Supplemental Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.

eAppendix. Inclusion and Exclusion Criteria and Outcomes

The inclusion criteria were as follows: (i) female patients staged I-III and aged at least 18 years; (ii) patients had histologically confirmed unilateral primary breast cancer without distant metastasis; (iii) patients who had been treated with surgery and sentinel lymph node biopsy or ALN dissection (ALND), and had been pathologically examined to determine axillary lymph node (ALN) status; (iv) preoperative dynamic contrast–enhanced magnetic resonance imaging (DCE-MRI) scan of breast tumor and/or ALN were conducted, including contrast-enhanced T1-weighted imaging (T1+C), T2-weighted imaging (T2WI), and diffusion-weighted imaging quantitatively measured apparent diffusion coefficients (DWI-ADC); the post-neoadjuvant therapy MRI was selected when the patients undergo preoperative systemic treatment. Key exclusion criteria were: (i) patients underwent biopsy at an external institution and pathological results were not available; (ii) patients previously had non-breast cancer without complete remission for more than 3 years; (iii) insufficient DCE-MRI quality to obtain measurements; and (iv) the correlation between the breast tumor and ALN in DCE-MRI and postoperative pathologic examination was uncertain. All patients were staged according to the 8th edition of the American Joint Committee on Cancer Staging Manual.¹

The primary endpoints included ALNM and disease-free survival (DFS). DFS were defined as the time from the diagnosis of breast cancer and ALND surgery to the first relapse at any site, or confirmed time of metastatic disease, or death due to any other cause, or the date of the last follow-up visit, whichever occurred first. Secondary endpoint included overall survival (OS), which was defined as the time from diagnosis of breast cancer to death from any cause.

eReferences

1. Amin MB, Edge S, Greene F, et al. AJCC cancer staging manual, 8th edn. New York, NY: Springer; 2016.

.eFigure 1. Patient Recruitment and Study Design



In total, 1214 patients with preoperative magnetic resonance imaging from four academic institutions were enrolled in this study for model construction and validation. DFS, disease-free survival; ALN, axillary lymph node.





0

Number at risk

24



48

72

Time since diagnosis (months)

96

120

144

DFS (A) and OS (B) for patients in the entire cohort. DFS, disease-free survival; OS, overall survival; HR, hazard ratio; CI, confidence interval.

eFigure 3. Kaplan-Meier Survival Analysis Stratified by ALN Metastasis Status in the Entire Cohort



A. DFS stratified by ALN metastasis status





(A) DFS stratified by ALN metastasis status for patients in the entire cohort. (B) OS stratified by ALN metastasis status for patients in the entire cohort. DFS, disease-free survival; ALN, axillary lymph node; OS, overall survival; HR, hazard ratio; CI, confidence interval.

eFigure 4. Unsupervised Clustering Analysis of MRI Multisequence Data of Axillary Region of Interest









(A) Heatmap illustrating clustered matrix of sample-wise similarities (Entire cohort) based on multi-sequence (T1+C, T2WI and DWI-ADC) radiomic profiles of axillary lymph nodes. (B) Distribution of ALN metastasis over patient clusters defined by similarities of radiomic profile (OR 1.79, 95% CI 1.30-2.46; *P* < .001). MRI, magnetic resonance imaging; ALN, axillary lymph node; T1+C, contrast-enhanced T1-weighted imaging; T2WI, T2-weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured apparent diffusion coefficients; OR, odds ratio; CI, confidence interval.



eFigure 5. Identification of Essential Radiomic Features of T1+C, T2WI and DWI-ADC Sequences for ALN Metastasis Prediction with LASSO Regression Analysis

(A-B) T1+C sequence. (C-D) T2WI sequence. (E-F) DWI-ADC sequence. T1+C, contrast-enhanced T1-weighted imaging; T2WI, T2weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured apparent diffusion coefficients; ALN, axillary lymph node; LASSO, Least absolute shrinkage and selection operator. The LASSO model was used to select 47, 21, and 21 key features from the T1+C, T2WI, and DWI-ADC MRI sequences, respectively.

eFigure 6. ROC Curves of Radiomic Signature for ALN Metastasis Prediction in the Development and Validation Cohorts Based on LASSO–Logistic Regression Model



B. T2WI sequence radiomic signature to predict ALN metastasis



C. DWI-ADC sequence radiomic signature to predict ALN metastasis





(A) T1+C sequence radiomic signature. (B) T2WI sequence radiomic signature. (C) DWI-ADC sequence radiomic signature. (D) Combination of features from T1+C, T2WI, and DWI-ADC sequences radiomic signature. ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve; T1+C, contrast-enhanced T1-weighted imaging; T2WI, T2-weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured apparent diffusion coefficients; ALN, axillary lymph node. The logistic regression model resulted in AUCs of 0.80 and 0.68 for the T1+C signature, 0.77 and 0.72 for the T2WI signature, and 0.80 and 0.72 for the DWI-ADC signature. In addition, this model showed the AUCs of 0.88 and 0.85 for the radiomic signature in the development and validation cohorts, respectively.

eFigure 7. ROC Curves of Clinical Signature for ALN Metastasis Prediction in the Development and Validation Cohorts



Clinical signature was built based on Logistic regression model. ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve; ALN, axillary lymph node.

eFigure 8. Clinical-Radiomic Nomogram Developed in the Development Cohort to Predict Axillary Lymph Node Metastasis

Points	0 	10	20	30	40	50	60	70	80	90	100
Radiomic signature	0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	
Clinical signature	0.1	0.2 0.3	0.4	0.5 0.6	0.7	0.8 0.9					
Total Points	г 0	20	40	60		, , , , , , , 30 10	00	120	140	160	 180
ALN metastasis probability	/		0.1	0.2 0.3 0.4	0.5 0.	6 0.7 0.8	0.9				

ALN, axillary lymph node.





ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve; ALN, axillary lymph node

eFigure 10. ROC Curves of Clinical-Radiomic Nomogram for ALN Metastasis Prediction in Different Molecular Subtype in the Development and Validation Cohorts



A. Nomogram to predict ALN metastasis in Luminal A patients

B. Nomogram to predict ALN metastasis in Luminal B patients

Development cohort AUC = 0.92

0.8

1.0

0.6

False positive rate

(A) Luminal A. (B) Luminal B. (C) HER2-positive. (D) Triple negative. ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve; ALN, axillary lymph node; HER2, human epidermal growth factor receptors 2.

Development cohort AUC = 0.97

0.8

1.0

Validation cohort AUC = 0.83

0.6

False positive rate

0.4

0.2

0.0

0.0

0.2

0.4

0.4

0.2

0.0

0.0

0.2

0.4

eFigure 11. Decision Curve Analysis for ALN Metastasis in the Development and Validation Cohorts





B. Validation cohort



(A) ALN metastasis prediction. (B) DFS prediction. ALN, axillary lymph node; DFS, disease-free survival.

eFigure 12. Unsupervised Clustering Analysis of MRI Multisequence Data of Primary Breast Tumors



A. Clustered matrix for multi-sequence profiles of primary breast tumors

B. DFS stratified by cluster of primary breast tumors



(A) Heatmap illustrating clustered matrix of sample-wise similarities (Entire cohort) based on multi-sequence (T1+C, T2WI and DWI-ADC) radiomic profiles of primary breast tumors. (B) Kaplan-Meier analysis of the MRI radiomic subgroups with DFS. MRI, magnetic resonance imaging; T1+C, contrast-enhanced T1-weighted imaging; T2WI, T2-weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured apparent diffusion coefficients; DFS, disease-free survival; HR, hazard ratio; CI, confidence interval.

eFigure 13. ROC Curves of T1+C Sequence Radiomic Cignature for 1-Year, 2-Year, and 3-Year DFS Prediction based on the Random forest-Cox Regression Model



A. Development cohort





(A) Development cohort. (B) Validation cohort. T1+C, contrast-enhanced T1-weighted imaging; DFS, disease-free survival; ROC, receiver operating characteristics curve. The top 30 features identified by the random forest algorithm were also selected and used to construct a model with the coefficients weighted using the penalized Cox model that showed AUCs for the 1-, 2-, and 3-year DFS of 0.81, 0.78, and 0.73, respectively in the development cohort, for T1+C signature; and also predicted AUCs of 0.58, 0.60, and 0.63 in the validation cohort, respectively.

eFigure 14. ROC Curves of T2WI Sequence Radiomic Signature for 1-Year, 2-Year, and 3-Year DFS Prediction based on the Random Forest–Cox Regression Model



A. Development cohort

B. Validation cohort



(A) Development cohort. (B) Validation cohort. T2WI, T2-weighted imaging; DFS, disease-free survival; ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve. The top 30 features identified by the random forest algorithm were also selected and used to construct a model with the coefficients weighted using the penalized Cox model that showed AUCs for the 1-, 2-, and 3-year DFS of 0.79, 0.79, and 0.76 for the T2WI signature in the development cohort, respectively; also predicted AUCs of 0.53, 0.53, and 0.53 in the validation cohort, respectively.

eFigure 15. ROC curves of DWI-ADC Sequence Radiomic Signature for 1-Year, 2-Year, and 3-Year DFS Prediction based on the Random Forest–Cox Regression Model



A. Development cohort

(A) Development cohort. (B) Validation cohort. DWI-ADC, diffusion-weighted imaging quantitatively measured apparent diffusion coefficients; DFS, disease-free survival; ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve. The top 30 features identified by the random forest algorithm were also selected and used to construct a model with the coefficients weighted using the penalized Cox model that showed AUCs for the 1-, 2-, and 3-year DFS of 0.75, 0.78, and 0.77 for the DWI-ADC signature in the development cohort, respectively; also predicted AUCs of 0.70, 0.72, and 0.70 in the validation cohort, respectively.

eFigure 16. The Performance of Radiomic Signature Combining T1+C, T2WI, and DWI-ADC Features in Predicting DFS based on the Random Forest–Cox Regression Model



A. Radiomic signature predicted DFS in development cohort

C. DFS according to radiomic signature in development cohort



B. Radiomic signature predicted DFS in validation cohort

D. DFS according to radiomic signature in validation cohort



ROC curves of radiomic signature for 1, 2 and 3-year DFS prediction in the development (A) and validation (B) cohorts, respectively. Kaplan-Meier plots for DFS according to radiomic signature in the development (C) and validation (D) cohorts, respectively. DFS, disease-free survival; HR, hazard ratio; CI, confidence interval; ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve.

eFigure 17. Univariate Association of Clinicopathological Characteristics with DFS

