

Supplementary Data for

USP7 Facilitates SMAD3 Autoregulation to Repress Cancer Progression in p53-deficient Lung Cancer

Yu-Ting Huang¹, An-Chieh Cheng¹, Hui-Chi Tang², Guo-Cheng Huang¹, Ling Cai^{3,4}, Ta-Hsien Lin^{1,5}, Kou-Juey Wu⁶, Ping-Hui Tseng¹, Greg G. Wang^{3,4}, Wei-Yi Chen^{1,7,*}

¹Institute of Biochemistry and Molecular Biology, National Yang Ming Chiao Tung University, Taipei 112, Taiwan

²Department of Life Sciences and Institute of Genome Sciences, National Yang Ming Chiao Tung University, Taipei 112, Taiwan

³Department of Biochemistry and Biophysics, University of North Carolina at Chapel Hill School of Medicine, Chapel Hill, NC, USA

⁴Lineberger Comprehensive Cancer Center, University of North Carolina at Chapel Hill School of Medicine, Chapel Hill, NC, USA

⁵Basic Research Division, Medical Research Department, Taipei Veterans General Hospital, Taipei 112, Taiwan

⁶Cancer Genome Research Center, Chang Gung Memorial Hospital at Linkou, Taoyuan, Taiwan

⁷Cancer Progression Research Center, National Yang Ming Chiao Tung University, Taipei 112, Taiwan

*Correspondence:

Wei-Yi Chen

Institute of Biochemistry and Molecular Biology, National Yang Ming Chiao Tung University, Taipei 112, Taiwan

Contact: chenwy@nycu.edu.tw

Phone: +886-2-2826-7328

Supplemental Figures

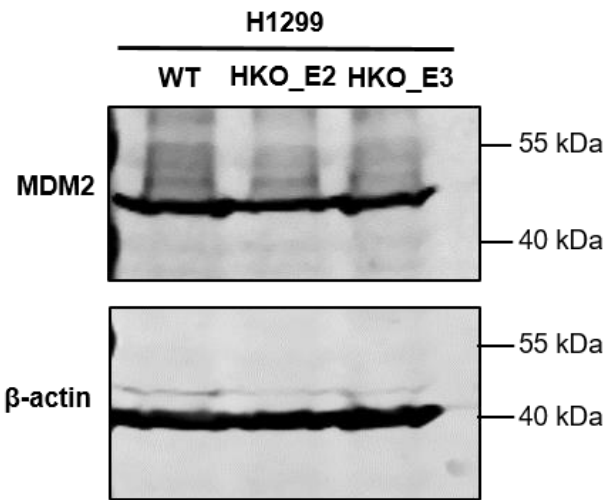


Figure S1. Comparable levels of MDM2 are expressed in wildtype and *USP7* KO H1299 cells.

Immunoblots of MDM2 in the cell lysates from wildtype (WT) and the indicated *USP7* KO H1299 cells. β -actin is the loading control.

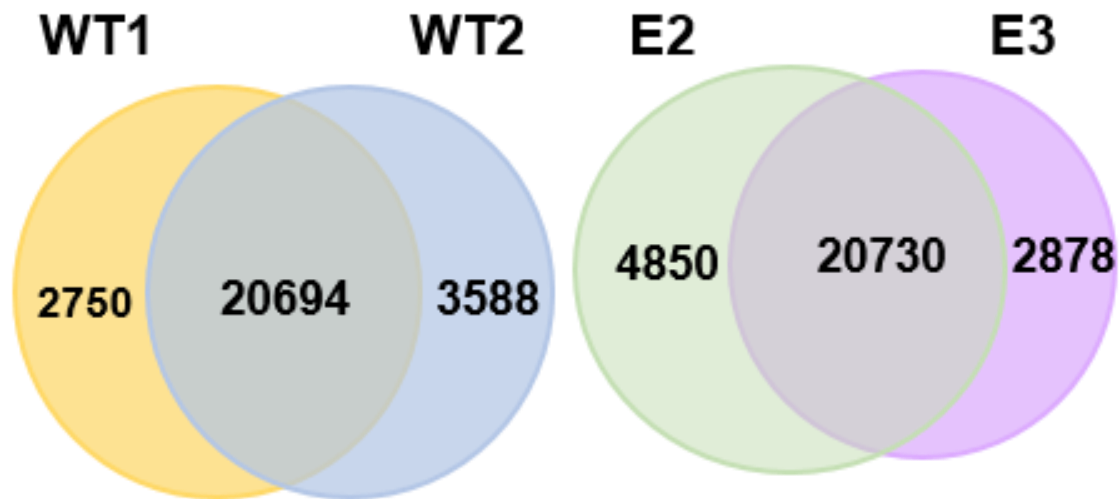


Figure S2. Genome-wide profiling of USP7-responsive enhancers in H1299 cells.

Venn diagrams showing the comparison of H3K27ac ChIP-seq peaks identified in wildtype (left panel, two biological experiments) or in *USP7* KO (right panel, two clonal lines: HKO-E2 and HKO-E3) H1299 lines. Peak overlapping analysis was performed using the *mergePeaks* of HOMER software with "-d given" parameter. The common regions of each genomic background were further analyzed for identifying the USP7-responsive enhancers in Fig. 2A and listed in dataset S1.

