

Supplements

1. There were total of 62 individuals included in the external validation cohort. And the basic information of external validation cohort were presented in the Table S1.

Table S1 The basic information of external validation cohort

	benign	malignancy	p.overall
	N=15	N=47	
gender:			0.049
F	6 (40.0%)	34 (72.3%)	
M	9 (60.0%)	13 (27.7%)	
pathology:			<0.001
benign	15 (100.00%)	5 (10.6%)	
LACC	0 (0.00%)	35 (74.5%)	
LACC	0 (0.00%)	2 (4.26%)	
NSCLC	0 (0.00%)	2 (4.26%)	
other_malignant	0 (0.00%)	3 (6.38%)	
up:			0.051
down/middle	12 (80.0%)	22 (46.8%)	
up	3 (20.0%)	25 (53.2%)	
GGN:			0.076
GGN	5 (33.3%)	30 (63.8%)	
non-GGN	10 (66.7%)	17 (36.2%)	
glitch:			0.052
glitch	0 (0.00%)	11 (23.4%)	
non-glitch	15 (100%)	36 (76.6%)	
age:			0.985
<=60	9 (60.0%)	26 (55.3%)	
>60	6 (40.0%)	21 (44.7%)	
stage:			<0.001

	benign	malignancy	p.overall
	N=15	N=47	
	0 (0.00%)	8 (17.0%)	
benign	15 (100%)	0 (0.00%)	
I	0 (0.00%)	36 (76.6%)	
II	0 (0.00%)	3 (6.38%)	
smoking:			0.016
ever/current	5 (33.3%)	3 (6.38%)	
never	10 (66.7%)	44 (93.6%)	
size:			0.667
<=3cm	14 (93.3%)	40 (85.1%)	
>3cm	1 (6.67%)	7 (14.9%)	

2. Comparison among SCHC model with other models

In order to compare the SCHC model with other models including classical and new models, we randomly selected 97 individuals from the development group, including 25 benign and 72 malignant patients. The basic information of the random cohort were displayed in the **Table S2**. A total of 5 models were used to calculate the probabilities, including VA model, MC model, BU model, TG model, PU model and SCHC model. And the probabilities calculated by 6 models were compared in **Table S2**. And the ROC curves were drawn to evaluate the diagnostic value. As shown in **Table S3** and **Figure S1**, the SCHC model exceeded the other 5 models with the AUC at 0.82.

The information of new models (TG model, PU model) was as follows:

The Tongji model (TG model) was developed by the Tongji University in 2017, a primary cohort was consisted of 1798 patients, and the formula to calculate the malignant probability was as follows:

$$P = e^x / (1 + e^x),$$

$$X = -5.4175 + 0.8149 \times \text{LgCEA} + 1.0447 \times \text{Nodule diameter (mm)} + 2.5978 \times \text{Cancer history} + 0.0518 \times \text{Age} + 1.7166 \times \text{Spiculation} + 0.3986 \times \text{Pleural indentation} - 2.2549 \times \text{calcification}.$$

In their original study, they compared the model with MC model, VA model, BU model and Beijing university. And their results showed that the AUC of Tongji model (0.85, 95%CI: 0.83-0.85) was higher than the other 4 models (0.8, 95%CI: 0.77-0.82; 0.65, 95%CI: 0.62-0.68; 0.83, 95%CI: 0.8-0.86; 0.8, 95%CI: 0.78-0.83). (DOI: 10.1002/jso.24704)

And the Peking University model (PU model) was developed by the Peking University in 2011, including 371 individuals. And the formula to calculate the malignant probability was as follows:

$$P = e^x / (1 + e^x),$$

$$X = -4.496 + (0.07 \times \text{Age}) + (0.676 \times \text{diameter}) + (0.736 \times \text{spiculation}) + (1.267 \times \text{family history of cancer}) - (1.615 \times \text{calcification}) - (1.408 \times \text{border}).$$

As they reported , the AUC of Peking University model was 0.888, which also exceeded than MC model (AUC 0.747) and VA model(AUC 0.707). (doi: 10.1016/j.clcc.2011.06.005)

