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Supporting Information

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Deubiquitylase OTUD6B Governs pVHL Stability in an Enzyme-Independent Manner and Suppresses Hepatocellular Carcinoma Metastasis

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Supporting Information

Deubiquitylase OTUD6B governs pVHL stability in an enzyme-independent manner and suppresses hepatocellular carcinoma metastasis

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Supplemental Figure 1. OTUD6B suppresses HCC metastasis. (A) Scatter plot of 98 members of DUBs mRNA expression in human HCC tissues from TCGA data of National Cancer Institute, USA. The X-axis represents the value of log2 (fold change of DUBs PKFM in tumor tissues (T) / non-tumor liver tissue (NT) in HCC patients, and the Y-axis represents the value of false positive rate (FDR). (B) Scatter plot of the protein levels of OTU members in human HCC tissues from CNHPP data. The X-axis represents the fold change of OTUs iBQ in tumor tissues (T) / non-tumor liver tissue (NT) in HCC patients, and the Y-axis represents the value of false positive rate (FDR). (C-K) Transwell assays were used to test the effect of depletion of OTU family DUB members, including OTUB1 (C), OTUB2 (D), OTUD2 (D), OTUD3 (E), OTUD4 (F), OTUD5 (G), OTUD6B (H), OTUD7B (I) or OTULIN (K) on cell migration in MHCC-LM3 cells. (L) Transwell assays were used to examine the effect of depletion of OTUD6B on cell migration in Bel7402 cell. Results are shown as mean \pm s.d. n=3 independent experiments. **, P < 0.01, ***, P < 0.001, student *t* test. (M) Immunoblot assays were conducted with indicated antibodies in HCC cells (Bel7402) with OTUD6B stable knockdown. (N, O) Real time Q-PCR assays were performed to test the mRNA level of OTUD6B and OTUD6A in MHCC-LM3 (N) and Bel7402 (O) cells. Results are shown as mean \pm s.d. n=3 independent experiments. **, P < 0.01, student t test. (P) MTS assays were used to examine cell proliferation of HCC cells with OTUD6B knockdown. (Q) 5×10^6 MHCC-LM3 cells with indicated shRNA were injected into nude mice subcutaneously. The mice were euthanized 6 weeks later by a cervical dislocation. Three dimensions of tumors were measured with caliper and tumor volume was calculated with formula length x width x depth x $0.52 \text{ (mm}^3)$. The tumor weight was calculated and shown. Results are shown as mean \pm s.d. n=5 independent experiments. (R) Immunohistochemistry (IHC) was performed with anti-CD31 antibody on tumor tissues. (S, T) The protein (S) and mRNA (T) level of OTUD6B in a panel of HCC cell lines. Results are shown as mean \pm s.d. n=3 independent experiments. *, P < 0.05, **, P < 0.01, ***, P < 0.001, student *t* test.









Supplemental Figure 2. OTUD6B negatively regulates HIF pathway. (A) Identification of the different expression genes (DEGs) was graphed in volcano plot. (B) Gene Ontology (GO) enrichment analysis for biological process, cell component, and molecular function of DEGs. The $-\log_{10}$ (Q value of enrichment) is shown on x axis; the numbers represent the number of associated proteins for each term. (C) The selected genes involved in cell motility, cell community and microenvironments are shown as a heatmap. (D) Real-time Q-PCR assays were used to confirm the results of RNA-Seq. (E) Real time Q-PCR was used to examine the mRNA level of HIF-1 α and HIF- 2α in MHCC-LM3 cells transfected with indicated shRNA. (F) Transwell assays were used to examine the effect of depletion of OTUD6B on cell migration in MHCC-LM3 cell under normoxia and hypoxia. (G) Fold change of the relative luciferase activity was examined by luciferase-reporter assay in OTUD6B knockdown and NC HCC cells which were incubated under normoxia or hypoxia for 24 hours. (H) Real-time Q-PCR assays were used to determine the expression of indicated genes in MHCC-LM3 cells transfected with indicated shRNA. (I) Real time Q-PCR was used to examine the mRNA level of HIF-1 α and HIF-2 α in SMMC7721 cells with ectopic OTUD6B overexpression. (J) Transwell assays were used to examine the effect of ectopic OTUD6B on cell migration in SMMC7721 cell. (K) Fold change of the relative luciferase activity was examined by luciferase-reporter assay in HCC cells transfected with indicated constructs. (L) Real time Q-PCR assays were used to determine the expression of indicated genes in SMMC7721 cells with stable overexpression of indicated genes. (Results are shown as mean \pm s.d. n=3 independent experiments. *, P < 0.05, **, P < 0.01, ***, P < 0.001, student *t* test.)