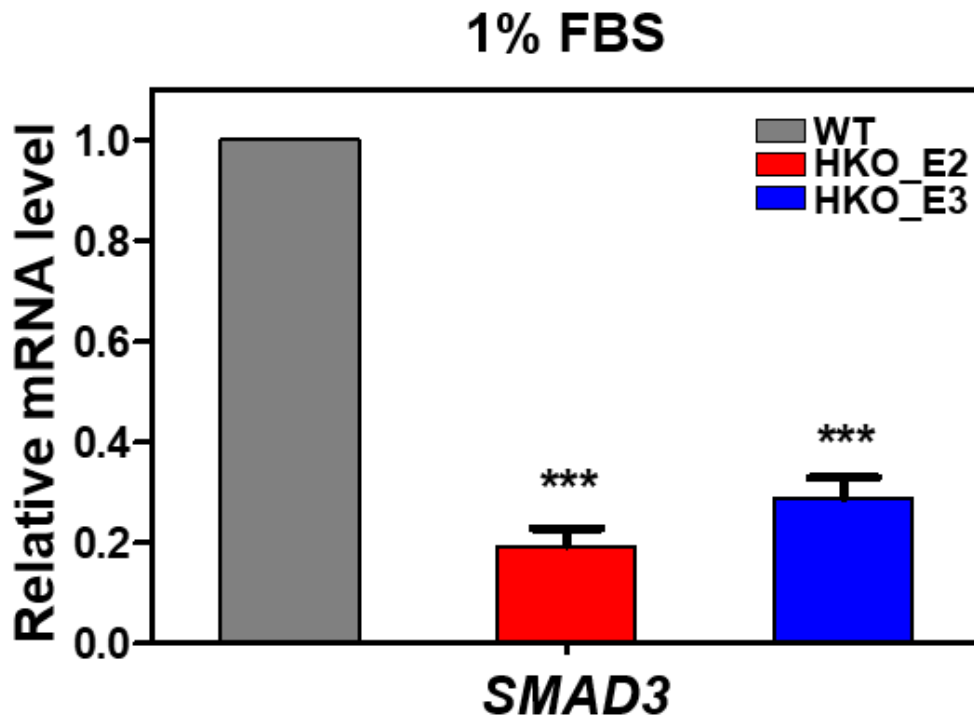


Figure S3. USP7 inactivation significantly downregulates the expression of SMAD3.

RT-qPCR assays showing the relative expression levels of *SMAD3* in wildtype (WT) or *USP7* KO (two independent clones: HKO_E2 and HKO_E3) H1299 cell lines treated with 1% FBS. Means \pm SD from three biological experiments are shown. Student's t-test, *** $p < 0.001$.

