

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 (<i>n</i>) 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☒ | ☐ 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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 <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	BD FACSDiva v8.01; Flowjo_v10.10.0 software; STAR aligner v2.7.10; edgeR v3.38.4; ComBat-seq v3.44.0; CellRanger v6.1.1; Scrublet v0.2.1; Generated single-cell RNA-seq data were analyzed using Seurat v3.0; Slingshot v2.4.0; Monocle v2.24.1; CellChat v1.6.1; UCell v2.0.1
Data analysis	RNA-seq raw sequencing reads were processed using STAR aligner v2.7.10 and raw counts normalization was conducted using CPM method. DE analysis with RNA-seq data was analyzed using edgeR v3.38.4 in R. Batch effect correction for raw count data was performed using ComBat-seq v3.44.0 in R. Single-cell RNA-seq raw sequencing reads were processed using CellRanger v6.1.1. Doublets were removed using Scrublet v0.2.1. Generated single-cell RNA-seq data were analyzed using Seurat v3.0 in R. Trajectory analyses were performed with Slingshot v2.4.0, and Monocle v2.24.1 in R. Cell-cell interaction analysis was performed by CellChat v1.6.1 in R. UCell v2.0.1 was used to calculate enrichment scores of custom gene sets. All source code for analyzing single-cell RNA sequencing is available at https://github.com/MinhoLee-DGU/2024.Myeong.et.al.NatureComms .

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](#)

All raw sequencing data (.fastq) generated in this study are available at the NCBI BioProject with the following Accession IDs: PRJNA963403, PRJNA963409, and PRJNA964006. Whole exome sequencing data generated in this study have been deposited at NCBI and are publicly available under the following accession codes: PRJNA1213881

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	Cervical tissue samples were collected only from female patients who agreed to donate parts of their excised specimen after surgery
Reporting on race, ethnicity, or other socially relevant groupings	The patients who donated their cervix samples are all Korean.
Population characteristics	Out of 31 Korean patients who donated their cervical tissues after surgery, 9 were diagnosed with adenomyosis, 13 with uterine myoma, and 9 with cervical dysplasia. The average age is 45.8, ranging from 36 to 56. Among 31 patients, 9 were confirmed to have HPV infection. Detailed clinical characteristics are summarized in the Supplementary Table .
Recruitment	Female patients with adenomyosis, uterine myoma, and cervical dysplasia were recruited from the Chilgok Kyungpook National University Hospital, Gyeongsangbuk-do, Korea, between April 2021 to Jun 2024. 22 HPV-uninfected, 8 patients diagnosed with HSIL, and 1 carcinoma in situ samples were collected. Each sample was dissociated into single cells for organoid culture or transplantation.
Ethics oversight	All patients signed separate informed consent forms for providing cervical normal, precancerous, or cancer samples resected by surgery for the treatment. All experiments using human materials were approved by the internal review boards of DGIST and Chilgok Kyungpook National University Hospital, Gyeongsangbuk-do, Korea, in accordance with all relevant ethical regulations (KNUCH-2020-12-020-001 and DGIST-20210401-BR-112-01).

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	Single-cell analysis was conducted on two samples. RNA sequencings were conducted with triplicates. Organoid formation experiments, cell cycle analysis, and gene expression analysis were conducted on three to five samples as indicated in the figure legend.
Data exclusions	Single-cell RNA-seq : Low quality cells with < 200 genes and >25% mitochondrial gene percentage were excluded from analyses. Doublet cells were also excluded.
Replication	All experiments were reliably reproduced, and each experiment was repeated at least three times independently to validate the findings, as indicated in the figure legend. Single-cell analysis was performed with two samples from two different patients.
Randomization	The in vitro cell or organoid experiments were not randomized. For in vivo tissue reconstitution experiments, mice were randomly assigned to each cell subpopulation group. For experiments with chemical inhibitors or activators and genetic silencing, cells or organoids were randomly allocated to control and treatment groups.
Blinding	The investigators who analyzed RNA sequencing data and WES data were blinded to the control or treatment. The investigator who processed tongues transplanted with different subpopulation of cells for tissue staining were blinded to the assignment. The investigators who performed organoid experiments were not blinded to the treatment status.

