

Figure S1 Interaction of WHSC1 with P4HB. (a) Measurement of candidate interacting proteins for WHSC1 in SMMC7721 cells with western blotting. (b) Measurement of candidate interacting proteins for WHSC1 in Hep3B cells with western blotting.

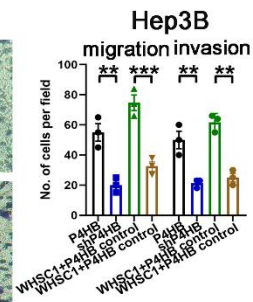
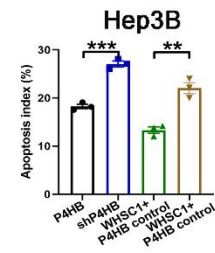
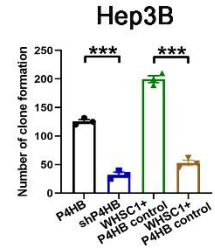
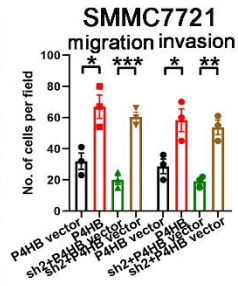
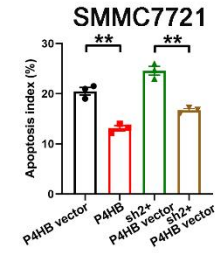
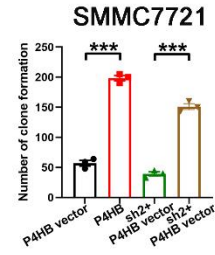
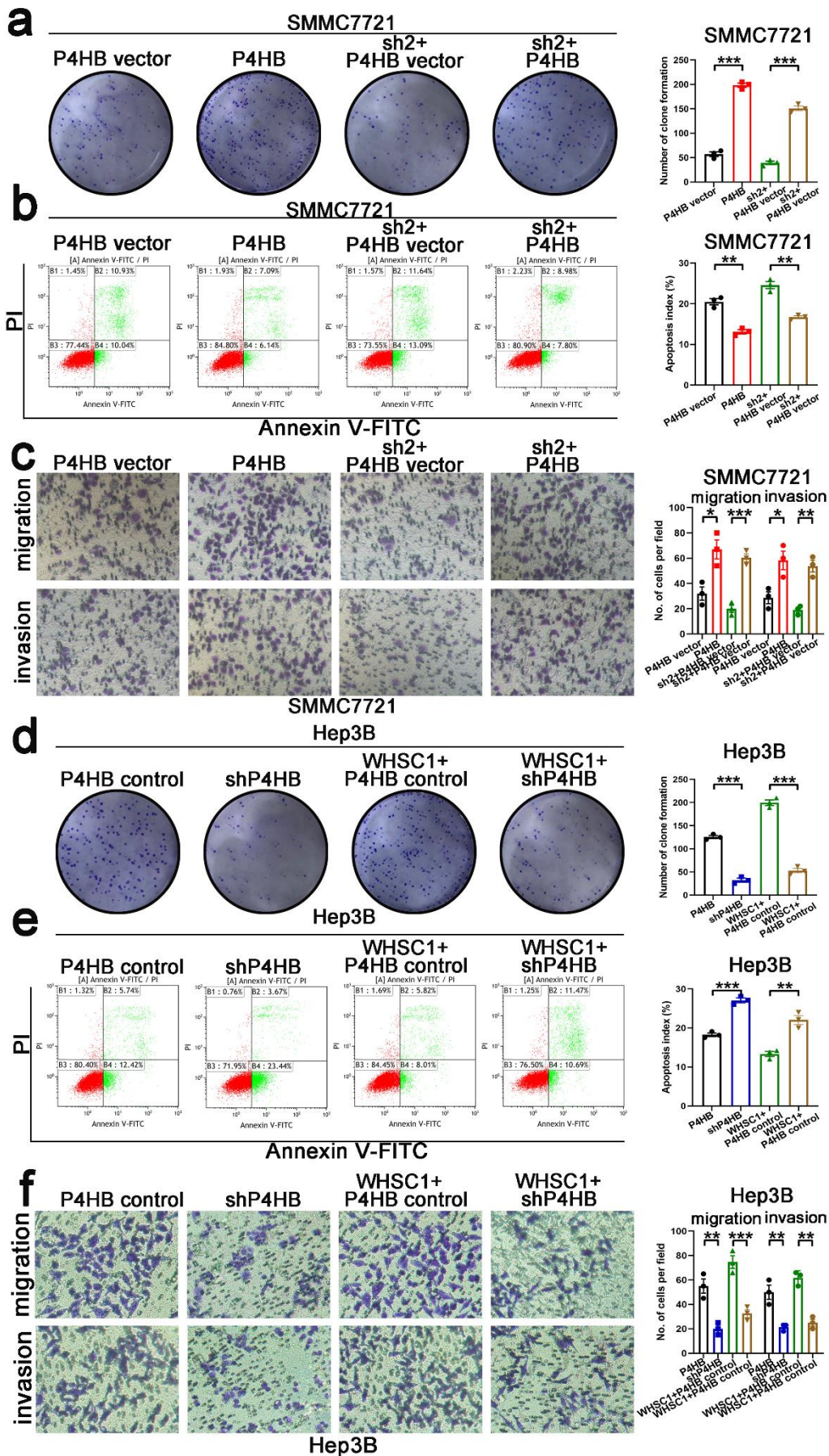