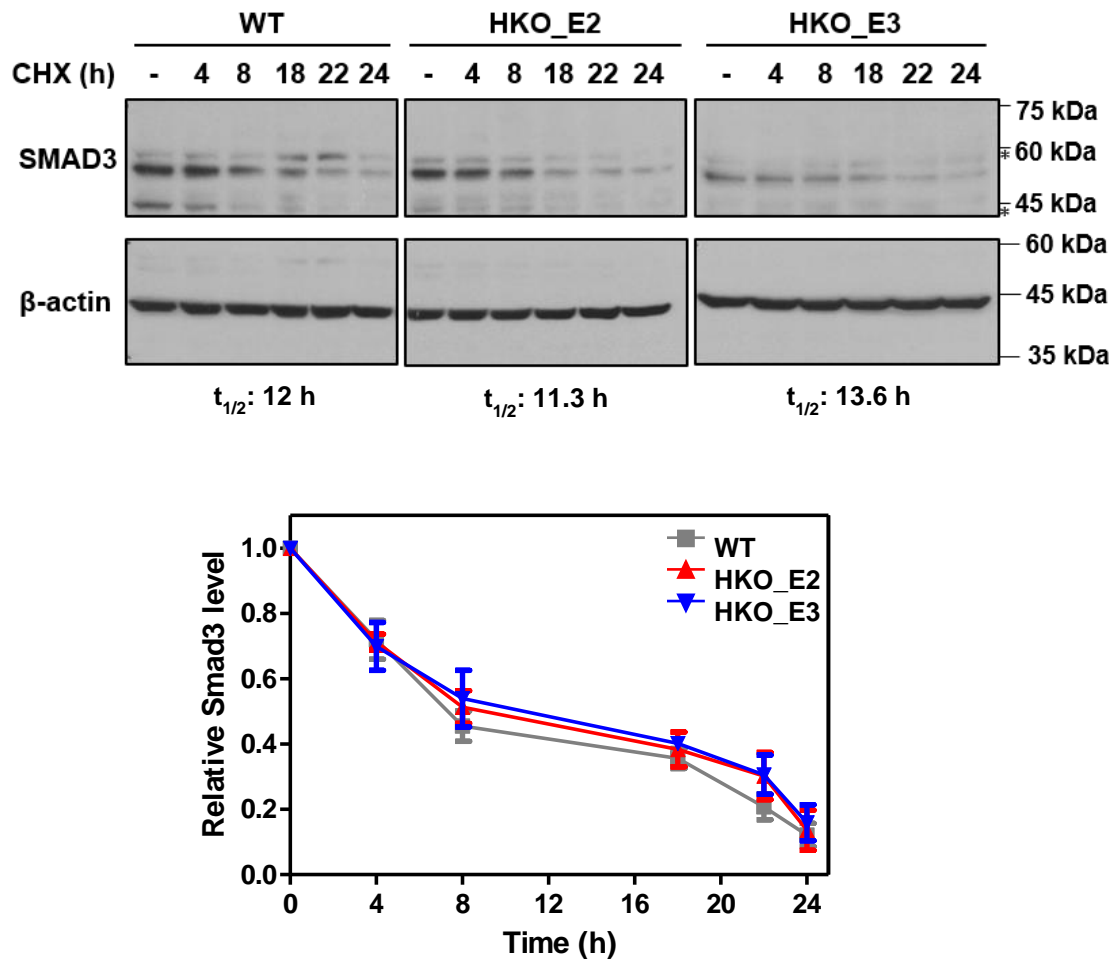


Figure S4. USP7 inactivation has no effects on the SMAD3 protein stability. (Upper) Representative immunoblots showing the stability of SMAD3 in wildtype or *USP7* KO H1299 lines. Cells were treated with cycloheximide (CHX, 20 μ g/mL) for indicated time (h) and cell lysates were subjected to immunoblotting assays with anti-SMAD3 antibody. β -actin as an internal control. Asterisks denote non-specific signals. Calculated half-lives ($t_{1/2}$) of SMAD3 in each cell line are indicated.

(Bottom) Decay curves for SMAD3 protein in the indicated cell lines. The SMAD3 levels were quantitated by the ImageJ software and the level in the control cells (without CHX treatment) was set to 1. Mean \pm SD from 3 independent experiments.

Supplemental Table S1. Oligos used in this study

RT-qPCR

<i>SMAD2</i>	F: GCTGGCCTGATCTTCACAGT
	R: CCAGAGGCGGAAGTTCTGTT
<i>SMAD3</i>	F: GCTGTCTACCAGTTGACCCG
	R: AGGACCTTGTCAAGCCACTG
<i>SMAD4</i>	F: GGACTGCACCATACACACCT
	R: AATGGGAGGCTGGAATGCAA

ChIP-qPCR

<i>SMAD3_EN1</i>	F: AACTGCTCCAGAACTCTCAA
	R: CACATGAAGCCCAAACCTGTG
<i>SMAD3_EN4</i>	F: TCTCTCTATCGCCAACGTGA
	R: TCCTGGCAGGCCTTTCCTTA
<i>SMAD3_EN9</i>	F: GTTGCTTTCGCCTAACTGGC
	R: AGCAAAGGGATCCACAGACG
<i>SMAD3_EN10</i>	F: GGAAGCAGAGTGGTATTCAGCA
	R: TAGGCAACATGGGGAAAATGGA

For reporter construction

<i>SMAD3_EN1</i>	F: CACATGCTATCTTCACAGTGTGATCGA
	R: GACAGAAAAAGAAAATAATGTTGACTTCAGTTTGCA
<i>SMAD3_EN2</i>	F: GAATCCTGGTTTTCCAAGTGTTTAGAGG
	R: GATCAGGAGGCCTCCAGCAG
<i>SMAD3_EN3</i>	F: TGTGTGCTTGCTCTGAAGATTCCA
	R: TTGCCTCTGTGCTGCCAAG
<i>SMAD3_EN4</i>	F: TTGCCTCTGTGCTGCCAAG
	R: AAAATGATTGCTTCCTGAGGTCTGGATG
<i>SMAD3_EN5</i>	F: GGTCTCCCCTTAAATGTCATCTAAGAGAG
	R: CGCGGGAGGTGGTGG
<i>SMAD3_EN6</i>	F: CTGTTCCCCCAGACCCTG
	R: ATAGCAAGACCTCTTCTCAACAGAAAAATACAAAAA
<i>SMAD3_EN7</i>	F: AAATCAAGGAACATTGCCCCATCTCC
	R: CTCGGTAAGCACCAGCACATCT

<i>SMAD3_EN8</i>	F: CTTGGCCTGTTGGTGGTGG
	R: GAAAGAATCCAACAACCTCAGATATGCAAAATTTTACC
<i>SMAD3_EN9</i>	F: CAGTAATTCTGCAGCCTCCCTCAC
	R: CCAGTCCCAGCTGAGATTCAGA
<i>SMAD3_EN10</i>	F: TCCATAGATCTGACTCTGGAAACACCG
	R: CCTGCCTGTGATTCACAAGTGT

