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Reporting Summary

Nature Portfolio 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 Portfolio policies, see our Editorial Policies and the Editorial Policy Checklist.

Statistics

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
☐	☒ 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. *F*, *t*, *r*) with confidence intervals, effect sizes, degrees of freedom and *P* value noted *Give P 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
☒	☐ Estimates of effect sizes (e.g. Cohen's *d*, Pearson's *r*), indicating how they were calculated

Our web collection on statistics for biologists contains articles on many of the points above.

Software and code

Policy information about availability of computer code

Data collection	For bulk and single-cell RNA-seq analysis, cDNA libraries were sequenced by using Novaseq 6000 (Illumina) or Ion Torrent Proton (Thermo Fisher) as described in Methods section. No commercial, open source or custom code was used to collect data.
Data analysis	For scRNA-seq analysis, pair-end Fastq data were processed as follows: Adapter trimming, homopolymer trimming, and quality filitering of sequencing data was performed by using cutadapt. Associated cDNA reads were mapped to Ensembl RNA (GRCm38.p6, release-101) by using bowtie2. Then, cell barcode information of each read was added to the bowtie2-mapped BAM files, and read counts of each gene in each cell barcode were counted by using mawk. Resulted count data was converted to genes x cells matrix file and inflection threshold of the knee-plot was detected by using DropletUtils package in R. In addition, we further estimate background beads by using emptyDrops formula in DropletUtils package. The resultant dataset was analyzed using R software package Seurat v4.0.4 in R 4.1.0. As quality control, doublets and cells with the mitochondrial gene proportion >20% were filtered out. The log-normalized gene counts were calculated using NormalizeData function (scale.factor = 1,000,000) and highly variable genes were defined by FindVariableFeatures function (selection.method="vst", nfeature=2000). Read counts were regressed out by the ScaleData function. Principal component analysis was performed on the variable genes, and principal components with their p-value <0.05 calculated by the jackstraw method were subjected to cell clustering and UMAP dimensional reduction. For Fig. 6, fibroblast clusters were subjected to re-clustering analysis. Differentially expressed genes were defined as those whose p-value, as calculated by the Wilcoxon rank sum test and adjusted by the Bonferroni method is <0.05 and whose log2FoldChange is >0.5 or <-0.5. GSEA was conducted by utilizing the R software package clusterProfiler v4.0.5. Pseudotime analysis was performed by utilizing slingshot v2.4.0 and tradeSeq. RNA velocity analysis was conducted by utilizing scVelo.

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 Portfolio guidelines for submitting code & software for further information.

Data

Policy information about availability of data

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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our policy

Transcriptomic data have been deposited in Gene Expression Omnibus (GEO) under accession number GSE221310.

Human research participants

Policy information about studies involving human research participants and Sex and Gender in Research.

Reporting on sex and gender	n/a
Population characteristics	n/a
Recruitment	n/a
Ethics oversight	n/a

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

Sample size	No statistical methods were used to determine sample size.
Data exclusions	No data were excluded from mice experiments.
Replication	All the experiments were successfully replicated at least three times.
Randomization	Animals used in this study were randomly assigned to their respective groups before the experiments were performed.
Blinding	Blinding was not achieved in this study due to requirements for cage identification and labeling for treatment purposes.

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

n/a	Involved in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☐	☒ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used: The following antibodies were purchased from BioLegend: APC-conjugated anti-CD200R3 (Ba13), APC-Cy7-conjugated anti-Ly6G (1A8), FITC-conjugated CD45 (30-F11), PacificBlue-conjugated anti-c-Kit (2B8), anti-CD11b (M1/70), BV421-conjugated PDL2 (TY25), BV605-conjugated anti-CD11b (M1/70), BV711-conjugated anti-F4/80 (BM8), BV785-conjugated anti-Ly6C (HK1.4), PE-conjugated anti-PDL2 (TY25), PE-Cy7-conjugated anti-CD49b (HMa2), anti-F4/80 (BM8), anti-PDL2 (TY25). The following antibodies were purchased from BD Biosciences: Alexa 647-conjugaed anti-Siglec-F (E50-2440), BV421-conjugated anti-Siglec-F (E50-2440), BV480-conjugated c-Kit (2B8). IgE mAb (IGELb4, ATCC-TIB141) specific to 2,4,6-trinitrophenol (TNP) was prepared in our laboratory.

Validation: Antibodies were used according to the manufacturer's instructions, based on their provided methods of validation.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals: 7-10 week-old mice were used in this study. BALB/c and C57BL/6J mice were purchased from Sankyo Labo Service Corporation, Inc, Japan. CD45.1 congenic C57BL/6 mice and Il4ra-/- BALB/c mice 31 were purchased from the Jackson Laboratory. Ccr2-/- BALB/c mice were kindly provided from W.A. Kuziel (External Scientific Affairs, Daiichi Sankyo Group, Edison, NJ) and N. Mukaida (Kanazawa University). Ccr2-/- C57BL/6 mice were generated by N. Mukaida (Kanazawa University) by backcrossing of Ccr2-/- BALB/c mice to C57BL/6 strain. Mice were maintained under specific pathogen-free conditions in our animal facilities. All animal studies were approved by the Institutional Animal Care and Use Committee of Tokyo Medical and Dental University (No. A2020-152C4).

Wild animals: n/a

Reporting on sex: Data presented here is based on female mice, but the findings presented in this study were not restricted to female mice.

Field-collected samples: n/a

Ethics oversight: All animal studies were approved by the Institutional Animal Care and Use Committee of Tokyo Medical and Dental University (No. A2020-152C4).

Note that full information on the approval of the study protocol must also be provided in the manuscript.

Flow Cytometry

Plots

Confirm that:

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

☒ 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).

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

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

Methodology

Sample preparation: For flow cytometric analyses, single cell suspensions were prepared from the ear skin by treating excised ears with collagenase (125 U/mL, Wako) in RPMI complete medium at 37°C for 2 h, followed by depletion of red blood cells. After pre-incubation with TruStain FcX™ PLUS antibody (anti-CD16/32 antibody; BioLegend) and normal rat serum (Merck Millipore) on ice for 10 min to prevent the non-specific binding of irrelevant Abs, cells were stained with indicated combination of Abs, and analyzed with FACSLyric (BD Biosciences) or sorted with FACSAriaIII (BD Biosciences).

Instrument: Flow-cytometric analysis was perfoemed using BD FACS Lyric flow cytometer (BD Biosciences). Cell sorting was performed using BD FACS AriaIII (BD Biosciences).

Software	Flow cytometry data were analyzed using FlowJo software (version 10.8.1, BD Biosciences)
Cell population abundance	Purity for all cell populations were confirmed to be greater than 95%.
Gating strategy	Each cell lineage was identified as follows: neutrophils (CD45+ Ly6G+ Siglec-F-), eosinophils (CD45+ Ly6Gint Siglec-F+), basophils (CD45int c-Kit- CD49b+ CD200R3+), Mo-Macs (CD45+ Ly6G- Siglec-F- CD11b+ F4/80+), and non-hematopoietic cells (CD45-).

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