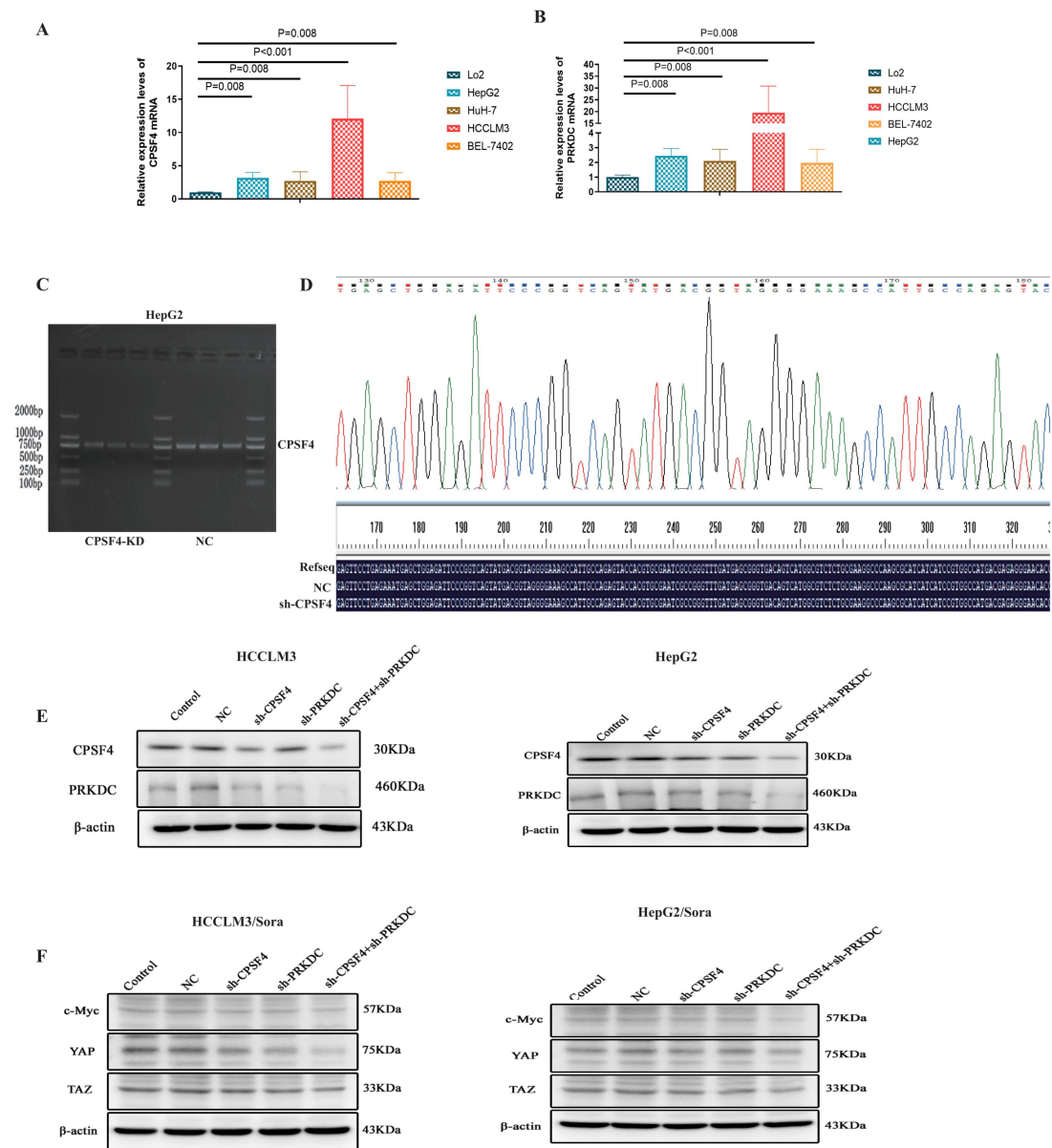


Supplementary materials

Supplementary Figure1(A-B)Expression of CPSF4 and PRKDC in different cell lines.(C-D)RIP assay and the transcript sequence of the selective splice site of PRKDC was amplified by PCR and the product analysis sequence was further validated.(E)western blot assay to analyze CPSF4 and PRKFC protein expression levels.(F)Effects of shCPSF4 and shPRKDC on c-MYC, YAP, and TAZ expression analyzed under sorafenib intervention



