

SUPPLEMENTARY FIGURE

In Silico Identification of ANKRD22 as a Theragnostic Target for Pancreatic Cancer and Fostamatinib's Therapeutic Potential

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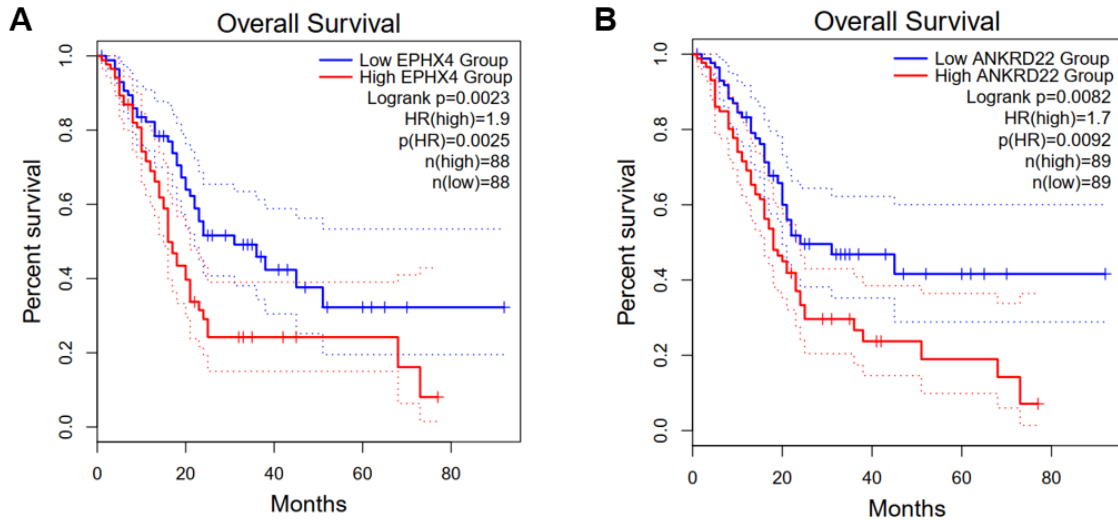
Corresponding authors: Alexander T.H. Wu and Chien-Hsin Chen

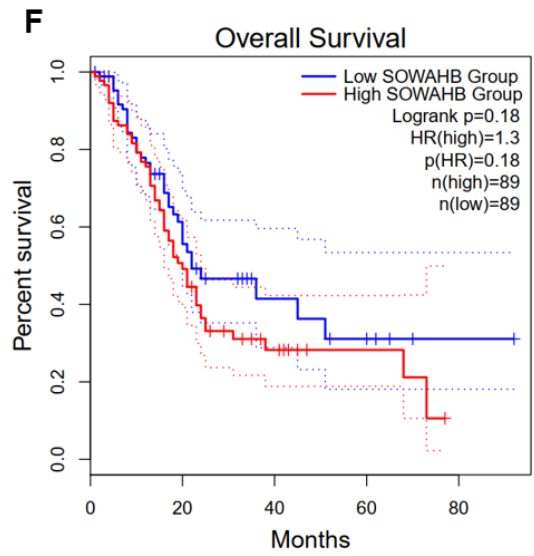
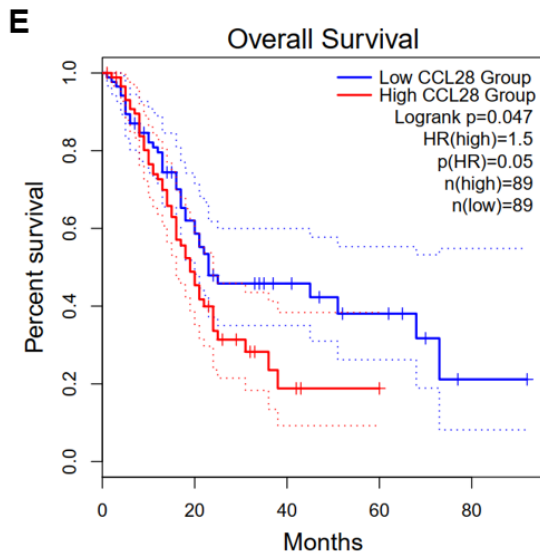
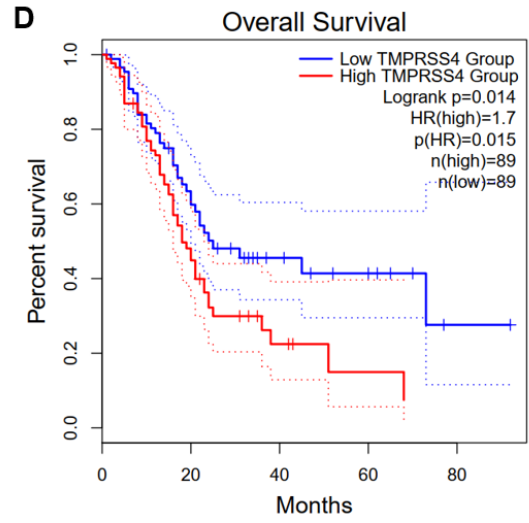
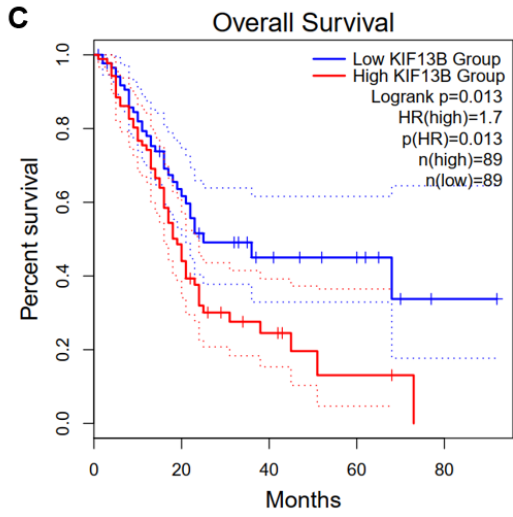
Supplementary table S1.

