Appendix 1

The performance of nomogram in the validation cohort

In accordance with the preceding results, the mean amide proton transfer value (APTmean), mean apparent diffusion coefficient value (ADCmean), and Prostate Imaging Reporting and Data System (PI-RADS) score of each patient in the validation cohort were acquired by one of two junior radiologists. The clinical and pathological characteristics of these participants are displayed in *Table 1*.

The APTmean, ADCmean, and PI-RADS scores of the validation cohort were imported into the trained nomogram. The result of receiver operating characteristic (ROC) analysis (*Figure S1*) demonstrated that the nomogram constructed based on PI-RADS score, APTmean, and ADCmean retained high diagnostic efficacy (area under the ROC curve: 0.835) in the validation cohort.

Table S1 Parameters of the MR sequences

Parameters	T2WI	DWI	DCE	APT
TR (ms)	3,280	3,623	4	2,100
TE (ms)	102	97.2	1.8	18.4
Slice-thickness/gap (mm)	4/1	4/1	4/none	5/none
NEX	2	1 (for T2)	1	1
Matrix	288×256	128×64	256×192	128×128
FOV (mm^2)	220×220	220×220	360×360	340×340
Acquisition time (min)	2.02	6.40	6.10	5.28

The b values of DWI were 0, 1,400, 2,000, and 3,000. MR, magnetic resonance; T2WI, T2-weighted imaging; DWI, diffusion-weighted imaging; DCE, dynamic contrast-enhanced; APT, amide proton transfer; TR, time of repetition; TE, time to echo; NEX, number of excitations; FOV, field of view.

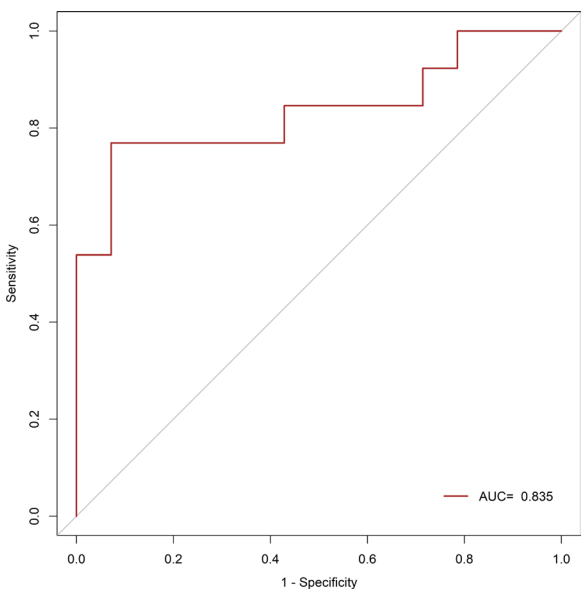

Figure S1 ROC analysis of the nomogram in differentiating csPCa. ROC, receiver operating characteristic; AUC, area under the ROC curve; csPCa, clinically significant prostate cancer.

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