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Appendix Table S1

Primers used for q-RT PCR	
TRINGS	FW:GGACAAGTATGCACTGCCCT
	RV:AAGAACGCATGAGCTGGTGA
Actin	FW:CTGTCCCTGTATGCCTCTG
	RV:ATGTCACGCACGATTTCC
U1	FW:GGGAGATACCATGATCACGAAGGT
	RV:CCACAAATTATGCAGTCGAGTTTCCC
STRAP	FW:GGCATCACGCCTTATGGGTA
	RV:CAGTGTTGCACCCCAAACAG
lncRNA-1	FW:CTCCCAGCCAGGAAGAAAGT
	RV:TCTTGGCCTCATTCCAAGTC
lncRNA-2	FW:CAGCACGTGGAGACAGTCAA
	RV:GCATGCGCTGATTGGTCTTG
lncRNA-3	FW:CGGAGCAGTCTGTGTCAAAA
	RV:TCTCCTCCCCGTGACAATAC
lncRNA-4	FW:AGAGATTTTCCAGGCCAAGC
	RV:TTGGATGGTTCTGTGGGTCT
lncRNA-5	FW:AGCCACTCTACTTGGCCTGA
	RV:GTAGGTCCCAGCGTGTCTGT
lncRNA-6	FW:ATTCTACCATGTCGGCATCCA
	RV:TCGGGATTCTCCTGTACCTCT
lncRNA-7	FW:CGTGGCCTACCTTGTCAGTT
	RV:CAGACCCAATGCCCTCAGTT
lncRNA-8	FW:GAAAGTGGTGAGCCAACGAT
	RV:GGCCTGAAAAACTGTTGCAT

lncRNA-9	FW:GGACAAGTATGCACTGCCCT
	RV:AAGAACGCATGAGCTGGTGA
lncRNA-10	FW:GGGTAGGTATTCACCTGCACT
	RV:TGTGCTGTTCCTGCACTTCA
Primers used for CHIP	
TRINGS	FW:TTATGGTTAAGGGAACAAAT
	RV:TAAAGCAAAATTAGGAATGCCTTT
Actin	FW:TCGATATCCACGTGACATCCA
	RV:GCAGCATTTTTTTACCCCCTC
p21	FW:CTGTCCTCCCCGAGGTCA
	RV:ACATCTCAGGCTGCTCAGAGTCT
Oligonucleotide sequence of shRNAs	
shTRINGS-1	GCACTGCCCTACTTACCTACT
shTRINGS-2	AACCAGGTAGTCGTACAGTGT
shSTRAP	GTCTGTTAGTAGTATGGAATA
shp53	GACTCCAGTGGTAATCTAC
shGSK3β	CCCAAATGTCAAACTACCAAA
Oligonucleotide sequence of DNA Probes for Biotin-pulldown	
sense	CCGAGAGACTCACCAAAGACATGAAGAGAA
Anti-sense	TTCTCTTCATGTCTTTGGTGAGTCTCTCGG
Oligonucleotide sequence of single-guide RNA	
sgRNA-1	TACTAAACAGACCCAGACTT
sgRNA-2	ATCTGGACACTCCCAAGTCT

Appendix Figure S1

(A) H1299 cells carrying a p53 tet-on system were treated with DMSO (Dox-) or doxycycline (Dox+, 1ug/ml) for indicated times. Total RNA were analyzed for evaluating indicated lncRNAs expression by real-time RT-PCR using primers against indicated lncRNAs.

(B) U2OS cells were incubated with 2.5 mM glucose starvation medium for 0 h, 12 h or 24 h, and total RNA was then isolated for measuring indicated lncRNAs by real-time RT-PCR.

(C) Schematic illustration of the intron-exon structure of *trings* on chromosome 4. Its corresponding nucleotide sequences are shown in the same color.

(D) Genomic location of TRINGS was shown in the ideogram of chromosome 4, and the genomic tracks with its neighborhood were also represented. Evolutionary conservation of TRINGS was illustrated using multiple alignments with phastCons and phyloP tracks of genome browser. Annotations were taken from UCSC genome browser.

Appendix Figure S2

(A) p53 dependent expression of TRINGS in different types of tumors as compared with mutant p53 in TCGA datasets, the information was extracted and plotted through TANRIC database.

(B-D) U2OS cells were incubated with DMEM medium deprived of FBS (A), Serine (B) or Glutamine (C) for indicated times. Total RNAs were isolated from cells exposed to indicate nutritional stresses and levels of TRINGS were determined by real-time RT-PCR, and cell lysates were analyzed by Western blotting with anti-p53 or anti-Actin antibodies.

(E)H1299 cells (without p53) were cultured under glucose starvation (2.5mM glucose) for the indicated time points. The cells were harvested for total RNA extraction subsequently analyzed by real time RT-PCR.