Supplemental Figure 3. OTUD6B deubiquitylates and stabilizes pVHL in an OTU-independent manner. (A) Real time Q-PCR was used to examine the mRNA level of pVHL in SMMC7721 cells with stable OTUD6B overexpression. (B) Real-time Q-PCR assays were used to determine the expression of VHL in MHCC-LM3 cells with OTUD6B depletion. (C) Immunoblot assays were conducted with indicated antibodies in HCC cells (Bel7402) with OTUD6B stable knockdown. (D) Real time Q-PCR was used to examine the mRNA level of pVHL in Bel7402 cells with stable OTUD6B knockdown. (E) Bel7402 HCC cells were treated with 10µg/ml cycloheximide (CHX), and collected at the indicated times for western blot. Quantification of pVHL levels relative to GAPDH is shown. Results are shown as mean \pm s.d. n=3 independent experiments. **, P <0.01, two-way ANOVA test. (F) Immunoblot assays were conducted with indicated antibodies in HCC cells (Bel7402) with OTUD6B stable knockdown. (G) Overview of the structures of OTUD6B wild type and different truncates. (H, I) HA-Ub was co-transfected together with indicated constructs into HEK293T cells. Cells were treated with MG132 for 8h before collection. Then pVHL was immunoprecipitated with anti-myc antibody and immunoblotted with anti-HA antibody. (J) Immunoblot assays were conducted with indicated antibodies in HCC cells (SMMC7721) with stable overexpression of OTUD6B wild type and different truncates. (K) Transwell assays were used to examine the effect of OTUD6B wild type and different truncates on cell migration in SMMC7721 cell. Results are shown as mean \pm s.d. n=3 independent experiments. **, P < 0.01, ***, P < 0.001, student *t* test.









Supplemental Figure 4. OTUD6B interacts with pVHL. (A) Immunofluorescence staining was performed in HCC cells (Bel7402) with anti-OTUD6B and pVHL antibodies to determine the co-localization of these two proteins in HCC cells (scale bar, $10 \mu m$). (B) The lysates of HEK293T cells transfected with indicated constructs were subjected to immunoprecipitation with anti-Flag. The immunoprecipitates or the eluates were then blotted.







Supplemental Figure 5. OTUD6B interacts with elongin B and enhances the binding of pVHL and elongin C. (A, B, C) Increasing amounts of myc or flag-OTUD6B were co-transfected together with indicated constructs into HEK293T cells and the lysates were subject to immunoprecipitation with anti-myc or flag antibody. The lysates and immunoprecipitates were then blotted. (D, E) The lysates of HEK293T cells transfected with indicated constructs were subjected to immunoprecipitation with anti-Myc. The immunoprecipitates or the eluates were then blotted. (F) MHCC-LM3 Cells with NC or OTUD6B knockdown were treated with MG132 for 8 hrs, and then lysed in 0.5 ml of CHAPS lysis buffer. 500 µl of the lysate was loaded onto a Superdex 200 10/300 GL column. Chromatography was performed on the AKTA-FPLC with CHAPS buffer. UV280 of different fractions was recorded. (G, H) Immunofluorescence staining was performed in HCC cells with anti-OTUD6B and anti-elonginB antibodies to determine the co-localization of these two proteins in MHCC-LM3 (G) and Bel7402 cells (H) (scale bar, 10 µm). (I, J) The lysates of HEK293T cells transfected with indicated constructs were subjected to immunoprecipitation with anti-Flag. The immunoprecipitates or the eluates were then blotted.

Figure S6



Supplemental Figure 6. pVHL mediates the inhibitory effect of OTUD6B on HCC cell migration. (A) Immunoblotting of pVHL and OTUD6B in human HCC tumor tissues (T) and the corresponding non-tumor liver tissues (NT). (B) Immunoblotting of pVHL and OTUD6B in HCC cells with stable overexpression or knockdown of indicated genes. (C) Transwell assays were performed to identify the capacity of migration in HCC cell with stable overexpression or knockdown of indicated genes. (D) Immunoblot assays were conducted with indicated antibodies in different types of tumor cells with OTUD6B stable knockdown. (E) Transwell assays were performed to examine the cell migration in indicated types of tumor cells. Results are shown as mean \pm s.d. n=3 independent experiments. *, P < 0.05, **, P < 0.01, ***, P < 0.001, student *t* test.



Supplemental Figure 7. OTUD6B plays as one of target genes of HIF-1/2 α in HCC cells. (A) Real time Q-PCR assays were used to determine the expression of indicated genes in HCC cells treated with Digoxin under normoxia or hypoxia. (B) Real time Q-PCR assays were used to determine the expression of indicated genes in HCC cells transfected with indicated shRNA under normoxia or hypoxia. (C) Immunoblot assays were conducted with indicated antibodies in HCC cells with HIF-1/2 α stable knockdown. (D) The HRE (hypoxia response element) motifs in OTUD6B promoter were shown. (E) Chip assay was used to determine the bind of HIF-1 α , HIF-2 α and HIF-1 β to the HRE sequence in OTUD6B promoter. (F) Cell lysates of HCC cells transfected with indicated constructs were subject to immunoprecipitation with anti-flag antibodies. The immunoprecipitates were then blotted with anti-flag antibody. Results are shown as mean \pm s.d. n=3 independent experiments. *, P < 0.05, **, P < 0.01, ***, P < 0.001, student *t* test.