The overlapping upregulated genes with the hazard ratio and p-value in the PAAD cohort (non-significant results)

SYMBOL	Gene name	<i>p</i>-value	HR
<i>SOWAHB</i>	Sosondowah ankyrin repeat domain family member B	0.18	1.3
<i>SPDEF</i>	SAM pointed to the domain containing the ETS transcription factor	0.22	1.3
<i>EPCAM</i>	Epithelial cell adhesion molecule	0.26	1.3
<i>SLC28A3</i>	Solute carrier family 28-member 3	0.37	1.2
<i>FEZF1</i>	FEZ family zinc finger 1	0.37	0.83
<i>ACE2</i>	Angiotensin-converting enzyme 2	0.55	1.1
<i>TMPRSS2</i>	Transmembrane serine protease 2	0.72	1.1

Supplementary Figure 1.





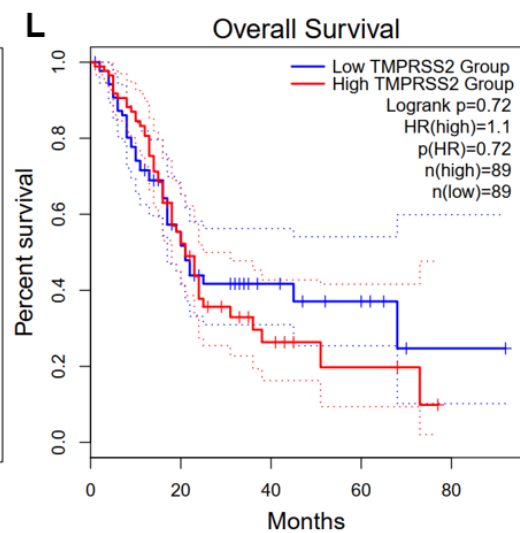
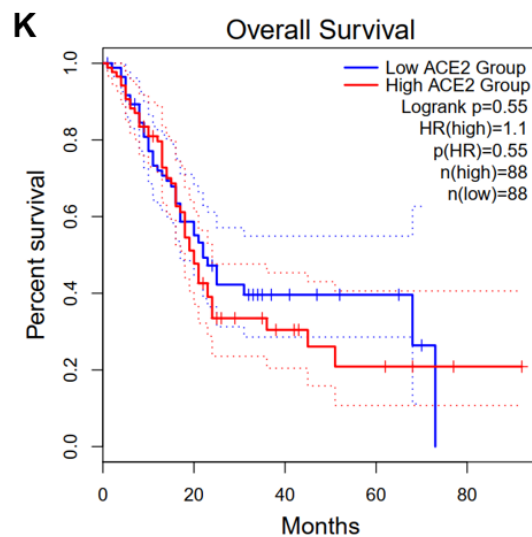
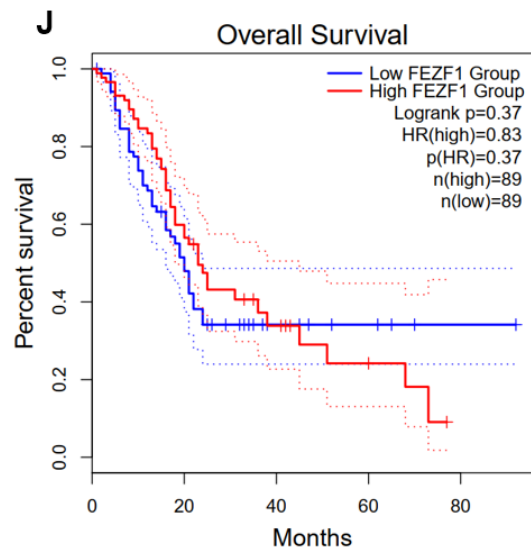
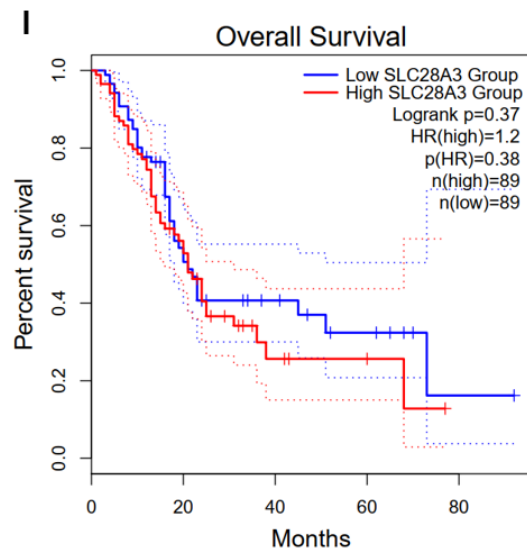
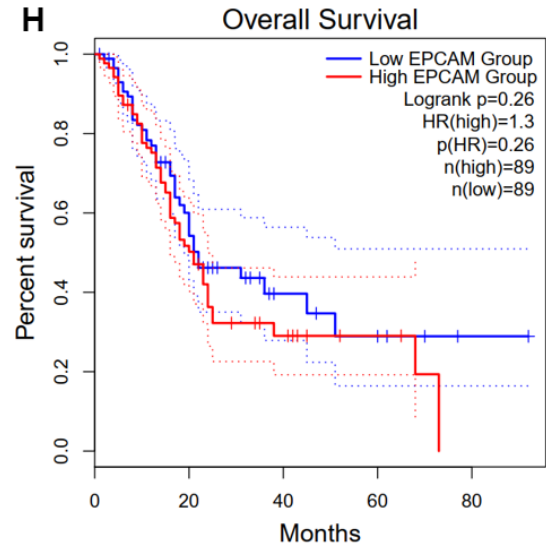
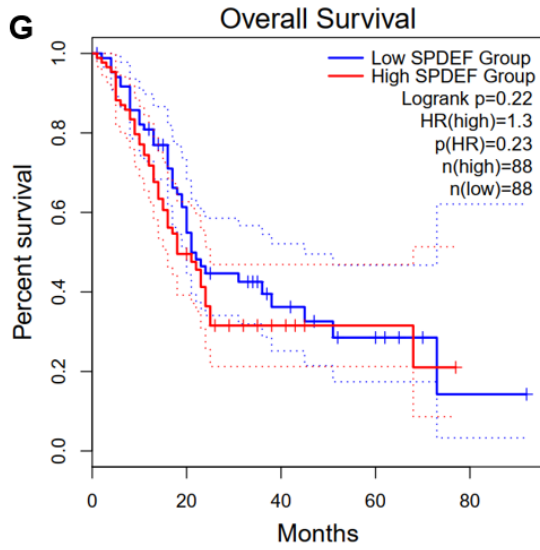


Figure S1. The overall survival rate of PC patients is based on overlapping upregulated gene expression. (A-L). OS rate for EPHX4, ANKRD22, KIF13B, TMPRSS4, CCL28, SOWAHB, SPDEF, EPCAM, SLC28A3, FEZF1, ACE2, and TMPRSS2, respectively.