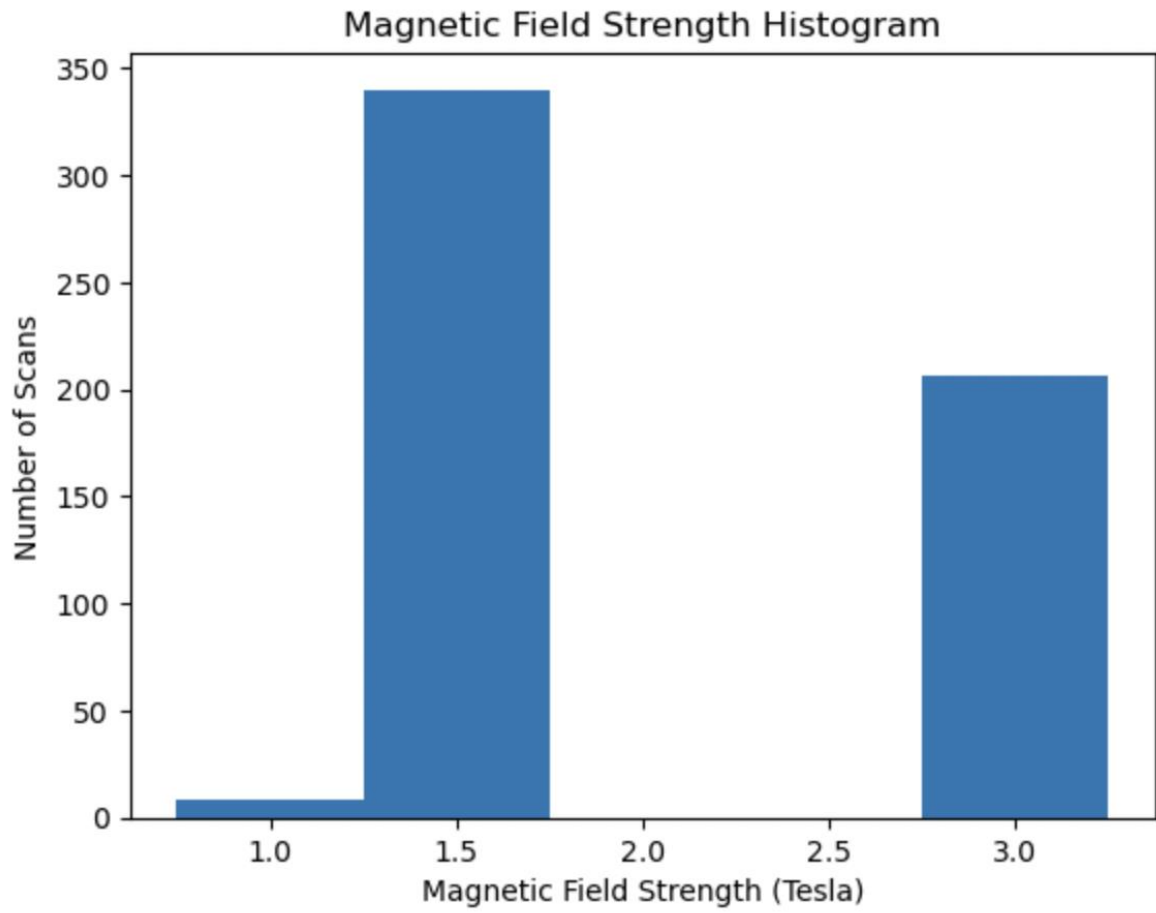
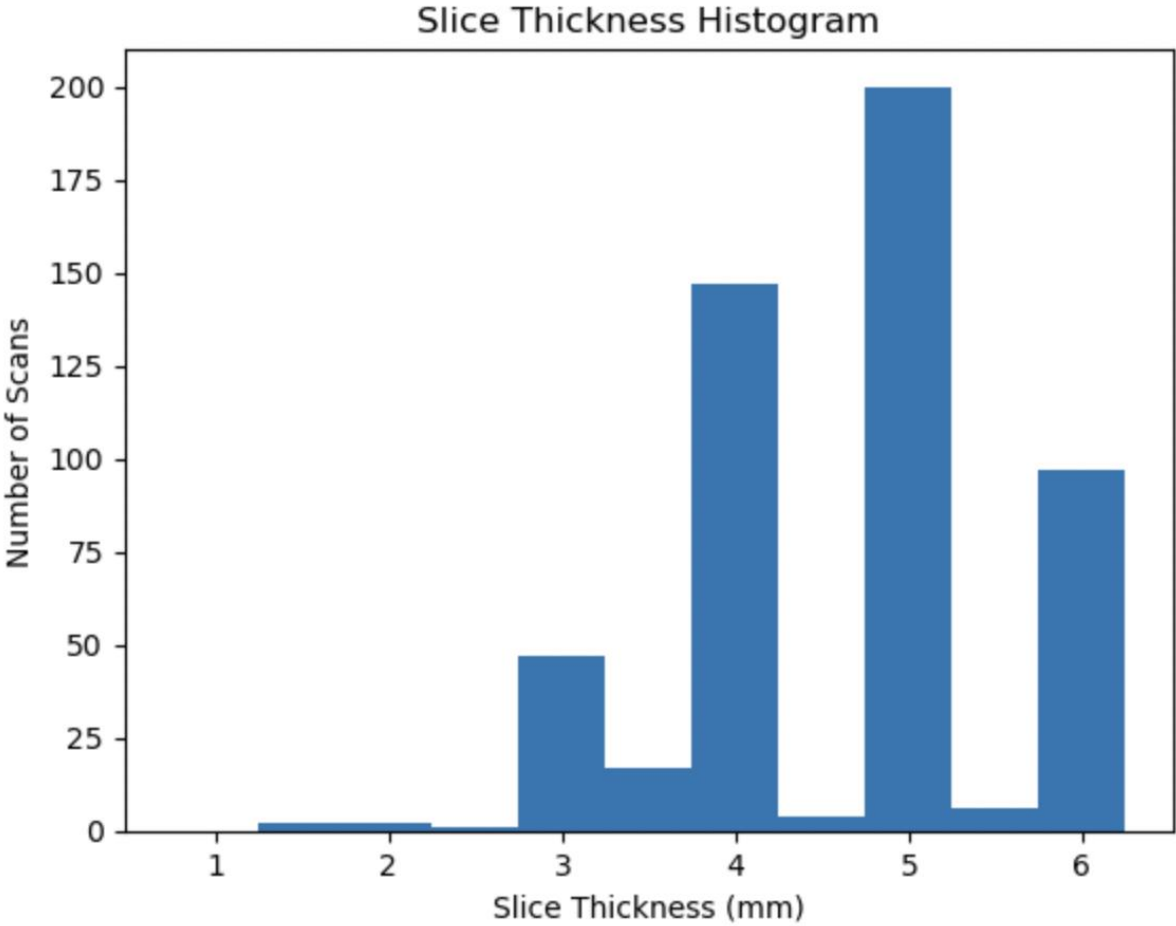


