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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	Nikon NIS Elements and 10X Genomics Cellranger 2.1.1 packages were used in acquiring experimental data.
Data analysis	The software is available under open source license in github repository, together with multiple analysis notebooks, at velocyto.org.

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

The data is available from short read sequencing archive, with accession numbers provided in the text.

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	sample size of each measurement was determined by the practical limitations of the protocol utilized. No statistical estimation of sample size was performed.
Data exclusions	cell types unrelated to the neurogenesis branches being analyzed were excluded from the final analysis, as described in the Methods. (however full dataset has been made available).
Replication	the approach was applied to multiple independent datasets, as presented in the manuscript. Multiple batches or timepoints served as replicates (showing consistency in all dataset). Similarly, the approach is implemented by two distinct pipelines (python and R version), which for a computational idea, served as another type of replication. In the analysis of the embryonic adrenal medulla, sample size was between 3-6 embryos derived from 1 to 2 independent litters to ensure reproducibility.
Randomization	bootstrap sampling across cells and genes was performed to assess sensitivity of results on individual datasets. Samples were not randomized across experiments.
Blinding	blinding is not applicable to the described experimental designs (i.e. single-cell measurements of a known normal tissue).

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

Animals and other organisms

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

Laboratory animals	For the oligodendrocyte dataset, we used male and female mice of the CD1 strain at postnatal days 20, 21 and 22. In the analysis of the embryonic adrenal medulla, wild type CD1 mice or transgenic Htr3a-EGFP mice were used (received from MMRRC and provided by J. Hjerling-Leffler laboratory (Karolinska Institutet, Sweden) (https://www.mmrrc.org/catalog/sds.php?mmrrc_id=273).
Wild animals	study did not involve wild animals.
Field-collected samples	study did not involve field-collected samples

Human research participants

Policy information about studies involving human research participants

Population characteristics	Human first trimester subcortical forebrain tissue was obtained from elective routine abortions (10 weeks postconception) with the written informed consent of the pregnant woman and in accordance with the ethical permit given by the Regional Ethics Vetting Board (Stockholm, Sweden). Human fetal forebrain tissue was collected and stored in hibernation media with addition of GlutaMAX and B-27 supplements according to the manufacture's instructions (overnight, 4oC, Hibernate-A, Thermo-Fisher). The

tissue was then cut into small cubic pieces of approximately 1-2mm length. Tissue was dissociated using a dissociation kit (Miltenyi, Neural Tissue Dissociation Kit (P)) according to manufacture's instructions. In short, tissue was prepared in the kit buffer containing 0.067mM beta-mercaptoethanol. After addition of enzyme mix 1 and 2, the tissue was mechanically dissociated using three increasingly smaller gauges of fire polished Pasteur pipettes, pipetted 20, 15 and 10 times up and down respectively. Ultimately, collected cells were stored on ice in PBS containing 1% BSA and immediately prepared for single cell library preparation. Single-cell RNA sequencing was performed using the 10X Genomics Chromium V2 kit, following the manufacturer's protocol, and sequenced on an Illumina Hiseq 2500.

Recruitment

Participants were recruited as part of routine clinical elective abortions. Self-selection bias is unlikely to have affected the results, as the embryos derived from elective abortions are likely to be normal.