Appendix Figure S3

(A-E) Control or p53 knockdown U87cells (A), Mel-CV cells (B), SMCC7721 cells (C), IMR90 cells (D) or MCF10A cells (E) were incubated with 2.5 mM glucose starvation medium for indicated time periods. Total RNA were analyzed by real-time RT-PCR to examine RNA level of TRINGS. Cell lysates were used to access p53 expression by Western blotting using anti-p53 antibody.

(F) Control shRNA (shctrl) or TRINGS knockdown (shTRINGS-1) U2OS cells were harvested for total RNA extraction, subsequently indicated lncRNAs expression level was measured by real time RT-PCR. Data shown are mean ± SD (n=3).

Appendix Figure S4

(A-C) Fluorescence microscopy images of control or TRINGS knockdown U87 cells (A), Mel-CV cells (B) or SMCC7721 (C) cells incubated with 2.5 mM glucose starvation medium for indicated times and followed by double staining with PI and Hochest 33342.

(D) U2OS cells were treated with 1mM H_2O_2 indicated time. The total RNA was analyzed for TRINGS expression by real time RT PCR. Data shown are mean ± SD (n=3). Cell lysates were also analyzed by Western blotting with anti-p53 and anti-Actin antibodies.

(E) U2OS cells containing control shRNA (shctrl), shTRINGS-1 or shTRINGS-2 were cultured in DMEM medium with 1mM H_2O_2 for 12 h. Cells were then stained with PI and Hochest33342 and visualized by fluorescent microscope.

(F) U2OS cells infected with control shRNA (shctrl), shTRINGS-1 or shTRINGS-1 plus shSTRAP were incubated in DMEM medium with 1mM H_2O_2 for 12 h. Cells were then stained with PI and Hochest33342, and visualized by fluorescent microscope. PI positive cells were counted from 300 Hochest33342 positive cells. Bars represent means ± SD of three independent experiments. Cell lysates were analyzed by Western blotting using anti-STRAP or anti-Actin antibody. (***, $p < 0.001$; error bars are ± S.E.).

(G) Control shRNA (shctrl) or shTRINGS U2OS cells were incubated with 2.5 mM glucose starvation medium with or without 5μM CHIR98014 (inhibitor of GSK3β activity) for 32 h. Cells were then stained with PI and Hochest33342, and visualized

by fluorescent microscope. PI positive cells were counted in 300 Hochest 33342 positive cells and plotted. Bars represent means ± SD of three independent experiments. (***, $p < 0.001$).

Appendix Figure S5

(A) Control shRNA (shctrl), shTRINGS-1 or shTRINGS-2 U2OS cells were incubated under normal condition, growth curves of cells were measured for the indicated periods of time. Data shown are mean ± SD (n=3).

(B) 10^3 shctrl, shTRINGS-1 or shTRINGS-2 U2OS cells were seeded into soft agar for each well of 6-well plate. Two weeks later, cells were subjected to crystal violet staining and photographs were taken.

(C) $2x10^6$ shctrl or shTRINGS-1 U2OS cells were then injected subcutaneously into nude mice (n = 8 for each group). Representative photographs of xenografts were taken 2 weeks after injection.

(D) Lysates from HCT116 cells expressing Flag or Flag-STRAP and Flag-STRAP mutants as indicated were used for coimmunoprecipitation (co-IP) using anti-Flag resin. Eluted products were used for examining TRINGS and STRAP by real-time RT-PCR and Western blotting analysis respectively.

Appendix Figure S6

(A) The distribution of strap was detected by western blot. H2A and GAPDH were used as markers for nucleus and cytosol, respectively.

(B)Control, p53 knockdown (shp53) or p53 overexpressed (Flag-p53) U2OS cells were harvested, and cell lysates were analyzed by Western blotting using indicated antibodies.

(C) Control or p53 knockdown U2OS cells were treated with 50μg/ml of cycloheximide (CHX) for indicated times. Subsequently cell lysates were analyzed by western blotting with anti-p53, anti-STRAP and anti-Actin antibodies. Total RNA was analyzed by real-time RT-PCR analysis for TRINGS expression. Data shown are mean ±SD (n=3).

(D) Control or p53 overexpression U2OS cells were treated with 50μg/ml of cycloheximide (CHX) for indicated times. Subsequently cell lysates were analyzed by western blotting with anti-p53, anti-STRAP and anti-Actin antibodies. Total RNA was analyzed by real-time RT-PCR analysis for TRINGS expression. Data shown are mean ±SD (n=3).

(E) Control shRNA (shctrl) or TRINGS knockdown U2OS cells were transfected with control vector or Flag-STRAP separately. 24 h after transfection, cell lysates were used for co-immunoprecipitation assay with anti-Flag coupled resin. The input and co-immunoprecipitates were analyzed by Western blotting using anti-Flag or anti-GSK3β antibodies. The intensity of STRAP-binding GSK3β bands was quantified by densitometry analysis.

(F) U2OS cells under normal condition or glucose starvation were harvested, and the cell lysates were used for co-immunoprecipitation assay with anti-GSK3β antibody. The input and co-immunoprecipitates were analyzed by Western blotting using anti-STRAP or anti-GSK3β antibodies. The intensity of GSK3β-binding STRAP bands were quantified by densitometry analysis.

