-based quantification.

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
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	The antibodies used in this study include: chicken anti-GFP (Aves, GFP-1020; 1:1000), mouse anti-human nuclear antigen (Novus, NBP2-34342; 1:100), rabbit anti-GABA (Millipore Sigma, A2052-100ul; 1:250), rabbit anti-NEUROD2 (Abcam, ab104430; 1:500), guinea pig anti-DCS (Millipore Sigma, AB2253; 1:200), rabbit anti-GFAP (abcam, ab7260; 1:1500), rabbit anti-SOX9 (Abcam, ab104430; 1:250), and mouse anti-OLIG2 (Millipore Sigma, MABN50; 1:200). Secondaries used include AlexaFluor anti-chicken 488 (Jackson Immunoresearch 703-545-155; 1:500) , anti-mouse 488 (ThermoFisher A-21042; 1:500), anti-rabbit 594 (ThermoFisher A-21207; 1:500) , anti-guinea pig 647 (Jackson Immunoresearch 706-605-148; 1:500), anti-mouse IgG1 488 (ThermoFisher A-21121; 1:500) , and anti-mouse IgG2a 647 (ThermoFisher A-21241; 1:500).
Validation	Aves, GFP-1020 (ch anti-GFP) Antibodies were analyzed by western blot analysis (1:5000 dilution) and immunohistochemistry (1:500 dilution) using transgenic mice expressing the GFP gene product. Western blots were performed using BlokHen® (Aves Labs) as the blocking reagent, and HRP-labeled goat anti-chicken antibodies (Aves Labs, Cat. #H-1004) as the detection reagent. Immunohistochemistry used tetramethyl rhodamine-labeled anti-chicken IgY. Novus, NBP2-34342 (ms anti-Human Nuclear Antigen) Publications using NBP2-34342 in the following applications: ICC/IF (6 publications), IHC (1 publication), IHC-Fr (1 publication) Millipore Sigma, A2052-100ul (rabbit anti-GABA) Expression of GABA in neucortical cells harvested from the brains of E19 day old rat embyros was detected by immunofluorescence using rabbit anti-GABA antibody. Triple IF staining was performed with the anti-GABA antibody and two anti-GAD antibodies. Expression of GABA was analyzed in cells isolated from the pallium of various animals including rats, mice, rabbits, guinea pigs, and

lizards by immunohistochemistry. IHC was performed using rabbit anti-GABA antibody at 1:1000 diluted in a solution of 0.0lM PBS ph 7.4 + 0.5% triton-xl00.

Abcam, ab104430 (rabbit anti-NEUROD2)
Tested applications: Suitable for IHC-P, IHC-Fr, WB

Abcam, ab104430 (rabbit anti-SOX9)
Tested applications: Suitable for IHC-P, IHC-Fr, WB

Millipore Sigma, MABNS0 (mouse anti-OLIG2)
Quality assurance: Evaluated by Western Blot in mouse brain lysate. Western Blot Analysis: 2 µg/ml of this antibody detected Olig2 on 10 µg of mouse brain lysate.

Santa Cruz, c-33664 (mouse anti-PTPRZl)
Previously used in: PMID: # 31901251 Cell Stem Cell. 26: 48-63.e6.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	NIH/3T3 (ATCC); Lenti-X HEK293T (Takara Bio)
Authentication	Cell lines were not authenticated.
Mycoplasma contamination	Cell lines were not tested for mycoplasma.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified lines used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	CB17.Cg-PrkdcscidLystbg-J/Crl mice, both male and female, ages postantal day 3-6 through day 90. Mice were housed in a barrier facility with 12hr light/12hr dark cycle and temperature and humidity control (70F, 50% rack humidity).
Wild animals	No wild animals were used in the study.
Field-collected samples	No field-collected samples were used int he study
Ethics oversight	All protocols and procedures followed the guidelines of the Laboratory Animal resource Center at the University of California, San Francisco and were conducted with IACUC approval.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Human tissue samples were collected without any identifying information including sex or race
Recruitment	No human participants were used int his study; human tissue was collected from elective terminations with the patient's prior consent.
Ethics oversight	All primary tissue was obtained and processed as approved by the UCSF Human Gamete, Embryo and Stem Cell research Committee (GESCR) approval 10-05113.

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

Flow Cytometry

Plots

Confirm that:

☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☒ All plots are contour plots with outliers or pseudocolor plots.

☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	PTPRZ1+ cells from germinal zone were prepared as described in the Methods.
Instrument	Becton Dickinson FACSAria
Software	FlowJo
Cell population abundance	60-70% of cells were PTPRZ1+
Gating strategy	No primary Ab negative control used to set gates for PtPRZ1+ cells.

☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.