Supplementary Tables**Supplementary Table 1.** First-strand cDNA synthesis configuration system

Component	Volume
Total RNA	Quantified at 800 ng
Random Primer (0.1 μ g/ μ l)	1 μ l
2 $\times$ TS Reaction Mix	10 μ l
TransScript [®] RT/RI Enzyme Mix	1 μ l
gDNA Remover	1 μ l
RNase-free Water	Up to 20 μ l

Supplementary Table 2 .Information on the primers used in the fluorescence-based quantitative mRNA assay

Primer name	Sequence, (5' to 3')	Product size (bp)
CPSF4-F	TATGCAAGAAAGGGGGACCAG	122
CPSF4-R	GATGTGCAGGAAGGGGACATT	
PRKDC-F	ACCTTGTTCTGGGCAGGATGTC	128
PRKDC-R	TCTGAGGACGAATTGCCTTT	
c-Myc-F	CATCAGCACAACTACGCAGC	169
c-Myc-R	CGTTGTGTGTTTCGCCTCTTG	
YAP-F	CAACTCCAACCAGCAGCAAC	227
YAP-R	ATTCCTGAGACATCCCGGGA	
TAZ-F	TCCCAGCCAAATCTCGTGATG	122
TAZ-R	AGCGCATTGGGCATACTCAT	
hsa GAPDH-F	TGTTGCCATCAATGACCCCTT	202
hsa GAPDH-R	CTCCACGACGTACTCAGCG	

Supplementary Table 3. Clinical correlation statistics

Characteristics	CPSF4.High_ PRKDC.High(N=116)	CPSF4.Low_ PRKDC.Low(N=116)	CPSF4.Low_ PRKDC.High(N=68)	CPSF4.High_ PRKDC.Low(N=68)	Total(N=368)	pvalue
age						0.2255
<60	57(15.49%)	54(14.67%)	31(8.42%)	23(6.25%)	165(44.84%)	
>=60	59(16.03%)	62(16.85%)	37(10.05%)	45(12.23%)	203(55.16%)	
gender						0.9826
female	36(9.78%)	38(10.33%)	22(5.98%)	23(6.25%)	119(32.34%)	
male	80(21.74%)	78(21.20%)	46(12.50%)	45(12.23%)	249(67.66%)	
pathologic_M						0.3636
M0	88(32.84%)	78(29.10%)	47(17.54%)	52(19.40%)	265(98.88%)	
M1	0(0.0e+0%)	2(0.75%)	0(0.0e+0%)	1(0.37%)	3(1.12%)	
pathologic_N						0.7615
N0	84(33.07%)	72(28.35%)	47(18.50%)	47(18.50%)	250(98.43%)	
N1	2(0.79%)	1(0.39%)	0(0.0e+0%)	1(0.39%)	4(1.57%)	
pathologic_T						0.2744
T1	48(13.15%)	69(18.90%)	34(9.32%)	31(8.49%)	182(49.86%)	
T2	34(9.32%)	21(5.75%)	19(5.21%)	18(4.93%)	92(25.21%)	
T3	30(8.22%)	21(5.75%)	12(3.29%)	15(4.11%)	78(21.37%)	
T4	4(1.10%)	3(0.82%)	2(0.55%)	4(1.10%)	13(3.56%)	
race						0.0488
american indian or alaska native	0(0.0e+0%)	1(0.28%)	0(0.0e+0%)	0(0.0e+0%)	1(0.28%)	
asian	63(17.60%)	37(10.34%)	25(6.98%)	32(8.94%)	157(43.85%)	
black or african american	8(2.23%)	4(1.12%)	3(0.84%)	2(0.56%)	17(4.75%)	
white	45(12.57%)	68(18.99%)	38(10.61%)	32(8.94%)	183(51.12%)	
neoplasm_histologic_grade						2.43E-05
G1	9(2.48%)	29(7.99%)	8(2.20%)	9(2.48%)	55(15.15%)	
G2	45(12.40%)	63(17.36%)	37(10.19%)	31(8.54%)	176(48.48%)	
G3	53(14.60%)	22(6.06%)	19(5.23%)	26(7.16%)	120(33.06%)	
G4	8(2.20%)	1(0.28%)	1(0.28%)	2(0.55%)	12(3.31%)	
tumor_stage						0.1308
stage i	48(13.95%)	64(18.60%)	32(9.30%)	28(8.14%)	172(50.00%)	
stage ii	29(8.43%)	20(5.81%)	18(5.23%)	18(5.23%)	85(24.71%)	
stage iii	33(9.59%)	20(5.81%)	13(3.78%)	17(4.94%)	83(24.13%)	
stage iv	0(0.0e+0%)	3(0.87%)	0(0.0e+0%)	1(0.29%)	4(1.16%)	
vascular_tumor_cell_type						0.1444
Macro	8(2.55%)	6(1.91%)	2(0.64%)	0(0.0e+0%)	16(5.10%)	
Micro	28(8.92%)	23(7.32%)	20(6.37%)	20(6.37%)	91(28.98%)	
None	54(17.20%)	74(23.57%)	40(12.74%)	39(12.42%)	207(65.92%)	

