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Reporting Summary

Nature Research 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 Research 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	Shimadzu Biotech MALDI-MS software (version 2.90.3000) was used to collect the data of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry.
Data analysis	Microsoft Excel 2019, OriginPro 2018, SPSS v24.0, Image J 1.51, Casa XPS (version 2.3.13), OMNIC 8, Shimadzu Biotech MALDI-MS software (version 2.90.3000) and TEG Analytical Software 4.2.3 software were used. For the mass-spectrometry-based proteomics study, the raw MS files were analyzed and searched against the uniprot-Sus scrofa protein database on the basis of the species of the samples using MaxQuant (1.5.6.5).

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

The main data supporting the results in this study are available within the paper and its Supplementary Information. The raw and analysed datasets generated during the study are too large to be publicly shared, yet they are available for research purposes from the corresponding authors on reasonable request.

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	As this proof-of-concept study involved the initial demonstration of new methodology, no sample-size calculations or power calculations were performed. Sample sizes were thus selected to ensure confidence in the reproducibility of the methodology as well as statistically testable results. The purpose of the experiments were to demonstrate the use of a pseudo-haemophilia model as an anticoagulant substitute in large-animal surgical models. An N of 3 animals was used for each condition in each experiment to ensure reproducibility. Sample sizes were determined on the basis of estimates from preliminary experiments, standard practice and prior experience in the field of blood purification. We considered that three biological repeats were sufficient to understand the reproducibility of our results.
Data exclusions	We did not exclude any samples.
Replication	At least 3 replications were performed for all the tests, and the attempts for replications were successful.
Randomization	All beagle dogs were randomly allocated into appropriate groups.
Blinding	The establishment of hemodialysis access for dogs were performed pairwise by 2 independent surgeons. The surgeons are blinded to the blood-thinning model during the surgery. During in vivo follow-up, the technicians acquiring data (that is, blood count assays, clotting time tests, biological parameters level assays and tissue evaluation) were also blinded to the groups. Characterizations of the microspheres (including Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, energy dispersive spectra, X-ray photoelectron spectroscopy, Fourier transform infrared spectroscopy, thermogravimetric analysis), hemocompatibilities (including serum protein electrophoresis, rapid thromboelastography, haemolysis ratio, blood count assay in vitro, mass quantification of individual coagulation factor, evaluation of complement activation, contact activation system and kallikrein/kinin system, evaluation of platelet activation and platelet adhesion), targeted quantitative proteomics technologies and mass-spectrometry-based proteomics were all conducted by an independent operator. The operator was blinded to group allocation during data collection and/or analysis. During data analysis, in particular, for image-based data analysis, at least two blinded graders performed the grading /evaluation (such as histology and SEMs).

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
☐	☒ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	For ELISA methods, antibody-coated wells (provided by ELISA kit) were used for detection. The antibody-coated wells from Human complement fragment 3a (C3a) kit, human complement fragment 5a (C5a) kit, human platelet factor 4 (PF4) kit and human bradykinin (BK) kit were purchased from Cusabio Biotech, China. The antibody-coated wells from thrombin-antithrombin Enzygnost TAT micro kit was purchased from Assay Pro, USA.
Validation	The antibodies were validated by the vendors; further validation was not performed.

Eukaryotic cell lines

Policy information about cell lines

Cell line source(s)	Human umbilical vein endothelial cells (ATCCPCS-100-010) were used. The cells were purchased from the Stem Cell Bank, Chinese Academy of Sciences.
Authentication	The cell line was authenticated by ATCC provided by the Stem Cell Bank, Chinese Academy of Sciences, at the time of purchase. No further authentication was performed.
Mycoplasma contamination	The cells were tested, and absence of mycoplasma contamination was confirmed.
Commonly misidentified lines (See ICLAC register)	No commonly misidentified cell lines were used.

Animals and other organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research

Laboratory animals	Healthy beagle dogs (2 years old, male, about 15–18 kg of weight, Laboratory Animal Center of West China Hospital Science Park, Sichuan University).
Wild animals	The study did not involve wild animals.
Field-collected samples	The study did not involve samples collected from the field.
Ethics oversight	All procedures involving the use of animals in this study were prospectively reviewed and approved by the Institutional Animal Care and Use Committee. This study was conducted in accordance with the National Institutes of Health Guide for the care and use of laboratory animals (NIH Publications No. 8023, revised 1978). This experiment conformed to the legal requirement in China and was approved by the ethical committee (No. K2016027) of West China Hospital, Sichuan University.

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

Human research participants

Policy information about studies involving human research participants

Population characteristics	Human fresh blood samples were collected from three 24-year-old healthy male donors without medical history.
Recruitment	The West China Hospital announced the recruitment of human research participants. These volunteers were recruited by voluntary registration and disease-history screening.
Ethics oversight	The experiments were approved and performed by West China Hospital, Sichuan University, and all the experiments were performed in compliance with the relevant laws and national guidelines (GB/T 16886.4-2003/ISO 10993-4:2002, General Administration of Quality Supervision, Inspection and Quarantine of the People's Republic of China, Standardization Administration of the People's Republic of China). Informed consent was obtained for any experimentation with human subjects, and all regulations (e.g. IRB) were fulfilled for using human blood.

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