

Performance Sensitivity Analysis of Brain Metastasis Stereotactic Radiosurgery Outcome Prediction using MRI Radiomics

Supplementary Material

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Table S1. Complete catalogue of the 119 features included within the study. The number for each feature is the “Feature Look-up Number” used elsewhere such as Figure S2 and Table S3. All features not with feature type “Clinical” are radiomic features computed from the pre-treatment T1w-CE MRI, with complete documentation of the features provided by the PyRadiomics project (<https://pyradiomics.readthedocs.io/en/latest/features.html>). Underlined numbers are only to aid the reader in looking-up feature numbers. Abbreviations: Gray-Level Co-occurrence Matrix (GLCM), Gray-Level Run Length Matrix (GLRLM), Gray-Level Dependence Matrix (GLDM), Gray-Level Size Zone Matrix (GLSZM), Neighbouring Gray Tone Difference Matrix (NGTDM).

#	Feature Type	Feature Name	#	Feature Type	Feature Name
1	First Order	10 th Percentile	57	GLRLM	Gray-Level Non-Uniformity
2	First Order	90 th Percentile	58	GLRLM	Gray-Level Non-Uniformity Normalized
3	First Order	Energy	59	GLRLM	Gray-Level Variance
4	First Order	Entropy	<u>60</u>	GLRLM	High Gray-Level Run Emphasis
5	First Order	Interquartile Range	61	GLRLM	Long Run Emphasis
6	First Order	Kurtosis	62	GLRLM	Long Run High Gray-Level Emphasis
7	First Order	Maximum	63	GLRLM	Long Run Low Gray-Level Emphasis
8	First Order	Mean Absolute Deviation	64	GLRLM	Low Gray-Level Run Emphasis
9	First Order	Mean	65	GLRLM	Run Entropy
<u>10</u>	First Order	Median	66	GLRLM	Run Length Non-Uniformity
11	First Order	Minimum	67	GLRLM	Run Length Non-Uniformity Normalized
12	First Order	Range	68	GLRLM	Run Percentage
13	First Order	Robust Mean Absolute Deviation	69	GLRLM	Run Variance
14	First Order	Root Mean Squared	<u>70</u>	GLRLM	Short Run Emphasis
15	First Order	Skewness	71	GLRLM	Short Run High Gray-Level Emphasis
16	First Order	Total Energy	72	GLRLM	Short Run Low Gray-Level Emphasis
17	First Order	Uniformity	73	GLDM	Dependence Entropy
18	First Order	Variance	74	GLDM	Dependence Non-Uniformity
19	Shape & Size	Elongation	75	GLDM	Dependence Non-Uniformity Normalized
<u>20</u>	Shape & Size	Flatness	76	GLDM	Dependence Variance
21	Shape & Size	Least Axis Length	77	GLDM	Gray-Level Non-Uniformity
22	Shape & Size	Major Axis Length	78	GLDM	Gray-Level Variance
23	Shape & Size	Maximum 2D Diameter Column	79	GLDM	High Gray-Level Emphasis
