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Reporting Summary

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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

We employed a 3.0T MRI scanner (Discovery MR750w, General Electric, Milwaukee, WI, USA) equipped with a 24-channel head coil. Bold fMRI data were collected utilizing a gradient echo single-shot echo planar imaging (GRE-SS-EPI) sequence. The imaging parameters were as follows: echo time (TE) = 30ms; repetition time (TR) = 2,000ms; matrix size = 64 x 64; flip angle = 90°; Field of View (FOV) = 220mm x 220mm; slice gap = 1mm; slice thickness = 3mm, 35 interleaved axial slices; 185 volumes; and acquisition time = 6 min 10 s. High-resolution three-dimensional T1-weighted structural images were acquired using the brain volume (BRAVO) sequence with the following parameters: TE = 3.2ms; TR = 8.5ms; Inversion time (TI) = 450ms; matrix size = 256 x 256; flip angle = 12°; FOV = 256 x 256 mm; no gap; slice thickness = 1mm; 188 sagittal slices; acquisition time = 4 min 56 s.

Data analysis

- ① All fMRI image preprocessing was conducted using the MATLAB 2022a platform (Mathworks, Sherborn, MA, USA) along with the RESTplus toolbox (<http://www.restfmri.net/forum>), which implements functions from the Statistical Parametric Mapping (SPM12, <http://www.fil.ion.ucl.ac.uk/spm/software/spm12/>) toolbox.
- ② VBM was performed using the Computational Anatomy Toolbox (CAT12, <http://dbm.neuro.uni-jena.de/cat/>).
- ③ Statistical analysis were conducted using GraphPad Prism 9.5 software (<https://www.graphpad.com/>).

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 datasets generated and/or analyzed during the current study are available from the corresponding author upon reasonable request. Due to ethical and privacy considerations, individual patient imaging and clinical data are not publicly available. However, de-identified aggregate data supporting the findings of this study can be shared with qualified researchers upon request and after approval by the local institutional ethics committee. No third-party datasets were used in this study. This study was approved by the Research Ethics Committee of the First Affiliated Hospital of Anhui Medical University (Approval No: PJ2022-01-12).

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

In this study, we classified participants based solely on biological sex (male and female) without distinguishing between sex and gender. Participants' sex was determined according to physiological characteristics, and informed consent was obtained from all patients for data collection and sharing. AS the study did not include gender-based analyses, we did not consider gender as a variable in the study design. In our study, in order to avoid the interference of sex factor, we have circumvented it as a covariate during the analyses. Finally, the study included 54 DCM patients (female/male = 25/29) and 57 HC (female/male = 28/29).

Reporting on race, ethnicity, or other socially relevant groupings

The participants in our study were all from China and of Han ethnicity. The inclusion and exclusion criteria for patients were applied without any discrimination.

Population characteristics

The study included 54 DCM patients (51.39 +/- 7.44) and 57 HC (50.84 +/- 4.61). Specifically, DCM patients received cervical and brain MRIs, as well as neurological assessments preoperatively and three months postoperatively, whereas HC underwent baseline MRI evaluations. Among the DCM patients, 41 underwent anterior cervical discectomy and fusion (ACDF), 8 received anterior cervical corpectomy and fusion (ACCF), 3 had a combined ACDF and ACCF procedure, and 2 underwent posterior open-door decompression of the cervical vertebral canal.

Recruitment

All DCM patients were recruited from the spine Department of our hospital, while HC were recruited from family members or the community. During the recruitment process, all participants signed informed consent forms.

Ethics oversight

This study was approved by the Research Ethics Committee of the First Affiliated Hospital of Anhui Medical University (Approval No: PJ2022-01-12).

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](https://www.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

In this study, the sample size was determined based on previous literature and similar studies in the field of DCM. We did not perform a formal statistical power calculation, but instead chose an appropriate sample size that was consistent with those used in comparable research. The rationale for this sample was to ensure the study had sufficient power to detect meaningful differences based on the observed effects in the literature. Given the effect sizes reported in prior studies, we believe the sample size is adequate to provide reliable and statistically meaningful results for our analysis.

