nature portfolio

Corresponding author(s): DAPR NCOMMS-24-12113B

Last updated by author(s): Jan 26, 2025

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	VisualSonic Vevo 2100 was used for echocardiography data collection and analysis. Immunofluorescent images were acquired using the fluorescence microscope Axio Imager M2 (Carl Zeiss). Real-time PCR data were obtained using the CFX 96Touch Real time Fluorescence Quantitative PCR Instrument (Bio Rad). Confocal microscopy images were captured with Laser confocal microscope FV-500 (Carl Zeiss).
Data analysis	Histology analysis: ImageJ software. Echocardiography analysis:VevoLab software (V3.1.0) Confocal microscopy images were processed using ZEN Microscopy Software software (Carl Zeiss) and Image J software. All statistical analyses and figure preparation were conducted with GraphPad Prism software (v8.0). Data analyses was assisted with Microsoft Excel (Microsoft Office 2019).

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

Al data associated with this study are present in the main text or the, suoplementary materials, Source data are provided with this paper

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	No sex specific-analyses were perfomed. Both sexes were included in the analyses.
Reporting on race, ethnicity, or other socially relevant groupings	No race, ethnicity and other socially relevant specific-analyses were perfomed.
Population characteristics	Clinicopathological characteristics of enrolled patients are presented in Table 1 and 2. Patients in this cohort were stratified according to the baseline tertile of plasma dsDNA levels (Table 1). Diabetes, hscTnT, and dsDNA concentrations were higher in patients with high plasma dsDNA levels, whereas other baseline characteristics were unrelated to dsDNA. During the 1-year clinical follow-up, MACE rate was at the top in patients in the highest peak dsDNA tertile, intermediate in the middle tertile, and the least in the lowest tertile. Moreover, higher peak plasma dsDNA levels were associated with increased risk of all-cause mortality (Table 2).
Recruitment	The present cohort comprised 230 patients diagnosed with STEMI from the General Hospital of Northern Theater Command, Shenyang Liaoning Province, China, between January 2016 and May 2017. Patients were included if they presented with acute chest pain and/or discomfort possibly indicating AMI with symptom onset within 24 h, were older than 18 years and were willing to participate in the study. Exclusion criteria included patients with known active inflammatory or autoimmune diseases, severe heart failure, hemodynamic instability, suspected myocarditis or pericarditis, diseases of the hematopoietic system, known severe kidney or liver disease, known malignancy, use of immunosuppressant agents, and previous coronary artery bypass graft surgery.
Ethics oversight	The written informed consent was obtained from all participants, and the Ethics Committee of General Hospital of Northern Theater Command Hospital approved the study protocols (No. k (2012) 17-1). This study followed the Strengthening the Reporting of Observational Studies in Epidemiology reporting guideline and Declaration of Helsinki.

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

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☒ Life sciences ☐ Behavioural & social sciences ☐ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see nature.com/documents/nr-reporting-summary-flat.pdf

Life sciences study design

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

Sample size	No statistical methods were used to predetermine sample size. Estimates were made based on our previous experience, availabiity and feasilbility required to obtain statistically significant results, This methodology was followed based on previously published research articles, e.g. Nature Communications DOI: s41467-018-04908-2, while complying with the 3Rs rule on reducing, replacing and refining the use of animals for scientific purpose. The simple size (n) for each experiment is provided in the figure legends.
Data exclusions	Data were not excluded from study reporting. Animals who suffered perioperative (same day) death and heart rupture were not included in study reporting.
Replication	Results shown are representative of several independently performed experiments. Each dot in the bar plots indicates a different animal.
Randomization	All studies were performed with randomization when possible. For all in vivo experiments, mice were preselected based on age and then randomly assigned to treatment groups.

Blinding	Investigators performing functional, histological or molecular analysis were blinded to the experimental conditions and to the genotype of the mice.

