

Figure S1. DEGs of dataset GSE62452. (A) Heatmap of all DEGs in dataset GSE62452. **(B)** Volcano plot of genes of GSE62452.

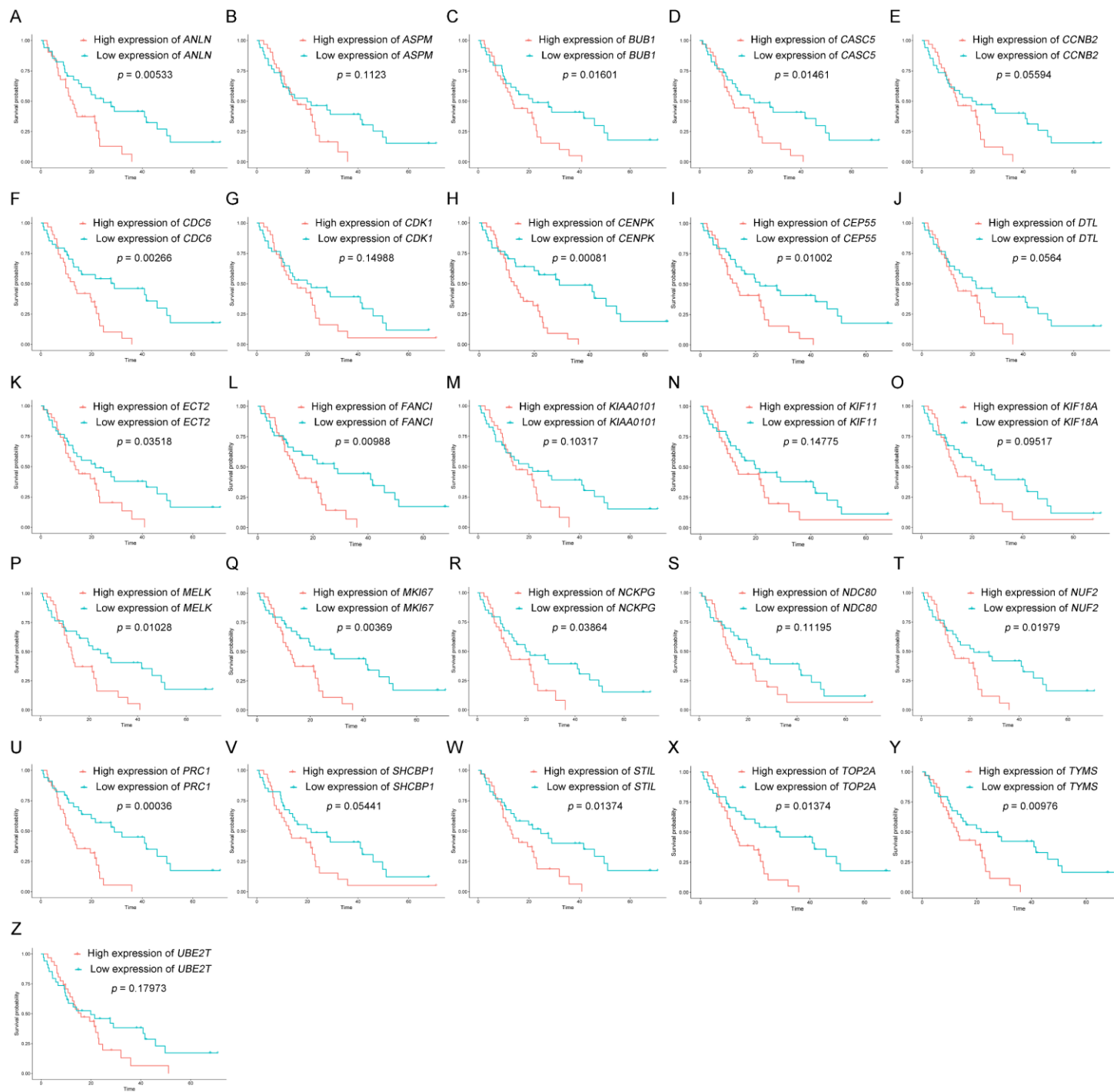


Figure S2. Survival analysis of the remaining 26 genes in the dataset GSE62452.

(A) ANLN. (B) ASPM. (C) BUB1. (D) CASC5. (E) CCNB2. (F) CDC6. (G) CDK1.

