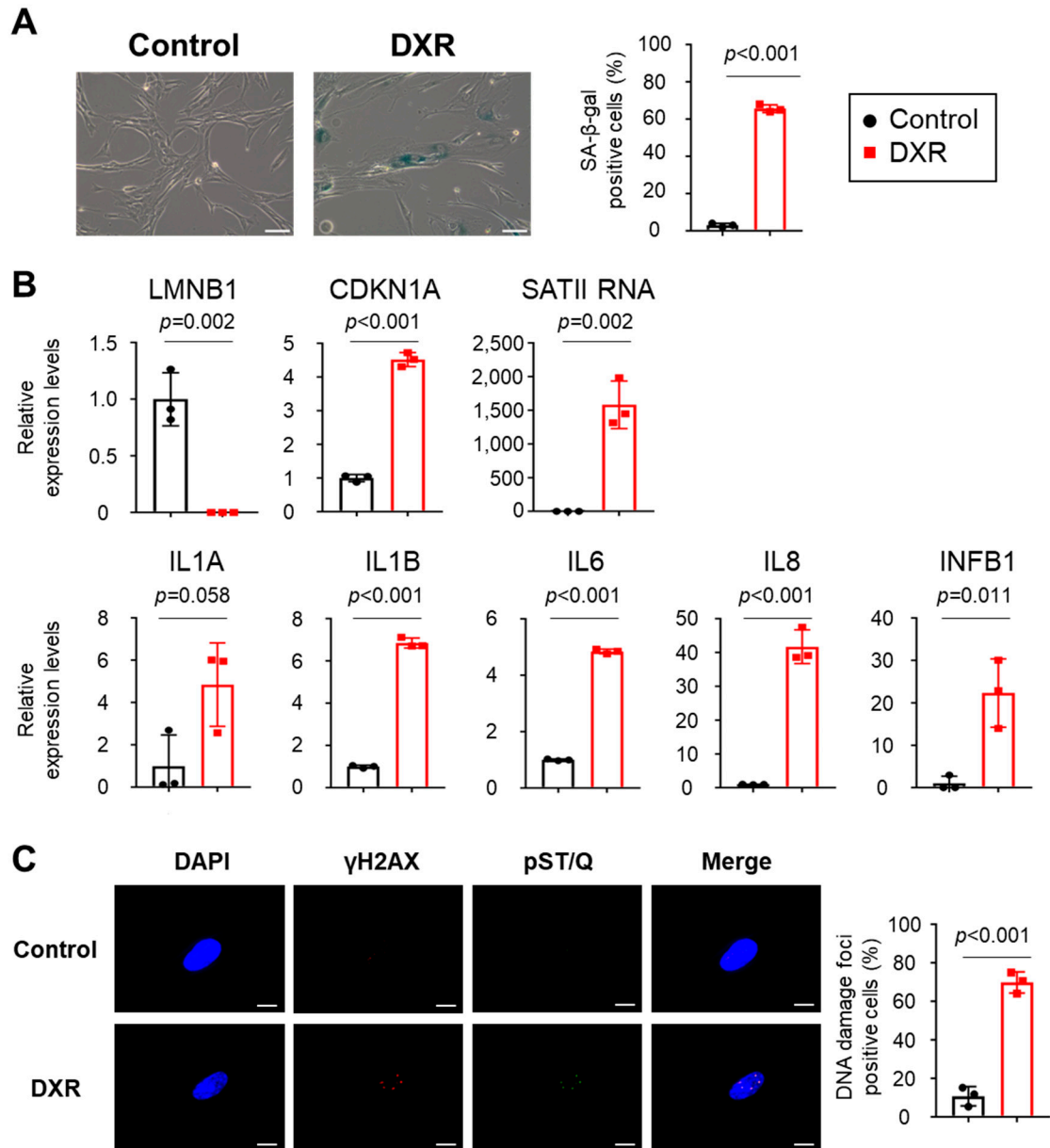


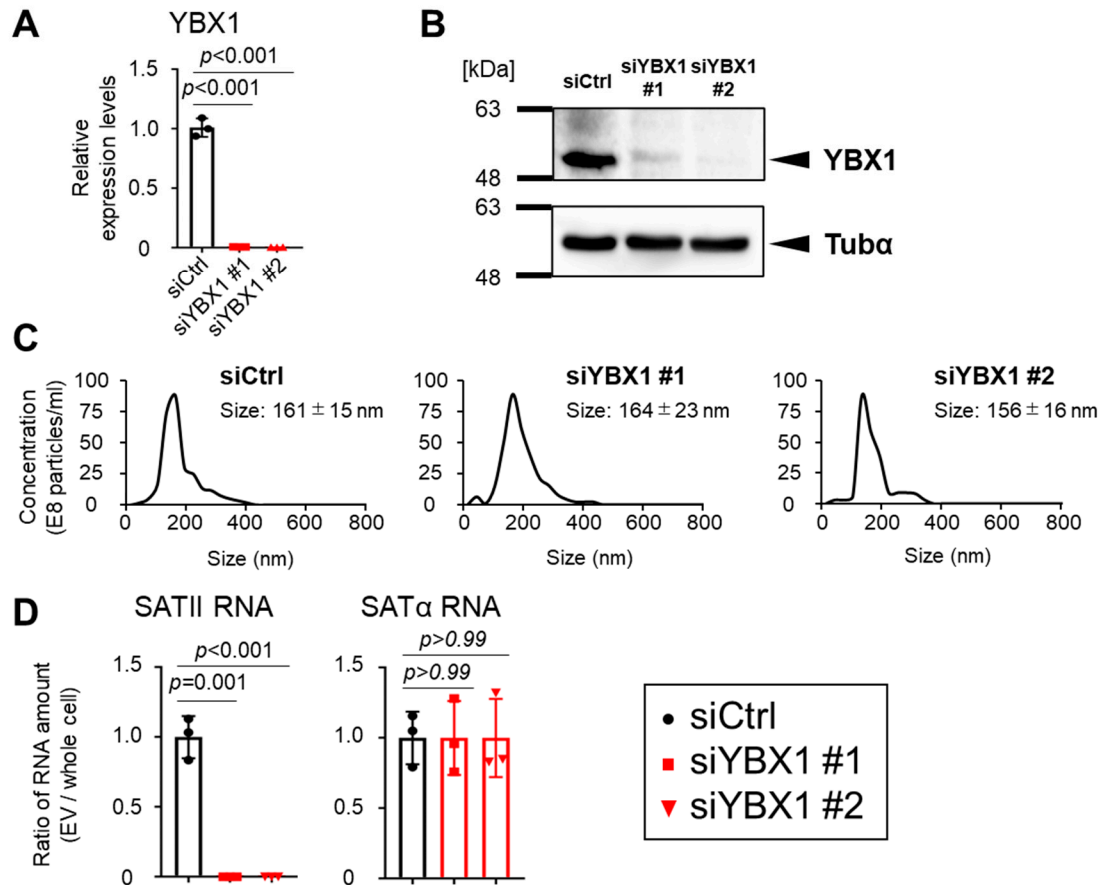
Cell type: IMR-90



**Figure S1.** Cellular senescence was induced by doxorubicin (DXR) treatment in IMR-90 cells. (A) IMR-90 cells were treated with 200 ng/mL DXR for 11 days to induce cellular senescence. Senescence-associated  $\beta$ -galactosidase (SA- $\beta$ -gal) staining of the cells before and after DXR treatment for 11 days. The bar graphs indicate the percentage of SA- $\beta$ -gal-positive cells. Scale bar = 100  $\mu$ m. (B) Relative RNA levels of *LMNB1*, *CDKN1A*, *IL1A*, *IL1B*, *IL6*, *IL8*, *INFB1*, and *SATII* RNA in control and irradiated cells by reverse transcription quantitative polymerase chain reaction. Relative quantitation data represent the mean  $\pm$  standard deviation (SD) normalized to actin  $\beta$ . (C) Immunofluorescence staining of DNA damage response markers  $\gamma$ H2AX (red), pST/Q (green), and 4',6-diamidino-2-phenylindole (blue) in the cells before and after doxorubicin

addition. The bar graphs indicate the percentage of nuclei containing more than two positive foci for both  $\gamma$ H2AX and pST/Q staining from at least 100 cells per condition for three independent experiments. Scale bar = 10  $\mu$ m. Results represent the mean  $\pm$  SD. *p*-Values were calculated by unpaired two-tailed Student's *t*-test in all panels.

#### Cell type: IMR-90



**Figure S2.** YBX1 knockdown reduced SATII RNA in sEVs released from IMR-90 cells. (A) Relative mRNA levels of *YBX1* in siCtrl cells and YBX1 knockdown IMR-90 cells were measured by reverse transcription quantitative polymerase chain reaction. Relative quantitation data represent the mean  $\pm$  standard deviation (SD) normalized to actin  $\beta$ . (B) Western blot analysis of whole cell lysate of siCtrl and YBX1 knockdown IMR-90 cells. (C) Nanoparticle tracking analysis for quantitative measurement of sEVs collected from siCtrl or YBX1 knockdown cells. (D) Ratio of the amount of SATII RNA and SAT  $\alpha$  RNA contained in sEVs divided by the amount contained in whole cells under treatment with YBX1 or control siRNA. Relative quantitation data represent the mean  $\pm$  SD. *p*-Values were calculated by one-way analysis of variance with Dunnett's multiple comparisons test in panels A and E.