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### Figures and figure supplements

Comprehensive machine-learning survival framework develops a consensus model in large-scale multicenter cohorts for pancreatic cancer

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Figure 1. The workflow of our research.



**Figure 2.** Construction and testing of the artificial intelligence-derived prognostic signature (AIDPS). (**A**) The C-indexes of 76 machine-learning algorithm combinations in the nine testing cohorts. (**B**) Discovery of 32 consensus prognosis genes from 10 independent multicenter cohorts. (**C**–J) The predictive performance of AIDPS was compared with common clinical and molecular variables in the PACA-AU-Array (**C**), TCGA-PAAD (**D**), PACA-AU-Seq (**E**), PACA-CA-Seq (**F**), E-MTAB-6134 (**G**), GSE62452 (**H**), GSE78229 (**I**), and GSE79668 (J). Z-score test: \*p<0.05, \*\*p<0.01, \*\*\*p<0.001, \*\*\*\*p<0.001.



Figure 3. Survival analysis and predictive performance evaluation of artificial intelligence-derived prognostic signature (AIDPS). (A, B) Kaplan–Meier survival analysis for overall survival (OS) (A) and relapse-free survival (RFS) (B) between the high and low AIDPS groups in the PACA-AU-Array. (C, D) Kaplan–Meier survival analysis for OS (C) and RFS (D) between the high and low AIDPS groups in the Meta-Cohort. (E, F) Multivariate Cox regression analysis of OS (E) and RFS (F) in the PACA-AU-Array. (G, H) Multivariate Cox regression analysis of OS (G) and RFS (F) in the PACA-AU-Array. (I, J) Calibration curve for predicting 1-, 2-, and 3-year OS in the PACA-AU-Array (I), and Meta-Cohort (J). (K, L) Time-dependent receiver-operator characteristic (ROC) analysis for predicting 1-, 2-, and 3-year OS in the PACA-AU-Array (K), and Meta-Cohort (L).



Figure 3—figure supplement 1. Survival analysis of artificial intelligence-derived prognostic signature (AIDPS) in the nine testing cohorts. (A– I) Kaplan–Meier survival analysis for overall survival (OS) between the high and low AIDPS groups in the TCGA-PAAD (A), PACA-AU-Seq (B), PACA-CA-Seq (C), E-MTAB-6134 (D), GSE62452 (E), GSE28735 (F), GSE78229 (G), GSE79668 (H), and GSE85916 (I). (J–M) Kaplan–Meier survival analysis for relapse-free survival (RFS) between the high and low AIDPS groups in the TCGA-PAAD (J), PACA-AU-Seq (K), PACA-CA-Seq (L), and E-MTAB-6134 (M). (N) Multivariate Cox regression analysis of OS in the TCGA-PAAD.

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Figure 3—figure supplement 2. Survival analysis of artificial intelligence-derived prognostic signature (AIDPS) in the nine testing cohorts. (A– F) Multivariate Cox regression analysis of overall survival (OS) in the PACA-AU-Seq (A), PACA-CA-Seq (B), E-MTAB-6134 (C), GSE79668 (D), GSE62452 (E), and GSE78229 (F). (G–J) Multivariate Cox regression analysis of relapse-free survival (RFS) in the TCGA-PAAD (G), E-MTAB-6134 (H), PACA-CA-Seq (I), and PACA-AU-Seq (J).

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Figure 3—figure supplement 3. Predictive performance of artificial intelligence-derived prognostic signature (AIDPS) in the nine testing cohorts. Timedependent receiver-operator characteristic (ROC) analysis for predicting 1-, 2-, and 3-year overall survival (OS) in the TCGA-PAAD (A), PACA-AU-Seq (B), PACA-CA-Seq (C), E-MTAB-6134 (D), GSE62452 (E), GSE28735 (F), GSE78229 (G), GSE79668 (H), and GSE85916 (I).





Figure 3—figure supplement 4. Survival analysis and predictive performance of artificial intelligence-derived prognostic signature (AIDPS) in the three external validation cohorts. (A) Univariate Cox regression analysis of AIDPS and 86 published signatures of pancreatic cancer (PACA) in three external validation cohorts. (B–D) Kaplan–Meier survival analysis for overall survival (OS) in the GSE21501 (B), GSE57495 (C), and GSE71729 (D) cohorts. (E–G) Time-dependent receiver-operator characteristic (ROC) analysis for predicting 1-, 2-, and 3-year OS in the GSE21501 (E), GSE57495 (F), and GSE71729 (G). (H–J) Calibration curve for predicting 1-, 2-, and 3-year OS in the GSE21501 (H), GSE57495 (I).

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**Figure 4.** Comparisons between artificial intelligence-derived prognostic signature (AIDPS) and 86 expression-based signatures. (**A**) Univariate Cox regression analysis of AIDPS and 86 published signatures of pancreatic cancer (PACA). (**B**) C-indexes of AIDPS and 86 published signatures in the PACA-AU-Array, TCGA-PAAD, PACA-AU-Seq, PACA-CA-Seq, E-MTAB-6134, GSE62452, GSE28735, GSE78229, GSE79668, GSE85916, and Meta-Cohort. Z-score test: \*p<0.05, \*\*p<0.01, \*\*\*p<0.001, \*\*\*p<0.0001.



Figure 4—figure supplement 1. Comparison of artificial intelligence-derived prognostic signature (AIDPS) with 86 published signatures in the three validation cohorts and with models constructed by other methods for nine AIDPS genes. (A) C-indexes of AIDPS and 86 published signatures in the GSE21501. (B) C-indexes of AIDPS and 86 published signatures in the GSE57495. (C) C-indexes of AIDPS and 86 published signatures in the GSE57495. (C) C-indexes of AIDPS and 86 published signatures in the GSE57495. (D) The C-indexes of AIDPS and models constructed by other methods for nine AIDPS genes in the nine testing cohorts and three external validation cohorts. (E) The C-indexes for the six-gene signature of Stratford JK in all 13 cohorts. (F) The C-indexes for the 15-gene signature of Chen DT in all 13 cohorts. (G) The C-indexes for the five-gene signature of Kim J in all 13 cohorts. Z-score test: \*p<0.05, \*\*p<0.01, \*\*\*p<0.001, \*\*\*\*p<0.0001.



