SUPPLEMENTARY FIGURE AND TABLE LEGENDS

Supplementary Figure 1. PI3K regulates BRCA expression. Western blot of cell lysates (7 days post transfection) from BT20 and BT549 cells transfected with control or *PIK3CA* siRNAs using the indicated antibodies. Tubulin was used as loading control.

Supplementary Figure 2. PI3K blockade suppresses BRCA1/2 transcription. qRT-PCR measuring both BRCA1 and BRCA2 mRNA levels in MDA-MB-231, HCC1143 and HCC70 cells treated with BKM120 for 4 days. Measurements were normalized to 18S mRNA levels and expressed as fold change compared to controls (Log_2 scale). Data are shown as mean ± S.E. of 3 independent replicates for each condition.

Supplementary Figure 3. Combined *PIK3CA* siRNA and PARP suppression in TNBC cell lines. **A**, Viability (assayed by Cell Titer-Glo)of BT20 cells transfected with control, *PIK3CA* or *BRCA1* siRNAs and plated in the absence or presence of olaparib for 7 days. IC-50 values were calculated using GraphPad Prism program. **B**, Clonogenic proliferation of MDA-MB-468 and BT549 cells transfected as in panel A and plated in the absence or presence of ABT888 for 14-18 days. IC50 values were calculated using GraphPad Prism program.

Supplementary Figure 4. Concordance in ER, PR, HER2, and PTEN expression between original patient tumors and the derived tumor grafts. Magnification10X.

Supplementary Figure 5. Western blot of cell lysates from MDA-MB-468 or PDC44 cells treated with 750nM and 500nM BKM120 respectively for 4 days using the indicated antibodies. Total ERK (tERK) is used as loading control.

Supplementary Figure 6. ERK and ETS1 downregulate BRCA1/2 expression. Western blot of protein lysates from MDA-MB-231 treated with control or ETS1 siRNA for 4 days and then probed using the indicated antibodies. Total ERK (tERK) is used as loading control. qRT-PCR measuring both BRCA1 and BRCA2 mRNA levels in MDA-MB-231 cells after 4 days of transfection with control and ETS1 specific siRNA.

Supplementary Table 1. Common *BRCA1* and *BRCA2* promoter putative transcription factors analysis. *BRCA1* and *BRCA2* promoter sequences were analyzed by JASPAR putative binding motif search at 95% alignment indentifying 51 and 40 motifs respectively. Seven common transcription factors in BRCA1 and BRCA2 were identified. The number of binding motifs for each of the BRCA1/2 putative common transcription factor is listed.