Behavioural & social sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Briefly describe the study type including whether data are quantitative, qualitative, or mixed-methods (e.g. qualitative cross-sectional, quantitative experimental, mixed-methods case study).
Research sample	State the research sample (e.g. Harvard university undergraduates, villagers in rural India) and provide relevant demographic information (e.g. age, sex) and indicate whether the sample is representative. Provide a rationale for the study sample chosen. For studies involving existing datasets, please describe the dataset and source.
Sampling strategy	Describe the sampling procedure (e.g. random, snowball, stratified, convenience). Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient. For qualitative data, please indicate whether data saturation was considered, and what criteria were used to decide that no further sampling was needed.
Data collection	Provide details about the data collection procedure, including the instruments or devices used to record the data (e.g. pen and paper, computer, eye tracker, video or audio equipment) whether anyone was present besides the participant(s) and the researcher, and whether the researcher was blind to experimental condition and/or the study hypothesis during data collection.
Timing	Indicate the start and stop dates of data collection. If there is a gap between collection periods, state the dates for each sample cohort.
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, provide the exact number of exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Non-participation	State how many participants dropped out/declined participation and the reason(s) given OR provide response rate OR state that no participants dropped out/declined participation.
Randomization	If participants were not allocated into experimental groups, state so OR describe how participants were allocated to groups, and if allocation was not random, describe how covariates were controlled.

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Briefly describe the study. For quantitative data include treatment factors and interactions, design structure (e.g. factorial, nested, hierarchical), nature and number of experimental units and replicates.
Research sample	Describe the research sample (e.g. a group of tagged <i>Passer domesticus</i> , all <i>Stenocereus thurberi</i> within Organ Pipe Cactus National Monument), and provide a rationale for the sample choice. When relevant, describe the organism taxa, source, sex, age range and any manipulations. State what population the sample is meant to represent when applicable. For studies involving existing datasets, describe the data and its source.
Sampling strategy	Note the sampling procedure. Describe the statistical methods that were used to predetermine sample size OR if no sample-size calculation was performed, describe how sample sizes were chosen and provide a rationale for why these sample sizes are sufficient.
Data collection	Describe the data collection procedure, including who recorded the data and how.
Timing and spatial scale	Indicate the start and stop dates of data collection, noting the frequency and periodicity of sampling and providing a rationale for these choices. If there is a gap between collection periods, state the dates for each sample cohort. Specify the spatial scale from which the data are taken
Data exclusions	If no data were excluded from the analyses, state so OR if data were excluded, describe the exclusions and the rationale behind them, indicating whether exclusion criteria were pre-established.
Reproducibility	Describe the measures taken to verify the reproducibility of experimental findings. For each experiment, note whether any attempts to repeat the experiment failed OR state that all attempts to repeat the experiment were successful.
Randomization	Describe how samples/organisms/participants were allocated into groups. If allocation was not random, describe how covariates were controlled. If this is not relevant to your study, explain why.
Blinding	Describe the extent of blinding used during data acquisition and analysis. If blinding was not possible, describe why OR explain why blinding was not relevant to your study.

Did the study involve field work? ☐ Yes ☐ No

Field work, collection and transport

Field conditions	<i>Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).</i>
Location	<i>State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).</i>
Access & import/export	<i>Describe the efforts you have made to access habitats and to collect and import/export your samples in a responsible manner and in compliance with local, national and international laws, noting any permits that were obtained (give the name of the issuing authority, the date of issue, and any identifying information).</i>
Disturbance	<i>Describe any disturbance caused by the study and how it was minimized.</i>

