

Supplementary material

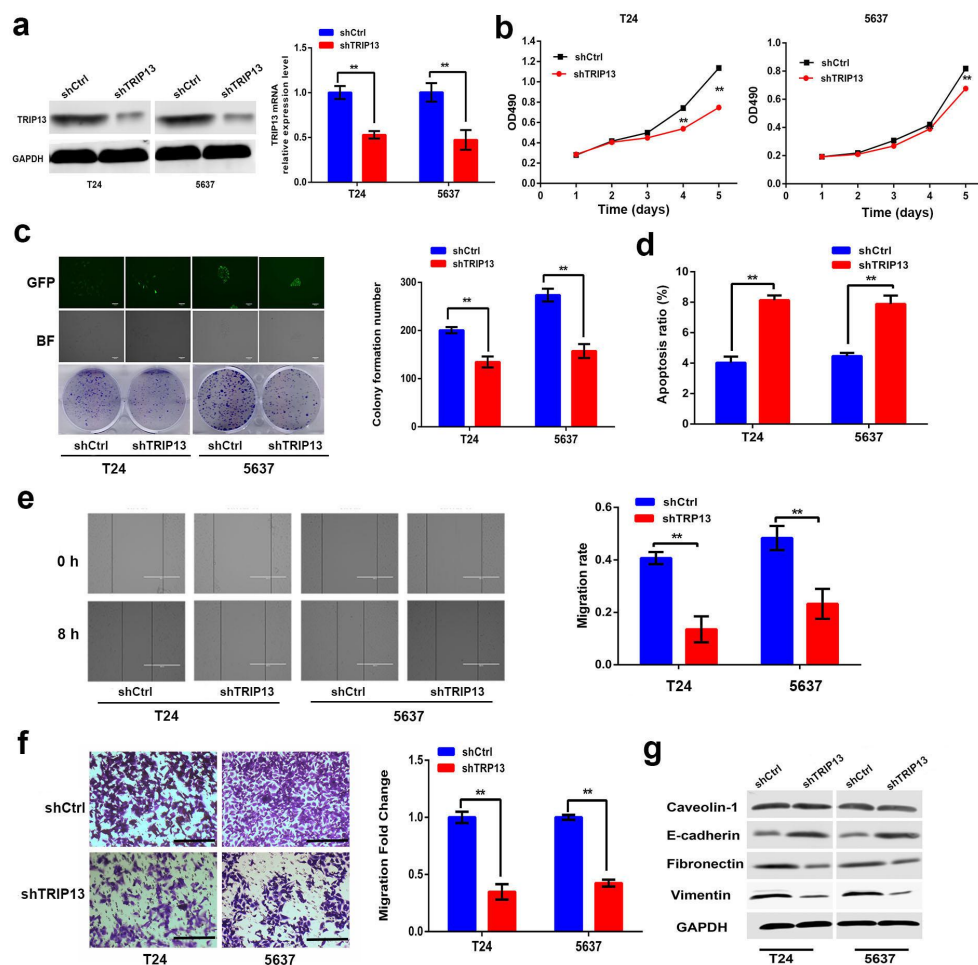


Figure S1: Inhibition of TRIP13 in bladder cancer cells suppresses proliferation, promotes apoptosis and impairs cell motility. (a) The efficiency of shTRIP13 knockdown in T24 and 5637 cells was confirmed by qPCR and western blot analyses. (b) The proliferation of T24 and 5637 cells transduced by lentiviruses expressing shCtrl or shTRIP13 was determined by the MTT assay. (c) Colony formation assay of T24 and 5637 cells transduced with lentiviruses expressing shCtrl or shTRIP13. BF: bright field; GFP: green fluorescent protein. Scale bar, 50 μ m. (d) Cell apoptosis was measured using flow cytometry in T24 and 5637 cells treated with lentiviruses expressing shCtrl or shTRIP13. The motility of T24 and 5637 cells transduced with

lentiviruses expressing shCtrl or shTRIP13 was determined by (e) wound-healing and (f) transwell assays. Scale bar, 50 μ m. (g) The expression of caveolin-1, E-cadherin, vimentin, and fibronectin was evaluated by western blot in T24 and 5637 cells after treatment with lentiviruses expressing shCtrl or shTRIP13. The data are presented as the mean \pm SD from three independent experiments. *, P<0.05, **, P<0.01.