	Events (n)/ patients (N) in patients with risk factor	Events (n)/ patients (N) in patients without risk factor	HR t	(95%CI)	<i>P</i> value	
Age (years)(≥40 vs <40)						_
Development cohort Validation cohort	44/702 18/286	16/147 8/79	0.59 0.66	(0.33-1.05) (0.29-1.51)	.070 .320	
Number of tumors (>1 vs 1)						
Development cohort Validation cohort	15/123 5/47	45/725 21/318	2.12 1.90	(1.18-3.80) (0.71-5.04)	.010 .190	
Histological type (Others vs Invasive ductal carcinoma)						
Development cohort Validation cohort	4/91 1/33	56/758 25/332	0.52 0.38	(0.19-1.44) (0.05-2.82)	.200 .320	
Histological grade (Grade3 (high) vs Grade1-2 (low-intermediate))						
Development cohort Validation cohort	31/328 16/139	19/383 6/183	2.00 3.73	(1.13-3.55) (1.46-9.56)	.015 .003	
Pathological T stage (T2-4 vs T1)						
Development cohort Validation cohort	36/435 18/176	24/408 7/188	1.44 2.78	(0.86-2.41) (1.16-6.65)	.170 .017	
Pathological N stage (N1-3 vs N0)	44/282	10/467	0.55	(1 49 4 40)	< 001	_
Validation cohort	19/162	7/203	2.55 3.75	(1.57-8.92)	.001	
Pathological TNM stage (II-III vs I)	49/570	10/050	4 74	(0.00.0.00)	002	_
Validation cohort	22/249	3/113	1.74 3.54	(1.06-11.84)	.083	
ER status (Positive vs Negative)	51/71/	0/133	1.05	(0.52-2.14)	800	
Validation cohort	19/302	7/60	0.52	(0.22-1.25)	.140	
PR status (Positive vs Negative)	34/608	26/238	0 40	(0 30 0 82)	005	_
Validation cohort	15/251	11/111	0.49	(0.26-1.25)	.160	
HER2 status (Positive vs Negative)	40/004	24/504	4 07	(0.70.0.05)	110	_
Validation cohort	13/114	12/206	2.19	(0.72-2.25) (1.00-4.82)	.044	
Ki67 status (≥30 vs <30)	34/370	25/464	1 08	(1 18-3 34)	009	_
Validation cohort	14/159	11/202	2.26	(1.02-5.02)	.040	
Molecular subtype (TN/HER2+ vs Lu Development cohort	i minal) 9/121	51/721	1,10	(0.54-2.23)	.800	
Validation cohort	6/55	19/306	1.79	(0.72-4.49)	.210	
Breast conversing surgery (Yes vs I	No)					
Development cohort Validation cohort	15/343 8/163	45/505 18/202	0.49 0.54	(0.27-0.87) (0.23-1.24)	.014 .140	
					Fa	vours control Favor risk
						$\longleftarrow \longrightarrow$

DFS, disease-free survival; TNM, tumor-node-metastasis; HER2, human epidermal growth factor receptors 2; ER, estrogen receptor; PR, progesterone receptors; TN, triple negative; HER2, human epidermal growth factor receptors 2; HR, hazard ratio; CI, confidence interval.



B. DFS according to clinical signature in validation cohort

eFigure 18. The Performance of Clinical Signature in Predicting DFS



A. DFS according to clinical signature in development cohort

C. Clinical signature predicted DFS in development cohort

D. Clinical signature predicted DFS in validation cohort



Kaplan-Meier plots for DFS according to clinical signature in the development (A) and validation (B) cohorts, respectively. ROC curves of clinical signature for 1, 2 and 3-year DFS prediction in the development (C) and validation (D) cohorts, respectively. DFS, disease-free survival; HR, hazard ratio; CI, confidence interval; ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve.

eFigure 19. Clinical-Radiomic Nomogram Developed in the Development Cohort to Predict 1-Year, 2-Year, and 3-Year DFS



DFS, disease-free survival.

eFigure 20. ROC Curves of Clinical-radiomic Nomogram for 1-Year, 2-Year, and 3-year DFS Prediction in Different Institutions



Kaplan-Meier plots for DFS according to clinical-radiomic nomogram in the SYSMH/SYSUCC (A) and SYSUTH/SMUSH (B) cohorts, respectively. ROC curves of clinical-radiomic nomogram for 1, 2 and 3-year DFS prediction in the SYSMH/SYSUCC (A) and SYSUTH/SMUSH (B) cohorts, respectively. DFS, disease-free survival; HR, hazard ratio; CI, confidence interval; ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve.

eFigure 21. ROC Curves of Clinical-Radiomic Nomogram for 1-Year, 2-Year, and 3-year DFS Prediction in Different Molecular Subtypes in the Entire Cohort



(A) Luminal A. (B) Luminal B. (C) HER2-positive. (D) Triple negative. DFS, disease-free survival; ROC, receiver operating characteristic; AUC, area under the receiver operating characteristics curve; HER2, human epidermal growth factor receptors 2.

eFigure 22. Decision Curve Analysis for DFS Prediction in the Development and Validation Cohorts



A. Development cohort

B. Validation cohort



(A) Development cohort. (B) Validation cohort. DFS, disease-free survival.

eTable 1. Information of 4 Institutions in Thi			
Institution	Investigator in Charge	No. of Patients Enrolled	Time of Patients Enrolled
Sun Yat-Sen Memorial Hospital	Herui Yao	622	November 17, 2011 to December 25, 2018
Sun Yat-Sen University Cancer Center	Chuanmiao Xie	381	July 03, 2007 to August 26, 2019
Tungwah Hospital of Sun Yat-Sen University	Jie Ouyang	90	July 08, 2013 to September 21, 2019
Shunde Hospital of Southern Medical University	Qiugen Hu	121	March 09, 2012 to December 18, 2018

Hospital	Scanner	Sequence	TR/TE (ms)	FOV (mm)	Matrix	Slice Thickness (mm)	Slice Gap (mm)	Slices	Flip Angle	Acquisition Time (min)	Scans
	Philips 1.5T	T2WI	4000/60	337×240	400×318	3	0	55	90°	4min	
	(Achieva)	DWI-ADC	7439/53	363×340	360×301	3	0	55	90°	4min35s	
		T1+C	3.3/1.54	320×250	217×172	1	0	55	10°	7min	55
	Philips 3.0T	T2WI	4000/60	337×240	400×318	3	0	55	90°	4min	
		DWI-ADC	7439/53	363×340	360×301	3	0	55	90°	4min35s	
SYSMH	(T1+C	3.3/1.54	320×250	217×172	1	0	55	10°	7min	55
	Siemens 1 5T	T2WI	2760/107	350×350	320×224	5	1	30	150°	2min46s	
	(Avanto)	DWI-ADC	5400/119	400×252	200×170	6	1.8	20	180°	2min34s	
	Siemens 3.0T	T1+C	4.95/2.2	380×269	288×216	3	0.6	48-72	10°	5-7min	50/70
		T2WI	7600/75	340×340	448×358	4	0.8	35	116°	3min42s	
		DWI-ADC	7620/64	360×310	192×192	4	0.8	35	180°	1min54s	
		T1+C	3.25/1.22	380×327	256×218	2.5	0.5	48-72	10°	5-7min	50/70

eTable 2. MR Scanning Parameters for the Patients

	United Imaging	T2WI	3600/74.34	340×340	336×335	5	1	24	90°	3min05s	
	3.0T	DWI-ADC	3597/67.2	350×350	350×190	6	1	24	90°	1min33s	
SYSUCC	(China)	T1+C	4.3/1.99	340×340	336×335	0.67	0	204	10°	9min58s	8
	GE 3.0T	T2WI	3912/107.64	380×380	416×256	5	1	28	111°	1min59s	
	(USA)	DWI-ADC	4168/60.2	380×380	128×160	5	1	48	-	1min40s	
		T1+C	4.3/1.7	360×360	256×320	1	0	204	5°	9min50s	8

