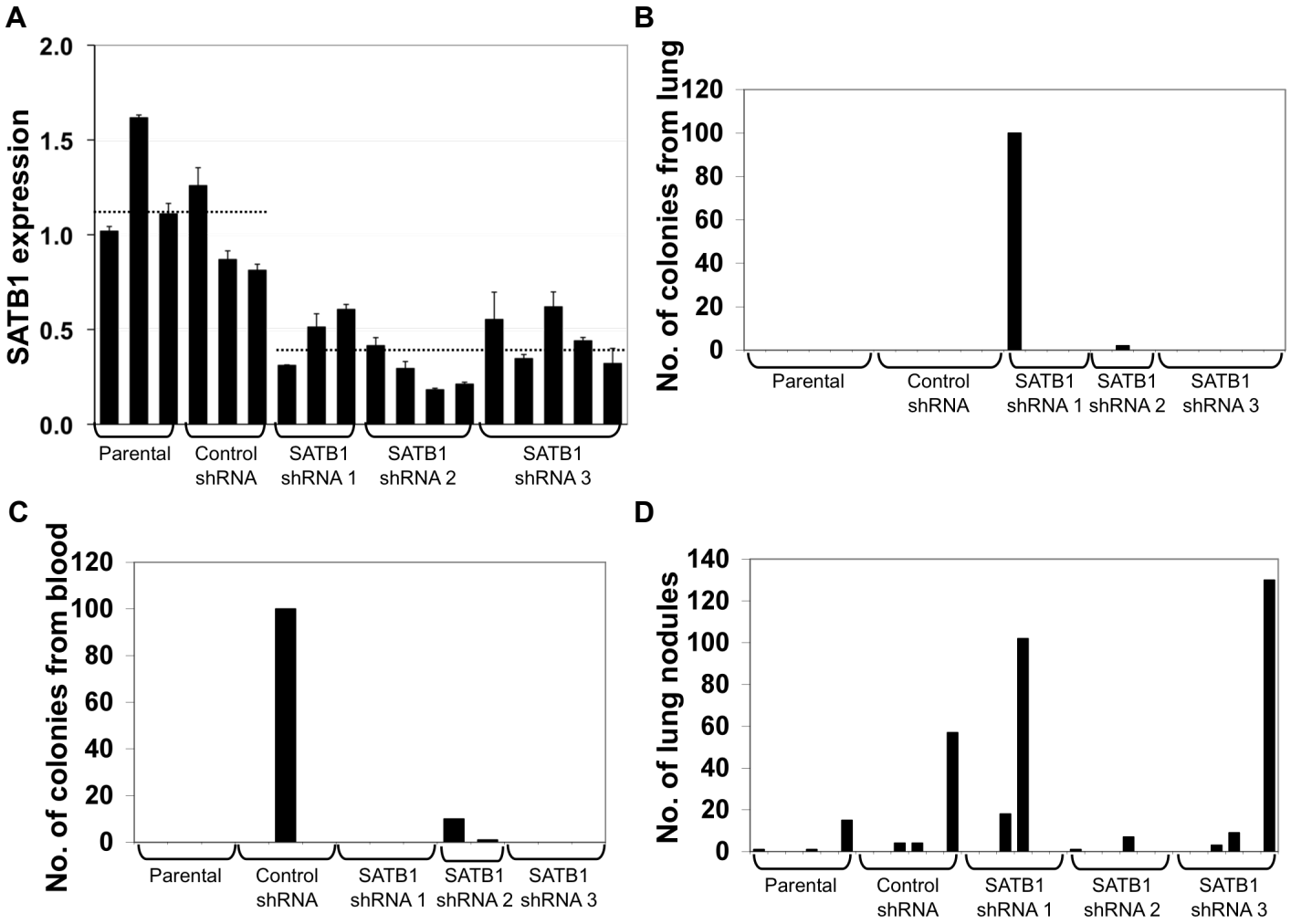
SUPPLEMENTARY FIGURE 2



Supplementary Figure 2. Effect of SATB1 depletion on the aggressive cancer cell phenotype in vivo. For these experiments, we used SATB1 short hairpin RNA (shRNA) 1, 2, and 3 MDA-MB-231 cells, control shRNA MDA-MB-231 cells, and parental MDA-MB-231 cells. Mice (n = six mice per group) were injected with 2 x 10^5 SATB1 shRNA cells, control shRNA cells, or parental MDA-MB-231 cells into the fourth mammary fat pad from flank to obtain one tumor per mouse. Tumor formation is described in Figure 2. **A)** SATB1 mRNA expression in tumors measured by quantitative real-time reverse transcription-polymerase chain reaction (qRT-PCR) analysis. Data are expressed as normalized SATB1 mRNA expression, calculated relative to expression of endogenous GAPDH mRNA control and adjusted relative to expression of GAPDH normalized SATB1 in tumor one, obtained from mouse one of the group injected with parental MDA-MB-231 cells. SATB1 mRNA experiments were repeated three times, with each point in triplicate. Error bars = 95% confidence intervals; dotted lines = mean normalized SATB1 expression in parental and control shRNA tumors (mean normalized SATB1 expression = 1.11) and SATB1 shRNA 1, 2, and 3 tumors (mean normalized SATB1 expression = 0.40). **B-D)** Data are from one measurement from each mouse, and each experiment was performed once. **B)** Numbers of colonies formed by cells isolated from lung samples of tumor-bearing mice from the experiment in panel A after 21 days of puromycin selection. **C)** Numbers of colonies formed by cells isolated from blood samples of the same tumor-bearing mice. **D)** Number of metastases in lungs of mice (n = 6 per group) 10 weeks after tail vein injection of 1 x 10^6 cells.