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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 *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	no software was used
Data analysis	no software was used

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 during and/or analysed during the current study are available from Bin Lv on reasonable request.

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	There is no specific reporting of gender in the manuscript. Only clinical samples were collected from gender-diverse populations, including 52 men and 38 women. All disclosures were made with patient consent
Reporting on race, ethnicity, or other socially relevant groupings	no reporting
Population characteristics	The inclusion criteria were as follows: confirmed diagnosis of AMI based on clinical, electrocardiographic, and echocardiographic findings, and biochemical features of the disease. The exclusion criteria were as follows: statin or anti-inflammatory drug therapy prior to AMI; diseases affecting the detection of inflammatory indicators, such as oncological, inflammatory, autoimmune, and infectious diseases during exacerbation; and prolonged treatment with corticosteroids.
Recruitment	Participants were recruited from the outpatient and inpatient departments of Tianjin Chest Hospital. All the participants enrolled in this clinical trial comprehensively understood the study procedures and signed an informed consent form. For the researchers, recruitment is blinding
Ethics oversight	The study was approved by the Medical Ethics Review Committee of Tianjin Chest Hospital, China (ethics approval number: 2022LW-007).

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	ased on the sample size estimation of the power test, determine the important parameters such as effect size and standard deviation, as well as the death of experimental animals, estimate the sample size and ensure that each group is included in the statistics n=9. The animal experiments followed The ARRIVE Guidelines.
Data exclusions	No data were excluded from the analysis.
Replication	We rehearsed several times and all attempts at replication were successful.
Randomization	Samples were randomly assigned to experimental groups.
Blinding	The investigators were blinded to group allocation during data collection and analysis.

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	anti-Cleaved caspase 3 (9664s, Cell signaling technology, MA, USA), anti-GCN5L2 (3305s, CST, MA, USA), anti-Histone H3 (4499s, CST, MA, USA), anti- Acetyl Histone H3 (Lys 9) (9649s, CST, MA, USA) and anti-β-actin (4970s, CST, MA, USA)
Validation	anti-Cleaved caspase 3 : Western blot analysis of extracts from C6 (rat), NIH/3T3 (mouse), and Jurkat (human) cells, untreated or treated with staurosporine #9953 (1uM, 3hrs) or etoposide #2200 (25uM, 5hrs) as indicated, using Cleaved Caspase-3 (Asp175) (5A1E) Rabbit mAb. Cleaved Caspase-3 (Asp175) (5A1) Rabbit mAb detects endogenous levels of the large fragment (17/19 kDa) of activated caspase-3 resulting from cleavage adjacent to Asp175. This antibody does not recognize full length caspase-3 or other cleaved caspases. Non-specific labeling may be observed by immunofluorescence in specific sub-types of healthy cells in fixed-frozen tissues (e.g. pancreatic alpha-cells). Cytoplasmic background may be observed in human and monkey samples.Species Reactivity: Human, Mouse, Rat, Monkey anti-GCN5L2 :Western blot analysis of extracts from various cell lines using GCN5L2 (C26A10) Rabbit mAb. GCN5L2 (C26A10) Rabbit mAb detects endogenous levels of total GCN5L2 protein. The antibody does not cross-react with the related PCAF protein. Species Reactivity:Human, Mouse, Rat, Monkey anti-Histone H3:Western blot analysis of extracts from various cell lines using Histone H3 (D1H2) XP® Rabbit mAb. Histone H3 (D1H2) XP® Rabbit mAb detects endogenous levels of total Histone H3 protein, including isoforms H3.1, H3.2, and H3.3. This antibody also detects the Histone H3 variant CENP-A. This antibody does not cross-react with other core histones. Species Reactivity: Human, Mouse, Rat, Monkey anti- Acetyl Histone H3 (Lys 9) :Western blot analysis of lysates from HeLa and NIH/3T3 cells, untreated or TSA-treated (400 nM for 18 hours) using Acetyl-Histone H3 (Lys9) (C5B11) Rabbit mAb. Acetyl-Histone H3 (Lys9) (C5B11) Rabbit mAb detects endogenous levels of histone H3 only when acetylated on Lys9. This antibody does not cross-react with other acetylated histones. Species Reactivity: Human, Mouse, Rat, Monkey, Zebrafish anti-β-actin : Western blot analysis of recombinant Actin isoforms using β-Actin (13E5) Rabbit mAb (upper) and Pan-Actin Antibody #4968 (lower). β-Actin (13E5) Rabbit mAb detects endogenous levels of total β-actin protein. Depsite the high sequence identity between the cytoplasmic actin isoforms, β-actin and cytoplasmic γ-actin, β-Actin (13E5) Rabbit mAb #4970 does not cross-react with cytoplasmic γ-actin, or any other actin isoforms. Species Reactivity: Human, Mouse, Rat, Monkey, Bovine, Pig

