

SUPPLEMENTARY FIGURE TITLES AND LEGENDS for

Rogers et. al., *Biomolecules*

“Cell type specific suppression of hyper-recombination by human RAD18 is linked to PCNA K164 ubiquitination.”

Figure S1. Loss of MLH1 expression does not increase SCEs in hTERT RPE-1 cell lines.

(A) Western blot analysis confirming loss of MLH1 expression in two independent RPE-1 *MLH1*^{-/-} clones and two independent *RAD18*^{-/-}/*MLH1*^{-/-} clones, with β -actin as the loading control. The asterisk indicates a nonspecific band recognized by the anti-RAD18 antibody. Quantification is based on densitometry using FIJI normalized to the loading control and WT lane, minus signal from the nonspecific RAD18 band.

(B) Average number of SCEs per chromosome in RPE-1 MLH1-proficient and -deficient cell lines. Black lines indicate mean values and significance was calculated using a Mann-Whitney test. No comparisons were statistically significant.

(C) Original western blot images related to Figure S1A.

Figure S2. Original western blot images related to Figure 1.

(A) Original western blot images related to Figure 1A.

(B) Original western blot images related to Figure 1B.

(C) Original western blot images related to Figure 1C.

(D) Original western blot images related to Figure 1I.

Figure S3. Original western blot images related to Figure 3.

Figure S4. Generation and characterization of HCT116 *PCNA*^{K164R/+} mutant cell lines.

(A) Sanger sequencing trace files from HCT116 *PCNA*^{K164R/+} cell lines. The dotted red box indicates the codon for the K164 residue. The dotted orange or pink boxes indicate the sequences for the diagnostic EcoRI or XcmI restriction enzyme recognition sites, respectively.

(B) (Left) Schematic of *PCNA* in HCT116 *PCNA*^{K164R/+} cells indicating that exon 2 was targeted by CRISPR-Cas9. The locations of the Cas9 cut site and primers used are indicated. Allele-specific frameshift mutations were determined by TOPO-TA cloning followed by Sanger sequencing of PCR amplicons. (Right) Table summarizing results of TOPO-TA cloning and sequencing analyses.

(C) Clonogenic survival of HCT116 wild-type and two *PCNA*^{K164R/+} cell lines following MMS treatment at the indicated dosages (5, 10 or 20 μ M). Error is indicated as standard deviation and significance was calculated using two-tailed students *t*-test with * > 0.05; ** > 0.01, *** > 0.001 across at least two biological replicates.

Figure S5. Original western blot and gel images related to Figure 4.

(A) Original gel image related to Figure 4B.

(B) Original western blot images related to Figure 4D.

Figure S6. Original western blot images related to Figure 5.

(A) Original western blot images related to Figure 5A.

(B) Original western blot images related to Figure 5E.

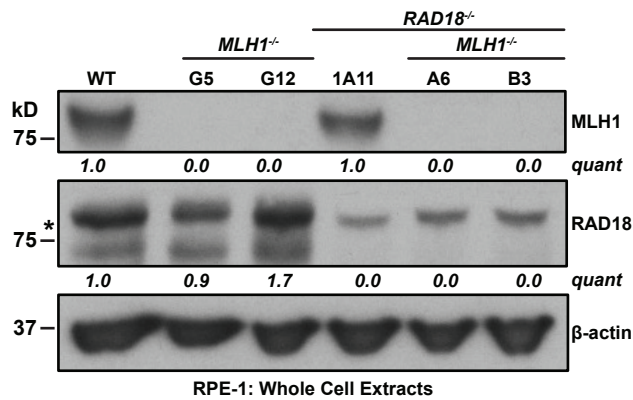
Figure S7. Expression of super-telomerase (ST) effectively lengthens telomeres in *PCNA*^{K164R/+} or reverted *PCNA*^{+/+} cell lines.

(A) Telomere restriction fragment length analyses of *PCNA*^{K164R/+} cell lines (top) or reverted *PCNA*^{+/+} cell lines (bottom) expressing ST. Yellow lines indicate the location of highest average peak intensity. Arrows indicate clones that were used for further studies.