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 following antibodies were used for immunostaining: rabbit anti-keratin 14 (1:1000, Abcam), mouse anti-keratin 14 (1:1000, Invitrogen), rabbit anti-keratin 1 (1:1000, Biolegend), rabbit anti-loricrin (1:100, Biolegend), mouse anti-keratin 7 (1:100, Invitrogen), rabbit anti-keratin 5 (1:200, Biolegend), rabbit anti-YAP (1:100, Cell Signaling Technology), mouse anti-ITGB4 (1:20, Santacruz), rabbit anti-Ki67 (1:100, Abcam), mouse APC anti-human CD24 (1:50, Biolegend), mouse FITC anti-human CD271 (NGFR) (1:50, Biolegend), mouse FITC anti-human HLA-A,B,C (1:25, Biolegend), and rabbit HRP-conjugated anti-p63 (1:100, Abcam), rat FITC anti-mouse ITGB4 (1:50, Biolegend), and rat APC anti-mouse CD24 (1:50, Biolegend). The following antibodies were used for flow cytometric analysis: FITC anti-human ITGB4 (1:50, Biolegend), PerCP-Cy5.5 anti-human CD24 (1:50, Biolegend), PE anti-human EpCAM (1:50, Biolegend), FITC anti-mouse ITGB4 (1:50, Biolegend), PE-Cy7 anti-mouse CD24 (1:50, Biolegend), and APC anti-mouse EpCAM (1:50, Biolegend).
Validation	All antibodies have been validated by the manufacturers using specific assay for human cells and have multiple citations for the human cells. Investigators independently validated antibodies by reproducible findings with biological replicates in this study. Primary and secondary antibody controls were used for immunofluorescence. Secondary antibody only controls or matched isotype controls were used for immunostaining. Matched isotype controls were used for flow cytometry.

Eukaryotic cell lines

Policy information about [cell lines and Sex and Gender in Research](#)

Cell line source(s)	SiHa and HeLa cell lines were purchased from the Korean cell line bank
Authentication	Both SiHa and HeLa cell lines are widely used cervical cancer cell lines. We purchased them for this study and used them in their early passage. Therefore, we did not authenticate in our side.
Mycoplasma contamination	There was no mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	Both SiHa and HeLa cell lines are widely used cervical cancer cell lines. We purchased them for this study and used them in their early passage.

Palaeontology and Archaeology

Specimen provenance	<i>Provide provenance information for specimens and describe permits that were obtained for the work (including the name of the issuing authority, the date of issue, and any identifying information). Permits should encompass collection and, where applicable, export.</i>
Specimen deposition	<i>Indicate where the specimens have been deposited to permit free access by other researchers.</i>
Dating methods	<i>If new dates are provided, describe how they were obtained (e.g. collection, storage, sample pretreatment and measurement), where they were obtained (i.e. lab name), the calibration program and the protocol for quality assurance OR state that no new dates are provided.</i>
☐ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	<i>Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.</i>

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

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	1-6 months old female C57BL/6J mice were used to harvest uterine cervix. 1-12 months old male and female NOD.Cg-Prkdcscid Il2rgtm1Wjl/SzJ (NSG) mice were used for the intralingual transplantation.
Wild animals	No wild animals were used in this study.
Reporting on sex	Cervical tissues were collected from female patients or female mice. However, when we transplanted cervical organoids or cells into NSG mice to test the in vivo tissue reconstitution, male and female NSG mice were used.
Field-collected samples	No field-collected samples were used in this study.
Ethics oversight	All experimental work complied with the Republic of Korea Animal Scientific Procedures Act. The animal study was approved by the Ethical Committee and the Institutional Animal Care and Use Committee at DGIST. Human materials were obtained in accordance with the approval of internal review boards of DGIST and Chilgok Kyungpook National University Hospital, Gyeongsangbuk-do, Korea, in accordance with all relevant ethical regulations. Informed consent was obtained from all patients.