Fig. 1B

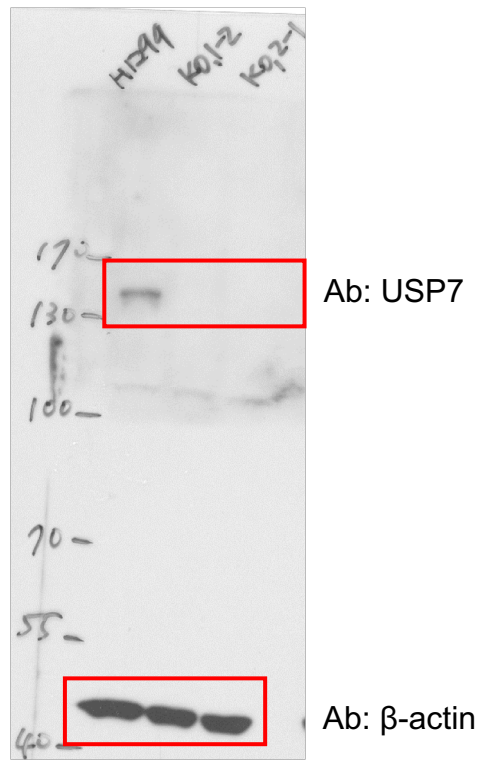


Fig. 3C

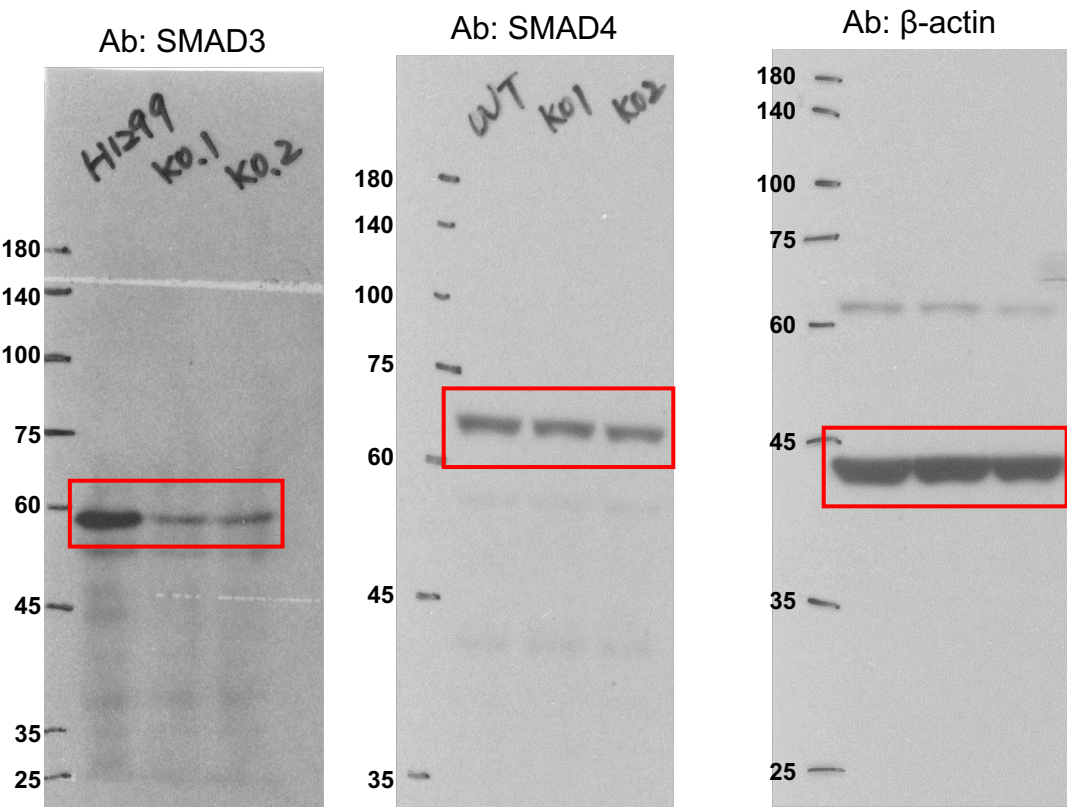
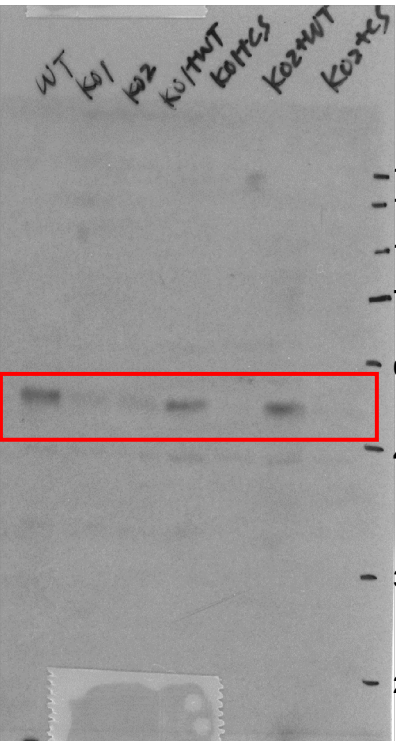
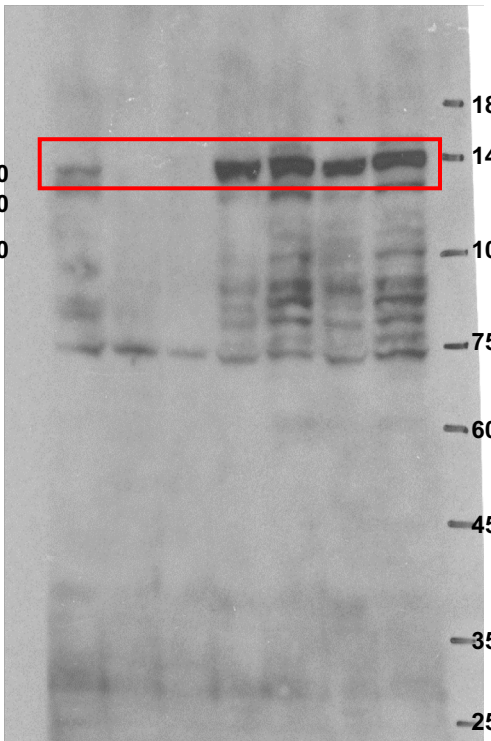


