

Appendix 1

The formulas for calculating the RS-Coms in both tasks.

Task1: RS-Com= $+0.787 * T2w\text{-wavelet}\text{-LLL_glcm_MCC} + 0.651 * original_firstorder_Minimum - 0.506 * T2w\text{-wavelet}\text{-LHH_firstorder_Median} + 0.487 * T2w\text{-wavelet}\text{-HLL_ngtdm_Contrast} + 0.446 * T2w\text{-wavelet}\text{-HHL_firstorder_Median} - 0.434 * original_glcm_JointEntropy - 0.397 * T2w\text{-wavelet}\text{-LHH_glcm_MaximumProbability} - 0.373 * wavelet\text{-LLL_glcm_SumEntropy} - 0.280 * T2w\text{-wavelet}\text{-LHL_glcm_Correlation} + 0.203 * wavelet\text{-HLL_gldm_DependenceVariance} + 0.185 * T2w\text{-wavelet}\text{-LHH_ngtdm_Strength} + 0.162 * wavelet\text{-LLL_firstorder_Kurtosis} + 0.120 * original_firstorder_Kurtosis} + 0.081 * wavelet\text{-LLL_glszm_ZoneVariance} - 2.058$

Task2: RS-Com= $+0.741 * wavelet\text{-LLL_glszm_ZoneVariance} - 0.736 * wavelet\text{-LLH_gldm_DependenceEntropy} - 0.633 * T2w\text{-wavelet}\text{-HLH_gldm_DependenceEntropy} + 0.620 * wavelet\text{-LLL_firstorder_Kurtosis} - 0.350 * original_glszm_LargeAreaEmphasis} + 0.263 * T2w\text{-wavelet}\text{-HLH_glcm_DifferenceAverage} - 0.242 * wavelet\text{-HLL_glcm_MaximumProbability} - 0.156 * wavelet\text{-LLL_glcm_JointEntropy} + 0.137 * wavelet\text{-LHL_glszm_ZoneVariance} + 0.055 * original_firstorder_Kurtosis} - 1.352$

Table S1 Comparison of multiparametric breast MRI sequences in two centers

Sequence	Center	TE (ms)	TR (ms)	Fat suppression	FOV (mm)	Matrix	slice gap (mm)	Slice thickness (mm)
T1WI	1	4.7	403	No	340*340	412*320	1	5.0
T2WI	2	8.6	509	No	340*340	384*384	1	4.0
DCE	1	78	6083	Yes	340*340	352*288	1	5.0
	2	58	4278	Yes	340*340	416*333	1	4.0
	1	2.4	6.2	Yes	320*320	256*256	0	2.4
	2	2.6	5.1	Yes	340*340	400*320	0	1.5

