Supplementary

Table S1 Oligonucleotide primers used for quantitative PCR analysis of LINC00705-regulated target genes

	Sequence	Exon location
LINC00705		
Forward primer	GAGAGGCTACTTCGCACACC	343–362 bp
Reverse primer	GAGGTTGGGTCACACTGAGC	522–541 bp
Gene sequence accession number	NR_015425.1	
Location	342–541 bp	
Length	199 bp	
GAPDH		
Forward primer	AGATCCCTCCAAAATCAAGTGG	
Reverse primer	GGCAGAGATGATGACCCTTTT	

GAPDH served as endogenous control.

Table S2 High-confidence miRNAs identified through bioinformatic analysis

hsa-miR-6845-3p
hsa-miR-1266-3p
hsa-miR-1182
hsa-miR-6799-5p
hsa-miR-4776-3p
hsa-miR-663b
hsa-miR-6794-5p
hsa-miR-146b-3p
hsa-miR-6891-3p
hsa-miR-7156-3p
hsa-miR-1266-5p
hsa-miR-4518
hsa-miR-3059-5p
hsa-miR-6732-5p
hsa-miR-6799-3p
hsa-miR-7111-5p
hsa-miR-6760-5p
hsa-miR-4722-3p
hsa-miR-6754-5p
hsa-miR-6825-5p
hsa-miR-5196-5p
hsa-miR-6865-3p
hsa-miR-3130-5p
hsa-miR-6870-5p
hsa-miR-6876-3p
hsa-miR-6826-3p
hsa-miR-6849-3p
hsa-miR-6769b-5p
hsa-miR-1296-5p
hsa-miR-3173-5p
hsa-miR-12128
hsa-miR-937-5p
hsa-miR-6884-3p
hsa-miR-550a-5p
hsa-miR-3667-3p
hsa-miR-3184-5p
hsa-miR-6880-5p
hsa-let-7e-5p
hsa-miR-632
hsa-miR-8071
hsa-miR-6892-3p
hsa-miR-4793-5p
hsa-miR-4449
hsa-miR-5001-3p
hsa-miR-1976
hsa-miR-3198
hsa-miR-3677-5p

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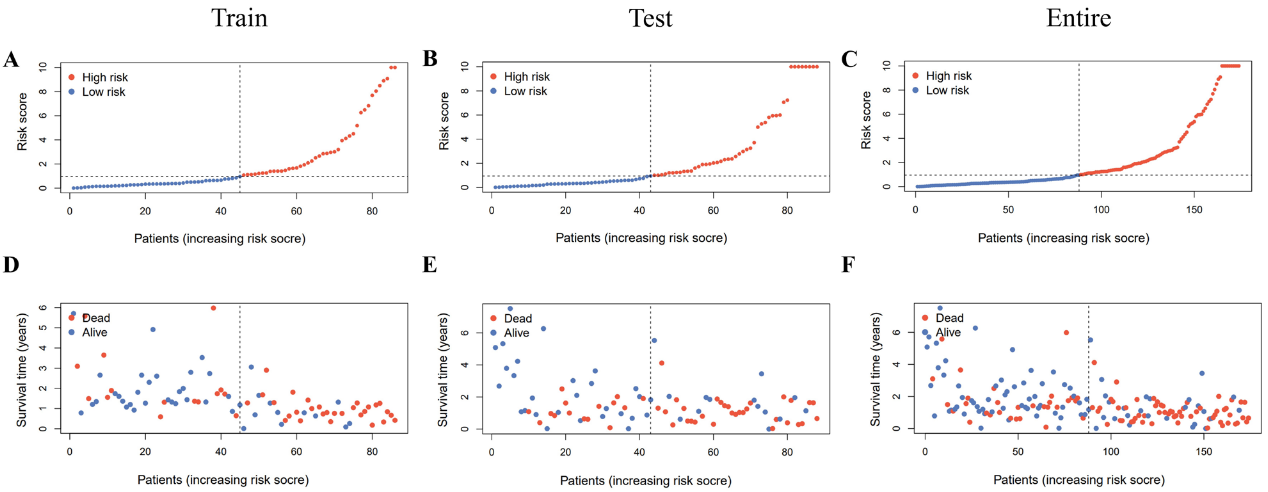

Figure S1 Risk score plots (A-C) represent the distribution of risk scores in the training, test, and entire groups. Survival scatterplots (D-F) reflect the relationship between risk scores and survival status in the Training, Test, and Entire groups.

