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 | Immunohistochemistry (IHC), immunofluorescence (IF), and hematoxylin and eosin (HE) micrographs were acquired utilizing the Zeiss Zen Blue edition software, version 3.4. Flow cytometry datasets were amassed via a CytoFLEX instrument from Beckman Coulter. Western Blot analyses were conducted and data collected employing a Tanon 5200 Intelligent Imaging System. Quantitative real-time polymerase chain reaction (qPCR) assays were executed using PerfectStart® Green qPCR SuperMix (AQ601, TransGen Biotech) on a Bio-Rad CXF96 Real-Time System (Bio-Rad, USA). |
| Data analysis | NovoExpress 2.0, Primer Premier Versions 5.00, Cell Ranger Versions 4.0.0, Seurat Versions 4.0.0, DoubletFinder Versions 2.0.3, SCENIC version 1.2.1, Limma Versions 3.52.2, Cellchat Versions 1.4.0, CellPhoneDB Versions 2.1.7, Scissor Versions 2.0.0, monocle3 Versions 1.3.1, CopyKat Versions 1.1.0, R software (version 4.0.0), jaspar(web page). All custom code and algorithms used in this study are available in a DOI-minting repository. The specific DOI for our code repository is https://zenodo.org/record/1306857554. Subsequent versions of the code will be managed in this repository under an open source initiative-approved license. |

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 sequencing data reported in this study (including 4 single-cell sequencing datasets from the pooled samples of 12 mice in Fig. 1, and 4 single-cell sequencing datasets from the individually sampled 4 mice in Fig. 4) have been deposited in the Genome Sequence Archive of the National Genomics Data Center (NGDC), with the accession number CRA011974. Consequently, all related data are freely available for download. The scRNA-seq data generated in this study have been deposited in the Genome Sequence Archive in the National Genomics Data Center under the accession number CRA011974 [https://ngdc.cncb.ac.cn/gsa/browse/CRA011974]. The publicly available data used in this study include the previously published HNSCC scRNA-seq data from the GEO database, specifically under accession codes GSE139324 [https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE139324] and GSE164690 [https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE164690]. The TCGA HNSCC data is available in the Genomic Data Commons (GDC) Data Portal under accession code TCGA-HNSC [https://portal.gdc.cancer.gov/projects/TCGA-HNSC]. The TCGA PanCancer data can be accessed under accession code TCGA [https://portal.gdc.cancer.gov]. The remaining data are available within the Article, Supplementary Information or Source Data file. Further information and requests for resources and reagents should be directed to and will be fulfilled by the corresponding author Demeng Chen (chendm29@mail.sysu.edu.cn). Source data are provided with this paper. All custom code and algorithms used in this study are available in a DOI-minting repository. The specific DOI for our code repository is https://zenodo.org/record/1306857554. Subsequent versions of the code will be managed in this repository under an open source initiative-approved license.

## 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 | *Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.*<br>*Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.*<br>*Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.* |
| Reporting on race, ethnicity, or other socially relevant groupings | *Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).*<br>*Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)*<br>*Please provide details about how you controlled for confounding variables in your analyses.* |
| Population characteristics | A cohort contained 81 HNSCC specimens was obtained from the Department of Oral and Maxillofacial Surgery, The First Affiliated Hospital of Sun Yat-sen University. |
| Recruitment | A cohort contained 81 HNSCC specimens was obtained from the Department of Oral and Maxillofacial Surgery, The First Affiliated Hospital of Sun Yat-sen University. |
| Ethics oversight | Tumor samples were collected with the patients' written informed consent and approved by the Department of Oral and Maxillofacial Surgery, The First Affiliated Hospital of Sun Yat-sen University. |

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 | For the C57BL/6N mouse experiments, we used n ≥ 6 biological independent samples per group. The sample sizes and treatment protocols were determined based on established methodologies and statistical guidelines detailed in related literature (PMID: 28285905, 33945793). These references provide comprehensive insights into the statistical methods employed, ensuring the robustness and reliability of our |

| | |
|---|---|
| | experimental design.In experiments involving flow cytometry sorting of immune cells, each group consisted of n ≥ 3 biological independent samples. Where possible, sample sizes were determined according to widely accepted protocols within the scientific community, ensuring sufficient power to detect significant differences while maintaining ethical standards for animal use. Mice were randomly assigned to different experimental groups to minimize selection bias. This was achieved by randomly selecting mice from the same cohort and ensuring that each group was comparable in terms of age, sex, and initial health status. The allocation and experimental design were guided by established protocols and relevant literature to ensure scientific validity and reproducibility. This approach helped in maintaining consistency and reliability across experiments. |
| Data exclusions | No data was excluded in this study. |
| Replication | Replicability of findings was confirmed through multiple biologically independent trials. The figure legends delineate the sample sizes and underscore the consistency of outcomes across these biologically independent experiments. |
| Randomization | Mice were randomly assigned to different experimental groups to minimize selection bias. This was achieved by randomly selecting mice from the same cohort and ensuring that each group was comparable in terms of age, sex, and initial health status. |
| Blinding | While the study design precluded the incorporation of blinding procedures, all experimental measures were conducted under standardized conditions. Specifically, data for both control and experimental groups were garnered within identical parameters. This methodological rigor substantially mitigates the potential for observer bias and subjective interpretation to influence the study's conclusions. |