Fig. 5C

Ab: SMAD3



Ab: USP7



Ab: β -actin

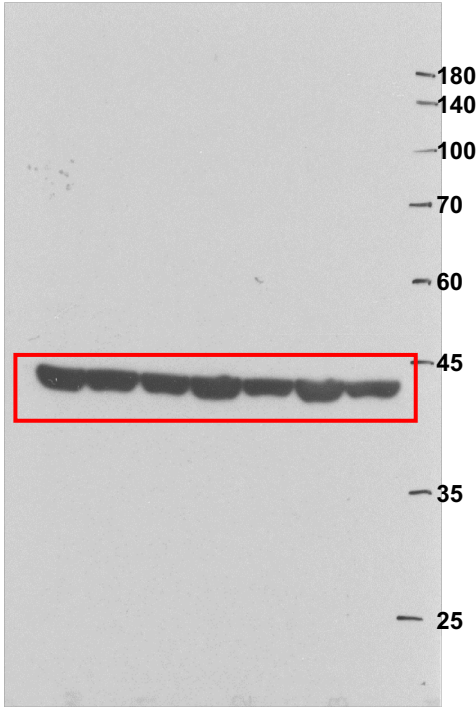
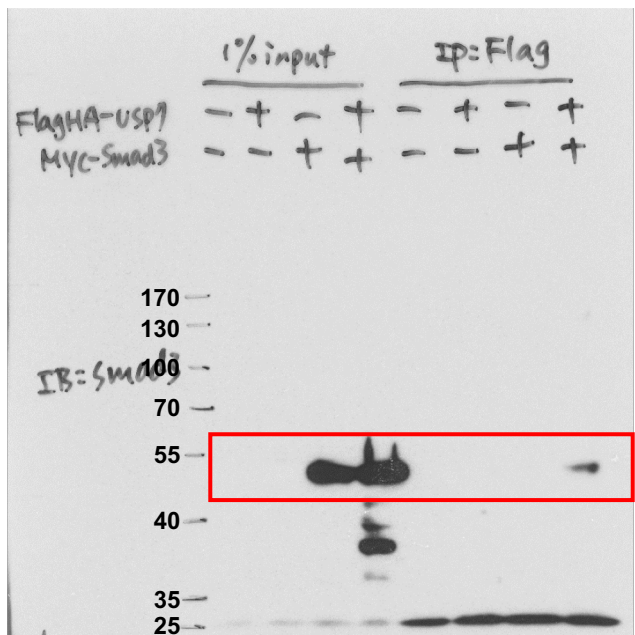
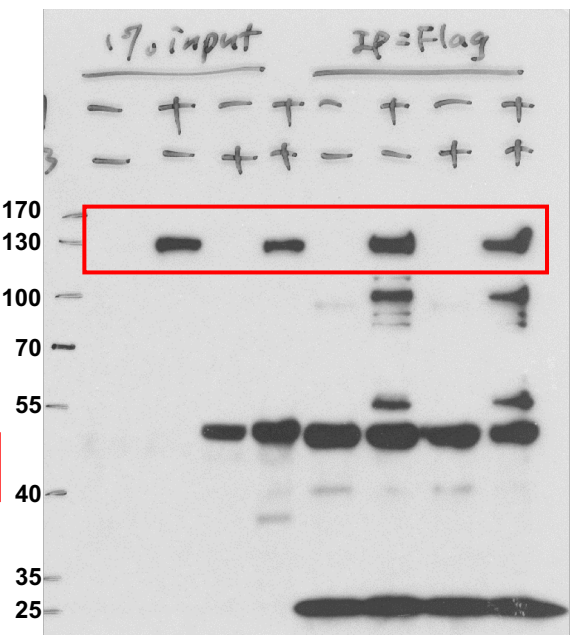


