***eLife’s* transparent reporting form**

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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
* You should state the statistical method of sample size computation and any required assumptions
* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn’t apply to your submission:

Sample-size estimation is a section in the Material and Methods. It was empirically determined.

**Replicates**

* You should report how often each experiment was performed
* You should include a definition of biological versus technical replication
* The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
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* Criteria for exclusion/inclusion of data should be clearly stated
* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Replicate information is indicated in text and figures wherever applicable. High-throughput sequence data is available on GEO (accession GSE165844). Filtered and processed scRNA-Seq data is available here:

[https://mouse-hsc.cells.ucsc.edu](https://urldefense.proofpoint.com/v2/url?u=https-3A__mouse-2Dhsc.cells.ucsc.edu&d=DwMFaQ&c=WO-RGvefibhHBZq3fL85hQ&r=s8aapmTnWzThB-rmLedTZVEFrtmbe0Bm_QRI9kU2B-k&m=wx10h0CSyLJUlhnFEqQaOME_W1bKMs1Pd8ZctIMKJAI&s=_4JEP044j0cqWyzkddVDvJgzEx_FIraItXL0JpIfAuU&e=)

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* Statistical analysis methods should be described and justified
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* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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An entire section of the Materials and Methods is dedicated to computational and statistical analyses. All statistical analysis code and outputs pertaining to the scRNA-Seq data is available on GitHub. Within the main text, figure legends and figure source tables, statistical tests, measures of centrality and dispersion are indicated.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

**Group allocation**

* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
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Group allocation is described in the Methods section “Mice and external stimulant treatment”

**Additional data files (“source data”)**

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
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Please indicate the figures or tables for which source data files have been provided:

Source tables are provided for figures 1-4. Source Files further contain data from which figures are derived. In addition, all code and output of the analysis is available on Github in the form of Jupyter notebooks.