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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	Retrospective CCTA data were collected from PACS systems of participating institutions. No additional software was used for data acquisition.
Data analysis	Data analysis was performed using Python (v3.12.4) with the following packages: matplotlib (v3.8.4), numpy (v2.1.3), pandas (v2.2.3), scipy (v1.14.1), seaborn (v0.13.2), SimpleITK (v2.4.0), and tqdm (v4.66.5). Custom code for automated plaque analysis (PLASMA) is available on GitHub and archived on Zenodo (DOI: 10.5281/zenodo.16741227).

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

A sample dataset and an interactive demo of PLASMA, which features automated coronary artery reconstruction and plaque analysis, are available at https://aidemo.united-imaging.com/ (username: demo; password: Uai@434254!). Statistical atlases of plaque characteristics derived from the cohort are shared in GitHub

and archived on Zenodo (https://zenodo.org/records/16741227). All shared data are fully anonymized to protect patient privacy in accordance with relevant legal requirements. Due to restrictions imposed by institutional review boards, the raw datasets used in this study are not publicly accessible. However, requests for access to aggregated data and supporting clinical documentation will be evaluated by an independent review panel based on the scientific merit of the request. For data access inquiries related to this study, please contact the corresponding author, Dinggang Shen (dinggang.shen@gmail.com). Requests will be reviewed and responded to within two months. 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	All analyses were stratified by biological sex (male and female). Sex information was obtained from anonymized CCTA records, where sex was originally self-reported by patients. Disaggregated sex data have been provided in the source data, with 9,520 males and 6,780 females included in the final analysis.
Reporting on race, ethnicity, or other socially relevant groupings	Race, ethnicity, and other socially constructed variables were not collected or analyzed in this study, as they were not relevant to the research objectives.
Population characteristics	The study involves demographic information on age and sex. Additional clinical characteristics were not included in the analysis.
Recruitment	Participants were identified retrospectively from clinical records of patients who underwent CCTA during the study period at participating hospitals. All eligible cases with available demographic data and CCTA images of sufficient quality for quantitative analysis were included. No active recruitment was conducted, minimizing selection bias.
Ethics oversight	The study protocol was approved under the umbrella ethical approval of Shanghai General Hospital Institutional Review Board (IRB 2023-049), with additional approvals obtained from other participating hospitals as listed in the manuscript.

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	The sample size consisted of 16,300 patients who underwent clinically indicated CCTA. No statistical method was used to predetermine sample size.
Data exclusions	Eligible subjects were included based on the availability of age and sex demographics, along with the requirement that CCTA images were of sufficient quality for quantitative plaque assessment. Specifically, image quality of original axial images was visually assessed by certified CT analysts using a 4-point scale—excellent (absence of artifacts, score 3), good (presence of mild artifact, score 2), sufficient (presence of moderate artifact, but still diagnostic, score 1), and poor (presence of severe artifact, non-diagnostic, score 0)—following established criteria (Dai X et.al., 2018). Cases with scores of 0 or 1 were excluded to ensure adequate image quality, and all four proximal coronary segments (RCA, LM, LAD, and LCx) were required to be readable for plaque evaluation. Exclusions were also made for patients under 25 years of age and those who had previously undergone PCI or CABG. Prior cardiac procedures were identified using a task-specific AI model that automatically detected the presence of stents or grafts in the CCTA images, with all findings subsequently confirmed through manual review.
Replication	Replication was not applicable as this was an observational study using existing clinical data. Analyses were performed on a large multi-center cohort with rigorous quality control and subgroup analyses to ensure the robustness and reproducibility of the findings.
Randomization	Randomization was not applicable, as this was a retrospective observational study and no experimental group allocation was involved.
Blinding	Blinding was not applicable, as this was a retrospective, anonymized study where group assignment and all analyses based on objective demographic variables (age and sex) with automatic tools.

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

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.