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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 single-cell RNA sequencing, chromium Single Cell 3' v3 (10x Genomics) libraries were prepared using the Chromium Controller according to the manufacturer's instructions, the resulting libraries were sequenced with the Illumina NovaSeq 6000 platform,and the trimmed data were processed using the CellRanger (version 3.0, 10x Genomics). For spatial transcriptomics, skin sections were prepared using a cryostat microtome and mounted onto Visium slides (Visium Spatial Tissue Optimization Slide & Reagent kit, 10x Genomics), the cDNA libraries were sequenced on the Illumina NovaSeq 6000 platform, the data were processed with the SpaceRanger (version 1.1.0, 10x Genomics) and mapped to the GRCh38-2020-A genome. Histological images were captured by a Leica DM2500 microscope. Immunofluorescent images were captured by a Leica STELLARIS 8 DIVE microscopy system. For Bulk RNA-seq, cDNA libraries were prepared using a VAHTS Universal V8 RNA-seq Library Prep Kit for Illumina (Vazyme cat. NR605-01) according to the manufacturer's instructions and sequenced on a NovaSeq 6000 (Illumina). The sequences were then aligned to GRCm38 using STAR and assembled using StringTie. Flow data were collected using a BD LSRFortessa™ or BD FACSymphony™ A3 cytometer and the FACSDiva software. ELISA data were collected using a Thermo MULTISKAN GO system. Mouse paw X-ray images were collected by microCT (Venus001, Pingseng Scientific).
Data analysis	The single-cell RNA sequencing data were analyzed using the Seurat package (version 4.3.0) and monocle 2. The spatial transcriptomics data were visualized using the Seurat package (version 4.3.0). Gene set enrichment analysis was performed using GSEA 4.3.2. The immunofluorescent images were visualized by Leica LAS X. Flow data were analyzed using FlowJo. Mouse paw X-ray images were analyzed by DataViewer (Bruker). Statistical analysis was performed using GraphPad Prism 9.

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

The sequencing data in this paper are deposited in Genome Sequence Archive (GSA) and Gene Expression Omnibus (GEO). The bulk RNA sequencing data are deposited under the accessions: CRA013603 and CRA013771; the mouse single-cell transcriptomics data are deposited under the accessions: CRA025637, CRA028265 and GSE205790; the human single-cell transcriptomics data are deposited under the accessions: HRA003418 and HRA006130; the human spatial transcriptomics data are deposited under the accession: HRA006129.

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	We generated single-cell transcriptomics data of six male patients with psoriasis and four healthy donors (1 male, 2 females, and 1 not known). We generated spatial transcriptomics data of 2 healthy donors (1 male, 1 female) and 3 patients with psoriasis (2 males, 1 female).
Reporting on race, ethnicity, or other socially relevant groupings	All samples were collected from Chinese.
Population characteristics	The patients with psoriasis vulgaris (age 27-59) and control healthy donors who had plastic surgeries (age 25-55) were recruited in this study for skin biopsy collection.
Recruitment	Psoriatic skin samples were obtained by punch biopsy from patients under local lidocaine anesthesia. Normal adult human skin specimens were obtained from healthy donors undergoing plastic surgery. All participants provided written informed consent. This study was performed in accordance with the principles of the Declaration of Helsinki and approved by the Research Ethics Boards of Shanghai General Hospital.
Ethics oversight	Ethics Committee of Shanghai General Hospital No. 2018KY239

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	Sample size is indicated in the figure legends. No statistical methods were used to predetermine sample sizes.
Data exclusions	Cells with fewer than 200 genes, more than 5,000 genes, or more than 5% mitochondria content were removed. Doublets were predicted using DoubletFinder and removed.
Replication	All mouse experiments were successfully repeated ≥2 times and where possible quantification and statistics were run on combined replicate experiments.
Randomization	Age and sex-matched mice were randomly assigned to experimental groups. All experiments involved control samples and the respective treatment conditions.
Blinding	Blinding was performed for microCT and bulk RNA-seq data collection.