Name	FC Mean	P value
	USP family	
USP49	7.869139194	1.09831E-07
USP54	3.989933303	0.000586991
USP21	3.714645962	2.90903E-11
USP35	3.669373819	7.15256E-07
USP46	2.842409008	3.37269E-08
USP22	2.838782231	1.05271E-11
USP1	2.684594767	0.000200946
USP31	2.630570425	7.24325E-07
USP27X	2.54864061	0.005831605
USP14	2.414225362	4.62075E-09
USP3	2.399001565	1.36805E-07
USP11	2.267834522	5.47469E-08
USP39	2.214987797	2.89526E-11
USP5	2.206641088	4.79505E-13
USP36	2.155383147	6.75756E-08
USP37	2.140295652	6.80989E-06
USP42	2.004362934	3.87037E-07
USP33	1.970531922	3.21092E-05
USP24	1.903860951	4.44187E-05
USP40	1.86603239	5.15633E-08
USP19	1.84826459	7.98074E-09
USP51	1.829917148	0.181272525
USP6	1.788081246	0.000309536
USP30	1.778839229	1.28833E-06
USP16	1.756498948	2.89561E-05
USP28	1.753369982	3.0596E-05
USP34	1.748864366	2.44737E-06
USP7	1.715657352	2.8628E-08
USP32	1.678044268	0.000160033
USP4	1.633647317	9.07146E-06
USP13	1.610067084	0.000530334
USP48	1.605525165	5.94223E-07
USP8	1.603138348	3.8408E-05
USP20	1.59637505	3.38606E-08
USP45	1.593446948	0.00163141
USP47	1.515399433	0.000118691
USP25	1.511177673	0.00197186
USP12	1.444762184	0.409306427
USP53	1.420120437	0.32520132

Supplemental table 1. The fold change of relative mRNA level of DUBs in HCC tissues and the non-tumor liver tissue.

USP10	1.415685614	0.000932035					
USP9X	1.413418676	0.000350617					
USP2	1.388377328	0.856827092					
USP9Y	1.364606219	0.367532674					
USPL1	1.266937596	0.120210293					
USP15	1.201895041	0.240381614					
OTUD4	1.174323133	0.449080733					
USP6NL	1.166292669	0.198634372					
USP18	1.159572212	0.381991178					
USP50	1	0.787503181					
USP38	0.993233066	0.194152828					
USP44	0.847593718	0.069908955					
USP43	0.846289658	0.312404287					
USP17	NA	NA					
USP17L2	NA	NA					
USP17L6P	NA	NA					
USP26	NA	NA					
USP29	NA	NA					
	OTU family						
OTUB2	7.188493266	1.49632E-09					
OTUD7A	3.398297586	9.92464E-06					
OTUD6B	3.308460973	2.21158E-08					
OTUD3	2.828913095	8.07502E-05					
OTUD7B	2.453160651	5.84104E-06					
ALG13	2.112971111	0.000001					
OTUB1	2.088885875	4.47514E-10					
OTULIN	2.015745576	0.000001					
VCPIP1	1.676041636	0.000167363					
ZRANB1	1.312428885	0.153661456					
OTUD1	1.058225329	0.439996236					
OTUD4	1.174323133	0.449080733					
OTUD5	1.553118509	3.47409E-07					
OTUD6A	NA	NA					
JAMM family							
PSMD14	2.054390897	8.66839E-07					
PSMD7	2.153836181	1.70315E-06					
PRPF8	2.088065448	0.000358897					
MPND	1.843564189	2.01357E-05					
MYSM1	1.57777778	0.000219769					
COPS6/CSN6	1.308472021	3.27852E-14					
STAMBPL1	0.453117352	2.76123E-06					
STAMBP	1.573292978	1.12825E-06					
BRCC3	1.234379562	1.15454E-06					

COPS5	1.263253397	1.53699E-10			
EIF3F	1.168754755	2.29492E-08			
EIF3H	1.594306541	6.65907E-08			
	MCPIP family				
ZC3H12A	1.051391466	0.14600871			
ZC3H12B	0.517522124	0.030769727			
ZC3H12C	1.130651558	0.837094549			
ZC3H12D	1.608	0.013614281			
NYNRIN	1.414326466	0.150998298			
KHNYN	0.964744058	3.96851E-08			
N4BP1	1.532289442	0.000332133			
	UCH family				
UCHL1	75.09866667	0.066840399			
UCHL3	3.15745614	0.11464283			
UCHL5	1.661445244	7.52876E-07			
BAP1	1.012614207	2.50874E-11			
MJD family					
ATXN3	0.962463768	0.001394892			
JOSD1	0.70458079	5.22817E-05			
JOSD2	1.006901141	3.36E-08			