(H) CENPK. (I) CEP55. (J) DTL. (K) ECT2. (L) FANCI. (M) KIAA0101. (N) KIF11.

(O) KIF18A. (P) MELK. (Q) MKI67. (R) NCKPG. (S) NDC80. (T) NUF2. (U) PRC1.

(V) SHCBP1. (W) STIL. (X) TOP2A. (Y) TYMS. (Z) UBE2T. Red lines represent high

expression of the real hub genes and blue lines represent low expression.

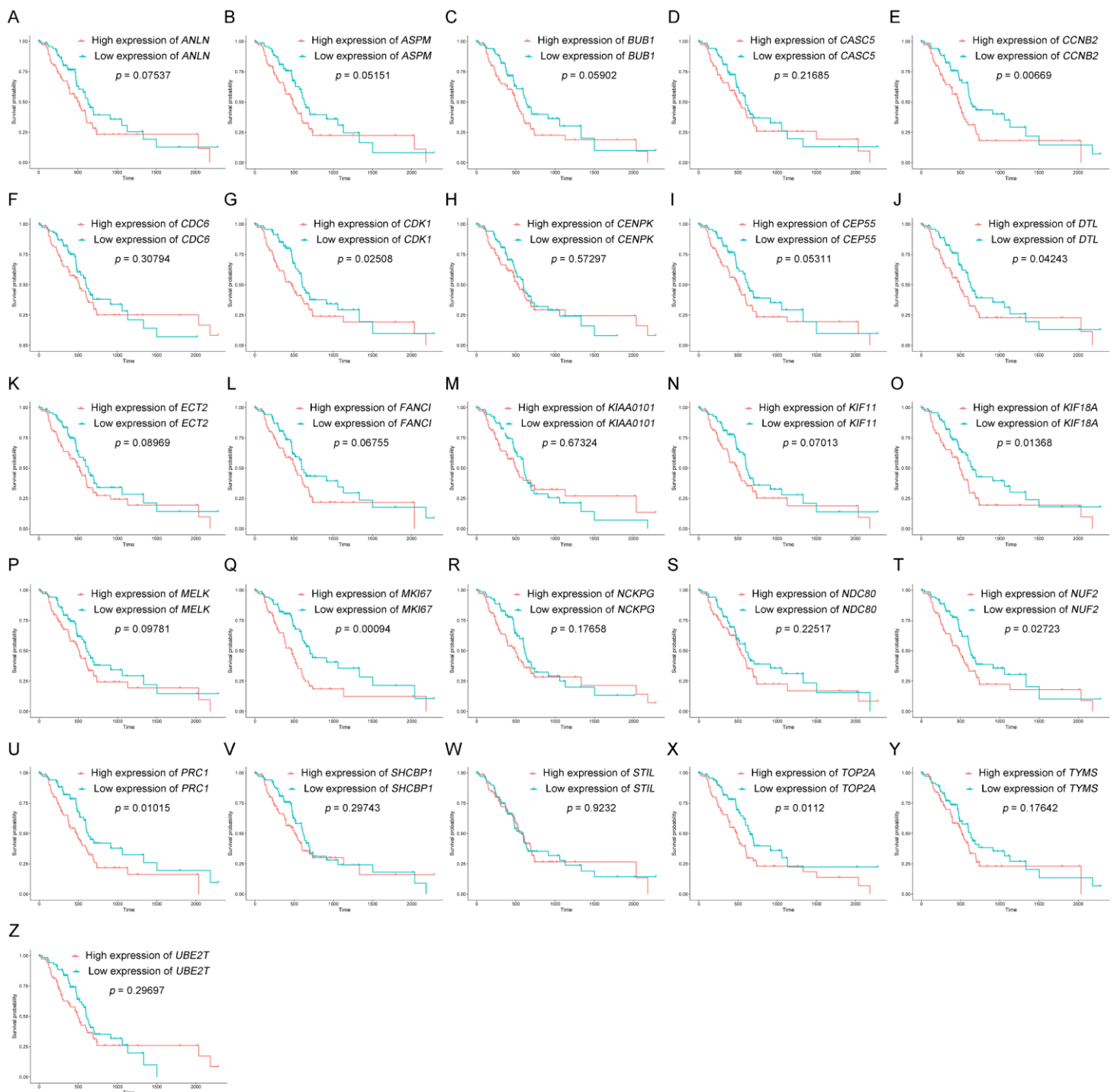


Figure S3. Survival analysis of the remaining 26 genes in the TCGA dataset. (A) ANLN. (B) ASPM. (C) BUB1. (D) CASC5. (E) CCNB2. (F) CDC6. (G) CDK1. (H) CENPK. (I) CEP55. (J) DTL. (K) ECT2. (L) FANCI. (M) KIAA0101. (N) KIF11. (O) KIF18A. (P) MELK. (Q) MKI67. (R) NCKPG. (S) NDC80. (T) NUF2. (U) PRC1. (V) SHCBP1. (W) STIL. (X) TOP2A. (Y) TYMS. (Z) UBE2T. Red lines represent high expression of the real hub genes and blue lines represent low expression.