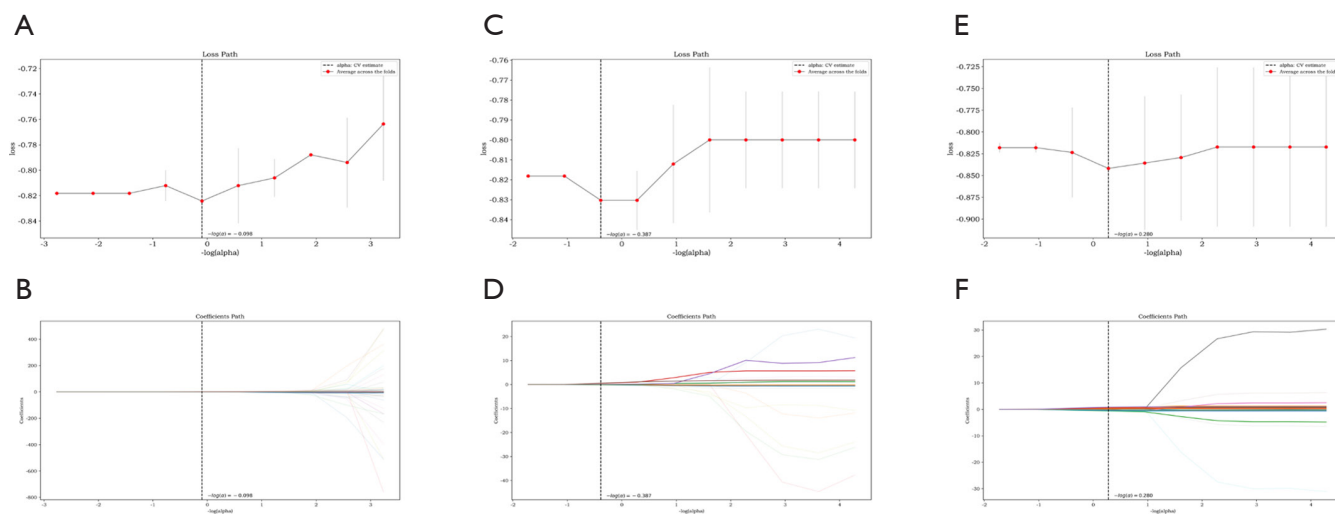


Figure S1 Radiomics feature selection via LASSO in Task 1 for DCE, T2WI, and combined sequences. LASSO coefficient analysis using the 1-standard error (1-SE) criterion and 10-fold cross-validation to select optimal $\log(\text{Lambda})$ for DCE (A), T2WI (C), and combined sequence (E). LASSO coefficients of selected features for DCE (B), T2WI (D), and combined sequence (F).

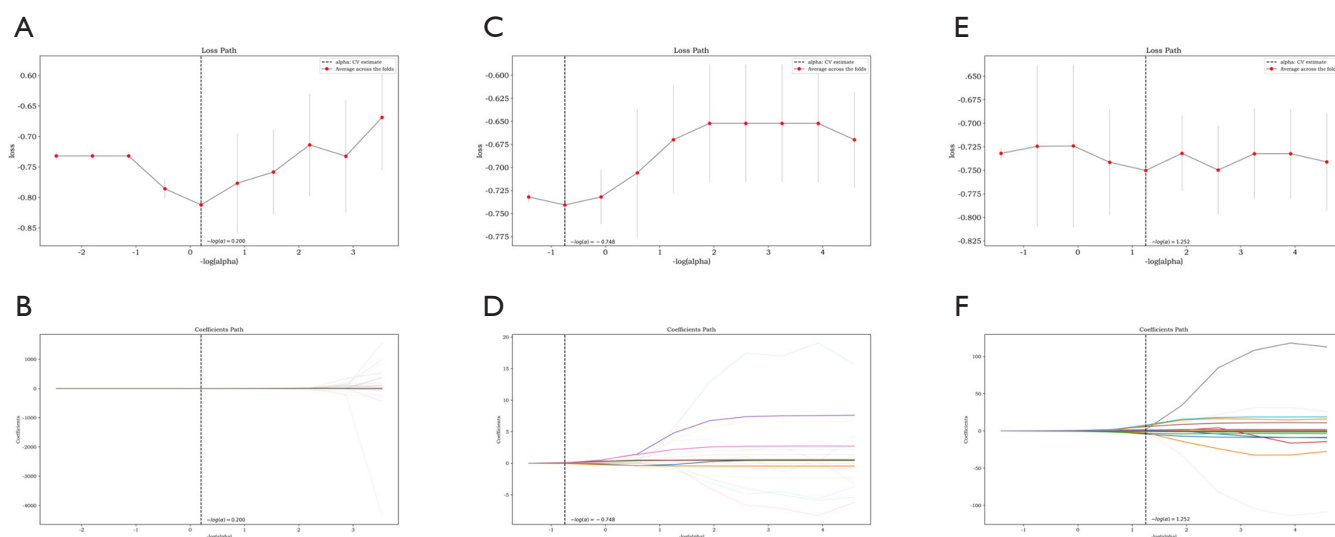


Figure S2 Radiomics feature selection via LASSO in Task 2 for DCE, T2WI, and combined sequences. LASSO coefficient analysis using the 1-standard error (1-SE) criterion and 10-fold cross-validation to select optimal $\log(\text{Lambda})$ for DCE (A), T2WI (C), and combined sequence (E). LASSO coefficients of selected features for DCE (B), T2WI (D), and combined sequence (F).