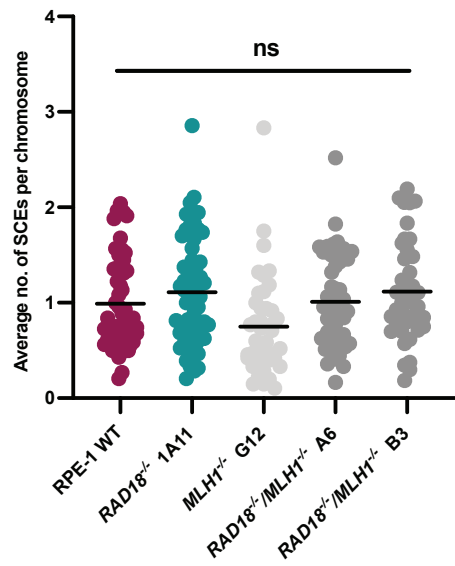
(B) Original TRF images related to Figure S7A.

Figure S1

A



B



C

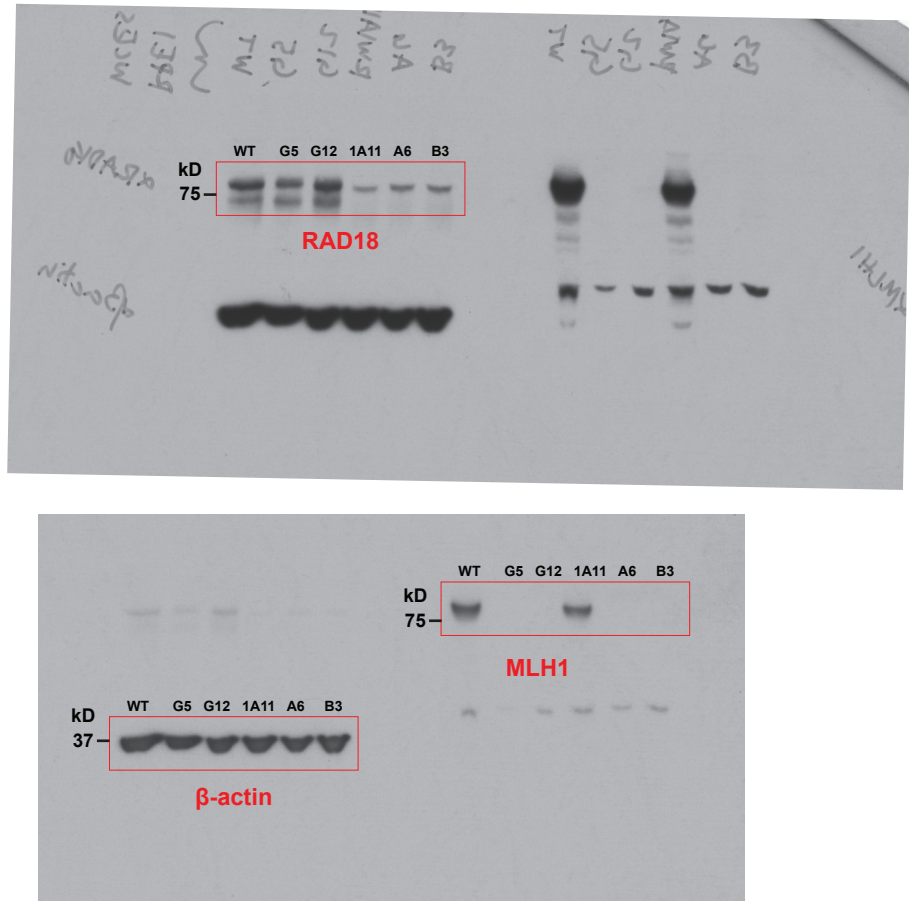


Figure S2

