

Life Sciences Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form is intended for publication with all accepted life science papers and provides structure for consistency and transparency in reporting. Every life science submission will use this form; some list items might not apply to an individual manuscript, but 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 sizes were chosen such that difference were confirmed at sufficiently high significance ($p < 0.005$) by Student's t-test.

2. Data exclusions

Describe any data exclusions.

No animals were excluded

3. Replication

Describe whether the experimental findings were reliably reproduced.

All experiments were performed in three biological replicates and independently reproduced as indicated in figure legends.

4. Randomization

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

Randomization was not used.

5. Blinding

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

Blinding techniques were not used.

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 in the Methods section if additional space is needed).

- | n/a | Confirmed |
|--------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The <u>exact sample size</u> (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A statement indicating how many times each experiment was replicated |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A description of any assumptions or corrections, such as an adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> A clear description of statistics including <u>central tendency</u> (e.g. median, mean) and <u>variation</u> (e.g. standard deviation, interquartile range) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> 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.

Statistical analyses were performed using GraphPad Prism 7.0. Limited dilution leukemia-initiating cell data was analyzed by ELDA software. Adobe Illustrator was used to assemble the figures.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► 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.

No restrictions

9. Antibodies

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

APC-Cy7 anti-CD4 (BD Pharmingen-552051) and PE-Cy7 anti-CD8a (eBiosciences-25-0081-82) were validated by manufacturers.

10. Eukaryotic cell lines

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

293T (ATCC), REH (ATCC), CUTLL1 (Columbia - Reference 29)

b. Describe the method of cell line authentication used.

STR fingerprint analysis

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

All lines were tested and found to be negative for mycoplasma (Mycoalert - Lonza).

d. If any of the cell lines used 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.

C57BL/6 females 6-8 weeks old were used for mouse experiments in Figures 1, 2, 4 and Extended Data Figure 6. Immunodeficient NRG (NOD.Cg-Rag1^{tm1Mom}/2rg^{tm1Wjl}/SzJ) mice were used for experiments in Extended Data Figure 6.

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.

n/a

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. | Methods Section ("Mice and animal procedures") |
| 6. Identify the instrument used for data collection. | Section ("Mice and animal procedures") |
| 7. Describe the software used to collect and analyze the flow cytometry data. | Section ("Mice and animal procedures") |
| 8. Describe the abundance of the relevant cell populations within post-sort fractions. | n/a |
| 9. Describe the gating strategy used. | No gating other than cell viability (FSC/SSC- DAPI) |

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