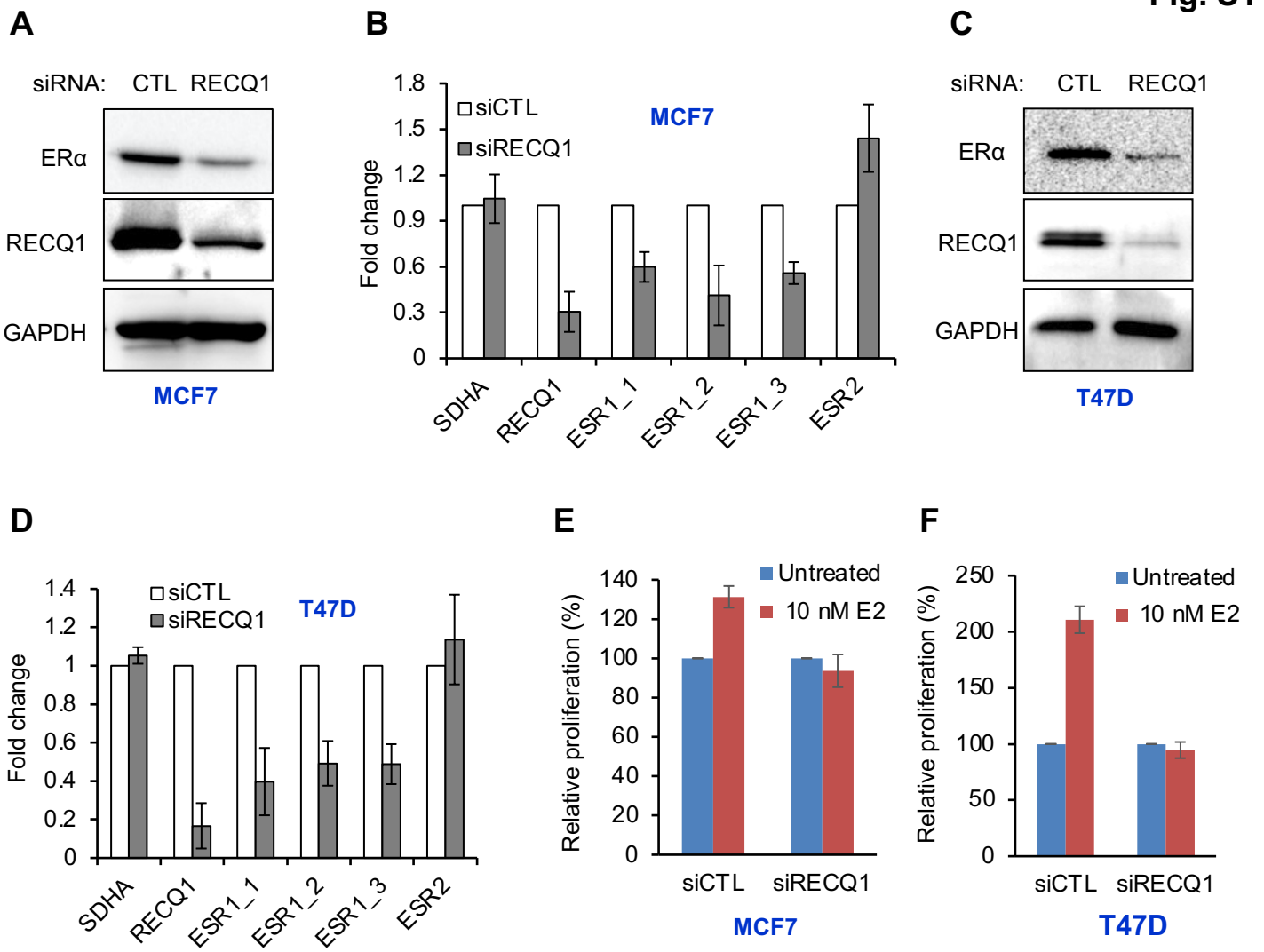
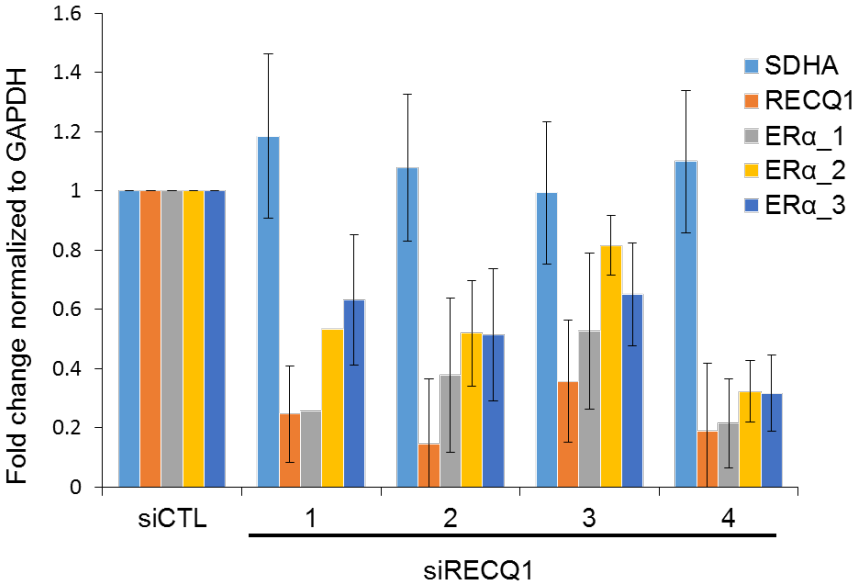


