Table S1. Sequences of primers used quantitative real-time PCR

Gene	Primer	Sequence (5'–3')
β-actin	Forward	CACGATGGAGGGGCCGGACTCATC
	Reverse	TAAAGACCTCTATGCCAACACAGT
SIM2	Forward	ACTGGAGAACTAGTC
	Reverse	CACATACAGCGGGCTC

Table S2. Univariate and multivariate cox analysis of SIM2 expression and other clinical pathological features

Characteristics	Total (N)	Univariate analysis		Multivariate analysis	
		Hazard ratio (95% CI)	P-value	Hazard ratio (95% CI)	P-value
Pathologic T stage	177		0.017		
T1 and T2	31	Reference		Reference	
T3 and T4	146	2.035 (1.079–3.838)	0.028	1.298 (0.656–2.567)	0.454
Pathologic N stage	174		0.002		
N0	50	Reference		Reference	
N1	124	2.161 (1.287–3.627)	0.004	2.005 (1.155–3.483)	0.013
Pathologic M stage	85		0.713		
M0	80	Reference			
M1	5	0.773 (0.185–3.227)	0.724		
Gender	179		0.320		
Female	80	Reference			
Male	99	0.813 (0.541–1.222)	0.319		
Age	179		0.230		
≤ 65	94	Reference			
> 65	85	1.285 (0.853–1.937)	0.230		
Histologic grade	177		0.017		
G1	31	Reference		Reference	
G2	96	1.974 (1.016–3.834)	0.045	1.469 (0.740–2.915)	0.272
G3 and G4	50	2.586 (1.288–5.192)	0.008	1.610 (0.780–3.324)	0.198
SIM2	179		0.003		
Low	89	Reference		Reference	
High	90	1.853 (1.220–2.814)	0.004	1.381 (0.883–2.161)	0.047

Table S3. The relationship between SIM2 mRNA expression and clinical parameters of patients with PC

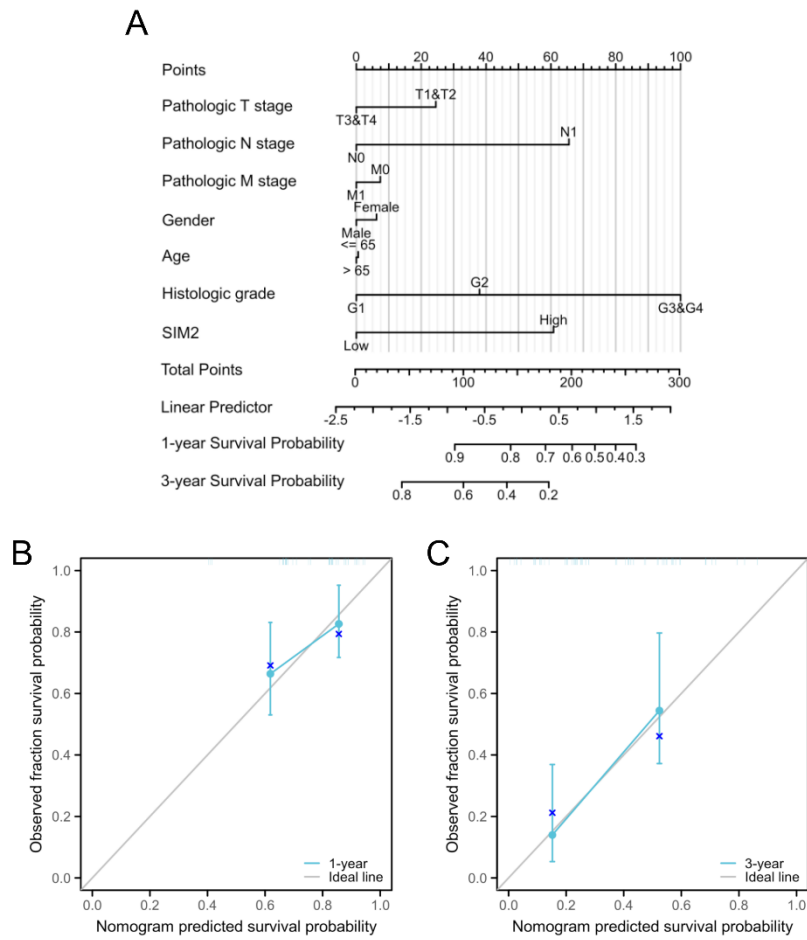| Characteristics	Low expression of SIM2	High expression of SIM2	P-value
N	89	90	
Pathologic T stage, n (%)			0.023
T1 and T2	21 (11.9)	10 (5.6)	
T3 and T4	66 (37.3)	80 (45.2)	
Pathologic N stage, n (%)			0.598
N0	26 (14.9)	24 (13.8)	
N1	59 (33.9)	65 (37.4)	
Pathologic M stage, n (%)			0.315
M0	43 (50.6)	37 (43.5)	
M1	1 (1.2)	4 (4.7)	
Pathologic stage, n (%)			0.742
Stage I and stage II	84 (47.7)	84 (47.7)	
Stage III and stage IV	3 (1.7)	5 (2.8)	
Gender, n (%)			0.332
Female	43 (24)	37 (20.7)	
Male	46 (25.7)	53 (29.6)	
Age, n (%)			0.115
≤ 65	52 (29.1)	42 (23.5)	
> 65	37 (20.7)	48 (26.8)	
Residual tumor, n (%)			0.005
R0	63 (38.2)	44 (26.7)	
R1 and R2	21 (12.7)	37 (22.4%)	
Histologic grade, n (%)			0.004
G1	23 (13)	8 (4.5)	
G2	46 (26)	50 (28.2)	
G4 and G3	18 (10.2)	32 (18.1)	
Anatomic neoplasm subdivision, n (%)			0.603
Body and tail	12 (6.7)	17 (9.5)	
Head	71 (39.7)	68 (38)	
Other	6 (3.4)	5 (2.8)	
Alcohol history, n (%)			0.053
No	38 (22.8)	27 (16.2)	
Yes	44 (26.3)	58 (34.7)	
History of diabetes, n (%)			0.141
No	48 (32.7)	61 (41.5)	
Yes	22 (15)	16 (10.9)	
History of chronic pancreatitis, n (%)			0.177
No	65 (45.8)	64 (45.1)	
Yes	4 (2.8)	9 (6.3%)	
Family history of cancer, n (%)			0.511
No	22 (19.8)	25 (22.5)	
Yes	34 (30.6)	30 (27)	
Radiation therapy, n (%)			0.400
No	60 (36.6)	59 (36)	
Yes	26 (15.9)	19 (11.6)	
Smoker, n (%)			0.125
No	36 (24.8)	30 (20.7)	
Yes	33 (22.8)	46 (31.7)	

Fig. S1. Validation of the nomogram in the validation set. (A) A nomogram for assessing the survival probability of 1-year and 3-year for PC. (B-C) Calibration curve of the SIM2 gene