

Figure S1. Time-dependent ROC curves for CXCR subunits in patients with pancreatic ductal adenocarcinoma. Time-dependent ROC curves for (A) overall survival and (B) disease-free survival. CXCR, C-X-C motif chemokine receptor; ROC, receiver operating characteristic; AUC, area under the curve.

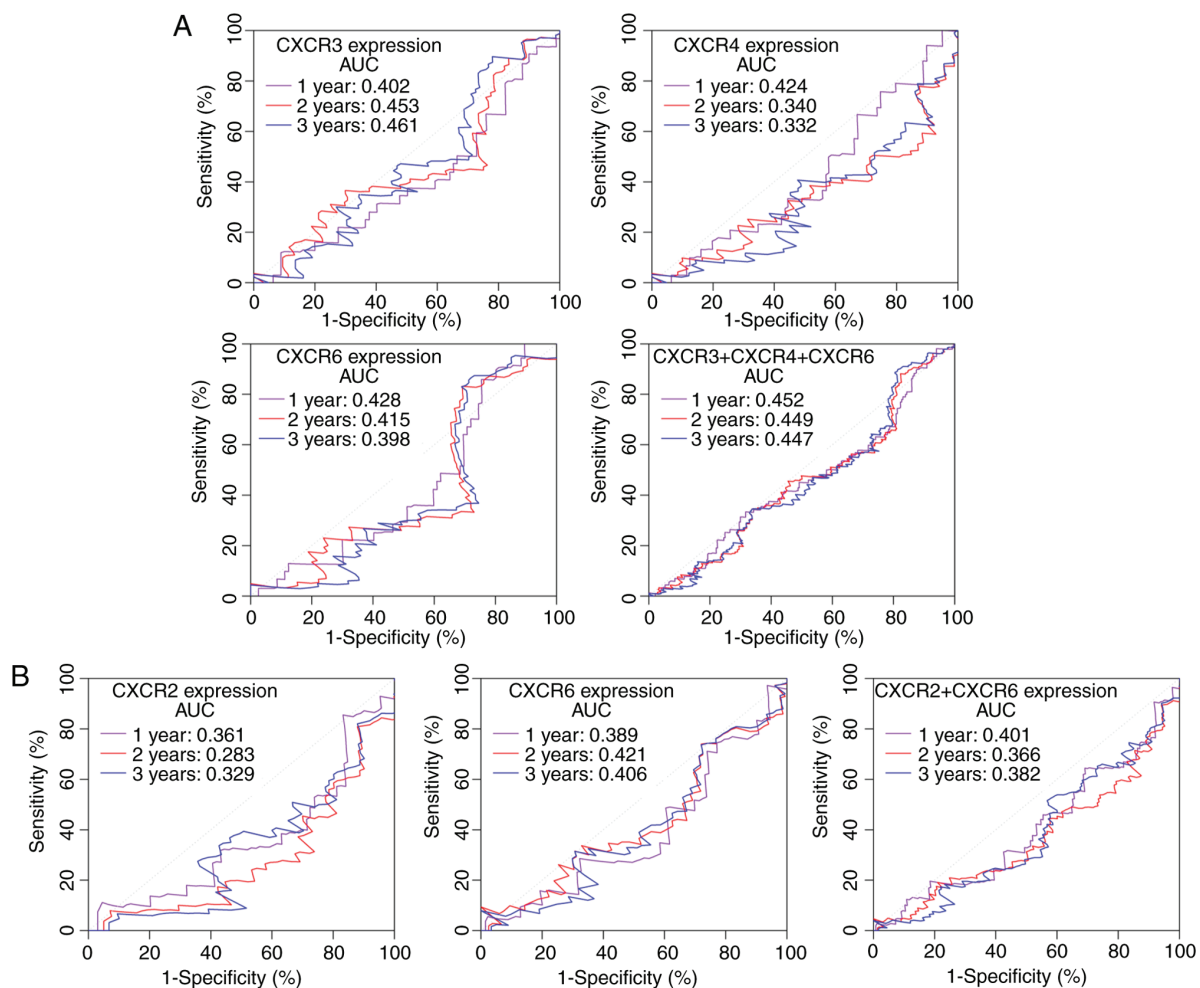


Figure S2. GSEA in patients with early-stage PDAC. GSEA reports of adhesion and differentiation of immune cells for high C-X-C motif chemokine receptor subunit expression levels using high- vs. low-risk groups. Enrichment plots for (A) regulation of adaptive immune response, (B) leukocyte cell to cell adhesion, (C) regulation of cell to cell adhesion, (D) lymphocyte differentiation and (E) T cell differentiation. These panels provide the genome-wide potential pathways and molecular mechanisms in patients with PDAC based on gene expression levels. NES, normalized enrichment score; GSEA, gene set enrichment analysis; PDAC, pancreatic ductal adenocarcinoma.