Fig. 6A

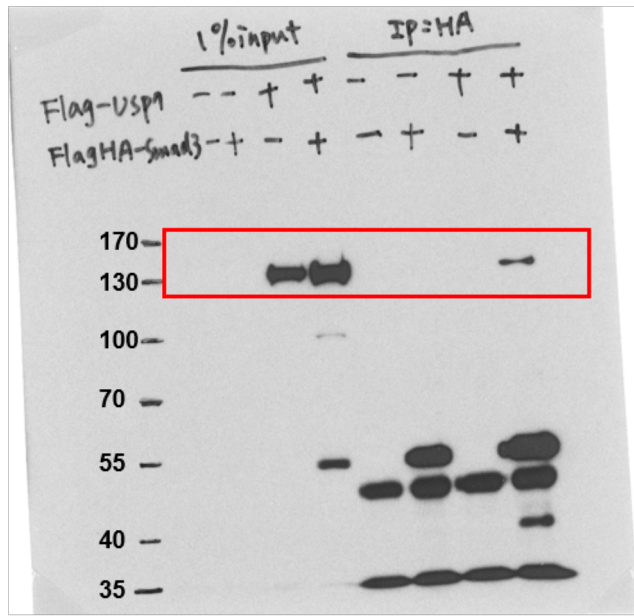
Ab: SMAD3



Ab: USP7



Ab: USP7



Ab: SMAD3

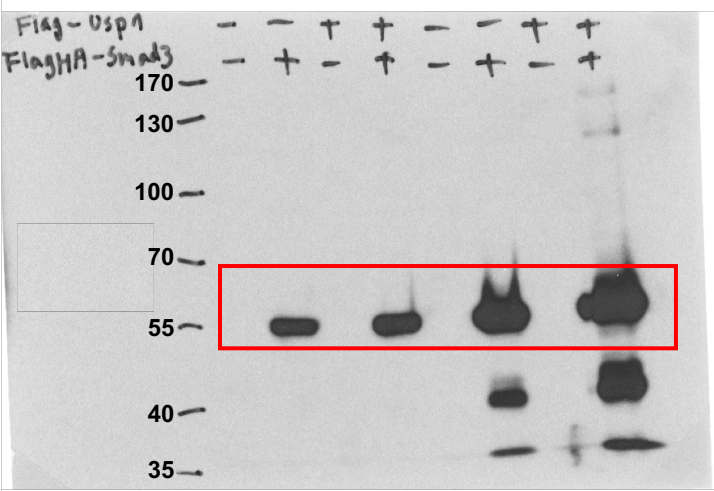


Fig. 6B

Ab: Myc

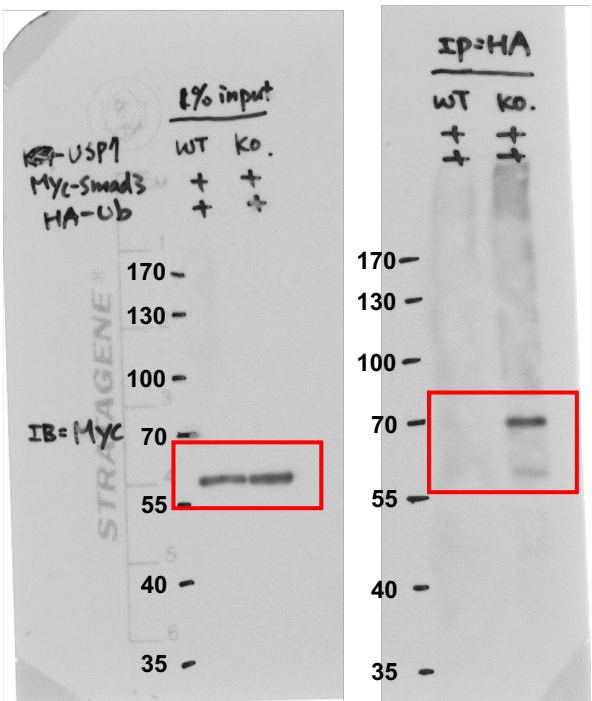