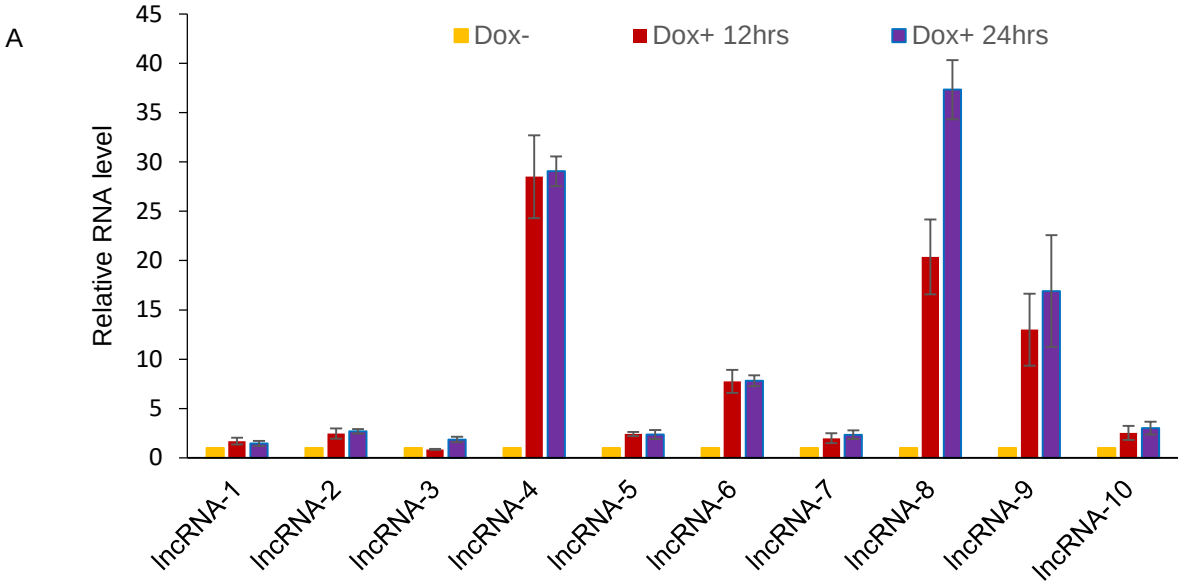
(G) Lysates from U2OS cells under normal condition or glucose starvation were used for co-immunoprecipitation (co-IP) using lgG or anti-STRAP antibody. Eluted products were used for assessing TRINGS and STRAP by real-time RT-PCR and Western blotting analysis respectively.

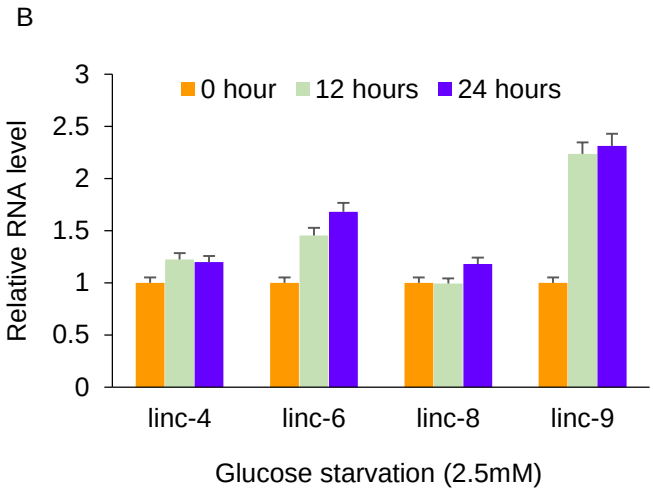
Appendix Figure S7

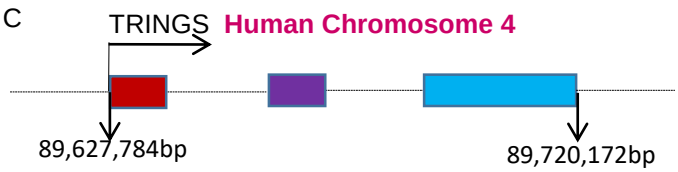
(A) U2OS cells expressing control shRNA (shctrl) or shTRINGS-1,-2 were treated with Doxorubicin (1μg/ml), Nutlin-3 (Mdm2 inhibitor) (20μM) or glucose starvation (2.5mM, 32h) individually, and the cell lysates were assayed by Western blotting using antibodies against PARP, p53 and Actin.

(B) U2OS cells were treated with DMSO (control), Doxorubicin (1μg/ml), Nutlin-3 (20μM) or glucose starvation (2.5mM, 32h), and the levels of TRINGS were measured by real time RT-PCR. Cell lysates were used for monitoring p53 activation by Western blot analysis.