Figure 5. The clinical signature and functional characteristics of the high and low artificial intelligence-derived prognostic signature (AIDPS) groups. (A–D) Composition percentage of the two groups in clinical characteristics such as age (A), gender (B), stage (C), and grade (D) in the PACA-AU-Array. (E–H) Kaplan–Meier survival analysis for overall survival (OS) in the TCGA-LIHC (E), TCGA-STAD (F), TCGA-COAD (G), and TCGA-READ (H). (I, J) The top five Gene Ontology (GO)-enriched pathways (I) and Kyoto Encyclopedia of Genes and Genomes (KEGG)-enriched pathways (J) in the high AIDPS groups. (K, L) The top five GO-enriched pathways (K) and KEGG-enriched pathways (L) in the low AIDPS groups.



Figure 5—figure supplement 1. The clinical characteristics of the high and low artificial intelligence-derived prognostic signature (AIDPS) groups. (A, E, I, M) Composition percentage of the two groups in clinical characteristics such as age (A), gender (E), stage (I), and grade (M) in the TCGA-PAAD cohort. (B, F, J, N) Composition percentage of the two groups in clinical characteristics such as age (B), gender (F), stage (J), and grade (N) in the PACA-AU-Seq cohort. (C, G, K, O) Composition percentage of the two subtypes in clinical characteristics such as age (C), gender (G), stage (K), and grade (O) in the Meta-Cohort cohort. (D, H, L) Composition percentage of the two groups on grade in the E-MTAB-6134 cohort.



**Figure 6.** Multi-omics analysis based on mutation, copy number alteration (CNA), and methylation. (**A**) Genomic alteration landscape according to artificial intelligence-derived prognostic signature (AIDPS). Tumor mutation burden (TMB), relative contribution of four mutational signatures, top 15 mutated genes and broad-level CNA (>20%), and selected genes located within chromosomes 8q24.21, 9p21.3, and 18q21.2 are shown from the top to the bottom panels. The proportion of the high and low AIDPS groups in each alteration is presented in the right bar charts. (**B**) Comprehensive comparison of mutation landscapes in 10 oncogenic signaling pathways across the high and low AIDPS groups. Genes are mutated at different frequencies (color intensity indicates the mutation frequency within the entire dataset) by oncogenic mutations (red) and tumor suppressor mutations

Figure 6 continued on next page

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#### Figure 6 continued

(blue). Each gene box includes two percentages representing the mutation frequency in the high and low AIDPS groups, and another box representing the statistical p-value. Genes are grouped by signaling pathways, with edges showing pairwise molecular interactions. (**C**) Comparison of the two groups in TMB. (**D**) Comparison of the two groups in arm and focal CNA burden. (**E**, **F**) Boxplot of DNA methylation level (**E**) and mRNA expression level (**F**) for methylation-driven genes in the high and low groups. (**G–J**) Kaplan–Meier survival analysis between the high and low methylation groups in the *MAP3K8* (**G**), *PCDH7* (**H**), *PCDHB1* (**I**), and *SPAG6* (**J**). \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.



**Figure 7.** The immune landscape in the high and low artificial intelligence-derived prognostic signature (AIDPS) groups. (**A**) The heatmap of 28 immune cell types in the high and low AIDPS groups. (**B**) Boxplot of relative infiltrate abundance of 28 immune cell types in patients with high and low AIDPS groups. (**C**) Boxplot of relative expression levels at 27 immune checkpoints profiles between the high and low AIDPS patients. \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.

