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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	The medical imaging data is the raw output of the CT machines, which is in the Digital Imaging and Communication in Medicine (DICOM) format. Clinical metrics did not include any software for the data collection.
Data analysis	Statistical analysis and figure generation were performed using GraphPad Prism (version 10.5.0). Medical image segmentation for the primary analysis was performed using the proprietary software iCurveE (version 1.0). For comparison, segmentations were also generated using the open-source nnU-Net framework (version 2.2) and TotalSegmentator (version 2.4.0).

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 source data underlying the figures, tables, and statistical analyses presented in this study are provided as a Source Data file with this paper. The primary clinical data of this study, including anonymized CT scans and the generated OAR contours, are available from the corresponding author upon 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	We collected data on participant sex. Both male and female participants were included in this prospective study. Sex was not considered as a variable in the primary analysis as sex-based differences in the study outcome were not anticipated. The demographic distribution of participant sex is provided in Table 1 of the manuscript.
Reporting on race, ethnicity, or other socially relevant groupings	Information on race or ethnicity of the participants was not collected as it was not considered a relevant variable for the study's primary endpoint and objectives.
Population characteristics	From September 30, 2022, to February 14, 2023, 500 patients were enrolled to undergo CT scanning for this trial, including 146 with lung cancer (non-small cell and small cell lung cancer), 35 with esophageal cancer, and 320 with breast cancer. Key demographic characteristics included a mean age of 54.0 years (s.d. = 12.46; range: 20.0–88.0) and a sex distribution of 363 females (72.6%) and 137 males (27.4%).
Recruitment	From September 30, 2022, to February 14, 2023, this prospective, multicenter, randomized clinical trial involved 500 patients with cancer from five hospitals in China: Tianjin Medical University Cancer Institute & Hospita, Wuhan Union Hospital,Shanxi Cancer Hospita, The Fifth Affiliated Hospital of Sun Yat-sen Universit, a nd Nanxishan Hospital of Guangxi Zhuang Autonomous Region. Written informed consent was obtained from all participants. Each participant was compensated RMB 300.
Ethics oversight	This study was conducted in accordance with the Declaration of Helsinki and received approval from the Institutional Review Boards of all participating centers (IRB Nos.: TMUCIH: E20220700; WHUH: [2022] L.SH.Z-0540; SXCH: QX-2022-011; FHSU: [2022] L.Z. Q200-1; and NXSH: 2022-003-01).

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	From September 30, 2022, to February 14, 2023, 500 patients were recruited consecutively from the radiotherapy departments of five hospitals. Sample size was determined based on a non-inferiority design (one-sided á=0.025, 90% power, margin=-0.05) with pre-specified superiority testing, enrolling 500 patients to meet the required 474 after accounting for a 10% dropout rate and a further safety margin. Potential self-selection bias was minimized due to the non-interventional and multicenter nature of the study.
Data exclusions	The exclusion criteria were as follows: (1) thoracic deformities caused by non-tumoral factors (e.g., congenital anomalies); (2) indiscernible anatomical structure contours due to artifacts and implants; (3) non-DICOM image; and (4) investigator-determined unsuitability.
Replication	The reproducibility and generalizability of the findings were ensured by using independent validation and test sets from two centers, followed by prospective end-user testing across five centers.
Randomization	Anonymized CT images were randomly assigned to two cohorts in a 1:1 ratio. Cohort 1 underwent initial manual delineation, followed by AI-assisted delineation after a washout period (>4 weeks), whereas Cohort 2 followed the inverse sequence.
Blinding	The investigators were not blinded to allocation during this trial due to the visible nature of the delineation methods.

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

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	NCT05787522
Study protocol	The full study protocol is available from the corresponding author upon reasonable request.
Data collection	Data were collected prospectively within a multicenter, randomized clinical trial conducted atat five academic medical centers in China: Tianjin Medical University Cancer Institute & Hospital (TMUCIH), Wuhan Union Hospital (WHUH), Shanxi Cancer Hospital (SXCH), The Fifth Affiliated Hospital of Sun Yat-sen University (FHSU), and Nanxishan Hospital of Guangxi Zhuang Autonomous Region (NXSH). The period for patient recruitment and data collection was from September 30, 2022, to February 14, 2023.
Outcomes	The primary endpoints were the volumetric Dice similarity coefficient (vDSC) and contouring time. Secondary endpoints included the 95% Hausdorff distance (HD95), surface Dice similarity coefficient (sDSC), and volumetric revision index (VRI).

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.*