Fig. S1. RECQ1 depletion results in decreased ERα expression and impaired estrogen-stimulated proliferation in ER-positive breast cancer cells.

(A-D) MCF7 and T47D cells grown in regular full medium were transfected with control (CTL) siRNA or *RECQ1* siRNAs for 48 hr. Immunoblotting was performed using GAPDH as loading control to determine the effect of *RECQ1* knockdown on ERα and RECQ1 protein levels (A and C). RT-qPCR was performed to measure the effect on mRNA levels of *RECQ1* and *ESR1* (the gene encoding ERα) (B and D). The housekeeping gene *SDHA* served as a negative control in RT-qPCR. Note that in panel B, ESR1_1, ESR1_2 and ESR1_3 are 3 primers different primer pairs to measure ESR1 expression. ESR2 encodes ERβ.

(E, F) 48 hr after siRNA transfection, MCF7 or T47D cells growing in phenol-red free medium containing 5% charcoal-stripped fetal bovine serum (i.e. hormone deprived medium) were treated with 10 nM 17β-estradiol (E2) or 0.1% ethanol and cell proliferation was measured by CCK8 assays after 48 hr. Note that in panel D, ESR1_1, ESR1_2 and ESR1_3 are 3 primers different primer pairs to measure ESR1 expression. ESR2 encodes ERβ.

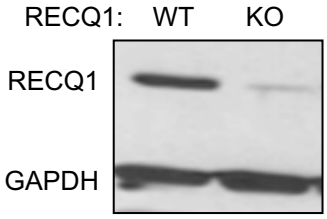
A



Target Sequences of siRNA:

1. GAGCUUAUGUUACCAGUUA
2. CUACGGCUUUGGAGAUAUA
3. GAUUAUAAGGCACUUGGUA
4. GGGCAAGCAAUGAAUAUGA

B



C

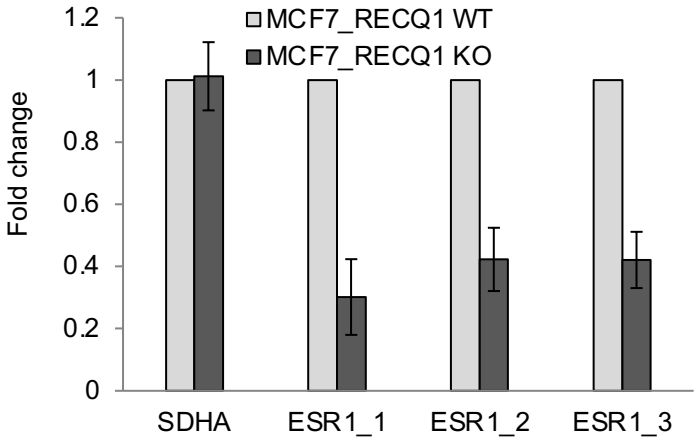


Fig. S2. Loss of RECQ1 in MCF7 cells leads to decreased ESR1 expression.

