

Table S1. Eighty-six texture features extracted from each tumour segmentation

Metrics	Features
Conventional features	1. Min
	2. Mean
	3. Std
	4. Max
	5. Q1
	6. Q2
	7. Q3
	8. Skewness
	9. Kurtosis
	10. Excess Kurtosis
	11. Peak Sphere 0.5 mL: discretised volume sought
	12. Peak Sphere 0.5 mL (value only for PET or MRI)
	13. Peak Sphere 1 mL: discretised volume sought
	14. Peak Sphere 1 mL (value only for PET or MRI)
	15. Calcium Agatston Score [only for CT]
	16. TLG (mL) [only for PET or MRI]
	17. RIM_min
	18. RIM_mean
	19. RIM_stdev
	20. RIM_max
	21. RIM_Volume (mL)
	22. RIM_Volume (vx)
	23. RIM_sum
Discretised features	1. Min
	2. Mean
	3. Std
	4. Max
	5. Q1
	6. Q2
	7. Q3
	8. Skewness
	9. Kurtosis
	10. Excess Kurtosis
	11. Peak Sphere 0.5 mL: discretised volume sought
	12. Peak Sphere 0.5 mL (value only for PET or MRI)
	13. Peak Sphere 1 mL: discretised volume sought
	14. Peak Sphere 1 mL (value only for PET or MRI)
	15. TLG (mL) [only for PET or MRI]
	16. RIM_min
	17. RIM_mean
	18. RIM_stdev
	19. RIM_max
	20. RIM_sum
	21. HISTO_Skewness
	22. HISTO_Kurtosis
	23. HISTO_Excess Kurtosis
	24. HISTO_Entropy_log10
	25. HISTO_Entropy_log2
	26. HISTO_Energy [=Uniformity]
Shape features	1. Volume (mL)
	2. Volume (vx)
	3. Sphericity [only for 3DROI]
	4. Surface(mm2) [only for 3DROI]

				5. Compacity [only for 3DROI]
Grey-Level Co-occurrence Matrix (GLCM)				1. Homogeneity [=Inverse Difference]
				2. Energy [=Angular Second Moment]
				3. Contrast [=Variance]
				4. Correlation
				5. Entropy_log10
				6. Entropy_log2 [= Joint Entropy]
				7. Dissimilarity
Grey-Level Run Length Matrix (GLRLM)				1. Short Run Emphasis (SRE)
				2. Long Run Emphasis (LRE)
				3. Low Grey Run Emphasis (LGRE)
				4. High Grey Run Emphasis (HGRE)
				5. Short Run Low Grey Emphasis (SRLGE)
				6. Short Run High Grey Emphasis (SRHGE)
				7. Long Run Low Grey Emphasis (LRLGE)
				8. Long Run High Grey Emphasis (LRHGE)
				9. Grey-Level Non-Uniformity (GLNU)
				10. Run Length Non-Uniformity (RLNU)
				11. Run Percentage (RP)
Grey-Level Zone Length Matrix (GLZLM)				1. Short-Zone Emphasis (SZE)
				2. Long-Zone Emphasis (LZE)
				3. Low Grey-Level Zone Emphasis (LGZE)
				4. High Grey-Level Zone Emphasis (HGZE)
				5. Short-Zone Low Grey-Level Emphasis (SZLGE)
				6. Short-Zone High Grey-Level Emphasis (SZHGE)
				7. Long-Zone Low Grey-Level Emphasis (LZLGE)
				8. Long-Zone High Grey-Level Emphasis (LZHGE)
				9. Grey-Level Non-Uniformity (GLNU)
				10. Zone Length Non-Uniformity (ZLNU)
				11. Zone Percentage (ZP)
Neighbouring Grey-Level Difference Matrix (NGLDM)				1. Coarseness
				2. Contrast
				3. Busyness

Table S2. Diagnostic performance of texture models using support vector machine (SVM) algorithm for training and validation sets in differentiating the chondroblastic pattern from non-chondroblastic patterns (8 vs. 26)

Lesion compartment	SVM models	Principal component	AUC of training set	AUC of validation set
Intraosseous lesions	T1_intra	PC1-4	0.92	0.17
	T2_intra	PC1-3	0.93	0.76
	CE-T1_intra	PC1-4	0.89	0.48
	3-Sequence_intra	PC1-6	1.00	0.47
Extraosseous lesions	T1_extra	PC1-4	0.98	0.72
	T2_extra	PC1-3	0.94	0.89
	CE-T1_extra	PC1-5	0.99	0.67

	3-Sequence_extra	PC1-6	0.99	0.70
Entire lesions	T1_entire	PC1-4	0.95	0.58
	T2_entire	PC1-3	0.97	0.80
	CE-T1_entire	PC1-4	0.98	0.57
	3-Sequence_entire	PC1-7	0.99	0.75

Table S3. Diagnostic performance of texture models using support vector machine (SVM) algorithm for training and validation sets to predict 3-year survival (survivors vs. non-survivors, 27 vs. 7)

Lesion compartment	SVM models	Principal component	AUC of training set	AUC of validation set
Intraosseous lesions	T1_intra	PC1-4	0.99	0.88
	T2_intra	PC1-3	0.88	0.52
	CE-T1_intra	PC1-4	0.86	0.46
	3-Sequence_intra	PC1-6	0.99	0.76
Extraosseous lesions	T1_extra	PC1-4	0.98	0.51
	T2_extra	PC1-3	0.89	0.50
	CE-T1_extra	PC1-5	1.00	0.63
	3-Sequence_extra	PC1-6	0.99	0.45
Entire lesions	T1_entire	PC1-4	0.87	0.38
	T2_entire	PC1-3	0.98	0.48
	CE-T1_entire	PC1-4	0.95	0.49
	3-Sequence_entire	PC1-7	0.99	0.45

Table S4. The confusion matrix and diagnostic performance of Model T2_extra for all cases in discriminating the chondroblastic pattern from non-chondroblastic pattern

Model T2_extra	Chondroblastic pattern (n =8)	Non-chondroblastic pattern (n =26)
Model Prediction Positive	8	4
Model Prediction Negative	0	22

Sensitivity: 100%; Specificity: 84.6%; Positive predictive value: 66.7%; Negative predictive value: 100%

Table S5. The confusion matrix and diagnostic performance of Model T1_intra for all cases in predicting 3-year survival

Model T1_intra	Non-Survivor (n = 7)	Survivor (n = 27)
Model Prediction Positive	6	2
Model Prediction Negative	1	25

Sensitivity: 85.7%; Specificity: 92.5%; Positive predictive value: 75.0%; Negative predictive value: 96.2%