Figure S2 WHSC1 promoting HCC malignancy through P4HB upregulation. (a) Colony-forming abilities of SMMC7721-P4HB control cells and SMMC7721-shP4HB cells with or without WHSC1 overexpression. (b) Flow cytometric analysis of SMMC7721-P4HB control cells and SMMC7721-shP4HB cells with or without WHSC1 overexpression. (c) Invasive and migratory abilities of SMMC7721-P4HB control cells and SMMC7721-shP4HB cells, with or without WHSC1 overexpression. (d) Colony-forming abilities of Hep3B-P4HB vector cells and Hep3B-P4HB cells with or without WHSC1 knockdown. (e) Flow cytometric analysis of Hep3B-P4HB vector cells and Hep3B-P4HB cells with or without WHSC1 knockdown. (f) Invasive and migratory abilities of Hep3B-P4HB vector cells and Hep3B-P4HB cells with or without WHSC1 knockdown. Data are presented as mean \pm SEM. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$. P-values were determined using a two tailed t-test.

a

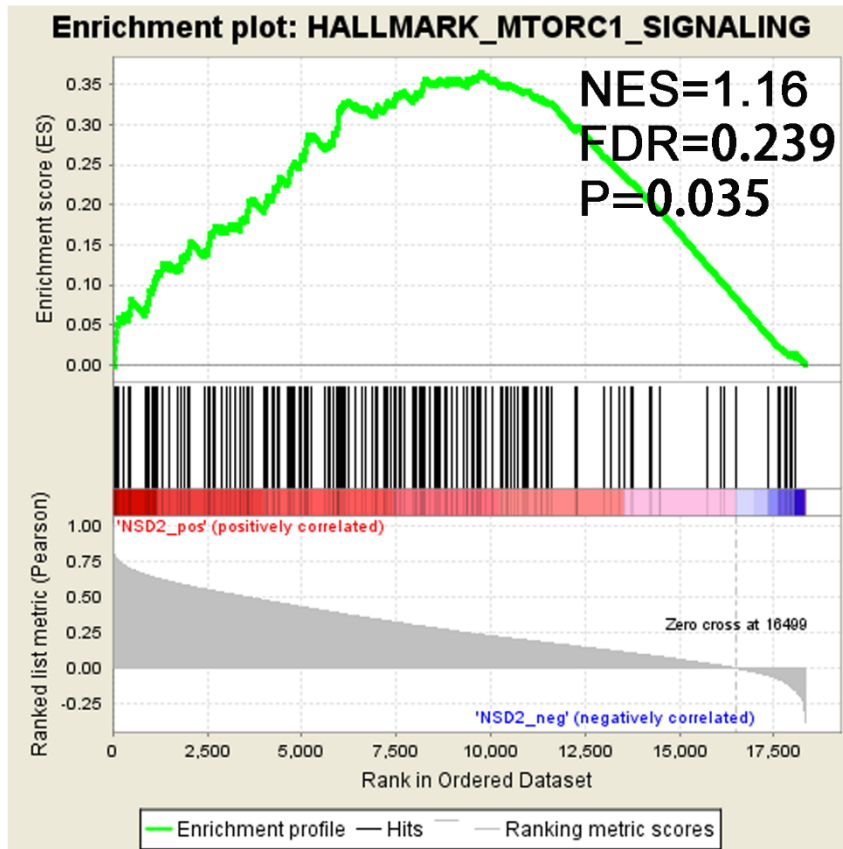


Figure S3 Positive regulation of mTORC1 signaling by WHSC1. (a) GSEA using data from TCGA to determine the signaling pathways influenced by WHSC1.

Supplementary Data 1:

WHSC1 shRNA Sequence (5'-3') Genn ID: 7468, NM_001042424.3

WHSC1 shRNA1: 5'-GCCAAGAGGGACATCAGAAAG-3'

WHSC1 shRNA2: 5'-GCACTTCCAGGATATCATTTG-3'

WHSC1 shRNA3: 5'-GCCTCCAATTGCAGTGGATTC-3'

P4HB shRNA Sequence (5'-3') Genn ID: 5034, NM_000918.4

P4HB shRNA1: 5'-GCCATCGATGACATACCATTT-3'

P4HB shRNA2: 5'-GCTTGTTGGGAAGAACTTTGA-3'

P4HB shRNA3: 5'-GGAAGACGATGATCAGAAAGC-3'

The sequences of primers used

WHSC1-F CCCACCATAACAAGCACAT

WHSC1-R TCAGACACTCCGAATCAAA

Supplementary Data 2:

First protein	Gene name	Description	Peptides	Sequence coverage [%]	Unique sequence coverage [%]	Mol. weight [kDa]	Sequence length	iBAQ treat
P55809	OXCT1	Succinyl-CoA:3-ketoacid coenzyme A transferase 1, mitochondrial	9	28.7	28.7	56.157	520	492250
Q9Y230	RUVBL2	RuvB-like 2	8	20.5	20.5	51.156	463	935980
E9PIR7	TXNRD1	Thioredoxin reductase 1, cytoplasmic	6	19.3	19.3	53.166	482	525730
E7ER27	HSD17B4	Peroxisomal multifunctional enzyme type 2	5	12.8	4.4	53.928	500	394130
I3L514	P4HB	Protein disulfide-isomerase	4	27.4	8.5	11.565	106	420900
P14618	PKM	Pyruvate kinase PKM	37	71.2	71.2	57.936	531	8544300
Q14152	EIF3A	Eukaryotic translation initiation factor 3 subunit A	8	6.3	6.3	166.57	1382	156600
P67936	TPM4	Tropomyosin alpha-4 chain	21	56	30.6	28.521	248	3174800