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	n/a
Data analysis	Graphpad Prism 9 was used for all statistical analysis in this study.

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

RNA-seq data reported in this papper are deposited in the Gene Expression Omnibus (GEO) database. The accession number is GSE240276. The mass spectrometry proteomics data have been deposited to the proteomeXchange Consortium (http://proteomecentral.proteomexchange.org) via the iProX partner repository with the dataset identifier IPX0006893000.

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	n/a
Reporting on race, ethnicity, or other socially relevant groupings	n/a
Population characteristics	Gastric cancer tissues were obtained from patients with gastric cancer who underwent gastrectomy.
Recruitment	Gastric cancer tissues were obtained from patients with gastric cancer who underwent gastrectomy between 2019 and 2020. Data on clinicopathological features and prognoses of the patients were collected and analyzed retrospectively.
Ethics oversight	Patients were signed informed consents for the use of the specimen. The study was performed in accordance with the Declaration of Helsinki and approved by the Huashan Hospital Institutional Review Board, Fudan University (approval ID, No.2017-222).

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 statistical methods were used to predetermine sample sizes and sample sizes were chosen empirically and are similar to those reported in previous studies.
Data exclusions	No data were excluded from the analysis.
Replication	At least two independent experiments were performed with similar results in our study.
Randomization	For in vivo experiments, all mice were randomly allocated into different experimental groups. For in vitro studies, no randomization was performed.
Blinding	The investigators were not blinded to allocation during experiments and outcome assessment.

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	Annexin A1 (Cell Signaling, #3299), OLFM4 (Cell Signaling, #14369), GAPDH (Cell Signaling, #5174), MST1 (Cell Signaling, #3682), MOB1(Cell Signaling, #13730), pMOB1(T35) (Cell Signaling, #8699), LATS1 (Cell Signaling, #3477), Histone H2A (Cell Signaling, #7631),

	pYAP(S127) (Cell Signaling, #92367), HA tag (Cell Signaling, #3724), IRF3 (Cell Signaling, #4962), p-IRF3 (Cell Signaling, #4947), STING (Cell Signaling, #13647), CD63 (Cell Signaling, #52090), YAP (Santa Cruz, sc-101199), EBNA-1 (Santa Cruz, sc-81581) and FAT1 (Santa Cruz, sc-517329), MMP2 (abcam, ab271866), β-actin (abcam, ab8226),Flag tag (Sigma-Aldrich, F3165), 6xHis tag (Proteintech, 66005)
Validation	The Research Resource Identifiers (RRIDs) for the antibodies used in our study are listed below: Annexin A1 (Cell Signaling, #3299), OLFM4 (Cell Signaling, #14369), GAPDH (Cell Signaling, #5174), MST1 (Cell Signaling, #3682), MOB1(Cell Signaling, #13730), pMOB1 (T35) (Cell Signaling, #8699), LATS1 (Cell Signaling, #3477), Histone H2A (Cell Signaling, #7631), pYAP(S127) (Cell Signaling, #92367), HA tag (Cell Signaling, #3724), IRF3 (Cell Signaling, #4962), p-IRF3 (Cell Signaling, #4947), STING (Cell Signaling, #13647), CD63 (Cell Signaling, #52090), YAP (Santa Cruz, sc-101199), EBNA-1 (Santa Cruz, sc-81581) and FAT1 (Santa Cruz, sc-517329), MMP2 (abcam, ab271866), β-actin (abcam, ab8226),Flag tag (Sigma-Aldrich, F3165), 6xHis tag (Proteintech, 66005)

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	GES-1, HGC-27, AGS, HEK293FT cells were purchased from the cell library of the Chinese Academy of Sciences.
Authentication	Cell line identity was confirmed with STR analysis by Shanghai Genening Biotechnologies Inc.
Mycoplasma contamination	All cell lines used in our study are negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No misidentified cell lines were used in our 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	4 weeks BALB/c nude mice mice were used in our study.
Wild animals	No wild animals were used in our study.
Reporting on sex	Male nude mice were used for subcutaneous experiment in our study.
Field-collected samples	No field-collected samples were used in our study.
Ethics oversight	The animal study was performed in accordance with the Institutional Animal Care and Use Committee of Fudan University (approval ID, IDM2022037) and the Institutional Animal Care and Use Committee guidelines of the Animal Core Facility of the Institute of Biochemistry and Cell Biology (Certificate SIBCB-NAF-14-004-S329-023).

Note that full information on the approval of the study protocol must also be provided in the manuscript.