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<br>*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<br>*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 | For scRNA-seq data, the Cel Ranger pipeline (v7.1.0) was used to preprocess the data. |
| Data analysis | The Seurat (4.3.01, http://satijalab.org/seurat/>) R toolkit was used to perform all analyses. Statistical analysis and data visualization were conducted using R language version 4.0.2 and GraphPad Prism version 6.0. |

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 amount of data generated during this research is extremely large. It will be made available to the public after the manuscript is accepted. Before that, the corresponding author can obtain the relevant data 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 | This study focused on ovarian cancer, so all the samples collected were from females. During the research process, we strictly followed the relevant ethical regulations and laws, and conducted thorough verification and analysis of the data. In the process of data analysis, we did not conduct gender-based analysis, but analyzed all the data as a whole. |
| Reporting on race, ethnicity, or other socially relevant groupings | The samples were all from Asian patients/participants. |
| Population characteristics | The participants were patients who underwent ovarian cancer surgery for removal. For detailed information, please refer to the Supplementary Information. |
| Recruitment | Ten surgical samples of patients with ovarian cancer were collected from Wuxi Maternal and Child Health Hospital. |
| Ethics oversight | All patients signed the informed consent form, and this study has been approved by the Institutional Review Board of Wuxi Maternal and Child Health Hospital, in accordance 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 | According to the requirements of scRNA-seq, the collected samples are approximately spherical particles with a diameter of 1-2 centimeters. We believe this is sufficient for scRNA-seq analysis. |
| Data exclusions | No data were excluded from the analyses. |
| Replication | At least three differential tests have been conducted, and all the repeated experiments were successfully completed (for details, see the figure/results section). |
| Randomization | All the samples were randomly assigned to the experimental group. The weights of the animals were equal and they were randomly distributed to each experimental group. |
| Blinding | During the data collection and preliminary analysis stage, the researchers were unaware of the group allocation. However, in the subsequent analysis process, the researchers would utilize the grouping information for comparative analysis, thus they no longer remained in a blind state. |

# 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

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|---|---|
| Antibodies used | anti-COL1A1 (1:300 dilution, catalog AF20100, AiFang biological), anti-CD163 (1:2,000 dilution, catalog ab182422, Abcam), anti-CD8 (1:1,000 dilution, catalog AF20211, AiFang biological), and anti-SMA (1:500 dilution, catalog AFMM0002, AiFang biological) in multiple immunohistochemistry (mIHC) staining. E-cadherin (1:1,000 dilution, catalog 60335-1-Ig, ProteinTech), N-cadherin (1:1,000 dilution, catalog A19083, abclonal), COL1A1 (1:1,000 dilution, catalog A24112, Abclonal, Wuhan, China), MMP2 (1:1,000 dilution, catalog 10373-2-AP, ProteinTech), MMP9 (1:1,000 dilution, catalog 10375-2-AP, ProteinTech), FAK (1:1,000 dilution, catalog #3285, Cell Signaling Technology), p-FAK (1:1,000 dilution, catalog #3283, Cell Signaling Technology), and GAPDH (1:10,000 dilution, catalog 10494-1-AP, ProteinTech) in Western blotting analysis. |
| Validation | The antibodies were used for multiple immunohistochemistry (mIHC) staining and Western blotting. The sources of the samples were human and mouse respectively. |

## Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

| | |
|---|---|
| Cell line source(s) | Human cancer cell lines SKOV3 and OVCAR3 cells were purchased from the American Type Culture Collection (ATCC). |
| Authentication | All the cells were authenticated by short tandem repeat (STR) profiling. |
| Mycoplasma contamination | All the cells showed negative results in the mycoplasma test. |
| Commonly misidentified lines (See ICLAC register) | No commonly misidentified cell lines were used in this study. |

## 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 | Six to eight weeks old female C57BL/6 mice were used in the study. |
| Wild animals | The study did not involve wild animals. |
| Reporting on sex | The study did not conduct any sex-related analysis. |
| Field-collected samples | The study did not involve the sample collected from the field. |
| Ethics oversight | All experimental mice were housed in specific pathogen-free conditions and all animal procedures were approved by the Institutional Animal Care and Use Committee of Jiangnan University (JN.No20240930c0400215[513]). |

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 | No clinical trial. |
| Study protocol | NA, this manuscript does not contain any clinical trial content. The clinical samples were collected by the doctors. This research has been approved by the Ethics Committee of Wuxi Maternal and Child Health Hospital, and all patients have signed the informed consent form. |
| Data collection | The data were extracted from the individual hospital databases. |
| Outcomes | Not applicable (No clear clinical assessment indicators have been set, this study focuses on molecular and transcriptome analysis) |

## Plants

| | |
|---|---|
| Seed stocks | The study did not involve plants. |
| Novel plant genotypes | The study did not involve plants. |
| Authentication | The study did not involve plants. |