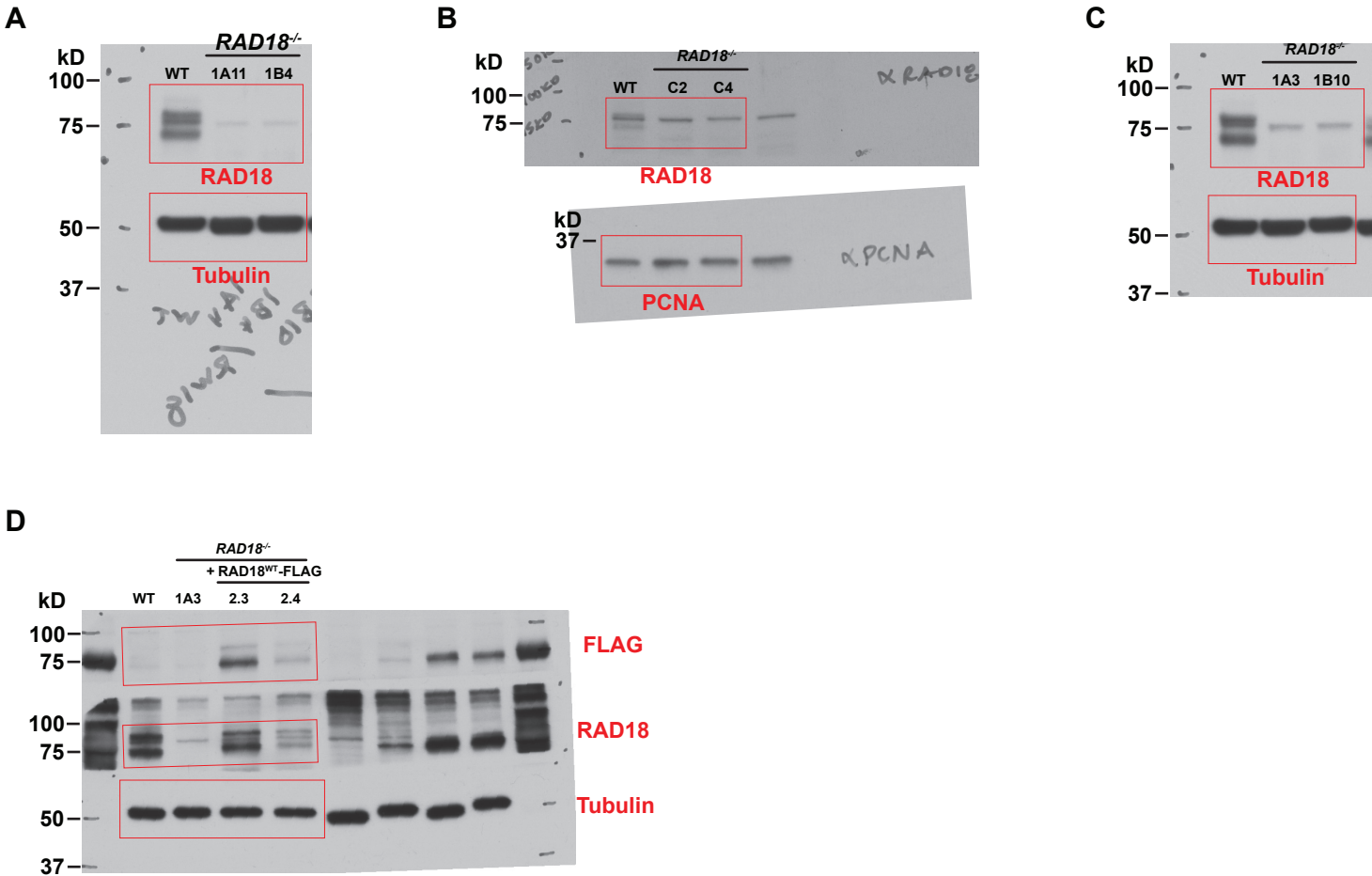


Figure S3

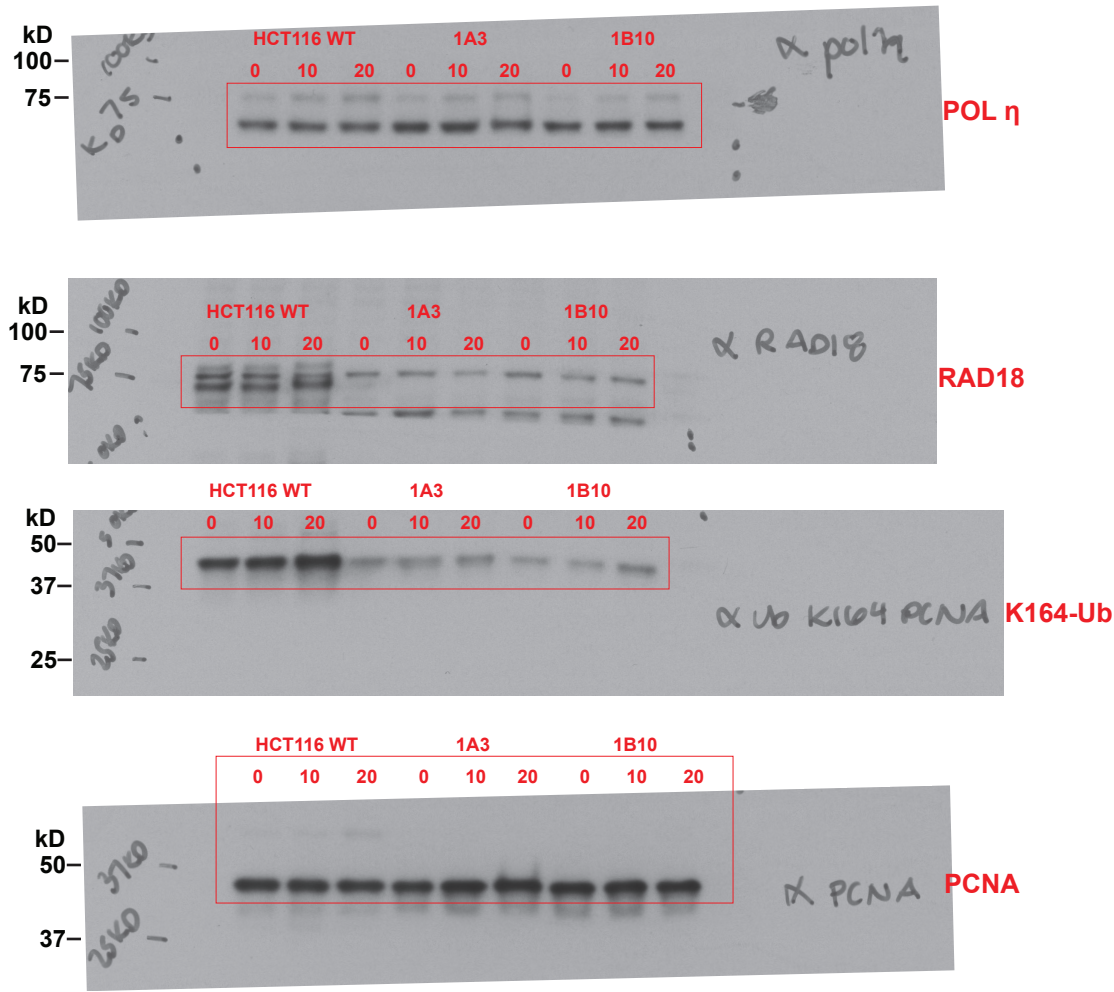


