Table S1. Cox analysis and expression level of LUC7L3, RBMX, and DDX17 in proteomic data.

DFS

GeneName	UniprotID	DFS.HR.average	Jiang's cohort		Gao's cohort		Xing's cohort	
			HR	Pvalue	HR	Pvalue	HR	Pvalue
LUC7L3	O95232	2.29	2.44 (1.19-5)	0.012	2.09 (1.27-3.45)	0.003	2.34 (1.59-3.43)	<0.001
RBMX	P38159	1.96	2.3 (1.08-4.92)	0.027	1.79 (1.1-2.91)	0.018	1.8 (1.26-2.57)	0.001
DDX17	Q92841	1.95	2.44 (1.17-5.07)	0.014	1.82 (1.11-2.98)	0.016	1.6 (1.09-2.33)	0.015

OS

GeneName	UniprotID	OS.HR.average	Jiang's cohort		Gao's cohort		Xing's cohort	
			HR	Pvalue	HR	Pvalue	HR	Pvalue
LUC7L3	O95232	3.39	4.16 (1.16-14.93)	0.017	3.03 (1.56-5.89)	0.001	2.98 (1.59-5.6)	<0.001
RBMX	P38159	3.10	4.59 (1.61-13.14)	0.002	2.34 (1.31-4.16)	0.003	2.38 (1.44-3.91)	<0.001
DDX17	Q92841	3.73	5.73 (2.01-16.37)	<0.001	2.98 (1.57-5.65)	<0.001	2.47 (1.51-4.03)	<0.001

T/P

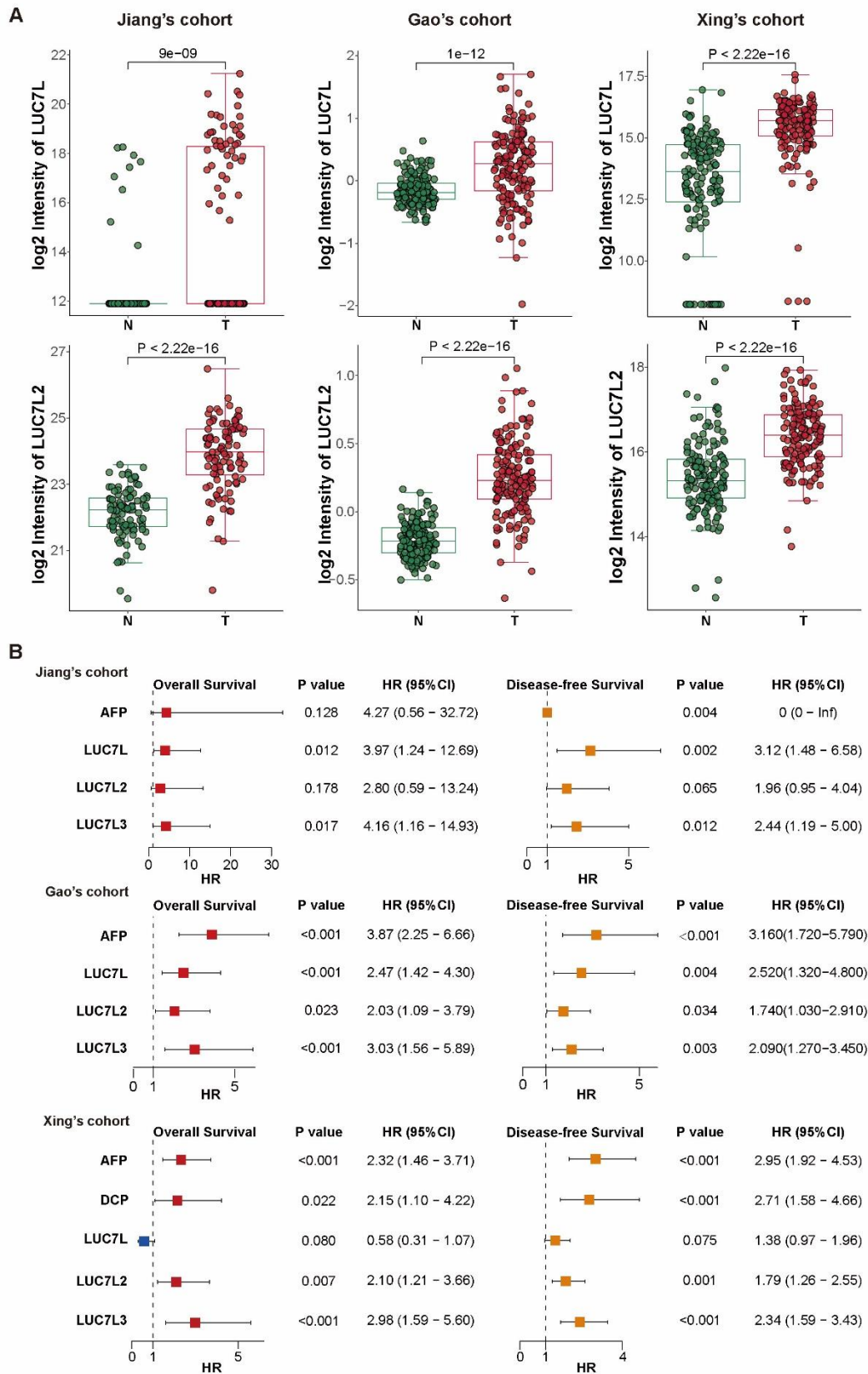| GeneName	UniprotID	logFC.average	Jiang's cohort		Gao's cohort		Xing's cohort	
			logFC	Padj	logFC	Padj	logFC	Padj
LUC7L3	O95232	1.81	2.111	<0.001	0.612	<0.001	2.706	<0.001
RBMX	P38159	1.25	1.658	<0.001	0.605	<0.001	1.475	<0.001
DDX17	Q92841	1.10	1.674	<0.001	0.604	<0.001	1.028	<0.001

Figure S1. LUC7L and LUC7L2 in the clinical proteomic data. (A) Box plots indicating that the expression of LUC7L and LUC7L2 are upregulated in HCC tumor tissue in all three clinical cohorts. (B) Forest plots depicting the Cox analysis of AFP, DCP, LUC7L, LUC7L2, and LUC7L3. AFP, alpha-fetoprotein; DCP, des-γ-carboxy prothrombin.
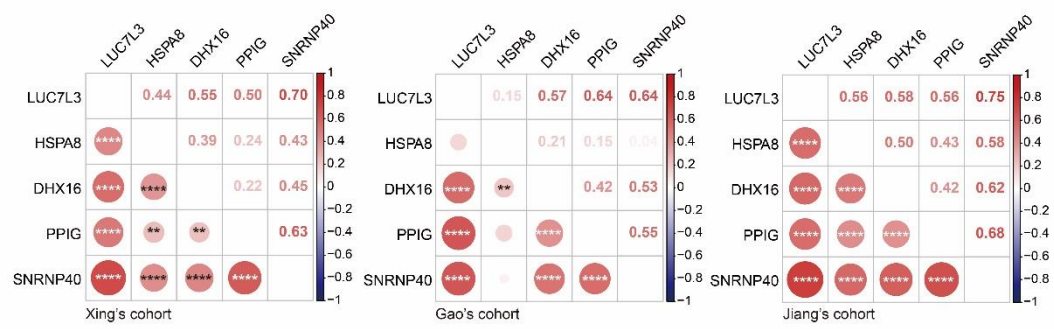
Figure S2. Correlation analysis between LUC7L3 and recognized alternative splicing-related proteins, including HSPA8, DHX16, PPIG and SNRNP40.