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

For flow cytometry
Anti-Human CD45 (Clone 2D1, BioLegend, Cat#368516 , 1:200 dilution);
Anti-Human CD45 (Clone HI30, BD Biosciences, Cat#562279, 1:200 dilution);
Anti-Human CD11c (Clone B-ly6, BD Biosciences, Cat#563787, 1:200 dilution);
Anti-Human CD200 (Clone MRC OX-104, BD Biosciences, Cat#562125, 1:200 dilution);
Anti-human CD1b (Clone SN13, BioLegend, Cat#329106, 1:200 dilution);
Anti-human IL-23p19 (Clone 23dcdp, eBioscience, Cat#50-7823-42, 1:100 dilution);
Anti-human IL-12/IL-23p40 (Clone eBioHP40, eBioscience, Cat#48-7235-42, 1:100 dilution);
Anti-Mouse CD45 (Clone 30-F11, BD Biosciences, Cat#562420, 1:200 dilution);
Anti-Mouse CD45 (Clone 30-F11, BioLegend, Cat#103128, 1:200 dilution);
Anti-Mouse CD11c (Clone N418, eBioscience, Cat#17-0114-82, 1:200 dilution);
Anti-Mouse MHC Class II (I-A/I-E) (Clone M5/114.15.2, eBioscience, Cat#11-5321-82, 1:200 dilution);
Anti-Mouse CD172a (Clone P84, eBioscience, Cat#46-1721-82, 1:200 dilution);
Anti-Mouse CD200 (Clone OX-90, BD Biosciences, Cat#565547, 1:200 dilution);
Anti-Mouse CD326 (Ep-CAM) (Clone G8.8, BioLegend, Cat#118227, 1:200 dilution);
Anti-Mouse/Rat XCR1 (Clone ZET, BioLegend, Cat#148220, 1:200 dilution);
Anti-Mouse/Rat XCR1 (Clone ZET, BioLegend, Cat#148204, 1:200 dilution);
Anti-Mouse CD64 (FcγRI) (Clone X54-5/7.1, BioLegend, Cat#139314, 1:200 dilution);
Anti-Mouse CD64 (FcγRI) (Clone X54-5/7.1, BioLegend, Cat#139319, 1:200 dilution);
Anti-Mouse Ly-6G (Clone 1A8 , BD, Biosciences, Cat#563979, 1:200 dilution);
Anti-Mouse CD3e (Clone 145-2C11, BD Biosciences, Cat#563123, 1:200 dilution);
Anti-Mouse CD3e (Clone 145-2C11, BD Biosciences, Cat#562286, 1:200 dilution);
Anti-Mouse CD19 (Clone 6D5 , BioLegend, Cat#115555 , 1:200 dilution);
Anti-Mouse TCR beta (Clone H57-597, eBioscience , Cat#17-5961-82, 1:200 dilution);
Anti-Mouse IL-17A (Clone TC11-18H10.1, BioLegend, Cat#506904, 1:100 dilution);
Anti-Mouse/Rat IL-17A (Clone eBio17B7, eBioscience, Cat#25-7177-82, 1:100 dilution);
Anti-Mouse CD8a (Clone S18018E, BioLegend , Cat#162304, 1:200 dilution);
Anti-Mouse CD4 (Clone RM4-5, BD Biosciences, Cat#561115, 1:200 dilution);
Anti-Mouse CD4 (Clone GK1.5, BioLegend , Cat#100412, 1:200 dilution);
Anti-Mouse/human CD44 (Clone IM7, BioLegend, Cat#103032, 1:200 dilution);
Anti-Mouse CD62L (Clone MEL-14, BD Biosciences, Cat#562404, 1:200 dilution);
Anti-Mouse CD16/32 (Clone 93, BioLegend, Cat#101328, 1:200 dilution).