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OS_TCGA_PAAD-	****	OS_GSE78229-		OS_E_MTAB_6134 -		OS_GSE62452 -	***	OS_TCGA_PAAD-	***
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OS_GSE85916-		OS_PACA_AU_Seq -		OS_GSE62452 -		OS_GSE71729-		OS_GSE21501 -	
OS_GSE79668-	****	OS_GSE71729-		OS_PACA_AU_Seq-	•	OS_GSE21501 -		OS_GSE79668 -	
OS_GSE28735-	••••••••••••••••••••••••••••••••••••••	OS_GSE28735 - 🛏		OS_GSE28735-	•	OS_PACA_CA_Seq-	<b>⊢</b>	OS_PACA_CA_Seq-	
DFS_TCGA_PAAD-	****	DFS_TCGA_PAAD-		DFS_TCGA_PAAD	**	DFS_TCGA_PAAD-		DFS_TCGA_PAAD-	**
RFS_PACA_AU_Array-	<b></b>	RFS_PACA_AU_Array		RFS_PACA_AU_Array	• • • • • • • • • • • • • • • • • • •	RFS_PACA_AU_Seq	••	RFS_PACA_AU_Seq-	
RFS_PACA_CA_Seq-		RFS_PACA_CA_Seq	· · · · · · · · · · · · · · · · · · ·	RFS_PACA_CA_Seq -	• • • • • • • • • • • • • • • • • • •	RFS_E_MTAB_6134 -	•	RFS_E_MTAB_6134 -	****
RFS_PACA_AU_Seq-		RFS_E_MTAB_6134	••••••••••••••••••••••••••••••••••••••	RFS_PACA_AU_Seq -		RFS_PACA_AU_Array-		RFS_PACA_AU_Array-	
RFS_E_MTAB_6134-	****	RFS_PACA_AU_Seq -		RFS_E_MTAB_6134-		RFS_PACA_CA_Seq-	<b></b>	RFS_PACA_CA_Seq-	<b></b>
DSS_TCGA_PAAD-	****	DSS_TCGA_PAAD-		DSS_TCGA_PAAD-		DSS_TCGA_PAAD-	•	DSS_TCGA_PAAD-	***
PFS_TCGA_PAAD -	****	PFS_TCGA_PAAD-		PFS_TCGA_PAAD-		PFS_TCGA_PAAD-	****	PFS_TCGA_PAAD-	****
	0.96 0.97 0.98 0.99 1.00 Hazard ratio	0	0.5 0.7 1.0 Hazard ratio	0.3	0.5 1.0 Hazard ratio		Hazard ratio		1 2 3 Hazard ratio
OS DFS	RFS DSS PFS	OS DFS RF	FS 📕 DSS 🔳 PFS	OS DFS R	FS 📕 DSS 🔳 PFS	OS DFS I	RFS 📕 DSS 🔳 PFS	OS DFS	RFS 📕 DSS 🔳 PFS
F UNC13D Cox	regression anlaysis	G EREG Cox re	egression anlaysis		egression anlaysis	CDCA4 Cox	regression anlaysis	s J TGM2 Cox	regression anlaysis
OS_GSE28735 -	regression anlaysis	G EREG Cox re	egression anlaysis	OS_E_MTAB_6134-	egression anlaysis	CDCA4 Cox OS_GSE21501-	regression anlaysis	s J TGM2 Cox OS_GSE78229-	regression anlaysis
OS_GSE28735- OS_GSE78229-	regression anlaysis	G EREG Cox re OS_GSE79668 - OS_GSE28735 -	egression anlaysis	ADM Cox re OS_E_MTAB_6134 - OS_GSE85916 -	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 -	regression anlaysis	s J TGM2 Cox OS_GSE78229- OS_GSE79668-	regression anlaysis
F UNC13D Cox OS_GSE28735- OS_GSE78229- OS_GSE62452-	regression anlaysis	G EREG Cox re OS_GSE79688 - OS_GSE28735 - OS_TCGA_PAAD -	egression anlaysis	ADM Cox re OS_E_MTAB_6134 - OS_GSE85916 - OS_GSE28735 -	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 - OS_GSE62452 -	regression anlaysis	s J TGM2 Cox OS_GSE78229- OS_GSE79668- OS_GSE85916-	regression anlaysis
CS_GSE28735- OS_GSE28735- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq-	regression anlaysis	G EREG Cox rr OS_GSE79668 - OS_GSE28735 - OS_TCGA_PAAD - OS_PACA_AU_Seq -	egression anlaysis	ADM Cox rr OS_E_MTAB_6134 - OS_GSE85916 - OS_GSE28735 - OS_GSE78229 -	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 - OS_GSE62452 - OS_GSE28735 -	regression anlaysis	S         J         TGM2 Cox           OS_GSE78229         OS_GSE79668         OS_GSE85916           OS_GSE62452         OS_GSE62452         OS_GSE62452	regression anlaysis
OS_GSE85916- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE85916-	regression anlaysis	G EREG Cox rd OS_GSE79668 - OS_GSE28735 - OS_TCGA_PAAD - OS_PACA_AU_Seq - OS_GSE78229 -	egression anlaysis	ADM Cox rd OS_E_MTAB_134 OS_GSE85916 OS_GSE28735 OS_GSE78229 OS_PACA_AU_Seq	egression anlaysis	CDCA4 Cox OS_GSE21501- OS_GSE78229- OS_GSE62452- OS_GSE62452- OS_GSE28735- OS_PACA_AU_Array-	regression anlaysis	S         J         TGM2 Cox           OS_GSE78229-         OS_GSE79668-         OS_GSE6916-           OS_GSE62452-         OS_TCGA_PAAD-	regression anlaysis
OS_GSE628735- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE65916- OS_GSE71729-	regression anlaysis	C EREG COX rd OS_GSE79668- OS_GSE28735- OS_TCGA_PAAD- OS_PACA_AU_Seq OS_GSE78229- OS_GSE62452-	agression anlaysis	H ADM Cox rr OS_E_MTAB_6134- OS_GSE85916- OS_GSE28735- OS_GSE78229- OS_PACA_AU_Seq- OS_GSE62452-	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 - OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79668 -	regression anlaysis	s         J         TGM2 Cox           OS_GSE78229         OS_GSE78685           OS_GSE85916         OS_GSE62452           OS_TCGA_PAAD         OS_PACA_AU_Array-	regression anlaysis
<ul> <li>UNC13D Cox</li> <li>OS_GSE28735-</li> <li>OS_GSE78229-</li> <li>OS_GSE62452-</li> <li>OS_PACA_AU_Seq-</li> <li>OS_GSE85916-</li> <li>OS_GSE71729-</li> <li>OS_PACA_AU_Array-</li> </ul>	regression anlaysis	C EREG COX K OS_GSE79668- OS_GSE28735- OS_TCGA_PAAD- OS_PACA_AU_Seq- OS_GSE78229- OS_GSE62452- OS_E_MTAB_6134-	egression anlaysis	ADM Cox re OS_E_MTAB_6134 OS_GSE85916- OS_GSE28735- OS_GSE78229- OS_PACA_AU_Seq OS_GSE62452- OS_GSE62452- OS_GSE79668-	egression anlaysis	CDCA4 Cox OS_GSE21501- OS_GSE78229- OS_GSE62452- OS_GSE28735- OS_PACA_AU_Array- OS_GSE79668- OS_PACA_AU_Seq-	regression anlaysis	<ul> <li>J TGM2 Cox</li> <li>OS_GSE78229-</li> <li>OS_GSE78688-</li> <li>OS_GSE85916-</li> <li>OS_GSE85916-</li> <li>OS_GSE82452-</li> <li>OS_TCGA_PAAD-</li> <li>OS_PACA_AU_Array-</li> <li>OS_PACA_AU_Seq-</li> </ul>	regression anlaysis
UNC13D Cox           OS_GSE28735-           OS_GSE78229-           OS_GSE62452-           OS_PACA_AU_Seq-           OS_GSE85916-           OS_GSE77229-           OS_PACA_AU_Array-           OS_PACA_AU_Array-           OS_GSE78686-	regression anlaysis	G         EREG Cox rt           OS_GSE79668         0S_GSE28735           OS_TCGA_PAAD         0S_TCGA_PAAD           OS_PACA_AU_Seq         0S_GSE78229           OS_GSE62452         0S_GSE62452           OS_E_MTAB_6134         0S_PACA_AU_MTAY	agression anlaysis	ADM Cox re OS_E_MTAB_0134 OS_GSE85916 OS_GSE28735 OS_GSE78229 OS_PACA_AU_Seq OS_GSE62452 OS_GSE62452 OS_GSE79668 OS_PACA_CA_Seq	egression anlaysis	CDCA4 Cox OS_GSE21501- OS_GSE78229- OS_GSE62452- OS_GSE28735- OS_PACA_AU_Array- OS_GSE79668- OS_PACA_AU_Seq- OS_TCGA_PAAD-	regression anlaysis	s         J         TGM2 Cox           OS_GSE78229         OS_GSE78688           OS_GSE6516         OS_GSE6516           OS_TCGA_PAAD         OS_PACA_AU_Array           OS_PACA_AU_Seq         OS_GSE28735	regression anlaysis
<ul> <li>UNC13D Cox</li> <li>OS_GSE28735-</li> <li>OS_GSE78229-</li> <li>OS_GSE62452-</li> <li>OS_PACA_AU_Seq-</li> <li>OS_GSE79729-</li> <li>OS_PACA_AU_Array-</li> <li>OS_GSE79668-</li> <li>OS_E_MTAB_6134-</li> </ul>	regression anlaysis	C EREG Cox re OS_GSE79668 - OS_GSE28736 - OS_TCGA_PAAD - OS_PACA_AU_Seq - OS_GSE78229 - OS_GSE62452 - OS_E_MTAB_6134 - OS_PACA_AU_Array - OS_GSE85916 -	agression anlaysis	H     ADM Cox rr      Os_E_MTAB_6134     Os_GSE85916     Os_GSE78229     Os_PACA_AU_Seq     Os_GSE78264     Os_GSE78664     Os_GSE78668     Os_GSE78668     Os_GSE78668     Os_GSE78668	egression anlaysis	CDCA4 Cox OS_GSE21501- OS_GSE78229- OS_GSE62452- OS_GSE62452- OS_PACA_AU_Array- OS_GSE79668- OS_PACA_AU_Seq- OS_TCGA_PAAD- OS_GSE85916-	regression anlaysis	<ul> <li>J TGM2 Cox</li> <li>OS_GSE78229</li> <li>OS_GSE79688</li> <li>OS_GSE62452</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_GSE28735</li> <li>OS_PACA_CA_Seq</li> </ul>	regression anlaysis