VCPIP1 NO. **OTUB1 OTUD4 OTUD5 OTUD6B OTUD7B OTULIN** ALG13 1 9.04 T^a.only T.only T.only T.only T.only T.only T.only 2 6.90 T.only T.only T.only T.only T.only T.only T.only 3 T.only 6.55 T.only T.only T.only T.only T.only T.only 4 6.25 T.only T.only T.only T.only T.only 327.82 T.only 5 5.87 T.only T.only T.only T.only T.only 175.47 T.only T.only 6 5.31 T.only T.only T.only T.only 86.73 T.only 7 5.18 T.only T.only T.only T.only T.only 73.36 T.only 8 4.89 T.only NA T.only T.only T.only 44.53 T.only 9 4.88 T.only NA T.only T.only T.only 31.82 T.only 10 4.68 T.only NA T.only T.only T.only 27.11 T.only T.only 11 4.35 T.only T.only T.only 20.89 T.only NA 12 4.21 T.only T.only T.only T.only 19.15 T.only NA 13 4.19 T.only NA T.only T.only T.only 18.98 T.only 14 4.12 T.only NA T.only T.only T.only 18.91 T.only 15 3.82 NA T.only T.only T.only 18.30 P.only T.only 16 3.73 T.only NA T.only T.only T.only 18.14 P.only 17 3.69 T.only NA T.only T.only T.only 17.28 P.only P^b.only 18 3.33 T.only NA T.only T.only 15.75 P.only 19 3.23 T.only NA T.only T.only NA 15.37 P.only 20 14.88 3.22 T.only NA T.only T.only 66.60 P.only 29.66 21 3.15 T.only NA T.only T.only 14.61 P.only 22 27.95 3.14 T.only NA T.only T.only 12.17 P.only 23 3.11 T.only NA T.only T.only 23.85 11.68 P.only 24 2.92 T.only NA T.only T.only 20.72 9.80 P.only 25 2.90 T.only NA T.only T.only 19.37 9.43 P.only 26 2.90 T.only NA T.only T.only 13.93 9.31 P.only 27 T.only T.only T.only 11.38 9.25 P.only 2.82 NA 9.12 28 2.75 T.only NA T.only T.only 10.21 P.only 29 2.72 T.only NA T.only T.only 10.17 8.94 P.only 30 2.70 T.only NA T.only T.only 7.74 8.92 P.only 31 2.68 NA T.only T.only 7.54 8.85 P.only T.only 32 2.68 T.only NA T.only T.only 7.30 8.21 NA 33 2.64 T.only NA T.only T.only 7.29 8.07 NA 7.17 34 2.58 T.only T.only T.only 7.86 NA NA 35 2.45 T.only NA T.only T.only 6.31 7.56 NA 5.93 36 2.32 T.only NA T.only T.only 7.53 NA 37 2.31 T.only NA T.only T.only 5.62 7.14 50.16 38 2.31 NA T.only 5.26 7.10 39.50 T.only T.only

Supplemental table 2. The fold change (FC) of relative protein level of OTU

DUBs in human HCC tissues and the non-tumor liver tissues.

39	2.30	T.only	NA	T.only	P.only	5.14	6.91	23.87
40	2.26	P.only	NA	T.only	P.only	4.90	6.87	16.60
41	2.25	P.only	NA	T.only	P.only	4.62	6.76	16.36
42	2.24	P.only	NA	T.only	NA	4.55	6.71	14.77
43	2.16	P.only	NA	T.only	NA	4.31	6.51	10.37
44	2.10	P.only	NA	T.only	74.92	4.28	6.28	9.19
45	2.09	P.only	NA	T.only	51.76	4.08	6.23	8.99
46	2.07	P.only	NA	T.only	42.10	3.84	6.23	8.96
47	2.06	P.only	NA	T.only	26.85	3.75	5.96	8.62
48	2.04	P.only	NA	T.only	26.52	3.37	5.76	8.61
49	2.02	P.only	NA	T.only	18.11	3.11	5.49	7.52
50	1.77	P.only	NA	T.only	17.41	2.95	5.28	6.79
51	1.76	P.only	NA	T.only	16.35	2.73	5.23	5.83
52	1.74	P.only	NA	T.only	15.20	2.55	5.18	5.73
53	1.73	NA	NA	T.only	12.82	2.55	4.93	5.68
54	1.72	NA	NA	T.only	12.61	2.55	4.90	5.41
55	1.71	NA	NA	T.only	11.28	2.48	4.61	5.32
56	1.68	NA	NA	T.only	11.22	2.40	4.43	4.98
57	1.64	NA	NA	T.only	10.46	2.39	4.13	4.79
58	1.62	NA	NA	T.only	10.16	2.33	4.12	4.30
59	1.61	NA	NA	T.only	9.88	2.20	4.11	3.98
60	1.61	NA	NA	T.only	9.41	2.16	4.06	3.71
61	1.60	NA	NA	T.only	8.85	2.14	3.73	3.65
62	1.58	NA	NA	T.only	7.90	2.10	3.61	3.40
63	1.54	NA	NA	P.only	7.43	2.07	3.47	3.31
64	1.54	NA	NA	P.only	7.07	2.05	3.47	2.49
65	1.54	NA	NA	P.only	6.77	2.01	3.38	2.43
66	1.53	NA	NA	P.only	6.68	1.89	3.34	2.36
67	1.53	NA	NA	P.only	6.51	1.87	3.27	2.30
68	1.52	NA	NA	NA	6.45	1.81	2.83	2.16
69	1.52	NA	NA	NA	5.98	1.79	2.75	1.91
70	1.51	NA	NA	NA	5.98	1.76	2.70	1.89
71	1.50	63.58	NA	NA	5.83	1.73	2.61	1.86
72	1.48	32.05	NA	NA	5.67	1.61	2.60	1.85
73	1.47	14.05	NA	NA	5.59	1.59	2.58	1.84
74	1.47	11.61	NA	NA	5.53	1.59	2.57	1.60
75	1.45	6.57	NA	NA	5.26	1.58	2.57	1.59
76	1.43	6.45	NA	NA	5.07	1.57	2.50	1.55
77	1.37	5.33	NA	NA	4.95	1.50	2.50	1.49
78	1.36	3.89	NA	NA	4.82	1.48	2.41	1.40
79	1.35	3.75	NA	NA	4.53	1.47	2.24	1.39
80	1.33	3.21	NA	NA	4.24	1.44	2.20	1.33
81	1.32	3.18	NA	NA	4.13	1.39	2.12	1.20

