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	All data in this study were derived from single-cell sequencing of clinical samples.The code is available on Github(http://github.com/chentingwei908/scRNA-seq-macrophage-uterine-adhesion)
Data analysis	All software used for bioinformatics analysis, including their versions and methodologies, has been detailed in the 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

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive(Genomics, Proteomics&Bioinformatics 2021)in National Genomics Data Center(Nucleic Acids Res 2024),China National Center for Bioinformation/Beijing Institute of Genomics, Chinese Academy of Sciences(GSA-

Human:HRA009746)that are publicly accessible at http://ngdc.cncb.ac.cn/gsa-human. Additional data are available from the corresponding author upon reasonable request.

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	All samples were collected from premenopausal women with menstrual cycles.
Reporting on race, ethnicity, or other socially relevant groupings	none
Population characteristics	All samples were in the proliferative phase of the menstrual cycle without exogenous hormonal treatment,the selection of patients was based on the clinical diagnosis of uterine adhesions and their severity.
Recruitment	The selection of patients was based on the clinical diagnosis of uterine adhesions and their severity.
Ethics oversight	This study was approved by the Ethics Committee of First People's Hospital of Yunnan Province(Ethics number:KHLL2021-KY049)affiliated with Kunming University of Science and Technology.

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	All samples were in the proliferative phase of the menstrual cycle without exogenous hormonal treatment,the number of samples we collected is detailed in Figure 1a ,Figure 1c and Supplementary Table S1.
Data exclusions	no data were excluded from the analysis
Replication	In this study, single-cell RNA sequencing was used to analyze cellular and molecular changes in intrauterine adhesions. To ensure consistency within disease groups, at least two samples were collected for each major group(see Figure 1c and Supplementary Table S1).For in vitro experiments,sufficient replicates were included to ensure reproducibility.
Randomization	In our article, the grouping is based on the presence of uterine adhesions in the endometrium and their severity. The specific grouping method is described in detail in the article figure 1c and supplementary tableS1.
Blinding	In this paper, the researchers selected samples based on the presence or absence of IUA, and the bioinformatic analysis required identifying each experimental group; therefore, blinding was not feasible.

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: The antibody information used in this article have been described in method immunohistochemistry section

Validation: All antibodies were validated for species specificity.Anti-CD68 antibody [KP1] ab955https://www.abcam.cn/products/primary-antibodies/cd68-antibody-kp1-ab955.html. The antibody has been referenced in 618 publications. RANTES Antibody - #DF7427https://www.affbiotech.com/goods-6221-DF7427-RANTES_Antibody.html. The antibody has been referenced in 1 publications.S100A8 Antibody - #DF6556https://affbiotech.cn/goods-5358-DF6556-S100A8_Antibody.html. The antibody has been referenced in 5 publications. Anti-MCP-1/CCL2 Antibody, Rabbit Polyclonalhttps://cn.sinobiological.com/antibodies/human-mcp-1-ccl2-10134-t26. The antibody has been referenced in 0 publications. Anti-alpha smooth muscle Actin antibody [EPR5368] ab124964https://www.abcam.cn/products/primary-antibodies/alpha-smooth-muscle-actin-antibody-epr5368-ab124964.html. The antibody has been referenced in 393 publications.Anti-Collagen I antibody [EPR7785] ab138492https://www.abcam.cn/products/primary-antibodies/collagen-i-antibody-epr7785-ab138492.html. The antibody has been referenced in 252 publications.

Plants

Seed stocks: none

Novel plant genotypes: none

Authentication: none