<ul> <li>UNC13D Cox</li> <li>OS_GSE28735-</li> <li>OS_GSE78229-</li> <li>OS_GSE62452-</li> <li>OS_FACA_AU_Seq-</li> <li>OS_GSE85916-</li> <li>OS_GSE71729-</li> <li>OS_PACA_AU_Array-</li> <li>OS_GSE79668-</li> <li>OS_E_MTAB_6134-</li> <li>OS_TCGA_PAAD-</li> </ul>	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_GSE28735           OS_TCGA_PAAD         OS_GSE78229           OS_GSE78229         OS_GSE62452           OS_PACA_AU_Seq1         OS_PACA_AU_Array           OS_PACA_AU_Array         OS_GSE85916           OS_GSE71729         OS_GSE71729	agression anlaysis	H     ADM Cox rr      Os_E_MTAB_6134     Os_GSE85916     Os_GSE78229     Os_PACA_AU_Seq     Os_GSE74262     Os_GSE74263     Os_GSE74966     Os_GSE57495     Os_PACA_AU_Array	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 - OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Seq - OS_TCGA_PAAD - OS_GSE85916 - OS_GSE85916 -	regression anlaysis	s         J         TGM2 Cox           OS_GSE78629         OS_GSE78689           OS_GSE85916         OS_GSE85916           OS_GSE85916         OS_GSE85452           OS_TCGA_PAAD         OS_TCGA_PAAD           OS_PACA_AU_Array-         OS_PACA_AU_Array-           OS_GSE28735         OS_PACA_CA_Seq           OS_PACA_CA_Seq         OS_SCSE57495	regression anlaysis
<ul> <li>UNC13D Cox</li> <li>OS_GSE28735-</li> <li>OS_GSE28735-</li> <li>OS_GSE62452-</li> <li>OS_PACA_AU_Seq-</li> <li>OS_GSE5916-</li> <li>OS_GSE79686-</li> <li>OS_EACA_AU_Array-</li> <li>OS_GSE79668-</li> <li>OS_E_MTAB_6134-</li> <li>OS_TCGA_PAAD-</li> <li>OS_GSE21501-</li> </ul>	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_GSE28735           OS_GSE28735         OS_TCGA_PAAD           OS_PACA_AU_Seq         OS_GSE62452           OS_GSE62452         OS_E_MTAB_6134           OS_PACA_AU_Array         OS_GSE85916           OS_GSE21501         OS_GSE21501	egression anlaysis	M ADM Cox re OS_E_MTAB_0134 OS_GSE589916 OS_GSE28735 OS_GSE78229 OS_GSE74229 OS_GSE74229 OS_GSE74968 OS_PACA_AU_Seq OS_GSE74968 OS_PACA_AU_Array OS_GSE71729	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 - OS_GSE62452 - OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Seq - OS_TCGA_PAAD - OS_GSE65916 - OS_GSE71729 - OS_GSE71729 -	regression anlaysis	<ul> <li>Cos_GSE78229</li> <li>OS_GSE78688</li> <li>OS_GSE85916</li> <li>OS_GSE62452</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_GSE28735</li> <li>OS_PACA_CA_Seq</li> <li>OS_GSE57495</li> <li>OS_GSE57495</li> </ul>	regression anlaysis
<ul> <li>UNC13D Cox</li> <li>OS_GSE28735-</li> <li>OS_GSE78229-</li> <li>OS_GSE62452-</li> <li>OS_PACA_AU_Seq-</li> <li>OS_GSE79686-</li> <li>OS_GSE79686-</li> <li>OS_E_MTAB_6134-</li> <li>OS_TCGA_PAAD-</li> <li>OS_PACA_CA_Seq-</li> <li>OS_PACA_CA_Seq-</li> </ul>	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_GSE28735           OS_TCGA_PAAD         OS_TCGA_PAAD           OS_PACA_AU_Seq         OS_GSE78229           OS_GSE62452         OS_GSE62452           OS_PACA_AU_Array         OS_GSE85916           OS_GSE71729         OS_GSE71729           OS_GSE21501         OS_GSE25495	agression anlaysis	M ADM Cox rt OS_E_MTAB_134- OS_GSE85916- OS_GSE28735- OS_GSE78229- OS_GSE78229- OS_GSE7828- OS_GSE7868- OS_PACA_AL_Seq- OS_GSE7868- OS_PACA_CA_Seq- OS_GSE77869- OS_GSE77729- OS_GSE71729- OS_CCA_PAAD.	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 - OS_GSE62452 - OS_GSE62452 - OS_GACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Seq - OS_GSE79668 - OS_GSE57495 -	regression anlaysis	<ul> <li>J TGM2 Cox</li> <li>OS_GSE78229</li> <li>OS_GSE7868</li> <li>OS_GSE62452</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_PACA_AU_Seq</li> <li>OS_PACA_AU_Seq</li> <li>OS_SE57495</li> <li>OS_GSE571729</li> <li>OS_E,MTAB_6134</li> </ul>	regression anlaysis
CS_CSE28735- OS_GSE28735- OS_GSE28735- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE65916- OS_GSE71729- OS_PACA_AU_Array- OS_GSE71729- OS_GSE770668- OS_E_MTAB_6134- OS_TCGA_PAAD- OS_GSE21501- OS_PACA_CA_Seq- OS_GSE57495-	regression anlaysis	C         EREG Cox rt           OS_GSE79668         0           OS_GSE28735         0           OS_TCGA_PAAD         0           OS_PACA_AU_Seq         0           OS_GSE78229         0           OS_GSE6452         0           OS_PACA_AU_Seq         0           OS_GSE6452         0           OS_PACA_AU_Array         0           OS_GSE5916         0           OS_GSE21501         0           OS_GSE21501         0           OS_GSE57495         0	agression anlaysis	► ADM Cox rt OS_E_MTAB_6134 OS_GSE85916 OS_GSE78229 OS_PACA_AU_Seq OS_GSE78229 OS_PACA_CA_Seq OS_SACA_CA_Seq OS_PACA_CA_Seq OS_PACA_AU_Array OS_GSE77495 OS_PACA_AU_Array OS_GSE77495 OS_PACA_AU_Array OS_GSE77495	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 - OS_GSE62452 - OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Seq - OS_TCGA_PAAD - OS_GSE5916 - OS_GSE5916 - OS_GSE571455 - OS_EMTAB_6134 - OS_GSE57495 -	regression anlaysis	<ul> <li>J TGM2 Cox</li> <li>OS_GSE78229</li> <li>OS_GSE79689</li> <li>OS_GSE65462</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_PACA_CA_Seq</li> <li>OS_GSE57495</li> <li>OS_GSE71729</li> <li>OS_E_MTAB_6134</li> <li>OS_GSE21501</li> </ul>	regression anlaysis
<ul> <li>UNC13D Cox</li> <li>OS_GSE28735-</li> <li>OS_GSE28735-</li> <li>OS_GSE62452-</li> <li>OS_FACA_AU_Seq-</li> <li>OS_GSE5916-</li> <li>OS_GSE571729-</li> <li>OS_PACA_AU_Array-</li> <li>OS_GSE71729-</li> <li>OS_PACA_AU_Array-</li> <li>OS_GSE71729-</li> <li>OS_FACA_AL_AU_Array-</li> <li>OS_GSE71729-</li> <li>OS_FACA_CA_SE1501-</li> <li>OS_PACA_CA_Seq-</li> <li>OS_GSE57496-</li> <li>DFS_TCGA_PAAD-</li> </ul>	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_GSE28735           OS_TCGA_PAAD         OS_TCGA_PAAD           OS_PACA_AU_Seq         OS_GSE2452           OS_GSE262452         OS_GSE262452           OS_PACA_AU_Array         OS_GSE262452           OS_PACA_AU_Array         OS_GSE262452           OS_PACA_AU_Array         OS_GSE262452           OS_GSE262452         OS_GSE262452           OS_GSE27495         OS_GSE27495           OS_PACA_CA_SEq         OS_GSE27495           OS_PACA_CA_SA_SEq         OS_GSE27495	agression anlaysis	ADM Cox rr           OS_E_MTAB_6134           OS_GSE85916           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_PACA_AU_Seq-           OS_GSE78289           OS_GSE79688           OS_GSE57495-           OS_PACA_AU_Array-           OS_GSE77729-           OS_GSE77729-           OS_GSE71729-           OS_GSE21501-           DFS_TCGA_PAAD	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 - OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79688 - OS_PACA_AU_Seq - OS_TCGA_PAAD - OS_GSE57169 - OS_E_MTAB_6134 - OS_GSE571495 - OS_PACA_CA_Seq - DFS_TCGA_PAAD -	regression anlaysis	<ul> <li>J TGM2 Cox</li> <li>OS_GSE78629</li> <li>OS_GSE78685</li> <li>OS_GSE65966</li> <li>OS_GSE65462</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Array</li> <li>OS_GSE28735</li> <li>OS_PACA_CA_Seq</li> <li>OS_GSE57495</li> <li>OS_GSE71729</li> <li>OS_GSE271729</li> <li>OS_GSE21501</li> <li>DFS_TCGA_PAAD</li> </ul>	regression anlaysis