82	1.32	2.87	NA	NA	3.96	1.38	1.98	1.14
83	1.31	2.82	NA	NA	3.81	1.29	1.90	1.13
84	1.31	2.76	NA	NA	3.52	1.28	1.86	1.06
85	1.27	2.32	NA	NA	3.46	1.27	1.85	1.05
86	1.24	2.25	NA	NA	3.41	1.24	1.79	0.98
87	1.22	2.05	NA	NA	3.15	1.20	1.74	0.91
88	1.22	1.95	NA	NA	3.11	1.18	1.73	0.90
89	1.18	1.80	NA	NA	3.05	1.18	1.67	0.75
90	1.17	1.54	NA	NA	3.02	1.17	1.63	0.75
91	1.17	1.50	NA	NA	2.61	1.16	1.62	0.71
92	1.16	1.38	NA	NA	2.40	1.12	1.61	0.66
93	1.16	1.26	NA	NA	2.19	1.10	1.59	0.66
94	1.14	1.26	NA	NA	2.12	1.05	1.50	0.62
95	1.07	1.21	NA	24.97	2.04	1.05	1.32	0.60
96	1.05	1.15	NA	16.78	2.03	0.98	1.31	0.58
97	1.05	1.13	NA	8.58	1.95	0.98	1.23	0.57
98	1.05	1.11	NA	8.16	1.89	0.95	1.21	0.52
99	1.04	0.97	NA	7.16	1.81	0.95	1.21	0.51
100	1.04	0.83	NA	7.13	1.72	0.94	1.18	0.46
101	0.98	0.83	NA	5.41	1.60	0.93	1.10	0.45
102	0.98	0.78	NA	5.16	1.53	0.92	1.00	0.42
103	0.97	0.74	NA	4.18	1.34	0.79	0.89	0.41
104	0.97	0.71	NA	3.84	0.91	0.78	0.86	0.39
105	0.95	0.71	NA	3.81	0.83	0.71	0.80	0.38
106	0.92	0.63	NA	3.22	0.82	0.63	0.80	0.38
107	0.88	0.52	NA	2.99	0.60	0.52	0.56	0.37
108	0.84	0.36	NA	2.50	0.60	0.50	0.52	0.35
109	0.70	0.20	NA	2.14	0.51	0.42	0.47	0.32
110	0.65	0.12	NA	1.32	0.51	0.38	0.24	0.27
111	0.42	0.05	NA	0.65	0.33	0.36	0.04	0.09

^{a)} Tumor; ^{b)} Peri-tumor

Supplemental table 3. Clinicopathological significance of OTUD6B in human

HCC tissues.

		No of nationts	Tumor OTUD6B Protein level				
Clinicopatholog	ical indexes	(%) $(n=89)$	Low(%)	mid(%)	High(%)		
			(n=18)	(n=52)	(n=19)	<i>p</i> value	
	≤50	40(44.9)	11(61.1)	20(38.5)	8.5) 9(47.4)		
Age(year)	>50	49(55.1)	7(38.9)	32(61.5)	10(52.6)	0.4181	
Gandar	Female	10(11.2)	2(11.1)	5(9.62)	3(15.8)	0.644	
Gender	Male	79(88.8)	16(88.9)	47(90.4)	16(84.2)	0.044	
LID: A a	Negative	18(20.5)	3(16.7)	10(19.2)	5(26.3)	0.4642	
повяд	Positive	70(79.5)	15(83.3)	41(78.8)	14(73.7)	0.4042	
LIDeAh	Negative	7(8.1)	2(11.1)	4(7.7)	1(5.3)	0.5422	
пысао	Positive	79(91.9)	16(88.9)	46(88.5)	17(89.5)	0.3422	
$\Delta ED (ng/m1)$	≤20	35(39.8)	2(11.1)	27(51.9)	6(31.6)	0 2262	
AFP (lig/lill)	>20	53(60.2)	16(88.9)	24(46.2)	13(68.4)	0.2262	
	≤54	51(58.0)	8(44.4)	27(51.9)	16(84.2)	0.0134	
001 (0/L)	>54	37(42.0)	10(55.6)	24(46.2)	3(15.8)	0.0134	
Liver airrhogia	No	9(10.2)	2(11.1)	5(9.6)	2(10.5)	0.4408	
	yes	79(89.8)	16(88.9)	31(59.6)	32(168.4)		
Tumor	≤5	62(69.7)	12(66.7)	34(65.4)	16(84.2)	0 2274	
size(cm)	>5	27(30.3)	6(33.3)	18(34.6)	3(15.8)	0.2374	
Tumor number	Single	78(87.6)	15(83.3)	46(88.5)	17(89.5)	0 5746	
	Multiple	11(12.4)	3(16.7)	6(11.5)	2(10.5)	0.3740	
Microvascular	absence	57(73.1)	11(61.1)	32(61.5)	14(73.7)	0 5395	
invasion	present	21(26.9)	4(22.2)	14(26.9)	3(15.8)	0.5575	
Tumor	complete	41(46.6)	7(38.9)	25(48.1)	9(47.4)	0.6121	
encapsulation	none	47(53.4)	11(61.1)	26(50)	10(52.6)	0.0131	
Histological	I+II	42(47.7)	5(27.8)	26(50)	11(57.9)	0.0021	
grade	III+IV	46(52.3)	12(66.7)	26(50)	8(42.1)	0.0921	
TNM stage	Ι	57(64.0)	11(61.1)	32(61.5)	13(68.4)	0 1001	
T INIVI stage	II+III	32(36.0)	7(38.9)	20(38.5)	5(26.3)	0.4004	
Daaumanaa	No	40(44.9)	6(33.3)	21(40.4)	13(68.4)	0.0204	
	Yes	49(55.1)	12(66.7)	31(59.6)	6(31.6)	0.0304	
Death	No	57(64.0)	9(50)	31(59.6)	17(89.5)	0.0117	
Death	Yes	32(36.0)	9(50)	21(40.4)	5(26.3)	0.011/	

