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

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see [EQUATOR Network](http://www.equator-network.org/%20)), life science research (see the [BioSharing Information Resource](https://biosharing.org/" \t "_blank)), or the [ARRIVE guidelines](http://www.plosbiology.org/article/info:doi/10.1371/journal.pbio.1000412) for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this 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:

RNA-seq studies were designed to yield sufficient cells based on the heterogeneity of our population to efficiently profile and perform differential expression tests across samples using common analysis tools and pipelines in Monocle and Seurat for scRNAseq. Additional experiments to test hypotheses were estimated using pilot data and literature analysis and <http://powerandsamplesize.com>. This is a validated, online sample size calculator. We assume a statistical power of 0.80 and a two sided alpha of 0.05 to calculate the numbers of animals in each group.

**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
* If you encountered any outliers, you should describe how these were handled
* 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)

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:

Each RNAseq experiment was performed one time, while all other experiments were repeated a minimum of 3-4 times with a representative example shown. Details regarding exclusion of <1% of contaminant cells after initial clustering in scRNA-seq can be found in the Methods section. All RNA-seq data has been uploaded to GEO, accession record GSE164476.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* 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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Statistical analysis, including test used, n per group and p value can be found in the figure legend for each accompanying figure. Further details regarding statistical analysis can be found in the Statistical Analysis subsection of the Methods section.

(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
* Indicate if masking was used during group allocation, data collection and/or data analysis

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:

Macrophages used in this study were grouped according to the age and/or genotype of the mouse from which they were harvested. Information regarding groups for each experiment can be found within the results section and each figure legend.

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

* We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
* 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
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

Fig. 1A, Fig. 1B, Fig. 1C, Fig. 1D, Fig. 1E, Fig.1-figure supplement 1, and Fig. 1-figure supplement 2

Fig. 2B, Fig. 2C, Fig. 2D, Fig. 2E, Fig. 2F

Fig. 3A,B,D,E, Fig. 3C, Fig. 3F, Fig. 3G, Fig. 3H, Fig. 3I, Fig. 3I, Fig. 3J, Fig. 3K

Fig. 4A, Fig. 4B-E, Fig. 4F, Fig. 4-figure supplement 1, Fig. 4-figure supplement 2