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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	RT-qPCR was performed on a StepOnePlus Real-Time PCR System (Applied Biosystem). RNA-Seq was performed on Hiseq (Illumina). Flow cytometry data were collected on FACSCelesta (BD Biosciences).
Data analysis	XPS analysis was conducted using Avantage (v5.9931) software. Gwyddion (v2.66) was used for AFM data visualization and analysis. Single-crystal X-ray diffraction data were collected on a Bruker D8 VENTURE diffractometer with a PHOTON III detector using Mo Kα radiation (λ = 0.71073 Å). Data reduction, integration and absorption correction were carried out using SAINT (v8.40B), and a multi-scan absorption correction was applied using SADABS (2016/2). The space group was assigned using XPREP in APEX6 (v2024.9-0). The structure was solved by direct methods with SHELXT-2018 and refined by full-matrix least-squares on F^2 using SHELXL-2019/3 within Olex2 (v1.5). All non-hydrogen atoms were refined anisotropically, and hydrogen atoms were placed in calculated positions using a riding model. Molecular docking was performed using AutoDock Tools v1.5.6 software. GraphPad Prism v10.0 was used for all statistical analyses. Flow cytometry data were analyzed by FlowJo v10.

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 are provided with this paper for Figures 1-8 and Supplementary Figures 3-11, 13, and 15-17.

Processed RNA-seq datasets were obtained from the GEO database, including GSE121212 (processed transcriptomes of psoriatic and atopic dermatitis skin samples) and GSE30768 (a publicly available cohort of psoriasis relapse samples from human lesional skin). In addition, differential expression of dsRNA-related genes in psoriasis-like mouse models compared with controls was analyzed using the publicly available GEO RNA-seq dataset GSE27628 and visualized as a dot plot.

RNA-seq data generated in this study from Mo90Ce10-treated HaCaT cells have been deposited in the NCBI Gene Expression Omnibus under accession number GSE270176.

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	Sex and gender were not considered in study design.
Reporting on race, ethnicity, or other socially relevant groupings	Race and ethnicity were not used for stratification or analytical grouping in this study. All participants were of Asian descent, and skin biopsies were obtained from healthy adult volunteers or patients clinically diagnosed with psoriasis, without further demographic subdivision. Race or ethnicity was not used as a proxy for biological or mechanistic inference, and these factors are not mechanistically relevant to the study's conclusions.
Population characteristics	Healthy adults aged 18–65 and patients diagnosed as having psoriasis in the same age range were included
Recruitment	All participants were enrolled in the study voluntarily, and each was fully informed of the study purpose and procedures before participation. Written informed consent was obtained from all individuals. All participants were recruited from Shanghai, China, and met the inclusion criteria of either being healthy adults or patients with clinically confirmed psoriasis.
Ethics oversight	The protocols were approved by the Ethics Review Committees of Shanghai Skin Disease Hospital (No. 2024-12).

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 formal statistical method was used to predetermine sample size. Sample sizes were selected based on commonly accepted practices in the field and our previous experience to provide sufficient reproducibility and statistical robustness for detecting meaningful biological differences. For animal studies, 3-6 biological replicates were included, and at least two independent experimental repeats were performed to confirm reproducibility. For in vitro experiments, three independent biological replicates were included, and experiments were independently repeated three times.
Data exclusions	No data was excluded from analysis.
Replication	All in vivo experiments were independently repeated a minimum of two times, and in vitro assays were performed in triplicate. Consistent results were obtained across all biological repeats. For each experiment, technical measurements were acquired once per replicate.
Randomization	For animal studies, mice were randomly assigned to experimental groups. For human skin tissue samples, samples were assigned to experimental groups where applicable. In both cases, investigators were not involved in group allocation. For in vitro experiments, cells were assigned to treatment groups under identical culture conditions. As all samples were handled under comparable conditions, no relevant covariates were identified that required control.
Blinding	In this study, data quantification and statistical analyses were performed with partial blinding. Specifically, the investigator responsible for

Blinding	image-based quantification and downstream statistical evaluation was unaware of sample group allocation, while animal modeling and sample processing were performed by the same researcher to ensure experimental consistency and reproducibility. Appropriate internal controls and standardized normalization procedures were applied throughout the study to minimize potential bias.