Appendix Figure S1







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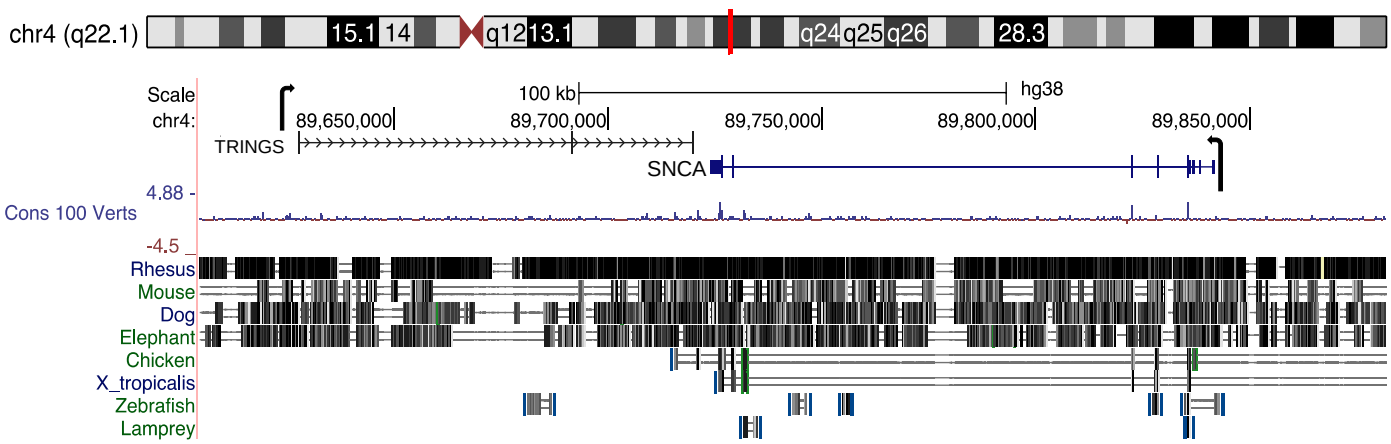
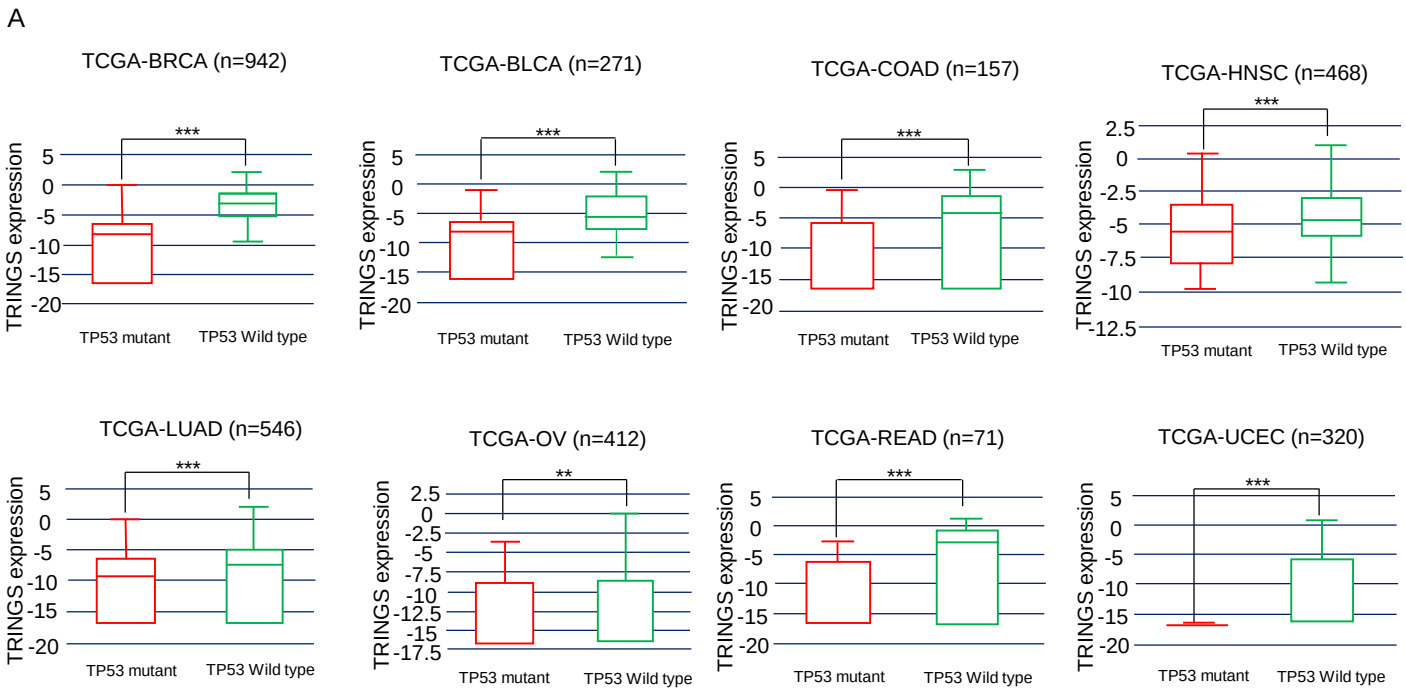
