Supplemental Information

Genome-wide Screening Identifies SFMBT1 as an Oncogenic Driver in Cancer with VHL Loss

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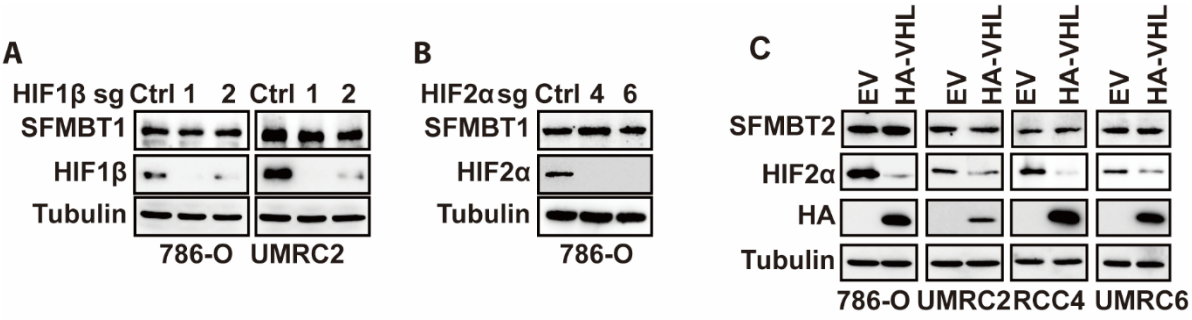


Figure S1. The regulation of SFMBT1 by pVHL was independent of HIF signaling, and SFMBT2 was not regulated by pVHL, related to Figure 1.

(A) Immunoblots for lysates from 786-O and UMRC2 cells transduced with lentivirus expressing control sgRNA (Ctrl) or HIF1β sgRNAs (1 and 2).

(B) Immunoblots for lysates from 786-O transduced with lentivirus expressing control sgRNA (Ctrl) or HIF2α sgRNAs (4 and 6).

(C) Immunoblots for lysates from cells transduced (786-O, UMRC2 and RCC4) with lentivirus expressing control (Ctrl) or HA-pVHL and cells transfected (UMRC6) with control vector (Ctrl) or HA-pVHL.