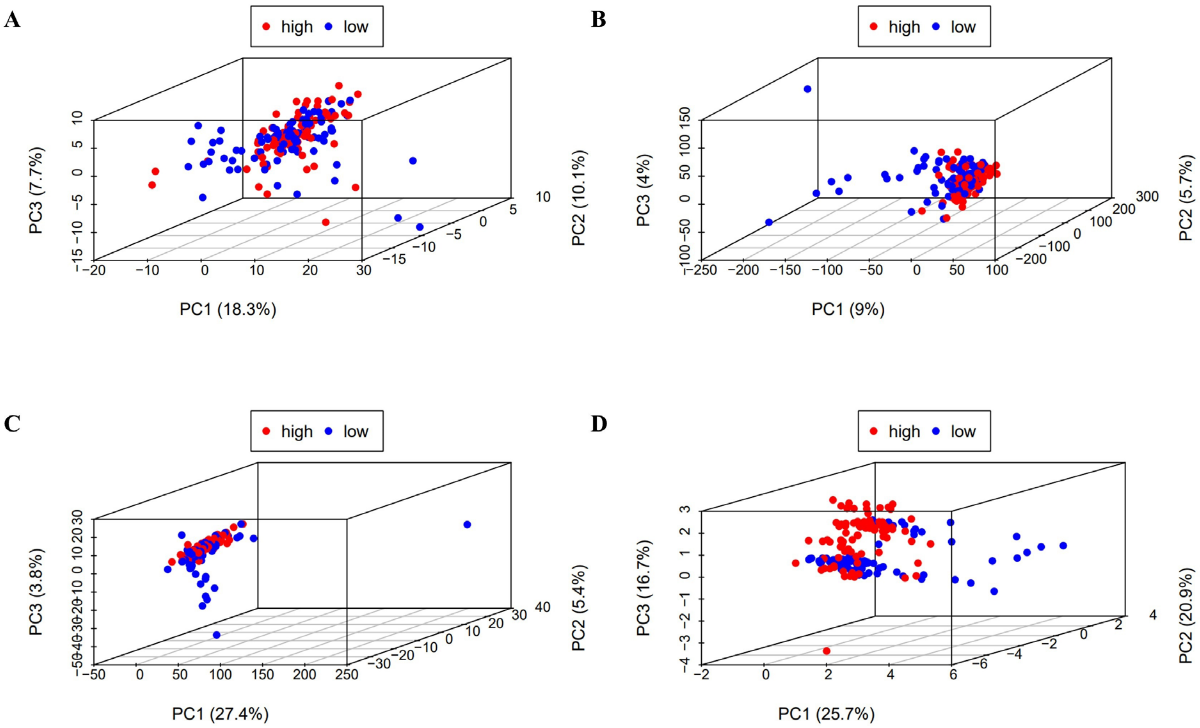

Figure S2 PCA analysis based on (A) ICD genes, (B) all lncRNAs, (C) ICD-associated DE lncRNAs, (D) the six selected ICD-associated lncRNAs.