Supplementary Material

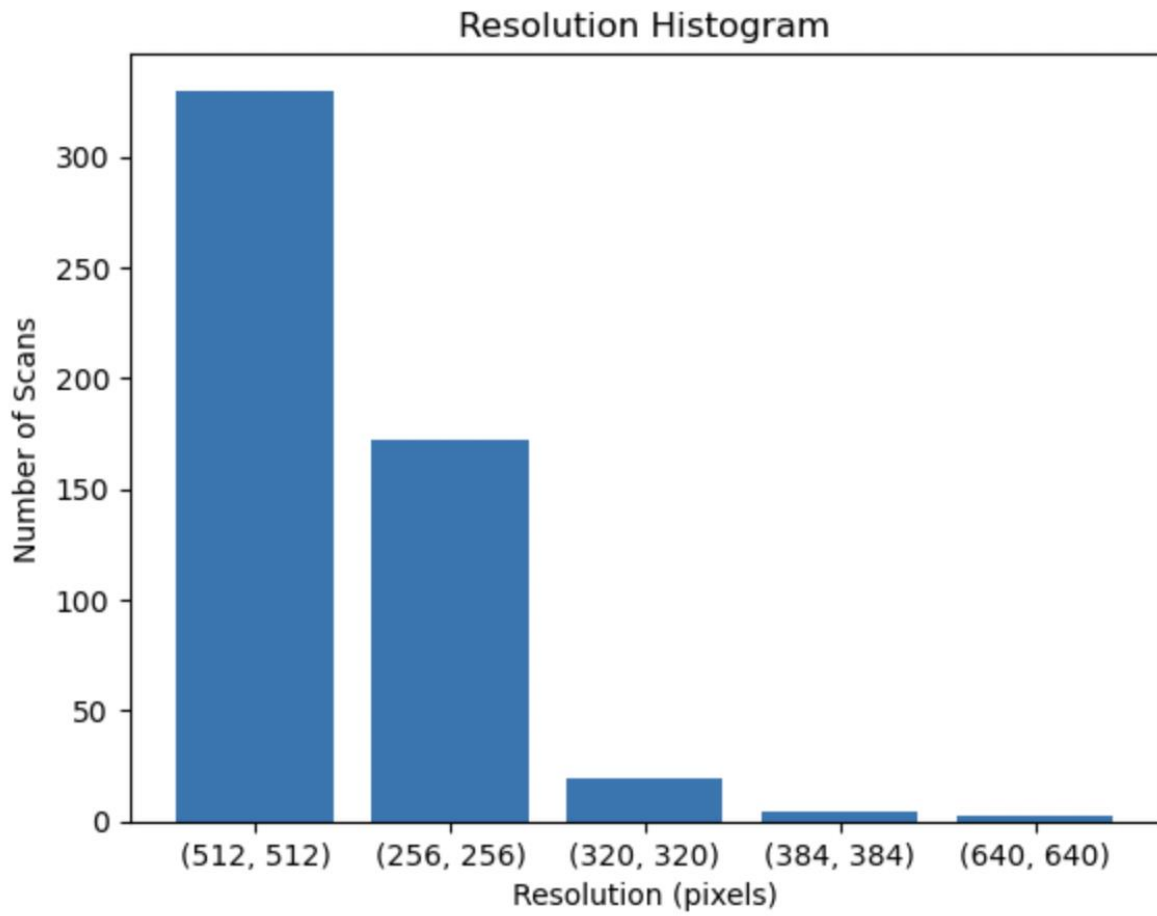
Supplementary Figure 1



Supplementary Figure 2

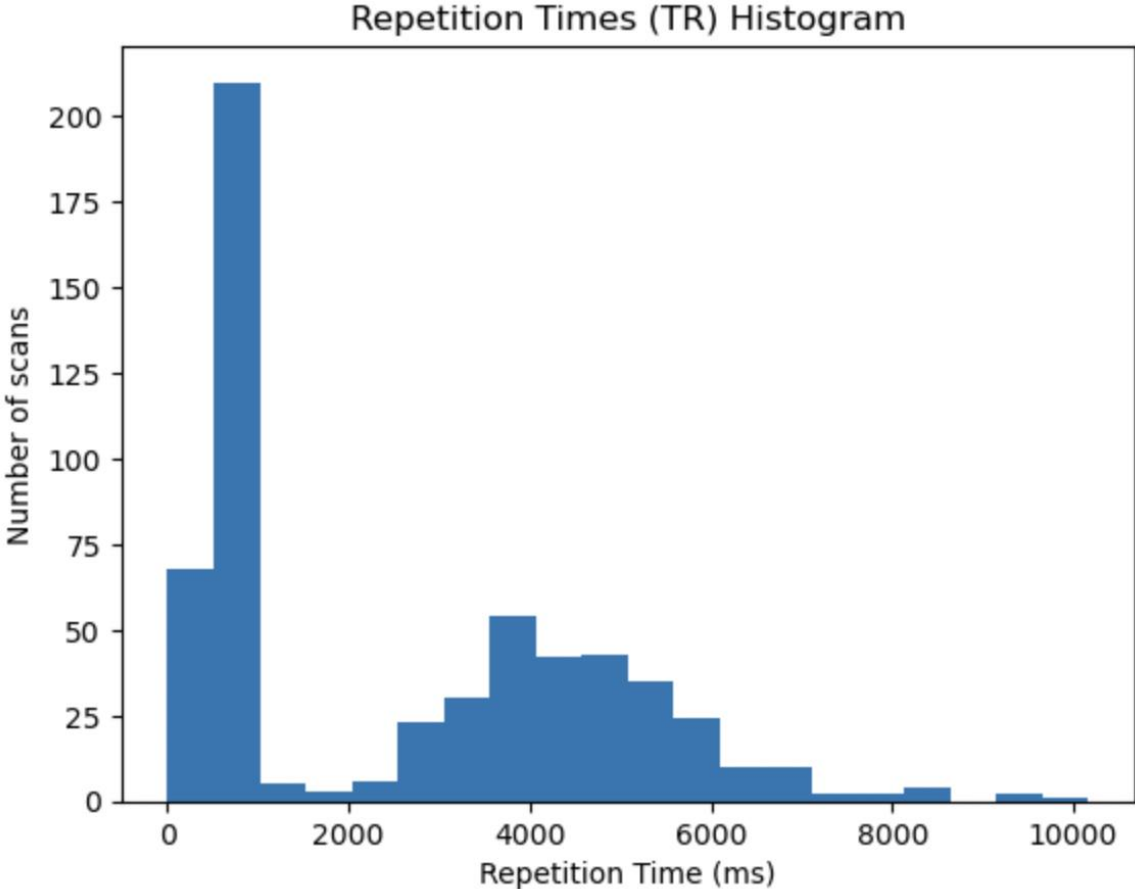


Supplementary Figure 3