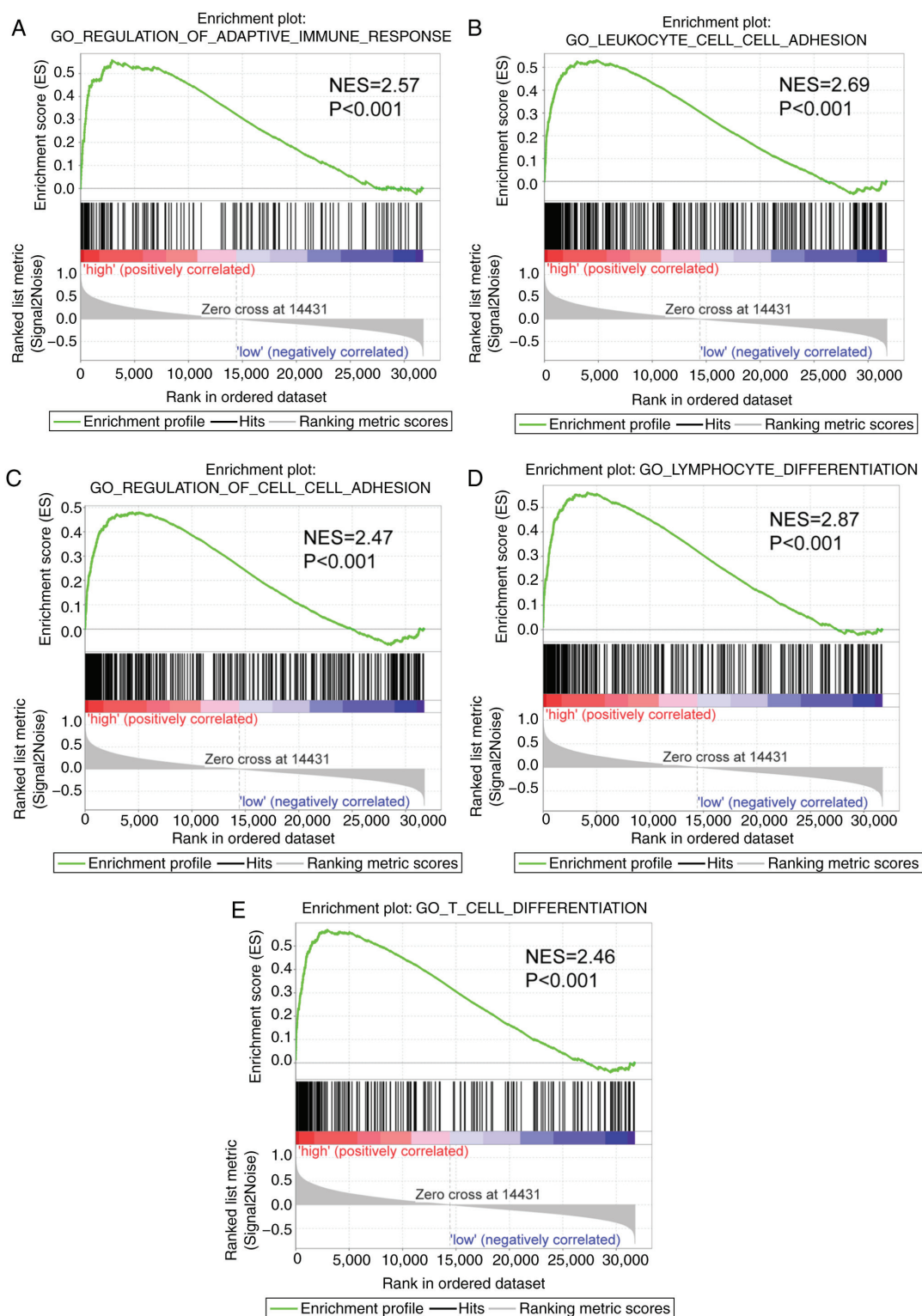


Figure S3. Comparisons of tumor infiltration levels among tumors with different SCNAs for CXCR2, CXCR3, CXCR4 and CXCR6. The infiltration level for each SCNA category defined by GISTIC 2.0 (deep deletion, arm-level deletion, arm-level gain and high amplification) was compared with the diploid/normal group using the two-sided Wilcoxon rank sum test with Bonferroni's correction. These figures provide the comparison of the abundance of immune infiltration among tumors with different SCNA category for given CXCR subunit groups. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. PAAD, pancreatic adenocarcinoma; CXCR, C-X-C motif chemokine receptor; SCNAs, somatic copy number alterations.