Fig. 6C

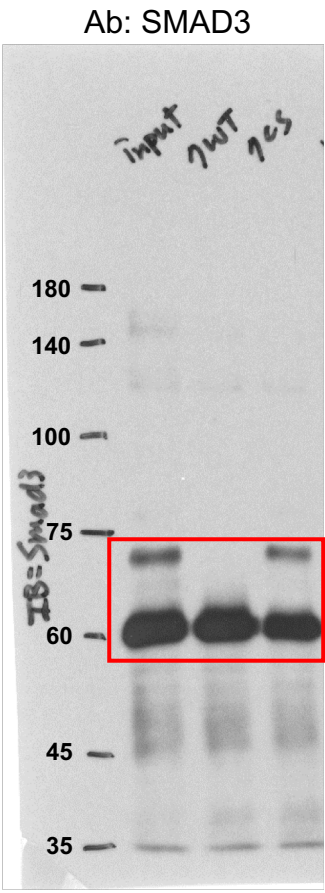


Fig. 7B

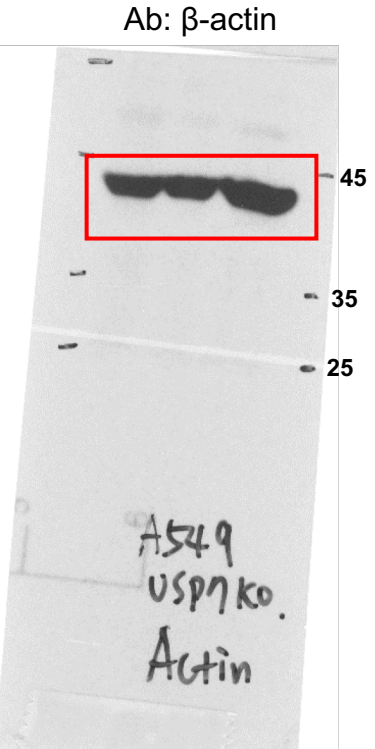
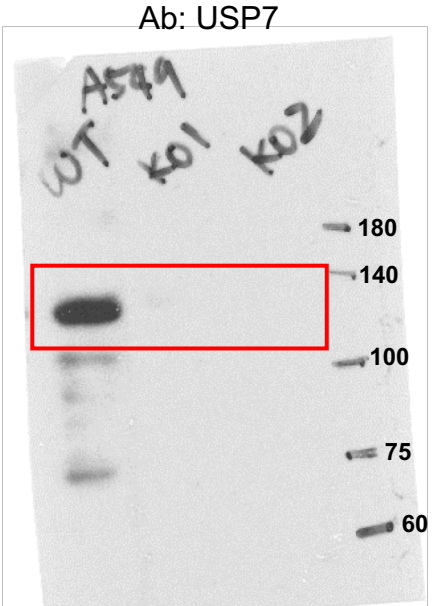
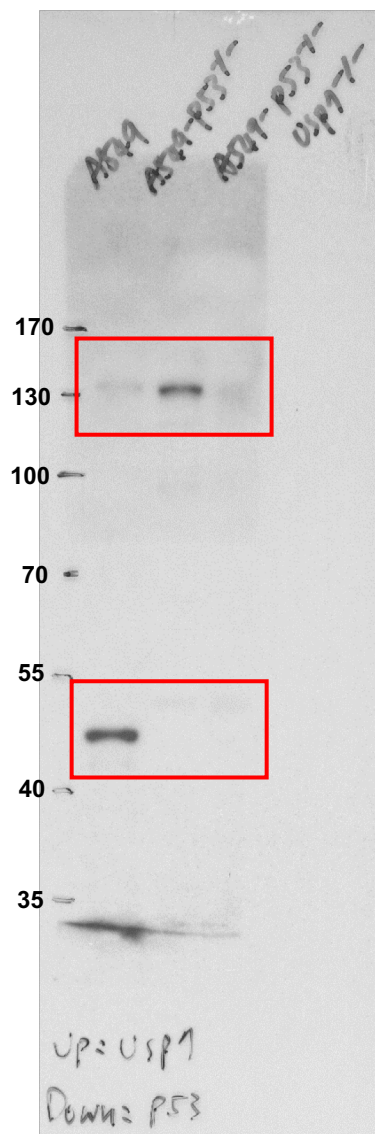