		e			
Gene ID	Ctrl	shOTUD6B	log2(shOTUD6B/	Qvalue(Ctrl-vs	Pvalue(Ctrl-vs-
	FPKM	FPKM	Ctrl)	-shOTUD6B)	shOTUD6B)
100529144	0.42	0.97	1.20	1.25E-12	3.66E-14
100532726	0.01	0.20	4.55	1.03E-07	5.64E-09
10098	0.01	0.11	3.81	4.47E-06	3.29E-07
101060179	0.26	0.66	1.36	3.78E-05	3.47E-06
10178	0.01	0.04	3.30	0.000523143	6.88E-05
10215	0.01	0.41	6.19	3.97E-17	7.37E-19
102723722	0.40	1.16	2.64	3.35E-23	3.80E-25
102724994	0.12	0.45	2.01	8.81E-09	4.16E-10
10278	0.00	0.08	5.00	0.000309659	3.75E-05
10391	0.01	0.26	4.37	9.89E-14	2.57E-15
10395	0.01	0.09	3.21	6.39E-07	4.06E-08
10485	0.09	0.53	2.52	6.02E-06	4.57E-07
10631	0.07	1.55	4.78	5.68E-81	1.44E-83
116448	0.02	0.40	4.44	1.82E-14	4.33E-16
1462	0.00	0.13	6.83	3.64E-13	1.00E-14
1634	0.70	1.97	1.49	1.28E-20	1.84E-22
165	0.04	0.16	1.94	4.35E-05	4.07E-06
1809	0.01	0.09	2.93	6.69E-06	5.15E-07
1848	0.47	1.22	1.38	4.38E-18	7.64E-20
220382	0.00	0.12	5.00	0.000309659	3.75E-05
221981	0.00	0.03	5.09	0.000183799	2.06E-05
2290	0.01	0.11	3.59	4.01E-05	3.73E-06
23266	0.00	0.05	4.25	0.000128334	1.38E-05
23302	0.01	0.09	3.09	3.28E-06	2.35E-07
2335	0.07	0.23	1.69	1.05E-10	3.74E-12
23767	0.01	0.09	3.17	3.43E-05	3.13E-06
2583	0.01	0.08	4.57	1.00E-05	8.02E-07
2841	0.05	0.18	2.05	0.000676782	9.36E-05
28951	0.01	0.31	5.02	2.52E-22	3.19E-24
2953	0.12	0.71	2.63	4.28E-09	1.93E-10
3400	0.00	0.12	5.09	3.33E-08	1.72E-09
341640	0.08	0.25	1.65	6.70E-23	7.71E-25
3485	0.09	2.09	4.89	4.07E-47	2.02E-49
3488	0.02	0.16	3.15	1.59E-12	4.74E-14
357	0.01	0.11	3.13	1.93E-06	1.31E-07
3690	0.04	0.15	2.03	4.73E-06	3.51E-07
3737	0.00	0.03	5.50	1.00E-05	7.97E-07
3800	0.00	0.06	4.80	3.11E-07	1.86E-08

Supplemental table 4. Differential gene expression in HCC cells with OTUD6B

knockdown and NTC

4133	0.02	0.14	2.49	5.78E-08	3.06E-09
4239	0.06	0.29	2.22	4.48E-05	4.22E-06
4313	0.03	0.13	2.32	0.000258269	3.04E-05
4323	0.06	0.41	2.91	5.82E-17	1.10E-18
441519	0.13	0.64	2.34	4.53E-06	3.35E-07
4684	0.03	0.11	1.93	0.000105985	1.11E-05
4811	0.01	0.12	4.03	1.63E-10	6.03E-12
4843	0.02	0.33	3.72	2.55E-18	4.40E-20
5098	0.01	0.22	4.23	2.54E-14	6.19E-16
51299	0.00	0.12	4.81	0.000896824	0.000128772
5156	0.03	0.13	2.44	1.51E-07	8.59E-09
51704	0.01	0.14	3.86	2.58E-06	1.79E-07
53826	0.07	0.52	3.04	3.21E-11	1.10E-12
5396	0.00	0.05	4.81	0.000881027	0.000126427
5453	0.03	0.15	2.34	0.000226626	2.62E-05
56140	0.05	0.14	1.44	0.000571728	7.66E-05
5625	0.23	0.72	1.75	1.21E-09	5.14E-11
56265	0.01	0.16	4.70	2.77E-06	1.96E-07
5629	0.00	0.02	4.81	0.000881027	0.000126427
56999	0.03	0.12	2.02	3.00E-07	1.79E-08
5803	0.02	0.63	4.86	2.84E-59	1.09E-61
5806	0.00	0.11	4.91	0.000522998	6.87E-05
6299	0.00	0.04	4.81	0.000881027	0.000126427
6507	0.01	0.23	4.42	3.19E-14	7.83E-16
653781	0.03	0.13	2.29	0.000906046	0.000130175
6657	0.06	0.54	3.25	5.81E-17	1.09E-18
6664	0.00	0.04	4.46	2.51E-05	2.19E-06
6678	0.10	1.50	3.87	1.79E-77	5.00E-80
6696	0.05	0.29	2.77	1.20E-05	9.78E-07
6925	0.05	0.22	2.08	3.70E-11	1.27E-12
7070	0.01	0.38	4.81	6.21E-13	1.77E-14
7345	0.06	0.71	3.49	7.75E-11	2.75E-12
752014	0.00	0.21	5.34	3.40E-05	3.07E-06
79870	0.03	0.18	2.89	2.56E-06	1.78E-07
81557	0.03	0.15	2.70	0.000207786	2.37E-05
81848	0.14	0.36	1.33	4.06E-08	2.14E-09
8293	0.61	6.68	2.92	8.52E-101	1.49E-103
8362	0.84	2.60	1.64	3.81E-05	3.51E-06
8404	0.05	0.39	3.12	1.44E-13	3.77E-15
8406	0.03	0.18	2.88	0.000460084	5.90E-05
84446	0.06	0.21	1.86	0.000246847	2.88E-05
85027	0.02	0.16	2.76	0.000125215	1.34E-05
8642	0.01	0.04	3.00	9.51E-06	7.53E-07

8671	0.05	0.19	2.03	6.12E-10	2.53E-11
8728	0.00	0.10	5.46	1.49E-10	5.47E-12
8840	0.00	0.05	5.00	0.000309659	3.75E-05
894	0.01	0.16	4.17	1.74E-15	3.72E-17
9500	0.22	0.56	1.36	7.15E-08	3.86E-09
9537	0.61	0.99	1.11	2.33E-08	1.18E-09
9715	0.09	0.29	1.74	2.07E-08	1.03E-09
9865	0.00	0.09	4.96	1.75E-07	1.00E-08
9900	0.03	0.18	2.88	2.31E-07	1.34E-08

Supplemental table 5. List of primers used for plasmids construction and target

Genes	Forward Primer 5'-3'	Reverse Primer 5'-3'	
Eukary	votic expression vector (pcDNA3.)	1-CMV backbone)	
	CCCAAGCTTATGGAGCCCC	CGCGGATCCTTAGCTGCAATT	
Flag-OTUD6B	GGGTGAG	TTCAGTAACT	
	CCCAAGCTTATGGAGCCCC	CGCGGATCCTTACACCAAGTT	
Flag-OTUD6B-△OTU	GGGTGAG	TGAAATGT	
	CCCAAGCTT	CGCGGATCCTTAGCTGCAATT	
Flag-O1UD6-△N	CTTGAGAATCAGCCACC	TTCAGTAACT	
Elas OTUDO C1999	CTATGTATAAAGCCATTGA	AGTGGCCATCAGATGGAATCT	
Flag-OTUD6-C1885	AGATCAACT	GT	
E_{1}^{1} OTUD(C_{1}^{1}	AGCAGGTTTCTTCTAGCGC	CCGGCTAGTAGGCACCTTCCA	
Flag-OTUD6-CT/S	GTGTGC	С	
	GCTTATAATTCGGTTACAC	TTCTCCTAAGCCATATGCATG	
Flag-OTOD0-ASA	GGTTG	TC	
Muo aVIII N	CGGAATTCGGATGCCCCGG	GGGGTACCTCATGGCAGTGTG	
wryc-p v HL-IN	AGGGCGG	ATATTGGCAAAAAT	
Muo »VIII C	CGGAATTCGGGTGTATACT	GGGGTACCTCAATCTCCCATC	
wiye-pvnL-C	CTGAAAGAGC	CGTTGATGTG	
Muo WSD1	GGAATTCGGATGGCCAGCT	CGGGGTACCCTAAATACGATA	
Myc-w SD1	TTCCCCCGAGGGT	CGAGAGAAACTCC	
Mua alanginD	CGGAATTCGGATGGACGTG	GGGGTACCTCACTGCACGGCT	
wryc-eiongnib	TTCCTCATGATCC	TGTTCATTG	
Mue alonginC	ACGCGTCGACCATGGATGG	GGGGTACCTTAACAATCTAAG	
wryc-ciolignic	AGAGGAGAAAACCT	AAGTTCGCAGCC	
Prokaryoti	c expression vector (pET-28a-His	or pGEX-6P-1-GST)	
His-OTUD6B	CGCGGATCCATGGAGCC	CCCAAGCTTTTAGCTGCAAT	
	CCGGAATTCATGGCCAGCT	ACGCGTCGACCTAAATACGAT	
HIS-WSB1	TTCCCCCGAG	ACGAGAGAAACT	
COT OTUDO	CGCGGATCCATGGAGCCCC	ACGCGTCGACTTAGCTGCAAT	
G21-010D0B	GGGT	TTTCAGTAACT	
CST aVIII	CGCGGATCCATGCCCGGAG	ACGCGTCGACTCAATCTCCCA	
USI-PVIL	GGC	TCCGTTGAT	
CST alamainD	CGCGGATCCATGGACGTGT	ACGCGTCGACTCACTGCACGGC	
GS1-elonginB	TCCTCATGATCC	TTGTTCATTG	
	Target sequences of shRN	NA	
	#1	#2	
shOTUB1	CACCACCAATCCGCACATC TT	TGTGGTTGTAAATGGTCCTAT	
shOTUB2	CCGTTTACCTGCTCTATAA	CTTCTGCACTCACGAAGTA	

sequence of shRNAs.