Supplementary figure D:

PRKDC protein kinase, DNA-activated, catalytic subunit [Homo sapiens (human)]

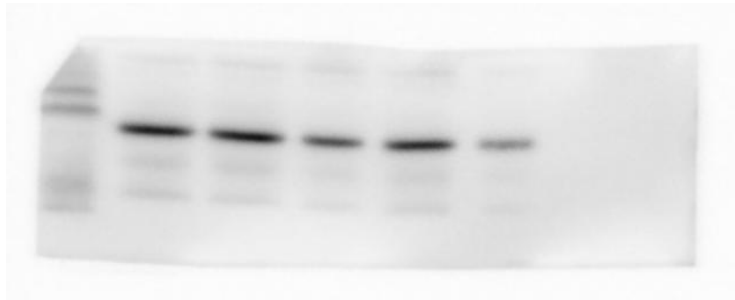
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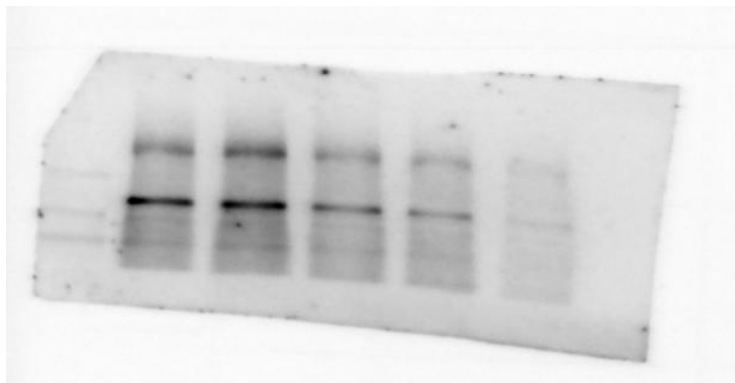
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Supplementary figure E:

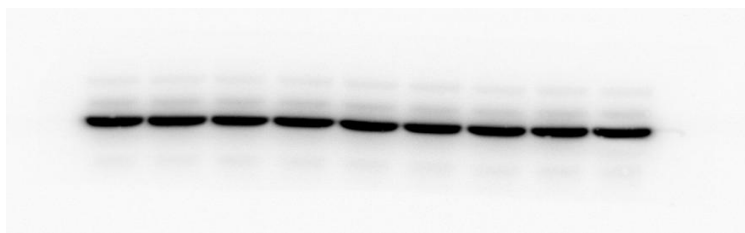
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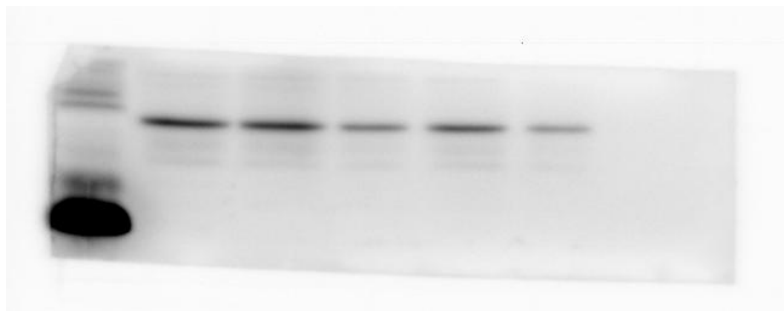
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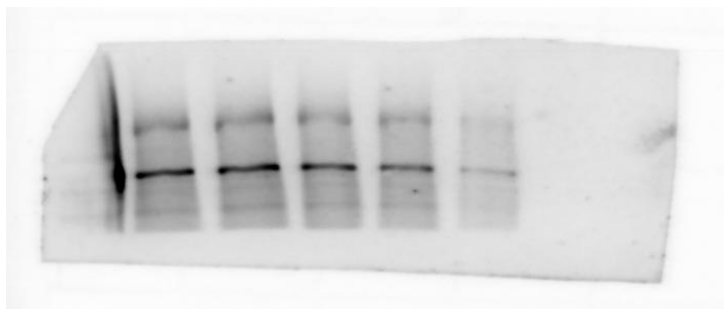
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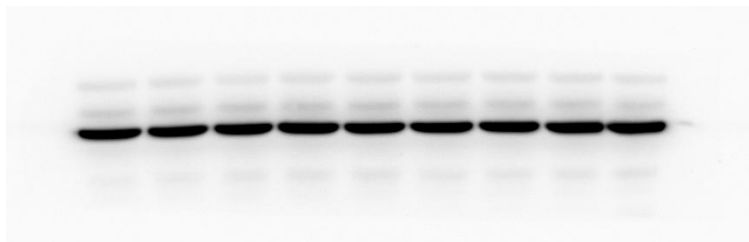
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HepG2-PRKDC:

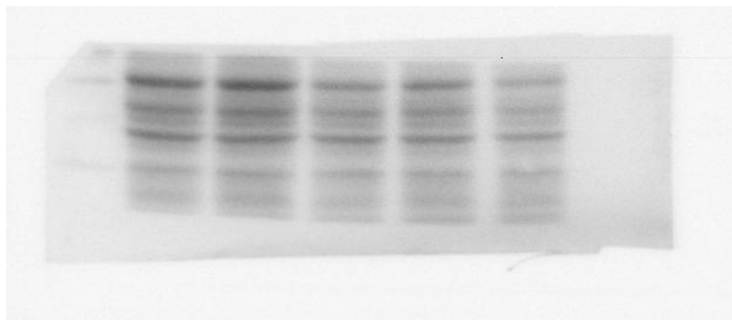


HepG2- β -actin:

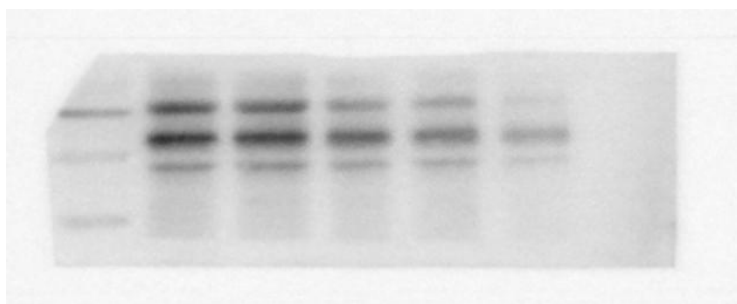


Supplementary figure F:

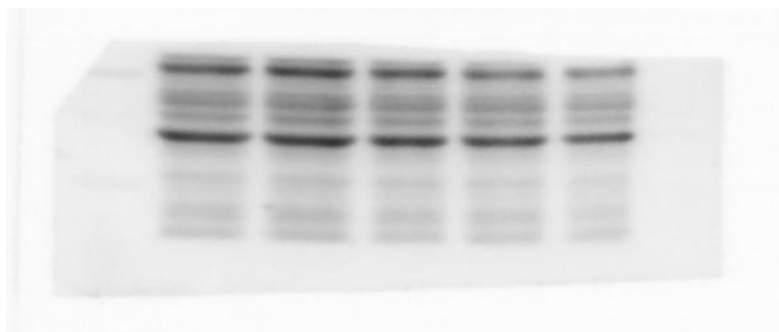
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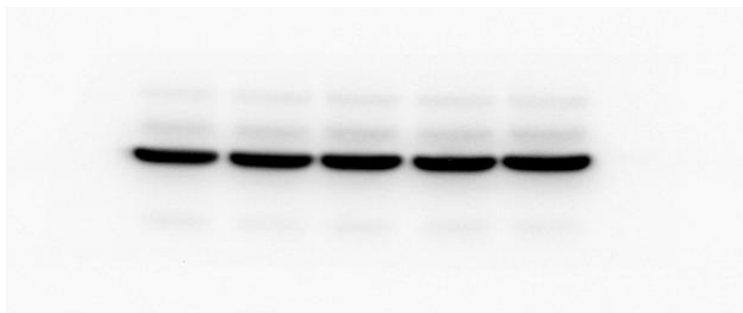
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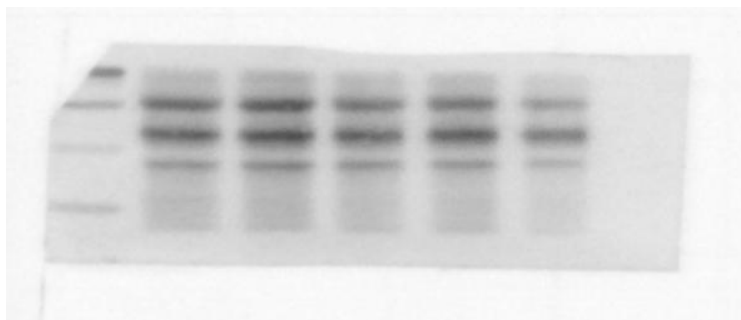
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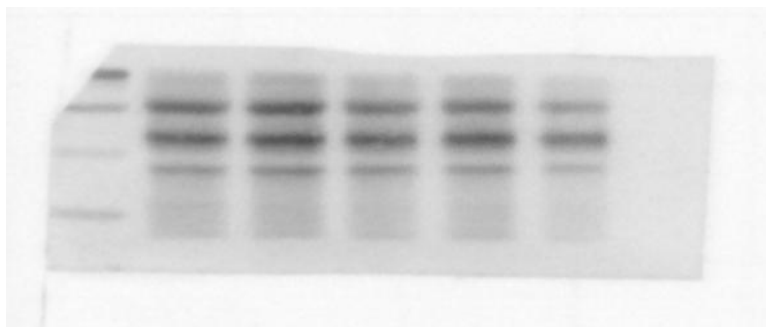
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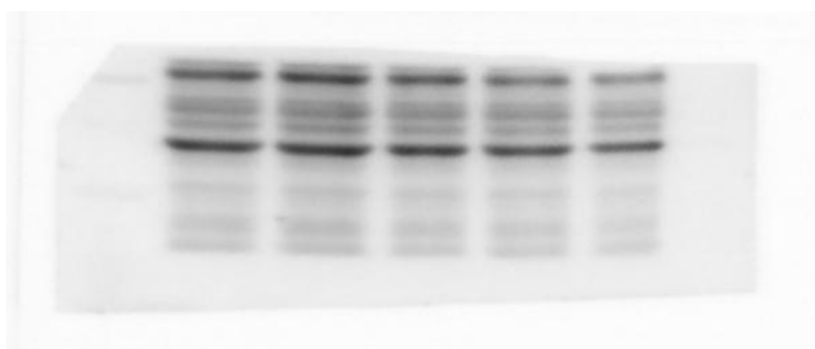
HepG2-c-Myc:



HepG2-YAP:



HepG2-TAZ:



HepG2- β -actin:

