

## 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

- |                                     |                                     |  |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | The statistical test(s) used AND whether they are one- or two-sided<br><i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i>   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | A description of all covariates tested   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons  |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> | For null hypothesis testing, the test statistic (e.g. $F$ , $t$ , $r$ ) with confidence intervals, effect sizes, degrees of freedom and $P$ value noted<br><i>Give <math>P</math> values as exact values whenever suitable.</i>                            |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/>            | 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

N/A

Data analysis

R ver4.2.3, Seurat 4.1.0., Catalyst package 1.22.0, FlowJo 10.4.2, Graphpad Prism 7

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](#)

Single-cell RNA-seq data will be uploaded to GEO and made publicly available when this manuscript is accepted for publication. Following is the accession and token for review: GSE274017, cfmnwymcjfwtfwr; GSE227209, kxgnkmokzjuxxyb.

## 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	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	Japanese, Caucasian
Recruitment	Nonallergic healthy volunteers and volunteers with seasonal allergy symptoms around the time of seasonal pollen dispersal were recruited at the Department of Pulmonary Medicine, Kagoshima University and the Benaroya Research Institute Registry and Repository. Healthy subjects with no nasal clinical history and no IgE for specific Japanese cedar pollen, cypress pollen, house dust mites, orchard grass pollen, or ragweed pollen were included as healthy controls. Subjects in cedar pollen-induced allergic rhinitis group had typical nasal symptoms during the cedar pollen season and elevated IgE specific for Japanese cedar pollen ( $\geq 0.70$ UA/mL).
Ethics oversight	Protocol IRB07109-431

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](https://www.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	Sample size calculation was not performed.
Data exclusions	No data were excluded from the analyses.
Replication	Reproducibility was confirmed by repeated experiments.
Randomization	Mice were either randomly assigned to treatment groups or assigned to groups based on genotype.
Blinding	Blinding was not performed.

## 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
<input type="checkbox"/>	<input checked="" type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input type="checkbox"/>	<input checked="" type="checkbox"/> Animals and other organisms
<input type="checkbox"/>	<input checked="" type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

### Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input type="checkbox"/>	<input checked="" type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging

## Antibodies

Antibodies used	All FACS antibodies used in this study are listed in supplementary table 2.
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Validation

All FACS antibodies were confirmed to exhibit a comparable pattern to the example on the manufacturer's website.

## 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	C57BL/6J was used in these experiments.
Wild animals	N/A
Reporting on sex	Experiments were performed on independent cohorts of male and female mice. No differences between sexes were observed and no analyses of the influence of sex were performed.
Field-collected samples	N/A
Ethics oversight	All experiments were conducted with the approval of the Tokyo University of Science and RIKEN IMS Institutional Animal Care and Use Committees.

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

## Clinical data

Policy information about [clinical studies](#)

All manuscripts should comply with the ICMJE [guidelines for publication of clinical research](#) and a completed [CONSORT checklist](#) must be included with all submissions.

Clinical trial registration	N/A
Study protocol	Protocol IRB07109-431
Data collection	Nonallergic healthy volunteers and volunteers with seasonal allergy symptoms around the time of seasonal pollen dispersal were recruited at the Department of Pulmonary Medicine, Kagoshima University and the Benaroya Research Institute Registry and Repository. Healthy subjects with no nasal clinical history and no IgE for specific Japanese cedar pollen, cypress pollen, house dust mites, orchard grass pollen, or ragweed pollen were included as healthy controls. Subjects in cedar pollen-induced allergic rhinitis group had typical nasal symptoms during the cedar pollen season and elevated IgE specific for Japanese cedar pollen ( $\geq 0.70$ UA/mL).
Outcomes	N/A

## Plants

Seed stocks	<i>Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.</i>
Novel plant genotypes	<i>Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.</i>
Authentication	<i>Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.</i>

## 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	Spleen and dLNs were collected, cut into small pieces, and digested in 10% FBS in RPMI containing 100mg/ml Liberase TL (Roche) and 100mg/ml DNase I (Roche) for 30min at 37°C and 200rpm in a shaking incubator. Skin cells were prepared from
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	the ears using the gentleMACSTM Octo Dissociator (Miltenyi Biotec) in the RPMI solution containing 250 mg/ml Liberase TL (Roche) and 50mg/ml DNase I (Roche). Single cells were isolated using a cell strainer.
Instrument	FACS Calibur, FACS Melody
Software	FlowJo 10.4.2
Cell population abundance	N/A
Gating strategy	The gating strategies are described in the supplementary files.

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