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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 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	Flow cytometry was performed on FACS Aria II (BD Biosciences).
Data analysis	AFM analysis was performed utilizing Nanoscope Analysis 1.9 Software. Software used for statistical analysis was Prism 7 GraphPad. Mouse gait was analyzed using the CatWalk XT (Noldus Information Technology, Wageningen, The Netherlands. FACS analysis was conducted using FlowJo v10 software. Raw microarray data were submitted to Gene Expression Commons (https://gexc.riken.jp) (Seita et al., 2012), where data normalization was computed against the Common Reference, which is a large collection of more than 11,939 mouse and 25,229 human array experiments deposited to the National Institutes of Health Gene Expression Omnibus (NIH GEO) database.

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 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 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	We use the minimum number of animals, depending on each experiment, necessary to achieve statistical significance. We determined required sample sizes by conducting power analyses using preliminary data from the mouse micfofracture and human mice xenografts .
Data exclusions	We exclude animals that unexpectedly become morbid during the course of the experiment.
Replication	All of our findings were replicated and reproduced multiple times. The only exceptions were incidents where animals died prematurely or unexpectedly before the requisite time point for analysis.
Randomization	Animals were allocated randomly into the different experimental group.
Blinding	Different, separate teams of investigators were used to perform procedures while others performed the analysis. Investigators performing analysis were blinded from on the procedure done to each animal to eliminate bias.

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
☐	☒ Human research participants
☐	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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

Antibodies

Antibodies used	CD45 (BioLegend, Cat#304029-BL, Lot#B256106), CD235a(BioLegend, Cat#306612-BL, Lot#B224562), CD31 (Thermo Fisher Scientific, Cat#13-0319-82, Lot#1994108), CD202b (Tie-2) (BioLegend, Cat#334204, Lot#B171579), CD146 (BioLegend, Cat#342010, Lot#B259888), PDPN (Thermo Fisher Scientific, Cat#17-9381-42, Lot#2065618), CD90 (THY1; BioLegend, Cat#328120, Lot#B263033), CD164 (BioLegend, Cat#324808), and CD73 (BioLegend, Cat#344016, Lot#B224216).
Validation	Antibodies were validated according to manufacture's description.

Animals and other organisms

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

Laboratory animals	9-week old, skeletally mature, male C57BL/6 or β Actin-CreERT/Rainbow mice were used to examine the effect of MF on the resident mSSC population. Immunodeficient NSG mice were used in xenograft experiments.
Wild animals	This study did not involve wild animals.
Field-collected samples	This study did not involve samples collected from the field.
Ethics oversight	The study protocol was approved by Stanford's Administrative Panel on Laboratory Animal Care.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Human fetal samples were obtained from Stemexpress (Folsom, CA) and shipped overnight. Samples ranged in age from 10 to 20 weeks of gestation with no restrictions on race or gender.
Recruitment	Adult femoral heads (58–74 years old) were obtained from Stanford Hospital. No restrictions were made regarding the race, gender, or age of the specimen's donor.
Ethics oversight	Fetal sample procurement and handling was in accordance with the guidelines set by the Institutional Review Board (IRB-35711). Adult femoral heads (58–74 years old) were obtained from Stanford Hospital in accordance with guidelines set by the Institutional Review Board (IRB-35711).

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	*Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.*
Study protocol	*Note where the full trial protocol can be accessed OR if not available, explain why.*
Data collection	*Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.*
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

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	Detailed sample preparation protocol is provided in methods section of the manuscript.
Instrument	Flow cytometry was performed on FACS Aria II (BD Biosciences). Gating schemes were established with fluorescence-minus-one (FMO: staining with all fluorophores except one) controls and negative propidium iodide (PI) (Sigma-Aldrich, Cat#P4170) staining (1 mg/ml) was used as a measure for cell viability.
Software	FlowJo was used to analyze FACS data.
Cell population abundance	Quantification of cell populations are provided in the manuscript.
Gating strategy	Gating Strategy is provided in diagrams in manuscript.

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