For immunofluorescence
Anti-CD161 (Clone 14F1F11, NOVUS, Cat#NBP2-14845, 1:50 dilution);
Anti-DC-LAMP (Clone 1010E1.01, NOVUS, Cat#DDX0191P-100, 1:50 dilution);
Anti-KRT17/CK17/Cytoketatin (Clone E3, LS Bio, Cat#LS-B7169 , 1:100 dilution);
Anti-KRT17/CK17/Cytoketatin (Polyclonal, LS Bio, Cat#LS-B7610, 1:100 dilution);
Anti-IL17RA (Polyclonal, Affinity Biosciences, Cat#DF3602, 1:50 dilution);
Anti-Krt6 (Polyclonal, Proteintech, Cat#10590-1-AP, 1:200 dilution);
Anti-Krt5 (Clone 2C2, Invitrogen, Cat#MA5-17057, 1:200 dilution);
Anti-Krt1/10 (Clone LH1, Santa Cruz, Cat#sc-53251, 1:200 dilution);
Anti-Ki67 (Clone Polyclonal, Servicebio, Cat#GB111499 , 1:500 dilution);
Anti-Filaggrin (Clone FLG01, GeneTex, Cat#GTX23137, 1:100 dilution);
Anti-CD200 (Clone E5I9V, Cell Signaling Technology, Cat#23451, 1:50 dilution);
Anti-IL-12p40 (Polyclonal, Invitrogen, Cat#PA5-23965, 1:40 dilution);
Anti-IL-23 (Polyclonal , Santa Cruz, Cat#sc-21079, 1:40 dilution);
Anti-IL-23p19 (Clone 242139G12, Proteintech, Cat#98392-1-RR , 1:40 dilution);
Anti-IL-12p40 (Clone C17.8, BioXCell, Cat#BE0051 , 1:40 dilution);
Anti-IL-17A (Polyclonal, Invitrogen, Cat#PA5-79470, 1:40 dilution);
HRP-labeled goat anti-mouse IgG (H+L), Beyotime, Cat#A0216, 1:1000 dilution);
HRP-labeled donkey anti-goat IgG (H+L), Beyotime , Cat#A0181, 1:1000 dilution);

HRP-labeled goat anti-rabbit IgG (H+L), Beyotime, Cat#A0208, 1:1000 dilution).

For neutralization
Anti-mouse/rat IL-17A (Clone 17F3, BioXCell, Cat#BE0173)
Anti-mouse IL-23 (p19) (Clone G23-8, BioXCell, Cat#BE0313)

Validation

All primary antibodies used in this study for the species and applications are validated by the manufactures.

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/6 mice were purchased from Shanghai SLAC Laboratory Animal Co., Ltd. Il4i1-2A-Cre (Il4i1cre) mice and R26-CAG-LSL-Il23a-IRES-EGFP (LSL-Il23a) mice were produced by Shanghai Model Organisms Co., Ltd. For Il4i1cre mice, a 2A-Cre-WPRE-polyA cassette was inserted via homologous recombination to replace the stop codon of Il4i1; for R26-CAG-LSL-Il23a-IRES-EGFP mice, a CAG-loxP-PGK-Neo-polyA-loxP-Il23a-IRES-EGFP expression cassette was targeted to the Rosa26 locus. ROSA26-LSL-DTR (ROSA26iDTR, stock# C001189) mice and Itgaxcre mice (stock# C001063) were obtained from Cyagen Co., Ltd. The mice were bred and maintained under specific pathogen-free (SPF) conditions.
Wild animals	The study did not involve wild animals.
Reporting on sex	Sex-matched mice (both males and females) were used in this study.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	Mouse experiments were conducted in accordance with the National Institutes of Health Guide for the Care and Use of Laboratory Animals with the approval (SYXK-2019-0028) of the Scientific Investigation Board of Shanghai General Hospital. Throughout these experimental studies, all efforts were made to alleviate any suffering and the mice were euthanized by CO2 inhalation.

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

Plants

Seed stocks	NA
Novel plant genotypes	NA
Authentication	NA

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	Single cell suspensions were generated from the skin of patients with psoriasis, healthy donors, Il4i1cre DTR mice, LSL-Il23a mice, Itgax-Il23aOE mice and Il4i1-Il23aOE mice. Fresh skin biopsies were placed in saline at 4℃ prior to processing. The epidermis was separated from the dermis by dispase II digestion overnight at 4℃. Single-cell suspensions were generated by enzyme digestion.
Instrument	Data acquisition was performed on a BD LSRFortessa™ or a BD FACSymphony™ A3 cytometer. Sorting was performed on a BD FACSAria™ III.

Software	BD FACSDiva and Flowjo (TreeStar)
Cell population abundance	The purity of sorted samples was typically >95%.
Gating strategy	FSC-A vs. SSC-A gates were used to identify population targeted viable cells. Singlet cells were separated from doublets using FSC-A vs. FSC-H gating. Live viability dye was used to eliminate dead cells. Target populations were further determined by specific antibodies, which were able to distinguish from negative populations.

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