Hospital	Scanner	Sequence	TR/TE (ms)	FOV (mm)	Matrix	Slice Thickness (mm)	Slice Gap (mm)	Slices	Flip Angle	Acquisition Time (min)	Scans
	Philips 1.5T	T2WI	3400/90	260×320	348×299	3	0.3	44	120°	4min4s	
	(Achieva)	DWI-ADC	2000/103	320×320	160×160	5	1	32	90°	1min36s	
SYSUTH	(ricine rd)	T1+C	5.4/2.4	300×320	300×320	1	0	300	15°	7min2s	6
	Philips 3.0T	T2WI	4495/70	280×340	332×377	3	0	52	90°	3min53s	
		DWI-ADC	7011/67	320×340	148×153	4	1	30	90°	1min24s	
		T1+C	4.8/2.1	280×340	280×339	1	0	300	12°	6min59s	6
	Philips 1.5T	T2WI	4518/70	320×260	256×159	4	0.07	36	120°	3min19s	
	(Achieva)	DWI-ADC	5837/67	365×221	124×73	3	1	36	90°	3min59s	
SMUSH		T1+C	6.0/2.9	350×255	252×243	2	1	150	10°	6min42s	9
Siriosit	Siemens 3.0T	T2WI	4290/78	128×332	332×128	4	1	30	180°	1min22s	
	(Skyra)	DWI-ADC	6560/49	340×172	66×130	4	0.8	37	180°	3min51s	
		T1+C	5.59/1.96	154×338	562×256	2	0.4	72	10°	7min15s	6

Abbreviations: FOV, field of view; TR, repetition time; TE, echo time; T1+C, contrast-enhanced T1-weighted imaging; T2WI, T2-weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured

apparent diffusion coefficients; SYSMH, Sun Yat-sen Memorial Hospital of Sun Yat-sen University; SYSUCC, Sun Yat-sen University Cancer Center; SYSUTH, Tungwah Hospital of Sun Yat-sen University; SMUSH, Shunde Hospital of Southern Medical University.

		Feature Selection	LASS	80	Ra	ndom Forest
Signature	Cohort	Classifer	Logistic Regression	SVM	Logistic Regression	SVM
			(AUC)	(AUC)	(AUC)	(AUC)
T1+C sequence radiomic signature						
	Development		0.80	0.81	0.77	0.77
	Validation		0.68	0.68	0.54	0.65
T2WI sequence radiomic signature						
	Development		0.77	0.82	0.79	0.79
	Validation		0.72	0.69	0.62	0.68
DWI-ADC sequence radiomic signature						
	Development		0.80	0.82	0.79	0.79
	Validation		0.72	0.74	0.71	0.75
Radiomic signature						
	Development		0.88	0.86	0.94	0.86

	Validation		0.8	5	0.74		0.53	0.75	
Abbreviations: LASSO, Least absolute shrinkage and selection operator; SVM, support vector machine; AUC, area under the receiver operating characteristics curve; T1+C, contrast-									
enhanced T1-weighted imaging; T2WI, T2-weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured apparent diffusion coefficients.									

eTable 4. The Performance of Different Region of Interest Constructed for Axillary Lymph Node Metastasis Prediction Based on LASSO–Logistic Regression Model

Signature Performance	ALN radiomic signature			Tumor radio	omic signature		Combination of tumor and ALN radiomic signature				
	Training Cohort	Validation Cohort		Training Cohort	ing Cohort Validation Cohort		Training Cohort	Validation Cohort			
AUC	0.88	0.85		0.86	0.60		0.90	0.71			
Abbreviations: AUC, area under the receiver operating characteristics curve; ALN, axillary lymph node.											

eTable 5. Essential Radiomic Features and Formula Composition for ALN									
Metastasis Prediction based on LASSO–Logistic Regression Model									
Model	Intercept/Feature Name	Coefficie nt							
T1+C sequence signature	Intercept=0.0117	β							
	wavelet-HHL-glrlm-LongRunEmphasis	0.8756							
	wavelet-LLL-glrlm-RunPercentage	-0.5771							
	wavelet-HHH-glrlm-RunPercentage	-1.1337							
	wavelet-LLH-gldm-LargeDependenceEmphasis	0.3085							
	wavelet-LHL-gldm-LargeDependenceEmphasis	-0.6641							

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wavelet-HHH-gldm- LargeDependenceLowGrayLevelEmphasis	0.2296
wavelet-LHH-gldm- LargeDependenceLowGrayLevelEmphasis	0.3373
wavelet-HLH-glszm-LargeAreaHighGrayLevelEmphasis	0.2097
wavelet-HHH-glszm-LargeAreaHighGrayLevelEmphasis	-0.4906
Intercept/Feature Name	Coefficie nt
wavelet-LHH-glrlm-RunLengthNonUniformity	-0.6072
wavelet-LHL-glrlm-GrayLevelNonUniformity	0.2640
	<pre>wavelet-HHH-gldm- LargeDependenceLowGrayLevelEmphasis wavelet-LHH-gldm- LargeDependenceLowGrayLevelEmphasis wavelet-HLH-glszm-LargeAreaHighGrayLevelEmphasis wavelet-HHH-glszm-LargeAreaHighGrayLevelEmphasis Intercept/Feature Name wavelet-LHH-glrlm-RunLengthNonUniformity wavelet-LHL-glrlm-GrayLevelNonUniformity</pre>