# 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

Treatment
InVivoMAb rat IgG1 isotype control BioXcell Cat#BE0088;
enoblituzumab, MedChemExpress Catalog #HY-P9966;
InVivoMAb anti-mouse PD-1 (CD279) BioXcell Cat# BE0146;
Anti-Integrin αvβ6 ADCC Enhanced Antibody Creative Biolabs Cat#AFC-431CL;
CX3CR1 antagonist MedChemExpress Cat# HY-123918;
InVivoPlus anti-mouse CD8α, BioXcell Catalog #BP0061;
InVivoPlus anti-mouse CD4, BioXcell Catalog #BE0119;
InVivoPlus mouse IgG2a isotype BioXcell Cat#BP0085;
InVivoMAb anti-mouse/human/rat CCL2 (MCP-1) Catalog #BE0185
anti-mouse CX3CL1 (Fractalkine) Antibody BioLegend Cat# 938903;
anti-mouse CX3CR1 Antibody GeneTex, Cat. No. GTX27200;
Recombinant Mouse CX3CL1/Fractalkine R&D Systems Cat# 458-MF;
Recombinant Mouse CXCL16 MCE cat#HY-P72961;
IHC, IF and WB
Novus NB500-170 https://www.novusbio.com/products/ki67-mki67-antibody_nb500-170 cited at least 160 times
CST 14058 https://www.cellsignal.com/products/primary-antibodies/b7-h3-d9m2l-xp-rabbit-mab/14058 cited at least 40 times
abclonal A17216 https://abclonal.com.cn/catalog/A17216 cited at least 10 times
Abcam ab229552 https://www.abcam.com/products/primary-antibodies/itgb6-antibody-ab229552 cited at least 60 times
CST 9661S https://www.cellsignal.com/products/primary-antibodies/cleaved-caspase-3-asp175-antibody/9661 cited at least 9591 times
abcam ab217344 https://www.abcam.com/products/primary-antibodies/cd8-alpha-antibody-epr21769-ab217344.html cited at least 96 times
abclonal A22993 https://abclonal.com.cn/catalog/A22993 cited at least 5 times
Abcam ab192869 https://www.abcam.com/products/primary-antibodies/caveolin-1-antibody-cav1-ab192869.html cited at least 100 times
Abcam ab119211 https://www.abcam.com/products/primary-antibodies/prnp-antibody-ab119211.html cited at least 50 times
CST 3285S https://www.cellsignal.com/products/primary-antibodies/fak-antibody-3285s cited at least 80 times

