## nature research

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## **Reporting Summary**

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see our Editorial Policies and the Editorial Policy Checklist.

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For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.				
n/a Confirmed				
$\square$ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement				
A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly				
The statistical test(s) used AND whether they are one- or two-sided Only common tests should be described solely by name; describe more complex techniques in the Methods section.				
A description of all covariates tested				
A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons				
A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)				
For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> values as exact values whenever suitable.				
For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings				
For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes				
$\square$ Estimates of effect sizes (e.g. Cohen's $d$ , Pearson's $r$ ), indicating how they were calculated				
Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.				
Software and code				
Policy information about <u>availability of computer code</u>				
Data collection Not applicable.				
Data analysis Not applicable.				
For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research guidelines for submitting code & software for further information.				
Data				

Policy information about <u>availability of data</u>

All manuscripts must include a data availability statement. This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

We indicated in Materials and Methods that RNA-seq data were deposited in the Gene Expression Omnibus with an accession number GSE166811.

Field-spe	ecific re	porting		
☐ Life sciences	В	s the best fit for your research. If you are not sure, read the appropriate sections before making your selection. sehavioural & social sciences		
Life scier	nces stu	udy design		
All studies must dis	All studies must disclose on these points even when the disclosure is negative.			
Sample size	This report is ar	n exploratory research with wild-type mice.		
Data exclusions	No data were e	No data were excluded from the analysis.		
Replication	All the mouse s	tudies were performed in 14 mice in each group. We indicated the number of mice for each figure legend.		
Randomization	Mice were rand	domly divided into the treated and untreated groups.		
Blinding	No subject mea	asures were employed in the current studies, and experimental data were not blinded.		
Reporting for specific materials, systems and methods  We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.  Materials & experimental systems    Methods				
Antibodies  Antibodies used	We sh	owed identities of all antibodies in Materials and Methods.		
Validation		All antibodies were commercial products. Validation data were provided by the manufacturers.		
validation	All diffe	isothes were commercial produces. Validation data were provided by the managed etc.		
Eukaryotic c	ell lines			
Policy information	about <u>cell lines</u>			
Cell line source(s	)	We used six mammalian cell lines, and their sources were indicated in Materials and Methods.		
Authentication	Cation We only used established cell lines.			
Mycoplasma contamination		We routinely examine the contamination by mycoplasma, and obtain negative results.		
Commonly misidentified lines (See ICLAC register)		We confirmed that we did not use misidentified cell lines.		

## Animals and other organisms

Policy information about <u>studies involving animals</u>; <u>ARRIVE guidelines</u> recommended for reporting animal research

Laboratory animals We describe

We described mouse strain, sex and age in Materials and Methods.

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Wild animals	Not applicable.
Field-collected samples	Not applicable.
Ethics oversight	All animal studies were performed after approval by the Animal Care and Use Committee of Nagoya University. We also followed relevant guidelines.
Note that full information on t	he approval of the study protocol must also be provided in the manuscript.
Flow Cytometry	
Plots	
Confirm that:	
The axis labels state t	he marker and fluorochrome used (e.g. CD4-FITC).
The axis scales are cle	early visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
All plots are contour p	plots with outliers or pseudocolor plots.
X A numerical value for	number of cells or percentage (with statistics) is provided.
Methodology	
Sample preparation	We described how we prepared samples in Materials and Methods.
Instrument	We showed the model name of the Flow Cytometry in Materials and Methods.
Software	We described the analysis software for Flow Cytometry data in Materials and Methods.

We counted more than 10,000 cells for each Flow Cytometry analysis.

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

We filtered out dead cells and cellular debris.

Cell population abundance

Gating strategy