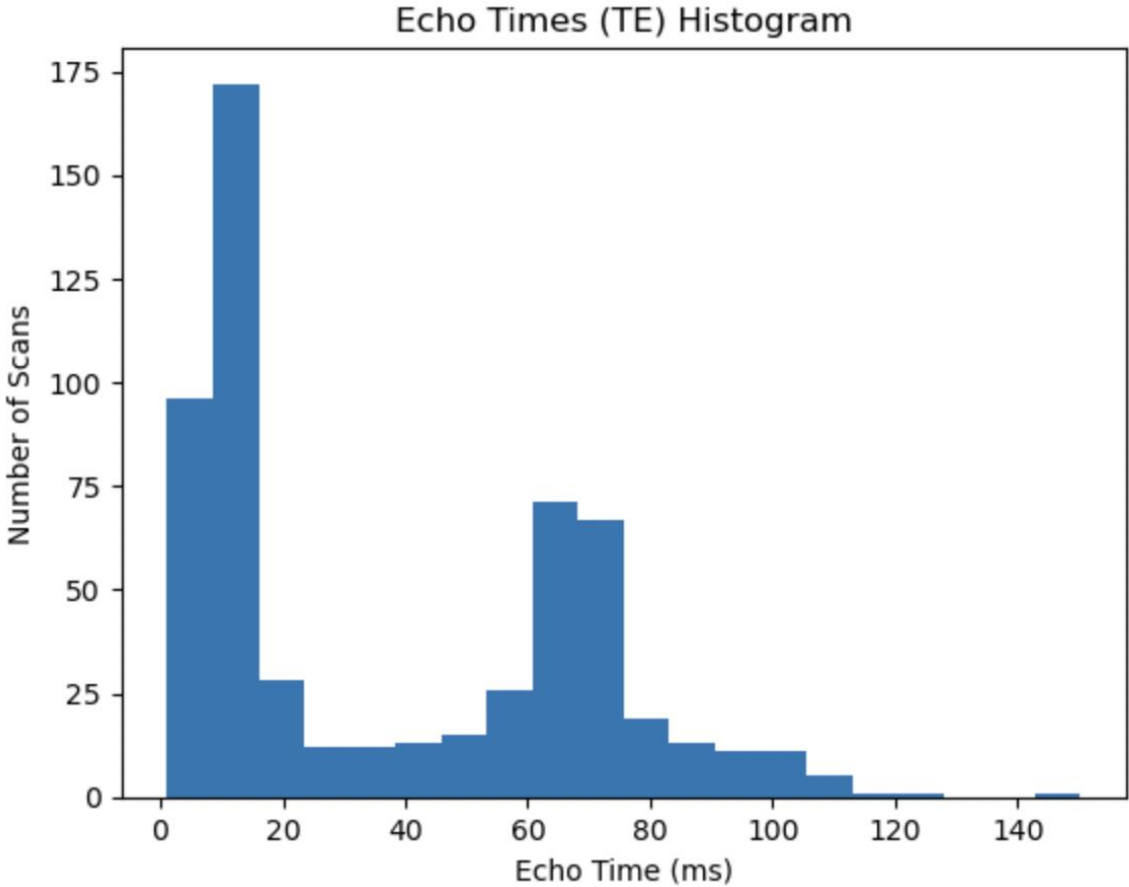


Note: N=528 as dimensions with a frequency of 1 or 2 are not depicted. In total 39 unique resolutions were included in our dataset.

