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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<u>Authors & Referees</u> and the<u>Editorial Policy Checklist</u>.

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	Сог	nfirmed			
	×	The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement			
	x	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			
	x	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)			
x		For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.			
X		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 <u>availability of computer code</u>						
Data collection	NIS Elements (Nikon Corporation), ZEN 2010 (Zeiss AG), QuantStudio 6(Applied Biosystems), NanoDrop 2000/2000c (Thermo Scientific)					
Data analysis	Fiji (v2.0.0-rc-69/1.52p) and custom plugins for image processing from Bioimaging Core Facility(BIOP, EPFL), Microsoft Excel 2011 (v14.5.5.) (Microsoft Corporation), GraphPad Prism (v9.1.2), Cutadapt (v2.1), Seurat (v3.1)					

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. 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

All data regarding image processing/quantification and RNA-se uencing analysis are available upon request.

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

Life sciences study design

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

Sample size	For EPI and TSC aggregates generated on microwells at 72 h, the sample size was >100. After transferring aggregates to 96 well plates, in general, the experiment design was to set 4 conditions with 24 aggregates per condition.		
Data exclusions	during medium exchange were excluded.		
Replication	All experiments were successfully replicated at least 3 times with similar results.		
Randomization	EPI and TSC aggregates with rounded morphology and no clear sign of apoptosis were picked and transfered together to form EpiTS embryoids.		
Blinding	Blinding was not performed.		

Reporting for specific materials, systems and methods

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	n/a	Involved in the study
	X Antibodies	×	ChIP-seq
	Eukaryotic cell lines	×	Flow cytometry
×	Palaeontology	×	MRI-based neuroimaging
×	Animals and other organisms		
×	Human research participants		
×	Clinical data		

Antibodies

Antibodies used	Primary antibodies used in this study:
	anti-E-cadherin Rabbit 1:500 #24E10 Cell Signaling Technology
	anti-Sox2 Rabbit 1:400 #ab97959 Abcam
	anti-Sox1 Goat 1:50 #af3369 R&D Systems
	anti-Otx2 Goat 1:25 #af1979 R&D Systems
	anti-Brachyury Goat 1:300 #sc-17745 (C-19) Santa Cruz
	anti-Brachyury Rabbit 1:100 #ab209665 Abcam
	anti-Oct4 Mouse 1:200 #sc-5270 (C-10) Santa Cruz
	anti-Nanog Rat 1:300 #14-5761-80 ThermoFisher
	anti-Cdx2 Rabbit 1:200 #ab76541 Abcam
	anti-Eomes Rabbit 1:200 #ab23345 Abcam
	anti-aPKC Mouse 1:100 #sc-17781 (H-1) Santa Cruz
	anti-Pax6 Rabbit 1:100 #901301 (Poly19013) BioLegend
	anti-Six1 Rabbit 1:200 #12891S (D4A8K) Cell Signaling Technology
	anti-Podocalyxin Rat 1:200 #MAB1556 (192703) R&D systems
	anti-Par6 Mouse 1:100 #sc-166405 (B-10) Santa Cruz
	anti-Tuj1 RAbbit 1:400 #ab18207 Abcam
	anti-Dppa3 Mouse 1:100 #AF2566-SP R&D systems
	Antibodies 58X474088474 5206 #2016 #2016 #2016 #2016 #2016 and in Beccari et. al and Turner et. al.
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	aPKC antiparty Reale 400 #10 11211 cher to the internation of SW 480 cells.
	Pax6 antibody was validated by Milad Klazitar (U.C. Irvine) for immunostanning of human iPSC derived neural rosettes. Ee have
	SIX1 ans Becondary and the manifecture of the provided by the manifecture of the provided by Historican. Podocalyxin antihody, was validated by the manifecturer for immunostaining of bEnd.3 Mouse Cell Line.
	Par6 antibody was validated by the manifacturer for immunostaining of human duodenum tissue.
	Tuj1 antibody was validated by the manifacturer for immunostaining of SK-N-SH (Human neuroblastoma cell line) cells.
	Dppa3 antibody was validated by the manifacturer for immunostaining of mouse ovary tissue.
	Foxa2 antibody was validated by the manifacturer for immunostaining of HT-29 cells.
	Tfap2c antibody was validated by the manifacturer for immunostaining of HeLa cells.
	Eya1 antibody was validated by the manifacturer for immunostaining of RH-30 cells.
	Laminin antibody was validated by the manifacturer for immunostaining of LS174T cells.
	Fibronectin antibody was validated by Früh et. al., 2015 for immunostaining of Normal Human Dermal Fibroblasts.
	Snai1 antibody was validated by Kunnen et. al., 2017 for immunostaining of Proximal Tubular Epithelial Cells (PTECs).
	mCherry antibody was validated by the manifacturer for immunostaining of mCherry transduced U2OS cells.

Eukaryotic cell lines

Policy information about <u>cell lines</u>	
Cell line source(s)	SBR ES cell line was generated and provided by David Suter Lab (Deluz et. al., 2016)
	TLC:mCherry line was generated by Ferrer Vaquer et. al., 2010 and provided by Alfonso Martinez-Arias.
Authentication	AR8:mCherry line was generated by Serup et. al., 2012 and provided by Alfonso Martinez-Arias.
	TS:GFP cells was generated by Tanaka et. al., 1998 and provided by Christian Schröter.
Mycoplasma contamination	SBR, TLC:mCherry and AR8:mCherry cell lines were authenticated by PCR genotyping following gene targeting.
Commonly misidentified lines (See ICLAC register)	TS:GFP cell line was authenticated in Tanaka et. al., Science, 1998. The authentication was done by chimera formation and GFP detection in only extraembryonic tissues.
	All cell lines were tested regularly and confirmed free of mycoplasma with in house mycoplasma test and MYCOPLASMACHECK service from GATC.

No cell lines used in this study are in the data-base of commonly misidentified cell lines.