wavelet-HHH-glszm-ZoneVariance	0.9074
original-gldm-LargeDependenceHighGrayLevelEmphasis	0.3005
wavelet-LLL-glszm-LargeAreaEmphasis	1.3307
wavelet-LHH-ngtdm-Coarseness	0.7035
wavelet-LHL-gldm-DependenceNonUniformity	0.3525
wavelet-HHH-glszm-LargeAreaEmphasis	-0.1849
wavelet-HLL-glrlm-RunPercentage	0.3038
wavelet-LLH-glrlm-RunLengthNonUniformity	0.5444
wavelet-HLH-glszm-LargeAreaLowGrayLevelEmphasis	0.6363
wavelet-HHL-glcm-MCC	0.3582

Model	Intercent/Feature Name	Coefficie
Model		nt
	wavelet-LHH-glrlm-RunPercentage	0.7261
	wavelet-LLH-glrlm-RunVariance	0.2819
	wavelet-LLH-gldm-	0 2947
	LargeDependenceHighGrayLevelEmphasis	0.2317
	original-glrlm-LongRunLowGrayLevelEmphasis	-1.0968
	wavelet-LHL-glcm-ldn	-0.4321
	wavelet-LHL-gldm-	-0.0675
	LargeDependenceLowGrayLevelEmphasis	0.0075
	original-firstorder-Maximum	0.0539

	wavelet-HLL-glrlm-ShortRunEmphasis	0.2819	
	wavelet-LLL-glrlm-RunVariance	0.6957	
	wavelet-LHH-gldm-SmallDependenceEmphasis	-1.1549	
	wavelet-LHL-gldm-	0.0572	
	LargeDependenceHighGrayLevelEmphasis	-0.0573	
	wavelet-HLL-gldm-	-0 1610	
	LargeDependenceHighGrayLevelEmphasis	0.1010	
	wavelet-LLH-glrlm-RunEntropy	0.5479	
Model	Intercent/Feature Name	Coefficie	
		nt	
	wavelet-LLH-gldm-	-0 1522	
	LargeDependenceLowGrayLevelEmphasis	-0,1322	

wavelet-LLL-glcm-InverseVariance					
wavelet-LHL-glcm-Imc2	0.0455				
wavelet-LLL-glcm-MCC	-0.1096				
wavelet-LLH-ngtdm-Coarseness	-0.1286				
wavelet-LLL-glcm-ClusterShade	-0.1054				
wavelet-HHL-glrlm-RunLengthNonUniformityNormalized	0.7591				
wavelet-HLH-gldm-SmallDependenceEmphasis	-0.3403				
original-shape-MajorAxisLength	-0.5406				
wavelet-LHH-glcm-Imc2	0.3851				
wavelet-LHH-gldm- LargeDependenceHighGrayLevelEmphasis	-0.3265				

	wavelet-HHL-gldm-DependenceVariance	-0.6298
Model	Intercept/Feature Name	Coefficie
		nt
T2WI sequence	Intercept=18.5770	β
signature		
	wavelet-HHH-glrlm-RunPercentage	0.0642
	wavelet-HHL-glrlm-LongRunEmphasis	0.1320
	original-gldm-LargeDependenceHighGrayLevelEmphasis	0.6104
	wavelet-HHL-glrlm-RunPercentage	-0.1379
	original-firstorder-RobustMeanAbsoluteDeviation	0.2757

	wavelet-LHH-glrlm-LongRunLowGrayLevelEmphasis	0.1135
	wavelet-HHL-glrlm-LongRunLowGrayLevelEmphasis	0.3070
	wavelet-LLH-glrlm-RunEntropy	-0.0844
	wavelet-LHL-firstorder-RobustMeanAbsoluteDeviation	0.8842
	wavelet-LLH-glrlm-LongRunEmphasis	0.3321
	wavelet-LLH-glcm-Imc2	0.3802
Model	Intercept/Feature Name	Coefficie
		nt
	original-glrlm-RunVariance	-0.0206
	wavelet-LLL-glszm-LargeAreaEmphasis	0.0775
	wavelet-HLL-firstorder-Entropy	0.2048

	original-glrlm-LongRunEmphasis	0.2054
	wavelet-LLL-glcm-MCC	0.1532
	wavelet-LLH-firstorder-RootMeanSquared	-0.1024
	original-shape-MajorAxisLength	-0.7563
	wavelet-LLH-firstorder-MeanAbsoluteDeviation	0.1581
	wavelet-LHL-glcm-InverseVariance	0.5645
	wavelet-LHL-ngtdm-Coarseness	506.9233
DWI-ADC		
sequence	Intercept=-0.0766	β
signature		

Model	Intercent/Feature Name	Coefficie
Model		
	wavelet-HHH-glrlm-RunPercentage	-0.5917
	diagnostics-Mask-interpolated-VoxelNum	0.2623
	wavelet-LLH-glcm-InverseVariance	0.1956
	wavelet-HLL-glcm-MCC	-0.0220
	wavelet-LLL-firstorder-Energy	0.3723
	wavelet-HLL-firstorder-RobustMeanAbsoluteDeviation	0.1601
	diagnostics-Mask-interpolated-VoxelNum	0.2623
	wavelet-LLH-glcm-InverseVariance	0.1956
	wavelet-HLL-glcm-MCC	-0.0220

	wavelet-LLL-firstorder-Energy	0.3723
	wavelet-HLL-firstorder-RobustMeanAbsoluteDeviation	0.1601
	wavelet-HHL-glcm-InverseVariance	0.2763
	wavelet-HLH-glszm-LargeAreaEmphasis	0.7292
Model	Intercept/Feature Name	Coefficie
		nt
	wavelet-HLH-glcm-InverseVariance	0.2603
	wavelet-HHH-glcm-InverseVariance	-0.0881
	wavelet-LHH-glszm-SmallAreaEmphasis	0.4704
	wavelet-LHH-glrlm-RunEntropy	0.0861
	wavelet-HLL-glszm-ZonePercentage	1.4259

	original-shape-MajorAxisLength						
	wavelet-LLL-glszm-LargeAreaHighGrayLevelEmphasis						
	wavelet-LLH-glcm-Imc2						
	wavelet-HLL-gldm-	0 5429					
	LargeDependenceLowGrayLevelEmphasis	0.5423					
	original-shape-Maximum3DDiameter	-0.9503					
	wavelet-HLL-ngtdm-Busyness	-0.7014					
	wavelet-LHL-glszm-LargeAreaHighGrayLevelEmphasis	0.7596					
	original-ngtdm-Coarseness	1.2341					
Model	Intercept/Feature Name						
		nt					