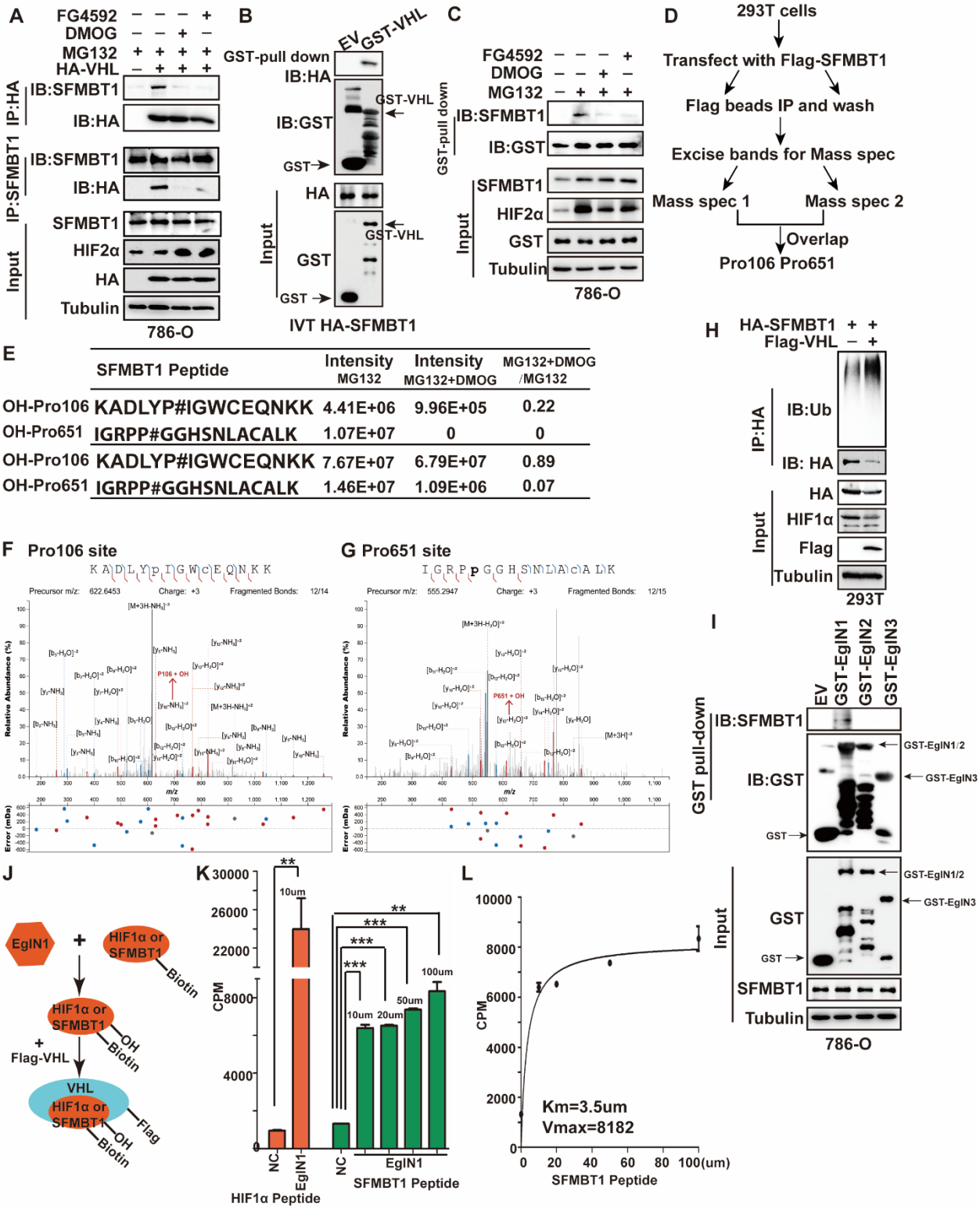

A
FG4592
DMOG
MG132
HA-VHL
IP:HA
IB:SFMBT1
IB:HA
IP:SFMBT1
IB:SFMBT1
IB:HA
Input
SFMBT1
HIF2α
HA
Tubulin
786-O
B
EV
GST-VHL
GST-pull down
IB:HA
IB:GST
GST-VHL
GST
Input
HA
GST-VHL
GST
GST
IVT HA-SFMBT1
C
FG4592
DMOG
MG132
GST-pull down
IB:SFMBT1
IB:GST
Input
SFMBT1
HIF2α
GST
Tubulin
786-O
D
293T cells
Transfect with Flag-SFMBT1
Flag beads IP and wash
Excise bands for Mass spec
Mass spec 1
Mass spec 2
Overlap
Pro106 Pro651
E
SFMBT1 Peptide
Intensity MG132
Intensity MG132+DMOG
MG132+DMOG /MG132
OH-Pro106 KADLYP#IGWCEQNKK 4.41E+06 9.96E+05 0.22
OH-Pro651 IGRPP#GGHSNLACALK 1.07E+07 0 0
OH-Pro106 KADLYP#IGWCEQNKK 7.67E+07 6.79E+07 0.89
OH-Pro651 IGRPP#GGHSNLACALK 1.46E+07 1.09E+06 0.07
F Pro106 site
K A D L Y P I G W C E Q N K K
Precursor m/z: 622.6453
Charge: +3
Fragmented Bonds: 12/14
P106 + OH
Relative Abundance (%)
m/z
Error (mDa)
G Pro651 site
I G R P P G G H S N L A C A L K
Precursor m/z: 555.2947
Charge: +3
Fragmented Bonds: 12/15
P651 + OH
H
HA-SFMBT1
Flag-VHL
IP:HA
IB:Ub
IB: HA
Input
HA
HIF1α
Flag
Tubulin
293T
I
EV
GST-EglN1
GST-EglN2
GST-EglN3
GST pull-down
IB:SFMBT1
IB:GST
GST-EglN1/2
GST-EglN3
GST
Input
GST
GST-EglN1/2
GST-EglN3
GST
SFMBT1
Tubulin
786-O
J
EglN1
HIF1α or SFMBT1
Biotin
HIF1α or SFMBT1
OH
Biotin
Flag-VHL
VHL
HIF1α or SFMBT1
Flag
OH
Biotin
K
CPM
10um
20um
50um
100um
NC
EglN1
HIF1α Peptide
NC
EglN1
SFMBT1 Peptide
L
CPM
Km=3.5um
Vmax=8182
SFMBT1 Peptide
100(um)

