

Appendix 1

Imaging protocol

DCE-MRI was performed at 3.0 T using a Signa HDxt 3.0 T MRI scanner (GE HealthCare, Chicago, IL, USA). All patients were in prone position and were scanned with a dedicated 8-channel double breast coil. First, the axial fat saturation T1-weighted precontrast scanning based on VIBRANT-VX technology was obtained. After intravenous injection of a contrast agent (Magnevist, Bayer Healthcare Pharmaceuticals, Berlin, Germany) at 4 mL/s and a dose of 0.15 mmol/kg body weight, 8 postcontrast scans were obtained under the following parameters: repetition time, 7.42 ms; flip angle, 15°; echo time, 4.25 ms; slice thickness, 2.20 mm; spacing between slices, 2.20 mm; field of view, 340×340 mm²; time per volume, 80s; and slice number, 78. Finally, 8 subtraction sequences were acquired by subtracting each precontrast scan sequence from the 8 postcontrast scan sequences.

Tumor segmentation

Two radiologists with 5 years (reader 1) and 10 years (reader 2) of working experience in breast MRI diagnosis evaluated the subtraction sequences of the fourth stage blinded to the pathological results of the patients; the section with the largest tumor cross-sectional area was selected from the image data of each patient for subsequent analysis. In case of judgment discrepancy, a third physician with 15 years (reader 3) of diagnostic experience made a final decision. MATLAB 2018b (MathWorks, Natick, MA, USA) was used to semiautomatically segment the selected slices to obtain the whole tumor region. First, readers 1 and 2 delineated an arbitrarily shaped region of interest (ROI) around the lesion area on the slice. Then, the pixel gray value in the ROI was normalized to average gray value of the pixels in the region of interest with a standard deviation of 3, and the region was quantized to 8 bits per pixel to change the signal-to-noise ratio of the texture results. Finally, the spatial fuzzy C-means (FCM) algorithm was applied to depict the contour boundary of the lesion according to the ROI, and the details were improved via morphological processing of the whole lesion area. In addition, for tumors near the edge of the breast or chest wall, a breast parenchyma ROI was manually created using ITK-SNAP software (www.itksnap.org) and loaded into MATLAB 2018b.

Pathologic assessment

ER, PR, and HER2 expression was detected with streptavidin peroxidase immunohistochemistry (IHC). The test results were interpreted by pathologists. ER or PR staining in at least 1% of tumor nuclei was defined as ER or PR positivity (60). HER2 expression results of a single negative or single positive were considered HER2 negative, triple positive was considered HER2 positive, and double positive was further verified with fluorescence *in situ* hybridization (61). According to ER and PR expression, cases were divided into luminal type (ER positive and/or PR positive) and nonluminal type (ER negative and PR negative).

Rad score calculation formula in predicting luminal and nonluminal breast cancer

$$\begin{aligned} \text{Rad-score} = & 0.6969 + \\ & -0.5428 \times \text{S-8_Rapid_Skewness} + \\ & 0.3935 \times \text{S-4_Rapid_SRHGLE}_0 + \\ & -0.3304 \times \text{S-4_Rapid_GLN}_{135} + \\ & -0.4182 \times \text{S-0_Rapid_Skewness} + \\ & 0.1870 \times \text{S-0_Rapid_Deubechies2}_4\text{H}_V \end{aligned}$$

References

60. Hammond ME, Hayes DF, Wolff AC, Mangu PB, Temin S. American society of clinical oncology/college of American

pathologists guideline recommendations for immunohistochemical testing of estrogen and progesterone receptors in breast cancer. *J Oncol Pract* 2010;6:195-7.

61. Wolff AC, Hammond MEH, Allison KH, Harvey BE, McShane LM, Dowsett M. HER2 Testing in Breast Cancer: American Society of Clinical Oncology/College of American Pathologists Clinical Practice Guideline Focused Update Summary. *J Oncol Pract* 2018;14:437-41.

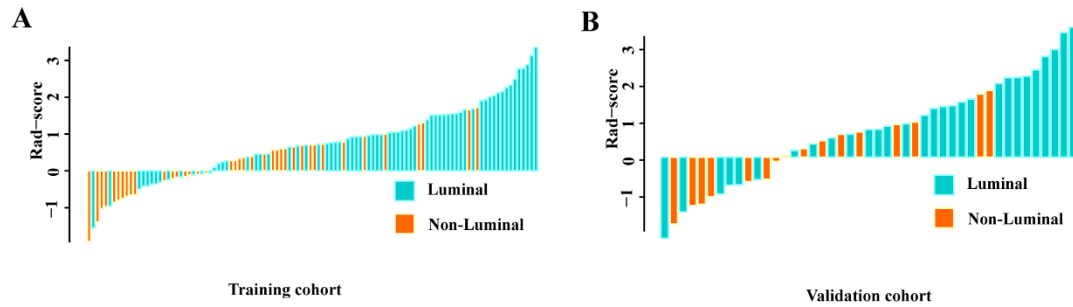


Figure S1 Bar graph of the radiomics score of each patient in the training (A) and validation cohorts (B). For a detailed description of the features we extracted, please refer to the pyradiomics website (<https://pyradiomics.readthedocs.io/en/latest/features.html>).

Table S1 Statistical comparison of AUC values between the 2 classifier models using the Delong test

Model	Cohort	Regions	Rapid	Medium	Slow	Combined	Whole lesion
SVM	Training	Rapid	/	0.126	0.629	0.120	0.322
		Medium	0.126	/	0.667	0.016	0.635
		Slow	0.629	0.667	/	0.177	0.177
		Combined	0.120	0.016	0.177	/	0.081
		Whole lesion	0.322	0.635	0.177	0.081	/
	Validation	Rapid	/	0.459	0.431	0.275	0.154
		Medium	0.459	/	0.886	0.930	0.631
		Slow	0.431	0.886	/	0.929	0.459
		Combined	0.275	0.930	0.929	/	0.422
		Whole lesion	0.154	0.631	0.459	0.421	/
LR	Training	Rapid	/	0.061	0.839	0.101	0.023
		Medium	0.061	/	0.039	0.001	0.744
		Slow	0.839	0.039	/	0.100	0.047
		Combined	0.101	0.001	0.100	/	0.003
		Whole lesion	0.023	0.744	0.047	0.003	/
	Validation	Rapid	/	0.261	0.288	0.254	0.254
		Medium	0.261	/	0.759	0.675	0.962
		Slow	0.288	0.759	/	0.725	0.735
		Combined	0.254	0.675	0.725	/	0.647
		Whole lesion	0.254	0.962	0.735	0.647	/

LR, logistic regression; SVM, support vector machine. The slash indicates that there is no data point here.