Radiomic signature	Intercept=-3.8489				
	T1+C sequence signature	4.7965			
	T2WI sequence signature	0.4580			
	DWI-ADC sequence signature	2.8023			
Clinical signature	Intercept=-2.9171	β			
	Clinical T stage	0.4001			
	Clinical N stage	1.8991			
	Histological grade	0.1638			
	Age	-0.0160			

	HER2 status	-0.1295		
Clinical- radiomic Nomogram	Intercept=-4.1190	β		
Model	Intercept/Feature Name			
		nt		
	Radiomic signature	4.5678		
	Radiomic signature Clinical signature	4.5678 4.1789		

	Deve	lopment coho	rt	Valie	dation cohort		E	ntire cohort	
Characteristic	Axillary Lymph Node Status		Axillary Lymph Node Status			Axillary Lymph Node Status			
	No. (%) Negative	No. (%) Positive	P value	No. (%) Negative	No. (%) Positive	<i>P</i> value	No. (%) Negative	No. (%) Positive	<i>P</i> value
Age, years			.007			.023			< .001
<40	66 (14.1)	81 (21.2)		35(17.2)	44 (27.2)		101 (15.1)	125 (23.0)	
≥40	401 (85.9)	301 (78.8)		168 (82.8)	118 (72.8)		569 (84.9)	419 (77.0)	
Number of tumors			.885			.027			.189
1	400 (85.7)	325 (85.3)		184 (90.6)	134 (82.7)		584 (87.2)	459 (84.5)	
>1	67 (14.3)	56 (14.7)		19 (9.4)	28 (17.3)		86 (12.8)	84 (15.5)	
Histological type			.123			.389			.385
Invasive ductal carcinoma	410 (87.8)	348 (91.1)		187 (92.1)	145(89.5)		597 (89.1)	493 (90.6)	
Others	57 (12.2)	34 (8.9)		16 (7.9)	17 (10.5)		73 (10.9)	51 (9.4)	
Histological grade			< .001			.576			< .001
Grade 1 (low)	14 (3.7)	4 (1.2)		12 (6.5)	3 (2.2)		26 (4.6)	7 (1.5)	
Grade 2 (intermediate)	211 (55.5)	154 (46.5)		92 (50.0)	76 (55.1)		303 (53.7)	230 (49.0)	

Grade 3 (high)	155 (40.8)	173 (52.3)		80 (43.5)	59 (42.8)		235 (41.7)	232 (49.5)	
Clinical T stage			< .001			< .001			< .001
T1	205 (44.0)	97 (25.4)		98 (48.3)	44 (27.2)		303 (45.3)	141 (25.9)	
T2	235 (50.4)	244 (63.9)		94 (46.3)	104 (64.2)		329 (49.2)	348 (64.0)	
Т3	19 (4.1)	32 (8.4)		9 (4.4)	9 (5.6)		28 (4.2)	41 (7.5)	
T4	7 (1.5)	9 (2.4)		2 (1.0)	5 (3.1)		9 (1.3)	14 (2.6)	
Clinical N stage			< .001			< .001			< .001
NO	391 (83.7)	160 (41.9)		158 (77.8)	66 (40.7)		549 (81.9)	226 (41.5)	
N1	74 (15.8)	185 (48.4)		44 (21.7)	85 (52.5)		118 (17.6)	270 (49.6)	
N2	2 (0.4)	33 (8.6)		0 (0.0)	9 (5.6)		2 (0.3)	42 (7.7)	
N3	0 (0.0)	4 (1.0)		1 (0.5)	2 (1.2)		1 (0.1)	6 (1.1)	
Clinical TNM stage			< .001			< .001			< .001
1	180 (38.6)	52 (13.6)		85 (41.9)	26 (16.0)		265 (39.6)	78 (14.3)	
11	270 (57.9)	268 (70.2)		112 (55.2)	115 (71.0)		382 (57.1)	383 (70.4)	
Ш	16 (3.4)	62 (16.2)		6 (3.0)	21 (13.0)		22 (3.3)	83 (15.3)	
ER status			.341			.632			.601
Negative	68 (14.6)	65 (17.0)		35 (17.4)	25 (15.5)		103 (15.5)	90 (16.6)	
ER status Negative	68 (14.6)	65 (17.0)	.341	35 (17.4)	25 (15.5)	.632	103 (15.5)	90 (16.6)	.60