A. MCF7 cells were transfected with CTL siRNA or 4 independent RECQ1 siRNAs for 48 hr and the effect on RECQ1 and ESR1 (using 3 different primers) was determined by RT-qPCR normalized to GAPDH. The housekeeping gene SDHA was used as a negative control.

B. CRISPR/Cas9 was used to deplete RECQ1 in MCF7 cells and the effect on RECQ1 protein was determined by immunoblotting from a wild-type clone (WT) and a RECQ1 knockout (KO) clone using GAPDH as loading controil. Note that this approach resulted in substantial decrease but not complete loss of RECQ1 protein.

C. RT-qPCR from MCF7 RECQ1 WT and isogenic RECQ1 KO cells shows substantial decrease in ESR1 expression using 3 independent primers. The housekeeping gene SDHA was used as negative control.

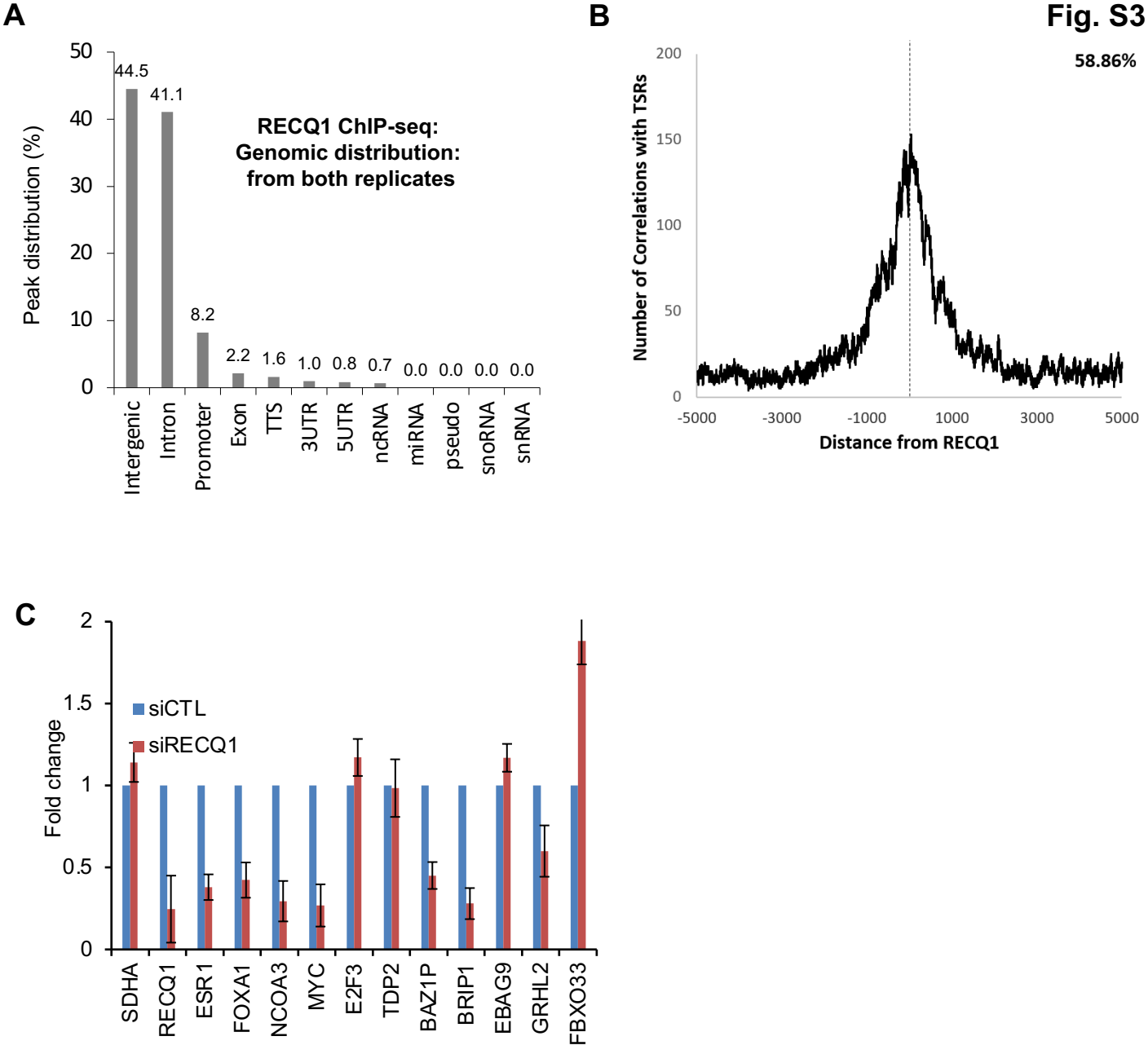


