nature portfolio

Corresponding author(s): Katalin Susztak

Last updated by author(s): 7/2/2026

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	Cell Ranger version7.2.0 (http://10xgenomics.com) was used to process scRNA-seq data. STARSolo (version 2.7.9a) was used to align scRNAseq to obtain spliced and unspliced matricesRNAvelocity
Data analysis	Custom scripts for data analysis are shared on https://github.com/jlevins2010/Fetal_atlas CellBender (version 0.2.0) was used to remove ambient RNA. scanpy (version 1.9.1) was used to import perform QC on scRNAseq data Clustering was performed using the Leiden algorithm (leidenalg version 0.8.10), with resolution 1.0. UMAPs were used to visualize cells in dimension reduced space (umap-learn version 0.5.3). RNA velocity was calculated using scVelo (version 0.2.5) CellRank (version 1.5.1) was used for calculating absorption probabilities to calculate trajectories of the single cell data. Age dependent DEGs were calculated using pyDESEQ2(56) (version 0.4.4) via pseudobuking each annotation by sample and plotted in matplotlib (version 3.6.3). The expression matrix and metadata from each CosMx run was exported from the AtoMx platform and was converted to a python object using squidpy(version 1.2.3) Raw counts of the initial object were used for SCVI batch correction (SCVI-colab version 0.11.0) Generalized additive models were constructed using pyGAM (version 0.8.0) and plotted using matplotlib (version 3.6.3). Pathway Analysis was done using GSEApy(58) (version 1.1.2) Cytosignal (version 0.2.0) and cellphonedb (version 5.0.0) were used to examine cell-cell interactions.

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

Raw data, processed data, and metadata from the scRNAseq and CosMx spatial transcriptomics has been deposited in Gene Expression Omnibus (GEO) with the accession code of GSE277893

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	Tissue from both male and female fetal human kidneys were examined. For scRNAseq, we identified sex looking at SRY and XIST expression. For spatial data, we designed probes for XIST and UTY, however these probes did not work well.
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	Human fetal kidneys were obtained from donors undergoing elective abortion at the Gynecology Clinic, University of Pennsylvania, Philadelphia and from the Sheba Medical Centre, Tel Aviv, Israel. Donors provided informed consent. Pediatric kidney tissue was obtained from surgical resections. Human pediatric kidney tissue was obtained retrospectively from surgical resections at the Children's Hospital of Philadelphia as part of the approved IRB protocol. Tissue was examined by an expert pathologist to ensure that it did not contain tumor cells. An honest broker deidentified the tissue and clinical information. Participants were not compensated.
Ethics oversight	All experimental procedures were approved by the Institutional Review Boards at the University of Pennsylvania (#832470) and at Sheba (approval number 8993-21-SMC), and at CHOP (#22-020263)

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	Sample size was determined based on tissue availability
Data exclusions	Samples with known congenital anomalies of the kidney and urinary tract were excluded.
Replication	Multiple samples were used in generating our datasets across gestational ages and modalities. 5 samples were used for single cell and 5 total for spatial analysis (4 fetal, 1 pediatric).
Randomization	N/A
Blinding	N/A

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
☒	☐ Plants

Methods

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

Antibodies

Antibodies used: Jag1 - goat (1:150, 1:200), (R&D, AF599-SP), Six2 - mouse (1:100) (proteintech, 66347-1-Ig), Cited1 - rabbit (1:50) (Invitrogen: PA5-65541), phospho-AKT 1 (1:50, CST#9271). Secondary antibodies used were the following: Donkey anti-Mouse – 555 (Invitrogen, A31570), Donkey anti-Goat – 405 (Invitrogen, A48257), Donkey anti-Rabbit - 647 (Invitrogen, A32795), Conjugated EpCAM (anti-Mo), FITC (Invitrogen, 11-5791-82, Alexaflor 555 goat-anti rabbit (Thermo #A-21428).

Validation: We used commercially available antibodies that have been internally validated by suppliers and are widely used in the field.

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 mice and e13 fetal CD1 mice.

Wild animals: N/A

Reporting on sex: Explants were obtained from fetuses irrespective of fetal sex.

Field-collected samples: N/A

Ethics oversight: Animal studies were approved by the University of Pennsylvania IACUC.

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

Plants

Seed stocks: N/A

Novel plant genotypes: N/A

Authentication: N/A