

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 ( <i>n</i> ) 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 type="checkbox"/>            | <input checked="" type="checkbox"/> A description of all covariates tested                                                                                                                                                                                                                     |
| <input type="checkbox"/>            | <input checked="" 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. <i>F</i> , <i>t</i> , <i>r</i> ) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted<br><i>Give P values as exact values whenever suitable.</i>                     |
| <input type="checkbox"/>            | <input checked="" 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 type="checkbox"/>            | <input checked="" type="checkbox"/> Estimates of effect sizes (e.g. Cohen's <i>d</i> , Pearson's <i>r</i> ), 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 | No custom code was used for data collection.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| Data analysis   | <p>We used the free software and frameworks at following URLs.</p> <p>SAIGE (version 1.1.3): <a href="https://saigegit.github.io/SAIGE-doc/docs/Installation.html">https://saigegit.github.io/SAIGE-doc/docs/Installation.html</a></p> <p>METAL (version released on 2011-03-25): <a href="https://csg.sph.umich.edu/abecasis/Metal/download/">https://csg.sph.umich.edu/abecasis/Metal/download/</a></p> <p>GCTA-COJO (version 1.94.1): <a href="https://github.com/jianyangqt/gcta">https://github.com/jianyangqt/gcta</a></p> <p>LAVA (version 0.1.0): <a href="https://github.com/josefin-werme/LAVA">https://github.com/josefin-werme/LAVA</a></p> <p>FUMA (version 1.6.0): <a href="https://fuma.ctglab.nl/">https://fuma.ctglab.nl/</a></p> <p>coloc (version 5.2.3): <a href="https://github.com/chr1swallace/coloc">https://github.com/chr1swallace/coloc</a></p> <p>S-Predixcan (version 0.7.4): <a href="https://github.com/hakymilab/MetaXcan">https://github.com/hakymilab/MetaXcan</a></p> <p>Seurat (version 5.1.0): <a href="https://satijalab.org/seurat/articles/install_v5">https://satijalab.org/seurat/articles/install_v5</a></p> <p>scDRS (version 1.0.2): <a href="https://github.com/martinjzhang/scDRS">https://github.com/martinjzhang/scDRS</a></p> <p>SMR (version 1.3.1): <a href="https://yanglab.westlake.edu.cn/software/smr/#Download">https://yanglab.westlake.edu.cn/software/smr/#Download</a></p> <p>hdWGCNA (version 0.4.1): <a href="https://github.com/smorabit/hdWGCNA">https://github.com/smorabit/hdWGCNA</a></p> <p>MultiNicheNet (version 2.1.0): <a href="https://github.com/saeyslab/multinichenetr">https://github.com/saeyslab/multinichenetr</a></p> <p>Custom scripts for this study are available on GitHub (<a href="https://github.com/HyeonbinJoHCho/Psoriasis_Jo2026">https://github.com/HyeonbinJoHCho/Psoriasis_Jo2026</a>) at Zenodo (<a href="https://zenodo.org/records/21256344">https://zenodo.org/records/21256344</a>)</p> |

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 UK Biobank data is available with a proper application process at. Access to the full, de-identified GWAS summary statistics from 23andMe was obtained through a data transfer agreement at <https://research.23andme.com/dataset-access/>. The GWAS datasets from Stuart et al. and FinnGen were directly accessible. Single-cell transcriptome datasets used in this study are freely available at Gene Expression Omnibus (GEO) website. GWAS from FinnGen r10 ([https://www.finnngen.fi/en/access\\_results](https://www.finnngen.fi/en/access_results)), GWAS from Stuart et al. (<https://www.ebi.ac.uk/gwas/studies/GCST90019016>), single-cell transcriptome data from Ma et al. (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE173706>), single-cell transcriptome data from Francis et al. (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE228421>), single-cell transcriptome data from Kim et al. (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE278330>), Spatial transcriptome data from Castillo et al. (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE202011>), 1000 Genomes phase 3 version 5 ([https://mathgen.stats.ox.ac.uk/impute/1000GP\\_Phase3.html](https://mathgen.stats.ox.ac.uk/impute/1000GP_Phase3.html)), Genotype-Tissue Expression database (GTEx, version 8) (<https://gtexportal.org/home/downloads/adult-gtex#qtl>), tractability information from Open Targets through the FTP site (<https://ftp.ebi.ac.uk/pub/databases/opentargets/platform/>).

## 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 used self-reported sex as a covariate for conducting genome-wide association study in UK Biobank. In the analysis, 187,771 males (45.95%) and 220,848 females (54.05%) were included. Other summary statistics are also adjusted for sex information as a covariate. For the single-cell data analysis, the lack of comprehensive demographic metadata in publicly available datasets precluded sex-stratified analyses. Furthermore, as these datasets were predominantly male-biased, the generalizability of our findings regarding sex-specific effects remains limited. Further discussion on these points and the associated limitations is provided in the Discussion section.

### Reporting on race, ethnicity, or other socially relevant groupings

UK Biobank data includes the self-reported ethnic background information as a data-field ID 21000. We used the individuals with white background for the GWAS analysis. Other GWAS analyses were also conducted in individuals of European ancestry.

### Population characteristics

We used age, sex, genotyping batch, and first 10 genetic principle components as covariates. In the downstream analyses, European-derived reference samples were used.

### Recruitment

All data in this study are publicly available (but with restricted access). Participant recruitment details can be found on each institution's website or related publications.

### Ethics oversight

The UK Biobank (UKB) received ethical approval from the National Research Ethics Committee (REC reference 11/NW/0382), and all research procedures were performed in accordance with the principles of the Declaration of Helsinki. For 23andMe data, GWAS data reported in a previous study was obtained. The UK Biobank analysis was approved under Application Number 33002. Participants provided informed consent under the 23andMe human subject protocol, which was reviewed and approved by Ethical & Independent Review Services.

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

In the GWAS meta-analysis, a total of 42,109 cases with psoriasis and 1,089,702 controls are included. Single-cell data from Ma et al. consists of 14 patients with psoriasis and 11 healthy controls. Single-cell data from Francis et al. consists of longitudinal samples from five patients with psoriasis. Single-cell data from Kim et al. consists of non-lesional, lesional samples at baseline and lesional sample after risankizumab treatment from 21 patients with psoriasis and 10 healthy controls. Spatial transcriptome data from Castillo et al. consists of skin tissues from 11 patients with psoriasis and three healthy controls.

### Data exclusions

We used UK Biobank samples with complete genotype and phenotype data. In the meta-analysis, common variants with minor allele

|                 |                                                                                                                                                                                                                                                                         |
|-----------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Data exclusions | frequencies > 5% in each GWAS dataset were included. For the single-cell analysis, quality control steps such as removing outlier cells and doublets were performed.                                                                                                    |
| Replication     | Replication is not applicable. However, we conducted a meta-analysis of various GWAS datasets and performed sensitivity analyses to robustly identify psoriasis-associated genes. We also used multiple single-cell datasets to support the robustness of our findings. |
| Randomization   | Randomization was not required because GWAS and single-cell analyses are based on observational data. Instead, all statistical tests included relevant covariates such as age, sex, and genetic principle components when possible.                                     |
| Blinding        | Blinding is not applicable because the researchers were not involved in participant recruitment.                                                                                                                                                                        |

## 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 checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies                    |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms   |
| <input checked="" type="checkbox"/> | <input 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 checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> 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, mosaicism, off-target gene editing) were examined.                                                                                                                                                                                                                                       |