shOTUD2	TGGTATGTCAGAAAGGATT	AGCAGATGAAGCTAGAAGA
shOTUD3	TGGAAATCAGGGCTTAAAT	GAGTTACACATCGCATATC
shOTUD4	ACGAAAAGACAAAGACTC	
SIIO I UD4	Т	AGGTTATCAGTACCATCGA
shOTUD5	AGATGCTAGAAGACAAGA	
SIIOTODS	А	ACCTAGACAGTATGAAGAA
shOTUD6P	GGTATTGACCGAAGAGCTT	GCTGAGAAGGCATCGCAAAG
SIIOTODOB	GA	А
shOTUD7P	GCAGCAGACACAGCAGAA	TGGTATACACAGAAGATGA
SIIOTUD/B	Т	IOUTATACACAGAAGATGA
shOTHI IN	ATCACCACGGACTCGCCGT	
SHOTOLIN	А	ACCACGGACTCGCCGTATGG
shHIF-1	GTTACGTTCCTTCGATCAG	/
abuie 2	CGACCTGAAGATTGAAGTG	
SIITIIF-2	AT	/
ahnVIII	GGAAAATACACGTGGGGT	
SIPVIL	GG	/
shNTC	TTCTCCGAACGTGTCACGT	/

Name	Cat#	Company	Dilution rate
OTUB1	ab175200	Abcame	1:1000 for WB
OTUB2	GTX83953	GeneTex	1:1000 for WB
OTUD2	HPA028400	Atlas	1:600 for WB
OTUD3	HPA028544	Atlas	1:500 for WB
OTUD4	MA5-31812	ThermoreFisher	1:800 for WB
OTUD5	HPA017375	Atlas	1:600 for WB
OTUD6B	NBP1-85652	Novas	1:800 for WB and IF; 1:150 for IHC
OTUD7B	16605-1-AP	Proteintech	1:2000 for WB
OTULIN	14127s	CST	1:1000 for WB
E-Cadherin	Ab1416	Abcame	1:1000 for WB
Snail	ab53519	Abcame	1:1000 for WB
HIF-1a	ab1	Abcam	1:800 for WB; 1:50 for Chip
HIF-2a	ab199	Abcam	1:800 for WB; 1:50 for Chip
HIF-1β		Abcam	1:50 for Chip
pVHL	NB100-485	Novas	1:500 for WB; 1:150 for IHC
pVHL	sc-55506	Santa Cruz	1:500 for IF
elonginB	ab168836	Abcam	1:1000 for WB
elonginB	sc-133090	Santa Cruz	1:500 for IF
elonginC	ab226831	Abcam	1:1000 for WB
Actin	sc-1616	Santa Cruz	1:1000 for WB
GAPDH	sc-25778	Santa Cruz	1:1000 for WB
Tubulin	TA-10	Zsbio	1:2500 for WB
HA	M180-3	MBL	1:2500 for WB
Мус	sc-374171	Santa Cruz	1:2500 for WB
Flag	sc-965	Santa Cruz	1:2500 for WB
His	sc8036	Santa Cruz	1:2500 for WB

Supplemental table 6. List of primary antibodies.

Gene name	Forward Primer 5'-3'	Reverse Primer 5'-3'
OTUD6B	TGAGAAGGCATCGCAAAGAGA	ATCTTCGGTGAGTTGCTTCCT
OTUD6A	ATGGATGATCCGAAGAGTGAACA	GGTCTTGGGGACCGAGTTTT
HIF-1a	TTCCCGACTAGGCCCATTC	CAGGTATTCAAGGTCCCATTTCA
HIF-2a	CGGAGGTGTTCTATGAGCTGG	AGCTTGTGTGTGTTCGCAGGAA
VEGF	GAGGAGCAGTTACGGTCTGTG	TCCTTTCCTTAGCTGACACTTGT
LOXL2	GGGTGGAGGTGTACTATGATGG	CTTGCCGTAGGAGGAGCTG
MMP2	TGACTTTCTTGGATCGGGTCG	AAGCACCACATCAGATGACTG
MMP14	GGCTACAGCAATATGGCTACC	GATGGCCGCTGAGAGTGAC
DCN	GACAAGGTCCGCCAGTTTATG	TCGTCTAGTCTCCACTCATTCTG
VCAN	GTAACCCATGCGCTACATAAAGT	GGCAAAGTAGGCATCGTTGAAA
NOS2	TGTGGAAGGACTACTTCAACCT	GGGACTTGGCTCCTCAATCT
pVHL	GGGAACGGGGTGGGTTTAG	GCTCGCGTGAGTTCACAGA
VEGF-HRE	ATCCGTCCTCAAGTTGCTTGT	TCGATCTCAGGCTATCTCGTG
OTUD6B-HRE	AATCCAGCGTGCGCCCTTCTGTTAA	CTCAATCCTTCTTATATCTTGTTTCC
Actin	CATCCTCACCCTGAAGTACCC	AGCCTGGATAGCAACGTACATG
GAPDH	TGCACCACCAACTGCTTAGC	GGCATGGACTGTGGTCATGAG

Supplememntal table 7. List of real-time Q-PCR primers.