Figure S2. SFMBT1 stability is regulated by pVHL through EglN1 hydroxylation, related to Figure 2.

(A) Immunoprecipitaiton and immunblots from 786-O cells transduced with lentivirus expressing either control vector (Ctrl) or HA-pVHL.

(B) GST-pull down assay between GST (EV) or GST-pVHL and IVT SFMBT1. Bands of GST-pVHL are indicated by arrows.

(C) GST-pull down assay between GST-pVHL and endogenous SFMBT1 from 786-O cells with indicated drugs treatment.

(D) Schematic diagram of SFMBT1 prolyl hydroxylation identification strategy by mass spectrometry.

(E) Intensity values of two potential prolyl hydroxylation sites (Pro106 and Pro651) identified in two independent mass spectrometry assays.

(F-G) MS/MS spectrum for identified hydroxylated SFMBT1 peptides at Pro106 (F) and Pro651 (G).

(H) Effect of Flag-pVHL on ubiquitination of transfected HA-SFMBT1 in 293T cells.

(I) GST-pull down assay between GST (EV) or GST-EglNs (EglN1, EglN2 and EglN3) and endogenous SFMBT1 in 786-O cell lysate. Bands of GST-EglNs are indicated by arrows.

(J) Schematic diagram of capture of biotinylated peptides by Flag-VHL after in vitro hydroxylation.

(K) CPM value with HIF1α and SFMBT1 peptide at the indicated concentration with the in vitro hydroxylation assay. NC denotes for negative control (With 10□m HIF1α peptide or 100 □m SFMBT1 peptide but without the EglN1). **, P<0.01; ***, P<0.001.

(L) Km and Vmax of SFMBT1 peptide.

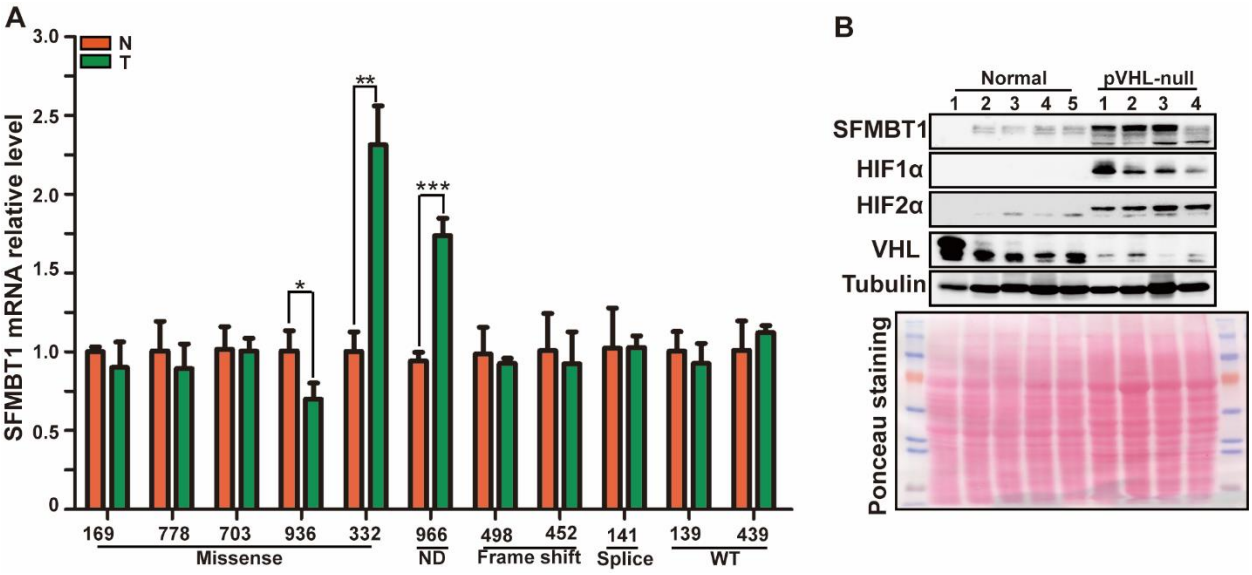


Figure S3. Related to Figure 3.