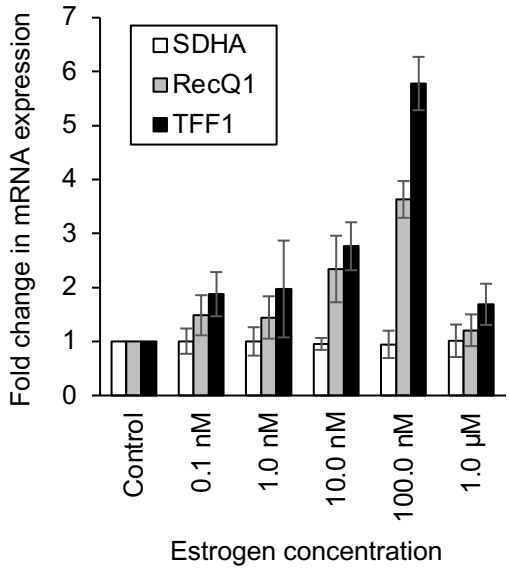
Fig. S3. Genomic distribution of RECQ1 ChIP-seq peaks.

A. Data from both RECQ1 ChIP-seq replicates show that RECQ1 peaks are mostly observed in introns and intergenic regions.

B. Colocalization of the RECQ1 binding sites with transcriptional start regions (TSRs). The histogram x axis extends 5-kb upstream and 5-kb downstream from the center of the RECQ1 peaks. The extent of colocalization (%) is measured as the fraction of RECQ1 peaks within the 5-kb window of the TSRs. (see the Materials and Methods section for details).

C. MCF7 cells were transfected with CTL siRNA or *RECQ1* siRNAs and the expression of genes validated by ChIP-qPCR (Figure 4B) was assessed by RT-qPCR normalized to *GAPDH.* The housekeeping gene *SDHA* was used as negative control.