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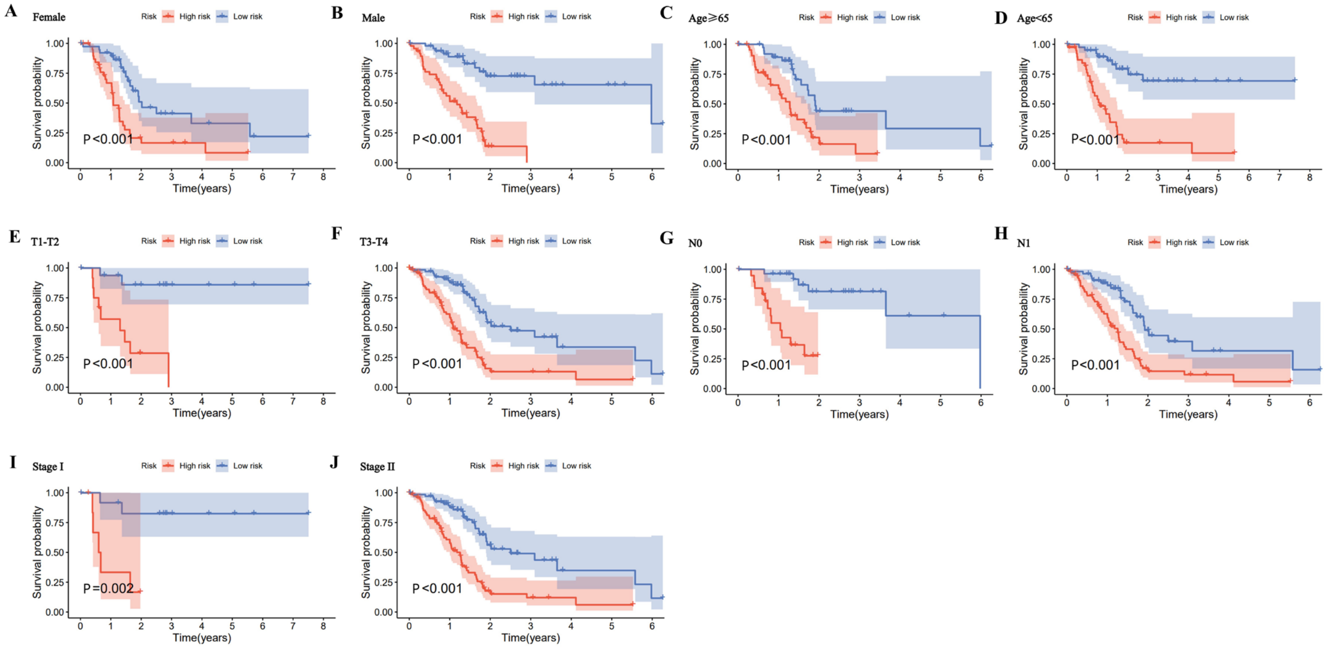

Figure S3 Overall survival comparison of PAAD patients with different clinical characteristics. (A,B) female and male; (C,D) age ≥65 and <65 years; (E,F) T1–2 and T3–4; (G,H) N0 and N1; (I,J) stage I and stage II.

