Figure S1 The heatmaps of the GEO data sets showing the expression of the differentially expressed m6A RNA methylation regulators and ferroptosis regulators in the PAAD and normal adjacent tissues. GEO, Gene Expression Omnibus; PAAD, pancreatic adenocarcinoma.

Table S1 Correlations between the 7-gene risk signature and the clinical characteristics of PAAD patients in TCGA

Characteristics	Level	High Risk n=88	Low Risk n=89	P value
Age (median [IQR])		64.50 [56.00, 73.00]	66.00 [60.00, 73.00]	0.31
N (%)	N0	20 (22.7)	29 (33.0)	0.176
	N1	66 (75.0)	57 (64.8)	
M (%)	M0	38 (43.2)	41 (46.1)	0.36
	M1	3 (3.4)	1 (1.1)	
T (%)	T1-2	9 (10.2)	22 (25.3)	0.01
	T3-4	79 (89.8)	65 (74.7)	
Stage (%)	Stage I	6 (6.9)	15 (17.2)	0.061
	Stage II-IV	81 (93.1)	72 (82.8)	
Gender (%)	female	37 (42.0)	43 (48.3)	0.451
	male	51 (58.0)	46 (51.7)	
Fustat (%)	Alive	32 (36.4)	53 (59.6)	0.003
	Dead	56 (63.6)	36 (40.4)	

IQR, interquartile range, PAAD, pancreatic adenocarcinoma; TCGA, The Cancer Genome Atlas.