A



B

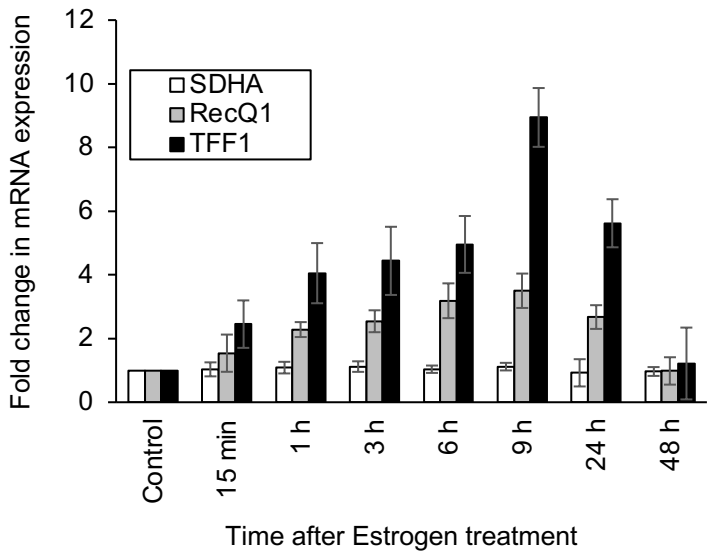
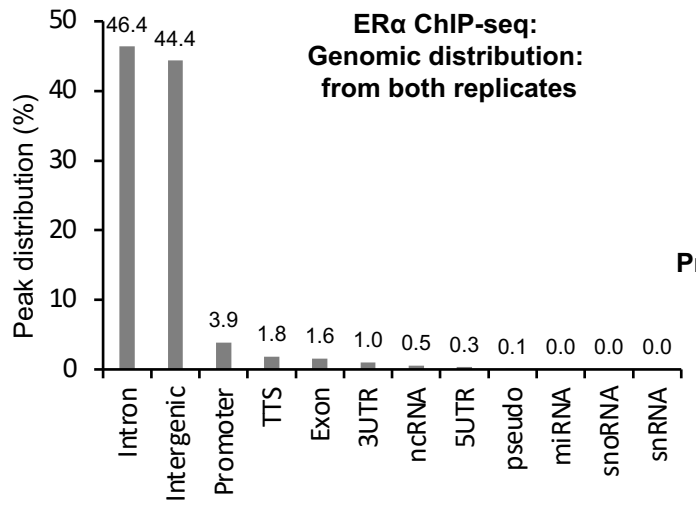
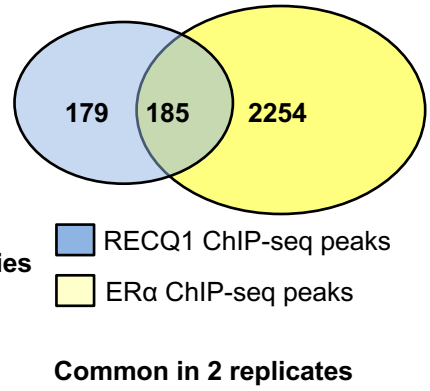


Fig. S4. Upregulation of RECQ1 by estrogen. MCF7 cells grown in hormone deprived medium cells were treated with 0.1% ethanol (control) or an indicated dose of 17β-estradiol (E2) for 6 hours (A), and with 10 nm of E2 for indicated time points (B). Expression levels of RECQ1 and TFF1 were measured by RT-qPCR. The housekeeping gene SDHA was used as negative control.