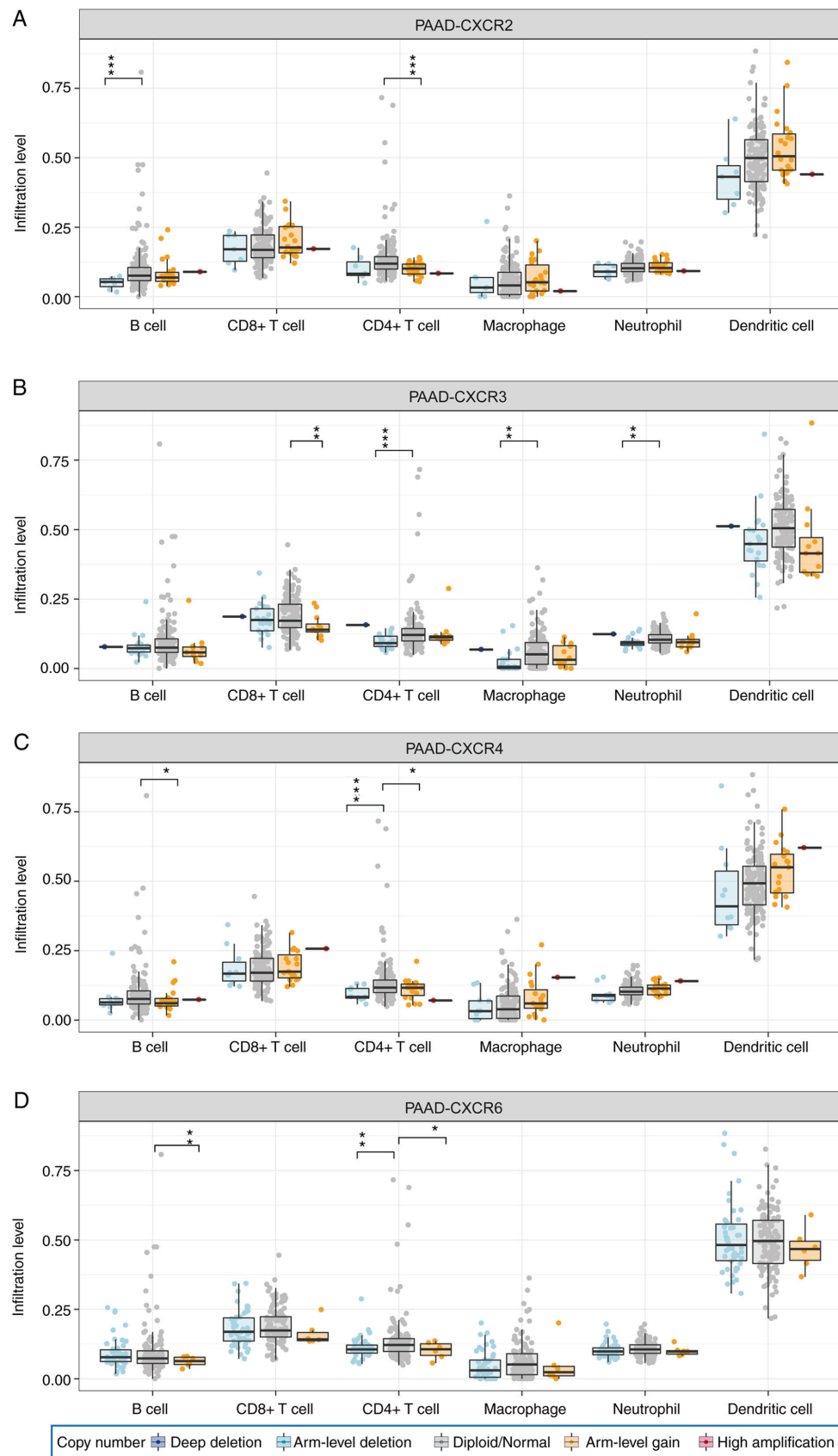


Table SI. Survival analysis of clinicopathological features in 112 patients with early-stage pancreatic ductal adenocarcinoma.

Clinicopathological feature	Patients	MST, days	Log-rank P-value	HR (95% CI)	MRT (days)	Log-rank P-value	HR (95% CI)
Age, years							
≤60	38	593	0.066	Ref.	716	0.549	Ref.
>60	74	485		1.64 (0.96-2.78)	581		0.81 (0.42-1.60)
Sex							
Female	53	511	0.523	Ref.	831	0.971	Ref.
Male	59	592		0.86 (0.53-1.38)	593		0.99 (0.51-1.93)
Alcohol addiction history							
No	43	592	0.349	Ref.	716	0.479	Ref.
Yes	61	511		1.28 (0.77-2.13)	593		1.29 (0.63-2.64)
Pathological stage							
Stage I	8	236	0.943	Ref.	NA	0.374	Ref.
Stage II	104	518		1.04 (0.38-2.87)	620		2.40 (0.33-17.61)
Pathological T stage							
T1/T2	14	498	0.466	Ref.	NA	0.249	Ref.
T3	98	518		1.34 (0.61-2.95)	593		1.99 (0.60-6.60)
Pathological N stage							
N0	21	634	0.091	Ref.	NA	0.020	Ref.
N1	91	511		1.82 (0.90-3.68)	581		3.74 (1.14-12.27)
Histological grade							
G1	15	518	0.034	Ref.	620	0.002	Ref.
G2	65	603		1.22 (0.54-2.76)	831		0.74 (0.27-2.03)
G3/G4	32	470		2.27 (0.96-5.34)	393		2.74 (0.94-8.02)
Radical resection							
No	44	381	0.009	Ref.	461	0.014	Ref.
Yes	66	603		0.51 (0.31-0.85)	831		0.40 (0.19-0.85)
Radiation therapy							
No	70	473	0.029	Ref.	716	0.697	Ref.
Yes	30	691		0.53 (0.29-0.95)	542		1.15 (0.56-2.36)
Targeted molecular therapy							
No	29	224	<0.001	Ref.	NA	0.470	Ref.
Yes	73	634		0.17 (0.10-0.30)	593		0.72 (0.29-1.78)

Alcohol addiction history information was unavailable for 8 patients, radical resection information was unavailable for 2 patients, radiation therapy information was unavailable for 12 patients and targeted molecular therapy information unavailable for 10 patients. MST, median survival time; MRT, median disease-free survival time; HR, hazard ratio; CI, confidence interval; Ref., reference; NA, not available.