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	<i>Provide the trial registration number from ClinicalTrials.gov or an equivalent agency.</i>
Study protocol	<i>Note where the full trial protocol can be accessed OR if not available, explain why.</i>
Data collection	<i>Describe the settings and locales of data collection, noting the time periods of recruitment and data collection.</i>
Outcomes	<i>Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.</i>

Dual use research of concern

Policy information about [dual use research of concern](#)

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

- | | |
|--------------------------|---|
| No | Yes |
| ☐ | ☐ Public health |
| ☐ | ☐ National security |
| ☐ | ☐ Crops and/or livestock |
| ☐ | ☐ Ecosystems |
| ☐ | ☐ Any other significant area |

Experiments of concern

Does the work involve any of these experiments of concern:

- | | |
|--------------------------|--|
| No | Yes |
| ☐ | ☐ Demonstrate how to render a vaccine ineffective |
| ☐ | ☐ Confer resistance to therapeutically useful antibiotics or antiviral agents |
| ☐ | ☐ Enhance the virulence of a pathogen or render a nonpathogen virulent |
| ☐ | ☐ Increase transmissibility of a pathogen |
| ☐ | ☐ Alter the host range of a pathogen |
| ☐ | ☐ Enable evasion of diagnostic/detection modalities |
| ☐ | ☐ Enable the weaponization of a biological agent or toxin |
| ☐ | ☐ Any other potentially harmful combination of experiments and agents |

Plants

- | | |
|-----------------------|--|
| Seed stocks | <i>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.</i> |
| Novel plant genotypes | <i>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.</i> |
| Authentication | <i>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.</i> |

ChIP-seq

Data deposition

- ☐ Confirm that both raw and final processed data have been deposited in a public database such as [GEO](#).
- ☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

- | | |
|--|--|
| Data access links
<i>May remain private before publication.</i> | <i>For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.</i> |
| Files in database submission | <i>Provide a list of all files available in the database submission.</i> |
| Genome browser session
(e.g. UCSC) | <i>Provide a link to an anonymized genome browser session for "Initial submission" and "Revised version" documents only, to enable peer review. Write "no longer applicable" for "Final submission" documents.</i> |

Methodology

- | | |
|-------------------------|--|
| Replicates | <i>Describe the experimental replicates, specifying number, type and replicate agreement.</i> |
| Sequencing depth | <i>Describe the sequencing depth for each experiment, providing the total number of reads, uniquely mapped reads, length of reads and whether they were paired- or single-end.</i> |
| Antibodies | <i>Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.</i> |
| Peak calling parameters | <i>Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.</i> |

Data quality

Describe the methods used to ensure data quality in full detail, including how many peaks are at FDR 5% and above 5-fold enrichment.

Software

Describe the software used to collect and analyze the ChIP-seq data. For custom code that has been deposited into a community repository, provide accession details.

Flow Cytometry

Plots

Confirm that:

- ☒ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☒ All plots are contour plots with outliers or pseudocolor plots.
- ☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

Human and mouse ectocervical tissues were incubated in dispase solution (2.4 U/ml of dispase, Gibco) at 37°C for 1 hour. Then, the epithelial layer was peeled off from connective tissue, incubated in TrypLE Express (Gibco) at 37°C for 5 min, and neutralized with blocking buffer (DPBS containing 2% bovine calf serum). After centrifugation, the pellets were incubated with 1X RBC lysis buffer and 1X DNase I (Enzymomics) at room-temperature (RT) for 5 min. After neutralization with the blocking buffer, the cell suspension was filtered through a 40 µm cell strainer. The dissociated cells were pelleted by centrifugation at 300 x g for 5 min and resuspended in the optimized medium for further experiments. Cells were suspended in PBS containing 2% FBS. Antibodies were added at the following ratios; FITC anti-human ITGB4 (1:50, Biolegend), PerCP-Cy5.5 anti-human CD24 (1:50, Biolegend), PE anti-human EpCAM (1:50, Biolegend), FITC anti-mouse ITGB4 (1:50, Biolegend), PE-Cy7 anti-mouse CD24 (1:50, Biolegend), and APC anti-mouse EpCAM (1:50, Biolegend). Dead cells were discriminated using Zombie dye (1:100, Biolegend) or propidium iodide (20 µg/ml, Sigma). For Cell cycle analysis, single cells were suspended in 150 µl of PBS, and 350 µl of absolute ethanol was added in a dropwise manner while vortexing. After incubating cells at 4°C for at least 2 hours, fixed cells were centrifuged at 1,500 x g for 3 min, and supernatant was removed. After washing with PBS, pellets were resuspended in staining solution containing 100 µg/ml RNase A and 50 µg/ml propidium iodide and incubated at RT for 30 min. After filtration through a cell strainer, cells were analyzed by the flow cytometer.

