nature portfolio

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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	BD FACSDiva Software v8.0.1, FlexiVent SCIREQ, Buxco Small Animal Whole Body Plethysmography
Data analysis	FlowJo V10.7, Biorad CFXMaestro V 2.3, Graphpad Prism 9.3.1, SlideViewer

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

Source data of all experiments are provided with this paper.

Research involving human participants, their data, or biological material

Policy information about studies with human participants or human data. See also policy information about sex, gender (identity/presentation), and sexual orientation and race, ethnicity and racism.

Reporting on sex and gender	This study did not involve human research participants.
Reporting on race, ethnicity, or other socially relevant groupings	This study did not involve human research participants.
Population characteristics	This study did not involve human research participants.
Recruitment	This study did not involve human research participants.
Ethics oversight	This study did not involve human research participants.

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 method was used to predetermine sample size. Sample sizes were chosen based on extensive experience with similar experiments in our laboratory. Wherever statistical tests were applied, we used at least n=4 to ensure non-parametric testing.
Data exclusions	In Figure 3-4-5 only one representative experiment is shown (Altogether: 2 experiments were done each with at least n=4)
Replication	All experiments were repeated at least three times with sufficient reproductibility.
Randomization	There were no allocation of test subjects in this study and thus, randomization was not applicable.
Blinding	The investigators were not blinded to allocation during experiments, since the same investigator performed analysis . The genotype of the mice were unkown for the technicians performing RNA-Isolation and qPCR.

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
☒	☐ Plants

Methods

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

Antibodies

Antibodies used	CD3 (17A2, rat IgG, Biolegend #100206; 1:200 dilution) CD4 (RM4-5, rat IgG, Biolegend #100568; 1:200 dilution) CD25 (PC61, rat IgG, Biolegend #102006; 1:100 dilution) CD45 (30-F11, rat IgG, Biolegend #103130 and #103132; 1:200 dilution) ST2 (DIH4, rat IgG, Biolegend #146610; 1:100 dilution) KLRG1 (2F1, syrian hamster IgG, Biolegend #138413; 1:200 dilution) GITR (DTA-1, rat IgG, Biolegend #126310; 1:100 dilution) CD11b (M1/70, rat IgG, Biolegend #101222; 1:400 dilution) SiglecF (S17007L, rat IgG, Biolgend #155509; 1:100 dilution) Ly6G (1A8, rat IgG, BD Biosciences #565964; 1:200 dilution) I-A/I-E (M5/114.15.2, rat IgG, Biolegend

#107635; 1:200 dilution) Foxp3 (FJK-16s, rat IgG, Thermo Fisher Scientific #50-5773-80; 1:100 dilution) GATA3 (TWAJ, rat IgG, Thermo Fisher Scientific #53-9966-41; 1:100 dilution) CD16/CD32 (Mouse BD Fc Block, 2.4G2, rat IgG, BD Biosciences # 553141; 1:50 dilution)

Validation

All antibodies were validated by their manufacturers. Statements for validation of antibodies can be found from these manufacturers websites.
CD3:https://www.biolegend.com/de-de/products/pe-anti-mouse-cd3-antibody-47
CD4:https://www.biolegend.com/de-de/products/apc-fire-750-anti-mouse-cd4-antibody-13560
CD25: https://www.biolegend.com/nl-nl/products/fitc-anti-mouse-cd25-antibody-422
CD45:https://www.biolegend.com/de-de/products/percp-anti-mouse-cd45-antibody-4265
CD45:https://www.biolegend.com/nl-nl/products/percp-cyanine5-5-anti-mouse-cd45-antibody-4264
ST2:https://www.biolegend.com/de-de/products/pe-cyanine7-anti-mouse-il-33ralpha-st2-antibody-15505
KLRG1:https://www.biolegend.com/de-de/products/brilliant-violet-421-anti-mouse-human-klrg1-mafa-antibody-7528
GITR:https://www.biolegend.com/de-de/products/pe-anti-mouse-cd357-gitr-antibody-4645
CD11b:https://www.biolegend.com/de-de/products/alexa-fluor-700-anti-mouse-human-cd11b-antibody-3388
SiglecF:https://www.biolegend.com/de-de/products/brilliant-violet-421-anti-mouse-cd170-siglec-f-antibody-17872
Ly6G:https://www.bdbiosciences.com/en-nz/products/reagents/flow-cytometry-reagents/research-reagents/single-color-antibodies-ruo/buv395-rat-anti-mouse-ly-6g.565964
I-A/I-E:https://www.biolegend.com/en-us/products/brilliant-violet-510-anti-mouse-i-a-i-e-antibody-7997?GroupID=BLG11931
Foxp3:https://www.thermofisher.com/antibody/product/FOXP3-Antibody-clone-FJK-16s-Monoclonal/14-5773-82
GATA3:https://www.thermofisher.com/antibody/product/Gata-3-Antibody-clone-TWAJ-Monoclonal/14-9966-82
CD16/CD32 (Mouse BD Fc Block):https://www.bdbiosciences.com/en-us/products/reagents/flow-cytometry-reagents/research-reagents/single-color-antibodies-ruo/purified-rat-anti-mouse-cd16-cd32-mouse-bd-fc-block.553141

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	For Treg-specific depletion of the CD83 gene, floxed CD83 animals were crossed with Foxp3-Cre mice (CD83 fl/fl Foxp3Cre+/- also called as CD83cKO). The corresponding Cre mice (CD83 wt/wt Foxp3Cre+/-) were used as controls (Ctrls) in all experiments.
Wild animals	This study did not involve wild animals.
Reporting on sex	In all experiments, we used an equal distribution of age-matched male and female mice.
Field-collected samples	This study did not involve field-collected samples.
Ethics oversight	All animal care and experimental procedures in this study followed the guidelines of the European Community Standards for Laboratory Animal Care and were approved by the local ethics committee. (Administration of Lower Franconia; Reference number 55.2-2532-2-633).

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

Plants

Seed stocks	This study did not involve plants.
Novel plant genotypes	This study did not involve plants.
Authentication	This study did not involve plants.

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	*Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
Instrument	BD FACS Canto II, BD FACS Fortessa, BD FACS Aria
Software	The FACS was running the BD FACS-Diva Software. Data were evaluated using Flowjo V10.
Cell population abundance	In healthy mice, we acquired 20,000 cells in the CD45+ gate (Treg analysis) or in the CD3+CD4+ T cell gate (Coculture experiments) for further analysis. In allergic asthma mice, 100,000 cells were aquired in the CD45+ gate.
Gating strategy	In all experiments, a standardized procedure was followed. We began by excluding doublets using forward scatter (FSC) area vs. height (FSC-A vs. FSC-H) gating. Subsequently, we proceeded to select living lymphocytes based on side scatter area (SSC-A) vs. FSC-A. In experiments aimed at analyzing the Treg (regulatory T cell) population, we initially identified CD45+ immune cells and further gated to isolate CD4+ T cells. Ultimately, Tregs were identified as (CD25+) Foxp3+ cells, and the expression of various surface receptors, including ST2, KLRG1, and GITR, was analyzed. In coculture experiments, double positive T cells were specifically gated using CD3 vs. CD4, and their proliferation was quantified through CTV-labeling. Data analysis was carried out using FlowJo. For experiments focusing on eosinophils, CD45+ immune cells were initially selected, and then gating was performed to isolate Ly6G- CD11b+ MHC-II- SiglecF+ eosinophils. Gating strategies are included in supplementary figures 1-3.

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