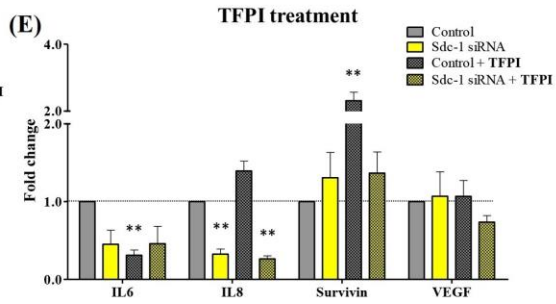
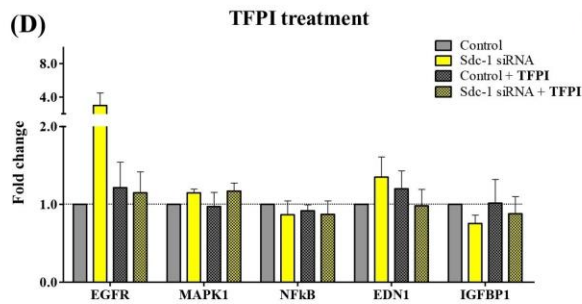
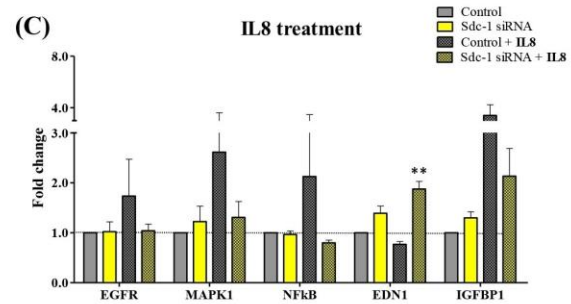
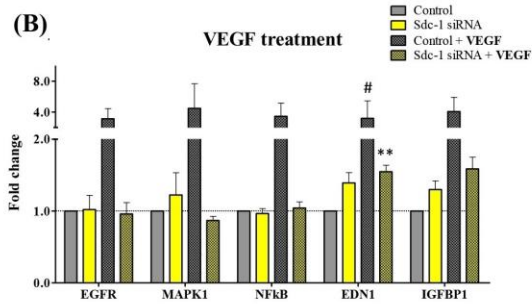
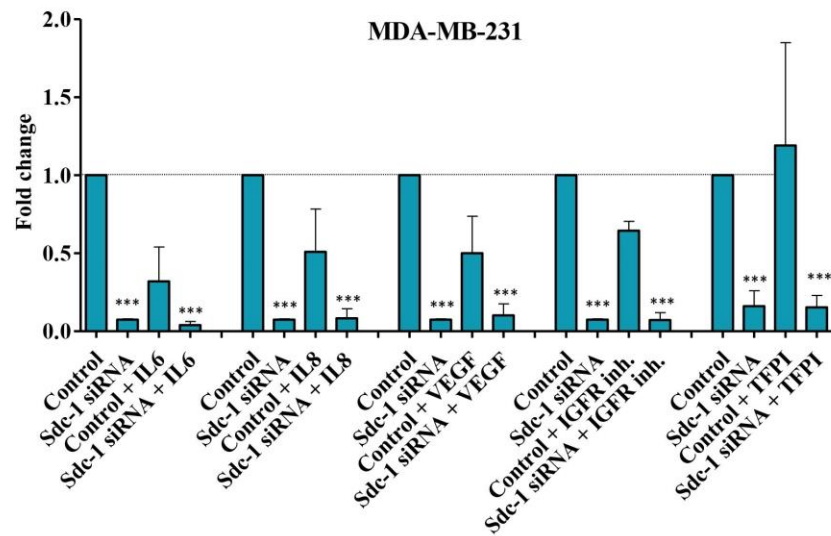
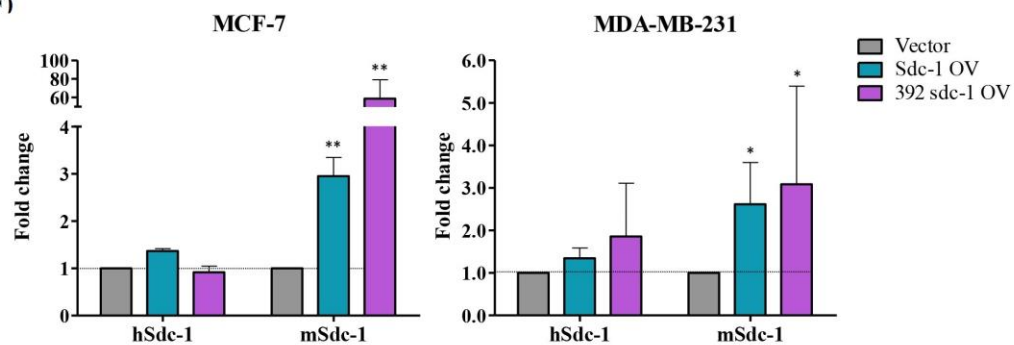


## Supplementary Figure

(A)



(F)



Supplementary Figure S1. qPCR analysis of gene expression changes in the breast cancer cells used in this study. (A) Sdc-1 siRNA transfection was confirmed by estimating the expression of Sdc-1 as determined by quantitative PCR after 72 h post-transfection and 48 h post-treatment with exogenous IL6 (100 ng/mL), IL8 (100 ng/mL), VEGF (20 ng/mL), TFPI (50 ng/mL) and the inhibition of IGFR with AG-1024 (20  $\mu$ M), normalized to  $\beta$ -ACTIN expression and plotted as fold change. (B–E) The expression of different genes was analyzed post-transfection and 48 h after (B) VEGF (20 ng/mL), (C) IL8 (100 ng/mL), and (D,E) 50  $\mu$ g/mL TFPI treatment via qPCR, normalized to  $\beta$ -actin expression, and shown as fold change (n = 3). Data represent the mean  $\pm$  SEM. Asterisks on the top of the bars indicate significant differences between the controls and all the conditions. The lines over the bars indicate significant differences (\*  $p$  < 0.05, \*\*  $p$  < 0.01, \*\*\*  $p$  < 0.001). (F) qPCR analysis of murine (mSdc-1) and human (hSdc-1) Sdc-1 expression. Sdc-1 expression was normalized to 18S rRNA. Error bars = SEM. Data represent the mean  $\pm$  SEM from three independent experiments. Asterisks represent comparisons with statistically significant differences (#  $p$  < 0.08, \*  $p$  < 0.05, \*\*  $p$  < 0.01, \*\*\*  $p$  < 0.001).