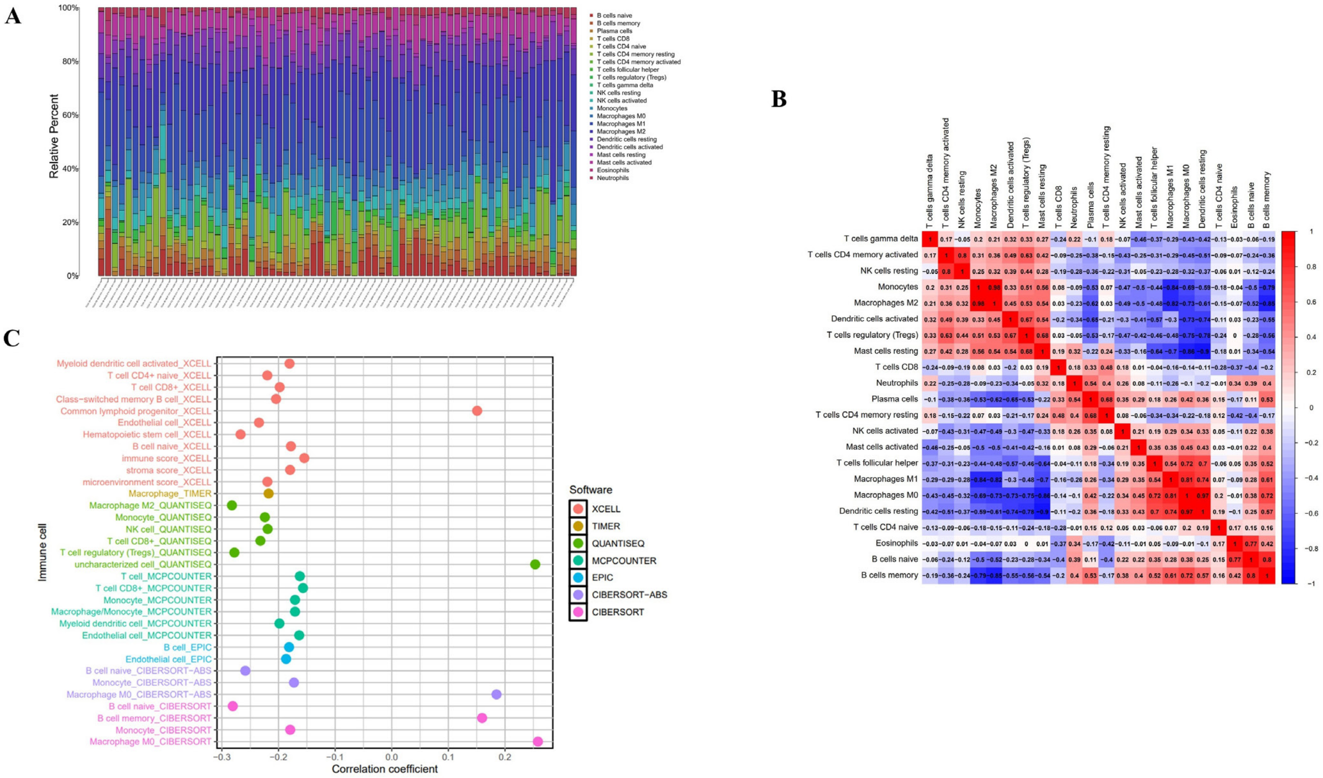

Figure S4 (A) The violet plot shows the proportion of tumor-infiltrating immune cells in PAAD patients. (B) Heatmap of the relationships between immune cells. (C) Bubble chart displaying immune infiltration analysis across seven different algorithms.