Supplementary Figure 4

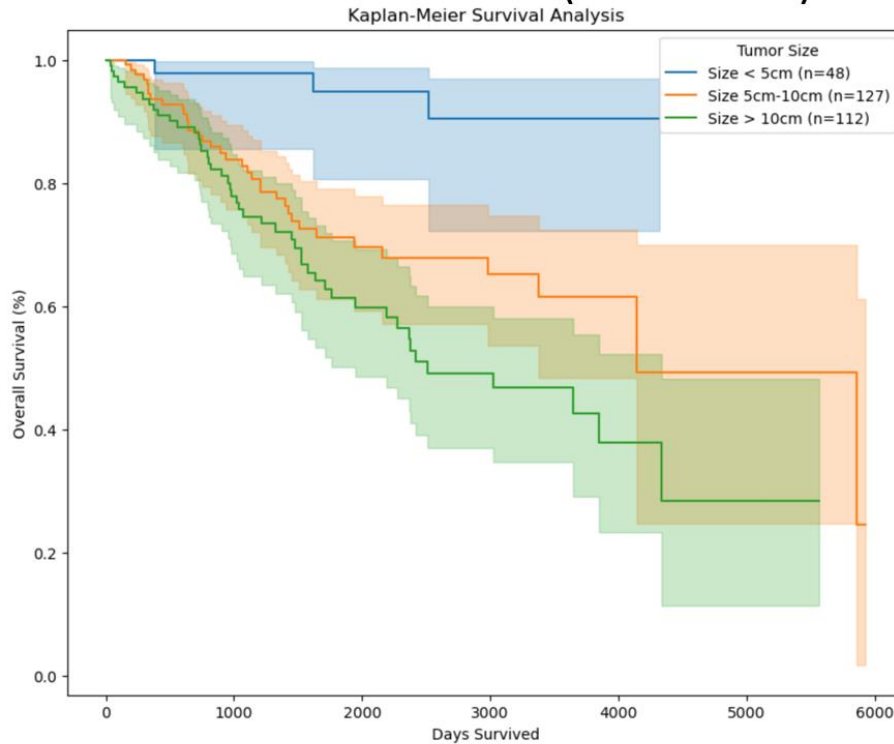


Supplementary Figure 5



Supplementary Figure 6: Kaplan-Meier survival analysis based on tumor size

Tumor Size and Vital Stats (Survival)



Groups: Size 5cm-10cm vs Size > 10cm, Corrected p-value: 0.18188228153158642
Groups: Size 5cm-10cm vs Size < 5cm, Corrected p-value: 0.0047070554048248845
Groups: Size > 10cm vs Size < 5cm, Corrected p-value: 3.698480366577247e-05

Supplementary Table 1

CLEAR Checklist

Section	No.	Item	Yes	No	n/a	Page/Section
Title						
	1	Relevant title, specifying the radiomic methodology Indicate the use of radiomics in the title. The following details can also be considered to be specified in the title: radiomic technique (e.g., hand-crafted, engineered, deep, delta, etc.), modality (e.g., computed tomography [CT], magnetic resonance imaging [MRI], ultrasound), important aspects of the scans (e.g., unenhanced, dynamic), use of machine learning (e.g., machine learning-based), external validation, and multi-center design.	X	<input type="checkbox"/>	<input type="checkbox"/>	Radiomics models
Abstract						
	2	Structured summary with relevant information Provide a structured summary of the purpose, methods, results, and conclusions, presenting only the most important aspects directly related to the purpose of the study. The abstract should be understandable on its own, without reading the main text. Considering the submission guidelines of the journals, it is recommended to specify the following items: the baseline characteristics (e.g., number of patients, scans, images, classes), data source (e.g., public, institutional), study nature (e.g., prospective, retrospective), segmentation technique (e.g., automated, semi-automated, or manual), feature extraction technique (e.g., hand-crafted, engineered, deep), dimensionality reduction techniques (e.g., feature selection, reproducibility analysis, multi-collinearity), modeling details (e.g., algorithms/models), validation technique (e.g., cross-validation), unseen testing (internal hold-out, external testing), model performance metrics (e.g., the area under the curve) with uncertainty measures (e.g., confidence intervals), number of the final set of features, traditional statistical methods with p-values, and open science status (e.g., public availability of data, code, and/or model).	X	<input type="checkbox"/>	<input type="checkbox"/>	Radiomics models
Keywords						
	3	Relevant keywords for radiomics List the primary keywords that indicate (e.g., radiomics, texture analysis) and characterize a radiomic study (e.g., machine learning, deep learning, computed tomography, magnetic resonance imaging, reproducibility), unless the journal requires exclusive use of certain terms (e.g., MeSH terms, which do not yet include radiomics-specific terms).	X	<input type="checkbox"/>	<input type="checkbox"/>	Radiomics models
Introduction						
	4	Scientific or clinical background Define the scientific or clinical problem with a summary of the related literature and knowledge gaps, including a short review of the current state of knowledge. Describe why the scientific question is technically or clinically important.	X	<input type="checkbox"/>	<input type="checkbox"/>	Background
	5	Rationale for using a radiomic approach Describe why a radiomic approach is considered. Performance and problematic aspects of currently used methods need to be described. Mention what the radiomics approach would offer to solve these problems. Clearly state how radiomics could affect clinical practice considering the study question.	<input type="checkbox"/>	<input type="checkbox"/>	X	
	6	Study objective(s) Describe the purpose of the study while focusing on the scientific problem. Mention the expected contributions to the current literature.	X	<input type="checkbox"/>	<input type="checkbox"/>	Background
Method						
Study Design	7	Adherence to guidelines or checklists (e.g., CLEAR checklist) Indicate that the CLEAR checklist was used for reporting and submit the checklist as supplemental data. Do the same with other checklists or guidelines if used in addition to the CLEAR checklist.	<input type="checkbox"/>	<input type="checkbox"/>	X	
	8	Ethical details (e.g., approval, consent, data protection) Describe the ethical questions to ensure that the study was conducted appropriately. Give information about ethical approval, informed consent, and data protection (e.g., de-identification) if the data is from private sources.	<input type="checkbox"/>	<input type="checkbox"/>	X	
	9	Sample size calculation Describe how the sample size or power was determined before or after the study (e.g., sample size/power calculation, based on availability).	<input type="checkbox"/>	<input type="checkbox"/>	X	
	10	Study nature (e.g., retrospective, prospective) Indicate whether the study is prospective or retrospective and case/control or cohort, etc. In the case of prospective studies, provide registration details if available.	X	<input type="checkbox"/>	<input type="checkbox"/>	Methods
	11	Eligibility criteria Define the inclusion criteria first. Then, specify the exclusion criteria. Avoid redundancies by using the opposite of the inclusion criteria as exclusion criteria. Specify the selection process (e.g., random, consecutive). Keep the numeric details of eligibility for the results.	X	<input type="checkbox"/>	<input type="checkbox"/>	Methods
	12	Flowchart for technical pipeline Provide a flowchart for summarizing the key methodological steps in the study. Due to the complex nature of the radiomic approaches, such flowcharts help readers better understand the methodology.	<input type="checkbox"/>	<input type="checkbox"/>	X	