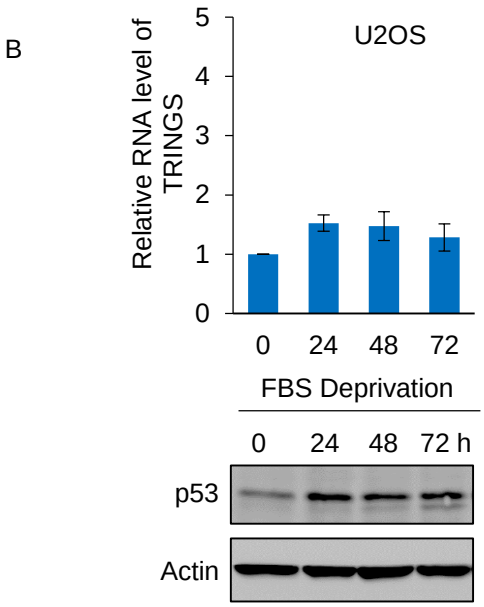
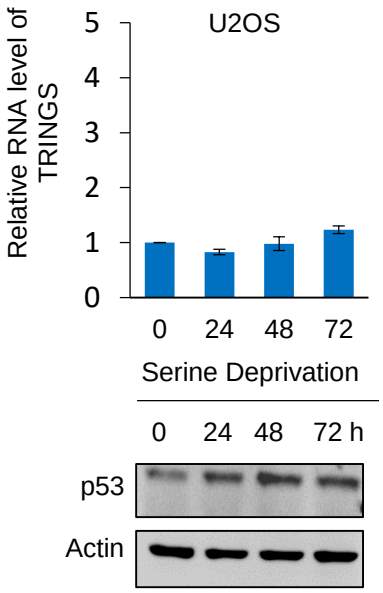
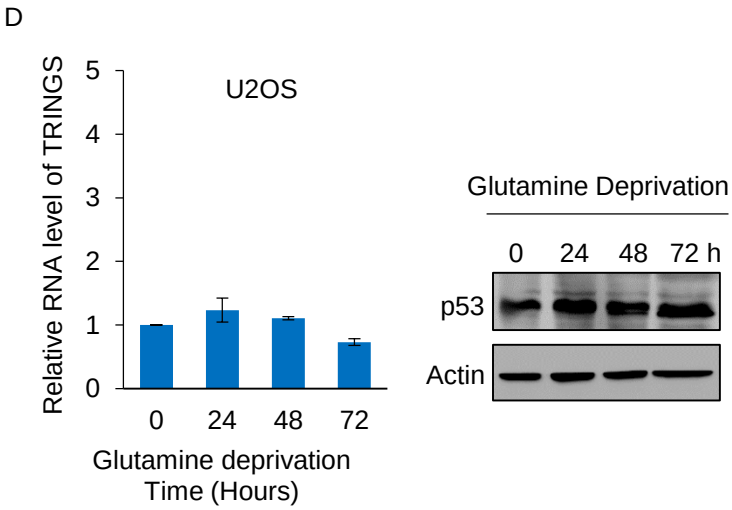