Positive	397 (85.4)	317 (83.0)		166 (82.6)	136 (84.5)		563 (84.5)	453 (83.4)	
PR status			.935			.754			.911
Negative	130 (28.0)	108 (28.3)		63 (31.3)	48 (29.8)		193 (29.0)	156 (28.7)	
Positive	334 (72.0)	274 (71.7)		138 (68.7)	113 (70.2)		472 (71.0)	387 (71.3)	
HER2 status			.337			< .001			< .001
Negative	296 (71.5)	228(68.3)		128 (72.3)	78 (54.5)		424 (71.7)	306 (64.2)	
Positive	118 (28.5)	106 (31.7)		49 (27.7)	65 (45.5)		167 (28.3)	171 (35.8)	
Ki67 status			.350			.867			.488
<15	125 (27.0)	87 (22.9)		54 (27.0)	36 (22.4)		179 (27.0)	123 (22.7)	
15-35	202 (43.6)	169 (44.5)		86 (43.0)	79 (49.1)		288 (43.4)	248 (45.8)	
35-55	61 (13.2)	66 (17.4)		24 (12.0)	25 (15.5)		85 (12.8)	91 (16.8)	
>55	75 (16.2)	58 (15.3)		36 (18.0)	21 (13.0)		111 (16.7)	79 (14.6)	
Molecular subtypes			.102			.489			.326
Luminal A	95 (21.2)	59 (16.1)		39 (20.1)	21 (13.5)		134 (20.9)	80 (15.3)	
Luminal B	291 (65.0)	248 (67.8)		121 (62.4)	114 (73.1)		412 (64.2)	362 (69.3)	
HER2-positive	33 (7.4)	31 (8.5)		12 (6.2)	16 (10.3)		45 (7.0)	47 (9.0)	
Triple negative	29 (6.5)	28 (7.7)		22 (11.3)	5 (3.2)		51 (7.9)	33 (6.3)	
		1	1		1	1		1	

Abbreviations: TNM, tumor-node-metastasis; HER2, human epidermal growth factor receptors 2; ER, estrogen receptor; PR, progesterone receptors; Ki67, proliferation marker protein Ki-67.

eTable 7. Multivariate Analysis of Axillary Lymph Node Metastasis in Relation to Clinical Signature and Radiomic Signature in the Development Cohort

alysis	Multivariate	Signatura	
P value	OR (95%CI)	Signature	
< .001	6.88 (3.90-12.33)	Radiomic signature (high-risk/low-risk)	
< .001	9.82 (5.22-19.29)	Clinical signature (high-risk/low-risk)	
	9.82 (5.22-19.29)	Clinical signature (high-risk/low-risk) Abbreviations: OR, Odds ratio; CI, confidence interval.	

eTable 8. The Performance of Each Signature Constructed With Different Algorithm for DFS Prediction

		Feature Selection	LASSO		Random	Forest
Signature	Signature Performance	Signature Building	Cox Regression		Cox Regr	ression
		Cohort	Development Cohort	Validation Cohort	Development Cohort	Validation Cohort
T1+C sequence radiomic signature						
	1-year AUC		0.84	0.44	0.81	0.58
	2-year AUC		0.80	0.50	0.78	0.60
	3-year AUC		0.75	0.53	0.73	0.63
T2WI sequence radiomic signature						
	1-year AUC		0.74	0.61	0.79	0.53
	2-year AUC		0.70	0.62	0.79	0.53
	3-year AUC		0.64	0.53	0.76	0.47
DWI-ADC sequence radiomic signature						
	1-year AUC		0.69	0.73	0.75	0.70
	2-year AUC		0.67	0.77	0.78	0.72
	3-year AUC		0.61	0.82	0.77	0.70
Radiomic signature						
	1-year AUC		0.83	0.54	0.80	0.68

	2-year AUC		0.82	0.64		0.83	0.74
	3-year AUC		0.78	0.66		0.81	0.73
Abbreviations: LASSO, Least absolute shrinkage and selection operator; AUC, area under the receiver operating characteristics curve; T1+C,							
contrast-enhanced T1-weighted imaging; T2WI, T2-weighted imaging; DWI-ADC, diffusion-weighted imaging quantitatively measured apparent							
diffusion coefficients.							

eTable 9. Essential Radiomic Features and Formula Composition for					
DFS Prediction					
Model	Feature Name	Coefficient			
T1+C sequence					
signature					
	wavelet-HLL-glszm-SizeZoneNonUniformity	0.8513			
	wavelet-HHH-glrlm-RunPercentage	-0.0566			
	wavelet-LHH-firstorder-Uniformity	-0.0849			
	wavelet-HHL-glszm-ZoneEntropy	-1.1890			
	wavelet-LHH-glszm-SizeZoneNonUniformity	0.8160			
	wavelet-LHL-glrlm-RunLengthNonUniformity	0.0644			

	wavelet-HHH-glszm-SizeZoneNonUniformity	0.4476
	wavelet-HLH-firstorder-Kurtosis	0.1274
	wavelet-HHL-glszm-GrayLevelNonUniformity	-2.1320
Model	Feature Name	Coefficient
	wavelet-LHH-glrlm-GrayLevelNonUniformity	0.2053
	wavelet-HHL-glszm-SizeZoneNonUniformity	47.7500
	wavelet-LHH-firstorder-Kurtosis	0.2448
	wavelet-HHL-glszm-	
	SizeZoneNonUniformityNormalized	-44.0300
	wavelet-LLH-glszm-	
	SmallAreaLowGrayLevelEmphasis	0.5448
	original-shape-Maximum2DDiameterColumn	0.5991

	wavelet-LLH-glcm-Contrast	-0.1834
	wavelet-LHH-ngtdm-Strength	-0.0083
	wavelet-HLH-glszm-SizeZoneNonUniformity	-1.0020
	wavelet-LHH-firstorder-10Percentile	-0.3406
	original-shape-MeshVolume	0.2630
	original-shape-Sphericity	0.2054
	wavelet-LLL-firstorder-Energy	-1.7020
	wavelet-LLH-firstorder-TotalEnergy	-0.4103
Model	Feature Name	Coefficient
	wavelet-HLH-firstorder-10Percentile	0.3420
	wavelet-HHL-ngtdm-Contrast	0.1668

	wavelet-LLH-glszm-ZoneEntropy	-0.0813
	wavelet-HHH-glszm-ZoneEntropy	-0.7329
	wavelet-LLH-firstorder-InterquartileRange	-1.1560
	wavelet-HLH-firstorder-Uniformity	-0.6731
	wavelet-HHH-firstorder-Kurtosis	0.5630
T2WI sequence		
signature		
	wavelet-HLL-glszm-GrayLevelNonUniformity	-0.0563
	wavelet-LHH-glrlm-GrayLevelNonUniformity	-0.6585
	wavelet-HHL-glszm-SizeZoneNonUniformity	3.7646
	wavelet-HHH-glszm-	
	SizeZoneNonUniformityNormalized	-2.0030