(A) Relative SFMBT1 mRNA level in indicated ccRCC paired patient normal (N) and tumor (T) tissues. *,P<0.05; **, P<0.01; ***, P<0.001.

(B) SFMBT1 expression level is upregulated in pVHL-null-induced renal cancer using a novel ccRCC mouse model (Bailey et al., 2017).

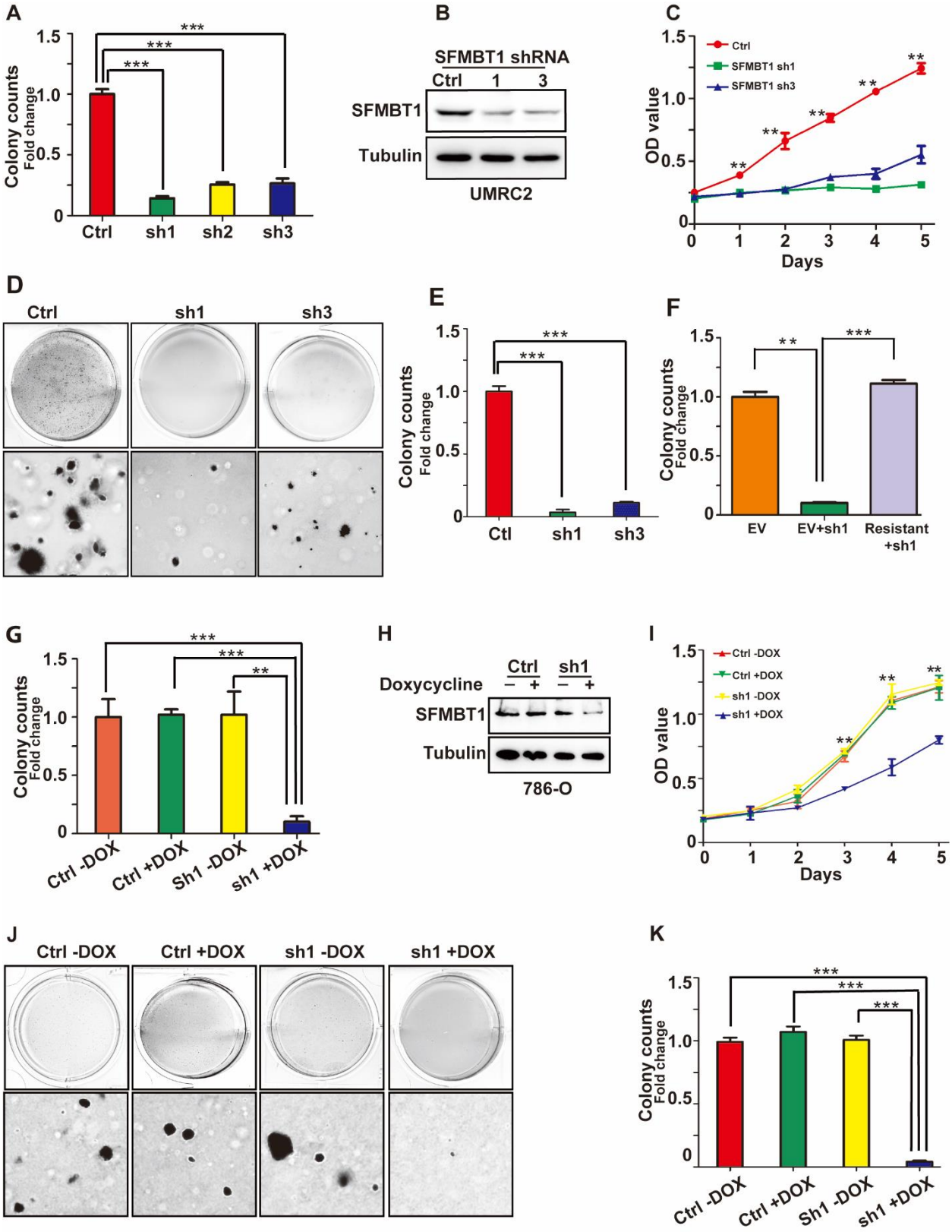

A
Colony counts
Fold change
1.5
1.0
0.5
0
***
***
***
Ctrl
sh1
sh2
sh3
B
SFMBT1 shRNA
Ctrl 1 3
SFMBT1
Tubulin
UMRC2
C
OD value
Ctrl
SFMBT1 sh1
SFMBT1 sh3
**
Days
D
Ctrl
sh1
sh3
E
Colony counts
Fold change
Ctl
sh1
sh3
F
Colony counts
Fold change
**
***
EV
EV+sh1
Resistant +sh1
G
Colony counts
Fold change
Ctrl -DOX
Ctrl +DOX
Sh1 -DOX
sh1 +DOX
H
Doxycycline
Ctrl sh1
– + – +
SFMBT1
Tubulin
786-O
I
OD value
Ctrl -DOX
Ctrl +DOX
sh1 -DOX
sh1 +DOX
Days
J
Ctrl -DOX
Ctrl +DOX
sh1 -DOX
sh1 +DOX
K
Colony counts
Fold change
Ctrl -DOX
Ctrl +DOX
Sh1 -DOX
sh1 +DOX

Figure S4. SFMBT1 regulates ccRCC cell proliferation, anchorage-independent growth, related to Figure 4.

(A) Quantification of soft agar assays of 786-O transduced with lentivirus expressing either control shRNA (Ctrl) or SFMBT1 shRNAs (sh1, sh2 and sh3).

(B-E) Immunoblots for lysates (B), cell proliferation assays (C), representative anchorage-independent growth assays (D) and quantification of soft agar assays(E) of UMRC2 cells transduced with lentivirus expressing either control shRNA (Ctrl) or SFMBT1 shRNAs (sh1 and sh3). * SFMBT1 sh1/sh3 vs Ctrl; **, $P<0.01$; ***, $P<0.001$.

(F) Quantification of soft agar assays of UMRC2 cells transduced with lentivirus expressing either control shRNA (Ctrl) or SFMBT1 sh1, followed by infection with lentivirus encoding empty vector (EV) or HA-SFMBT1 sh1-resistant (resistant). **, $P<0.01$; ***, $P<0.001$.