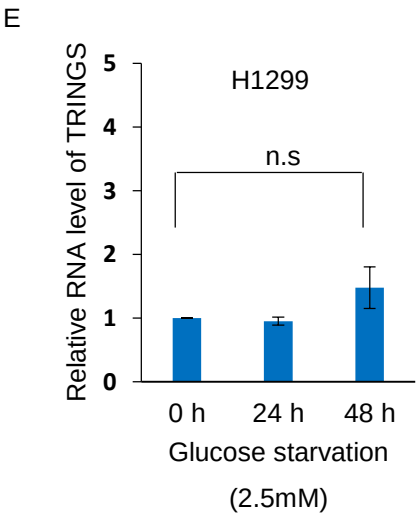
Appendix Figure S2



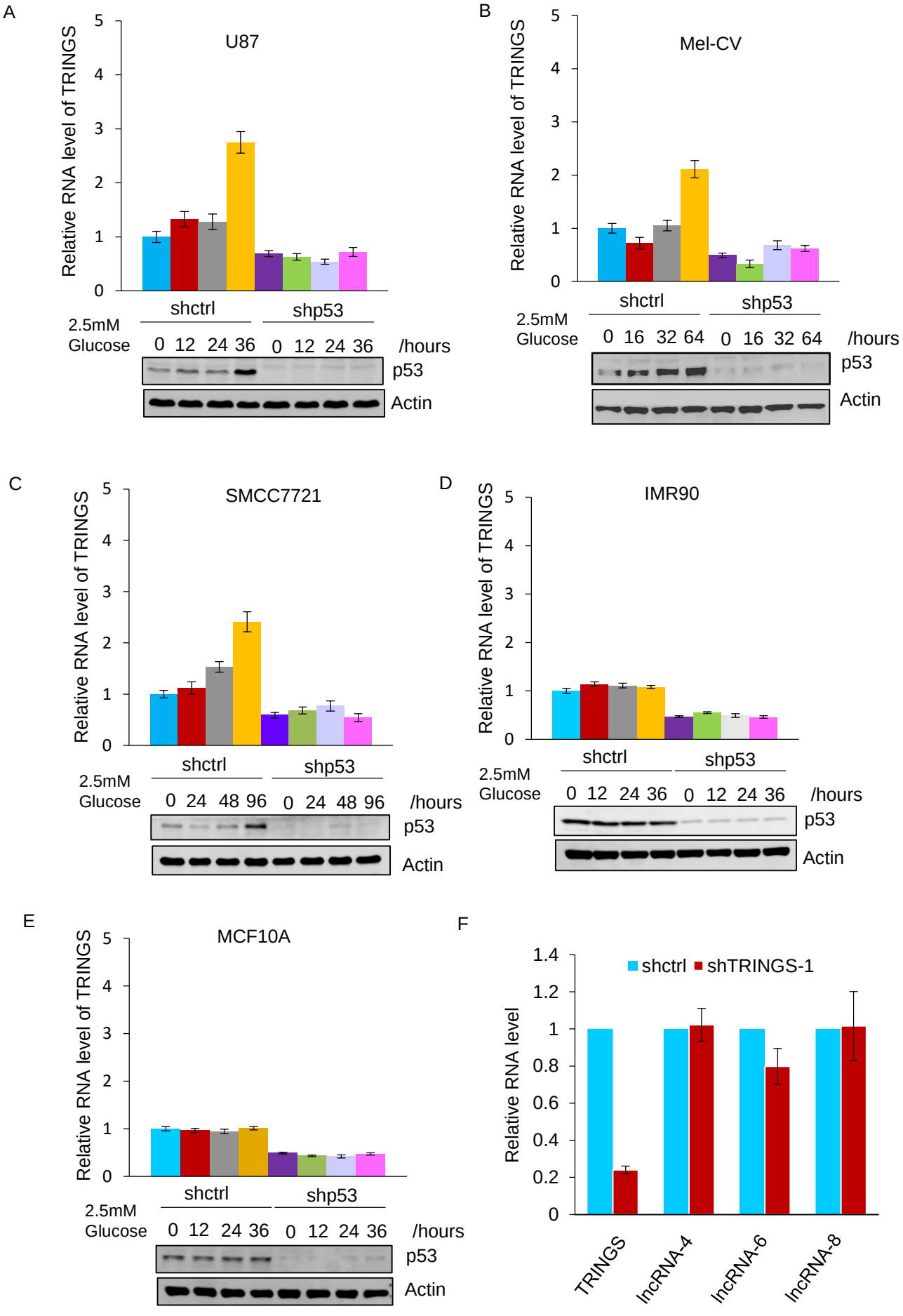