	wavelet-HLL-firstorder-Mean	-4.9581
Model	Feature Name	Coefficient
	original-shape-Sphericity	0.0977
	wavelet-HLL-firstorder-Uniformity	1.1684
	wavelet-LLH-glszm-SizeZoneNonUniformity	1.1128
	wavelet-HLL-firstorder-Kurtosis	-0.2916
	wavelet-HHH-glszm-ZoneEntropy	1.8131
	wavelet-LHL-firstorder-TotalEnergy	4.1148
	original-shape-Maximum2DDiameterColumn	3.9735
	wavelet-HHL-glrlm-	
	LongRunHighGrayLevelEmphasis	0.4227
	wavelet-HHH-glrlm-RunLengthNonUniformity	-1.9274

	original-shape-MeshVolume	0.1625
	wavelet-HHL-glszm-ZoneEntropy	0.9950
	wavelet-HLH-glrlm-RunLengthNonUniformity	2.7230
	wavelet-HHL-glrlm-GrayLevelNonUniformity	0.7743
	wavelet-LLH-glszm-ZoneEntropy	0.7662
Model	Feature Name	Coefficient
	wavelet-HHH-glrlm-RunPercentage	-0.0494
	wavelet-HHH-glrlm-GrayLevelNonUniformity	0.6484
	wavelet-HLH-glszm-SizeZoneNonUniformity	-0.8657
	wavelet-HHL-glszm-GrayLevelNonUniformity	-0.2980
	wavelet-HLH-glrlm-GrayLevelVariance	0.6176

	wavelet-HLH-firstorder-Kurtosis	-0.0233
	wavelet-LLH-firstorder-TotalEnergy	-3.7440
	wavelet-HLH-glrlm-GrayLevelNonUniformity	-0.1860
	wavelet-HLH-firstorder-Uniformity	-1.1006
	wavelet-LHH-firstorder-Kurtosis	-0.8432
	wavelet-HLH-glszm-ZoneEntropy	-5.0645
DWI-ADC		
sequence		
signature		
Model	Feature Name	Coefficient
	wavelet-LHL-glrlm-	
	RunLengthNonUniformityNormalized	-0.1017

wavelet-HHL-glszm-GrayLevelNonUniformity	-0.6127
wavelet-HHL-gldm-DependenceNonUniformity	-0.0277
wavelet-LLH-glcm-JointEntropy	-2.2394
wavelet-HHH-glrlm-RunLengthNonUniformity	1.8230
wavelet-HHH-glszm-SizeZoneNonUniformity	-3.0838
wavelet-LHL-glszm-ZoneEntropy	1.6147
wavelet-LHH-glrlm-RunLengthNonUniformity	-0.1816
original-firstorder-Mean	0.2905
wavelet-HLL-firstorder-TotalEnergy	1.1169
wavelet-LHH-ngtdm-Contrast	0.1275
wavelet-HLL-firstorder-Mean	0.1465

	wavelet-HLH-glszm-SizeZoneNonUniformity	1.3711
	wavelet-HLH-firstorder-Kurtosis	-0.0953
Model	Feature Name	Coefficient
	wavelet-LLH-glrlm-	
	GrayLevelNonUniformityNormalized	-0.2268
	wavelet-LHL-firstorder-Uniformity	-0.4446
	wavelet-HHL-ngtdm-Contrast	0.0941
	wavelet-HLL-glrlm-RunLengthNonUniformity	-0.4508
	wavelet-HHL-firstorder-TotalEnergy	-1.8425
	wavelet-HLH-glszm-	
	LargeAreaLowGrayLevelEmphasis	0.2196
	diagnostics-Mask-interpolated-BoundingBox	-0.7884

	wavelet-HHL-glszm-ZoneEntropy	3.7485
	wavelet-LLH-firstorder-Kurtosis	0.1644
	wavelet-HHL-glszm-	
	LargeAreaLowGrayLevelEmphasis	0.4181
	wavelet-HLL-glszm-ZoneEntropy	-2.7319
	wavelet-HLH-glszm-GrayLevelNonUniformity	-0.0254
	wavelet-LHH-gldm-LargeDependenceEmphasis	0.1046
	wavelet-LLH-firstorder-Uniformity	-1.3138
Model	Feature Name	Coefficient
	original-shape-MinorAxisLength	0.4667
	original-shape-Sphericity	0.4792

Radiomic		
signature		
	T1+C sequence signature	0.5075
	T2WI sequence signature	0.2717
	DWI-ADC sequence signature	0.6309
Clinical		
signature		
	Number of tumors	0.9420
	Histological grade	0.3346
	Pathological T stage	-0.0160
	Pathological N stage	0.8280
	PR status	-0.4022

	Ki-67 expression level	0.3440
Model	Feature Name	Coefficient
	Type of surgery	-0.5657
Clinical-		
radiomic		
Nomogram		
	Radiomic signature	0.7085
	Clinical signature	0.6444
Abbreviation: DFS, dise	ease-free survival; T1+C, contrast-enhanced T1-weighted imaging; T2	WI, T2-weighted
imaging; DWI-ADC, dif	fusion-weighted imaging quantitatively measured apparent diffusior	n coefficients; PR,
progesterone receptor	s; Ki-67, proliferation marker protein Ki-67.	

eTable 10. Multivariate Analysis of Clinical Signature and Radiomic Signature With DFS in the Development Cohort

Signature	Multivariate Analysis		
	HR (95%CI)	<i>P</i> value	
Radiomic signature (low-risk/high-risk)	0.16 (0.07-0.36)	< .001	
Clinical signature (low-risk/high-risk)	0.16 (0.07-0.40)	< .001	
Abbreviations: DFS, disease-free survival; HR, Hazard	ratio; CI, confidence interval.		