

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 (<i>n</i>) 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 <i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>
☒	☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted <i>Give P values as exact values whenever suitable.</i>
☒	☐ 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 <i>d</i> , Pearson's <i>r</i>), 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	The software and instruments used for data collection are described in the Materials and Methods section. Brightfield and epifluorescence images were acquired using an Olympus BX43 microscope, and confocal images were obtained with a Leica Stellaris 8 confocal microscope. Flow cytometry data were acquired on a BD LSRFortessa, cell sorting on a BD FACSAria II Fusion, and spectral analysis using a Cytex Biosciences Aurora Spectral Analyzer. qPCR data were obtained using a QuantStudio™ 3 System. RNA sequencing was performed on a NovaSeq 6000 SP v1.5 platform.
Data analysis	Data analysis was performed using Microsoft Excel 365 and GraphPad Prism v10.3.1. Image analysis was carried out with ImageJ v1.54q. Flow cytometry data were analyzed with FlowJo v10.10 (BD Biosciences). Bulk RNA-seq data were processed using CLC Genomics Workbench (Qiagen), and enrichment analysis was conducted with the NIH DAVID Bioinformatics Functional Annotation Tool. scRNA-seq data were analyzed using the Scanpy v1.9.0 package in Python.

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](#)

The data sets generated were deposited in the Gene Expression Omnibus (GEO) with the accession number GSE284270 and GSE284713.

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

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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](https://www.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

Data exclusions

Replication

Randomization

Blinding

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

For immunohistochemistry assays we used: Myh11(Abcam, AB224804, 1:100), EpCAM/CD326 (ThermoFisher, 14579185, 1:100), CD31 (BD Biosciences, 553370, 1:100), CD45 (BD Biosciences, 550539, 1:100), NG2 (Abcam, AB5320, 1:100), Alexa Fluor 488-conjugated goat anti-rat (ThermoFisher, A11006, 1:500) or anti-rabbit (ThermoFisher, A11008, 1:500), and Alexa Fluor 647 goat anti-rat (ThermoFisher, A21247, 1:500) or anti-rabbit (ThermoFisher, A21244, 1:500)

For flow cytometry we used: APC anti-mouse CD45 (BioLegend, 103112, 1:100), CD31 (BioLegend, 102409, 1:100) and EpCAM/CD326 (BioLegend, 118214, 1:100), Alexa Fluor 647 anti-NG2 antibody (Abcam, AB283639; 1:100), CD326 RB780 (BD Biosciences, 568737, 1:400), CD31 BV711 (BioLegend, 102449, 1:300), CD140a PE-Cy7 (ThermoFisher, 25-1401-82, 1:200), CD45 AF532 (ThermoFisher, 58-0451-80, 1:1000), F4/80 eFlour 450 (ThermoFisher, 48-4801-82, 1:200), CD11b BUV661 (BD Biosciences, 612977, 1:400), Ly6G PE-Fire 810 (BioLegend, 127673, 1:200), CD170 eFlour 660 (ThermoFisher, 50-1702-82, 1:200), FcεR1a APC-eFlour 780 (ThermoFisher, 47-5898-82, 1:200), I-A/I-E PerCP (BioLegend, 107624, 1:2000), CD3e RY586 (BD Biosciences, 568158, 1:800), CD45R BV570 (BioLegend, 103237, 1:3000), CD19 BUV737 (BD Biosciences, 612782, 1:400), and NK1.1 BB700 (BD Biosciences, 566502, 1:200).

Validation

Validation of the antibodies was based on the manufacturer's information and previous use in our laboratory

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)

Puman Pulmonary Fibroblasts (HPF) from 74 yo/male - PromoCell (Cat.No. C-12360, Lot:502Z022.12)

Authentication

Cells were expanded twice and cryopreserved upon arrival. Their identity and purity were supported by the manufacturer's Certificate of Analysis and further confirmed by consistent fibroblast morphology and detection of fibroblast markers, including Pdgfra and Col1a1.

Mycoplasma contamination

No mycoplasma contamination was detected

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

This study used 12-16-week-old mice purchased from The Jackson Laboratory: Rosa26-tdTomato (B6.Cg-Gt(rosa)26Sortm14(CAG-tdTomato)Hze/J; JAX Strain #:007914), Rosa26-DTA (B6.129S6(Cg)-Gt(ROSA)26Sortm1(DTA)pmb/J; JAX Strain #:032087), Pdgfra-CreERT2 (B6.129S-Pdgfratm1.1(cre/ERT2)Blh/J; JAX Strain #:032770), and Pdgfra-eGFP (B6.129S4-Pdgfratm11(EGFP)Sor/J; JAX Strain #:007669)

Wild animals

This study did not involve wild animals

Reporting on sex

Experiments were performed in both male and female mice. No sex-based differences were observed, and therefore data from both sexes were pooled and no sex-specific analyses are reported.

Field-collected samples

The study did not involve field-collected samples

Ethics oversight

All mouse studies were conducted in accordance with the Guide for the Care and Use of Laboratory Animals of the National Research Council. The animal use protocol was approved by the Institutional Animal Care and Use Committee (IACUC) at the University of Cincinnati.

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

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	Lungs were harvested from mice as described in the Methods section. Briefly, tissues were digested at 37 °C for 35 min in digestion buffer and processed using a MACS™ Dissociator (Miltenyi Biotec, 130-093-235). Red blood cells were removed by incubation with Red Cell Lysis Buffer (eBioscience, 00-4300-54), and the remaining cells were resuspended in FACS buffer (Dulbecco's PBS supplemented with 2% fetal bovine serum) and stained with the desired antibody.
Instrument	Flow cytometry analysis was conducted using a BD LSRFortessa and sorting performed on a BD FACSAria II Fusion. Spectral flow cytometry was performed using a Cytex Bioscience Aurora Spectral Analyzer.
Software	FlowJo v.10.10 software (BD Biosciences)
Cell population abundance	PostnLin cells represent approximately 0.1% of the viable stromal population. The purity of this population was confirmed by bulk RNA-seq analysis of the sorted cells, which showed high expression of Postn and undetectable expression of markers associated with other lineages, including Cd45 (hematopoietic cells), CD326 (epithelial cells), and Cd31 (endothelial cells). Additional details are provided in the manuscript.
Gating strategy	Samples were gated to exclude debris and doublets. Viable cells were selected by excluding those labeled with the dead cell staining marker. Because PostnLin cells represent a rare population, additional gating excluded CD45+, CD326+ and CD31+ cells to enrich for the fibroblast population of interest. Details of the gating strategy are provided in Supplementary Figures 5 and 6.

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