UNC13D Cox OS_GSE28735- OS_GSE28735- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE5916- OS_GSE79686- OS_EACA_AU_Array- OS_GSE79668- OS_ECA_AAU_Array- OS_GSE79668- OS_GSE79668- OS_GSE795- OS_FACA_CA_Seq- OS_GSE57495- DFS_TCGA_PAAD- RFS_E_MTAB_6134-	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_OS_CSE28735           OS_TCGA_PAAD         OS_OS_CSE28735           OS_DS_ACA_AU_Seq         OS_OS_GSE62452           OS_GSE62452         OS_GSE62452           OS_PACA_AU_Array         OS_OS_CSE85916           OS_GSE71729         OS_GSE21501           OS_GSE21501         OS_GSE2452           OS_PACA_CA_Seq         OS_GSE27495           OS_PACA_CA_Seq         OS_FACA_CA_Seq           DFS_TCGA_PAAD         OS           RFS_E_MTAB_6134         OS	egression anlaysis	ADM Cox rr           OS_E_MTAB_6134         OS_OSE28736           OS_GSE28736         OS_OSE78229           OS_GSE78229         OS_OSE78229           OS_GSE78229         OS_OSE7829           OS_GSE7829         OS_OSE7829           OS_GSE7829         OS_OSE7829           OS_GSE7829         OS_OSE7829           OS_DACA_CA_Seq         OS_OSE7829           OS_PACA_CA_Seq         OS_OSE7829           OS_CSE79688         OS_OSE7829           OS_CSE79688         OS_OSE7829           OS_CSE7829         OS_OSE7829           OS_CSE7898         OS_OSE7829           OS_CSE7829         OS_OSE7829           OS_CSE7829         OS           OS_TCGA_PAAD         OS_GSE21501           DFS_TCGA_PAAD         OS           RFS_E_MTAB_8134         OS	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 - OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Seq - OS_TCGA_PAAD - OS_GSE71729 - OS_ES71729 - OS_ES71729 - OS_SE85916 - OS_GSE71729 - OS_CSE7465 - OS_PACA_CA_Seq - DFS_TCGA_PAAD - RFS_PACA_CA_Seq -	regression anlaysis	<ul> <li>CRM2 Cox</li> <li>OS_GSE78229</li> <li>OS_GSE7868</li> <li>OS_GSE85916</li> <li>OS_GSE62452</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_GSE28735</li> <li>OS_PACA_CA_Seq</li> <li>OS_GSE267495</li> <li>OS_GSE71729</li> <li>OS_GSE71729</li> <li>OS_GSE27129</li> <li>OS_GSE27129</li> <li>OS_GSE27129</li> <li>OS_GSE27129</li> <li>OS_GSE21501</li> <li>DFS_TCGA_PAAD</li> <li>RFS_PACA_U_Seq</li> </ul>	regression anlaysis
UNC13D Cox OS_GSE28735- OS_GSE78229- OS_GSE62452- OS_FACA_AU_Seq- OS_GSE5916- OS_GSE79680- OS_PACA_AU_Array- OS_GSE79668- OS_E_MTAB_6134- OS_TCGA_PAAD- OS_GSE57495- DFS_TCGA_PAAD- RFS_E_MTAB_6134- RFS_FACA_AU_Seq-	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_OSE28736           OS_TCGA_PAAD         OS_TCGA_PAAD           OS_TCGA_PAAD         OS_OSE27329           OS_GSE78229         OS_GSE6452           OS_GSE6452         OS_GSE6452           OS_PACA_AU_Array         OS_GSE58916           OS_GSE71729         OS_GSE21501           OS_GSE57495         OS_GSE57495           OS_PACA_CA_Seq         DFS_TCGA_PAAD           RFS_E_MTAB_6134         RFS_PACA_CA_Seq	egression anlaysis	ADM Cox rr         OS_E_MTAB_134-         OS_GSE85916-         OS_GSE78229-         OS_OS_FACA_AL_S60-         OS_SCR78628-         OS_SCR78628-         OS_SCR78628-         OS_SCR7868-         OS_SCR7868-     <	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 - OS_GSE62452 - OS_GSE78688 - OS_PACA_AU_Array - OS_GSE79668 - OS_PACA_AU_Seq - OS_TCGA_PAAD - OS_GSE85916 - OS_GSE71729 - OS_E_MTAB_6134 - OS_GSE57495 - OS_PACA_CA_Seq - DFS_TCGA_PAAD - RFS_PACA_CA_Seq - RFS_PACA_CA_Seq -	regression anlaysis	<ul> <li>J TGM2 Cox</li> <li>OS_GSE78629</li> <li>OS_GSE7868</li> <li>OS_GSE62462</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_PACA_AU_Seq</li> <li>OS_GSE57495</li> <li>OS_GSE57495</li> <li>OS_GSE71729</li> <li>OS_E_MTAB_6134</li> <li>OS_GSE21501</li> <li>DFS_TCGA_PAAD</li> <li>RFS_PACA_AU_Seq</li> <li>RFS_PACA_AU_Seq</li> </ul>	regression anlaysis
UNC13D Cox OS_GSE28735- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE55916- OS_GSE71729- OS_GSE719	regression anlaysis	C         EREG Cox rt           OS_GSE79668         0           OS_GSE2735         0           OS_TCGA_PAAD         0           OS_GSE78229         0           OS_GSE78229         0           OS_GSE78229         0           OS_GSE6452         0           OS_GSE78229         0           OS_GSE78229         0           OS_GSE782916         0           OS_GSE782916         0           OS_GSE71729         0           OS_GSE21501         0           OS_GSE21501         0           OS_PACA_CA_Seq1         0           OS_PACA_CA_Seq2         0           RFS_PACA_CA_SA         0           RFS_PACA_CA_SA         0	agression anlaysis	ADM Cox rr           OS_E_MTAB_6134         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE68916         OS_GSE78028         O	egression anlaysis	CDCA4 Cox OS_GSE21501- OS_GSE78229 OS_GSE62452- OS_GSE28735- OS_PACA_AU_Array- OS_GSE79668- OS_PACA_AU_Seq OS_TCGA_PAAD- OS_GSE571629 - OS_EMTAB_6134- OS_GSE571729 - OS_EMTAB_6134- OS_GSE57495- OS_PACA_CA_Seq DFS_TCGA_PAAD- RFS_PACA_AU_Seq RFS_PACA_AU_Seq RFS_EMTAB_6134-	regression anlaysis	<ul> <li>CRM2 Cox</li> <li>OS_GSE78629</li> <li>OS_GSE78689</li> <li>OS_GSE65462</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Array</li> <li>OS_GSE28735</li> <li>OS_PACA_CA_Seq</li> <li>OS_GSE57495</li> <li>OS_GSE71729</li> <li>OS_E_MTAB_6134</li> <li>OS_GSE21501</li> <li>DFS_TCGA_PAAD</li> <li>RFS_PACA_AU_Array</li> <li>RFS_PACA_AU_Array</li> </ul>	regression anlaysis