Instrument

FACSAriaTMIII

Software

BD FACSDiva v8.01; Flowjo_v10.10.0 software

Cell population abundance

The sorted ITGB4+CD24-, ITGB4-CD24-, and ITGB4-CD24+ cells were approximately 30%, 40%, and 25%, respectively, of total live/CD31-/CD45- cells in normal human ectocervix. In the murine ectocervix, sorted ITGB4+CD24-, ITGB4-CD24-, and ITGB4-CD24+ cells were approximately 15%, 70%, and 10%, respectively. Small portions of sorted cells were run through the machine to confirm purity of over 90%.

Gating strategy

Cells were selected using FSC/SSC scatter profile to remove debris. Doublets were excluded using FSC-W/FSC-H. Dead cells were removed using Zombie NIRTM Fixable Viability Kit. Blood and endothelial cells were removed using CD45 and CD31 antibodies. Viable (Zombie negative) and CD31/CD45 negative cells were gated with ITGB4 and CD24 antibodies.

- ☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type

Indicate task or resting state; event-related or block design.

Design specifications

Specify the number of blocks, trials or experimental units per session and/or subject, and specify the length of each trial or block (if trials are blocked) and interval between trials.

Behavioral performance measures

State number and/or type of variables recorded (e.g. correct button press, response time) and what statistics were used to establish that the subjects were performing the task as expected (e.g. mean, range, and/or standard deviation across subjects).

Acquisition

Imaging type(s)	<i>Specify: functional, structural, diffusion, perfusion.</i>
Field strength	<i>Specify in Tesla</i>
Sequence & imaging parameters	<i>Specify the pulse sequence type (gradient echo, spin echo, etc.), imaging type (EPI, spiral, etc.), field of view, matrix size, slice thickness, orientation and TE/TR/flip angle.</i>
Area of acquisition	<i>State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.</i>
Diffusion MRI	☐ Used ☐ Not used

Preprocessing

Preprocessing software	<i>Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).</i>
Normalization	<i>If data were normalized/standardized, describe the approach(es): specify linear or non-linear and define image types used for transformation OR indicate that data were not normalized and explain rationale for lack of normalization.</i>
Normalization template	<i>Describe the template used for normalization/transformation, specifying subject space or group standardized space (e.g. original Talairach, MNI305, ICBM152) OR indicate that the data were not normalized.</i>
Noise and artifact removal	<i>Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).</i>
Volume censoring	<i>Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.</i>

Statistical modeling & inference

Model type and settings	<i>Specify type (mass univariate, multivariate, RSA, predictive, etc.) and describe essential details of the model at the first and second levels (e.g. fixed, random or mixed effects; drift or auto-correlation).</i>
Effect(s) tested	<i>Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.</i>
Specify type of analysis:	☐ Whole brain ☐ ROI-based ☐ Both
Statistic type for inference	<i>Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.</i>
(See Eklund et al. 2016)	
Correction	<i>Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).</i>

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis
Functional and/or effective connectivity	<i>Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).</i>
Graph analysis	<i>Report the dependent variable and connectivity measure, specifying weighted graph or binarized graph, subject- or group-level, and the global and/or node summaries used (e.g. clustering coefficient, efficiency, etc.).</i>
Multivariate modeling and predictive analysis	<i>Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.</i>