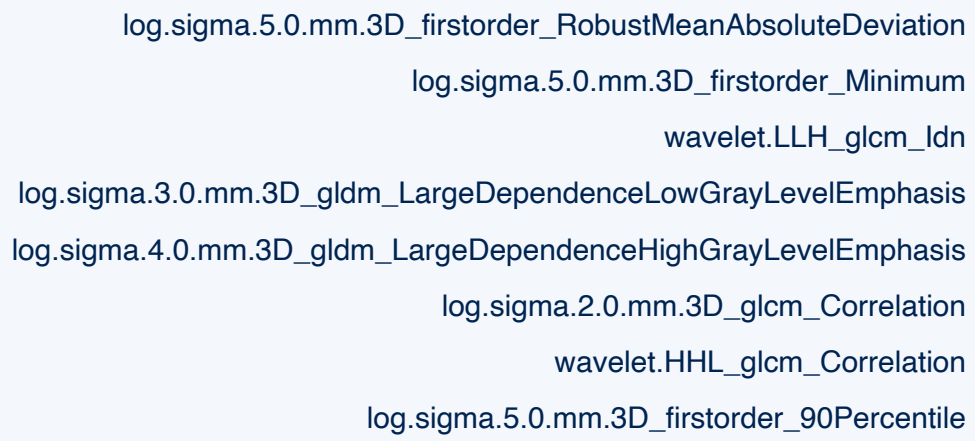


Supplementary Figure 1

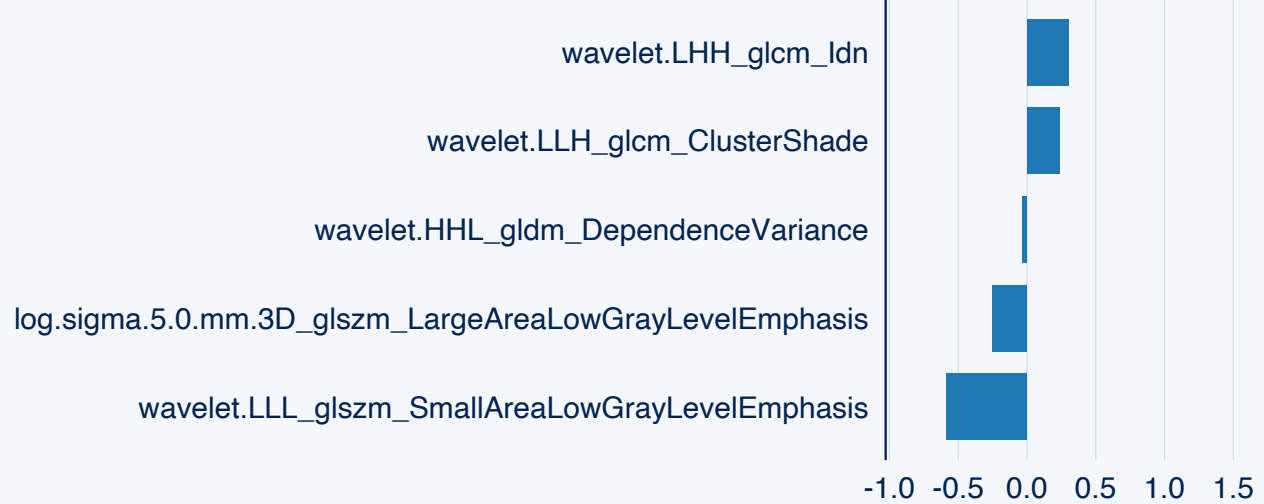
Rad\_Tumoral



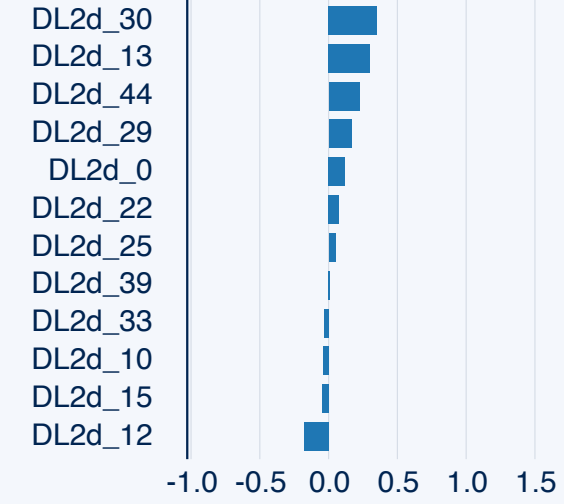
Rad\_Peritumoral\_3u



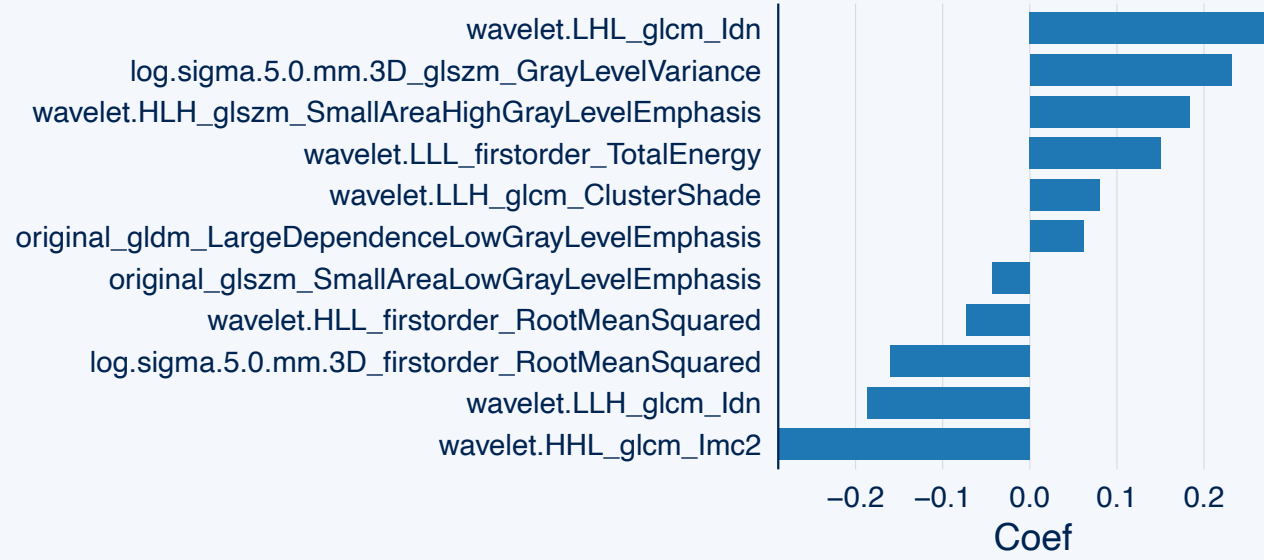
Rad\_Peritumoral\_6u



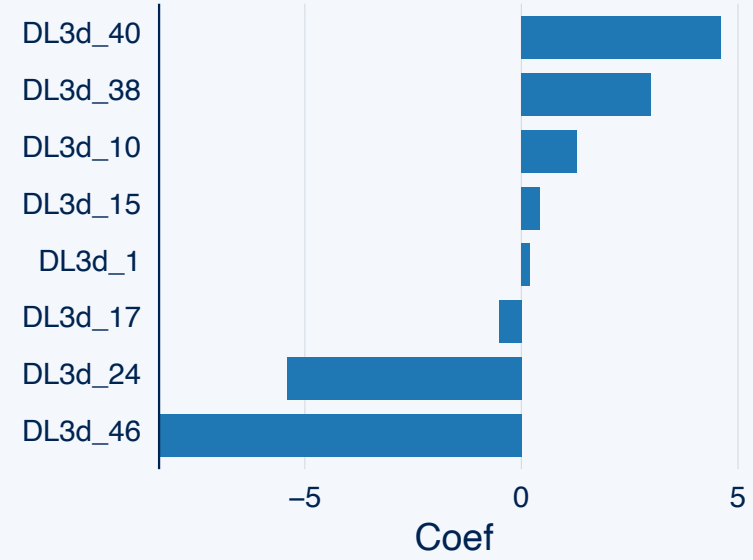