Data	13	Data source (e.g., private, public) State the data source (e.g., private, public, mixed [both private and public]). State clearly which data source is used in different data partitions. Provide web links and references if the source is public. Give the image or patient identifiers as a supplement if public data is used.	X	<input type="checkbox"/>	<input type="checkbox"/>	Methods
	14	Data overlap State if any part of the dataset was used in a previous publication. Describe the differences between the current study and previous studies in terms of study purpose and methodology.	<input type="checkbox"/>	<input type="checkbox"/>	X	
	15	Data split methodology Describe the data split into training, validation, and test sets. Mention that multiple splits are created (e.g., k-fold cross-validation or bootstrapping). Specify how the assignment was done (e.g., random, semi-random, manual, center-wise, chronological order). Indicate the ratio of each partition, with class proportions. Describe at which level the data is split (e.g., patient-wise, image-wise, study-wise, scanner-wise, institution-wise). Clearly state the measures undertaken to avoid information leakage across datasets (e.g., creating the hold-out test set before feature normalization, feature selection, hyperparameter optimization, and model training) [23]. Note that any test data should only be used once for evaluation of the final model to prevent optimistic biases. Declare the systematic differences among the data partitions.	X	<input type="checkbox"/>	<input type="checkbox"/>	Statistical analysis and model evaluation
	16	Imaging protocol (i.e., image acquisition and processing) Provide the imaging protocol and acquisition parameters with post-processing details. Define physical pixel and voxel dimensions. Clearly state whether single or multiple or various scanners are used, with the number of instances for each protocol. Define the timing of the phase if a contrast medium was used. State the patient preparation (drug administration, blood sugar control before the scans, etc.) if performed.	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
	17	Definition of non-radiomic predictor variables Describe the data elements appearing as non-radiomic predictors. Non-radiomic variables might be demographic characteristics (e.g., age, gender, ethnicity), widely used traditional laboratory biomarkers (e.g., carcinoembryonic antigen), or traditional approaches used in daily clinical practice (e.g., radiologist's qualitative reading, Hounsfield Unit evaluation, Response Evaluation Criteria in Solid Tumors [RECIST], Response Assessment in Neuro-Oncology [RANO] criteria). It would be helpful to know how these predictors were identified (e.g., based on a literature review). If applicable, describe any transformation of predictors (e.g., binarization of continuous predictors, the grouping of levels of categorical variables).	X	<input type="checkbox"/>	<input type="checkbox"/>	Patients
	18	Definition of the reference standard (i.e., outcome variable) Describe the reference standard or outcome measure that the radiomic approach will predict (e.g., pathological grade, histopathological subtypes, genomic markers, local-regional control, survival, etc.). Provide the rationale for the choice of the reference standard (e.g., higher reproducibility rates). Clearly state the reproducibility concerns, potential biases, and limitations of the reference standard.	X	<input type="checkbox"/>	<input type="checkbox"/>	Background
Segmentation	19	Segmentation strategy Indicate which software programs or tools are used for segmentation or annotation. Specify the version of the software and the exact configuration parameters. Provide reference and web link to the software. Describe the segmentation method (e.g., automatic, semi-automatic, manual). Provide the rules of the segmentation (e.g., margin shrinkage or expansion from the visible contour, included/excluded regions). Provide figures to show the segmentation style. Provide image registration details (e.g., software, version, link, parameters) if segmentation is propagated for multi-modal (e.g., CT and MR), multi-phase (e.g., unenhanced, arterial, venous phase CT), or multi-sequence (e.g., T2-weighted, post-contrast T1-weighted, diffusion-weighted imaging) analyses. If radiomic features are extracted from 2D images on a single slice, please explain with which criteria the slice is chosen. In the case of several lesions, explain if all the lesions are segmented and describe how the feature values are aggregated. If only one lesion is chosen, describe the criteria (e.g., the primitive or the most voluminous).	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
	20	Details of operators performing segmentation State how many readers performed the segmentation, as well as their experience. In the case of multiple readers, describe how the final form of segmentation is achieved (e.g., the consensus of readers, intersection of segmentations, independent segmentation for further reproducibility analysis, sequential refinements from numerous expert raters until convergence), which is particularly important for the training data because the segmentation process on the test data should be as close to the clinical practice as possible, that is, the segmentation of a single reader.	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
Pre-processing	21	Image pre-processing details Indicate which software programs or tools are used for pre-processing. Specify the version of the software and the exact configuration parameters. Provide reference and web link to the software, if available. Describe all pre-processing techniques and associated parameters applied to the image including the normalization (e.g., minimum-maximum normalization, standardization, logarithmic transformation, bias field correction), de-noising, skull stripping (also known as brain extraction), interpolation to create uniform images (e.g., in terms of slice thickness), standardized uptake value conversion, and registration. Also, state if an image or feature-based harmonization technique was used.	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
	22	Resampling method and its parameters Specify the resampling technique (e.g., linear, cubic b-spline) applied to the pixels or voxels. Provide the physical pixel and voxel dimensions after resampling.	<input type="checkbox"/>	<input type="checkbox"/>	na	