Data exclusions

The exclusion criteria were as follows: (1) Individuals with a history of alcoholism, smoking, or drug use; (2) Accompanied by severe systemic diseases, such as hypertension, diabetes, heart disease, or history of chronic diseases; (3) Peripheral neuropathy; (4) Claustrophobia; (5) Pregnant women; (6) Presence of MRI-incompatible metal implants in the body. Ultimately, the study included 54 DCM patients and 57 HC.

Replication

To ensure the reproducibility of our experimental findings, we implemented several measures during the study design and analysis phases. First, we followed standardized protocols for data collection, imaging, and analysis, ensuring consistency across all participants' assessments. Second, all data processing steps, including statistical analysis and neuroimaging techniques, were performed using widely accepted methods.

and software with documented reliability.

We also conducted internal validation by performing repeat analysis on a subset of the data, which confirmed the consistency of the results. In terms of replication, all attempts to reproduce the key findings, including functional and structural changes in the brain following cervical decompression surgery, were successful. No findings were identified that could not be reproduced.

Randomization

In this study, participants were not randomly allocated into experimental groups. Instead, they were assigned based on clinical criteria, specifically individuals diagnosed with DCM who were scheduled for cervical decompression surgery. The control group consisted of healthy individuals matched for age, sex, and other relevant demographic factors to minimize confounding variables. TO control for potential covariates, these covariates were carefully considered during the statistical modeling to ensure that observed effects were not biased by these factors. Given the nature of the study, random allocation was not feasible due to the clinical and surgical requirements of the DCM cohort. However, the matching process and statistical controls were designed to minimize bias and ensure robust comparisons between the DCM and control groups.

Blinding

In this study, blinding during data collection and analysis was not possible due to the nature of the research. Participants were diagnosed with DCM and underwent cervical decompression surgery, which inherently made it clear which group they belonged to. As a result, the investigators involved in the data collection were aware of group allocation.

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

Methods

- 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

- n/a Involved in the study
- ☒ ☐ ChIP-seq
- ☒ ☐ Flow cytometry
- ☐ ☒ MRI-based neuroimaging

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

This study has been submitted for registration with the Chinese Clinical Trial Registry (ChiCTR). Due to time constraints, the registration number has not been assigned yet. Once the registration is completed and the number is issued, we will provide the trial registration number as an update.

Study protocol

The full trial protocol is currently not publicly available. This is because the trial has not yet been registered with the clinical trial registry, and the protocol is still under review. Once the trial is officially registered and the protocol is finalized, we will make it available upon request or provide a link to the registry where it can be accessed.

Data collection

Data collection for this study took place at the First Affiliated Hospital of Anhui Medical University in Hefei/China. The data were collected between 2022 and 2024, corresponding to the recruitment and treatment period for the participants diagnosed with DCM. The clinical assessments, neuroimaging (e.g., MRI), and follow-up evaluations were conducted at the hospital, while all analysis were performed in a dedicated research lab. Given the clinical nature of the study, data collection occurred in a controlled medical environment to ensure accurate diagnosed and standardized procedures. Participants underwent preoperative and postoperative assessments, with follow-up evaluations conducted at three months post-surgery.

Outcomes

In this study, the primary and secondary outcome measures were pre-defined based on the study objectives and relevant clinical endpoints.

Primary Outcome Measure: The primary outcome of this study was the changes in brain function and structure following cervical decompression surgery in patients with DCM. This was assessed using three key measure:

1. zALFF from resting-state fMRI to evaluate function brain activity in specific regions.
2. FC: we measured the brain's FC using seed-based analysis, focusing on networks relevant to sensory and processing. These were compared between pre- and post-surgery scans.
3. GMV changes in key brain regions assessed via structural MRI to investigate structural remodelling.

Secondary Outcome Measures:

Clinical Neurological Function: This was assessed using standard clinical scales such as the mJOA score, which administered before and after surgery.

Plants

Seed stocks	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.
Novel plant genotypes	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.
Authentication	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.