CST 3284S https://www.cellsignal.com/products/primary-antibodies/phospho-fak-tyr925-antibody-3284s cited at least 70 times
Affinity Biosciences AF6161 https://affbiotech.cn/goods-14439-AF6161-SRC_Antibody.html cited at least 10 times
Affinity Biosciences AF3162 https://affbiotech.cn/goods-14439-AF3162-Phospho_SRC_Antibody.html cited at least 8 times
Abclonal A19566 https://abclonal.com/catalog/A19566 cited at least 30 times
Abclonal AP0474 https://abclonal.com/catalog/AP0474 cited at least 20 times
Proteintech 10176-2-AP https://www.ptglab.co.jp/Products/AKT-Antibody-10176-2-AP.htm cited at least 50 times
Proteintech 66444-1-Ig https://www.ptglab.co.jp/Products/Phospho_AKT-Antibody-66444-1-Ig.htm cited at least 40 times
CST 9252 https://www.cellsignal.com/products/primary-antibodies/sapk-jnk-antibody-9252 cited at least 400 times
CST 9251 https://www.cellsignal.com/products/primary-antibodies/phospho-sapk-jnk-antibody-9251 cited at least 350 times
CST 9102 https://www.cellsignal.com/products/primary-antibodies/erk1-2-antibody-9102 cited at least 600 times
CST 9101 https://www.cellsignal.com/products/primary-antibodies/phospho-erk1-2-antibody-9101 cited at least 500 times
CST 9212 https://www.cellsignal.com/products/primary-antibodies/p38-mapk-antibody-9212 cited at least 300 times
CST 9211 https://www.cellsignal.com/products/primary-antibodies/phospho-p38-mapk-antibody-9211 cited at least 200 times
Affinity Biosciences AF6241 https://affbiotech.cn/goods-14439-AF6241-PI3K_p85_alpha_Antibody.html cited at least 5 times
Affinity Biosciences AF3241 https://affbiotech.cn/goods-14439-AF3241-Phospho_PI3K_p85_alpha_Antibody.html cited at least 10 times
CST 8242 https://www.cellsignal.com/products/primary-antibodies/nf-kb-p65-antibody-8242 cited at least 200 times
CST 3033 https://www.cellsignal.com/products/primary-antibodies/phospho-nf-kb-p65-antibody-3033 cited at least 100 times
Abcam ab25093 https://www.abcam.com/products/primary-antibodies/cx3cl1-antibody-ab25093 cited at least 500 times
Proteintech 13885-1-AP https://www.ptglab.co.jp/Products/CX3CR1-Antibody-13885-1-AP.htm cited at least 30 times
Abcam ab303494 https://www.abcam.com/products/primary-antibodies/pf4-antibody-ab303494 cited at least 15 times
Abcam ab215036 https://www.abcam.com/products/primary-antibodies/klf4-antibody-ab215036.html cited at least 50 times
Flow Cytometry
Anti-Mouse F4/80 PerCP/Cy5.5 (Thermo Fisher Cat#45-4801-80) has been previously validated by the manufacturer (more information is available at https://www.thermofisher.com/antibody/product/F4-80-Antibody-clone-BM8-Monoclonal/45-4801-80) and cited at least 198 times.
Anti-Mouse CD45 PE-Cyanine7 (Tonbo Cat#60-0451) has been previously validated by the manufacturer (more information is available at https://www.tonbobio.com/products/flow-cytometry/pe-cyanine7-anti-mouse-cd45-30-f11) and cited at least 50 times.
Anti-Mouse CD3 APC (Tonbo Cat#20-0032) has been previously validated by the manufacturer (more information is available at https://www.netascientific.com/primary-antibodies/tb-20-0032-u100) and cited at least 45 times.
Anti-Mouse CD4 violet FluorTM 450 (Tonbo Cat#75-0041) has been previously validated by the manufacturer (more information is available at https://www.biocompare.com/9776-Antibodies/9246604-violetFluor-450-Anti-Mouse-CD4-GK1-5) and cited at least 4 times.
Anti-Mouse CD8a FITC (Tonbo Cat#35-0081) has been previously validated by the manufacturer (more information is available at https://www.thermofisher.cn/antibody/product/CD8a-Antibody-clone-53-6-7-Monoclonal/35-0081-82) and cited at least 82 times.
Anti-Mouse PDCD1 PE-Cyanine5 (Tonbo Cat#55-5773-U100) has been previously validated by the manufacturer (more information is available at https://www.tonbobio.com/products/flow-cytometry/pe-cyanine5-anti-mouse-pd-1-rmp1-30) and cited at least 5 times.
Anti-Mouse GZMB PerCP/Cy5.5 (Biolegend Cat#372211) has been previously validated by the manufacturer (more information is available at https://www.biolegend.com/en-us/products/pe-anti-mouse-human-nhp-granzyme-b-372211) and cited at least 10 times.
Anti-Mouse CXCR6 PE (Biolegend Cat#151103) has been previously validated by the manufacturer (more information is available at https://www.biolegend.com/en-us/products/pe-anti-mouse-cxcr6-151103) and cited at least 15 times.
Anti-Mouse PF4 violet FluorTM 450 (Abcam Cat#ab303494) has been previously validated by the manufacturer (more information is available at https://www.abcam.com/products/primary-antibodies/pf4-antibody-ab303494) and cited at least 15 times.
Ghost DyeTM Red 780 (Tonbo Cat#13-0865) has been previously validated by the manufacturer (more information isavailable at https://cytekbio.com/products/ghost-dye-red-780) and cited at least 22 times.

Validation

All primary antibodies were used according to the manufacturer's recommended dilutions and buffers. All antibodies purchased were verified by the company from whom they were obtained according to the manufacturer's website.

## Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

| | |
|---|---|
| Cell line source(s) | Moc1 (Mouse oral squamous cell carcinoma cells); SCC15(Squamous Cell Carcinoma) |
| Authentication | The mouse Moc1 cell line was purchased from KERAFAST, INC. (Boston, MA, USA,Cat#EWL001-FP) and HNSCC cell lines SCC15 were provided by Cheng Wang from Department of Maxillofacial Surgery, Guanghua Stomatological Hospital, Sun Yat-sen University, with the cell line STR authentication report. |
| Mycoplasma contamination | All the cells were tested negative for mycoplasma. |
| Commonly misidentified lines (See ICLAC register) | No commonly misidentified cell lines were used. |