	23	<p>Discretization method and its parameters Specify the discretization method (e.g., fixed bin width, fixed bin count method, or histogram equalization) used for hand-crafted radiomic feature extraction. Report the rationale for using a particular discretization technique. Indicate the number of grey levels for the fixed bin count method or the bin width as well as the value of the first level (or minimum and maximum bounds) for the fixed bin width method. Any experimental detail with different discretization methods and values is important to declare.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing and in our Responses to reviewer comments
	24	<p>Image types (e.g., original, filtered, transformed) Provide the image types from which the radiomic features are extracted, e.g., original or images with convolutional filters (e.g., Laplacian of Gaussian edge enhancement, wavelet decomposition) [24]. Also, give nuances about the parameters of transformed image types (e.g., sigma values of Laplacian of Gaussian filtering).</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
Feature extraction	25	<p>Feature extraction method Indicate which software programs or tools are used for radiomic feature extraction. Specify the version of the software and the exact configuration parameters (also see Item#55). Provide reference and web link to the software. Indicate if the software adheres to the benchmarks/certification of IBSI [25]. Specify the general feature types, such as deep features, hand-crafted features, engineered features, or a combination. Refer to the mathematical formulas of the hand-crafted and engineered features. Provide formulas and code if new hand-crafted features are introduced. Present the architectural details for deep feature extraction. Provide details of any feature engineering performed. Specify whether radiomic features are extracted in a two-dimensional (2D) plane, 2D tri-planar, or three-dimensional (3D) space. If 2D features are extracted from 3D segmentation, provide reasons (e.g., large slice thickness) as to why such an approach is followed.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
	26	<p>Feature classes Provide the radiomic feature classes (e.g., shape, first-order, grey-level co-occurrence matrix). Use IBSI terminology for feature classes [25]. Specify the number of features per feature class. Mention if any feature class is excluded with reason.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Responses to reviewer comments
	27	<p>Number of features Indicate the total number of features per instance. If applicable, provide the number of features per imaging modality and its components (e.g., phase for CT, sequence for MRI, etc.).</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Radiomics models
	28	<p>Default configuration statement for remaining parameters After providing all modified parameters of pre-processing and radiomic feature extraction, state clearly that all other parameters remained as a default configuration.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Responses to reviewer comments
Data preparation	29	<p>Handling of missing data State if, and how much, missing data are present in the study. If so, provide details as to how it was addressed (e.g., deletion, substitution, or imputation).</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Methods
	30	<p>Details of class imbalance Indicate the balance status of the classes according to the reference standard. Provide details about how class imbalance is handled. Specify the techniques (e.g., synthetic minority over-sampling, simple over-sampling through replication, under-sampling) used to achieve the class balance. Clearly state these data augmentation and under-sampling strategies are applied only in the training set.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Methods
	31	<p>Details of segmentation reliability analysis Describe the reliability analysis done to assess the influence of segmentation differences. An intra- and inter-rater reproducibility analysis must be considered in manual and semi-automatic methods. Provide details about the statistical tests used for the reliability analysis (e.g., intraclass correlation coefficient along with types) [26]. Mention the independence of assessment. Clearly state the reliability analysis is performed using the training set only.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Image Acquisition, Definition of Volumes of Interest, and Preprocessing
	32	<p>Feature scaling details (e.g., normalization, standardization) If applicable, describe the normalization technique applied to the radiomic feature data (e.g., minimum-maximum normalization, standardization, logarithmic transformation, ComBat normalization [choice of the batch, parametric or not, with or without empirical Bayes]). Specify the normalization scale. It is important to emphasize that this procedure is applied to the numeric radiomic feature data, not the images, in the training set and independently applied to the validation and test sets.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Radiomics models
	33	<p>Dimension reduction details Specify the dimension reduction methods used, if applicable (e.g., collinearity analysis, reproducibility analysis, algorithm-based feature selection). Provide details about the statistical methods used. For example, provide the relevant statistical cut-off values for each step (e.g., features with intraclass correlation coefficient ≤ 0.9 are excluded). Clearly state the dimension reduction that is performed using the training set. Specify how the final number of features is achieved, for instance, the "rule of thumb" of ten features maximum for each instance.</p>	<input type="checkbox"/>	<input type="checkbox"/>	X	