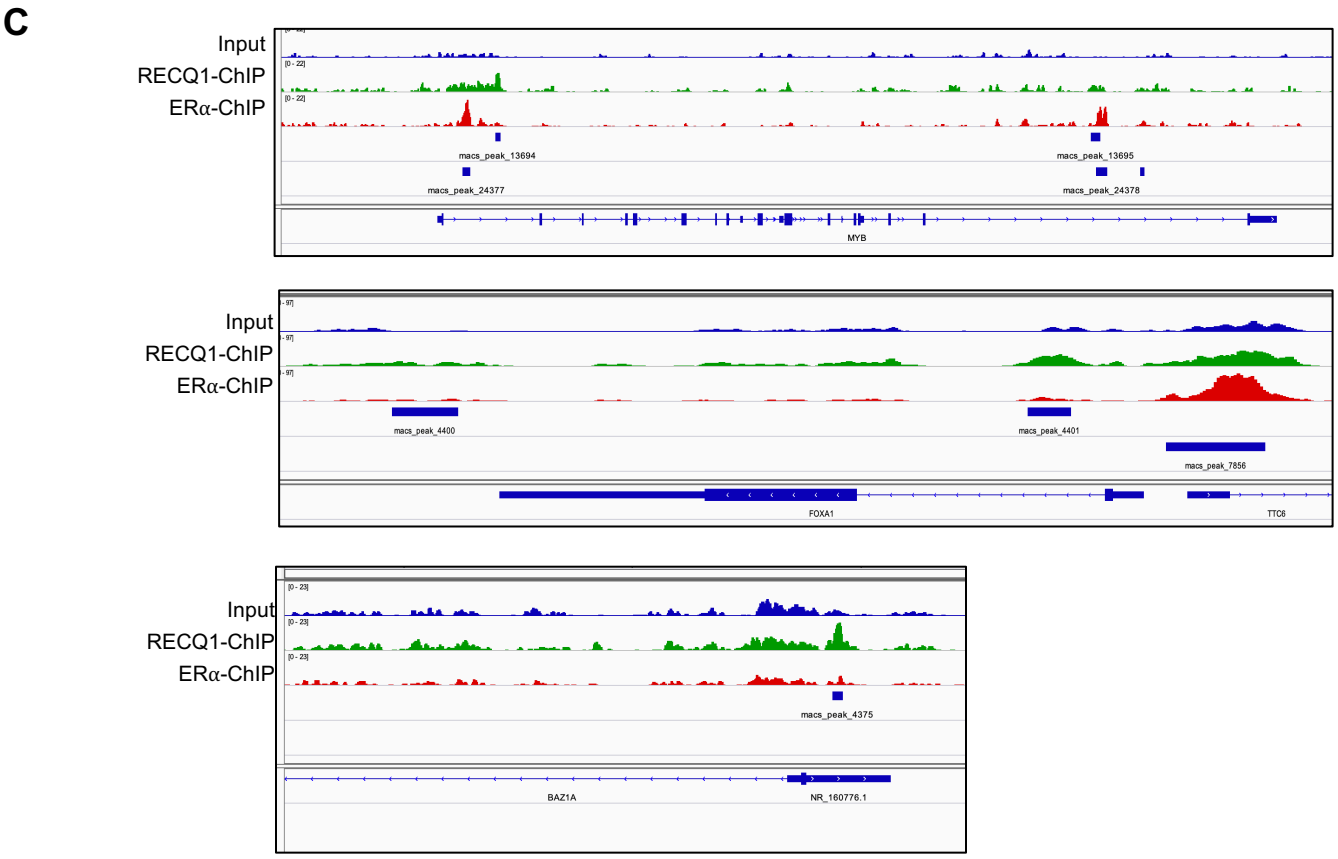


Fig. S5. Genomic distribution of ERα ChIP-seq peaks.

A. Data from both ERα ChIP-seq replicates show that ERα peaks are mostly observed in introns and intergenic regions.

B. Venn diagram shows the comparison of Erα and RECQ1 ChIP-seq peaks at promoters and gene bodies from 2 replicates.

C. IGV snapshots is shown for binding of RECQ1 and ERα at the promoters or gene bodies of of select RECQ1 target genes (MYB, FOXA1 and BAZ1A). These genes were also validated by ChIP-qPCR for RECQ1 in Fig. 3B.

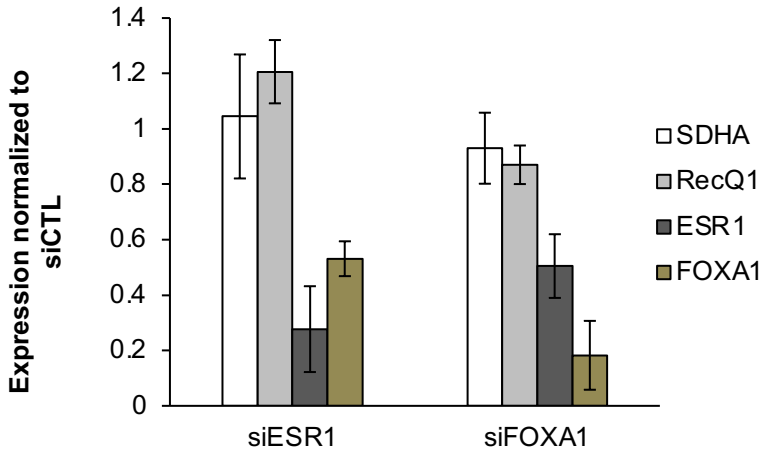


Fig. S6. FOXA1 or ERα knockdown has no impact on expression of RECQ1 in MCF-7 cell line.
MCF7 cells were transfected with CTL siRNA or FOXA1 siRNAs (Smartpool) for 48 hr and the effect on RECQ1, ESR1 and FOXA1 mRNA was determined by RT-qPCR normalized to GAPDH. The housekeeping gene SDHA was used as a negative control.