Figure S4

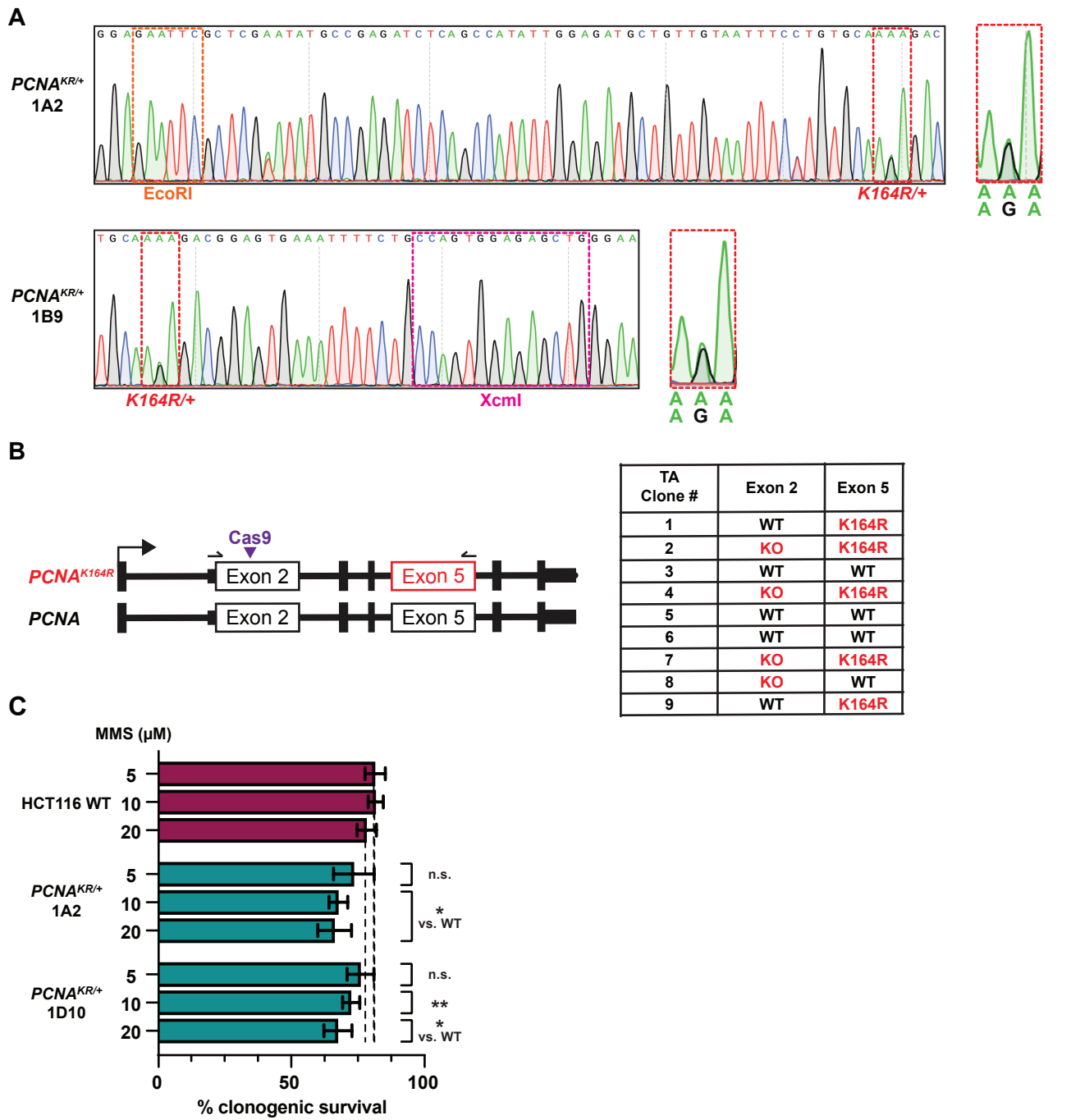
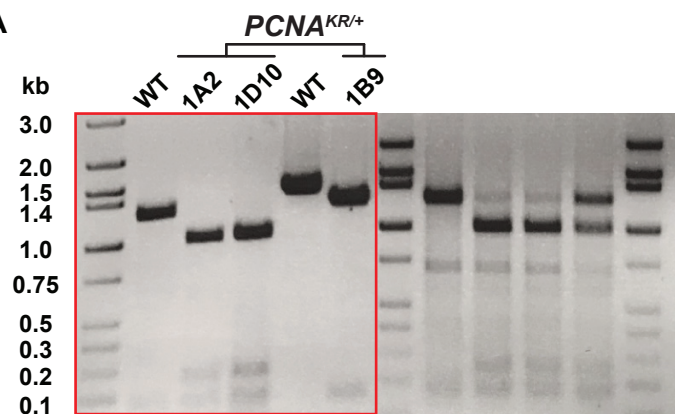


