nature research

Corresponding Author: Gokhan Hotamisligil

Date: Dec 5, 2017

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work we publish. This form is published with all life science papers and is intended to promote consistency and transparency in reporting. All life sciences submissions use this form; while some list items might not apply to an individual manuscript, all fields must be completed for clarity.

For further information on the points included in this form, see Reporting Life Sciences Research. For further information on Nature Research policies, including our data availability policy, see Authors & Referees and the Editorial Policy Checklist.

Experimental design

1. Sample size

Describe how sample size was determined.

Sample sized was estimated by pilot experiments that showed trends of effects and their sizes. In most cases, an n=6 was the minimal amount used, only where effect size was large an n=4 yielded significant results.

2. Data exclusions

Describe any data exclusions.

Mice were excluded for poor body condition (e.g. after surgery or during feeding studies).

3. Replication

Describe whether the experimental findings were reliably reproduced.

All replications were successful.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Mice were randomly allocated to groups. Only criteria were sex and age as explained in the methods.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

No blinding was performed.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or the Methods section if additional space is needed).

n/a	Confirmed	
☐	☒	The exact sample size (*n*) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
☐	☒	A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.
☐	☒	A statement indicating how many times each experiment was replicated
☐	☒	The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
☐	☒	A description of any assumptions or corrections, such as an adjustment for multiple comparisons
☐	☒	The test results (e.g. *p* values) given as exact values whenever possible and with confidence intervals noted
☐	☒	A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
☐	☒	Clearly defined error bars

See the web collection on statistics for biologists for further resources and guidance.

Software

Policy information about availability of computer code

7. Software

Describe the software used to analyze the data in this study.	We used Microsoft Excel, Graphpad Prism as well as Computational GESA and CPDB analysis as explained in the Methods section.

For all studies, we encourage code deposition in a community repository (e.g. GitHub). Authors must make computer code available to editors and reviewers upon request. The *Nature Methods* guidance for providing algorithms and software for publication may be useful for any submission.

Materials and reagents

Policy information about availability of materials

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.	All unique materials are available.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).	The antibody details are found in Supplementary Table 6.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.	This information can be found in the Materials and Methods section for human and mouse cells used in this study.
b. Describe the method of cell line authentication used.	We used newly generated cell lines.
c. Report whether the cell lines were tested for mycoplasma contamination.	We tested for mycoplasma contamination and found no contamination.
d. If any of the cell lines used in the paper are listed in the database of commonly misidentified cell lines maintained by ICLAC, provide a scientific rationale for their use.	N/A

Animals and human research participants

Policy information about studies involving animals; when reporting animal research, follow the ARRIVE guidelines

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.	The exact details following the ARRIVE guidelines can be found the Materials and Methods section.

Policy information about studies involving human research participants

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.	The exact details can be found the Materials and Methods section.

nature research

Corresponding author(s): Gokhan Hotamisligil

☐ Initial submission ☐ Revised version ☒ Final submission

Flow Cytometry Reporting Summary

Form fields will expand as needed. Please do not leave fields blank.

Data presentation

For all flow cytometry data, confirm that:

☒ 1. The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☒ 2. 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).

☒ 3. All plots are contour plots with outliers or pseudocolor plots.

☒ 4. A numerical value for number of cells or percentage (with statistics) is provided.

Methodological details

5. Describe the sample preparation.	The interscapular BAT depot from individual mice was minced and incubated in DMEM containing collagenase I and II (Calbiochem, 2 mg/ml each) for 40 min at 37 °C with 120 rpm shaking. The reaction was stopped with FACS buffer (PBS containing 5% FBS) and the suspensions were filtered through 100 µm cell strainers (BD Falcon). The cell suspensions were centrifuged at 2500 rpm for 5 min. The pellet was re-suspended in FACS buffer and filtered with 40 µm cell strainer (BD Falcon). The cell suspension was centrifuged at 3500 rpm for 5 min and the pellet was incubated for 5 min in erythrocyte-lysing buffer (Sigma). Finally, the cells were suspended in FACS buffer.
6. Identify the instrument used for data collection.	BC FACS Calibur
7. Describe the software used to collect and analyze the flow cytometry data.	Flowjo v10
8. Describe the abundance of the relevant cell populations within post-sort fractions.	sorting was not performed
9. Describe the gating strategy used.	After excluding the PI positive dead cell population, the live cell population was identified. Then, the macrophage population was identified as CD11b +F4/80+ cells. finally, M1-like cells were identified as CD11b+F4/80 +CD11chigh cells and M2-like cells were identified as CD11b+F4/80 +CD11clow cells

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