Supplementary Figure S1 Differential expression analysis of PSMC1 (A), PSMC2 (B), PSMC3 (C), PSMC4 (D), PSMC5 (E), and PSMC6 (F) in normal liver tissues compared to HCC tissues from HCC patients with different aetiologies in TCGA. HCC: Hepatocellular carcinoma, PSMC: Proteasome 26S Subunit, ATPase, TCGA: The Cancer Genome Atlas database.

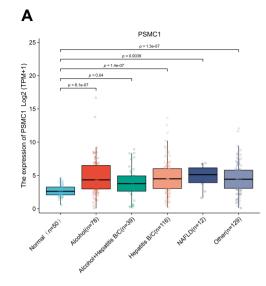
Supplementary Figure S2 The magnified immunohistochemical images indicating the intracellular localization of PSMC1 (A), PSMC2 (B), PSMC3 (C), PSMC4 (D), PSMC5 (E), and PSMC6 (F) in HCC tissues. All representative IHC staining images are from the HPA server. PSMC: Proteasome 26S Subunit, ATPase, HCC: Hepatocellular carcinoma, IHC: Immunohistochemistry, HPA: Human Protein Atlas.

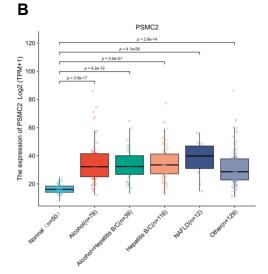
Supplementary Figure S3 The diagnostic value of PSMC1 (A), PSMC2 (B), PSMC3 (C), PSMC4 (D), PSMC5 (E), and PSMC6 (F) for identifying individuals with HCC in the TCGA cohort. HCC: Hepatocellular carcinoma, PSMC: Proteasome 26S Subunit, ATPase, TCGA: The Cancer Genome Atlas database.

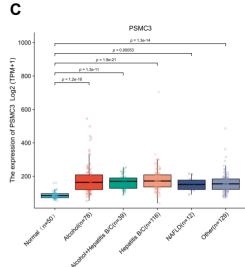
Supplementary Figure S4 The associations between PSMC gene expression levels in HCC tissues and pathologic T stage (A-F), pathologic stage (G-L), and histologic grade (M-R) in the TCGA-HCC cohort. HCC: Hepatocellular carcinoma, PSMC: Proteasome 26S Subunit, ATPase, TCGA: The Cancer Genome Atlas database.

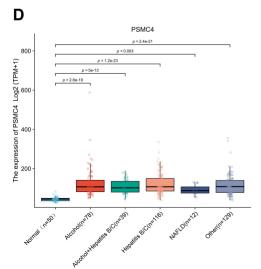
Supplementary Figure S5 Survival curves of DSS and PFI in the TCGA-HCC cohort: between PSMC1-high and -low patients with HCC (A, B), between PSMC2-high and -low patients with HCC(C, D), between PSMC3-high and -low patients with HCC(E, F), between PSMC4-high and -low patients with HCC(G, H), between PSMC5-high and - low patients with HCC(I, J), between PSMC6-high and -low patients with HCC(K, L).DSS: Disease-specific survival, PFI: Progress-free interval, HCC: Hepatocellular carcinoma, PSMC: Proteasome 26S Subunit, ATPase, TCGA: The Cancer Genome Atlas database.

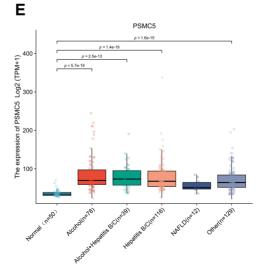
Supplementary Figure S6 Kaplan-Meier survival curves of overall survival in the TCGA-HCC cohort: between ATP5PD-high and -low patients with HCC (A), between PMPCB-high and -low patients with HCC(B), between PSMA3-high and -low patients with HCC(C), between PSMD13-high and -low patients with HCC(D), between SLIRP-high and -low patients with HCC(E), between TIMM50-high and -low patients with HCC(F). HCC: Hepatocellular carcinoma, TCGA: The Cancer Genome Atlas database.