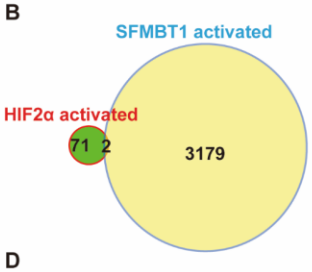
(G) Quantification of soft agar assays of UMRC2 luciferase stable cells infected with lentivirus encoding either Teton control shRNA (Ctrl) or Teton-SFMBT1 shRNA1 (sh1) and treated with or without doxycycline as indicated. **, $P<0.01$; ***, $P<0.001$.

(H-K) Immunoblots for lysates (H), cell proliferation assays (I), representative anchorage-independent growth assays (J) and quantification of soft agar assays(K) of 786-O luciferase stable cells infected with lentivirus encoding either Teton control shRNA (Ctrl) or Teton-SFMBT1 sh1 and treated with or without doxycycline as indicated. * sh1+DOX vs Ctrl-DOX/Ctrl+DOX/sh1-DOX; **, $P<0.01$; ***, $P<0.001$.

A

Fraction of... \ That overlap...	SFMBT1	H3K27ac	H3K4me3	H3K4me1	HIF1β	HIF2α
SFMBT1	1.00	0.91	0.85	0.12	0.12	0.05
H3K27ac	0.09	1.00	0.39	0.34	0.05	0.03
H3K4me3	0.18	0.92	1.00	0.32	0.08	0.03
H3K4me1	0.02	0.83	0.28	1.00	0.03	0.02
HIF1β	0.18	0.95	0.61	0.30	1.00	0.38
HIF2α	0.17	0.95	0.52	0.36	0.86	1.00

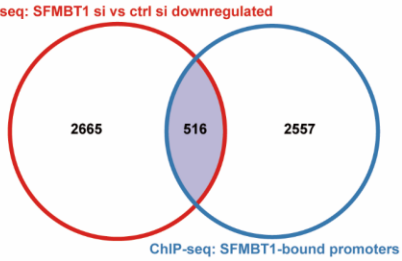
B



C

Motif	TF family	%target	%bkg	-log$_{10}$ p-value
	RBPJ1	80	52	204
	PCBP1	81	56	170
	MYC	84	60	170
	AP-1	78	56	130
	ELF/ETS	78	56	128
	SP3/C2H2 Zinc Finger	88	70	112
	FOXD3	76	59	84

D



E

Gene	SFMBT1 si vs Ctrl	LogFC value	Peaks in promoter	Tumor vs Normal	Kaplan-Meier survival	H3k4me3 promoter	H3k27ac promoter
MAP1LC3C	Down	-3.56259139315287	Yes	Higher	poorer	Yes	Yes
RRAD	Down	-2.06101492274293	Yes	Higher	poorer	Yes	Yes
SEMA3A	Down	-1.87089177390015	Yes	Higher	poorer	Yes	Yes
EPHA6	Down	-1.5040555460055	Yes	Higher	poorer	Yes	Yes
MC1R	Down	-1.2394707935514 5	Yes	Higher	poorer	Yes	Yes
TGFB3	Down	-1.0033773028615	Yes	Higher	poorer	Yes	Yes
SLC7A11	Down	-0.756284348422694	Yes	Higher	poorer	Yes	Yes
RUNX2	Down	-0.71450616091121	Yes	Higher	poorer	Yes	Yes
ARHGAP4	Down	-0.644301350731426	Yes	Higher	poorer	Yes	Yes
TMEM132A	Down	-0.636949315496535	Yes	Higher	poorer	Yes	Yes
ABCC3	Down	-0.590134032687698	Yes	Higher	poorer	Yes	Yes
TP53INP1	Down	-0.554533421067639	Yes	Higher	poorer	Yes	Yes
DUSP10	Down	-0.4635027620791 8	Yes	Higher	poorer	Yes	Yes
BBC3	Down	-0.450409773053357	Yes	Higher	poorer	Yes	Yes
CCDC57	Down	-0.436658683211758	Yes	Higher	poorer	Yes	Yes
FGD6	Down	-0.426806513482767	Yes	Higher	poorer	Yes	Yes
SPHK1	Down	-0.3986883 1680562	Yes	Higher	poorer	Yes	Yes
TET3	Down	-0.37373489661307	Yes	Higher	poorer	Yes	Yes
CNPY3	Down	-0.354376041133043	Yes	Higher	poorer	Yes	Yes
SH3KBP1	Down	-0.228340428319598	Yes	Higher	poorer	Yes	Yes

F

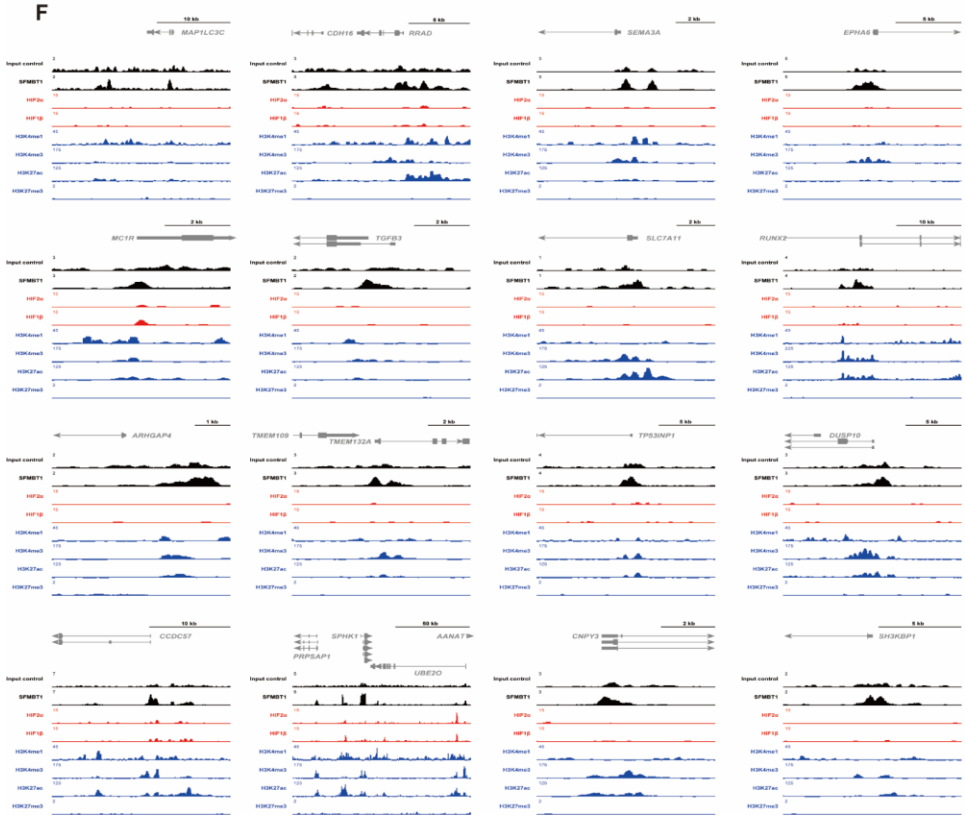


Figure S5. Identification of critical SFMBT1 direct target genes in ccRCC, related to Figure 5 and Figure 6.

