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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 <u>Editorial Policies</u> and the <u>Editorial Policy Checklist</u>.

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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> value noted Give <i>P</i> 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						
\square Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated						
Our web collection on <u>statistics for biologists</u> contains articles on many of the points above.						
Software and code						
Policy information about <u>availability of computer code</u>						
Data collection No code was used.						
a analysis All statistical analyses were conducted with GraphPad Prism (version 9.0; GraphPad Software).						
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 <u>availability of data</u> All manuscripts must include a <u>data availability statement</u> . 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

Provide your data availability statement here.

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Research	involving	human	narticir	nants	their	data	or l	aiole	gical	mate	ria
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,		with <u>human participants or human data</u> . See also policy information about <u>sex, gender (identity/presentation),</u> thnicity and racism.		
Reporting on sex	and gender	The sex of the participants was reported as a number and percentage of the total number of participants. The sex and birth gender was based on self-reporting.		
Reporting on race other socially relegroupings		All participants are asian-pacific.		
healthy as		All participants were included with age between 28 years to 65 years. Other than CKD, the participants were otherwise healthy as determined by the investigator or medically qualified designee based on a medical evaluation including medical history, physical examination, and laboratory tests.		
		The participants were recruited from the clinical sites using a combination of internal database searching and advertising as needed. The participant selection was based on strict inclusion/exclusion criteria that were prespecified in the protocol.		
Ethics oversight	Human sample collection for research was conducted in accordance with the recognized ethical guideline of Decla Helsinki.			
Note that full informa	tion on the appr	oval of the study protocol must also be provided in the manuscript.		
	_			
Field-spe	cific re	porting		
Please select the or	ne below that is	s the best fit for your research. If you are not sure, read the appropriate sections before making your selection.		
X Life sciences	В	ehavioural & social sciences		
For a reference copy of th	ne document with	all sections, see <u>nature.com/documents/nr-reporting-summary-flat.pdf</u>		
_				
_ife scien	ices stu	udy design		
All studies must disc	close on these	points even when the disclosure is negative.		
Sample size		ethods were used to pre-determine sample size, but our sample sizes are similar to those reported in previous publications 67) and based on internal historical studies/data.		
Data exclusions	No data were excluded from analysis.			
Replication	All data are rep	roduced in n>=3 independent experiments.		
Randomization		nanually sorted so that there was no statistically significant differences in sorting parameters prior to study start. No program termine group size, this was based on internal historical studies/data.		
Blinding	Investigators w	ere not blinded.		
Reporting	g tor sp	pecific materials, systems and methods		
		about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each materia your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.		
Materials & exp	perimental s	ystems Methods		
n/a Involved in the		n/a Involved in the study		
Antibodies	0 0 0 0 0 0 0 0	ChIP-seq		
Eukaryotic	cell lines	Flow cytometry		
Palaeontolo	ogy and archaeol	ogy MRI-based neuroimaging		
Animals and	d other organism	is		
Clinical data	Э			
Dual use re	search of concer	n		
⊠ Plants				

Antibodies

Antibodies used The primary antibodies used were: Chemerin (sc-373797; Santa Cruz Biotechnology, USA), CMKLR1 (SC-398769; Santa Cruz

Biotechnology, USA), TNFa (60291-1-Ig; Proteintech, USA), IL-6 (21865-1-AP; Proteintech, USA), ACSL4 (22401-1-AP; Proteintech, USA), TNFa (60291-1-Ig; Proteintech, USA), IL-6 (21865-1-AP; Proteintech, USA), ACSL4 (22401-1-AP; Pr USA), GPX4 (67763-1-Ig; Proteintech, USA), SLC7A11 (ab175186; Abcam, USA), p-NRF2 (PA5-67520; Invitrogen, USA), NRF2 (80593-1-RR; Proteintech, USA), AQP1 (ab168387; Abcam, USA), and Cytokeratin 19 (CK19; 60187-lg; Proteintech, USA).

Validation

Validations of these commercial antibodies are provided in manufacturer production information.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s) TCMK-1 cells were obtained from ATCC.

Authentication Cell line was not independently authenticated.

Cell line test negative for mycoplasma contamination. Mycoplasma contamination

Commonly misidentified lines (See ICLAC register)

None.

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Male C57BL/6 mice $(21 \pm 3 \text{ g}; 8 - 12 \text{ weeks})$ were used in this study. Laboratory animals

Wild animals No wild animals were used in this study.

Male mice were used in this study. Reporting on sex

Field-collected samples No field-collected samples were used in this study.

Animal procedures were approved by the Animal Experimentation Ethics Committee of the Nantong University (SYXK [SU] Ethics oversight

2017-0046).

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 ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

2022-138-01 Clinical trial registration

This study completed May 10, 2023 with the study protocol, which is provided in the manuscript. Study protocol

Data collection The clinical study was conducted at the affiliated hospital of Nantong University. The recruitment starts from August 2022 and

completed in December 2022. The data were collected in May, 2023.

The blood samples were used for measuring serum chemerin, blood urea nitrogen, and creatinine. Outcomes

Plants

Seed stocks	N/A

N/A Novel plant genotypes

N/A Authentication

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

Instrument

Sample preparation Mice were sacrificed at different time points (6, 12, 24 and 72 h) post-ischemia, and blood and kidney samples were collected

for further analysis. For transmission electron microscopy, kidney sections were fixed in electron microscope fixative (Servicebio, G1102, China) for 24 h. The samples were then incubated in 1% osmium acid for 2 h at room temperature, followed by dehydrated using a gradient ethanol series. Afterward, the samples were embedded in epoxy resin and sectioned into 70 nm slices. The samples were subsequently stained with 3% citrate–uranyl acetate. For H&E staining, tissue samples were fixed in formalin, embedded in paraffin and sectioned into $5~\mu m$ thick slices.

were fixed in formalin, embedded in paraffin and sectioned into 5 µm thick slice:

Software Samples were analyzed by Flow Cytometry using a BD LSRFortessa analyzer (BD Biosciences). Data were acquired using BD

for Flow cytometry Acquisition: BD FACSCelesta, Multicolor Flow Cytometer

FACSDiva software.

Cell population abundance The cell population and abundance were determined by the Flow cytometry core personnel.

Gating strategy

We gated FSC to determine C11 BODIPY fluorescence intensity. We excluded doublets and then by using a fixable viability

dye we excluded dead cells. Then, gating on the live cells we assessed the cells for the markers of interest.

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