Table S2 The basic information of appendix cohort

		benign	malignancy	p
Total		25	72	
gender	female	9	37	0.246
	male	16	35	
age	>60	6	38	0.019
	<=60	19	34	
pathology	benign	25		0.000
	LACC		59	
	NSCLC		5	
	LSCC		6	
	other_malignant		2	
stage	benign	25		
	I		41	
	II		10	
size	<=3cm	24	56	0.063
	>3cm	1	16	
VA_P		0.9955	0.9983	0.014
MC_P		0.0097	0.0375	0.000
BU_P		0.0372	0.2114	0.000
XGB_P		0.6224	0.7587	0.000
TG_P		0.9993	1	0.001
PU_P		0.9918	0.9999	0.000

Table S3 The ROC results of 6models in appendix cohort

Index	value-VA	value-MC	value-BU	value-XGB	value-TG	value-PU
AUC(%)	66.64	76.00	75.56	81.89	72.23	74.44
Best Cut-off Value	1.00	0.03	0.10	0.74	1.00	1.00
Sensitivity	75.00	58.33	72.22	61.11	82.86	83.33
Specificity	60.00	88.00	80.00	92.00	60.00	64.00
Negative Predictive Value	45.45	42.31	50.00	45.10	55.56	57.14
Positive Predictive Value	84.38	93.33	91.23	95.65	85.29	86.96
True Positive Rate	75.00	58.33	72.22	61.11	82.86	83.33
False Positive Rate	40.00	12.00	20.00	8.00	40.00	36.00
True Negatice Rate	60.00	88.00	80.00	92.00	60.00	64.00
False Negative Rate	25.00	41.67	27.78	38.89	17.14	16.67
False Discovery Rate	15.63	6.67	8.77	4.35	14.71	13.04
Accuracy	71.13	65.98	74.23	69.07	76.84	78.35
Precision	84.38	93.33	91.23	95.65	85.29	86.96

Youden Index	135.00	146.33	152.22	153.11	142.86	147.33
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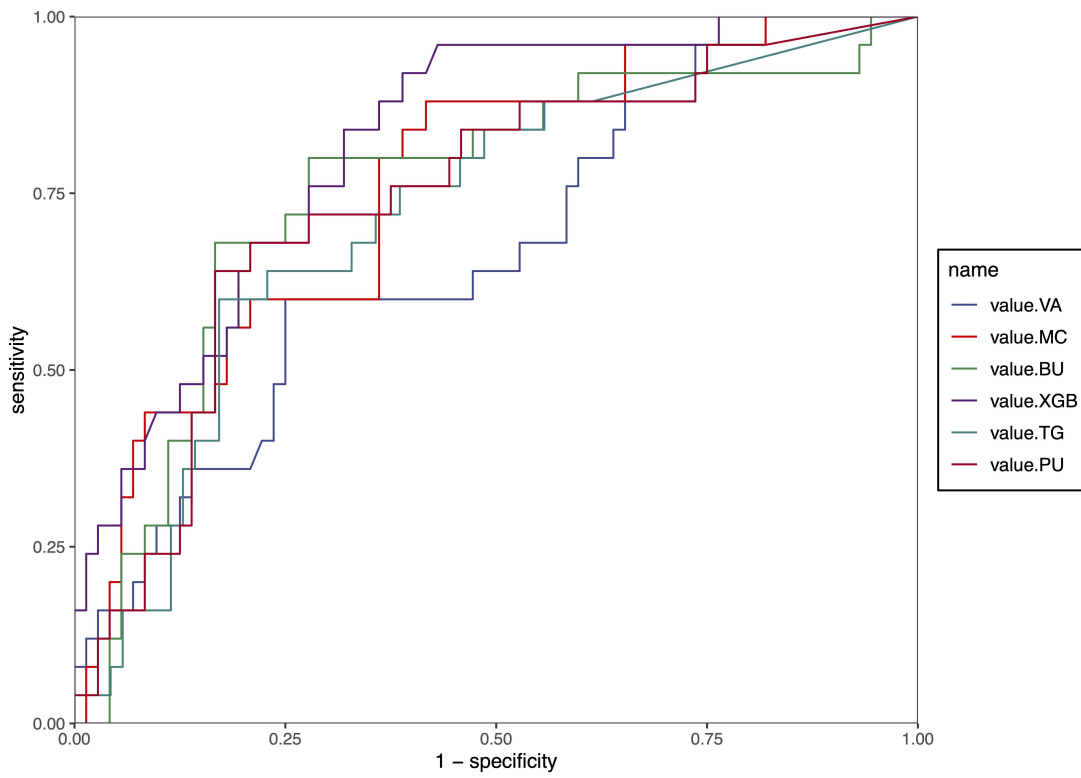


Figure S1 The ROC of 6 models in the appendix cohort