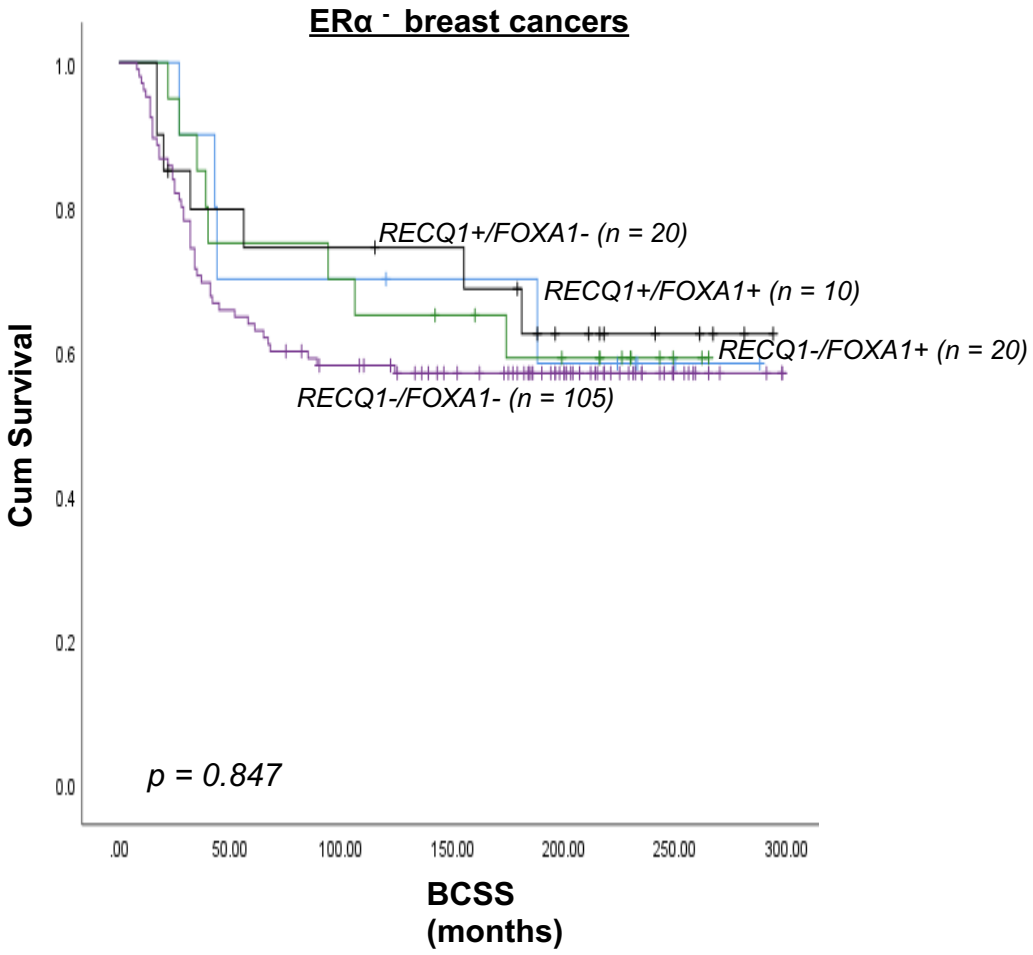


Fig. S7. Kaplan Meier curves for RECQ1/FOXA1 co-expression and breast cancer-specific survival (BCSS) in ERα- breast cancers.