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 Passer domesticus, all Stenocereus thurberi 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	*Describe the study conditions for field work, providing relevant parameters (e.g. temperature, rainfall).*
Location	*State the location of the sampling or experiment, providing relevant parameters (e.g. latitude and longitude, elevation, water depth).*
Access & import/export	*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).*
Disturbance	*Describe any disturbance caused by the study and how it was minimized.*

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

Western blotting primary antibodies:
1. S100A12 (Abcam, ab37657, 1:1000);
2. Histone H3 (citrulline R2 + R8 + R17) (Abcam, ab5103, 1:1000);
3. Neutrophil Elastase [EPR28386-66](Abcam, ab310335, 1:1000), (Santa cruz, sc-9520, 1:250);
4. Annexin V [EPR3980] (Abcam, ab108194, 1:2000);
5. MPO (CST, #79623, 1:1000);
6. GAPDH (CST, #2118S, 1:5000);
7. ERK1/2 (Proteintech, 11257-1-AP, 1:1000);
8. phospho-ERK1/2 (Thr202/Tyr204) (Proteintech, 28733-1-AP, 1:1000);
9. PAD4 (Proteintech, 17373-1-AP, 1:1000);
10. Cleaved-caspase3 (CST, #9661, 1:1000);
11. Caspase3 (CST, #9662, 1:1000);
12. Bax (CST, #2772, 1:1000);
13. Bcl2 (CST, #4223, 1:1000);
14. CaMKII-α (6G9) (CST, #50049, 1:1000);
15. Phospho-CaMKII (Thr286) (D21E4) (CST, #12716, 1:1000);

Immunostaining primary antibodies:
1. S100A12 (E1032, Sigma-Aldrich, 1:100);
2. Cleaved-caspase3 (Proteintech, 68773-1-Ig, 1:100);
3. Histone H3 (citrulline R2 + R8 + R17) [RM1001] (Abcam, ab281584, 1:100);
4. Ly-6G (E6Z1T) (CST, #87048, 1:100);
5. MPO (Proteintech, 66177-1-Ig, 1:100);
6. ANXA5[1F4-1A5] (Abcam, ab54775, 1:200);
7. α-actinin (Abcam, ab90421, 1:200)

Immunostaining secondary antibodies:
1. Goat anti-rabbit Alexa Fluor-488 (Thermo Fisher Scientific, # A-11008, 2 ug/ml)
2. Goat anti-rabbit Alexa Fluor-594 (Thermo Fisher Scientific, # A-11012, 2 µg/ml)

3. Goat anti-mouse Alexa Fluor-594 (Thermo Fisher Scientific, #A-11005, 2 ug/ml)
4. Goat anti-mouse Alexa Fluor-488 (Thermo Fisher Scientific, #A-11006 2 ug/ml).