Figure S5

A



B

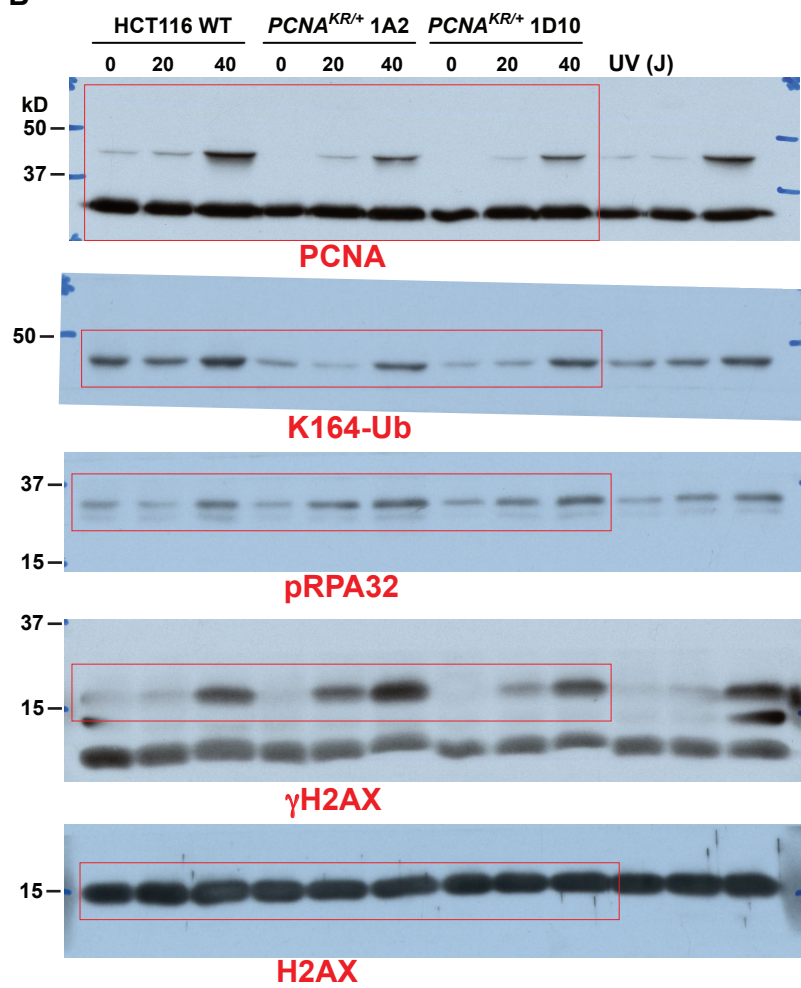


Figure S6

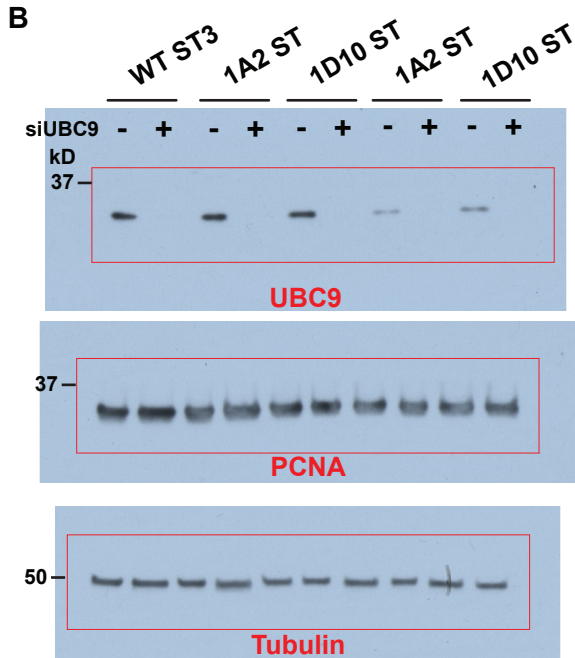
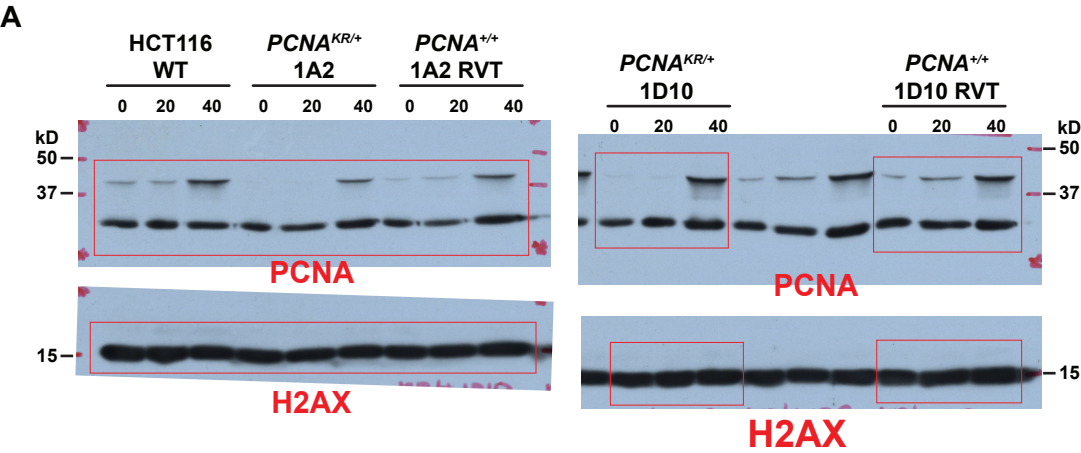


Figure S7