UNC13D Cox OS_GSE28735- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE5916- OS_GSE71729- OS_PACA_AU_Array- OS_GSE71729- OS_PACA_AU_Array- OS_GSE7168- OS_E_MTAB_6134- OS_GSE57498- DFS_TCGA_PAAD- RFS_PACA_AU_Seq- RFS_PACA_AU_Seq- RFS_PACA_AU_Array-	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_GSE79668           OS_GSE28735         OS_TCGA_PAAD           OS_TCGA_PAAD         OS_GSE78229           OS_GSE78229         OS_GSE78229           OS_GSE78229         OS_GSE78229           OS_GSE64524         OS_GSE78291           OS_GSE78291         OS_GSE78291           OS_GSE71729         OS_GSE71729           OS_GSE57495         OS_GSE7495           OS_PACA_CA_Seq         OS_GSE7495           OS_PACA_CA_Seq         OS_FACA_CA_Seq           RFS_PACA_CA_Seq         C           RFS_PACA_AU_Array         C           RFS_PACA_AU_Array         C	agression anlaysis	ADM Cox rr           OS_E_MTAB_6134           OS_GSE28735           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78296           OS_GSE78296           OS_GSE79688           OS_GSE57495           OS_GSE57495           OS_GSE71729           OS_GSE21501           DFS_TCGA_PAAD           OS_GSE21501           DFS_TCGA_PAAD           RFS_PACA_AU_Array           RFS_PACA_AU_Array           RFS_PACA_AU_Array           RFS_PACA_AU_Array	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE78229 OS_GSE62452 OS_GSE28735 OS_PACA_AU_Array - OS_GSE79688 OS_PACA_AU_Seq OS_TCGA_PAAD OS_GSE57169 OS_ECTCGA_PAAD OS_GSE57169 OS_EXTAB_6134 OS_GSE57495 OS_PACA_CA_Seq DFS_TCGA_PAAD FFS_PACA_AU_Seq RFS_PACA_AU_Seq RFS_E_MTAB_6134 FFS_PACA_AU_Array -	regression anlaysis	<ul> <li>CRES_PACA_CA_Seq</li> <li>CS_CSE77629</li> <li>CS_CSE77668</li> <li>CS_CSE77668</li> <li>CS_CSE77668</li> <li>CS_CSE85746</li> <li>CS_CSE857495</li> <li>CS_PACA_AU_Array</li> <li>CS_PACA_AU_Array</li> <li>CS_CSE57495</li> <li>CS_CSE57405</li> <li>CS_CSE57405</li></ul>	regression anlaysis
UNC13D Cox OS_GSE28735- OS_GSE78229- OS_GSE62452- OS_PACA_AU_Seq- OS_GSE5916- OS_GSE71729- OS_PACA_AU_Array- OS_GSE71668- OS_E_MTAB_6134- OS_TCGA_PAAD- OS_GSE57495- DFS_TCGA_PAAD- RFS_PACA_AU_Seq- RFS_PACA_AU_Seq- RFS_PACA_AU_Array- DSS_TCGA_PAAD- OS_STCGA_PAAD-	regression anlaysis	C         EREG Cox rt           OS_GSE79668         OS_OS_CSE28735           OS_TCGA_PAAD         OS_OS_CSE28735           OS_DS_ACA_AU_Seq         OS_OS_GSE62452           OS_GSE62452         OS_OS_CSE85916           OS_DS_CSE25101         OS_GSE7495           OS_GSE7495         OS_GSE7495           OS_PACA_CA_Seq         OS_GSE7495           OS_PACA_CA_Seq         OS_SCA_SCA_SE4           OS_SCA_CA_SE4         OS_GSE7495           OS_GSE7495         OS_GSE7495           OS_PACA_CA_SE4         OS_GSE7495           OS_SPACA_CA_SE4         OS_GSE7495           OS_SPACA_CA_SE4         OS_GSE7495           OS_SPACA_CA_SE4         OS_GSE7495           OS_SPACA_CA_SE4         OS_GSE7495           OS_SPACA_AU_ARR4         OS_GSE7495	egression anlaysis	ADM Cox rr           OS_E_MTAB_6134           OS_GSE28736           OS_GSE28736           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE78229           OS_GSE7829           OS_PACA_AU_Seq           OS_PACA_AL_ARR           OS_GSE7429           OS_GSE7429           OS_GSE7495           OS_CSE7495           OS_CSE740           OS_CSE740	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 OS_GSE28735 OS_PACA_AU_Array - OS_GSE79668 OS_PACA_AU_Seq OS_TCGA_PAAD OS_GSE85916 OS_GSE71729 - OS_GSE71729 - OS_GSE57465 OS_PACA_CA_Seq DFS_TCGA_PAAD DFS_TCGA_PAAD RFS_PACA_CA_Seq RFS_PACA_CA_Seq RFS_PACA_AU_Seq RFS_PACA_AU_Seq RFS_PACA_AU_Seq RFS_PACA_AU_Seq RFS_PACA_AU_Seq RFS_PACA_AU_Array - DS_TCGA_PAAD	regression anlaysis 	<ul> <li>CGA_PACA_CA_Seq</li> <li>OS_GSE78629</li> <li>OS_GSE78689</li> <li>OS_GSE78689</li> <li>OS_GSE85916</li> <li>OS_GSE85916</li> <li>OS_GSE82452</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_GSE71729</li> <li>OS_GSE71729<td>regression anlaysis</td></li></ul>	regression anlaysis
UNC13D Cox OS_GSE28735- OS_GSE78229- OS_GSE78229- OS_GSE78229- OS_GSE78229- OS_FACA_AU_Seq- OS_GSE5916- OS_GSE79680- OS_PACA_AU_Array- OS_GSE79680- OS_E_MTAB_6134- OS_GSE21501- OS_PACA_CA_Seq- OS_GSE57495- DFS_TCGA_PAAD- RFS_PACA_AU_Seq- RFS_PACA_AU_Seq- RFS_PACA_AU_Seq- RFS_PACA_AU_Seq- RFS_PACA_AU_Array- DSS_TCGA_PAAD- PFS_TCGA_PAAD-	regression anlaysis	C         EREG Cox r           OS_GSE79668         OS_GSE28735           OS_GSE28735         OS_GSE28735           OS_GSE28735         OS_GSE28735           OS_GSE28735         OS_GSE28735           OS_TCGA_PAAD         OS_GSE78228           OS_GSE62452         OS_GSE62452           OS_GSE62452         OS_GSE62452           OS_PACA_AU_Array         OS_GSE571729           OS_GSE571729         OS_GSE57496           OS_PACA_CA_Seq         OS_GSE57496           OS_PACA_CA_Seq         OS_PACA_CA_Seq           DFS_TCGA_PAAD         CRFS_PACA_AU_Array           RFS_PACA_AU_Array         OS_STCGA_PAAD           DSS_TCGA_PAAD         PFS_TCGA_PAAD	egression anlaysis	H     ADM Cox rr      OS_E_MTAB_9134     OS_GSE28735     OS_GSE78229     OS_GSE78229     OS_GSE78264     OS_GSE78264     OS_GSE78688     OS_PACA_CA_Seq     OS_GSE57488     OS_PACA_CA_Seq     OS_GSE71729     OS_TCGA_PAAD     OS_GSE21501     OS_GSE21501     OS_GSE21601     OS_GSE2160     OS_GSE2160     OS_GSE2160     OS_GSE2160     OS_GSE2160     OS_GSE2160	egression anlaysis	CDCA4 Cox OS_GSE21501 - OS_GSE78229 OS_GSE62452 OS_GSE28735 - OS_PACA_AU_Array - OS_GSE79668 OS_PACA_AU_Seq OS_TCGA_PAAD OS_GSE71729 - OS_ES71729 - OS_ES71729 - OS_GSE57465 OS_PACA_CA_Seq DFS_TCGA_PAAD RFS_PACA_CA_Seq - RFS_PACA_CA_Seq - RFS_PACA_AU_Seq - RFS_FACA_AU_Seq - RFS_FACA_AU_Seq - DSS_TCGA_PAAD - PFS_TCGA_PAAD -	regression anlaysis	<ul> <li>TGM2 Cox</li> <li>OS_GSE78229</li> <li>OS_GSE78685</li> <li>OS_GSE78685</li> <li>OS_GSE65966</li> <li>OS_GSE62452</li> <li>OS_TCGA_PAAD</li> <li>OS_PACA_AU_Array</li> <li>OS_PACA_AU_Seq</li> <li>OS_GSE28735</li> <li>OS_PACA_CA_Seq</li> <li>OS_GSE287495</li> <li>OS_GSE71729</li> <li>OS_GSE71729</li> <li>OS_GSE217501</li> <li>OFS_TCGA_PAAD</li> <li>RFS_PACA_AU_Seq</li> <li>RFS_PACA_AU_Seq</li> <li>RFS_PACA_AU_Seq</li> <li>RFS_PACA_AU_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>RFS_PACA_CA_Seq</li> <li>DSS_TCGA_PAAD</li> <li>PFS_TCGA_PAAD</li> <li>PFS_TCGA_PAAD</li> </ul>	regression anlaysis
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**Figure 7—figure supplement 1.** Integrated Cox regression analysis of survival variables for artificial intelligence-derived prognostic signature (AIDPS) and nine AIDPS genes in 13 cohorts. (**A**–**J**) Univariate Cox regression analysis of overall survival (OS), disease-free survival (DFS), relapse-free survival (RFS), disease-specific survival (DSS), and progression-free survival (PFS) for AIDPS (**A**), *SELENBP1* (**B**), *PLCB4* (**C**), *DCBLD2* (**D**), *PRR11* (**E**), *UNC13D* (**F**), *EREG* (**G**), *ADM* (**H**), *CDCA4* (**I**), and *TGM2* (**J**) in the training cohort, nine testing cohorts, and three external validation cohorts.

