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	RNA-seq: Fastq files were generated on an illumina HiSeq instrument and bcl2fastq (Illumina).
Data analysis	All analysis in this study were performed using published softwares. STAR were used for alignment of sequencing data. R (version 3.6.3) was used for statistical analysis and visualization. The detail of the package used in this study are found in Methods section.

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

New unique reagents were not generated in this study. The RNA-seq data generated in this study have been deposited in the National Bioscience Database Center (NBDC) Human Database under accession code JGAS000780. The RNA-seq data are available under restricted access for issue on privacy in informed consent by participants, access can be obtained by application for hum0413 at the NBDC. All data are included in the Supplementary Information or available from the authors. The raw numbers for charts and graphs are available in the Supplementary Information or the Source Data file whenever possible.

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 (biological attribute) of the study subjects was determined based on self-reporting. 110 males and 46 females with atopic dermatitis, 14 males and 4 females with psoriasis and 19 males and 7 female healthy subjects were analyzed as described in the manuscript.
Reporting on race, ethnicity, or other socially relevant groupings	All the participants were japanese as described in the manuscript.
Population characteristics	For all subjects with atopic dermatitis and psoriasis and healthy controls, people aged 15 or over who live in Japan were eligible as participants in the study. The detail of age and sex information is shown in Table 1.
Recruitment	Patients with AD, plaque-type psoriasis visiting Keio University Hospital, Nippon Medical School Hospital, and Tokyo Teishin Hospital between 2018 and 2022 were invited to participate. Normal control skin was obtained from healthy volunteers who were recruited at Keio University Hospital, defined as individuals with no inflammatory skin diseases.
Ethics oversight	The study protocol was approved by the Keio University School of Medicine Ethics Committee (Approval Numbers: 20160377, 20150325, and 20130384), Nippon Medical School Ethics Committee (29-03-916), Tokyo Teishin Hospital (1054), and RIKEN Yokohama Ethics Review Committee (Approval Number H28-24), aligning with the Declaration of Helsinki.

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 sample size calculations were performed. As an exploratory study on patient endotypic heterogeneity, sample size were set larger than previous studies on AD based on transcriptome analysis (PMID 33453290, PMID 32615169, PMID 35182548).
Data exclusions	Patients were excluded if they were under systemic therapy with JAK inhibitors. For skin tissue RNA-seq, we filtered samples by sequence quality criteria. Details of our quality control procedures are provided in the methods section of the manuscript.
Replication	The samples taken from same patients at different time points were analyzed in the cross-sectional study and we found no significant differences in the molecular profiles between the samples.
Randomization	No randomization of subjects was performed.
Blinding	No blinding was performed in data collection nor analysis since this study is an observational study without predefined patient groups.

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

Plants

Seed stocks

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.

Novel plant genotypes

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.

Authentication

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, mosiacism, off-target gene editing) were examined.