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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	IN Cell Analyzer 6000; IN Cell Developer Toolbox version 1.9.2; LSM880; EVOS FL Cell Imaging System; BD FACSAria IIu
Data analysis	Microsoft Excel 2019; GraphPad Prism version 8.4.3; IN Cell Developer Toolbox version 1.9.2; BD FACSDiva software version 6.1.3; ImageJ version 2.0.0; R version 3.6.0

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 data are available from the corresponding authors upon reasonable requests. All reasonable requests will be promptly reviewed by the corresponding authors to determine whether the request is subject to any intellectual property or confidentiality obligations.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research.](#)

Reporting on sex and gender	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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 statistical method was employed to predetermine sample size. To ensure reproducibility of the quantitative data, independent experiments were conducted three times. Statistical significance was determined using t-test for two-group comparisons or Tukey test for multiple-group comparisons.
Data exclusions	No data were excluded.
Replication	To ensure reproducibility of the quantitative data, independent experiments were conducted three times. The screening experiments for cell culture conditions were conducted once, but after selecting the conditions, independent experiments were performed three times to confirm their reproducibility.
Randomization	Randomization is not applicable to this study because we did not conduct any experiments involving treatment and control groups that would require random assignment among the subjects.
Blinding	The quantification analysis of the images was conducted in a blinded manner, where the quantifier conducting the analysis was unaware of the experimental conditions.

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

Methods

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

Antibodies

Antibodies used	anti-Wilms' tumor-1 (WT1; ab89901, Abcam plc. / sc-7385, Santa Cruz Biotechnology Inc.); anti-cytokeratin 8 (CK8 (TROMA-I); DSHB); anti-human nuclei (HuNu; MAB4383, Merck Millipore); anti-Ku80 (2180S, Cell Signaling Technology, Inc.); anti-lotus tetragonolobus

lectin (LTL; B-1325, Vector Laboratories, Inc.); anti-E-cadherin-1 (ECAD; 610181, BD Biosciences); anti-nephrin (GP-N2, Vector Laboratories, Inc.); anti-podocalyxin (PODXL; AF1658, R&D Systems, Inc.); anti-Jagged 1 (JAG1; sc-390177, Santa Cruz Biotechnology Inc.); anti-cadherin 6 (CDH6; AF1658, R&D Systems, Inc.); anti-aquaporin 1 (AQP1; ab9566, Abcam plc.); anti-megalin (sc-515772, Santa Cruz Biotechnology Inc.); anti-Dolichos biflorus agglutinin (DBA; B-1035, Vector Laboratories, Inc.); anti-sodium-chloride cotransporter (NCC; AB3553, Merck Millipore); anti-integrin alpha 8(ITGA8; BAF4076, R&D Systems, Inc.); anti-platlet-derived growth factor receptor alpha (PDGFRA; 323506, BioLegend, Inc.)

Validation	All antibodies used in this study are commercially available and have been validated by the manufacturer.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Human iPSC line iPSC-S09 was established by Sumitomo Pharma Co., Ltd. from peripheral blood cells using Sendai virus vectors. Human iPSC line 201B7 was established from dermal fibroblasts using retrovirus vectors at Kyoto University. Human iPSC line 317-12-Ff was generated by Kyoto University through fluorescent labeling of the 201B7 cell line. For further details, please refer to the following article: Fabian Oceguera-Yanez et al. Methods. 15;101:43-55. (2016).
Authentication	Human iPSC line iPSC-S09 was authenticated by the short tandem repeat (STR) pattern anlaysis. Human iPSC line 201B7 and 317-12-Ff were authenticated by Kyoto University.
Mycoplasma contamination	The cell lines were tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	N/A

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	Pregnant female C57BL/6NCrSlc mice on embryonic day 13.5 were purchased from Japan SLC, Inc. Pregnant female Microminipigs on embryonic day 30 were purchased from Fuji Micra, Inc.
Wild animals	No wild animals were used.
Reporting on sex	Embryonic animals were used, at a stage where sex is not visibly determinable and thus information on the sex of animals was not collected.
Field-collected samples	No field-collected samples were used.
Ethics oversight	The experiments were conducted in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals. Experiments involving the collection of fetuses from pregnant pigs were conducted in the laboratory of IVTeC Co., Ltd. (Tokyo, Japan) with the approval of the Animal Experiment Ethics Committee of IVTeC Co., Ltd. (approval numbers: IVT22-191 and IVT23-95). Experiments related to organoids were conducted in the laboratory of Sumitomo Pharma Co., Ltd. with the approval of the Institutional Animal Care and Use Committee of Sumitomo Pharma Co., Ltd. (approval number: AN14292). Experiments related to humanized xenogeneic kidneys were conducted in the laboratory of the Jikei University School of Medicine with the approval of the Institutional Animal Care and Use Committee of the Jikei University School of Medicine (approval numbers: 2018-066 and D2021-070). We have complied with all relevant ethical regulations for animal use. Every effort was made to minimize animal suffering.

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	Biotinylated anti-ITGA8, allophycocyanin-labeled streptavidin, and phycoerythrin-labeled anti-PDGFRA were used for cell staining.
Instrument	BD FACSAria IIu

Software	BD FACSDiva software
Cell population abundance	We conducted cell sorting targeting ITGA8-positive cells. Cell populations obtained after sorting exceeded a positivity rate of 80% and a count of 5.0 x10^5, which we subsequently used in the experiment.
Gating strategy	We identify the target cells by reacting them with anti-ITGA8 antibodies, followed by APC labeling of the anti-ITGA8 antibodies. In our culture system, ITGA8-positive and ITGA8-negative cells were clearly segregated and exhibited bimodal separation on the histogram plot. We set the cut-off value at the boundary between these peaks. Additionally, we confirmed the reliability of the cut-off value by analyzing cells not treated with anti-ITGA8 antibodies as a negative control.

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