24	Shape & Size	Maximum 2D Diameter Row	<u>80</u>	GLDM	Large Dependence Emphasis
25	Shape & Size	Maximum 2D Diameter Slice	81	GLDM	Large Dependence High Gray-Level Emphasis
26	Shape & Size	Maximum 3D Diameter	82	GLDM	Large Dependence Low Gray-Level Emphasis
27	Shape & Size	Mesh Volume	83	GLDM	Low Gray-Level Emphasis
28	Shape & Size	Minor Axis Length	84	GLDM	Small Dependence Emphasis
29	Shape & Size	Sphericity	85	GLDM	Small Dependence High Gray-Level Emphasis
<u>30</u>	Shape & Size	Surface Area	86	GLDM	Small Dependence Low Gray-Level Emphasis
31	Shape & Size	Surface Volume Ratio	87	GLSZM	Gray-Level Non-Uniformity
32	Shape & Size	Voxel Volume	88	GLSZM	Gray-Level Non-Uniformity Normalized
33	GLCM	Autocorrelation	89	GLSZM	Gray-Level Variance
34	GLCM	Cluster Prominence	<u>90</u>	GLSZM	High Gray-Level Zone Emphasis
35	GLCM	Cluster Shade	91	GLSZM	Large Area Emphasis
36	GLCM	Cluster Tendency	92	GLSZM	Large Area High Gray-Level Emphasis
37	GLCM	Contrast	93	GLSZM	Large Area Low Gray-Level Emphasis
38	GLCM	Correlation	94	GLSZM	Low Gray-Level Zone Emphasis
39	GLCM	Difference Average	95	GLSZM	Size Zone Non-Uniformity
<u>40</u>	GLCM	Difference Entropy	96	GLSZM	Size Zone Non-Uniformity Normalized
41	GLCM	Difference Variance	97	GLSZM	Small Area Emphasis
42	GLCM	Inverse Difference	98	GLSZM	Small Area High Gray-Level Emphasis
43	GLCM	Inverse Difference Moment	99	GLSZM	Small Area Low Gray-Level Emphasis
44	GLCM	Inverse Difference Moment Normalized	<u>100</u>	GLSZM	Zone Entropy
45	GLCM	Inverse Difference Normalized	101	GLSZM	Zone Percentage
46	GLCM	Informational Measure of Correlation 1	102	GLSZM	Zone Variance
47	GLCM	Informational Measure of Correlation 2	103	NGTDM	Busyness
48	GLCM	Inverse Variance	104	NGTDM	Coarseness
49	GLCM	Joint Average	105	NGTDM	Complexity
<u>50</u>	GLCM	Joint Energy	106	NGTDM	Contrast
51	GLCM	Joint Entropy	107	NGTDM	Strength
52	GLCM	Maximal Correlation Coefficient	108	Clinical	Gender
53	GLCM	Maximum Probability	109	Clinical	Age
54	GLCM	Sum Average	<u>110</u>	Clinical	Primary Cancer Active
55	GLCM	Sum Entropy	111	Clinical	Primary Cancer Site
56	GLCM	Sum Squares	112	Clinical	Primary Cancer Histology
			113	Clinical	Systemic Metastases Status
			114	Clinical	Systemic Therapy Status
			115	Clinical	Steroid Status
			116	Clinical	WHO Score
			117	Clinical	Gross Tumour Volume (GTV) Volume
			118	Clinical	Brain Metastasis (BM) Location
			119	Clinical	Dose and Fractionation