![](_page_16_Figure_0.jpeg)

# Figure 7—figure supplement 2. The correlation of artificial intelligence-derived prognostic signature (AIDPS) and its nine genes with immune molecules and immune cell types. (A–C) The correlation between AIDPS and its nine genes at expression level in the whole (A), high AIDPS (B) and low AIDPS (C) TCGA-PAAD cohort. (D–F) The correlation of AIDPS and its nine genes with 27 immune checkpoint molecules in the whole (D), high AIDPS (E), and low AIDPS (F) TCGA-PAAD cohort. (G–I) The correlation of AIDPS and its nine genes with 28 immune cell types in the whole (G), high AIDPS (H), and low AIDPS (I) TCGA-PAAD cohort.

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![](_page_17_Figure_2.jpeg)

**Figure 7—figure supplement 3.** The relevance of artificial intelligence-derived prognostic signature (AIDPS) and its nine genes with mutation and copy number alteration. From top to bottom panels, the AIDPS and expression of nine AIDPS genes *SELENBP1*, *PLCB4*, *DCBLD2*, *PRR11*, *UNC13D*, *EREG*, *ADM*, *CDCA4*, and *TGM2* for each sample; top 15 mutated genes and broad-level copy number alterations (>20%), and selected genes located within chromosomes 8q24.21, 9p21.3, and 18q21.2 are shown in the high and low AIDPS TCGA-PAAD cohort. The proportion of the high and low AIDPS groups in each alteration is presented in the right bar charts.

