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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	Structural characterizations were conducted on Tecnai 12 TEM instrument (Philips), scanning electron microscope (SEM, Ultra 55 microscope, Zeiss), Ultima III (Rigaku), D8 advance (Bruker), FT-IR (Thermo Scientific) spectrometer, STA449F3A-0061M (NETZSCH), and Nexsa G2 system (Thermo Scientific) instruments. Tensile strength measurement were performed on on a universal testing machine (Instron-1121). Fracture toughness measurement were performed on an Izod impact test machine (XJU-2.75, Chengde Testing Machine Factory). Tribological property measurement were performed using a UMT TriboLab (Bruker). Absorbance was quantified through a microplate reader (Molecular Device). The resultant oxygen generation was quantified using an oxygen electrode (SevenExcellence, Mettler Toledo). Hydroxyl radical was quantitatively assessed using electron paramagnetic resonance spectroscopy (EPR, EMX PLUS, Bruker)The detection of intracellular ROS levels using flow cytometry (CytoFLEX, Beckman Coulter) and fluorescence microscopy (DMi8, Leica). Micro-CT scanning was performed using a VivaCT 80 scanner (SCANCO Medical AG, Switzerland). The distribution of CZPE and PE particles was observed using a polarizing microscope (Eclipse LV100N POL, Nikon). The cerium content was quantified using Inductively Coupled Plasma Optical Emission Spectrometry (ICP-OES, iCAP 7200, Thermo /Avio 220 Max, PerkinElmer). Tissues slides were scanned using a Pannoramic MIDI slide scanner (3DHISTECH). RNA purity and concentration were assessed using a NanoDrop 2000 spectrophotometer (Thermo Scientific), while RNA integrity was evaluated using a 2100 Bioanalyzer (Agilent). Sequencing was performed on an Illumina Novaseq 6000 system (Illumina). QRT-PCR amplifications were performed on an Applied Biosystems StepOne™ real-time PCR (Thermo Scientific) machine. Western blots were visualized on a Tanon 5200 Multi Chemiluminescent Imaging System (Tanon). Cell counting was subsequently performed using a BC-2800vet automatic cell analyzer (Mindray).
Data analysis	Statistical analysis was performed with GraphPad Prism v.9.3.1. and Microsoft Excel 2021. Fluorescence intensity was quantified using Fiji 15.4d ImageJ software. Gene Set Enrichment Analysis (GSEA) was performed using GSEA software. The number of target cells and the area of the ROI were quantified using CaseViewer software. Flow cytomery analysis was performed using FlowJo_v10.8.1. 3D model was conducted by Geomagic Wrap 2021. Transcriptome sequencing was performed by Shanghai OE Biotech Co., Ltd (Shanghai, China), the package are

follows: HISAT2 (version 2.1.0), DESeq2 (version 1.20.0), Htseq (version 0.11.2), fastp (version 0.20.1), RseQC (version 4.0.0), R (version 3.5.1) and Clusterprofile (version 4.6.0)

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 main data that support the findings of this study are available within the paper and its Supplementary Information. Accession codes of transcriptomic data will be available before publication. Further datasets are available from the corresponding author(s) on reasonable request. Source Data are provided with this paper.

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	No sex- and gender-based analyses have been performed.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, or other social groupings were not considered in this study.
Population characteristics	No particular population characteristics was involved in this study, except for the progression of aseptic loosening. The Ctrl sample for the single-cell RNA sequencing was obtained from a 64-year-old male who had experienced a hip dislocation but did not exhibit aseptic loosening. The AL sample was derived from a 76-year-old male with confirmed aseptic loosening and periprosthetic osteolysis.
Recruitment	Tissue donors were recruited in the second affiliated hospitals of Zhejiang University school of Medicine following study protocol. There is no potential self-selection in the volunteer tissue donation process. Patients who met one of the following conditions were excluded: 1) suffering from other serious underlying diseases; 2) involuntary, or voluntary but strongly opposed by family members; and 3) less than 10 years since joint replacement surgery. Under the auspices of the Institutional Review Board of the Second Affiliated Hospital of Zhejiang University School of Medicine, written informed consent was obtained from all patients participating in the study.
Ethics oversight	This study was done in accordance with the Declaration of Helsinki, the study protocol of patient samples was reviewed and approved by the Institutional Review Boards of the Second Affiliated Hospital of Zhejiang University School of Medicine (Approval number: 2024LSYD0555). This study complies with all the approval policies and requirements set by China's Ministry of Science and Technology for this work.