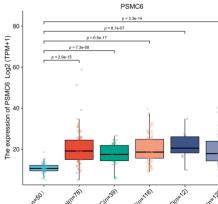




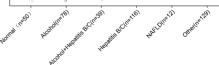


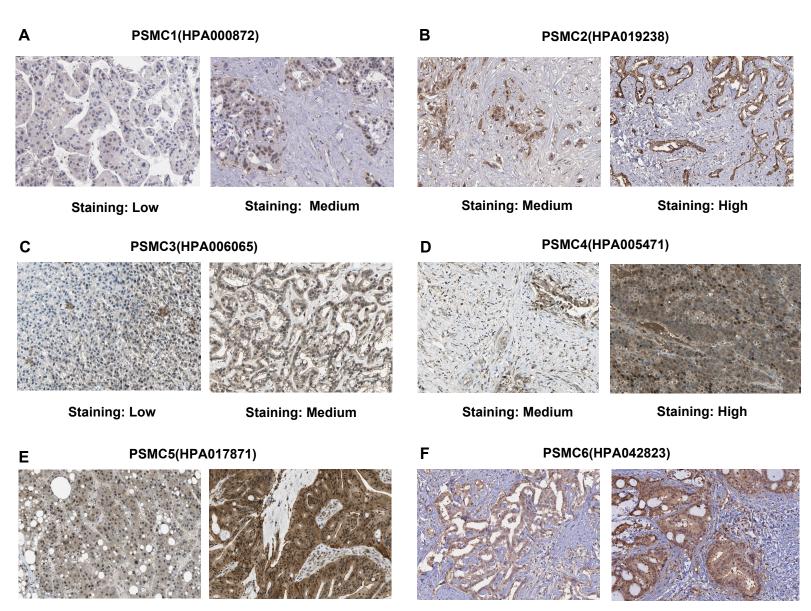






F



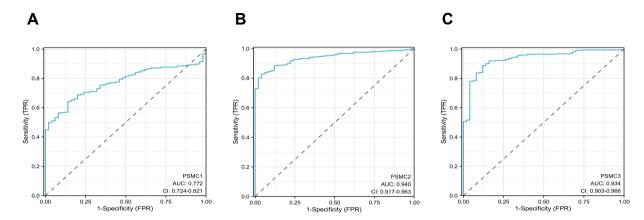


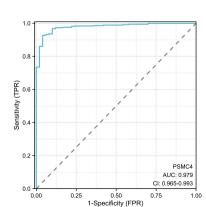
Staining: Medium

Staining: High

Staining: Low

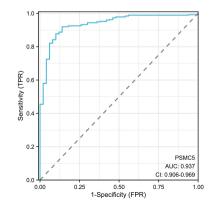
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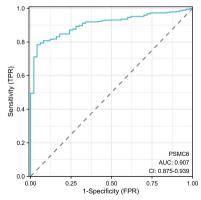