![](_page_18_Figure_2.jpeg)

**Figure 8.** Evaluating therapeutic drug benefits. (A) Boxplot of Tumour Immune Dysfunction and Exclusion (TIDE) score between the high and low artificial intelligence-derived prognostic signature (AIDPS) groups. (B) Percentage of immunotherapy responses at high and low AIDPS groups. (C) Submap analysis of the two groups and 47 pretreated patients with comprehensive immunotherapy annotations. For Submap analysis, a smaller p-value implied a more similarity of paired expression profiles. (D) Barplot of ouabain and panobinostat CMap scores in patients with high AIDPS. (E) Schematic outlining the strategy to develop potential therapeutic agents with higher drug sensitivity in the high AIDPS group. (F) Comparison of estimated gemcitabine's sensitivity between high and low *PAK1* expression groups. (G, H) The results of Spearman's correlation analysis of Cancer Therapeutics Response Portal (CTRP)-derived compounds (G) and profiling relative inhibition simultaneously in mixtures (PRISM)-derived compounds (H). (I, J) The results of differential drug response analysis of CTRP-derived compounds (I) and PRISM-derived compounds (J), the lower values on the y-axis of boxplots imply greater drug sensitivity. CMap, Connectivity Map \*p<0.05, \*\*p<0.01, \*\*\*p<0.001.