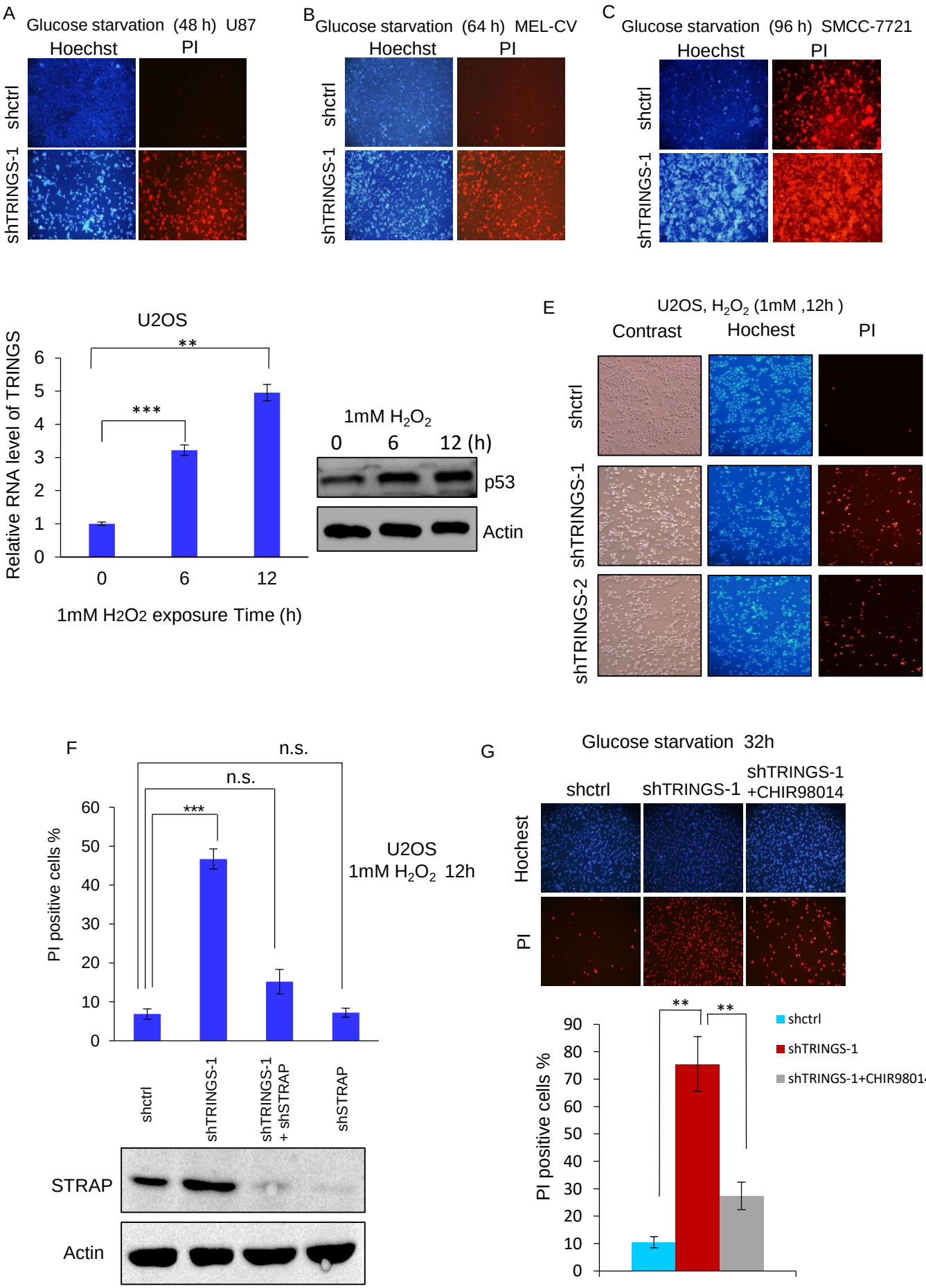




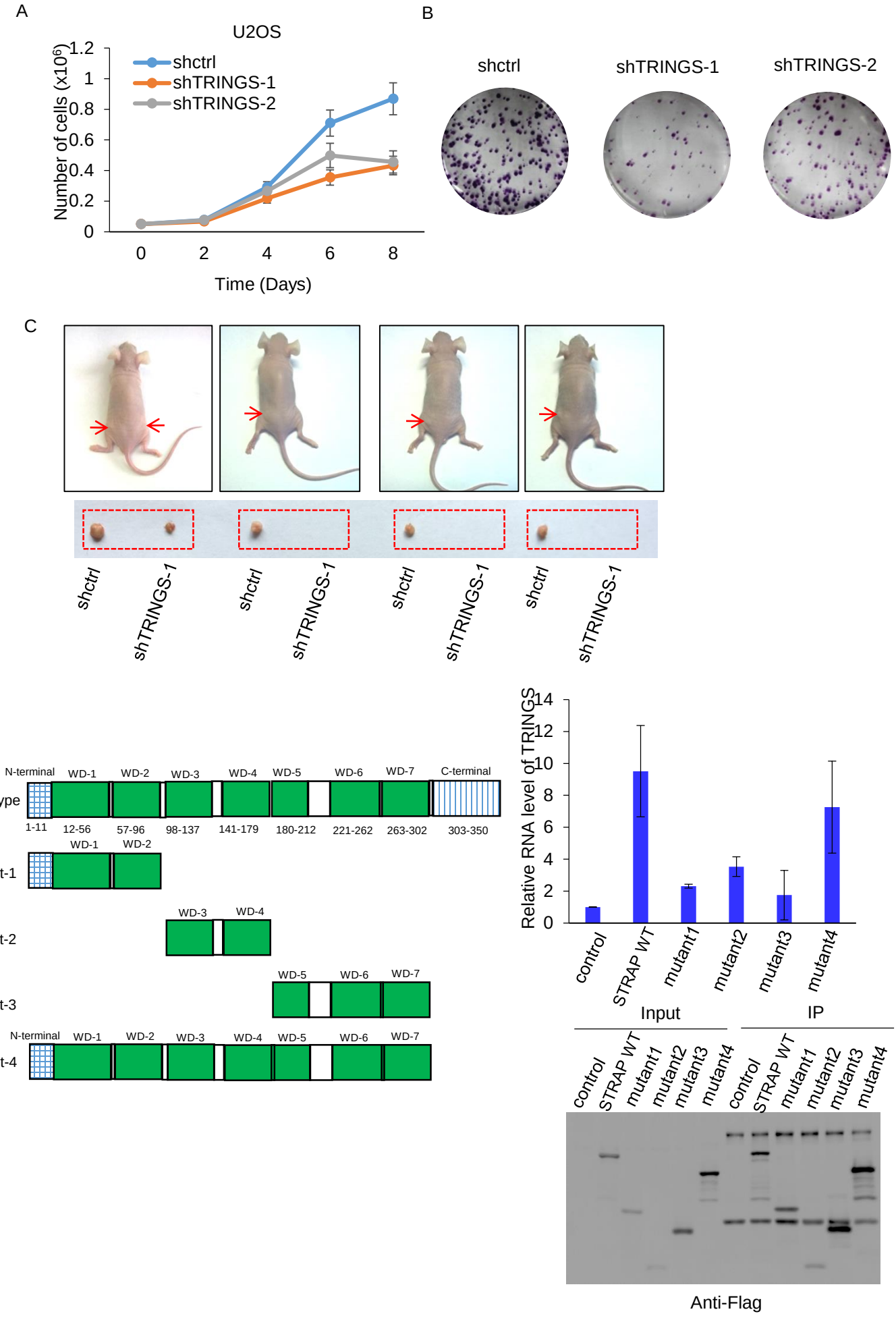
Appendix Figure S3