## 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 | WT C57BL/6, Itgb6fl/fl , Cx3cl1fl/fl and PF4CreERT2 mice were purchased from The GemPharmatech (Nanjing, China). K14CreER |

| | |
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| | (005107) mice were purchased from The Jackson Laboratory (Bar Harbor, ME, USA). All animal subjects were accommodated under specific pathogen-free conditions, maintained on a 12-hour light/dark circadian cycle, and granted ad libitum access to sustenance and hydration. All animal protocols received ethical clearance from the Institutional Animal Care and Use Committee (IACUC) of the First Affiliated Hospital of Sun Yat-sen University, under the protocol number SYSU-IACUC-2023-000861. For the induction of oral carcinogenesis, mice aged beyond four weeks were administered 4-nitroquinoline 1-oxide (4NQO) via drinking water at a concentration of 10 mg/mL. |
| Wild animals | No wild animals were used in this study. |
| Reporting on sex | Experimental procedures were designed to be gender-neutral, incorporating both male and female mice without distinction. |
| Field-collected samples | Experimental procedures were designed to be gender-neutral, incorporating both male and female mice without distinction. |
| Ethics oversight | All animal experiments were approved by the Animal Ethics Committee of the First Affiliated Hospital of Sun Yet-sen University (protocol number SYSU-IACUC-2023-000861). |

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

# 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 | Single-cell suspensions derived from mouse head and neck squamous cell carcinomas (HNSCC) were prepared as previously outlined. Prior to immunostaining, cells were re-suspended at a density of 1 × 10^7 cells/mL following a wash in a staining buffer containing 2% bovine growth serum in phosphate-buffered saline (PBS). The cells were then incubated with specific antibodies and re-suspended in the staining buffer for a two-hour period at 4°C for the purpose of extracellular staining. Data analysis was conducted utilizing NovoExpress software, and flow cytometric evaluations were performed using a CytoFLEX instrument from Beckman Coulter, version 2.0, . |
| Instrument | FC Cell Sorters: BD LSRFOrtessa.<br>FC Analysers: CytoFLEX, Beckman Coulter |
| Software | NovoExpress 2.0 and CytoFLEX2.0. |
| Cell population abundance | According to the estimated size and particle size of the forward and lateral scattering cells, as well as the accompanying positive or negative signals, the cell population is established for flow analysis. |
| Gating strategy | NONE |

☒ 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 | All mice were examined using a 3.0T MR scanner (MAGNETOM Vida, Siemens Healthcare, Erlangen, Germany) and a 16-channel mouse coil (CG-MUC48-H300-AS, Shanghai Chenguang Medical Technology Co., Ltd., Shanghai, China). The scan protocol includes axial T2WI TSE, coronal T2WI TSE and axial T1WI StarVIBE. |
| Design specifications | All mice were examined using a 3.0T MR scanner (MAGNETOM Vida, Siemens Healthcare, Erlangen, Germany) and a 16-channel mouse coil (CG-MUC48-H300-AS, Shanghai Chenguang Medical Technology Co., Ltd., Shanghai, China). The scan protocol includes axial T2WI TSE, coronal T2WI TSE and axial T1WI StarVIBE. |
| 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) *Specify: functional, structural, diffusion, perfusion.*

Field strength *Specify in Tesla*

Sequence & imaging parameters *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.*

Area of acquisition *State whether a whole brain scan was used OR define the area of acquisition, describing how the region was determined.*

Diffusion MRI ☐ Used ☒ Not used

## Preprocessing

Preprocessing software *Provide detail on software version and revision number and on specific parameters (model/functions, brain extraction, segmentation, smoothing kernel size, etc.).*

Normalization *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.*

Normalization template *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.*

Noise and artifact removal *Describe your procedure(s) for artifact and structured noise removal, specifying motion parameters, tissue signals and physiological signals (heart rate, respiration).*

Volume censoring *Define your software and/or method and criteria for volume censoring, and state the extent of such censoring.*

## Statistical modeling & inference

Model type and settings *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).*

Effect(s) tested *Define precise effect in terms of the task or stimulus conditions instead of psychological concepts and indicate whether ANOVA or factorial designs were used.*

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference *Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*

(See Eklund et al. 2016)

Correction *Describe the type of correction and how it is obtained for multiple comparisons (e.g. FWE, FDR, permutation or Monte Carlo).*

## Models & analysis

| n/a | Involved in the study |
|---|---|
| ☒ | ☐ Functional and/or effective connectivity |
| ☐ | ☒ Graph analysis |
| ☒ | ☐ Multivariate modeling or predictive analysis |

Graph analysis

Sequence Field of view (FOV, mm) Slice thickness (mm) Average Repetition time (TR, ms) Echo time (TE, ms) Resolution Flip angle (°)
axial T2WI TSE 40 1.5 8 3860 62 256×192 150
coronal T2WI TSE 40 1 8 2160 56 128×89.6 120
axial T1WI StarVIBE 60 1.5 2 9 4.38 224×192 130