Rad\_DeepL\_2d



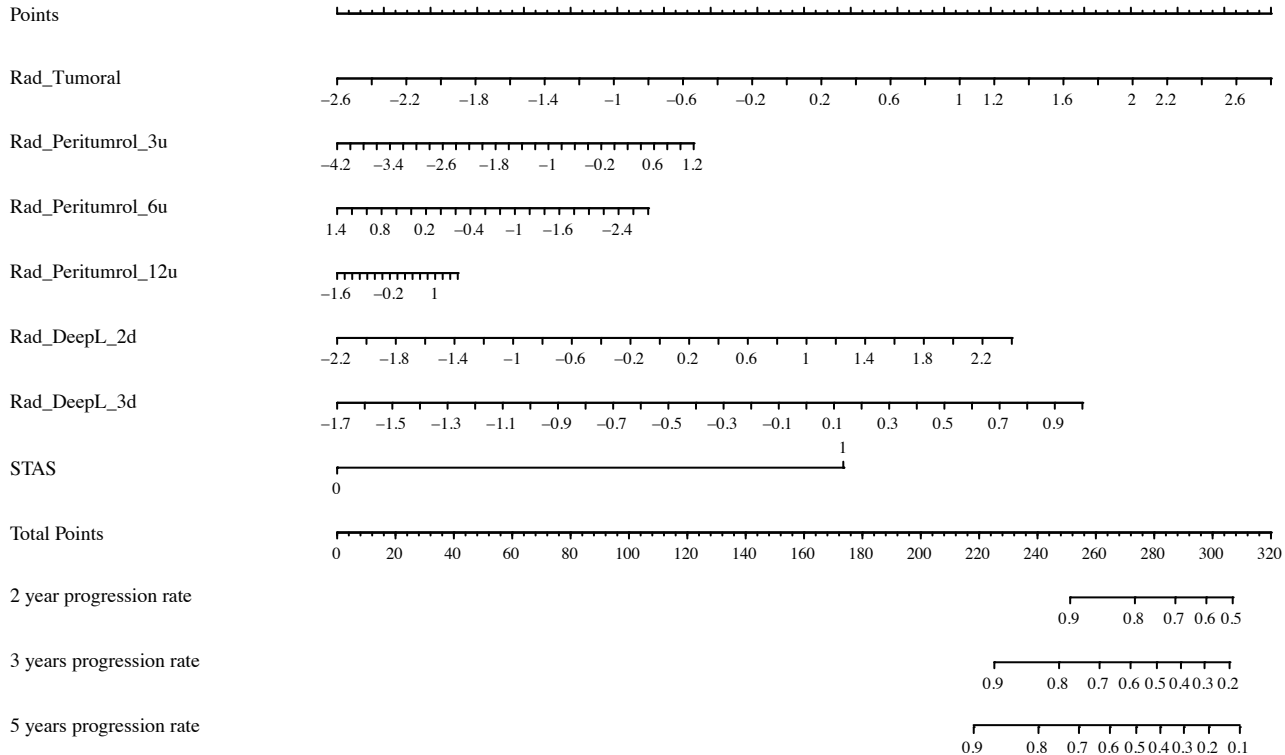
Rad\_Peritumoral\_12u



Rad\_DeepL\_3d



# Supplementary Figure 2



# Supplementary Figure 3

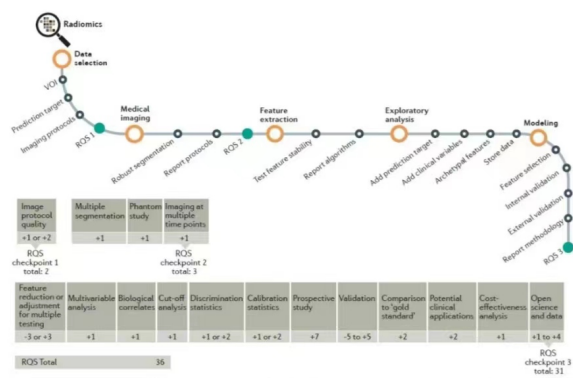


Figure 1 | Flowchart depicting the workflow of radiomics and the application of the RQS. The workflow includes the necessary steps in a radiomic analysis. The RQS both rewards and penalizes the methodology and analyses of a study, consequently encouraging the best scientific practice. RQS, radiomics quality score; VOI, volume of interest.