Table S2 Performance of the selected radiomics features of RS-Com in distinguishing HER2-low and -positive versus HER2-zero breast cancers

Features	Sources	Feature_scores
wavelet-LLL_glcM_MCC	T2WI	0.85
original_glcM_JointEntropy	DCE	0.78
original_firstorder_Minimum	DCE	0.72
wavelet-HLL_ngtdm_Contrast	T2WI	0.53
wavelet-LHH_firstorder_Median	T2WI	0.51
wavelet-HHL_firstorder_Median	T2WI	0.50
wavelet-LHH_glcM_MaximumProbability	T2WI	0.41
wavelet-LHL_glcM_Correlation	T2WI	0.28
wavelet-HLL_gldm_DependenceVariance	DCE	0.15
wavelet-LHH_ngtdm_Strength	T2WI	0.15
wavelet-LLL_glcM_SumEntropy	DCE	0.14
wavelet-LLL_firstorder_Kurtosis	DCE	0.14
original_firstorder_Kurtosis	DCE	0.11
wavelet-LLL_glszm_ZoneVariance	DCE	0.08
wavelet-HLL_glcM_MaximumProbability	DCE	0.02

Table S3 Performance of the selected radiomics features of RS-Com in distinguishing HER2-Low from HER2-negative breast cancers

Features	Sources	feature_scores
wavelet-HLH_glcM_InverseVariance	T2WI	8.56
wavelet-HLH_glcM_Correlation	T2WI	8.27
wavelet-LLL_firstorder_Kurtosis	DCE	5.30
original_firstorder_Kurtosis	DCE	3.97
wavelet-HLH_gldm_DependenceEntropy	T2WI	3.22
original_glszm_LargeAreaEmphasis	DCE	2.28
wavelet-LLL_glszm_ZoneVariance	DCE	1.54
wavelet-LHL_glszm_ZoneVariance	DCE	1.28
wavelet-HLH_gldm_DependenceNonUniformityNormalized	T2WI	0.99
wavelet-HLH_gldm_DependenceVariance	T2WI	0.95
wavelet-LLH_gldm_DependenceEntropy	DCE	0.94
wavelet-HLL_glcM_Correlation	T2WI	0.46
wavelet-LLL_glcM_JointEntropy	DCE	0.14
wavelet-HLL_glcM_MaximumProbability	DCE	0.08
wavelet-HLH_glcM_DifferenceAverage	T2WI	0.04

Table S4 DeLong test between training cohort, internal validation cohort, and external validation cohort in Task 1

	Model A	Model B	Model C	Model D	Model E
Training cohort					
Model A	1	0.445	0.448	0.013*	<0.001*
Model B	–	1	0.978	0.067	0.009*
Model C	–	1	1	0.077	0.008*
Model D	–	1	1	1	0.112
Model E	–	–	–	–	1
Internal validation cohort					
Model A	1	0.704	0.779	0.395	0.013*
Model B	–	1	0.541	0.668	0.036*
Model C	–	1	1	0.278	<0.001*
Model D	–	1	1	1	0.084
Model E	–	–	–	–	1
External validation cohort					
Model A	1	0.915	0.911	0.123	0.003*
Model B	–	1	0.839	0.031*	0.016*
Model C	–	1	1	0.235	0.140
Model D	–	1	1	1	0.601
Model E	–	–	–	–	1

P is derived from DeLong test between each of the models, and *P<0.05 is considered statistically significant. Model A: the model was constructed based on the clinical characteristics. Model B: the model was constructed based on the radiomics signature selected features from DCE. Model C: the model was constructed based on the radiomics signature selected features from T2WI. Model D: the model was constructed based on the combined radiomics signature selected features from DCE and T2WI. Model E: the model was constructed based on the combined clinical characteristics and radiomics signature selected features from DCE and T2WI.

