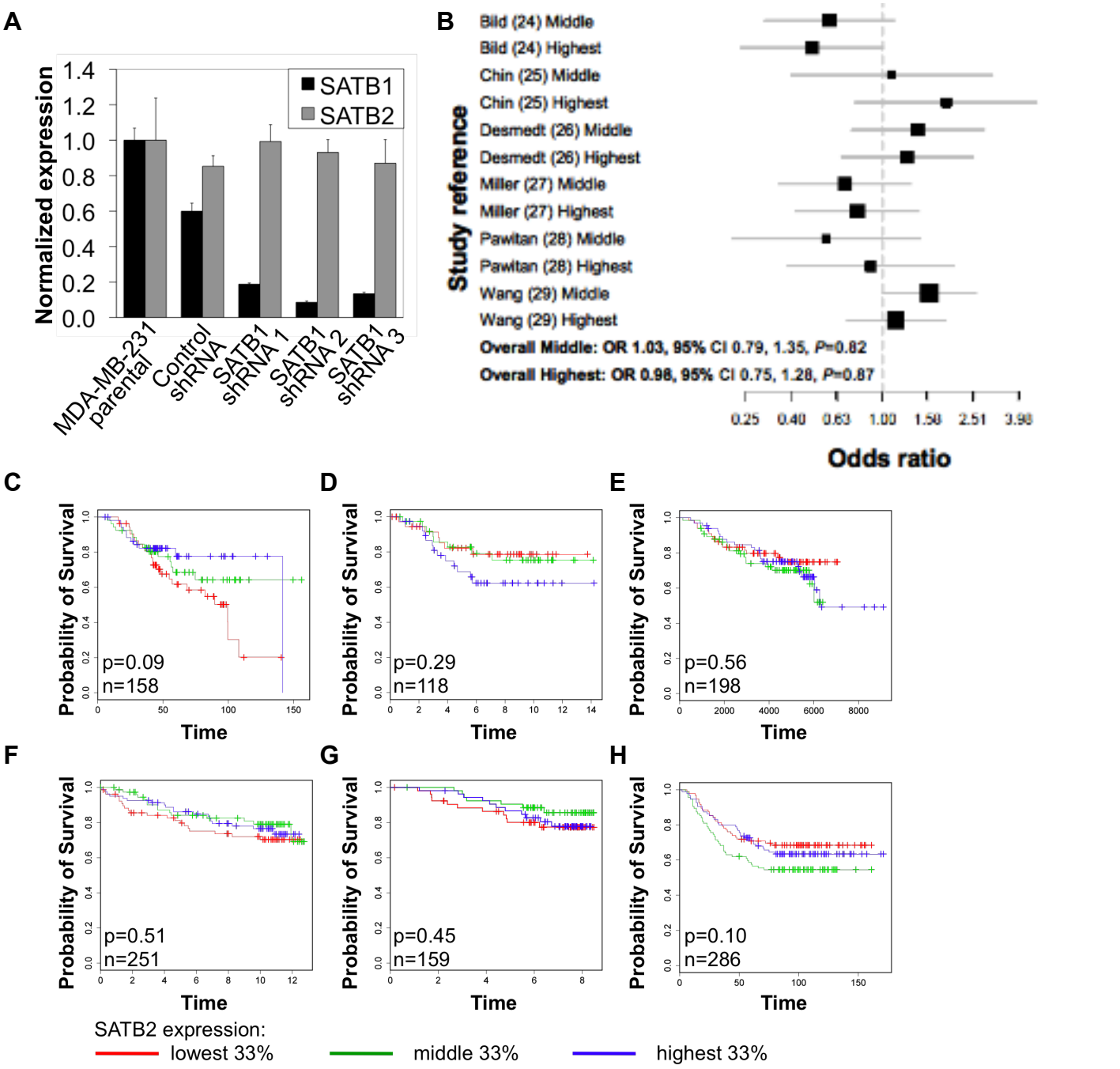
## SUPPLEMENTARY FIGURE 7




**Supplementary Figure 7. SATB2 expression in breast cancer cell lines and primary tumors from patients with breast cancer. A)** SATB1 and SATB2 mRNA expression. For these experiments, we used SATB1 short hairpin RNA (shRNA) 1, 2, and 3 MDA-MB-231 cells, control MDA-MB-231 cells, and parental MDA-MB-231 cells. SATB1 and SATB2 mRNA expression were determined by quantitative real-time reverse transcription-polymerase chain reaction (qRT-PCR) analysis. Data are expressed as normalized expression of SATB1 or SATB2 mRNA, calculated relative to expression of endogenous GAPDH mRNA control and adjusted relative to the expression of GAPDH normalized SATB1 or SATB2 in parental MDA-MB-231 cells. mRNA expression experiments were repeated three times, with each point in triplicate. Error bars = 95% confidence intervals. Black bars = SATB1 mRNA; grey bars = SATB2 mRNA. **B)** Forest plot of overall survival of patients with ductal breast carcinoma, stratified by SATB2 expression level. Expression data from the six independent microarray studies [24-29], as described in Figure 6, were stratified by tertiles of SATB2 expression. Middle or highest SATB2 expressing groups were compared with the lowest SATB2 expressing group. Squares = odds ratios (size of squares indicates the sample size); whiskers = 95% confidence intervals. **C-H)** Kaplan–Meier plots of overall survival of patients with ductal breast carcinomas stratified by SATB2 expression level from the following six independent microarray studies. **C)** Bild et al. [24]. **D)** Chin et al. [25]. **E)** Desmedt et al. [26]. **F)** Miller et al. [27]. **G)** Pawitan et al. [28]. **H)** Wang et al. [29]. Cox proportional hazard models were fitted to the data and chi-square tests were used to assess statistical significance. All statistical tests were two-sided.