Validation

1. S100A12 (Abcam, ab37657, 1:1000); Application: IHC-Fr, WB. Bouvet GF et al. DNA Methylation Regulates RGS2-induced S100A12 Expression in Airway Epithelial Cells. Am J Respir Cell Mol Biol 59:601-613 (2018).
2. Histone H3 (citrulline R2 + R8 + R17) (Abcam, ab5103, 1:1000); Application: PepArr, IP, WB. Meyers S et al. Neutrophils Protect Against Staphylococcus aureus Endocarditis Progression Independent of Extracellular Trap Release. Arterioscler Thromb Vasc Biol 43:267-285 (2023).
3. Neutrophil Elastase [EPR28386-66] (Abcam, ab310335, 1:1000), 1:1000); Application: WB, IHC-P, Flow Cyt (Intra). Knockout validated.
4. Annexin V [EPR3980] (Abcam, ab108194, 1:2000); Application: WB, ICC/IF, Flow Cyt (Intra). Knockout validated. Jiang F et al. Cannabinoid receptor-2 attenuates neuroinflammation by promoting autophagy-mediated degradation of the NLRP3 inflammasome post spinal cord injury. Front Immunol 13:993168 (2022).
5. MPO (CST, #79623, 1:1000); Application: WB. Li T et al. Cellular communication network factor 1 promotes retinal leakage in diabetic retinopathy via inducing neutrophil stasis and neutrophil extracellular traps extrusion. Cell Commun Signal. 2024 May 16;22 (1):275.
6. GAPDH (CST, #2118S, 1:5000); Application: WB, IHC, IF/ICC, Flow Cyt. Park SH et al. Crosstalk between bone metastatic cancer cells and sensory nerves in bone metastatic progression. Life Sci Alliance. 2024 Dec;7(12).
7. ERK1/2 (Proteintech, 11257-1-AP, 1:1000); Application: WB, IHC, IF/ICC, FC (Intra), ELISA. Chen Y et al. Aggresome formation promotes ASK1/JNK signaling activation and stemness maintenance in ovarian cancer. Nat Commun. 2024 Feb 13;15(1):1321.
8. phospho-ERK1/2 (Thr202/Tyr204) (Proteintech, 28733-1-AP, 1:1000); Applications: WB, IP, ELISA. Pan Z et al. Cholesterol promotes EGFR-TKIs resistance in NSCLC by inducing EGFR/Src/Erk/SP1 signaling-mediated ERRα re-expression. Mol Cancer. 2022 Mar 18;21 (1):77.
9. PAD4 (Proteintech, 17373-1-AP, 1:1000); Applications: WB, IHC, IF/ICC, FC (Intra), IP, ELISA. Török S et al. Investigation of H2S Donor Treatment on Neutrophil Extracellular Traps in Experimental Colitis. Int J Mol Sci. 2021 Nov 25;22(23).
10. Cleaved-caspase3 (CST, #9661, 1:1000); Applications: WB, IP, IHC, IF. Geng P et al. HIF-1α-HPRT1 axis promotes tumorigenesis and gefitinib resistance by enhancing purine metabolism in EGFR-mutant lung adenocarcinoma. J Exp Clin Cancer Res. 2024 Sep 30;43(1):269.
11. Caspase3 (CST, #9662, 1:1000); Applications: WB, IP, IHC. Liu J et al. HDAC1 and FOXK1 mediate EGFR-TKI resistance of non-small cell lung cancer through miR-33a silencing. J Transl Med. 2024 Aug 28;22(1):793.
12. Bax (CST, #2772, 1:1000); Applications: WB, IP. Zhang L et al. CRISPR screen of venetoclax response-associated genes identifies transcription factor ZNF740 as a key functional regulator. Cell Death Dis. 2024 Aug 27;15(8):627.
13. Bcl2 (CST, #4223, 1:1000); Applications: WB, IP. Kim Y et al. Discovery of New Anti-Cancer Agents against Patient-Derived Sorafenib-Resistant Papillary Thyroid Cancer. Int J Mol Sci. 2023 Nov 16;24(22).
14. CaMKII-α (6G9) (CST, #50049, 1:1000); Applications: WB, IHC, IF. Xue SG et al. Enhanced TARP-γ8-PSD-95 coupling in excitatory neurons contributes to the rapid antidepressant-like action of ketamine in male mice. Nat Commun. 2023 Dec 2;14(1):7971.