Magnetic resonance imaging

Experimental design

Design type	In this study, resting-state fMRI was used to assess brain function, specifically focusing on the zALFF and FC in various brain regions associated with sensory and motor processing. Resting-state fMRI allows for the evaluation of brain activity in the absence of a specific task, providing insights into spontaneous neural fluctuations. No task-based paradigms were used in this study; instead, we focused on resting-state data to investigate the baseline brain activity and its changes post-surgery.
Design specifications	As this study utilized resting-state fMRI, there were no specific or trials as seen in task-based fMRI designs. Instead, participants underwent resting-state scans where they were instructed to remain still with their eyes closed, minimizing external stimulation, for the duration of the scan. Each resting-state scan lasted approximately 6-8 minutes, during which data were collected continuously. There were no intervals between trials, as there was no explicit task; rather, the focus was on the natural, spontaneous fluctuations in brain activity. In total, two resting-state sessions were conducted per participant: one at baseline (preoperative) and one at the 3-month follow-up (postoperative). These sessions provided data for the analysis of functional brain activity and connectivity changes over time.
Behavioral performance measures	Neurological function was evaluated using the mJOA score, where lower scores indicate greater neurological impairment.

Acquisition

Imaging type(s)	1. Function MRI (fMRI): we employed resting-state fMRI to assess brain function, specifically measuring zALFF and FC. There variables provided insights into spontaneous brain activity and connectivity between brain regions associated with motor and sensory processing. 2. Structural MRI: we used structural MRI to measure GMV changes in key brain regions. These measurements allowed us to evaluate structural remodelling following cervical decompression surgery.
Field strength	3.0T
Sequence & imaging parameters	1. BOLD fMRI data were collected utilizing a gradient echo single-shot echo planar imaging (GRE-SS-EPI) sequence. The imaging parameters were as follows: echo time(TE) = 30ms; repetition time(TR) = 2,000ms; matrix size = 64 x 64; flip angle = 90°; Field of VIEW (FOV) = 220mm x 220mm; slice gap = 1mm; slice thickness = 3mm, 35 interleaved axial slices; 185 volumes; and acquisition time = 6 min 10 s. 2. High-resolution three-dimensional T1-weighted structural images were acquired using the brain volume (BRAVO) sequence with the following parameters: TE = 3.2ms; TR = 8.5ms; Inversion time (TI) = 450ms; matrix size = 256 x 256; flip angle = 12°; FOV = 256 x 256mm; no gap; slice thickness = 1mm; 188 sagittal slices; acquisition time = 4 min 56 s.
Area of acquisition	whole brain scan was used
Diffusion MRI	☐ Used ☒ Not used

Preprocessing

Preprocessing software	All fMRI image preprocessing was conducted using the MATLAB 2022a platform (Mathworks, Sherborn, MA, USA) along with the RESTplus Toolbox (http://www.restfmri.net/forum), which implements functions from the Statistical Parametric Mapping (SPM12, http://www.fil.ion.ucl.ac.uk/spm/software/spm12/) toolbox. The data preprocessing steps are as follows: (1) The first 10 time points of the time series were removed to reduce the impact of magnetic field instability during the initial scanning period; (2) Slice timing correction was applied to the functional images to correct for temporal offsets between different slices; (3) Motion correction was performed to exclude subjects with head movement parameters exceeding 3 mm or 3° in the X, Y, or Z axis; (4) Images were registered to MNI standard space using DARTEL registration techniques. Resampled to 3 x 3 x 3 mm; (5) Smoothing was applied using a Gaussian kernel with full-width half-maximum (FWHM) = 6 mm; (6) Confounding covariates (including head motion parameters, white matter signals, and cerebrospinal fluid signals)
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were removed from the regression calculations, and linear drift was also removed.

VBM was performed using the Computational Anatomy Toolbox (CAT12, <http://dbm.neuro.uni-jena.de/cat/>). Preoperative and postoperative T1-weighted scan data were preprocessed through CAT12's longitudinal preprocessing pipeline. This tool is integrated within SPM12 (<http://www.fil.ion.ucl.ac.uk/spm/software/spm12/>) and employs a projected thickness approach to automatically measure cortical thickness (CT) and the central surface of the cerebral hemispheres. Previous studies have demonstrated that CAT12 reliably and accurately estimates the GMV and CT. The preprocessing of the VBM data was conducted using default parameter settings were used, including realignment, bias correction, tissue classification, and spatial normalization with the AAL3 brain atlas template. The images were segmented into gray matter, white matter, and cerebrospinal fluid, and subsequently smoothed using an 8 mm full-width at half maximum (FWHM) Gaussian kernel. The data were normalized to the Montreal Neurological Institute (MNI) space, and the total intracranial volume (TIV) was calculated. The gray matter volume (GMV) was calculated through the modulation of gray matter tissue probability maps with the nonlinear deformation field in the normalization procedure. Subsequently, separate quality control measures were implemented, comprising visual inspection and outlier identification via the homogeneity checking function in CAT12 (<http://dbm.neuro.uni-jena.de/cat/>), to verify that all data were devoid of artifacts and abnormal brain structures. CAT12 is a neuroimaging analysis toolkit developed on the SPM platform, specifically designed for the processing of structural MRI (sMRI) data. This toolkit provides a comprehensive array of features that facilitate rapid and efficient brain morphometric analysis, as well as investigations into structural-functional connectivity 7, 8. Finally, employing the general linear models and algorithms available in the SPM12 software (<http://www.fil.ion.ucl.ac.uk/spm/software/spm12/>), we conducted intergroup two-sample t-tests and intragroup paired sample t-tests. Age, sex, education, and TIV were incorporated as covariates in the analysis.

