Oshi et al. "A novel 4-gene score to predict pathologically complete (R0) resection and survival in pancreatic cancer"

- 1. Table S1: Comparison of clinical and pathological features between low and high 4-gene score with pancreatic cancer in the TCGA cohort.
- 2. Table S2: Comparison of pathological features between low and high 4-gene score with pancreatic cancer in the GSE62452 cohort.
- 3. Table S3: Comparison of pathological feature between low and high 4-gene score with pancreatic cancer in the GSE57495 cohort.
- 4. Table S4: Pancreatic cancer cell lines
- 5. Figure S1: Gene set enrichment analysis (GSEA) of high 4-gene score pancreatic cancer in the TCGA, GSE62452, and GSE57495 cohorts.

TCGA (<i>n</i> = 176)	Low (88)	High (88)	<i>p</i> -value
Age			0.602
Median	66	65	
IQR	58-72	57-73	
Race			0.450
White	80	75	
Black	2	4	
Asian	4	7	
Unknown	2	2	
Histological type	_		0.112
PDAC*	68	77	
Other	20	11	
Tumor site			0.68
Body/Tail	15	13	
Head	66	71	
Unknown	7	4	
T-category	_		0.017
T1	3	4	
T2	18	5	
Т3	64	77	
T4	1	2	
Unknown	2	0	
N-category	_		0.178
N-	28	21	
N+	55	67	
Unknown	5	0	
M-category	_		1.00
M-	36	42	
M+	2	2	
Unknown	50	44	

Table S1. Comparison of clinical and pathological features between low and high 4-gene score with pancreatic cancer in the TCGA cohort.

*PDAC: pancreatic ductal adenocarcinoma.

GSE62452 (<i>n</i> = 69)	Low (34)	High (35)	<i>p</i> -value
Grade			0.024
1	2	0	
2	21	14	
3	10	20	
unknown	1	1	
Stage			0.706
I	3	1	
II	23	23	
III	5	8	
IV	3	3	
Unknown	0	0	

Table S2: Comparison of pathological features between low and high 4-gene score with pancreaticcancer in the GSE62452 cohort.

Table S3. Comparison of pathological feature between low and high 4-gene score with pancreaticcancer in the GSE57495 cohort.

GS57495 (<i>n</i> = 63)	Low (31)	High (32)	<i>p</i> -value
Stage			0.889
Ι	0	2	
IB	7	5	
IIA	8	9	
IIB	26	17	
Unknown	0	0	

Primary	Metastasis	
BXPC3	ASPC1	
CAPAN2	CAPAN1	
HPAC	CFPAC1	
KP2	HPAFII	
MIAPACA2	HS766T	
PANC0203	HUPT3	
PANC0327	HUPT4	
PANC0403	KP3	
PANC0504	KP4	
PANC0813	L33	
PANC1005	PATU8988S	
PATU8902	PATU8988T	
PK45H	PK1	
PSN1	PK59	
QGP1	SNU410	
SW1990	SU8686	
	SUIT2	
	TCCPAN2	
	YAPC	

Table S4. Pancreatic cancer cell lines.



Figure S1. Gene set enrichment analysis (GSEA) of high 4-gene score pancreatic cancer in the TCGA, GSE62452, and GSE57495 cohorts. Enrichment plots along with normalized enrichment score (NES) and false discovery rate (FDR) are shown for cancer aggressiveness-related Hallmark gene sets, including MTORC1 signaling, PI3K/AKT/MTOR signaling, DNA repair, unfolded protein response, notch signaling, and hypoxia. NES and FDR were determined with the classical GSEA method, where FDR < 0.25 is considered significant.