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Reporting Summary

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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	Reported on page 30 (Methods Section)
Data analysis	R computer software for Windows (version 3.3.2) was used for statistical analysis

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

The data that support the findings of this study are available from the corresponding author upon reasonable 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

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	The number of animals was derived from a Power calculation based on our preliminary data for differences in means, standard deviations, and assuming power=0.8 and alpha =0.05
Data exclusions	Animals with urogenital, reproductive, or clinical problems were not included in the study
Replication	Technical replicates were performed 3 times
Randomization	Animals were randomly assigned to experimental groups upon arrival to the animal facility
Blinding	Investigators were blinded during histological and morphometrical data analysis

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
☐	☒ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

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

Antibodies

Antibodies used	Anti-pan cytokeratin (AE1/AE3, 1:50, ab28028; Abeam), vimentin (1:100, ab28028; Abeam), smooth muscle myosin heavy chain 11 (MHC, 1:250 ab683; Abeam), calponin (1:100, C2687; Sigma-Aldrich), anti-a-SMA (1:40, ab18147; Abeam), anti-uteroglobin (7G4E9, 1:100, ab50711; Abeam), anti-CD31/PECAM-1 (C31.7, NBP2-15188; Novus biological), anti-estrogen receptor alpha (sc-5002; Santa Cruz), and anti-progesterone receptor (sc-811; Santa Cruz), biotinylated goat anti-mouse lgG (BA 9200, 1:300; Vector laboratories), goat anti-mouse Alexa Fluor 488 (1:500, All0l 7; ThermoFisher), Alexa Fluor 594 (1:100, A11020; ThermoFisher), R-phycoerythrin-conjugated CD9 (1:100, CBL162P; Millipore), fluorescein isothiocyanate (FITC)-conjugated lgG (1:250, ab79092; Abeam), phycoerythrin-labeled mouse lgG2b, K lsotype (559529; BD Pharmingen), and FITC mouse lgG2a (ab79092; Abeam), anti ?-actin (1:200, sc-47778; Abeam), Anti-a-SMA (1:200, ab-7187; Abeam), and bovine anti-goat secondary antibody (1:1000, sc-2378; Santa Cruz Biotechnology)
Validation	Primary antibodies were validated in normal rabbit uterine tissue (anti-pan cytokeratin (AE1/AE3), vimentin, mooth muscle myosin heavy chain 11, calponin, anti-a-SMA, anti-estrogen receptor alpha, and anti-progesterone receptor, and CD9), rabbit aorta (anti-CD31/PECAM-1) and rabbit lung tissue (anti-uteroglobin) , respectively according to the manufactures' website.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Adult female New Zealand white rabbits (3.5-4 kg)
Wild animals	The study did not involve wild animals
Field-collected samples	The study did not involve samples collected from the field
Ethics oversight	All animal experiments were performed with the approval of the Institutional Animal Care and Use Committee and in accordance with all federal guidelines. Rabbits were euthanized according to the guidelines set forth by the American Veterinary Medicine Association.

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	Reported on pages 22-23 (Methods Section)
Instrument	FACSCalibur instrument (Becton Dickinson Immunocytometry Systems)
Software	BD Cell Quest Pro software (version 5.1)
Cell population abundance	Cell were not sorted in this study
Gating strategy	Cell populations were gated out on the basis of scatter properties, excluding debris and doublets

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