15. Phospho-CaMKII (Thr286) (D21E4) (CST, #12716, 1:1000); Applications: WB. Xue SG et al. Enhanced TARP-γ8-PSD-95 coupling in excitatory neurons contributes to the rapid antidepressant-like action of ketamine in male mice. Nat Commun. 2023 Dec 2;14 (1):7971.
16. S100A12 (E1032, Sigma-Aldrich, 1:100); Application: IHC, WB.
17. Cleaved-caspase3 (Proteintech, 68773-1-Ig, 1:100); Applications: WB, IHC, IF/ICC, FC (Intra), IP, ELISA. Chen Y et al. Structural Characterization and Anti-breast Cancer Activity in vitro of a Novel Polysaccharide from Cymbopogon citratus. Front Nutr. 2022; 9: 911838.
18. Histone H3 (citrulline R2 + R8 + R17) [RM1001] (Abcam, ab281584, 1:100); Applications: IP, PepArr, ICC/IF, Flow Cyt (Intra), WB, Dot blot. Luo X et al. PAD4-dependent citrullination of nuclear translocation of GSK3β promotes colorectal cancer progression via the degradation of nuclear CDKN1A. Neoplasia 33:100835 (2022).
19. Ly-6G (E6Z1T) (CST, #87048, 1:100); Applications: WB, IHC. Guo Y et al. Nanomedicine-based co-delivery of a calcium channel inhibitor and a small molecule targeting CD47 for lung cancer immunotherapy. Nat Commun. 2023 Nov 11;14(1):7306.
20. MPO (Proteintech, 66177-1-Ig, 1:100); Applications: WB, IHC, IF-P, ELISA. Li T et al. Fasting-mimicking diet alleviates inflammatory pain by inhibiting neutrophil extracellular traps formation and neuroinflammation in the spinal cord. Cell Commun Signal. 2023 Sep 21;21(1):250.
21. ANXA5[1F4-1A5] (Abcam, ab54775, 1:200); Applications: IP, WB, ICC/IF, IHC-P, Flow Cyt. Martínez-Lagunas K et al. In vivo detection of programmed cell death during mouse heart development. Cell Death Differ 27:1398-1414 (2020).
22. α-actinin (Abcam, ab90421, 1:200); Applications: WB, ICC/IF, IHC-P. Feng Y et al. OSMR deficiency aggravates pressure overload-induced cardiac hypertrophy by modulating macrophages and OSM/LIFR/STAT3 signalling. J Transl Med 21:290 (2023).
23. Goat anti-rabbit Alexa Fluor-488 (Thermo Fisher Scientific, #A-11008, 2 ug/ml); immunofluorescence analysis of many tissues using this antibody has been reported on the manufacturer website (https://www.thermofisher.cn/cn/zh/antibody/product/Goat-anti-Rabbit-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-11008).
24. Goat anti-rabbit Alexa Fluor-594 (Thermo Fisher Scientific, # A-11012, 2 µg/ml); immunofluorescence analysis of many tissues using this antibody has been reported on the manufacturer website (https://www.thermofisher.cn/cn/zh/antibody/product/Goat-anti-Rabbit-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-11012).
25. Goat anti-mouse Alexa Fluor-594 (Thermo Fisher Scientific, #A-11005, 2 ug/ml); immunofluorescence analysis of many tissues using this antibody has been reported on the manufacturer website (https://www.thermofisher.cn/cn/zh/antibody/product/Goat-anti-Mouse-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-11005)
26. Goat anti-mouse Alexa Fluor-488 (Thermo Fisher Scientific, #A-11006 2 ug/ml); immunofluorescence analysis of many tissues using this antibody has been reported on the manufacturer website (https://www.thermofisher.cn/cn/zh/antibody/product/Goat-anti-Rat-IgG-H-L-Cross-Adsorbed-Secondary-Antibody-Polyclonal/A-11006).