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	Primary rat myocardial cells were obtained by the laboratory.
Authentication	ALL cell lines were authenticated using cell line STR genotyping.
Mycoplasma contamination	All cell lines tested negative for mycoplasma contamination
Commonly misidentified lines (See ICLAC register)	No misidentified cell lines

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	Male Sprague-Dawley rats (6-8 weeks) of body weights of 240–270 g; KAT2A-/- mice of body weights of 25-30 g
Wild animals	The study did not involve wild animals.
Reporting on sex	In this study, the sex of the animals had no effect on the experimental results, and in the previous studies on AMI, there were no specific requirements for the gender, and animals of different genders could be used as research objects. Therefore, half-male and half-female mice were chosen. We did not collect data on animals of different genders, because it has been confirmed in previous studies that gender has no effect on AMI.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	This study was reviewed by the Animal Experimental Ethics Committee of the Tianjin University of Traditional Chinese Medicine (ethics approval number: TCM-LAEC2019045).

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

Plants

Seed stocks	N/A
Novel plant genotypes	N/A
Authentication	N/A

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	Immune cells in the blood, spleen, and heart were collected 3, 5, and 7 days after AMI and analyzed by flow cytometry. Blood was collected by ocular blood sampling, placed in an EP tube filled with 3 mg/ml heparin sodium, lysed with red blood cell lysis buffer, and stained with immunity antibodies. The fresh spleen and left ventricle were cut into small pieces and washed with cold PBS. The cellular suspension was prepared using the Multi Tissue Dissociation Kit 2, and was subsequently lysed with erythrocytic lysate and colored with immune cell antibodies. The suspension of colored cells was analyzed for cell populations using flow cytometry, and the results were analyzed using FlowJo. The following fluorochrome-labeled anti-mouse antibodies were used for flow cytometry analysis: anti-CD115 (CSF-1R, 135524); anti-Ly-6G (127614); anti-Ly-6C (128008); anti-F4/80 (123128); anti-CD11b (101206). All antibodies were purchased from BioLegend (San Diego, CA). Cells were washed in PBS, resuspended in 500 µl of ANX-V binding buffer and then stained with 5 µl of Annexin-V-fluorescein isothiocyanate (FITC) for 15 min on ice in the dark, according to the manufacturers instructions. Subsequent to staining, the cells were incubated with 10 µl of propidium iodide (PI) for 5 min on ice in the dark.
Instrument	BD FACS AriaIII
Software	FlowJo
Cell population abundance	total immune cells and other cell populations were isolated by CD45 antibody, so that the obtained cell populations were immune cells. Then the immune cell subsets were isolated by different antibodies
Gating strategy	Blank control: No staining control can help determine the location of negative population at voltage; Isotype control: An antibody with the same subtype and fluorescence as the antibody, which helps to identify non-specific binding of the antibody; FMO control: Fluorescence minus one control, that is, one fluorescent antibody is reduced, and other fluorescent antibodies are added to the control, to help identify the positive cell location. In addition, CD45 and SSC markers were used to identify immune cells and remove debris and dead cells. First level gating was completed by loose shot (FSC/SSC) according to cell size and particle size. Subsequently, specific cell populations were isolated using specific population gates and visualized by compensation.

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