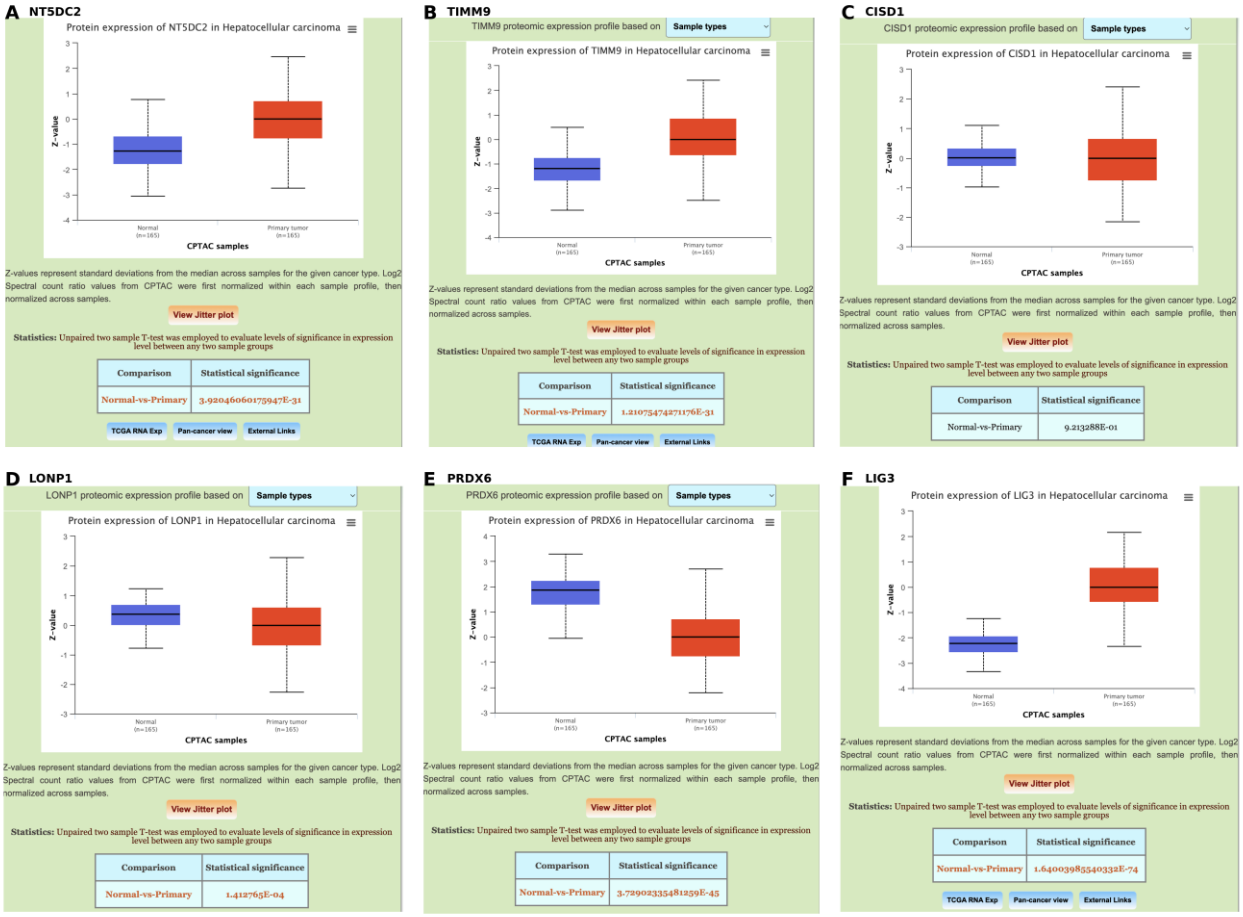
Supplementary Material



Supplementary Figure 1 Public UALCAN-CPTAC protein-level assessment of the six-gene signature in hepatocellular carcinoma. Panels show protein abundance for (A) NT5DC2, (B) TIMM9, (C) CISD1, (D) LONP1, (E) PRDX6, and (F) LIG3 in normal liver tissues and primary hepatocellular carcinoma tissues. Protein abundance is presented as Z-values. The UALCAN-CPTAC comparison included 165 normal samples and 165 primary tumor samples. P values were generated using the unpaired two-sample t test implemented in UALCAN. These public proteomic data are presented as exploratory protein-level observations and do not constitute in-house experimental validation.

Supplementary Table 1 Public UALCAN-CPTAC protein-level comparison of the six-gene signature in hepatocellular carcinoma

Gene	Database	Cancer type	Tumor vs normal protein abundance	P value	Interpretation
NT5DC2	UALCAN-CPTAC	Hepatocellular carcinoma	Higher in primary HCC tissues	3.92×10^{-31}	Significantly higher protein abundance
TIMM9	UALCAN-CPTAC	Hepatocellular carcinoma	Higher in primary HCC tissues	1.21×10^{-31}	Significantly higher protein abundance
CISD1	UALCAN-CPTAC	Hepatocellular carcinoma	No significant difference	0.921	No significant difference in protein abundance
LONP1	UALCAN-CPTAC	Hepatocellular carcinoma	Lower in primary HCC tissues	1.41×10^{-4}	Significantly lower protein abundance
PRDX6	UALCAN-CPTAC	Hepatocellular carcinoma	Lower in primary HCC tissues	3.73×10^{-45}	Significantly lower protein abundance
LIG3	UALCAN-CPTAC	Hepatocellular carcinoma	Higher in primary HCC tissues	1.64×10^{-74}	Significantly higher protein abundance

Note: CPTAC, Clinical Proteomic Tumor Analysis Consortium; HCC, hepatocellular carcinoma. P values were obtained from the public UALCAN-CPTAC portal. The table summarizes exploratory public protein-level observations rather than experimental validation performed in the present study.