(A) Chip-Seq binding sites overlap for indicated transcription factors SFMBT1, HIF2α, and HIF1β, as well as H3K4me1, H3K4me3, H3K27ac and H3K27me3.

(B) Overlap between SFMBT1 and HIF2 activated genes derived from RNA-seqs. HIF2α activated target genes in 786-O were analyzed from HIF2α siRNA RNA-seq data available online (GSE102097) (Yao et al., 2017).

(C) Over-enriched transcription factor motifs for sites unique to SFMBT1. The general family of transcription factors is shown alongside the -log10 p-value of enrichment compared to nearby background sequence.

(D) Overlap between SFMBT1 binding sites and genes that are positively regulated by SFMBT1 from RNA-seq.

(E) SFMBT1 direct target gene list.

(F) ChIP-Seq binding sites of SFMBT1, HIF2α, and HIF1β, as well as H3K4me1, H3K4me3, and H3K27Ac for 16 target genes.

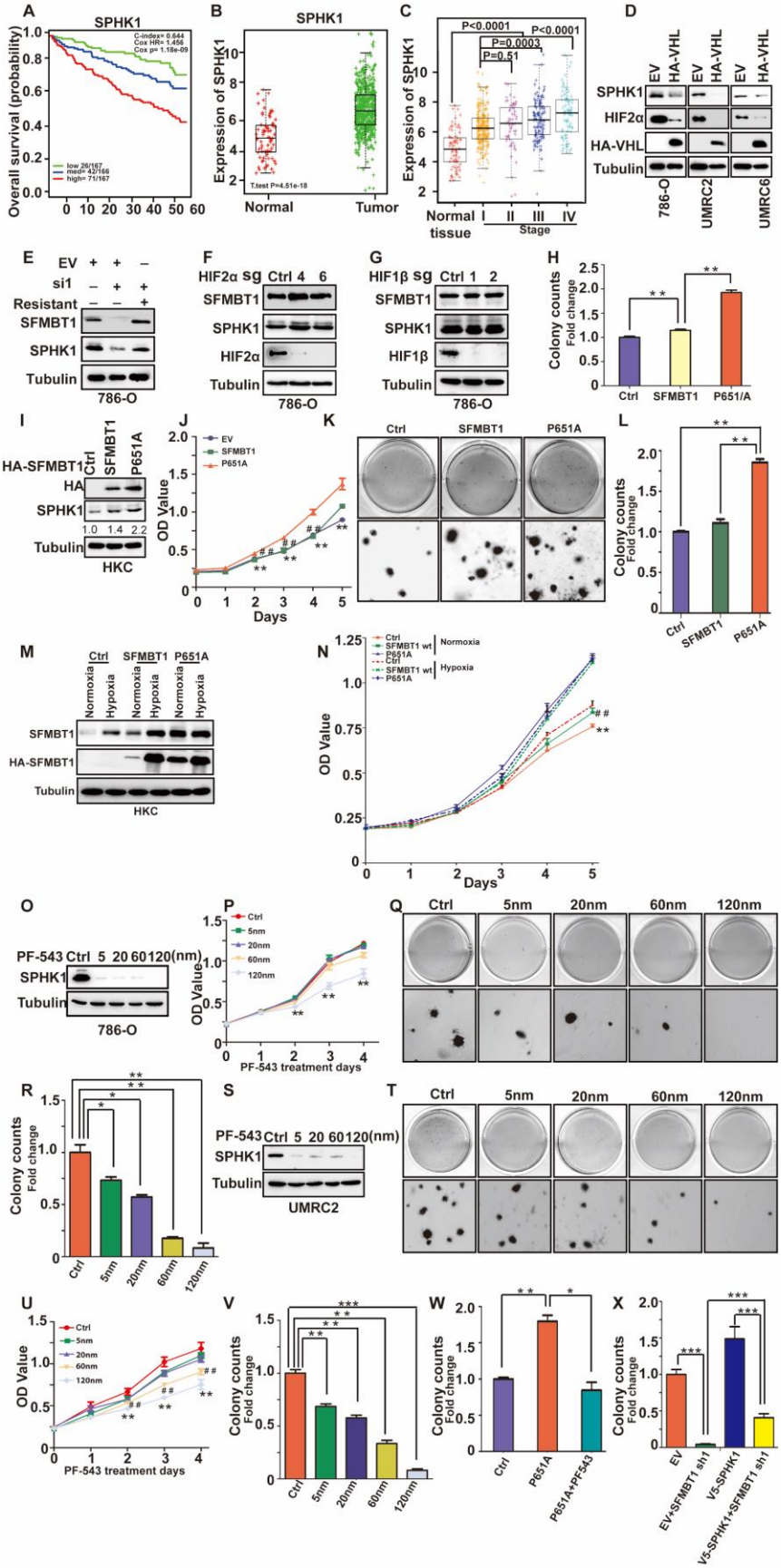

A
SPHK1
Overall survival (probability)
B
SPHK1
Expression of SPHK1
Normal
Tumor
C
P<0.0001
P<0.0001
P=0.0003
P=0.51
Expression of SPHK1
Normal tissue
Stage
D
EV
HA-VHL
SPHK1
HIF2α
HA-VHL
Tubulin
786-O
UMRC2
UMRC6
E
EV
si1
Resistant
SFMBT1
SPHK1
Tubulin
786-O
F
HIF2α sg Ctrl 4 6
SFMBT1
SPHK1
HIF2α
Tubulin
786-O
G
HIF1β sg Ctrl 1 2
SFMBT1
SPHK1
HIF1β
Tubulin
786-O
H
Colony counts
Fold change
Ctrl
SFMBT1
P651/A
I
HA-SFMBT1
Ctrl
SFMBT1
P651A
HA
SPHK1
1.0 1.4 2.2
Tubulin
HKC
J
EV
SFMBT1
P651A
OD Value
Days
K
Ctrl
SFMBT1
P651A
L
Colony counts
Fold change
Ctrl
SFMBT1
P651A
M
Ctrl
SFMBT1
P651A
Normoxia
Hypoxia
SFMBT1
HA-SFMBT1
Tubulin
HKC
N
Ctrl
SFMBT1 wt
P651A
Normoxia
Hypoxia
OD Value
Days
O
PF-543 Ctrl 5 20 60 120(nm)
SPHK1
Tubulin
786-O
P
Ctrl
5nm
20nm
60nm
120nm
OD Value
PF-543 treatment days
Q
Ctrl
5nm
20nm
60nm
120nm
R
Colony counts
Fold change
Ctrl
5nm
20nm
60nm
120nm
S
PF-543 Ctrl 5 20 60 120(nm)
SPHK1
Tubulin
UMRC2
T
Ctrl
5nm
20nm
60nm
120nm
U
Ctrl
5nm
20nm
60nm
120nm
OD Value
PF-543 treatment days
V
Colony counts
Fold change
Ctrl
5nm
20nm
60nm
120nm
W
Colony counts
Fold change
Ctrl
P651A
P651A+PF543
X
Colony counts
Fold change
EV
EV+SFMBT1 sh1
V5-SPHK1
V5-SPHK1+SFMBT1 sh1

Figure S6. SPHK1 is an SFMBT1 direct target gene in ccRCC, related to Figure 6.

(A) Box plots of SPHK1 expression between normal and ccRCC tumors in TGCA.

(B) Kaplan–Meier (K-M) plot of SPHK1 in TCGA Kidney Clear Cell Carcinoma (KIRC) data set.

(C) Box plots of SPHK1 expression between different stages of ccRCC tumors.

(D) Immunoblots for lysates from cells transduced (786-O and UMRC2) with lentivirus expressing either control (Ctrl) or HA-pVHL and cells transfected (UMRC6) with control vector (Ctrl) or HA-pVHL.

(E) Immunoblots for lysates from 786-O cells transduced with lentivirus expressing either empty vector (EV) or SFMBT1 si1-resistant, followed by transfection with control siRNA or SFMBT1 si1.

(F) Immunoblots for lysates from 786-O cells transduced with lentivirus expressing either HIF2α control sgRNA (Ctrl) or sgRNAs (4 and 6).

(G) Immunoblots for lysates from 786-O cells transduced with lentivirus expressing either HIF1β control sgRNA (Ctrl) or sgRNAs (1 and 2).

(H) Quantification of soft agar assays in Flag-VHL-UMRC2 cells transduced with lentivirus expressing either empty vector (EV), HA-SFMBT1 or P651A. **, P<0.01.

(I-L) Immunoblots for lysates (I), cell proliferation assays (J), representative anchorage-independent growth assays (K) and quantification of soft agar assays (L) in HKC cells transduced with lentivirus expressing either empty vector (EV), HA-SFMBT1 or P651A. * EV vs P651A; $^{\#}$ SFMBT1 vs P651A. **/$^{\#\#}$, P<0.01.

(M-N) Immunoblots for lysates (M) and cell proliferation assays (N) in HKC cells infected with lentivirus encoding either empty vector (EV), HA-SFMBT1 (SFMBT1) or P651A mutant under normoxia or hypoxia.* Hypoxia Ctrl vs Normoxia Ctrol; $^{\#}$ Hypoxia SFMBT1 wt vs Normoxia SFMBT1 wt. **/$^{\#\#}$, P<0.01.

(O-R) Immunoblots for lysates (O), cell proliferation assays (P), representative anchorage-independent growth assays (Q) and quantification of soft agar assays (R) in 786-O cells treated with indicated concentration of SPHK1 inhibitor PF543. *120nm vs Ctrl; **, P<0.01.

(S-V) Immunoblots for lysates (S), cell proliferation assays (T), representative anchorage-independent growth assays (U) and quantification of soft agar assays (V) in UMRC2 cells treated

with indicated concentration of SPHK1 inhibitor PF543. *120nm vs Ctrl; # 60nm vs Ctrl; **/# #, P<0.01.

(W) Quantification of soft agar assays in Flag-VHL-UMRC2 cells infected with lentivirus encoding either empty vector (EV), P651A or P651A with PF543 treatment. *, P<0.05; **, P<0.01.

(X) Quantification of soft agar assays in 786-O cells transduced with lentivirus expressing either SFMBT1 shRNA control (Ctrl) or SFMBT1 sh1, followed by infection with lentivirus encoding either empty vector (EV) or v5-SPHK1. ***, P<0.001

