Materials Design Analysis Reporting (MDAR)
Checklist for Authors

The MDAR framework establishes a minimum set of requirements in transparent reporting applicable to studies in the life sciences (see Statement of Task: doi:10.31222/osf.io/9sm4x.). The MDAR checklist is a tool for authors, editors, and others seeking to adopt the MDAR framework for transparent reporting in manuscripts and other outputs. Please refer to the MDAR Elaboration Document for additional context for the MDAR framework.

For all that apply, please note where in the manuscript the required information is provided.

Materials:

Newly created materials	indicate where provided: section/legend	n/a
The manuscript includes a dedicated "materials availability statement" providing transparent disclosure about availability of newly created materials including details on how materials can be accessed and describing any restrictions on access.		X

Antibodies	indicate where provided: section/legend	n/a
For commercial reagents, provide supplier name, catalogue number and RRID, if available.	All antibodies used for this study are listed in the Table S2.	

DNA and RNA sequences	indicate where provided: section/legend	n/a
Short novel DNA or RNA including primers, probes: Sequences should be included or deposited in a public repository.		X

Cell materials	indicate where provided: section/legend	n/a
Cell lines: Provide species information, strain. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID.		X
Primary cultures: Provide species, strain, sex of origin, genetic modification status.	For murine primary culture : Informations about strain, sex, and age are in the "Mice" section of the methods. The genetic modification status of the analysis is mentioned in the figure and legends of each experiment using primary murine cells. For human primary culture: informations about gender and age are detailed in the Table S1.	

Experimental animals	indicate where provided: section/legend	n/a
Laboratory animals or Model organisms: Provide species, strain, sex, age, genetic modification status. Provide accession number in repository **OR** supplier name, catalog number, clone number, **OR** RRID.	Informations about strain, sex, and age are in the "Mice" section of the methods We provided RRID for the different mouse linges in the "Mice" sections.	
Animal observed in or captured from the field: Provide species, sex, and age where possible.		X

Plants and microbes	indicate where provided: section/legend	n/a
Plants: provide species and strain, ecotype and cultivar where relevant, unique accession number if available, and source (including location for collected wild specimens).		X
Microbes: provide species and strain, unique accession number if available, and source.		X

Human research participants	indicate where provided: section/legend;	n/a

	or state if these demographics were not collected	
If collected and within the bounds of privacy constraints report on age, sex and gender or ethnicity for all study participants.	Age and sex/gender are provided in the table S1. Informations on ethnicity were not collected during this study.	

Design:

Study protocol	**indicate where provided: section/legend**	**n/a**
If study protocol has been pre-registered, provide DOI. For clinical trials, provide the trial registration number **OR** cite DOI.		X

Laboratory protocol	**indicate where provided: section/legend**	**n/a**
Provide DOI **OR** other citation details if detailed step-by-step protocols are available.	The detailed protocol containing primary murine periosteal cell culture, in vitro differentiation, flow cytometry, murine tibial fracture, cell transplantation, and histological analysis of tibial callus is available : DOI: 10.21769/BioProtoc.4107.	

Experimental study design (statistics details)		
For in vivo studies: State whether and how the following have been done	**indicate where provided: section/legend. If it could have been done, but was not, write not done**	**n/a**
Sample size determination	This is mentioned in the “Study design” section of the methods.	
Randomisation	This is mentioned in the “Study design” section of the methods..	
Blinding	This is mentioned in the “Study design” section of the methods.	
Inclusion/exclusion criteria	This is mentioned in the “Study design” section of the methods.	

Sample definition and in-laboratory replication	**indicate where provided: section/legend**	**n/a**
State number of times the experiment was replicated in laboratory.	For each experiment, sample were obtained from at least 2 independent experiments. This is mentioned in the “Statistical analyses” and “Study design” sections of the methods.	
Define whether data describe technical or biological replicates.	The type of replicates used for the different experiments are listed in the “Statistical analyses” section of the methods.	

Ethics	**indicate where provided: section/legend**	**n/a**
Studies involving human participants: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	All information regarding approval of human sample collection are available in the methods, section “Human tissue sample collection”, subsection “Cohort and Ethical approval”.	
Studies involving experimental animals: State details of authority granting ethics approval (IRB or equivalent committee(s), provide reference number for approval.	All information regarding approval of experimentation using mouse models are available in the methods, section “Mice”.	
Studies involving specimen and field samples: State if relevant permits obtained, provide details of authority approving study; if none were required, explain why.		X

Dual Use Research of Concern (DURC)	**indicate where provided: section/legend**	**n/a**
If study is subject to dual use research of concern regulations, state the authority granting approval and reference number for the regulatory approval.		X

Analysis:

Attrition	indicate where provided: section/legend	n/a
Describe whether exclusion criteria were preestablished. Report if sample or data points were omitted from analysis. If yes report if this was due to attrition or intentional exclusion and provide justification.	We describe exclusion criteria in the "Study design" section of the methods.	

Statistics	indicate where provided: section/legend	n/a
Describe statistical tests used and justify choice of tests.	All details on the statistical analyses are provided in the "Statistical analyses" section of the discussion.	

Data availability	indicate where provided: section/legend	n/a
For newly created and reused datasets, the manuscript includes a data availability statement that provides details for access or notes restrictions on access.	All reusued datasets are publicly available. All newly created dataset are deposited and will be publicly available at time of publication. All information to access the data are available in the "Data and materials availability" section.	
If newly created datasets are publicly available, provide accession number in repository **OR** DOI **OR** URL and licensing details where available.	Our newly generated datasets are deposited and all informations to access it are in the section "Data and materials availability".	
If reused data is publicly available provide accession number in repository **OR** DOI **OR** URL, **OR** citation.	All reused data are listed in the methods in "Single nuclei RNA sequencing analysis" section and in Data and materials availability.	

Code availability	indicate where provided: section/legend	n/a
For all newly generated custom computer code/software/mathematical algorithm or re-used code essential for replicating the main findings of the study, the manuscript includes a data availability statement that provides details for access or notes restrictions.	All reused code and packages are publicly available and listed in the methods, in "Single nuclei RNA sequencing analysis" section.	
If newly generated code is publicly available, provide accession number in repository, **OR** DOI **OR** URL and licensing details where available. State any restrictions on code availability or accessibility.		X
If reused code is publicly available provide accession number in repository **OR** DOI **OR** URL, **OR** citation.	All reused code and packages are listed in the methods, in "Single nuclei RNA sequencing analysis" section.	

Reporting

MDAR framework recommends adoption of discipline-specific guidelines, established and endorsed through community initiatives. Journals have their own policy about requiring specific guidelines and recommendations to complement MDAR.

Adherence to community standards	**indicate where provided: section/legend**	**n/a**
State if relevant guidelines (e.g., ICMJE, MIBBI, ARRIVE) have been followed, and whether a checklist (e.g., CONSORT, PRISMA, ARRIVE) is provided with the manuscript.		X