

Figure S1. The rate of DNA synthesis remains relatively constant in cultures before beginning to decline at 100 minutes after the beginning of our experiment. Growing cultures were pulse-labeled with  $[^3\text{H}]$ thymidine for 2 min and the relative amount of  $^3\text{H}$  incorporated into the DNA is plotted over time. Fresh overnight cultures were diluted 1:100 in 50 ml of DGcthy medium and grown to an OD600 of 0.3 in a 37 shaking incubator. At the indicated times, 1 Ci/ml  $[^3\text{H}]$ thymidine (77.8 Ci/mmol) was added to duplicate 0.5-ml aliquots for 2 min at 37, before the cells were lysed and DNA precipitated in 5 ml of cold 5% TCA and filtered onto Millipore glass fiber prefilters. The amount of  $^3\text{H}$  on each filter was determined by liquid scintillation counting.

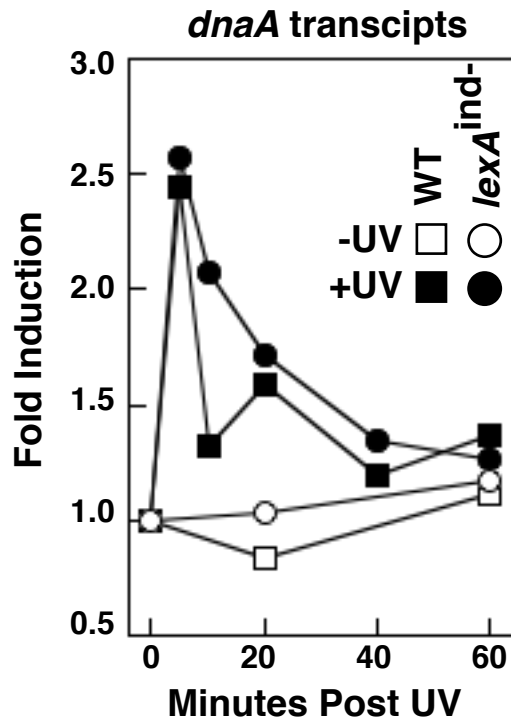


Figure S2. Transcriptional induction following UV irradiation of *dnaA*. The change in transcript levels for *dnaA* is plotted over time in wild type and *lexA1* mutants. Wild type (squares); *lexA1* (circles); UV irradiated (filled symbols); mock irradiated (open symbols). Cells were grown in Davis medium plus 0.4% glucose. Cultures were inoculated at a 1:200 dilution from a fresh overnight culture and grown to an OD600 of 0.4 before UV irradiation or mock irradiation. RNA was prepared and relative mRNA levels were determined by parallel two-color hybridization to cDNA microarrays representing 4101 open reading frames (ORFs). cDNA arrays were manufactured and transcript abundance was analyzed as described in (Courcelle et al. 2001). Time course samples were analyzed directly by comparing the abundance of each gene's transcripts relative to the time 0 sample. RNA samples taken during the time course were labeled with Cy-5, and RNA at Time 0 was labeled with Cy-3.

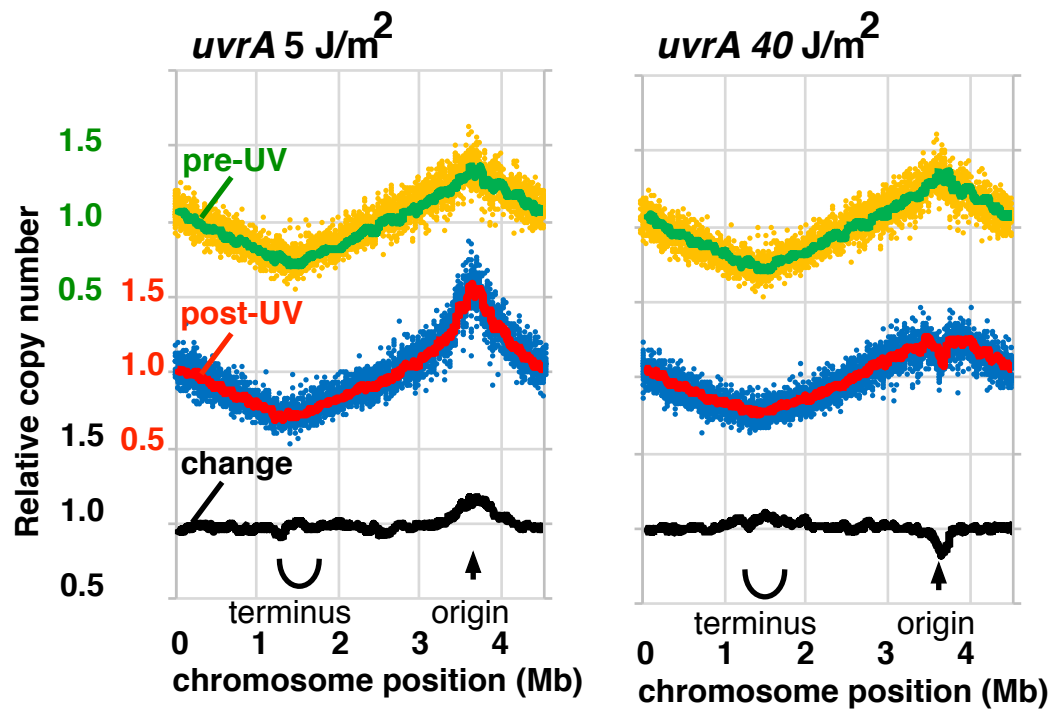


Figure S3. Comparative replication profiles of *uvrA* mutants irradiated with 5 and 40 J/m<sup>2</sup>. Replication profiles of *uvrA* mutants prior to UV (top green), 90 min post-UV (middle red), and the change between these times (bottom black) are plotted at the indicated dose. Profiles were analyzed as in Fig. 3. Data for 40 J/m<sup>2</sup> is reproduced from Figure 5 for the purposes of comparison and controls.