Table S1 Primer sequences for qPCR

Gene	Forward (5'-3')	Reverse (3'-5')
TRIP13	ACTGTTGCACTTCACATTTTCCA	TCGAGGAGATGGGATTTGACT
CTHRC1	CAATGGCATTCCGGGTACAC	GTACACTCCGCAATTTTCCCAA
TSP1	AGACTCCGCATCGCAAAGG	TCACCACGTTGTTGTCAAGGG
COL4A1	GGA CTACCTGGAACAAAAGGG	GCCAAGTATCTCACCTGGATCA
MYD88	AGCGACATCCAGTTTGTGC	CCTTCTAGCCAACCTCTTTTC
ANGPTL4	GGCTCAGTGGACTTCAACCG	CCGTGATGCTATGCACCTTCT
KLF4	CGGACATCAACGACGTGAG	GACGCCTTCAGCACGAACT
MAPK9	AGCCAACTGTGAGGAATTATGT	GCTTGTCAGGATCAATCACTAAC
MTSS1	ACTGGGAATCTGACCACTAT	GACCTGACTGCTAAGGGAC
HMOX1	AAGACTGCGTTCCTGCTCAAC	AAAGCCCTACAGCAACTGTGCG
ID3	AGCCAGGTGGAAATCCTAC	AAGCTCCTTTTGTGCGTTGG
ITGA2	CCTACAATGTTGGTCTCCCAGA	AGTAACCAGTTGCCTTTTGGATT
LOX	ACTCTGACGACAACCCTTAT	ATCTGCCCTGTATGCTGTAC
JAG1	GTCCATGCAGAACGTGAACG	GCGGGACTGATACTCCTTGA
F2R	GCGCATTACTCATTCTTTC	AGACGTACCTCTGGCACTCA
BMP2	CAGAATCAAGAACGGCTATGTG	GGATCTCCAATGTGAGACCAAC
CDKN1A	CTGTCACTGTCTTGTACCCTTGT	AAATCTGTCATGCTGGTCTGC
ID1	GTA AACGTGCTGCTCTACGACATGA	AGCTCCA ACTGAAGGTCCTGA
RUNX2	GGAATGCCTCTGCTGTTATG	GGATTTGTGAAGACGGTTATGG
Slug	CAAGGACACATTAGAACTCACAC	CTACACAGCAGCCAGATTCC
Cox-2	CTCCTGTGCCTGATGATTGC	CAGCCCGTTGGTGAAAGC

MET	AGTCATAGGAAGAGGGCATT	CTTCACTTCGCAGGCAGA
JUN	CGCCAAGAACTCGGACCTC	CCTCCTGCTCATCTGTCACG
EGFR	GGTGACCGTTTGGGAGTT	CCTGAATGACAAGGTAGCG
EGR1	CAGCAGCCTTCGCTAACC	CCACTGGGCAAGCGTAA
FOS	GAAGCCAAGACTGAGCCG	GCGGGTGAGTGGTAGTAAG AG
F3	CAAACCCGTCAATCAAGTCTAC	CTTCACATCCTTCACAATCT CG
F2RL1	GGGTTTGCCAAGTAACGGC	GGGAACCAGATGACAGAGA GG
LAMA5	GGAAGTGCAGGCCACCG	TGGCCATTGCTCAGGAAGAG
LAMB2	TGCGAGCAGTGTCAGGATTT	TGGGTCACGGTAGAAGAAG G
CREB1	ACTGTAACGGTGCCAACTCC	GCTGTGCGAATCTGGTATGT
GAPDH	TGACTTCAACAGCGACACCCA	CACCCTGTTGCTGTAGCCAA A

Table S2 Mass spectrometry analysis of potential proteins that bind to TRIP13 (with top scores)

Accession	Description	Score	% Coverage	Unique Peptides	Peptides	Peptide Spectrum Matches
Q15645	Pachytene checkpoint protein 2 homolog	241155.69	83.80	69	69	9060
P68104	Elongation factor 1-alpha 1	20689.76	57.58	22	22	908
P68371	Tubulin beta-4B chain	18299.29	59.55	2	25	738
P07437	Tubulin beta chain	18263.27	58.78	5	24	707
Q9BQE3	Tubulin alpha-1C chain	16705.45	49.22	6	21	657
P60709	Actin, cytoplasmic 1	16302.36	81.60	11	29	661
P04350	Tubulin beta-4A chain	15278.62	52.48	2	21	606
Q13885	Tubulin beta-2A chain	14140.76	65.84	5	25	604
P68366	Tubulin alpha-4A chain	13594.89	39.51	2	17	567
Q13509	Tubulin beta-3 chain	13211.89	57.11	7	22	493

P04264	Keratin, type II cytoskeletal 1	9766.27	58.85	37	43	431
Q9BUF5	Tubulin beta-6 chain	9142.58	57.62	10	23	407
P68032	Actin, alpha cardiac muscle 1	8977.45	59.95	6	24	460
P08238	Heat shock protein HSP 90-beta	8916.86	51.52	27	50	446
Q01813	ATP-dependent 6-phosphofructokinase, platelet type	8812.21	37.24	30	35	375
Q00325	Phosphate carrier protein, mitochondrial	7822.11	38.95	22	22	428
P49411	Elongation factor Tu, mitochondrial	7482.84	56.86	26	26	301
P13645	Keratin, type I cytoskeletal 10	6744.24	45.03	24	28	309
P05023	Sodium/potassium-transporting ATPase subunit alpha-1	6702.08	39.30	43	43	328
P23396	40S ribosomal protein S3	6610.77	71.60	25	25	321

Table S3 Mass spectrometry analysis of potential proteins that bind to TRIP13 (full list)