Modeling	34	Algorithm details Provide the name and version of software programs or packages used for modeling. Refer to the related publication of the software if available. Specify the algorithms used to create models with architectural details including inputs, outputs, and all intermediate components. The description of the architecture should be complete to allow for exact replication by other investigators (also see Item#55 and Item#56). When a previously described architecture is used, refer to the previous work and specify any modification. If the final model involved an ensemble of algorithms, specify the type of ensemble (e.g., stacking, majority voting, averaging, etc.).	X	<input type="checkbox"/>	<input type="checkbox"/>	Clinical models, Radiomics models and Neural network models
	35	Training and tuning details Describe the training process with adequate detail. Specify the augmentation technique, stopping criteria for training, hyperparameter tuning strategy (e.g., random, grid-search, Bayesian), range of hyperparameter values used in tuning, optimization techniques, regularization parameters, and initialization of model parameters (e.g., random, transfer learning). If transfer learning is applied, clearly state which layers or parameters are frozen or affected.	X	<input type="checkbox"/>	<input type="checkbox"/>	Model training
	36	Handling of confounders Describe the method (e.g., directed acyclic graphs) for the detection of potential confounders (e.g., differences in tumor size between cohorts, different image acquisition parameters such as slice thickness, and differences in patient populations between primary and secondary hospitals) [27, 28]. Please describe how confounding was addressed (e.g., covariate adjustment).	<input type="checkbox"/>	<input type="checkbox"/>	X	
	37	Model selection strategy Describe how the final model was selected. Two broad categories for these are probabilistic (e.g., Akaike information criterion, Bayesian information criterion) and resampling methods (e.g., random train-test split, cross-validation, bootstrap validation) [12, 29]. Clearly state that only the training and validation sets are used for model selection. State if the model complexity is considered in selection, for instance, the “one standard error rule” [30]. Specify which performance metrics were used to select the final model.	X	<input type="checkbox"/>	<input type="checkbox"/>	Methods
Evaluation	38	Testing technique (e.g., internal, external) Clearly state whether the model was internally or externally tested. The term “external testing” should only be used for the process that involves data usage from different institutions. In the case of external testing, specify the number of sites providing data and further details about whether they are used for multiple testing or in a single test. Describe the data characteristics and state if there are any differences among training, validation, internal testing, and external testing datasets (e.g., different scanners, different readers for segmentation, different ethnicity). Again, note that any test data should only be used once for evaluation to prevent biased performance metric estimates.	X	<input type="checkbox"/>	<input type="checkbox"/>	Patients, Image Acquisition, Definition of Volumes of Interest, and Preprocessing
	39	Performance metrics and rationale for choosing Specify the performance metrics to evaluate the predictive ability of the models. Justify the selected metrics according to the characteristics of the data (e.g., class imbalance). Beware of the potential pitfalls and follow recommendations when selecting the appropriate performance metrics [7, 31].	X	<input type="checkbox"/>	<input type="checkbox"/>	Statistical analysis and model evaluation
	40	Uncertainty evaluation and measures (e.g., confidence intervals) Describe the uncertainty evaluation (e.g., robustness, sensitivity analysis, calibration analysis if applicable) and measures of uncertainty quantification (e.g., confidence intervals, standard deviation).	X	<input type="checkbox"/>	<input type="checkbox"/>	Results
	41	Statistical performance comparison (e.g., DeLong’s test) Specify the statistical software and version used. Indicate which method was used for the comparison of the model performance such as the DeLong’s test [32, 33], McNemar’s test [34], or Bayesian approaches [35]. Provide a statistical threshold for the comparison (e.g., $p < 0.05$) along with confidence intervals if applicable to the method or metric. Also, state if multiplicity is considered and corrected when comparing multiple models (e.g., p-value adjustment, Bonferroni correction, false-discovery rate). Report threshold values to stratify data into groups for statistical testing (e.g., the operating point on the receiver operating characteristic [ROC] curve to define the confusion matrix, and cut-off values for defining strata in survival analysis).	X	<input type="checkbox"/>	<input type="checkbox"/>	Results, Discussion
	42	Comparison with non-radiomic and combined methods Indicate whether comparisons with non-radiomic approaches (e.g., clinical parameters, laboratory parameters, traditional radiological evaluations) are performed. Non-radiomic approaches can be combined with radiomic data as well (e.g., clinical-radiomic evaluation). Explain how the clinical utility is assessed, such as with decision curve analysis [36].	X	<input type="checkbox"/>	<input type="checkbox"/>	Predictions, Performance compared to other models
	43	Interpretability and explainability methods Describe the techniques used to increase the interpretability and explainability of the models created, if applicable [37]. Figures (e.g., class activation maps, feature maps, SHapley Additive exPlanations, accumulated local effects, partial dependence plots, etc.) related to the interpretability and explainability of the proposed radiomic model can be provided.	X	<input type="checkbox"/>	<input type="checkbox"/>	Model interpretation
Results						
	44	Baseline demographic and clinical characteristics Provide the baseline demographic, clinical, and imaging characteristics in text and/or tables. Report the information separately for training, validation (i.e., cross-validation), and test datasets, along with grouping based on the reference standard or non-radiomic variables. Associated statistical tests should also be provided to identify if the sets are identical or not. Provide whether any confounder is detected and handled appropriately.	X	<input type="checkbox"/>	<input type="checkbox"/>	Results (Table 1)

	45	Flowchart for eligibility criteria Provide a flowchart for summarizing eligibility criteria with the number of included and excluded instances. If more than one data source is involved, please give details for each source separately.	<input type="checkbox"/>	<input type="checkbox"/>	na	
	46	Feature statistics (e.g., reproducibility, feature selection) Give statistical information (e.g., distribution of features based on outcome variables) of the selected features for inclusion into the model. Provide the name and number of reproducible features (e.g., for segmentation reproducibility, for reproducibility against image perturbations). Create a table for the selected features with details of feature name, class, and image type. Also, provide results of reproducibility statistics. Reproducibility metrics of selected features can be presented in tables or supplementary files. Figures (e.g., boxplots, correlation matrix, feature importance plots) and tables of descriptive summaries of features can be provided.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Patients, clinical variable models, Radiomics models. Also KM curves and correlation
	47	Model performance evaluation Provide the performance metrics for training, validation (e.g., multiple splits like cross-validation, bootstrapping, etc.), and unseen test data, separately. A summary of the most important findings should be given in the text. Provide the 'no information rate' as well. Details can be provided in figures (e.g., ROC curves, precision-recall curves) and tables. It is a good practice to provide figures for calibration statistics to show the robustness of model performance. Present additional figures to showcase examples of true and false predictions to help readers better understand the strengths and limitations of the proposed strategy.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Predictions
	48	Comparison with non-radiomic and combined approaches Give the results about the comparison of radiomic approaches with non-radiomic (e.g., visual analysis, clinical only parameters) or combined approaches in the text and preferably on a table. Present the results for training, validation, and test data, separately. Provide uncertainty measures (e.g., confidence intervals, standard deviation, etc.) and statistical comparison results with p-values for each. Confusion matrices must also be provided. Aside from the predictive performance, specify which model is superior to others in terms of clinical utility. The clinical utility can be presented with a decision curve analysis. For the decision curve analysis, quantify the net benefit according to optimal probability thresholds, with multiple cut-points associated with different clinical views. Also, provide the rationale for why a specific threshold could be appropriate and clearly state what is meant by all and none strategies.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Performance compared to other models
Discussion						
	49	Overview of important findings Provide a summary of the work and an overview of the most important findings. No statistical information is needed. Try to position the study into one of the following categories: proof of concept evaluation, technical task-specific evaluation, clinical evaluation, and post-deployment evaluation [38]. Summarize the contribution to the literature.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Discussion
	50	Previous works with differences from the current study Provide the most important and relevant previous works. Mention the most prominent differences between the current study and the previous works.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Background, Discussion
	51	Practical implications Summarize the practical implications of the results. Describe the key impact of the work on the field. Highlight the potential clinical value and role of the study. Discuss any issues that may hamper the successful translation of the study into real-world clinical practice. Also, provide future expectations and possible next steps that others might build upon the current work.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Discussion
	52	Strengths and limitations (e.g., bias and generalizability issues) Clearly state the strengths and the limitations of the current work. Any issue that may lead to potential bias, uncertainty, reproducibility, robustness, and generalizability problems should be declared.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Discussion
Open Science						
Data availability	53	Sharing images along with segmentation data [Please note this item is "not essential" but "recommended"] Provide relevant raw or processed image data considering the regulatory constraints of the institutions involved. Segmentation data can also be shared unless the segmentation is done as part of the workflow. In situations where sharing of the entire dataset is not possible, an end-to-end analysis workflow applied to a representative sample, or a public dataset with similar characteristics can facilitate the ability of the readers in reproducing key components of the analysis [39]. Also, specify the reason if the data is not available.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Github site with code, but no images and clinical data can be shared
	54	Sharing radiomic feature data Share selected radiomic feature data along with clinical variables or labels with the public, if possible (i.e., in accordance with the regulatory constraints of the institute). Specify the reason if the radiomic feature data is not available.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Github site with code, but no images and clinical data can be shared
Code availability	55	Sharing pre-processing scripts or settings Share the pre-processing and feature extraction parameter scripts or settings (e.g., YAML file in PyRadiomics or complete textual description). If it is not available in a script format, then the parameter configuration as appeared in the software program can be shared as a screenshot.	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Github site with code

