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.
   - The sample size chosen for our animal experiments in this study was estimated based on our prior experience of performing similar sets of experiments.

2. Data exclusions
   - Describe any data exclusions.
   - No data were excluded from the analysis.

3. Replication
   - Describe whether the experimental findings were reliably reproduced.
   - We at least independently repeated all the data once. All attempt to reproduce the results were successful.

4. Randomization
   - Describe how samples/organisms/participants were allocated into experimental groups.
   - All animal results were included and no method of randomization was applied.

5. Blinding
   - Describe whether the investigators were blinded to group allocation during data collection and/or analysis.
   - Binding is not relevant to our study, as we need to know the genotypes of the mouse strains.

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).

<table>
<thead>
<tr>
<th>n/a</th>
<th>Confirmed</th>
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<tbody>
<tr>
<td>☑</td>
<td>The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)</td>
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<td>☑</td>
<td>A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly.</td>
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<td>☑</td>
<td>A statement indicating how many times each experiment was replicated</td>
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<td>☑</td>
<td>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)</td>
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<td>A description of any assumptions or corrections, such as an adjustment for multiple comparisons</td>
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<td>☑</td>
<td>The test results (e.g. p values) given as exact values whenever possible and with confidence intervals noted</td>
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<tr>
<td>☑</td>
<td>A summary of the descriptive statistics, including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)</td>
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<tr>
<td>☑</td>
<td>Clearly defined error bars</td>
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</table>

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. RNA-seq was analyzed by Tophat & Cuffdiff & R package 'ggplot2'; Ribosome Profiling by tuxedo suit & R package; s4U Seq by STAR & HTSeq-count & R package INSPEcT/corrplot/maSigPro/pheatmap. All those information has been detailed in the method part.

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.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

b. Describe the method of cell line authentication used.

c. Report whether the cell lines were tested for mycoplasma 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.

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.

We used both male and female C57BL/6 mice of all ages, we isolate T cells from mouse spleen and lympha nodes. The transgenic mouse lines we used include: Mettl3-f/f, Mettl14-f/f, CD4-Cre, RAG2-/-.

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 research did not involve human research participants.
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.

   Cells from thymus, peripheral lymph nodes, mesenteric lymph nodes and spleen were isolated and used for FACS analysis. For sample preparation from spleen, erythrocytes were lysed and removed before FACS analysis.

6. Identify the instrument used for data collection.

   The LSR II Flow Cytometer from BD Bioscience were used for FACS data collection.

7. Describe the software used to collect and analyze the flow cytometry data.

   The FlowJo Software (Version 7.6.1) was used for FACS data analysis.

8. Describe the abundance of the relevant cell populations within post-sort fractions.

   The purity of sorted cells was detected via flow cytometry immediately after sorting and samples with purity higher than 95% were used.

9. Describe the gating strategy used.

   A FSC-H/FSC-A gate was used to determine single-cell populations. The boundaries between "positive" and "negative" were determined by the clear cell subpopulations and unstained negative controls.

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