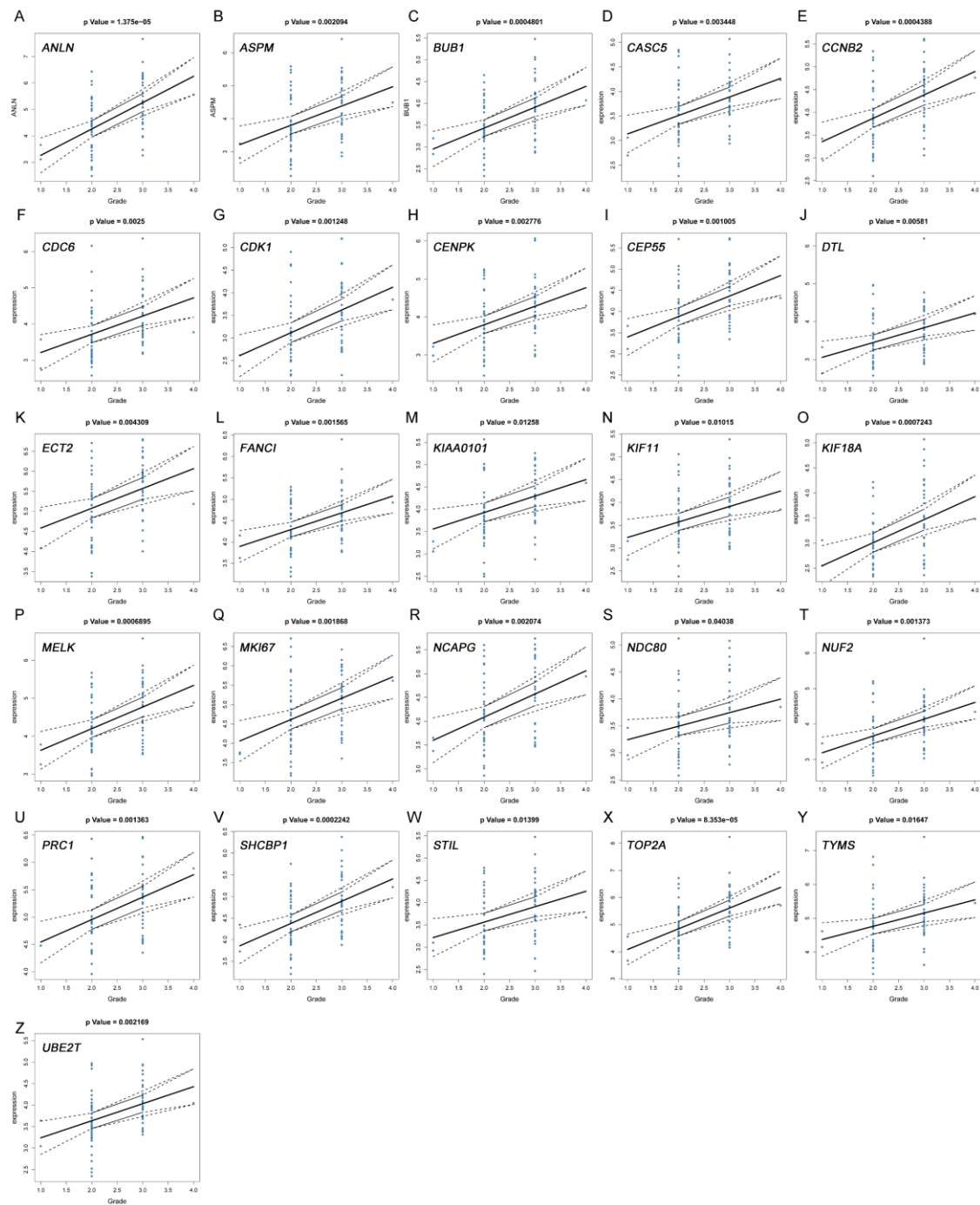


Figure S4. The correlation between the expression levels of the remaining 26 genes in the dataset GSE62452 and the disease progression of PDAC. (A) *ANLN*. (B) *ASPM*. (C) *BUB1*. (D) *CASC5*. (E) *CCNB2*. (F) *CDC6*. (G) *CDK1*. (H) *CENPK*. (I) *CEP55*. (J) *DTL*. (K) *ECT2*. (L) *FANCI*. (M) *KIAA0101*. (N) *KIF11*. (O) *KIF18A*. (P) *MELK*. (Q) *MKI67*. (R) *NCAPG*. (S) *NDC80*. (T) *NUF2*. (U) *PRC1*. (V) *SHCBP1*. (W) *STIL*. (X) *TOP2A*. (Y) *TYMS*. (Z) *UBE2T*. Grade means histological grade.