Image protocol quality - well-documented image protocols (for example, contrast, slice thickness, energy, etc.) and/or usage of public image protocols allow reproducibility/replicability	<input checked="" type="checkbox"/> protocols well documented <input type="checkbox"/> public protocol used <input type="checkbox"/> none
Multiple segmentations - possible actions are: segmentation by different physicians/algorithms/software, perturbing segmentations by (random) noise, segmentation at different breathing cycles. Analyse feature robustness to segmentation variabilities	<input checked="" type="radio"/> yes <input type="radio"/> no
Phantom study on all scanners - detect inter-scanner differences and vendor-dependent features. Analyse feature robustness to these sources of variability	<input checked="" type="radio"/> yes <input type="radio"/> no
Imaging at multiple time points - collect images of individuals at additional time points. Analyse feature robustness to temporal variabilities (for example, organ movement, organ expansion/shrinkage)	<input type="radio"/> yes <input checked="" type="radio"/> no
Feature reduction or adjustment for multiple testing - decreases the risk of overfitting. Overfitting is inevitable if the number of features exceeds the number of samples. Consider feature robustness when selecting features	<input checked="" type="radio"/> Either measure is implemented <input type="radio"/> Neither measure is implemented
Multivariable analysis with non radiomics features (for example, EGFR mutation) - is expected to provide a more holistic model. Permits correlating/inferencing between radiomics and non radiomics features	<input checked="" type="radio"/> yes <input type="radio"/> no
Detect and discuss biological correlates - demonstration of phenotypic differences (possibly associated with underlying gene-protein expression patterns) deepens understanding of radiomics and biology	<input type="radio"/> yes <input checked="" type="radio"/> no
Cut-off analyses - determine risk groups by either the median, a previously published cut-off or report a continuous risk variable. Reduces the risk of reporting overly optimistic results	<input checked="" type="radio"/> yes <input type="radio"/> no
Discrimination statistics - report discrimination statistics (for example, C-statistic, ROC curve, AUC) and their statistical significance (for example, p-values, confidence intervals). One can also apply resampling method (for example, bootstrapping, cross-validation)	<input checked="" type="checkbox"/> a discrimination statistic and its statistical significance are reported <input type="checkbox"/> a resampling method technique is also applied <input type="checkbox"/> none
Calibration statistics - report calibration statistics (for example, Calibration-in-the-large/slope, calibration plots) and their statistical significance (for example, P-values, confidence intervals). One can also apply resampling method (for example, bootstrapping, cross-validation)	<input type="checkbox"/> a calibration statistic and its statistical significance are reported <input type="checkbox"/> a resampling method technique is applied <input checked="" type="checkbox"/> none
Prospective study registered in a trial database - provides the highest level of evidence supporting the clinical validity and usefulness of the radiomics biomarker	<input type="radio"/> yes <input checked="" type="radio"/> no
Validation - the validation is performed without retraining and without adaptation of the cut-off value, provides crucial information with regard to credible clinical performance	<input type="checkbox"/> No validation <input checked="" type="checkbox"/> validation is based on a dataset from the same institute <input type="checkbox"/> validation is based on a dataset from another institute <input type="checkbox"/> validation is based on two datasets from two distinct institutes <input type="checkbox"/> the study validates a previously published signature <input type="checkbox"/> validation is based on three or more datasets from distinct institutes
Comparison to 'gold standard' - assess the extent to which the model agrees with/is superior to the current 'gold standard' method (for example, TNM-staging for survival prediction). This comparison shows the added value of radiomics	<input type="radio"/> yes <input checked="" type="radio"/> no
Potential clinical utility - report on the current and potential application of the model in a clinical setting (for example, decision curve analysis).	<input checked="" type="radio"/> yes <input type="radio"/> no
Cost-effectiveness analysis - report on the cost-effectiveness of the clinical application (for example, QALYs generated)	<input type="radio"/> yes <input checked="" type="radio"/> no
Open science and data - make code and data publicly available. Open science facilitates knowledge transfer and reproducibility of the study	<input checked="" type="checkbox"/> scans are open source <input checked="" type="checkbox"/> region of interest segmentations are open source <input type="checkbox"/> the code is open sourced <input checked="" type="checkbox"/> radiomics features are calculated on a set of representative ROIs and the calculated features and representative ROIs are open source