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	ScRNA-seq of single-cell suspensions was performed using the Chromium Single Cell 3 Reagent Kits v3 (10X Genomics, Pleasanton, CA, USA) and sequenced on a NovaSeq platform (Illumia)
Data analysis	Cell Ranger (10x Genomics, Pleasanton, CA, USA)

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 original scRNA-seq data are accessible in NCBI's Gene Expression Omnibus (GSE243716). The following secure token has been created to allow review of record GSE243716 while it remains in private status: mdoxaucylbgbxu.

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	Patient for scRNA-Seq：1 Female (sex) Patients for validation experiments：11 Males and 9 Females (sex) The sex of patients was determined by self-reporting.
Reporting on race, ethnicity, or other socially relevant groupings	All patients are Han Chinese (provided by the participates) and the method used to classify people was self-reporting.
Population characteristics	Patients participating in the study included 13 males and 7 females, all between the ages of 20-45 years.7 males and 3 females were diagnosed with keloids;4 males and 6 females were diagnosed with hypertrophic scars; and one female patient was diagnosed with both hypertrophic scar and keloid.
Recruitment	Patients were recruited from outpatient surgical patients undergoing pathological scar excision in Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine.
Ethics oversight	Ethics Committee of Shanghai Ninth People's Hospital, Shanghai Jiao Tong University School of Medicine (Approval No: SH9H-2021-T204-2)

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	This single-cell analysis study is a rare case of a patient with both hypertrophic scar and keloid wh ho underwent surgical excision only.
Data exclusions	No data were excluded from the analyses.
Replication	Single-cell sequencing analyses were not replicated, which was due to limitations of sample uniqueness (but all conclusions were validated by public data). Three technical replicates of the RT-PCR experiments were performed and all three replicat tes yielded the same results.
Randomization	Samples from a single patient source cannot be grouped.
Blinding	The study was a single-cell sequencing analysis that did not involve grouping or blinding.

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

FN1 (Abcam,CatNO :ab2413, Rabbit polyclonal to Fibronectin)
CD90(Protintech,Cat NO : 66766-1-Ig, Mouse monoclonal to CD90)
CD31(Abcam,Cat NO : ab9498, Mouse monoclonal [JC/70A] to CD31)
KRT14(Protintech,CatNO:60320-1-Ig, Mouse monoclonal to Cytokeratin 14)
APOE(Protintech,Cat NO :18254-1-AP, Rabbit polyclonal to apolipoprotein E)
YAP(Protintech,Cat NO :13584-1-AP, Rabbit polyclonal to Yes-associated protein 1)

Validation

FN1(KD/KO Validated, Reactivity: Human and Mouse; Applications:ICC/IF,WB,IHC-P)
CD90(KD/KO Validated, Reactivity: Human, Pig, Rat, Rabbit, Mouse; Applications: IF/ICC, IHC, WB, ELISA)
CD31 (KD/KO Validated, Reactivity: Human; Applications:IHC-Fr, WB, IHC-P, Flow Cyt, ICC/IF)
KRT14 (KD/KO Validated, Reactivity: Human, Mouse and Rat; Applications:FC, IF/ICC, IHC, IP)
APOE (KD/KO Validated, Reactivity: Human and More; Applications:WB, IF/ICC, FC, ELISA)
YAP(KD/KO Validated, Reactivity: Human, Mouse and Rat; Applications:WB, IHC, IF/ICC, IF-P, IP, ELISA)

Plants

Seed stocks

No seed was used in this study.

Novel plant genotypes

No plant was used in this study.

Authentication

No plant was used in this study.