nature portfolio

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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	BD FACSDiva software was used to collect FACS data.
Data analysis	graphpad prism 10

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

Provide your data availability statement here.

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	Through screening, we ultimately enrolled 20 patients on the waiting list, including 10 in the non-transplant group and 10 in the renal transplant group. No statistically significant differences were observed between the two groups regarding age, sex, dialysis duration, dialysis modality, comorbidities, primary kidney disease, or serum parameters such as urea nitrogen and creatinine.
Ethics oversight	The clinical studies were approved by the Ethics Committee of the First Affiliated Hospital of Zhengzhou University (No. 2021-KY-0781-001), informed consent was obtained from all individual participants included in the study, all ethical regulations relevant to human research participants were followed.

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 sample-size calculation was performed, the sample sizes were chosen by according to the similar studies have been published.
Data exclusions	No data were excluded. No sample-size calculation was performed, the sample sizes were chosen by according to the Similar studies have been published.
Replication	All attempts at replication were successful.
Randomization	*Describe how samples/organisms/participants were allocated into experimental groups. If allocation was not random, describe how covariates were controlled OR if this is not relevant to your study, explain why.*
Blinding	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
[ ]	[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
[ ]	[x] ChIP-seq
[ ]	[x] Flow cytometry
[ ]	[ ] MRI-based neuroimaging

Antibodies

Antibodies used: Elf-1 Antibody (C-4): sc-133096 X, Santa Cruz;Western Blotting:p-P65 (3033, Cell Signaling Technology), P65 (6956, Cell Signaling Technology), NLRP3 (15101, Cell Signaling Technology), GBP4 (AB232689, Abcam) or β-actin (A5441, Sigma).Flow cytometry: anti-CD11b (15-0112-83, ThermoFisher) , anti-F4/80 antibodies (123110, BioLegend) , anti-TNF-α antibody (12-7321-82, ThermoFisher), anti-CD86 antibodies (105006, eBioscience), anti-CD206 antibodies (141703, BioLegend), anti-CD45 antibodies (103112, BioLegend), anti-CD45.1 antibodies (110730, BioLegend) and anti-CD45.2 antibodies (109827, BioLegend).

Validation: Elf-1 Antibody (C-4) is recommended for detection of Elf-1 of mouse, rat and human origin by WB, IP, IF, IHC(P) and ELISA; TransCruz reagent for ChIP application (sc-133096 X, 200 µg/0.1 ml).Other flow cytometry and Western blot antibodies also have clear references published previously.

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s): *State the source of each cell line used and the sex of all primary cell lines and cells derived from human participants or vertebrate models.*

Authentication: *Describe the authentication procedures for each cell line used OR declare that none of the cell lines used were authenticated.*

Mycoplasma contamination: *Confirm that all cell lines tested negative for mycoplasma contamination OR describe the results of the testing for mycoplasma contamination OR declare that the cell lines were not tested for mycoplasma contamination.*

Commonly misidentified lines (See ICLAC register): *Name any commonly misidentified cell lines used in the study and provide a rationale for their use.*

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: C57BL/6N mice were purchased from Vital River Laboratory Animal Technology Co., Ltd. (Beijing, China). ELF-1 knockout (ELF-1 KO) mice with complete deletion of the ELF-1 gene were generated as previously described (Saiye, Guangzhou, China).

Wild animals	*Provide details on animals observed in or captured in the field; report species and age where possible. Describe how animals were caught and transported and what happened to captive animals after the study (if killed, explain why and describe method; if released, say where and when) OR state that the study did not involve wild animals.*
Reporting on sex	The renal ischemia-reperfusion injury (IRI) model takes into account gender differences and uses male mice exclusively.
Field-collected samples	*For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.*
Ethics oversight	These animal experiments were approved by the Ethics Committee of Zhengzhou University (IACUC No.ZZU-LAC20200703). We have complied with all relevant ethical regulations for animal use.

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.

Clinical trial registration	The clinical studies were approved by the Ethics Committee of the First Affiliated Hospital of Zhengzhou University (No. 2021-KY-0781-001)
Study protocol	According to the inclusion and exclusion criteria, this study plan aims to include a total of 20 recipients. Among them, 10 cases are in the non-transplant group and 10 cases are in the kidney transplant group. Based on the principle of informed and voluntary consent from the patients, relevant peripheral blood samples were collected.PBMC was isolated by Ficoll centrifugation, and mononuclear cells were sorted by magnetic beads. After a series of inductions, M0/M1 type macrophages were obtained.
Data collection	The medical record data of patients during their hospitalization registration are collected through the hospital's medical record management system. This includes the age, gender, BMI, dialysis duration, dialysis method, serum creatinine value, serum urea nitrogen value, complications and primary diseases of the patients in the waiting list.
Outcomes	*Describe how you pre-defined primary and secondary outcome measures and how you assessed these measures.*

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 — *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, mosiacism, off-target gene editing) were examined.*

ChIP-seq

Data deposition

[x] Confirm that both raw and final processed data have been deposited in a public database such as GEO.

