CAN-10-0475 Supplementary Data
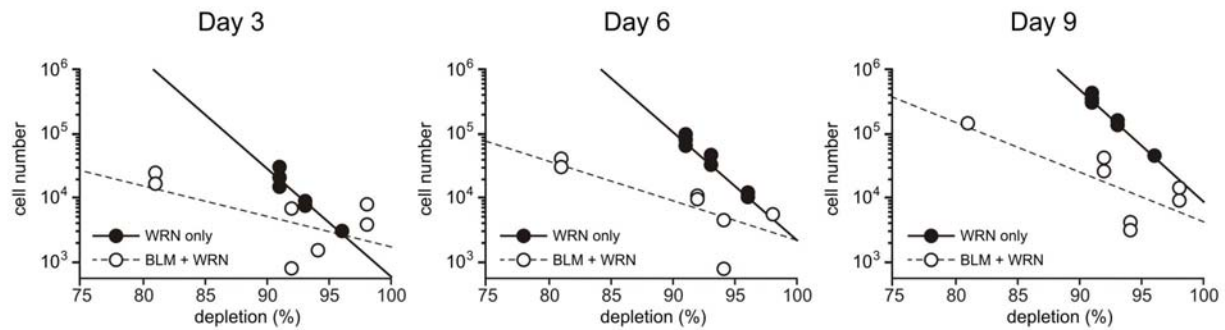
'The human WRN and BLM RecQ helicases differentially regulate cell proliferation and survival after chemotherapeutic DNA damage'

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**SUPPLEMENTARY FIG. 1. Suppression of cell proliferation in WRN and WRN/BLM-depleted GM639 cells as a function of percent depletion and time.** Plots show cell proliferation of GM639 human fibroblasts 3, 6 or 9 days after depletion of WRN or WRN/BLM. Proliferation of WRN-depleted versus WRN/BLM co-depleted cells was significantly different on all three days (p<0.01 for all days). WRN-depleted cell data are represented by open triangles in all panels (◇), and WRN/BLM co-depleted cells by '+' signs.
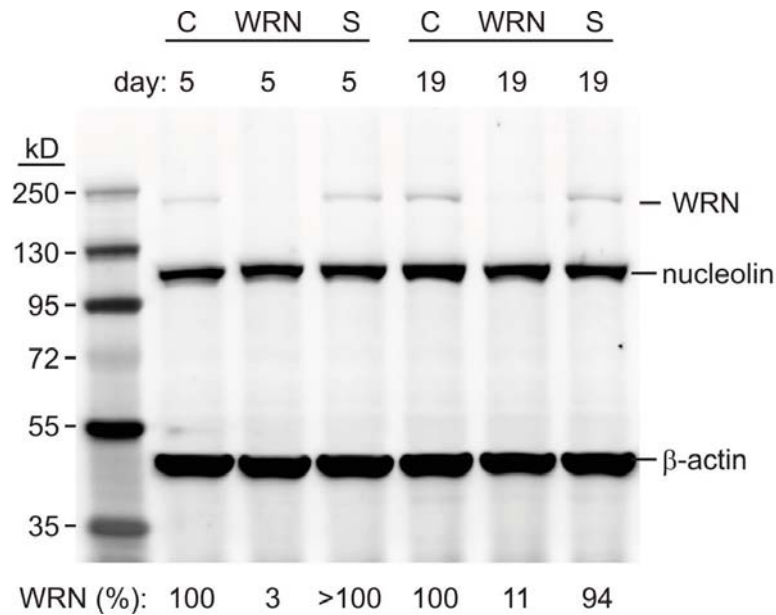
Supplementary Figure 2: Persistent shRNA-mediated depletion of WRN from human GM639 SV40 fibroblast cells. Cells were transduced with either a lentiviral control vector (C) or the same vector expressing a WRN-specific shRNA (WRN) or a scrambled shRNA (S) with no known target in the human genome. Cells were analyzed by Western blot 5,19 or 25 (not shown) days after transduction to determine the amount of WRN protein remaining versus nucleolin and β-actin controls. The data shown, from Days 5 and 19, document the persistent depletion of WRN protein over the time course of all analyses reported in our ms.

comparison samples†		difference‡	p value§
S1	S2	(S2-S1)	
C	W	2.7	0.0054*
C	B	5.9	1.8×10^{-8}*
C	WB	7.2	2.6×10^{-13}*
W	B	−3.2	0.0016*
W	W	−4.5	2.8×10^{-6}*
B	W	−1.3	0.18
C	scrambled	−1.4	0.27

SUPPLEMENTARY TABLE 1. Statistical analysis of γ-H2AX straining differences in WRN and/or BLM-depleted GM639 cells versus controls. key: †, sample pairs tested for significance: C = pLKO.1 vector-transduced; scrambled = pLKO.1 vector expressing a scrambled shRNA with no known target in the human genome; W = WRN-depleted; B = BLM-depleted; WB = WRN+BLM-depleted. ‡, average difference in fold induction between samples after adjusting for a significant linear increase in staining as a function of time ($p = 5.4 \times 10^{-6}$). This increase did not differ between controls and any treatment group (p > 0.5). §, the p value for significance after Bonferroni correction for 7 pairwise comparisons was <0.0071. Significant differences are marked with an asterisk (*).

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