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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 Authors & Referees and the Editorial Policy Checklist.

## Statistical parameters

When statistical analyses are reported, confirm that the following items are present in the relevant location (e.g. 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 |
| ☐ | ☒ | An indication of 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<br>*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 statistics 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<br>*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 |
| ☐ | ☒ | Clearly defined error bars<br>*State explicitly what error bars represent (e.g. SD, SE, CI)* |

*Our web collection on statistics for biologists may be useful.*

## Software and code

Policy information about availability of computer code

| | |
|---|---|
| Data collection | VGStudio MAX 2.2 |
| Data analysis | CATIA V5(R21), VGStudio MAX 2.2, GraphPad Prism 6, and Wolfram Mathematica 9 (for analytical modeling). |

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 upon request. 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 authors declare that all data supporting the findings of this study are available within the paper and its supplementary information.

# Field-specific reporting

Please select 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/authors/policies/ReportingSummary-flat.pdf

# Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

| | |
|---|---|
| Sample size | Experiments were performed with a sample size of 3. The experiments were repeated independently to enlarge the sample size when the preliminary experiment showed an effect, but this was limited by the sample size. |
| Data exclusions | None |
| Replication | All the experiments have been repeated in multiples independently. The number of replicates are mentioned in the paper. |
| Randomization | Device samples were prepared in advance and selected randomly from the pool of devices during experiments (force measurements, ex vivo, and in vivo). |
| Blinding | In all the experiments performed, a cavity was targeted using the device, and the operator was blinded to the depth of the target cavity. For the in vivo experiments, there was a single group of animals to test the feasibility of the device; hence, blinding was not needed. |

# Reporting for specific materials, systems and methods

## Materials & experimental systems

| n/a | Involved in the study |
|---|---|
| ☒ | ☐ Unique biological materials |
| ☒ | ☐ Antibodies |
| ☐ | ☒ Eukaryotic cell lines |
| ☒ | ☐ Palaeontology |
| ☐ | ☒ Animals and other organisms |
| ☒ | ☐ Human research participants |

## Methods

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

## Eukaryotic cell lines

Policy information about cell lines

| | |
|---|---|
| Cell line source(s) | Primary MSCs we purchased from Lonza http://www.lonza.com/products-services/bio-research/stem-cells/adult-stem-cells-and-media/human-mesenchymal-stem-cells-media/hmsc-human-mesenchymal-stem-cells.aspx |
| Authentication | Not applicable. |
| Mycoplasma contamination | Yes. They were tested for negative mycoplasma contamination, both by Lonza and lab tests. |
| Commonly misidentified lines (See ICLAC register) | Not applicable. |

## Animals and other organisms

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

| | |
|---|---|
| Laboratory animals | Dutch Belted rabbits (2–3kg body weight). |
| Wild animals | The study did not involve wild animals. |

| | |
|---|---|
| Field-collected samples | The study did not involve samples collected from field. |

## 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 | MSCs were cultured under standard media conditions. Prior to injection, cells were stained with a cell dye (DiD or CellTrace Violet). Stained cells (1 million) were injected into the SCS using i2T2, and recovered after few minutes through a recovery port placed diametrically opposite to the injection site (Fig. 5d in the paper). An excess amount of saline was pushed through the first needle, and effluent containing the cells was collected through the recovery port. Collected samples were pooled together and analyzed with a flow cytometer. |
| Instrument | BD LSR II |
| Software | FACSDiva for data acquisition and FlowJo 6 for data analysis |
| Cell population abundance | There were ~10K cells in the final gate (FSC vs. 7AAD). The purity of the cells was confirmed by CellTrace Violet positive staining before cell injection and after cell retrieval. |
| Gating strategy | FSC vs. SSC was used to gate out doublets, cell aggregates or dead/dying cells. Live cells (i.e. 7AAD-negative) were defined by Y-axis with value below 400. |

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