nature portfolio

Corresponding author(s): DBPR NCOMMS-23-59187B

Last updated by author(s): 2024.08.30

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	Bulk transcriptome data were derived from the publicly accessible dataset GSE52093 from GEO database.
Data analysis	R package Seurat was used for cell filtration, normalization, principal component analysis, variable genes finding, clustering analysis, and Uniform Manifold Approximation. The integrated analysis was performed using the Scissor algorithm.

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 data of single-cell RNA transcriptome data has been deposited in the GEO database with the accession code GSE254132. Proteome data is available from MassIVE with accession code MSV000093736. Requests for custom code can be directed to the corresponding authors, and the code will be provided within 30 days and without restrictions.

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	Our study included both male and female subjects. We ensured balanced representation of sexes in our experimental design and accounted for potential sex-based differences in our analysis.
Reporting on race, ethnicity, or other socially relevant groupings	Our study included only Asian subjects. As a result, the findings may be most applicable to Asian populations, and caution should be exercised when generalizing to other racial or ethnic groups.
Population characteristics	Our study population consisted of Asian subjects, including both male and female participants. The age range of the subjects was 46-57 year-old. Patients were included if they were diagnosed with complicated type B AD, which was confirmed through computed tomography angiography (CTA) and had signed informed consent for TEVAR. Detailed demographic and clinical characteristics are provided in Supplementary Tables.
Recruitment	We prospectively collected and analyzed the clinical data of patients with type B aortic dissection who underwent endovascular therapy in the Zhongshan Hospital of Fudan University between November 2016 and November 2020. Patients were included if they were diagnosed with complicated type B AD, which was confirmed through computed tomography angiography (CTA) and had signed informed consent for TEVAR. Patient demographics and baseline information were recorded by medical record. The blood samples were collected before TEVAR.
Ethics oversight	This study was approved by the Ethics Committee of Zhongshan Hospital of Fudan University (IRB number B2019-231R). Healthy normal aortas and dissected aortas were collected from participants with informed written consent, and under approval of local medical ethnics from Zhongshan Hospital Fudan 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	The sample size of n = 12 per group was determined based on a power analysis conducted using GPower. The analysis was designed to detect a disease incidence with a power of 0.8 and a two-sided significance level of 0.05.
Data exclusions	No data were excluded from analyses.
Replication	All experiments were conducted using standardized protocols to ensure consistency across all groups. Detailed protocols were followed for animal handling, treatment administration, data collection, and analysis.
Randomization	Animals were randomly assigned to experimental groups using a computer-generated random number sequence to ensure unbiased allocation. The randomization was stratified by weight to balance this variable across groups.
Blinding	To reduce bias, experiments were conducted in a blinded manner. Researchers responsible for data collection and analysis were unaware of the group allocations during the study.

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
[ ]	[x] Antibodies
[ ]	[ ] Eukaryotic cell lines
[ ]	[ ] Palaeontology and archaeology
[ ]	[x] Animals and other organisms
[ ]	[x] 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

Human aortic tissue samples were then permeabilized and stained with rabbit MPO antibody (ab208670, Abcam, Ltd., Cambridge, UK) at 1 mg/mL, polyclonal rabbit CitH3 antibody (ab5103, Abcam, Ltd., Cambridge, UK) at 1 mg/mL, rabbit CXCL3 antibody (AV07037, Sigma-Aldrich Co., St. Louis, MO, USA) at 1 mg/mL, and with rabbit CXCR2 antibody (ab225732, Abcam, Ltd., Cambridge, UK) at 1 mg/mL. Mouse aortic tissue samples were then permeabilized and stained with rabbit Ly6G antibody (ab238132, Abcam, Ltd., Cambridge, UK) at 2 mg/mL, rabbit CitH3 antibody (ab5103, Abcam, Ltd., Cambridge, UK) at 1 mg/mL, rabbit CXCL3 antibody (ab220431, Abcam, Ltd., Cambridge, UK) at 1 mg/mL, and with rabbit CXCR2 antibody (bs-12257R, Bioss Inc. Woburn, Massachusetts, USA) at 1 mg/mL.
As for in vivo study, the challenged mice were treated with either isotype control antibody (n = 12) or rabbit CXCL3 antibody (2 mg/kg, AF5568, R&D systems, Minneapolis, MN, USA) (n = 12) or CXCR2 antibody (2 mg/kg, MAB2164-100, R&D systems, Minneapolis, MN, USA) (n = 12)

Validation

The primary antibody used in this study was validated for its specificity in mouse through western blot analysis, which confirmed specific binding and no cross-reactivity with other proteins. The antibody was validated for use in immunohistochemistry by testing on tissue sections known to express the target protein and by including appropriate positive and negative controls.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	This study did not utilize any cell lines. All experiments were conducted using animal models and patient samples.
Authentication	This study did not utilize any cell lines.
Mycoplasma contamination	This study did not utilize any cell lines.
Commonly misidentified lines (See ICLAC register)	This study did not utilize any cell lines.