[x] 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.

the ChIP-seq data has been submitted to the CNCB database (OMIX018272).

Files in database submission

OMIX018272-01, IP_Elf1 KO_VS_IN_Elf1 KO.peak_annotation, OMIX018272-02, IP_WT_VS_IN_WT.peak_annotation

Genome browser session
(e.g. UCSC)

N/A

Methodology

Replicates

BMDMs from WT or ELF-1 KO mice were induced by LPS for 6 hours to obtain M1 macrophages for ChIP-seq assay.

Sequencing depth

The amount of sequencing data of each sample was 6G. Sample1: IN_WT (RawReads: 55184940, CleanReads: 55184940, mappedReads: 54489359, paired: 53339498, single: 53869), IP_WT (RawReads: 47472320, CleanReads: 46974542, mappedReads: 46062025, paired: 45572750, single: 45843). Sample2: IN_Elf1_KO (RawReads: 55774780, CleanReads: 55100736, mappedReads: 55017141, paired: 53868790, single: 58835), IP_Elf1_KO (RawReads: 47612334, CleanReads: 47117518, mappedReads: 46348820, paired: 45849288, single: 42944).

Antibodies

Elf-1 Antibody (C-4): sc-133096 X, Santa Cruz

Peak calling parameters

callpeak -t IP_WT.clean.uniq.rmdup.bam -c IN_WT.clean.uniq.rmdup.bam -f BAMPE -p 0.001 -g 2725537669 -m 5 50 --keep-dup 1;callpeak -t IP_Elf1_KO.clean.uniq.rmdup.bam -c IN_Elf1_KO.clean.uniq.rmdup.bam -f BAMPE -p 0.001 -g 2725537669 -m 5 50 --keep-dup 1.

Data quality

Trimmomatic (version 0.36) was used to filter out low-quality reads. ILLUMINACLIP:adapters.fa:2:30:10 LEADING:3 TRAILING:3 SLIDINGWINDOW:4:15 MINLEN:20.When the threshold of peak for screening significance is pvalue < 0.001,*peaks are screened.

Software

Trimmomatic (version 0.36) was used to filter out low-quality reads. Clean reads were mapped to the GRCm38 genome by Bowtie2. Samtools rmdup was used to remove potential PCR duplicates. The results were visualized using IGV_Win_2.3.92.

Flow Cytometry

Plots

Confirm that:

[ ] The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

[x] 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).

[x] All plots are contour plots with outliers or pseudocolor plots.

[x] A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation

BMDMs or PEMs isolated from WT or ELF-1 KO mice were stimulated with LPS (100 ng/mL, Escherichia coli 0111: B4; Sigma) and GolgiPlug (100ng/mL, 555029, BD) for 6 h to induce M1 macrophages. Cells were stained with anti-CD11b (15-0112-83, ThermoFisher) and anti-F4/80 antibodies (123110, BioLegend) for surface markers. For intracellular TNF-α detection, cells were fixed, permeabilized (BD Cytofix/Cytoperm), and stained with anti-TNF-α antibody (12-7321-82, ThermoFisher). The kidney tissue cells were also stained with anti-CD86 antibodies (105006, eBioscience), anti-CD206 antibodies (141703,

	BioLegend), anti-CD45 antibodies (103112, BioLegend), anti-CD45.1 antibodies (110730, BioLegend) and anti-CD45.2 antibodies (109827, BioLegend).
Instrument	Data were acquired on a BD FACSVerse.
Software	The acquired data were analyzed with FlowJo_V10 software
Cell population abundance	Renal macrophages (CD45+F4/80+CD11b+) were sorted by flow cytometry for RNA extraction for subsequent qPCR analysis;Bone marrow monocytes (Ly6CHiCD11b+) from WT mice were sorted by flow cytometry and resuspended in cDMEM medium. In vitro, we induced BMDMs and PEMs with or without LPS separately, and analyzed the cellular changes using surface markers and cytokine flow antibody staining.
Gating strategy	It was shown in the supplementary Figures.

☒ 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 (See Eklund et al. 2016)	*Specify voxel-wise or cluster-wise and report all relevant parameters for cluster-wise methods.*
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.*