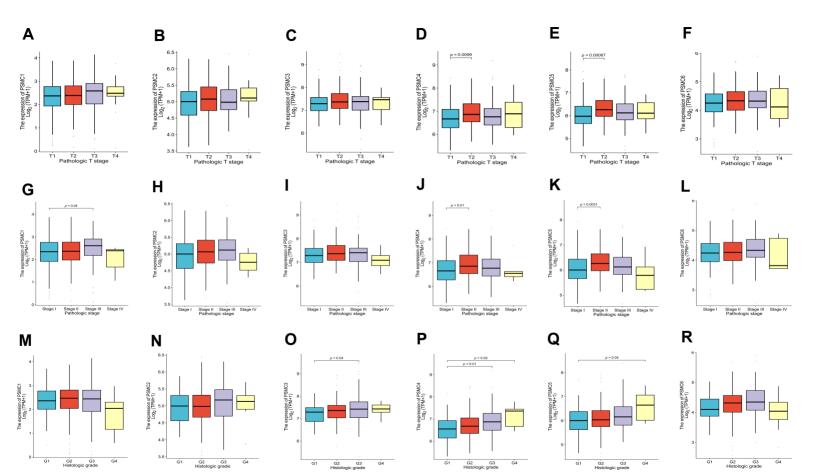
D

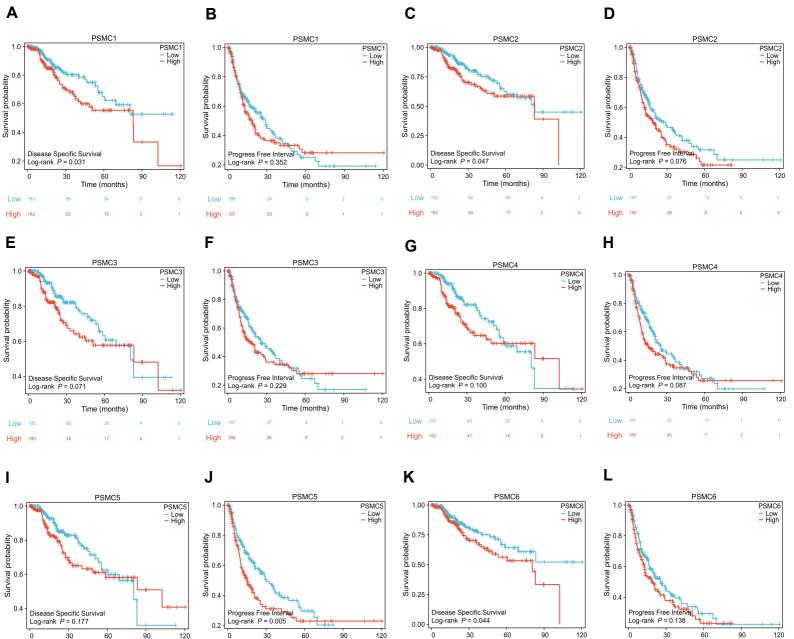
Ε



F



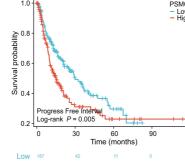




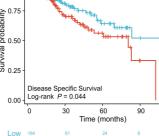
Time (months)

Low

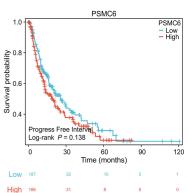
High 180

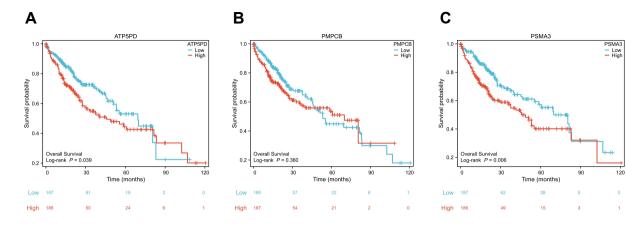


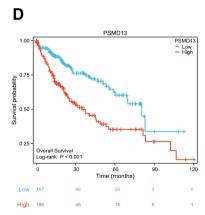
High



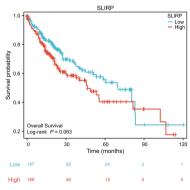
High



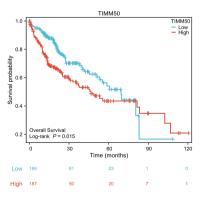












Genes	Forward Primer(5' -> 3')	Reverse Primer(5' -> 3')
PSMC1	CACACTCAGTGCCGGTTAAAA	GTAGACACGATGGCATGATTGT
PSMC2	GAGCACTTACTCTAGGCAGATCA	GTACACCTGGCAACCTGTAAAG
PSMC3	CGAGCAAGATGGAATTGGGGA	GCTCATGGGTGACTCTCAACA
PSMC4	CCGCTGGTCATCGGACAATTT	GCGCACATAATAGTTGGAGCCT
PSMC5	AGGCACAGAGGAACGAACTAA	AGGATGTACCTTGACCAACACTT
PSMC6	ATATGTTGTGGGGTTGTCGTCG	TCTGTTCTGATAGCCCTCCAAT

Supplementary Table 1 The primer sequences of PSMCs