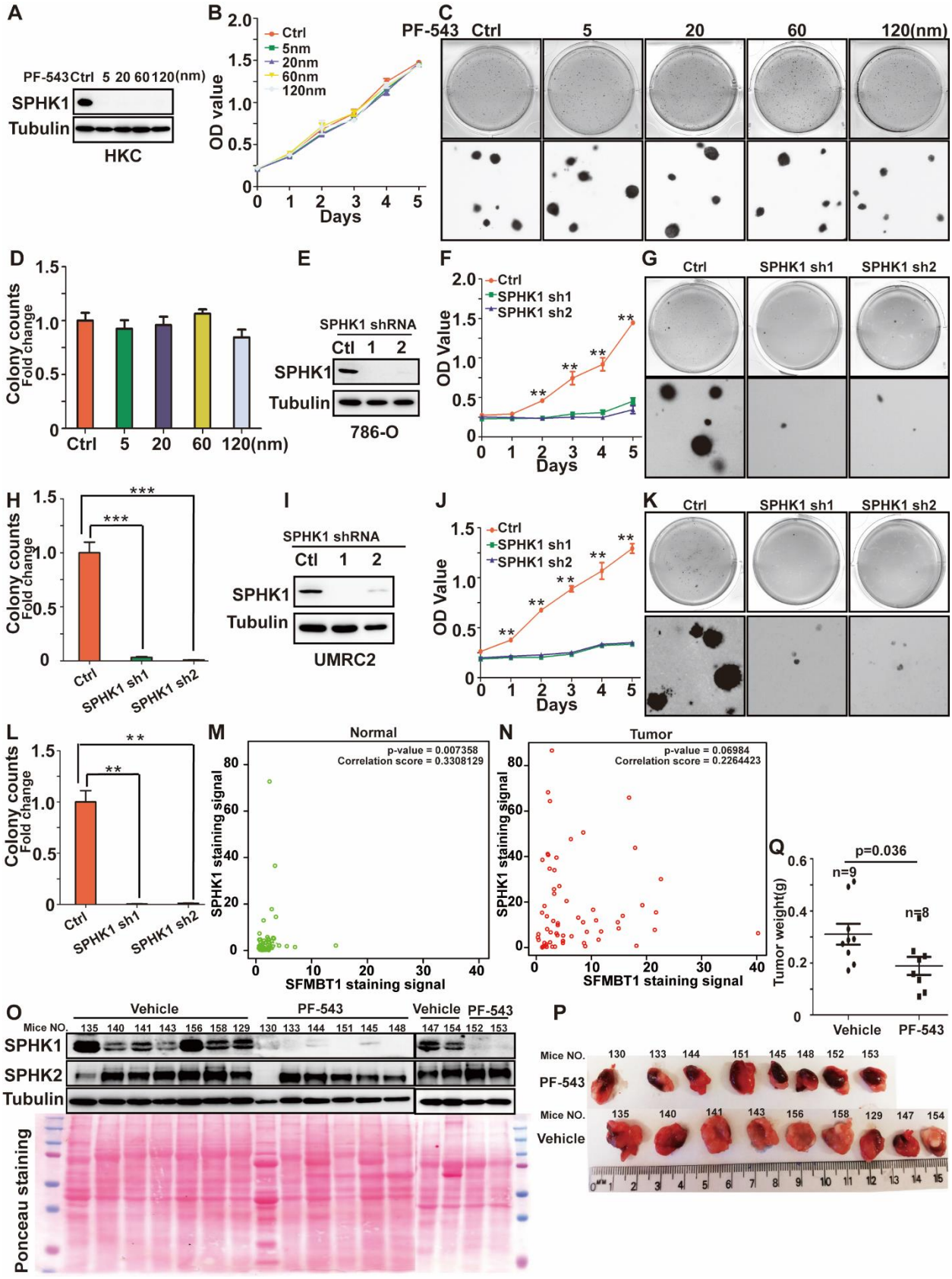

A
PF-543 Ctrl 5 20 60 120(nm)
SPHK1
Tubulin
HKC
B
Ctrl
5nm
20nm
60nm
120nm
OD value
Days
C
PF-543 Ctrl
5
20
60
120(nm)
D
Colony counts
Fold change
Ctrl 5 20 60 120(nm)
E
SPHK1 shRNA
Ctl 1 2
SPHK1
Tubulin
786-O
F
Ctrl
SPHK1 sh1
SPHK1 sh2
OD Value
Days
G
Ctrl
SPHK1 sh1
SPHK1 sh2
H
Colony counts
Fold change
Ctrl
SPHK1 sh1
SPHK1 sh2
I
SPHK1 shRNA
Ctl 1 2
SPHK1
Tubulin
UMRC2
J
Ctrl
SPHK1 sh1
SPHK1 sh2
OD Value
Days
K
Ctrl
SPHK1 sh1
SPHK1 sh2
L
Colony counts
Fold change
Ctrl
SPHK1 sh1
SPHK1 sh2
M
Normal
p-value = 0.007358
Correlation score = 0.3308129
SPHK1 staining signal
SFMBT1 staining signal
N
Tumor
p-value = 0.06984
Correlation score = 0.2264423
SPHK1 staining signal
SFMBT1 staining signal
Q
p=0.036
n=9
n=8
Tumor weight(g)
Vehicle
PF-543
O
Vehicle
PF-543
Vehicle
PF-543
Mice NO.
135 140 141 143 156 158 129
130 133 144 151 145 148
147 154
152 153
SPHK1
SPHK2
Tubulin
Ponceau staining
P
Mice NO.
130 133 144 151 145 148 152 153
PF-543
Mice NO.
135 140 141 143 156 158 129 147 154
Vehicle

Figure S7. SPHK1 regulates ccRCC cell proliferation, anchorage-independent growth and tumorigenesis, related to Figure 7.

(A-D) Immunoblots for lysates (A), cell proliferation assays (B), representative anchorage-independent growth assays (C) and quantification of soft agar assays (D) in HKC cells treated with indicated concentration of SPHK1 inhibitor PF543.

(E-H) Immunoblots for lysates (E), cell proliferation assays (F), representative anchorage-independent growth assays (G) and quantification of soft agar assays (H) in 786-O cells transduced with lentivirus expressing either control shRNA (Ctrl) or SPHK1 shRNAs (sh1 and sh2). * SPHK1 sh1/sh2 vs Ctrl.

(I-L) Immunoblots for lysates (I), cell proliferation assays (J), representative anchorage-independent growth assays (K) and quantification of soft agar assays (L) in UMRC2 cells transduced with lentivirus expressing either control shRNA (Ctrl) or SPHK1 shRNAs (sh1 and sh2). * SPHK1 sh1/sh2 vs Ctrl.

(M-N) Correlation analysis between SFMBT1 and SPHK1 expression level in non-tumor (N) (E) and tumor (T) (F) tissues.

(O) Immunoblots of lysates from gross tumors at necropsy of mice injected with 786-O cells treated with Vehicle or PF-543for SPHK1/2.

(P) Gross tumors (including kidney and tumor tissue) at necropsy of mice injected with 786-O cells treated with Vehicle or PF-543.

(Q) Plot of gross tumor weights at necropsy of mice injected with 786-O cells treated with Vehicle or PF-543.

TABLE S1. SHRNA SEQUENCES, REAL-TIME PCR PRIMER SEQUENCES, CHIP-QPCR PRIMERS, related to STAR Methods section.