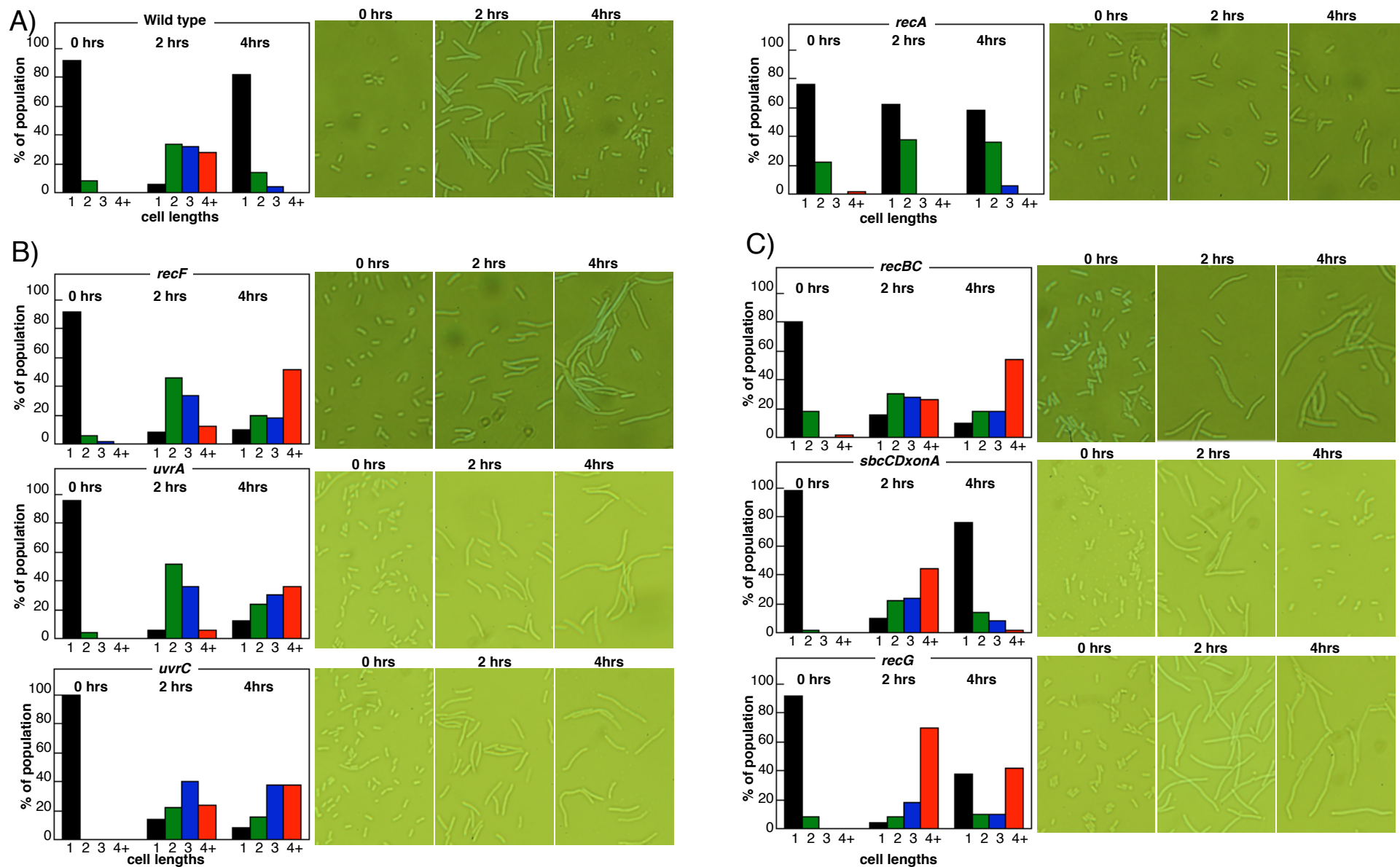


Figure S4. UV-irradiated wild type cells remain filamentous at 2 hours, but have returned to their normal size by 4 hours, suggesting that the chromosomal abnormalities have been resolved by this time. UV-irradiated *recA* mutants do not filament, which is under RecA control as part of the SOS response (Lutkenhaus et al. 1983). In mutants that are impaired in their ability to resume replication, the filamentous phenotype persisted out to at least 4 hours, and correlated with greater than 99% lethality in all cases, consistent with the idea that the partially replicated chromosomes persist and fail to resume. In mutants with an impaired ability to complete chromosome replication, the phenotype varied. The filamentous phenotype persisted through 4 hours in *recBC* and *recG* mutants and correlated with greater than 99% cell lethality, arguing that in these cases, the chromosomal imbalances cannot be resolved. In *sbcCDxonA* mutants, the filamentous cells had returned to normal size with 4 hours, and cells survived similar to wild type cultures, suggesting that the chromosomal imbalances in this mutant can be resolved in a manner that promotes survival. We have previously shown that *sbcCDxonA* mutants maintain viability by shunting the completion reaction through an aberrant recombinational pathway that leads to amplifications and instability in this region (Wendel et al., 2018; Hamilton et al., 0219). Plots represent the distribution of 100 cells counted at each time, with representative images shown next to each plot. Cells were prepared and imaged as in Fig.3C.

## Supplemental references

Courcelle, J., A. Khodursky, B. Peter, P. O. Brown, and P. C. Hanawalt, 2001 Comparative gene expression profiles following UV exposure in wild-type and SOS-deficient *Escherichia coli*. *Genetics* 158: 41-64.

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