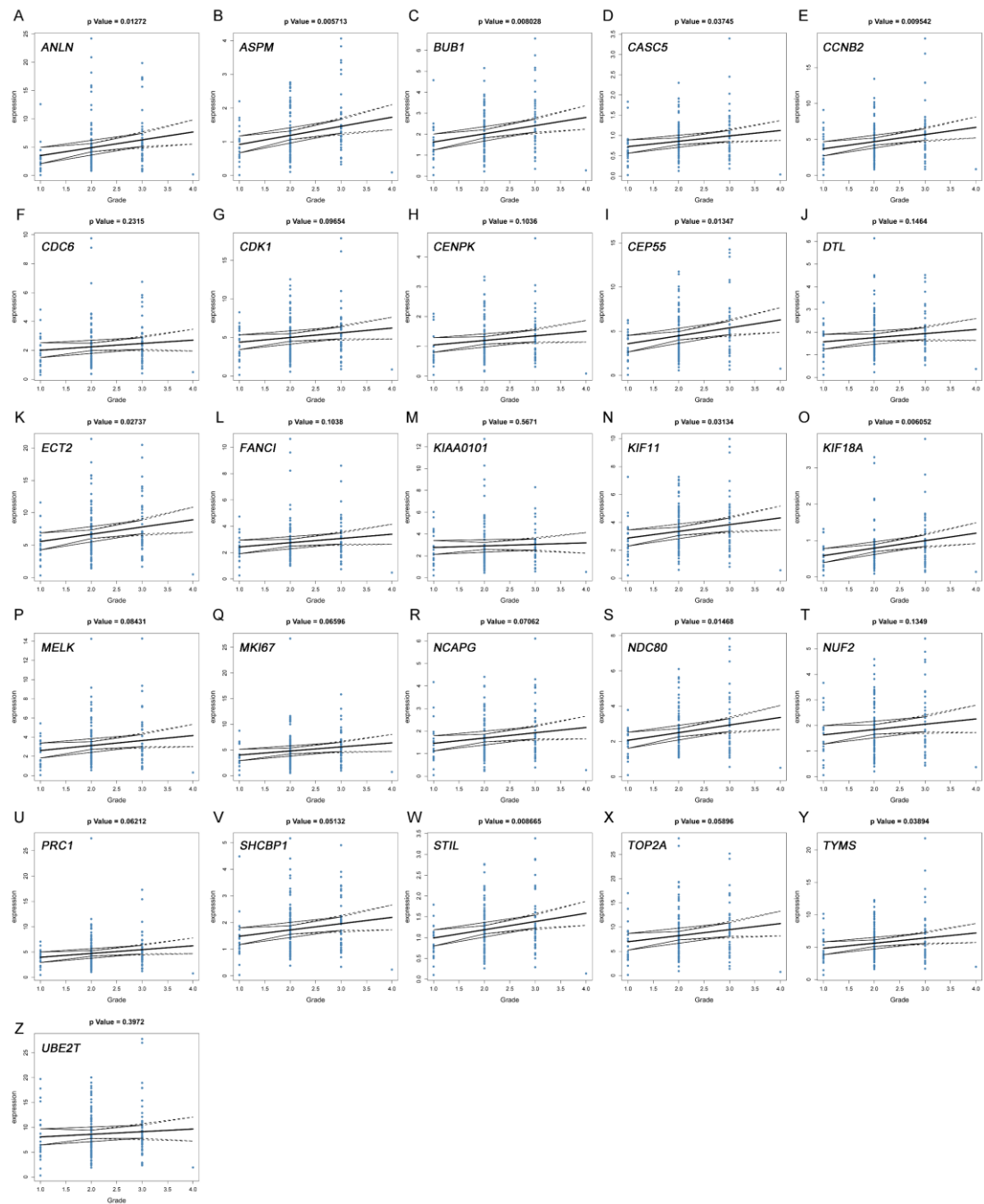


Figure S5. The correlation between the expression levels of the remaining 26 genes in the TCGA dataset and the disease progression of PDAC. (A) ANLN. (B) ASPM. (C) BUB1. (D) CASC5. (E) CCNB2. (F) CDC6. (G) CDK1. (H) CENPK. (I) CEP55. (J) DTL. (K) ECT2. (L) FANCI. (M) KIAA0101. (N) KIF11. (O) KIF18A. (P) MELK. (Q) MKI67. (R) NCAPG. (S) NDC80. (T) NUF2. (U) PRC1. (V) SHCBP1. (W) STIL. (X) TOP2A. (Y) TYMS. (Z) UBE2T. Grade means histological grade.

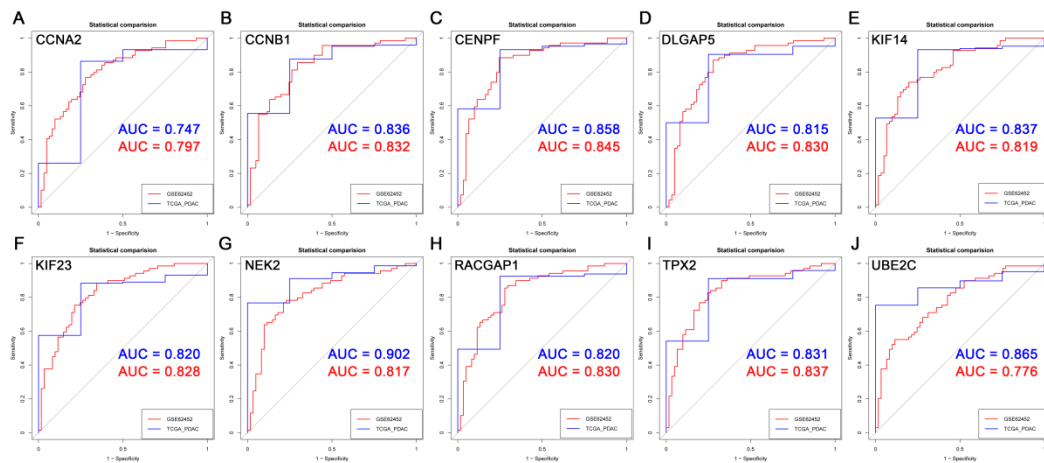


Figure S6. ROC analysis to distinguish normal and cancer tissues using TCGA and GSE62452. (A) *CCNA2*. (B) *CCNB1*. (C) *CENPF*. (D) *DLGAP5*. (E) *KIF14*. (F) *KIF23*. (G) *NEK2*. (H) *RACGAP1*. (I) *TPX2*. (J) *UBE2C*. Receiver operating characteristic (ROC) curves and area under the curve (AUC) statistics is to evaluate the capacity of distinguishing recurrent and non-recurrent PDAC.

Table S1. Clinical information of IHC in Human Protein Atlas database.

Gene symbol	Tissue type	ID	Age	Gender	Staining
CCNA2	normal	4156	57	male	low
	cancer	3851	63	male	Medium
CCNB1	normal	2032	35	female	Not detected
	cancer	317	66	female	Medium
CENPF	normal	2032	35	female	Medium
	cancer	1098	75	female	High
DLGAP5	normal	2329	66	male	Not detected
	cancer	3004	71	female	High
KIF14	normal	2220	43	female	Medium
	cancer	3592	59	male	High
KIF23	normal	2032	35	female	High
	cancer	729	70	male	High
NEK2	normal	3320	70	female	Not detected
	cancer	3548	60	female	High
RACGAP1	normal	2162	74	female	Not detected
	cancer	3004	71	female	High
TPX2	normal	2032	35	female	Not detected
	cancer	3004	71	female	medium
UBE2C	normal	3320	70	female	High
	cancer	1647	63	male	High