Fig. 7G

Ab: USP7
p53



Ab: β -actin

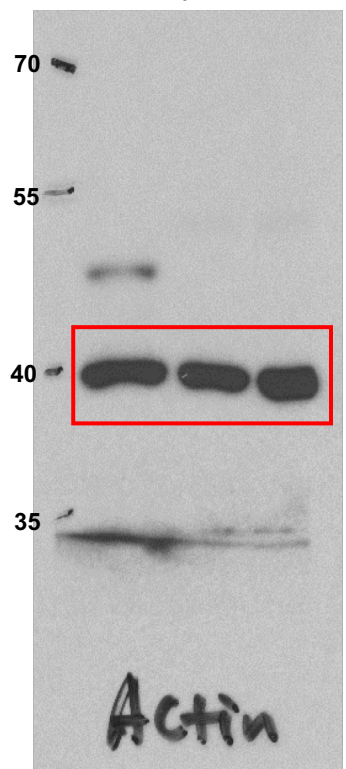


Figure S1

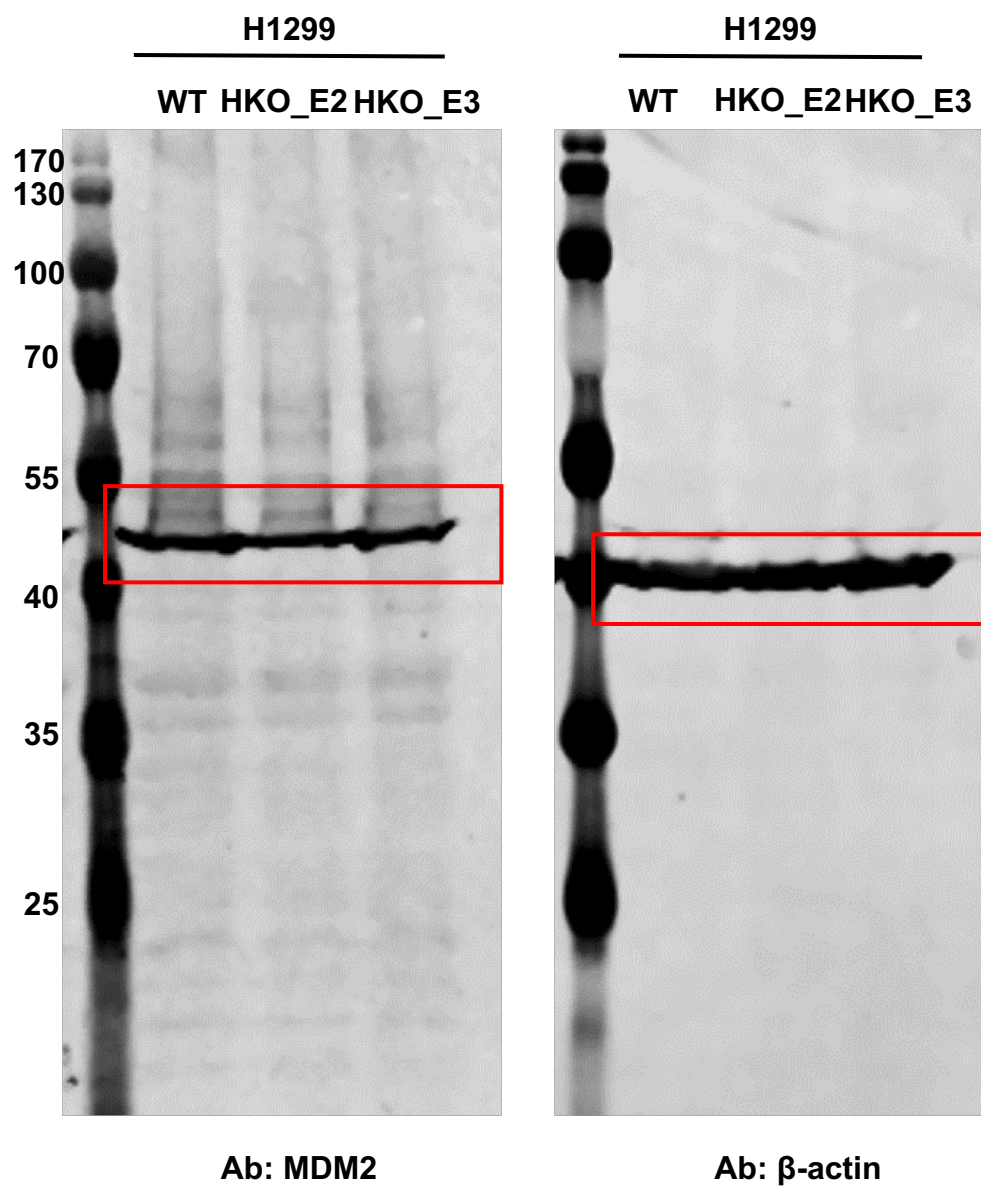
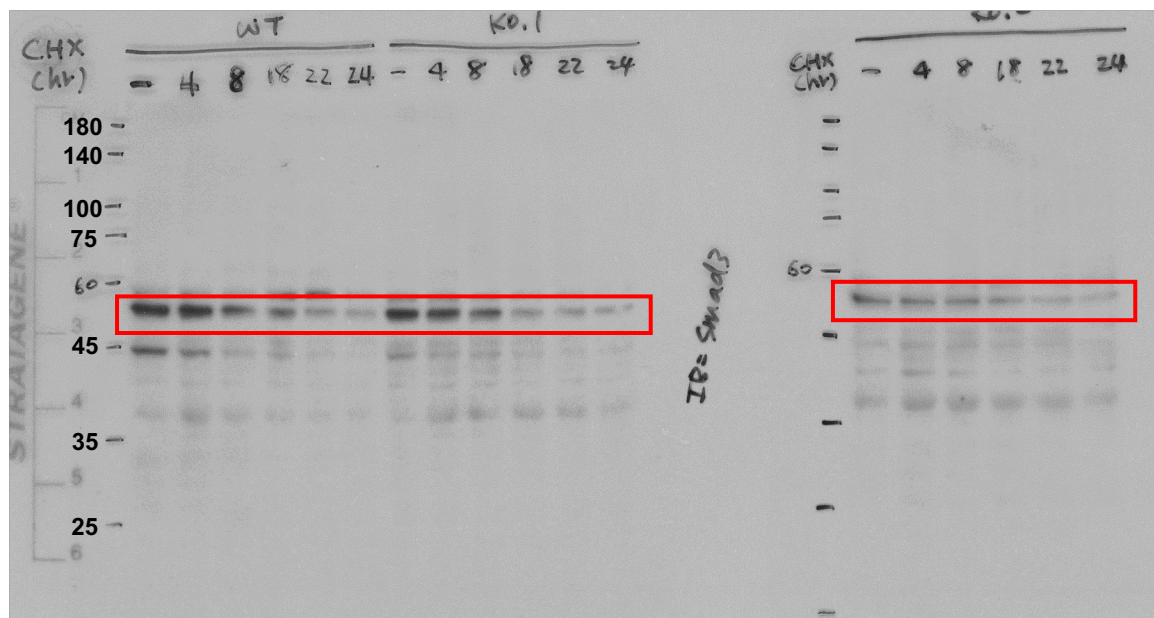


Figure S3

Ab: SMAD3



Ab: β -actin