Table S5 DeLong test between training cohort, internal validation cohort, and external validation cohort in Task 2

	Model A	Model B	Model C	Model D	Model E
Training cohort					
Model A	1	0.287	0.223	0.038*	0.002*
Model B	–	1	0.971	0.472	0.146
Model C	–	1	1	0.326	0.103
Model D	–	1	1	1	0.496
Model E	–	–	–	–	1
Internal validation cohort					
Model A	1	0.846	0.901	0.763	0.025*
Model B	–	1	0.948	0.628	0.032*
Model C	–	1	1	0.712	0.035*
Model D	–	1	1	1	0.096
Model E	–	–	–	–	1
External validation cohort					
Model A	1	0.570	0.847	0.335	0.040*
Model B	–	1	0.399	0.675	0.319
Model C	–	1	1	0.228	0.047*
Model D	–	1	1	1	0.165
Model E	–	–	–	–	1

P is derived from DeLong test between each of the models, and *P<0.05 is considered statistically significant. Model A: the model was constructed based on the clinical characteristics. Model B: the model was constructed based on the radiomics signature selected features from DCE. Model C: the model was constructed based on the radiomics signature selected features from T2WI. Model D: the model was constructed based on the combined radiomics signature selected features from DCE and T2WI. Model E: the model was constructed based on the combined clinical characteristics and radiomics signature selected features from DCE and T2WI.

Table S6 Univariate and multivariate logistic regression analyses of the clinical parameters for distinguishing HER2-low and -positive versus HER2-zero status in the training cohort

parameters	Univariate logistic regression		Multivariate logistic regression	
	OR (95% CI)	P	OR (95% CI)	P
Age	1.013 (0.978–1.049)	0.473		
Size	0.993 (0.967–1.020)	0.620		
Location	0.718 (0.321–1.605)	0.420		
PR status	0.219 (0.095–0.503)	<0.001*	0.308 (0.118–0.803)	0.016*
ER status	0.190 (0.083–0.439)	<0.001*	0.050 (0.004–0.564)	0.015*
Ki-67 index	0.298 (0.131–0.677)	0.004*	2.069 (0.390–10.971)	0.393
ALN	0.423 (0.187–0.958)	0.039*	4.103 (0.491–34.296)	0.193
Histological grade	0.837 (0.331–2.117)	0.707		
Menstrual history	0.515 (0.232–1.143)	0.103		
Family history	0.722 (0.198–2.629)	0.622		
Reproductive history	0.432 (0.180–1.040)	0.061		

*P<0.05.

Table S7 Univariate and multivariate logistic regression analyses of the clinical parameters for distinguishing HER2-low from HER2-negative in the training cohort

Parameters	Univariate logistic regression		Multivariate logistic regression	
	OR (95% CI)	P	OR (95% CI)	P
Age	1.017 (0.979–1.057)	0.394		
Size	1.013 (0.976–1.051)	0.503		
Location	1.460 (0.631–3.381)	0.377		
PR status	0.219 (0.090–0.536)	<0.001*	0.310 (0.113–0.853)	0.023*
ER status	0.215 (0.085–0.546)	<0.001*	0.329 (0.111–0.970)	0.044*
Ki-67 index	0.410 (0.173–0.972)	0.043*	0.426 (0.156–1.162)	0.096
ALN	0.336 (0.30–0.958)	0.024*	0.436 (0.151–1.254)	0.123
Histological grade	0.483 (0.116–1.411)	0.184		
Menstrual history	0.465 (0.199–1.086)	0.077		
Family history	1.407 (0.329–6.023)	0.645		
Reproductive history	0.773 (0.295–2.027)	0.601		

*P<0.05.