Palaeontology and Archaeology

Specimen provenance	This study did not involve the use of biological specimens that require provenance documentation.
Specimen deposition	This study did not involve the use of biological specimens that require provenance documentation.
Dating methods	This study did not involve the use of biological specimens that require provenance documentation.

[ ] Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight	This study did not involve the use of biological specimens that require provenance documentation.

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	Wild-type C57BL/6J male 3-week-old mice were used in this study and were purchased from the Beijing Vital River Laboratory Animal Technology.
Wild animals	The study did not involve wild animals.
Reporting on sex	We focused on male mice since sexual dimorphism has been reported in aortic dissection (AD) formation in humans and mice. In humans, AD has been more prevalent in men than in women. Likewise, in several mouse models, the incidence and severity of aortic

	pathologies are sexually dimorphic, with greater severity in male mice. While no studies have reported sexual dimorphism when β-Aminopropionitrile (BAPN) is administered alone, a few studies have indicated a lower incidence of AD in female mice co-administered BAPN and Angiotensin-II. Taking these factors into consideration, similar to other studies published in top-tier cardiovascular journals, we chose to use male mice for our experiments.
Field-collected samples	The study did not involve samples collected from field.
Ethics oversight	All animal experiments were approved by the Institutional Animal Care and Use Committee at Zhongshan Hospital.

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 ICMJEguidelines for publication of clinical research and a completedCONSORT checklist must be included with all submissions.

Clinical trial registration	This study did not involve a clinical trial. The research was conducted using observational studies.
Study protocol	This study did not involve a clinical trial. The research was conducted using observational studies.
Data collection	This study did not involve a clinical trial. The research was conducted using observational studies.
Outcomes	This study did not involve a clinical trial. The research was conducted using observational studies.

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	This study did not involve the use of seed stocks.
Novel plant genotypes	This study did not involve the use of seed stocks.
Authentication	This study did not involve the use of seed stocks.

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 *May remain private before publication.*	This study did not involve the use of CHIP-seq.
Files in database submission	This study did not involve the use of CHIP-seq.
Genome browser session (e.g. UCSC)	This study did not involve the use of CHIP-seq.

Methodology

Replicates	This study did not involve the use of CHIP-seq.
Sequencing depth	This study did not involve the use of CHIP-seq.
Antibodies	This study did not involve the use of CHIP-seq.
Peak calling parameters	This study did not involve the use of CHIP-seq.
Data quality	This study did not involve the use of CHIP-seq.
Software	This study did not involve the use of CHIP-seq.

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	This study did not involve the use of flow cytometry.
Instrument	This study did not involve the use of flow cytometry.
Software	This study did not involve the use of flow cytometry.
Cell population abundance	This study did not involve the use of flow cytometry.
Gating strategy	This study did not involve the use of flow cytometry.

☐ 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	This study did not involve the use of magnetic resonance imaging.
Design specifications	This study did not involve the use of magnetic resonance imaging.
Behavioral performance measures	This study did not involve the use of magnetic resonance imaging.

Acquisition

Imaging type(s)	This study did not involve the use of magnetic resonance imaging.
Field strength	This study did not involve the use of magnetic resonance imaging.
Sequence & imaging parameters	This study did not involve the use of magnetic resonance imaging.
Area of acquisition	This study did not involve the use of magnetic resonance imaging.

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software	This study did not involve the use of magnetic resonance imaging.
Normalization	This study did not involve the use of magnetic resonance imaging.
Normalization template	This study did not involve the use of magnetic resonance imaging.
Noise and artifact removal	This study did not involve the use of magnetic resonance imaging.
Volume censoring	This study did not involve the use of magnetic resonance imaging.

Statistical modeling & inference

Model type and settings	This study did not involve the use of magnetic resonance imaging.
Effect(s) tested	This study did not involve the use of magnetic resonance imaging.

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

Statistic type for inference (See Eklund et al. 2016)	This study did not involve the use of magnetic resonance imaging.
Correction	This study did not involve the use of magnetic resonance imaging.

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	This study did not involve the use of magnetic resonance imaging.
Graph analysis	This study did not involve the use of magnetic resonance imaging.
Multivariate modeling and predictive analysis	This study did not involve the use of magnetic resonance imaging.