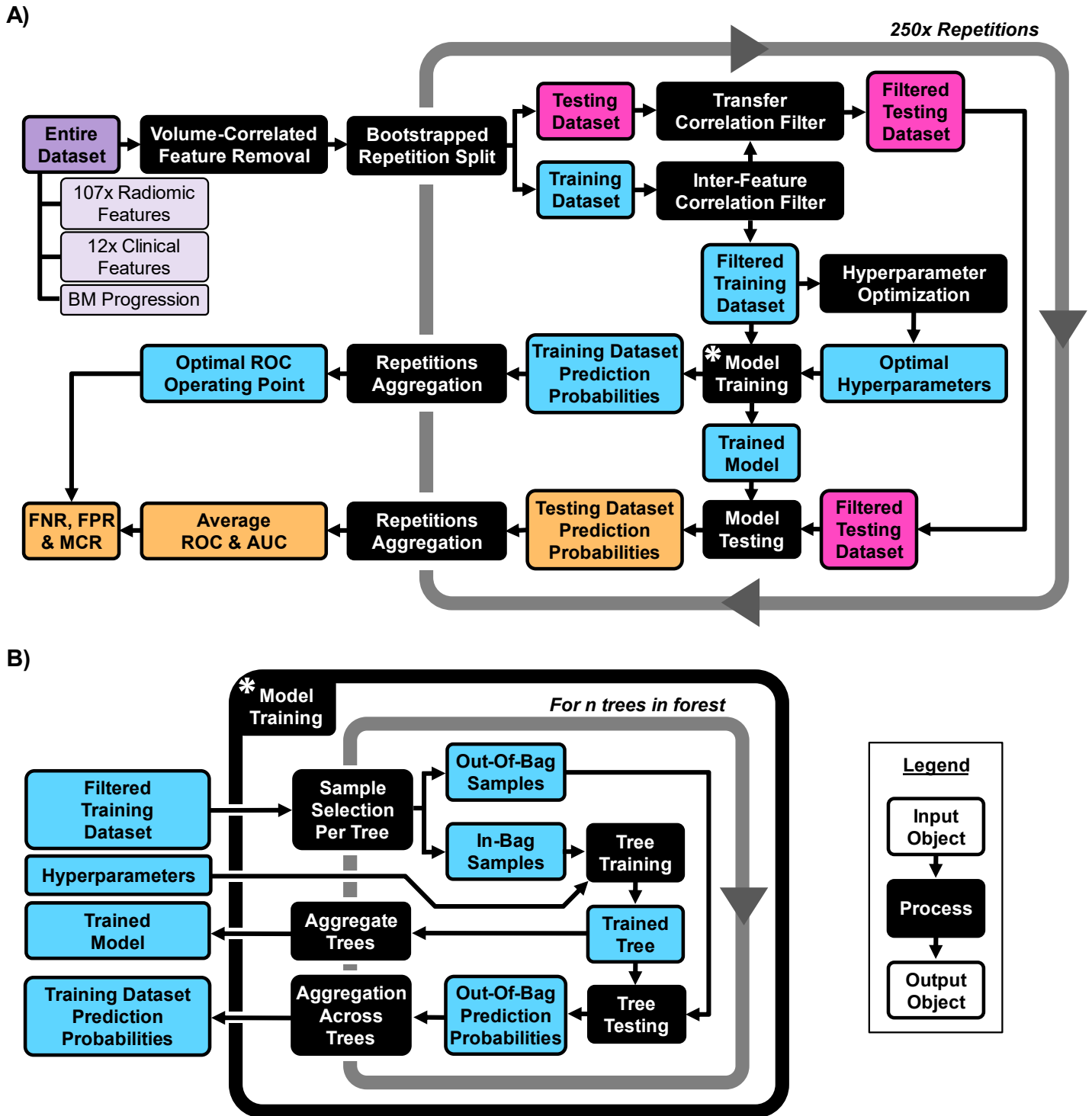


Figure S1. Schematic diagram of the machine learning experimental method technique used in the study. A) shows the overall experimental method, while B) provides enhanced detail of the model training to show how the out-of-bag samples from each tree in the random decision forest are used to produce the aggregated training dataset prediction probabilities. The colouring of the objects in the diagram is used to illustrate the separation of the entire dataset into training and testing datasets, the isolation of objects derived from each of the datasets during feature filtering and hyperparameter optimization (to prevent overfitting), and the recombination of objects from the datasets only during model testing and error metrics calculation. The inter-feature correlation filter used hierarchical clustering on the training dataset alone to determine groups of correlated features with a correlation coefficient >0.8 . For each group of correlated features, the feature most strongly correlated to BM progression was retained. This filtering of features was then transferred to the testing dataset, ensuring the testing dataset did not inform the selected features. For the experiments investigating primary cancer site and BM volume effects, the methodology shown would remain identical, except that after the “Repetitions Aggregation” processes shown in A), the training and testing dataset prediction probabilities would be grouped by the associated BMs’ primary cancers and volumes. This would lead to an optimal ROC operating point, and average ROC, AUC, MCR, FNR, and FPR per primary cancer or volume group.

Table S2. Hyperparameters for the random decision forest model used. For hyperparameters that underwent optimization, the optimization domain and search transform are provided. Numerical domains are indicated with minimum and maximum values in square brackets. Hyperparameter optimization was performed using 50 iterations of Bayesian optimization using the expected-improvement-plus acquisition function. The AUC on the out-of-bag samples was used as the optimization objective function. For hyperparameters that were not optimized, their value and justification are provided. For further descriptions of the hyperparameters, see the documentation for the *TreeBagger* function provided in Matlab 2019b.