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	HL-60:National Collection of Authenticated Cell Cultures HL-1: National Collection of Authenticated Cell Cultures 293T:National Collection of Authenticated Cell Cultures
Authentication	Referred to the manufacturer's website.
Mycoplasma contamination	All cells tested negative for mycoplasma contamination.
Commonly misidentified lines (See ICLAC register)	No misidentified line was used in this study.

Palaeontology and Archaeology

Specimen provenance	*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.*
Specimen deposition	*Indicate where the specimens have been deposited to permit free access by other researchers.*
Dating methods	*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.*

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

Ethics oversight	*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.*

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	Transgenic mice were purchased from Nanjing GemPharmatech Co., LTD. All mice were 8-12 weeks of age at the time of experimentation. Under approval from the Ethics Committee of General Hospital of Northern Theater Command Hospital, all mice were housed in 12:12 light:dark cycles at room temperatures ranging between 20~24 degrees and humidities between 40~60%. Food and water were available ad ibitum to the mice. Regular diet (BARASTOc) was provided. All animals displayed normal behaviour directly after recovery from anaesthesia. At any significant sign of distress or at the end of the experiments,animals were euthanized by cervical vertebra dislocation or isoflurane anesthesia.
Wild animals	No wild animals were used.
Reporting on sex	Male mice were used for surgeries in this study. Female mice would have provided further insight on the gender differences in response to the treatment. However, due to consistency and to ensure that the treatment variabilities are not due to gender differences we chose to utilize only male mice for surgery.
Field-collected samples	No field-collected samples used.
Ethics oversight	Animal experiments were performed in accordance with guidelines and protocols approved by the Ethics Committee of General Hospital of Northern Theater Command Hospital (No. 2022-17).

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	None

Study protocol	The experiment using patients' plasma samples was approved by theEthics Committee of General Hospital of Northern Theater Command Hospital. All patients provided written informed consent for the use of anonymized samples and the publication of the clinical information in accordance with the Declaration of Helsinki.
Data collection	The clinical information of patients was collected through the medical record. Blood samples were obtained at the time of arrival at the emergency department for all patients. Plasma S100A12 levels were detected using ELISA, and hscTnT, CK-MB and hs-CRP levels were detected respectively. Three independent cardiologists reviewed all available medical records. AMI was defined in accordance with current guidelines and required a typical rise and fall in cardiac biomarkers (troponins and/or CK-MB) with ECG evolution. STEMI was differentiated from NSTEMI by the presence of ST-segment elevation in at least two contiguous leads or true posterior infarction with anterior ST-segment depression.
Outcomes	All confirmed STEMI patients were followed via telephone or outpatient clinic visits at 6 months and 1 year after discharge. The primary outcome was major adverse cardiac and cerebral events (MACCE) at 1 year, a composite of all-cause death, repeat myocardial infarction (MI), stroke, or hospitalization for heart failure. Major secondary outcomes were the individual components of MACCE. MI was defined according to the Third Universal Definition of Myocardial Infarction. Stroke was defined as acute focal dysfunction of the brain, retina, or spinal cord lasting longer than 24 h, or of any duration if focal infarction or hemorrhage was confirmed by neuro-imaging. All clinical events were adjudicated by physicians blinded to the biomarker analysis results.

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	No seed stocks and other plant materials were used in this study
Novel plant genotypes	No samples of any novel plant genotypes were used in this study.
Authentication	No seed stocks were used and novel plant genotypes were generated in this study.

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.*	*For "Initial submission" or "Revised version" documents, provide reviewer access links. For your "Final submission" document, provide a link to the deposited data.*
Files in database submission	*Provide a list of all files available in the database submission.*
Genome browser session (e.g. UCSC)	*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.*

Methodology

Replicates	*Describe the experimental replicates, specifying number, type and replicate agreement.*
Sequencing depth	*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.*
Antibodies	*Describe the antibodies used for the ChIP-seq experiments; as applicable, provide supplier name, catalog number, clone name, and lot number.*
Peak calling parameters	*Specify the command line program and parameters used for read mapping and peak calling, including the ChIP, control and index files used.*
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	*Describe the sample preparation, detailing the biological source of the cells and any tissue processing steps used.*
Instrument	*Identify the instrument used for data collection, specifying make and model number.*
Software	*Describe the software used to collect and analyze the flow cytometry data. For custom code that has been deposited into a community repository, provide accession details.*
Cell population abundance	*Describe the abundance of the relevant cell populations within post-sort fractions, providing details on the purity of the samples and how it was determined.*
Gating strategy	*Describe the gating strategy used for all relevant experiments, specifying the preliminary FSC/SSC gates of the starting cell population, indicating where boundaries between "positive" and "negative" staining cell populations are defined.*

☐ 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)

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

Functional and/or effective connectivity

Report the measures of dependence used and the model details (e.g. Pearson correlation, partial correlation, mutual information).

Graph analysis

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.).

Multivariate modeling and predictive analysis

Specify independent variables, features extraction and dimension reduction, model, training and evaluation metrics.