Normalization

In the preprocessing pipeline of this study, the normalization step was performed using the standard procedures implemented in the RESTplus toolbox. Specifically, each participant's functional images were first realigned to their corresponding T1-weighted structural images. Subsequently, the images were normalized to the Montreal Neurological Institute (MNI) standard space using DARTEL, with voxel resampling to a resolution of 3×3×3 mm³. This step ensured spatial consistency of brain images across subjects, providing a standardized basis for subsequent group-level comparisons and statistical analyses.

Normalization template

DARTEL template

Noise and artifact removal

During fMRI data preprocessing, we employed the RESTplus toolbox to standardize the removal of noise and artifacts, thereby ensuring signal stability and reliability. The specific steps were as follows:

1. Slice timing correction and realignment were performed to eliminate temporal and spatial artifacts arising from inter-slice acquisition delays and minor head movements during scanning.
2. Nuisance regression was conducted to remove physiological noise and non-neuronal confounds by regressing out head motion parameters (Friston-24 model), white matter signals, cerebrospinal fluid (CSF) signals, and global brain signals.
3. Linear trend removal and temporal band-pass filtering (0.01–0.08 Hz) were applied to retain typical low-frequency BOLD fluctuations and suppress high-frequency noise.
4. Functional images were normalized to the Montreal Neurological Institute (MNI) space and spatially smoothed using a 6 mm full-width at half-maximum (FWHM) Gaussian kernel to enhance the signal-to-noise ratio and mitigate inter-individual anatomical variability.

Volume censoring

Although we did not apply a volume-scrubbing approach in the present study, we rigorously controlled for head motion artifacts. Specifically, motion correction was performed to exclude participants whose translational or rotational movements exceeded 3 mm or 3° in any of the X, Y, or Z axes. During preprocessing, we implemented Friston-24 head motion parameter regression, temporal detrending, and low-pass filtering to minimize the impact of motion-related artifacts. In future studies, we plan to incorporate volume censoring strategies to further enhance robustness against motion-related confounds.

Statistical modeling & inference

Model type and settings

Statistical analyses of the fMRI data were performed using SPM12. At the first-level analysis, a general linear model (GLM) was employed to model task-related brain activity. The following indicators such as ALFF and FC are calculated using RESTplus tools. Our analysis accounted for covariates including age, sex at birth, years of education, and TIV.

Effect(s) tested

1. We tested the main effect of time (pre-operative vs post-operative) in patients with cervical spondylotic myelopathy (CSM), using a within-subject paired design to assess longitudinal changes in brain activity/connectivity.
2. We tested the main effect of group (CSM vs healthy controls), aiming to identify brain regions showing significant differences in functional metrics (e.g., ALFF, ReHo, FC) between patients and controls.

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

Statistic type for inference

We concentrated on assessing the zALFF, FC, and GMV across all brain regions

(See [Eklund et al. 2016](#))

Correction

FDR/FWE

Models & analysis

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

Functional and/or effective connectivity

We used the seed-to-voxel correlation to calculate the FC values between the seed regions and the whole brain. FC maps were generated by assessing the linear correlations between the seed regions and other brain voxels, with Fisher's z transformation applied to obtain zFC maps for further group-level analysis. Seeds were selected from zALFF clusters that exhibited significant differences either intergroup or intragroup differences, and the relevant calculations were performed using the RESTplus toolbox for subsequent clinical analyses.