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	A precise value of 'n' were provided in the legends of figures. Sample size was chosen to ensure reproducibility of the experiments in accordance with the replacement, reduction and refinement principles of animal ethics regulation.
Data exclusions	No data was excluded from the analysis.
Replication	For property measurement experiments, samples were replicated and tested independently for 3-6 times and after analysis the standard deviation was displayed. For each experiment the statistical analysis is indicated in the figure legends.
Randomization	Randomization was used to divide up the animals for in vivo treatment study.
Blinding	No blinding was employed as the researcher performing the treatment was also responsible for the analysis. Our readouts consist of objective measurements.

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
[ ]	[x] Antibodies
[ ]	[x] Eukaryotic cell lines
[x]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[x]	[ ] Clinical data
[x]	[ ] Dual use research of concern
[x]	[ ] Plants

Methods

n/a	Involved in the study
[x]	[ ] ChIP-seq
[ ]	[x] Flow cytometry
[x]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used	Anti-IL-1β antibody (Servicebio #GB11113), anti-B220 antibody (Servicebio #GB113886), anti-CD138 antibody (Abcam #ab128936), anti-β-actin antibody (HRP conjugated, Servicebio ZB15001-HRP); anti-IL-6 antibody (Servicebio #GB11117), anti-TNF-α antibody (Servicebio # GB11188), anti-α-SMA (Servicebio # GB111364)
Validation	The antibodies listed above are standard reagents used in the field and validated in the literature as cited on the manufacturers websites, as well as by the manufacturers data sheets themselves https://www.servicebio.cn/goodsdetail?id=1391 https://www.servicebio.cn/goodsdetail?id=7318 https://www.abcam.cn/products/primary-antibodies/syndecan-1-antibody-epr6454-ab128936.html https://www.servicebio.cn/goodsdetail?id=21609 https://www.servicebio.cn/goodsdetail?id=1393 https://www.servicebio.cn/goodsdetail?id=4760 https://www.servicebio.cn/goodsdetail?id=3743

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	RAW264.7 cells and MT3T3-E1 cells were obtained from the Cell Bank of the Chinese Academy of Sciences. U266B1 myeloma cells sourced from the China Center for Type Culture Collection. THP-1 cells were a gift from Nanjing Drum Tower Hospital. Mouse synovial fibroblasts and bone marrow derived monocytes were isolated from 8-week-old male ICR mice.
Authentication	Cell lines have been authenticated by short tandem repeat profiling, and the results were compared with reference database.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

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	Institute of Cancer Research (ICR) mice were purchased from Beijing Vital River Laboratory Animal Technology Co., Ltd. NOD-Prkdcem1Il2rgem2 (NCG) mice were purchased from Hangzhou Ziyuan Laboratory Animal Technology Co., Ltd.
Wild animals	N/A
Reporting on sex	All the mice used within this manuscript were male.
Field-collected samples	N/A
Ethics oversight	All animal studies were performed under a protocol approved by the Science and Technology Ethics Committee of Nanjing University and approved by the Institutional animal care and use committee (IACUC) of Nanjing University.

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	First, RAW264.7 cells were seeded at a density of 2 × 10^5 cells per well in a 12-well plate and incubated for 12 h. CZPE and PE particles with concentrations of 0.2, 0.4, and 0.8 mg/mL were then dispersed in DMEM containing 10% FBS. This suspension was added to the wells, ensuring complete filling of each well, and sealed with parafilm. The plate was then inverted to maximize contact between the particles and cells. After 24 h of incubation, the plates were repositioned upright, and the medium containing particles was removed. The wells were washed thrice with PBS to eliminate residual particles. Cells were then incubated with 10 µM dichlorofluorescein diacetate (DCFH-DA, Sigma Aldrich) probe in the dark for 30 min, followed by the detection of intracellular ROS levels using flow cytometry (CytoFLEX, Beckman Coulter).
Instrument	CytoFLEX (Beckman Coulter)
Software	FlowJo_v10.8.1
Cell population abundance	The purity of post-sort fractions is regularly measured by the software.
Gating strategy	Cells untreated with CZPE/PE particles stained with probe were used as negative control and FSC-H/SSC-H was used to gate singlet. FITC-A was used to detect fluorescence signal.

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