Table S1. qPCR primer sequence

Gene	F	R
PHKG1	CACCTTGAGTGAGAAGGAAACC	GAGTTTGTGCAAGGTGCAGAT
HOXA4	CACCAGGGAAAGCACAAAC	AAGATTATATGGAGGAGGGAACG
ISL2	CATCAAGTGCGCCAAGTG	TCGATGTGGTACACGCTGTC
DMRT3	CCAAGCCAGATTTGACTG	CCTTACTCTTTGCCACAT
TRA2A	TCTGAATCCCATTCTCGATCA	GGATCTGGATCGAGTGTAACG
ACTB	GTGGCCGAGGACTTTGATTG	CCTGTAACAACGCATCTCATATT

Table S2. Patient demographics of the long-term survivor and common clinical course patients in TCGA PDAC cohort

	Long-term survivor (n=4)	Common clinical course (n=76)	*P*
Sex			
Male	2 (50.0%)	37 (487%)	>0.999
Female	2 (50.0%)	39 (51.3%)	
Age	66.0±4.2	65.3±11.1	0.797
Race			
CA	3 (75.0%)	68 (91.9%)	0.319
others	1 (25.0%)	6 (8.1%)	
Primary Site			
Body/Tail	1 (25.0%)	11 (14.5%)	0.485
Head	3 (75.0%)	65 (85.5%)	
Residual Tumor			
R0	2 (100%)	40 (56.3%)	0.505
R1/2	0 (0%)	31 (43.7%)	
Tumor Size	3.47±0.64	3.98±1.55	0.299
Grade			
G1	1 (25.0%)	8 (10.5%)	0.386
G2/3	3 (75.0%)	68 (89.8%)	
pT			
pT1/2	0 (0%)	10 (13.2%)	>0.999
pT3/4	4 (100%)	66 (86.8%)	
pN			
pN0	1 (25.0%)	15 (20.0%)	>0.999
pN1	3 (75.0%)	60 (80.0%)	
Stage			
Stage I	0 (0%)	6 (7.9%)	>0.999
Stage II	4 (100%)	67 (88.2%)	
Stage III/IV	0 (0%)	3 (76.0%)	

CA: Caucasian American.

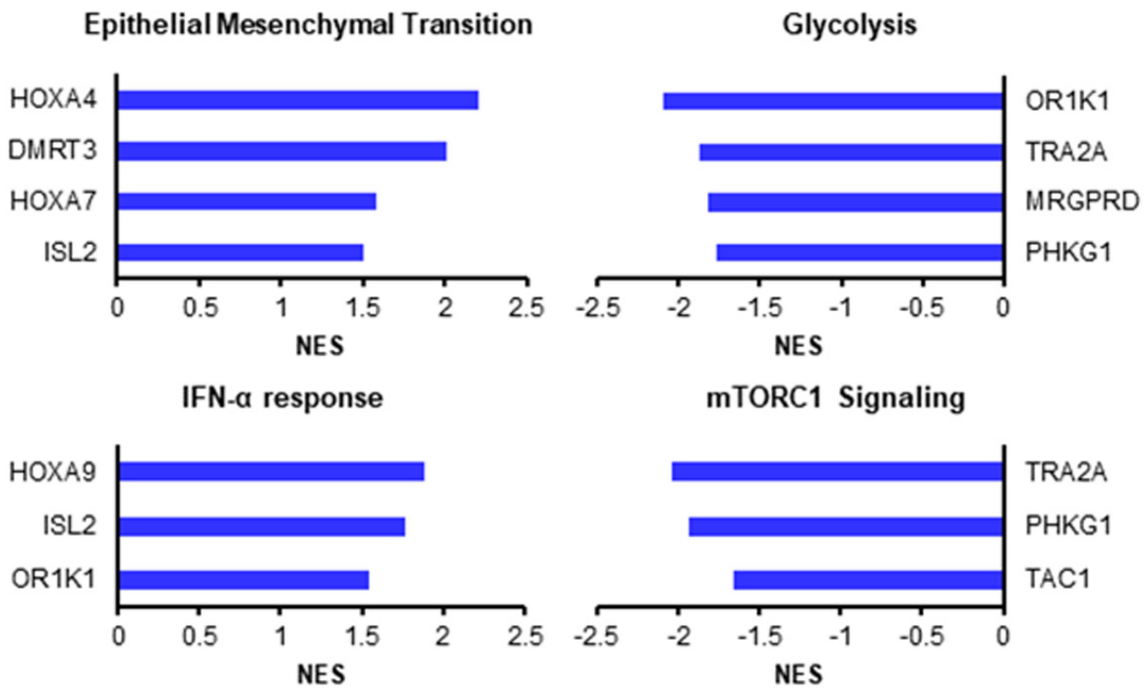

Figure S1. Gene set enrichment analysis (GSEA) of genes which were highly expressed in the long-term survivor. NES: normalized enrichment score.

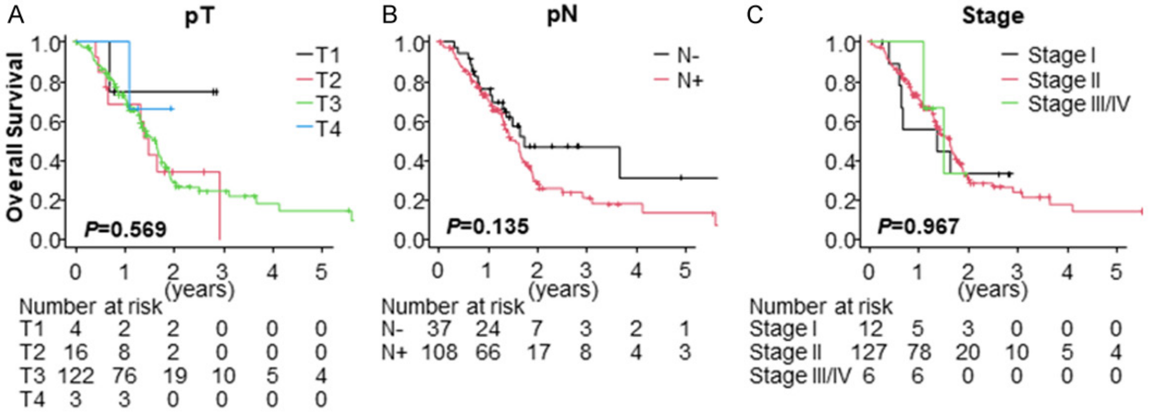

Figure S2. The relationship of the AJCC staging system and overall survival in TCGA PDAC cohort. A. Overall survival by pT classification. B. Overall survival by pN classification. C. Overall survival by stage.