Hyperparameter	Optimization Domain	Optimization Domain Search Transform
Number of trees	[10, 1000]	logarithmic
Number of features to sample	[1, number of features]	linear
Minimum leaf size	[1, number of features / 2]	logarithmic
Maximum number of decision splits	[1, number of samples – 1]	logarithmic
Feature selection	curvature, interaction curvature	categorical
Decision split criterion	Gini's diversity index, deviance	categorical
	Value	Justification
In-bag fraction	1	produces in-bag dataset that is the same size as the training dataset
Sample with replacement	on	allows for out-of-bag samples to be reserved for evaluating trained model using the training dataset
Cost per SRS response	equal for each response	false negatives and positives given equal cost
Prior	empirical	allows priors to be optimized for the study population
Algorithm for categorical features	exact	all combinations of categories for categorical features investigated at decision splits
Merge leaves	off	leaf merging not needed as trees are not pruned
Prune	off	tree pruning not needed as the maximum number of decision splits hyperparameter was optimized
Surrogate decision splits	10	not all surrogate splits investigated to decrease model training time
Weights	equal for each sample	all samples given equal importance during training

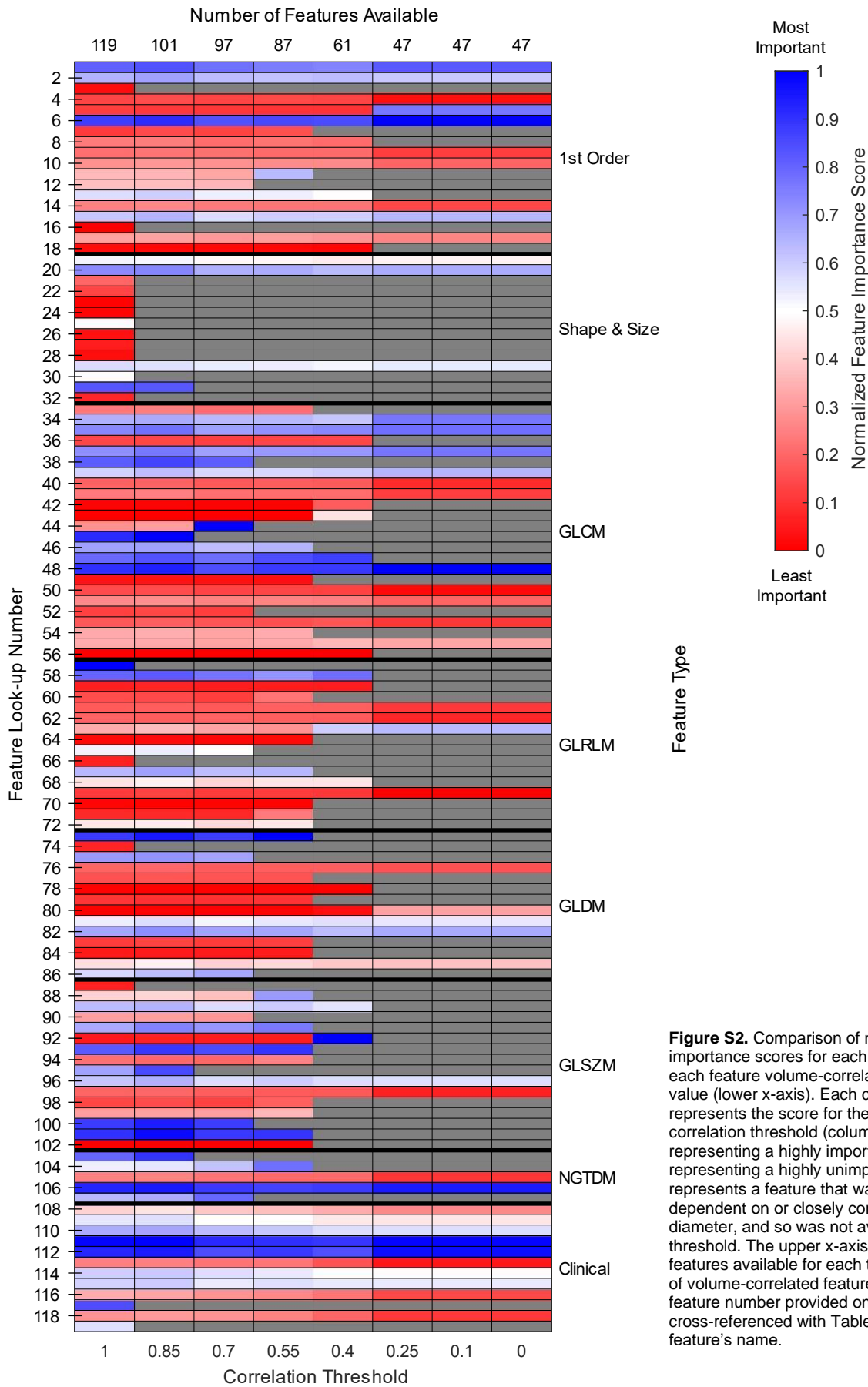


Figure S2. Comparison of normalized feature importance scores for each feature (y-axis) and for each feature volume-correlation coefficient threshold value (lower x-axis). Each colour-coded box represents the score for the given feature (row) and correlation threshold (column), with blue (1) representing a highly important feature and red (0) representing a highly unimportant feature. A grey box represents a feature that was removed due to it being dependent on or closely correlated to BM volume or diameter, and so was not available at a given threshold. The upper x-axis shows the number of features available for each threshold after the removal of volume-correlated features was performed. The feature number provided on the left y-axis can be cross-referenced with Table S1 to retrieve the given feature's name.