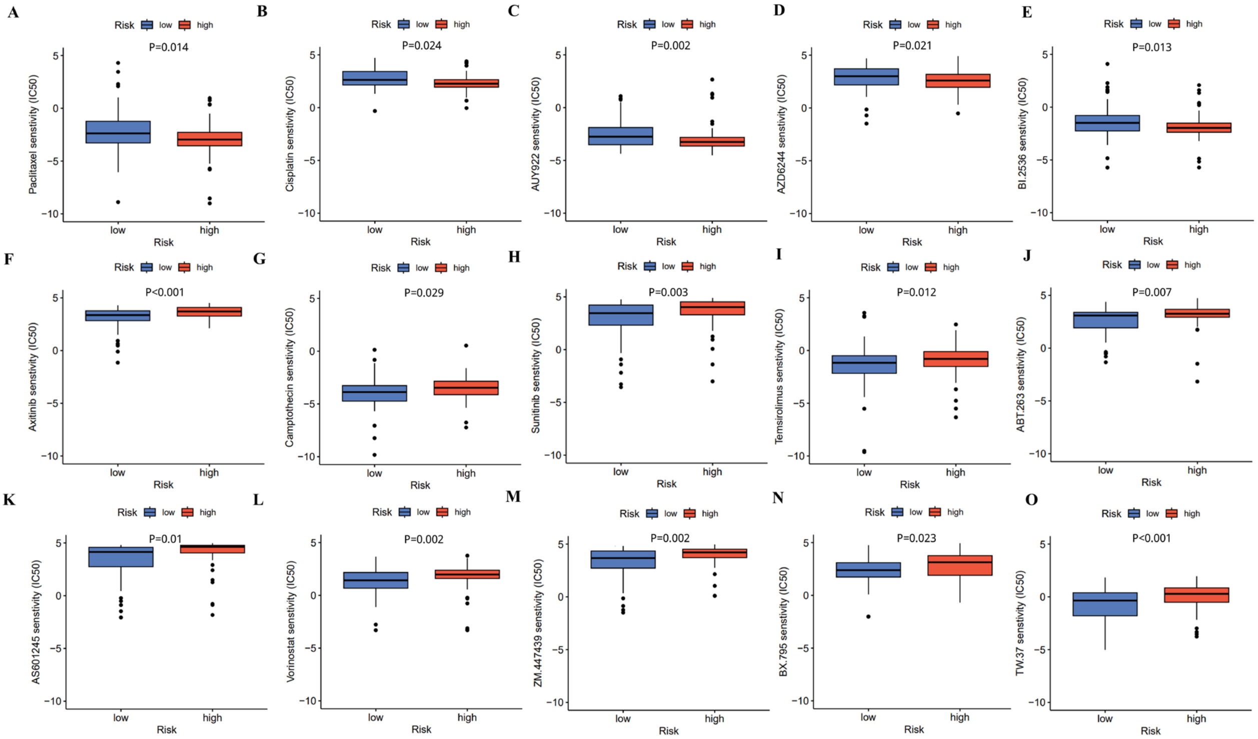

Figure S5 Prediction of sensitive drugs for high-risk populations. (A-E) Drugs sensitive in the high-risk group of PAAD patients. (F-O) Drugs sensitive in the low-risk group of PAAD patients.

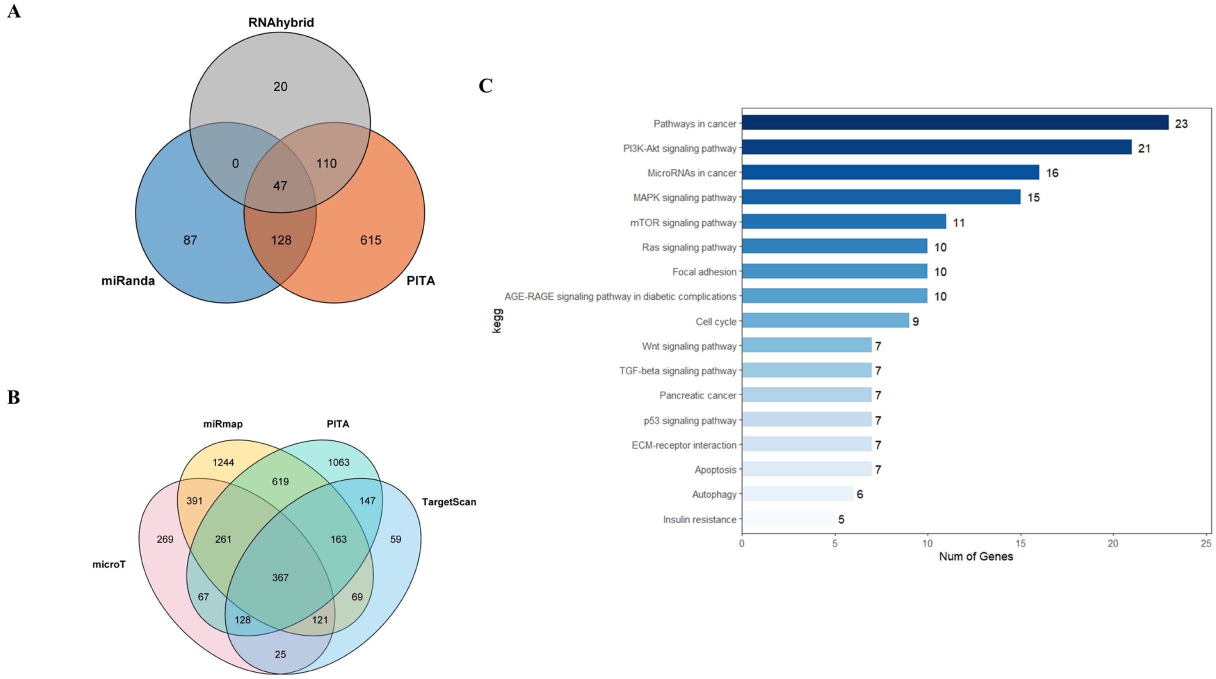

Figure S6 LINC00705-centered ceRNA network and functional consequences. (A) miRNA interactors of LINC00705 identified through intersection analysis. (B) Target genes of the consensus miRNAs. (C) KEGG pathway enrichment of the 367 target genes.

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