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

Antibodies for Immunochemistry staining:
Anti-Ki67: Abcam, Cat#ab16667, Clone#SP6, Lot#1015296-29, 1:200
Anti-Loricrin: Abcam, Cat#ab176322, Clone#EPR7148(2)(B), Lot#1002196-1, 1:250
Anti-Filaggrin: Abcam, Cat#ab81468, Lot#GR3276014-1, 1:1000
Anti-Cytokeratin 10: Abcam, Cat#ab76318, Lot#1057212-46, 1:2500
Anti-Ly6g: Abcam, Cat#ab238132, Clone#EPR22909-135, Lot#1073751-8, 1:200
Anti-dsRNA(J2): Sigma-Aldrich, Cat#MABE1134, Lot#4098878, 1:50

Antibodies for FACS:
Brilliant Violet 510™ anti-mouse CD45: Biolegend, Cat#103138, Clone#30-F11, Lot#B386738, 1:100
PerCP/Cyanine5.5 anti-mouse CD3: Biolegend, Cat#100218, Clone#17A2, Lot#B365335, 1:100
Alexa Fluor® 488 anti-mouse/human CD11b: Biolegend, Cat#101217, Clone#M1/70, Lot#B375700, 1:100
APC anti-mouse CD11c: Biolegend, Cat#117310, Clone#N418, Lot#372999, 1:100
PE anti-mouse F4/80: Biolegend, Cat#123110, Clone#BM8, Lot#B340064, 1:100
APC anti-mouse CD45: Biolegend, Cat#103112, Clone#30-F11, Lot#386153, 1:100
PerCP/Cyanine5.5 anti-mouse CD90.2 (Thy-1.2): Biolegend, Cat#140322, Clone#53-2.1, Lot#B311547, 1:100
PE anti-mouse TCR γ/δ: Biolegend, Cat#118108, Clone#GL3, Lot#B335874, 1:100
APC-Cyanine7 Anti-Mouse Ly6G (1A8): Tonbo bioscience, Cat#25-1276-U100, Clone#1A8, Lot#C1276070920253, 1:100
Brilliant Violet 421™ anti-mouse CD45: Biolegend, Cat#103133, Clone#30-F11, Lot#B383535, 1:100
Alexa Fluor® 700 anti-mouse CD3: Biolegend, Cat#100216, Clone#17A2, Lot#B376387, 1:100
Alexa Fluor® 488 anti-mouse/human CD11b: Biolegend, Cat#101219, Clone#M1/70, Lot#B375701, 1:100
Brilliant Violet 605™ anti-mouse Ly-6G/Ly-6C (Gr-1): Biolegend, Cat#108439, Clone#RB6-8C5, Lot#B393490, 1:100
APC anti-mouse CD11c: Biolegend, Cat#117309, Clone#N418, Lot# B356824, 1:100
Brilliant Violet 785™ anti-mouse CD326 (Ep-CAM): Biolegend, Cat#118245, Clone#G8.8, Lot#B368888, 1:100
Brilliant Violet 650™ anti-mouse F4/80: Biolegend, Cat#123149, Clone#BM8, Lot#B372797, 1:100
PerCP/Cyanine5.5 anti-mouse CD19: Biolegend, Cat#115533, Clone#, Lot#B341098, 1:100
PE anti-mouse FcεRIα: Biolegend, Cat#134307, Clone#6D5, Lot#B351057, 1:100
PE/Dazzle™ 594 anti-mouse CD117 (c-kit): Biolegend, Cat#135127, Clone#ACK2, Lot#B396288, 1:100
Zombie Aqua™ Fixable Viability Kit: Biolegend, Cat#423102, Lot#B393166, 1:100

