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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	The ZEN (Zeiss) and BZ-X Analyzer (KEYENCE) softwares were used for acquiring microscopy data. The BD Rhapsody software was used for single-cell gene expression. Electrophysiology data was collected using a 1550A digitizer (Molecular Devices), a 700B patch-clamp amplifier (Molecular Devices) and the pClamp 10.6 software (Molecular Devices).
Data analysis	The GraphPad Prism Version 7.0 was used for statistical analyses. ImageJ was used for image quantification. Clampfit (Molecular Devices) and Origin (OriginLab) were used for the analysis of electrophysiology data. QuantStudio Software v1.1 was used for Real-Time PCR data analysis and STAR v2.5.2b, Picard v2.5.0, GATK v3.3, featureCounts v1.5.1 and plink v1.08 were used for RNA-seq analyses. R version 3.3.2 and 3.4.0 with the following packages tidyverse v1.2.1, WGCNA v1.61, sva v3.22.0 edgeR v3.20.9, limma v3.34.9 were used for RNA-seq analyses.

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

Gene expression data are available in the Gene Expression Omnibus (GEO) under accession numbers GSE93811 and GSE107771. The data supporting the findings of this study are available upon request from the corresponding author.

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	The hiPSC lines used in each experiment are described in Supplementary Table 1. For most experiments, at least 4 hiPSC lines were used. For the electrophysiological experiments, 2 hiPSC lines were used. Sample sizes were determined empirically.
Data exclusions	Data was not excluded. However, some ventralization (forebrain) was observed in one of the 12 hiPSC lines tested in the qPCR experiments as shown in Figure 1d, and because the main goal of our analyses were on dorsal forebrain/hCS, this line was not used for immunohistochemistry analyses.
Replication	hiPSC lines were differentiated in multiple differentiation experiments to assess reliability of the methods. Success of differentiation is quantified in Figure 1e.
Randomization	The hiPSC lines used in each experiment are described in Supplementary Table 1. At least 4 hiPSC lines were used for most analyses, except for electrophysiological analysis: 2 hiPSC lines were used for the experiment. All hiPSC lines were derived from healthy individuals; no group comparisons were performed.
Blinding	Samples for RNA-seq were blinded. Most other experiments did not involve comparison accross groups, and blinding was not used.

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

Mouse anti-SATB2 (Abcam, AB51502), used 1:50
Rat anti-CTIP2 (Abcam, AB18465), used 1:300
Rabbit anti-TBR1 (Abcam, AB31940), used 1:300
Chicken anti-TBR1 (Millipore, AB2261, Lot. NG1820262), used 1:200
Mouse anti-TLE4 (Santa Cruz, sc-365406, Lot. C0218), used 1:200
Mouse anti-HOPX (Santa Cruz, sc-398703, Lot. F1615), used 1:100
Mouse anti-RELN (MBL, D223-3), used 1:200

Rabbit anti-BRN2 (GeneTex, GTX114650), used 1:250
Rabbit anti-cCas3 (CST, #9661, Lot. 45), used 1:200
Rabbit anti-SOX2 (CST, #3579, Lot. 5). used 1:200
Mouse anti-TBR2 (R&D, MAB6166), used 1:100
Rabbit anti-GFAP (DAKO, Z0334, Lot. 20035993), used 1:1000
Rat anti-GFAP (Thermo Fisher Scientific, 13-0300), used 1:1000

Validation

We have used or validated some of the antibodies in previous studies (Pasca et al., Nature Methods 2015; Sloan et al., Neuron 2017; Birey et al., Nature 2017; Sloan et al., Nature Protocols, 2018), such as SATB2, CTIP2, TBR1, HOPX, RELN, BRN2, SOX2, TBR2, GFAP in human cells. Moreover, most of these antibodies have been used in other studies:
The mouse anti-SATB2 (Abcam, AB51502) has been used in 87 studies according manufacturer's website, and tested for immunofluorescence staining in human fetal brains (Ozai et al., 2018).
The rat anti-CTIP2 (Abcam, AB18465) has been used in 240 studies according manufacturer's website, and tested for immunofluorescence staining in human fetal brains (Ozai et al., 2018).
The rabbit anti-TBR1 (Abcam, AB31940) has been used in 157 studies according manufacturer's website, and tested for immunofluorescence staining in human fetal brains (Ozai et al., 2018).
The chicken anti-TBR1 (Millipore, AB2261) has been tested in IHC and used in 1 study as stated on the manufacturer's website, and also tested for immunocytochemistry in human cells (Parween et al., 2017).
The mouse anti-TLE4 (Santa Cruz, sc-365406) has been used in 6 studies according manufacturer's website, and tested for immunofluorescence staining in human cells (Yang et al., 2015).
The mouse anti-HOPX (Santa Cruz, sc-398703) has been tested in IHC and used in 1 study as stated on the manufacturer's website.
The mouse anti-RELN (MBL, D223-3) has been used in 11 studies according manufacturer's website.
The rabbit anti-BRN2 (GeneTex, GTX114650) has been used in 6 studies, and tested for immunofluorescence staining in human cells according manufacturer's website.
The rabbit anti-cCas3 (CST, #9661) has been used in 3048 studies according manufacturer's website, and also tested for immunocytochemistry in human cells (Imaizumi et al., 2018).
The rabbit anti-SOX2 (CST, #3579) has been used in 93 studies according manufacturer's website, and tested for immunofluorescence staining in human cells (Kogut et al., 2018).
The mouse anti-TBR2 (R&D, MAB6166) has been used in 1 study according manufacturer's website.
The rabbit anti-GFAP (DAKO, Z0334) has been used in 8 studies according manufacturer's website, and tested for immunofluorescence staining in human cells (HD iPSX Consortium, 2017).
The rat anti-GFAP (Thermo Fisher Scientific, 13-0300) has been used in 115 studies according manufacturer's website, and tested for immunofluorescence staining in human fetal tissue (Errede et al., 2014).

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)

H20961 line was obtained from the Gilad laboratory.
TUBA1B-mEGFP (AICS-0012) and LMNB1-mEGFP (AICS-0013) lines were purchased from Coriell Institute.

Authentication

iPSC lines were authenticated by SNP arrays.

Mycoplasma contamination

All iPSC lines used in this study were tested for Mycoplasma free.

Commonly misidentified lines
(See ICLAC register)

No commonly misidentified cell lines were used.