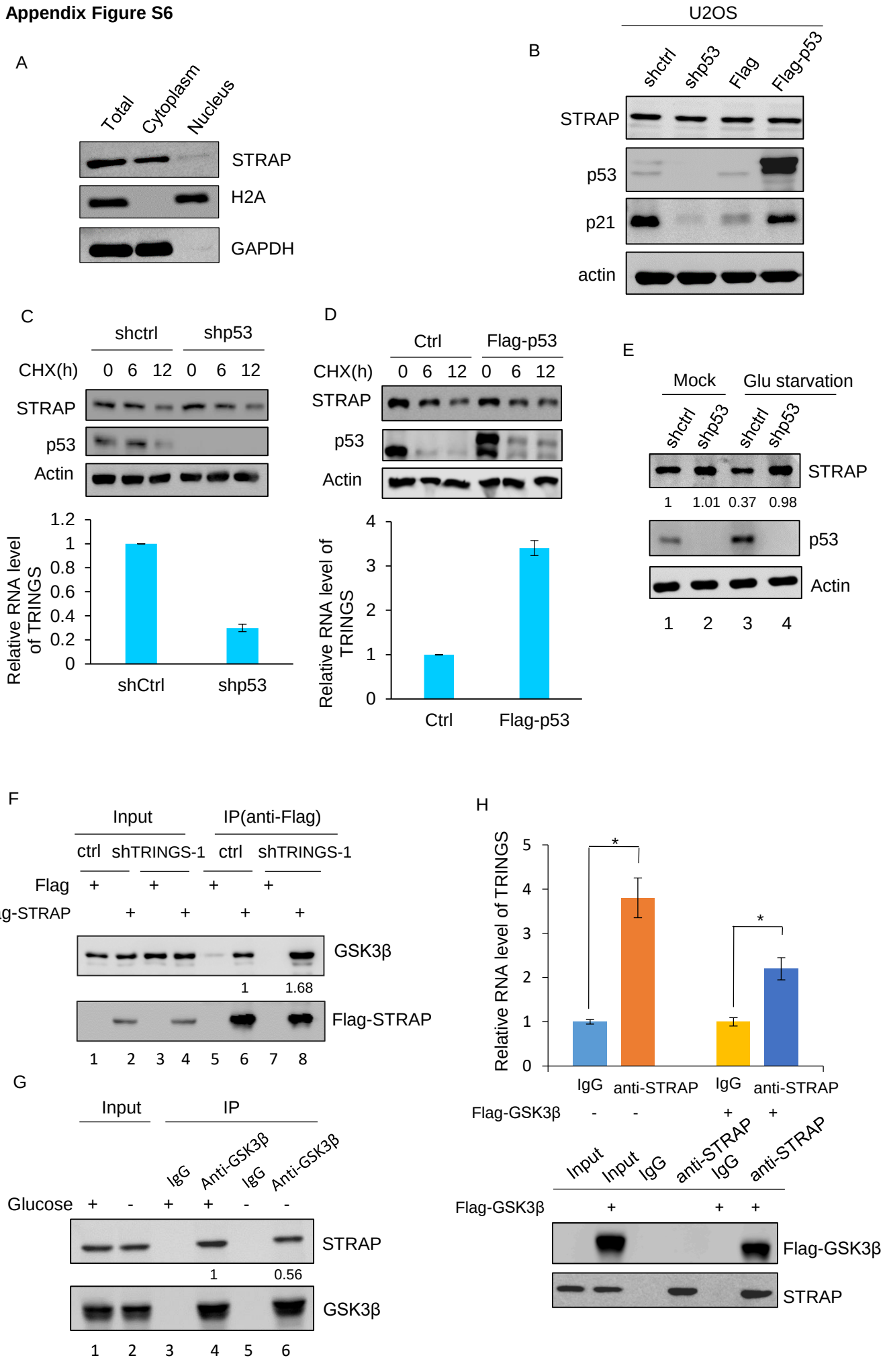
Appendix Figure S4



Appendix Figure S5



Appendix Figure S6



Appendix Figure S7