Validation

All of the above commercial antibodies have been thoroughly validated by the manufacturer. The specificity and validation were supplied in the manufacturer's technical datasheets and have been confirmed in literature. For technical details and further information, please consult the spec sheets on the vendors' websites, using the catalog numbers provided.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	The immortalized human keratinocyte cell line HaCaT (Catalog #CBP6033, Cobioer) and human dermal fibroblasts HDFs (Catalog #HXXFB-00001, Oricell) were obtained from commercial vendors and used in this study. NHEKs (Catalog #PCS-200-010, ATCC) were purchased from ATCC and used at passages 3–6 as recommended.
Authentication	All cell lines used in this study were authenticated by their respective vendors using morphology assessment, karyotyping, and PCR-based identity verification assays.
Mycoplasma contamination	All cell lines were tested for mycoplasma contamination and the results were negative.

Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

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 mice were obtained from the Shanghai Laboratory Animal Center. The mice aged at 7-8 weeks old were used in all experiments.
Wild animals	No wild animals were used in this study.
Reporting on sex	Male mice were used to study the imiquimod-induced psoriasis mouse model, while female mice were used to investigate the MC903-induced AD mouse model.
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	All animal experiments in this study followed protocols approved by the Animal Care and Use Committee of Shanghai Skin Disease Hospital, School of Medicine, Tongji University (Protocol No. 2024-02).

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	Protocol No. 2024-12
Study protocol	No study protocol is available online, as this study did not involve a registered clinical trial. Human skin biospecimens were collected with approval from the Ethics Committee of Shanghai Skin Disease Hospital, School of Medicine, Tongji University (Protocol No. 2024-12). Participants were recruited from individuals with psoriasis vulgaris and patients undergoing surgical procedures at the same institution. As participation was voluntary and based on written informed consent, a degree of self-selection bias may be present. In addition, recruitment from a single clinical center may introduce selection bias.
Data collection	Skin samples were obtained from patients undergoing surgery after written informed consent was obtained. The tissues were immediately placed in sterile saline for subsequent ex vivo culture experiments.
Outcomes	Following culture under the indicated conditions, skin tissues were collected for RNA extraction. Total RNA was isolated and subjected to qRT-PCR to assess the expression levels of CXCL1, CXCL2, CXCL8, IL36G, DHX58, and DDX58.

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

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	To obtain a whole skin cell suspension, mouse skin was meticulously minced after the removal of subcutaneous fat using fine scissors. The minced tissue was then digested in 2 mL of RPMI 1640 Medium (Catalog # 11875093, Gibco) supplemented with 0.25% collagenase (Catalog # C9091, Sigma), 0.01 M HEPES (Catalog # BP310, Thermo), 0.001 M sodium pyruvate (Catalog # BP356, Thermo), and 0.1 mg/mL DNase (Catalog # DN25, Sigma), with rotation at 37 °C for 1-1.5 hours. The digestion was halted by adding 1 mL of FBS to each sample. Subsequently, the digested cells were filtered through a 40 µm filter, centrifuged, and resuspended in FACS buffer (2% fetal bovine serum in PBS). Skin cells were then incubated with TruStain FcX™ antibody to block Fc receptors for 10 minutes at room temperature. Next, the isolated cells were stained with various cell surface markers for 30 minutes at 4 °C. Counting beads (10,000 beads/sample, Catalog # C36950, Invitrogen) were added to each sample prior to analysis. Notably, for IMQ-induced psoriasis-like skin lesions, cells were incubated with SYTOX™ Blue Dead Cell Stain (Catalog # S34857, Invitrogen) for an additional 5 minutes prior to analysis.
Instrument	FACSCelesta (BD Biosciences)
Software	FlowJo v10
Cell population abundance	All frequencies of cells are stated in the representative graphs and quantifications.
Gating strategy	The gating strategy is presented in the manuscript in Extended Data Fig. 7 and Extended Data Fig. 9.

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