## Supplementary material

Supplementary Figure 1 Univariate and multivariate regression analysis of other XPO5 clinicopathologic parameters and OS in patients with HCC



Supplementary Figure 2 Immunology and drug susceptibility analysis of



XPCS expression

2 4 XPOS expression Copyright ⓒ The Author(s) 2024.

## Supplementary Figure 3 These correlations were then validated (A). Further analysis showed that XPO5 was associated with immune checkpoint molecules in various cancers (B).



Supplementary Figure 4 Positively correlated with tumor mutation burden (r = 0.27, P < 0.05) (A). TME analysis revealed that the low XPO5 expression group had higher stromal, immune, and ESTIMATE scores, indicating the impact of XPO5 on the TME (B).

A

В

![](_page_3_Figure_1.jpeg)

Supplementary Figure 5 Stratification by PD1 and CTLA4 status showed significant differences in the IPS between the XPO5 expression groups (A),

with a negative correlation between XPO5 expression and chemotherapeutic sensitivity (B).

![](_page_4_Figure_1.jpeg)

Supplementary Figure 6 Evaluation of prognosis in patients with HCC using machine learning and mechanism prediction.

![](_page_5_Figure_0.jpeg)

Supplementary Figure 7 KICH and KIRC cells exhibited decreased XPO5 expression.

![](_page_6_Figure_0.jpeg)

Supplementary Figure 8 Further analysis, supported by immunohistochemistry data from the Human Protein Atlas, showed that XPO5 was substantially upregulated in the nucleus and cytoplasm of tumor cells, in contrast to the para-cancer and HCC tissues

![](_page_7_Figure_0.jpeg)

Primers	Sequence $(5' \rightarrow 3')$	
XPO5	Forward	5'-CTCAGACCCATGCTTCGTGT-3'
	Reverse	5'-GGGCTTCATAGTGCTCTGGG-3'
GAPDH	Forward	5'-GGTCTCCTCTGACTTCAACA-3'
	Reverse	5'-GTGAGGGTCTCTCTCTCTCT-3'

Supplementary Table 1 Primers used in Quantitative Real-Time PCR