Oligonucleotides		
Control shRNA: AACAGTCGCGTTTGCGACTGG	This paper	N/A
SFMBT1 shRNA1: GCTACTGTTGAGATAGTGAAA	This paper	N/A
SFMBT1 shRNA2: CCTTCAGCCATTAGACATCTA	This paper	N/A
SFMBT1 shRNA3: GAAGCCTATACCTGAATGTAT	This paper	N/A
SFMBT1 siRNA1: TGGCAGACGTTGTGCGGTT	This paper	N/A
SFMBT1 siRNA2: GGAAAGAGTTATCGGGCTA	This paper	N/A
SPHK1 shRNA1: GCAGCTTCCTTGAACCATTAT	This paper	N/A
SPHK1 shRNA2: GCAGGCATATGGAGTATGAAT	This paper	N/A
Real-Time PCR Primer: B-Actin F: AGAAAATCTGGCACCACACC R:GGGGTGTTGAAGGTCTCAAA	This paper	N/A
Real-Time PCR Primer: SFMBT1 F: ACG GAT GTG GGG AAG TCC TA R: GGC AGA ATT CAG TCA CCC GA	This paper	N/A
Real-Time PCR Primer: TGFB3 F:ACTTGGAGGAGAACTGCTGTG R: GCAGATGCTTCAGGGTTCAG	This paper	N/A
Real-Time PCR Primer: MCIR F: CTTAAAGGCGCTGTCACCCT R: GCATTGCAGATGATGAGGGC	This paper	N/A
Real-Time PCR Primer: MAPLC3C F: GCTGGTGAACAACAAGAGCC R: TCCAGGCAGCCAAATGTCTC	This paper	N/A
Real-Time PCR Primer: RRAD1 F: CTGTTTGAAGGTGTCGTGCG R: GCCTTTTTGCCAAGGCTCTC	This paper	N/A
Real-Time PCR Primer: SEMA3A F: GCAATTACCTCTGCCATGCG R: ACCAGACCTTCTGGCTAGGT	This paper	N/A
Real-Time PCR Primer: EPHA6 F: CTATGAGAAAGAACATGAGCAGC R: CGCAGTTCTCACTCGGATGT	This paper	N/A

Real-Time PCR Primer: SLC7A11 F: TCCATGAACGGTGGTGTGTT R: TGGTAGAGGAGTGTGCTTGC	This paper	N/A
Real-Time PCR Primer: RUNX2 F: TCTGGCCTTCCACTCTCAGTA R: GGACATGCCTGAGGTGACTG	This paper	N/A
Real-Time PCR Primer: TMEM132A F: AGTCTGCCAACACACAGGTC R: GGTGTCGGTGAGCTCGATAC	This paper	N/A
Real-Time PCR Primer: TP53IN1 F: AGTCCCAGAGTGGAAGCTCA R: TGGCGACGAAGGCTATTTCT	This paper	N/A
Real-Time PCR Primer: DUSP10 F: ATGAGCCAAGCCGAGTGATG R: TCTTGGAGCTGGAGGGAGTT	This paper	N/A
Real-Time PCR Primer: CCDC57 F: CTTGAGGAGCTCGACGGTGA R: TGCTCCCTCTTCCGCATTTT	This paper	N/A
Real-Time PCR Primer: CNPY3 F: GAGGAGAACGACTGGGTTCG R: CTGACTTCAGCTCCACAGCA	This paper	N/A
Real-Time PCR Primer: SH3KBP1 F: GACGATCAGCGTGGGTGAAA R: CAGGGGCTTTTCTGGAGCTT	This paper	N/A
Real-Time PCR Primer: SPHK1 F: CCGGTAGATGCACACCTTGT R: TGGGTGCAGCAAACATCTCA	This paper	N/A
Real-Time PCR Primer: ARHGAP4 F: CAAGCTGGGTTTCTCGTGC R: AGCAGTCCATGAGGTCCAAG	This paper	N/A
ChIP-qPCR primers: TGFB3 F: TTTGCGAGTCCTCTCGTTCG R: AACGTGTGGCAGGAGTGATT	This paper	N/A
ChIP-qPCR primers: MCIR F: ATGGAGGTGGCTTGTGAGTG R: ACCGCATCAGGGTTTTCAGT	This paper	N/A
ChIP-qPCR primers: MAPLC3C F: TGACTCAGCGTGAGTGTTAGG R: AAGACACCACTGGACTTCCG	This paper	N/A
ChIP-qPCR primers: RRAD1 F: GAGAGAGAGAGCGAGGTTGC R: AGAATTCAGTCTCACGGGGC	This paper	N/A

ChIP-qPCR primers: SEMA3A F: GCCAGGCACCGGATAATGAG R: GATTAGAGACTGCCACCGGC	This paper	N/A
ChIP-qPCR primers: EPHA6 F: GCCACTTTCCAGCCTCATGT R: AAACTTGACCAGCAGAGCGA	This paper	N/A
ChIP-qPCR primers: SLC7A11 F: ATTCTCCACCTCCTCGTTCCA R: GTGACAGGCAGGCGCTTAAA	This paper	N/A
ChIP-qPCR primers: RUNX2 F: ACCCCATTCCAAGCTGCAAA R: TGCCGGAGTCTTTGGAACAC	This paper	N/A
ChIP-qPCR primers: TMEM132A F: TCAGAAGCTTCCGTGAGGGAG R: GTCCCTGGAAGCAACAGAGGA	This paper	N/A
ChIP-qPCR primers: TP53IN1 F: GCTGTCTTCGGAGATGCGT R: GGAGTTTGGTCTCTGCCTCC	This paper	N/A
ChIP-qPCR primers: DUSP10 F: ATCACCGTCCCTAGTGGGAA R: CGCGAATTTTGGCTTAGCGT	This paper	N/A
ChIP-qPCR primers: CCDC57 F: CCCGCACCTCACCCTAACG R: GGACCCCGTTTCCTGTCGG	This paper	N/A
ChIP-qPCR primers: CNPY3 F: GAGGGAAGTGACGTTCGAGG R: CCTCAGCGACCTATGGCAAA	This paper	N/A
ChIP-qPCR primers: SH3KBP1 F: CAAGTGGGAGTGAATGGGGG R: GTCCACTTCAGCCTTGAGGG	This paper	N/A
ChIP-qPCR primers: SPHK1 F: GCCTTCTAGCCAGACGCCTA R: CCACGAGCTGGTTCCCG	This paper	N/A
ChIP-qPCR primers: ARHGAP4 F: ATCAGAGCCTGGGAACGAAC R: TTGGCTTAAGACGTGGGCTT	This paper	N/A