	56	<p>Sharing source code for modeling Share the modeling scripts [40]. Code scripts should include sufficient information to replicate the presented analysis (e.g., to train and test pipeline), with all dependencies and relevant comments to easily understand and build upon the method. Even if the actual input dataset used cannot be shared, in situations where a similar dataset is available publicly, it should be used to share an example workflow with all pre- and post-processing steps included. Specify the reason in case the source code is not available.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Github site with code
<i>Model availability</i>	57	<p>Sharing final model files Share the final model files for internal or external testing [40]. Describe how inputs should be prepared to use the model. Also, include the source code that was used for pre-processing the input data. Specify the reason in case the final model data is not available.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Github site with code
	58	<p>Sharing a ready-to-use system [Please note this item is “not essential” but “recommended”] An easy-to-use tool (e.g., standalone executable applications, notebooks, websites, virtual machines, etc.) can be created and shared with or without source code that is based on the model created [40]. The main aim is to be able to test or validate the model by other research groups. With this approach, users even without experience in machine learning or coding can also test the proposed models.</p>	X	<input type="checkbox"/>	<input type="checkbox"/>	Github site with code

Yes, details provided; **No**, details not provided; **n/a**, not applicable

Supplementary Table 2

CLAIM: Checklist for Artificial Intelligence in Medical Imaging

Section / Topic	No.	Item	
TITLE / ABSTRACT			
	1	Identification as a study of AI methodology, specifying the category of technology used (e.g., deep learning)	X
	2	Structured summary of study design, methods, results, and conclusions	X
INTRODUCTION			
	3	Scientific and clinical background, including the intended use and clinical role of the AI approach	X
	4	Study objectives and hypotheses	X
METHODS			
<i>Study Design</i>	5	Prospective or retrospective study	X
	6	Study goal, such as model creation, exploratory study, feasibility study, non-inferiority trial	
<i>Data</i>	7	Data sources	X
	8	Eligibility criteria: how, where, and when potentially eligible participants or studies were identified (e.g., symptoms, results from previous tests, inclusion in registry, patient-care setting, location, dates)	X
	9	Data pre-processing steps	X
	10	Selection of data subsets, if applicable	NA
	11	Definitions of data elements, with references to Common Data Elements	NA
	12	De-identification methods	NA
	13	How missing data were handled	NA
<i>Ground Truth</i>	14	Definition of ground truth reference standard, in sufficient detail to allow replication	X
	15	Rationale for choosing the reference standard (if alternatives exist)	
	16	Source of ground-truth annotations; qualifications and preparation of annotators	X
	17	Annotation tools	X
	18	Measurement of inter- and intrarater variability; methods to mitigate variability and/or resolve discrepancies	X
<i>Data Partitions</i>	19	Intended sample size and how it was determined	NA
	20	How data were assigned to partitions; specify proportions	NA
	21	Level at which partitions are disjoint (e.g., image, study, patient, institution)	NA
<i>Model</i>	22	Detailed description of model, including inputs, outputs, all intermediate layers and connections	X
	23	Software libraries, frameworks, and packages	X
	24	Initialization of model parameters (e.g., randomization, transfer learning)	X

<i>Training</i>	25	Details of training approach, including data augmentation, hyperparameters, number of models trained	X
	26	Method of selecting the final model	X
	27	Ensembling techniques, if applicable	NA
<i>Evaluation</i>	28	Metrics of model performance	X
	29	Statistical measures of significance and uncertainty (e.g., confidence intervals)	X
	30	Robustness or sensitivity analysis	NA
	31	Methods for explainability or interpretability (e.g., saliency maps), and how they were validated	X
	32	Validation or testing on external data	NA
RESULTS			
<i>Data</i>	33	Flow of participants or cases, using a diagram to indicate inclusion and exclusion	X
	34	Demographic and clinical characteristics of cases in each partition	X
<i>Model performance</i>	35	Performance metrics for optimal model(s) on all data partitions	NA
	36	Estimates of diagnostic accuracy and their precision (such as 95% confidence intervals)	X
	37	Failure analysis of incorrectly classified cases	NA
DISCUSSION			
	38	Study limitations, including potential bias, statistical uncertainty, and generalizability	X
	39	Implications for practice, including the intended use and/or clinical role	X
OTHER INFORMATION			
	40	Registration number and name of registry	X
	41	Where the full study protocol can be accessed	X
	42	Sources of funding and other support; role of funders	X

Mongan J, Moy L, Kahn CE Jr. Checklist for Artificial Intelligence in Medical Imaging (CLAIM): a guide for authors and reviewers. *Radiol Artif Intell* 2020; 2(2):e200029. <https://doi.org/10.1148/ryai.2020200029>