Table S3. Comparison of the normalized feature importance score and rank for all features with an importance score ≥ 0.75 for either correlation threshold = 1 (no features removed) or threshold = 0.25 (volume-correlated features removed). Shaded rows indicate features that were not highly important at threshold = 1, but became highly important at threshold = 0.25. Clinical features are underlined only to differentiate them more clearly against the radiomic features. The feature look-up number is provided to cross-reference this table with Figure S2, in which these look-up numbers correspond to the indices along the y-axis. Lastly, it should be noted that rows in this table are sorted according to the feature importance score/rank for correlation threshold = 0.25, and since the relative importance of the features changes at each threshold, the features are not in sorted order with respect to the threshold = 1 importance scores.

Feature Look-up Number	Feature Type	Feature Name	Correlation Threshold = 1 (No Feature Removal)		Correlation Threshold = 0.25	
			Importance Score	Importance Rank	Importance Score	Importance Rank
6	Radiomic – First Order	Kurtosis	0.878	10	1.000	1
48	Radiomic – GLCM	Inverse Variance	0.908	6	0.999	2
111	<u>Clinical</u>	<u>Primary Cancer Site</u>	0.990	2	0.992	3
112	<u>Clinical</u>	<u>Primary Cancer Histology</u>	0.926	4	0.972	4
106	Radiomic – NGTDM	Contrast	0.929	3	0.947	5
1	Radiomic – First Order	10 th Percentile	0.811	15	0.825	6
35	Radiomic – GLCM	Cluster Shade	0.736	19	0.784	7
34	Radiomic – GLCM	Cluster Prominence	0.654	28	0.769	8
37	Radiomic – GLCM	Contrast	0.720	21	0.768	9
5	Radiomic – First Order	Interquartile Range	0.122	90	0.767	10
57	Radiomic – GLRLM	Gray-Level Non-Uniformity	1.000	1	<i>No feature importance score available since these features were removed due to being volume-correlated at this correlation threshold value</i>	
45	Radiomic – GLCM	Inverse Difference Normalized	0.915	5		
101	Radiomic – GLSZM	Zone Percentage	0.902	7		
73	Radiomic – GLDM	Dependence Entropy	0.884	8		
100	Radiomic – GLSZM	Zone Entropy	0.882	9		
117	<u>Clinical</u>	<u>GTV Volume</u>	0.847	11		
31	Radiomic – Shape & Size	Surface Volume Ratio	0.832	12		
93	Radiomic – GLSZM	Large Area Low Gray-Level Emphasis	0.824	13		
38	Radiomic – GLCM	Correlation	0.818	14		
103	Radiomic – NGTDM	Busyness	0.803	16		
58	Radiomic – GLRLM	Gray-Level Non-Uniformity Normalized	0.800	17		
47	Radiomic – GLCM	Informational Measure of Correlation 2	0.795	18		