**Supplementary Figure S1.** An example of *BRCA1* reversion detected in one patient’s baseline tumor biopsy (platinum-sensitive cohort). *BRCA1* exonic figure was adapted from IGV (hg19 NM\_997294) and *BRCA1* protein domain structure from OncoKB.

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**Supplementary Figure S2.** Gene expression values in archival versus baseline samples. (A) Significantly increased expression of *RAD51C* in post-PARP inhibitor (baseline) versus pre-PARP inhibitor (archival) specimens. (B) No change in *RAD51D* expression.

FPKB, fragments per kilobase million; PARP, poly (ADP-ribose) polymerase.

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**Supplementary Figure S3.** Efficacy in patients with homologous recombination mutations with no reversion plus a *CCNE1* amplification in baseline samples versus all other patients (i.e., *CCNE1* amplified and wild-type homologous recombination or reversion and no *CCNE1* amplification and homologous recombination mutated, or no *CCNE1* amplification and wild-type homologous recombination or reversion). (A) PFS and (B) OS.

\*The upper-bound of the 95% CI interval for median PFS in the homologous recombination mutated and *CCNE1-*amplified group could not be accurately estimated due to small sample number.

AMP, amplified; CI, confidence interval; NA, not applicable; HR, homologous recombination; OS, overall survival; PFS, progression-free survival.

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**Supplementary Figure S4.** Absolute number of fusion gene pairs detected per sample.

Bars are colored by sample type (archival, baseline, or progression) with *BRCA* reversion cases denoted below the x axis.

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**Supplementary Figure S5.** Gene set enrichment (GSVA) scores for (A) DNA repair and (B) angiogenesis pathways using RNA sequencing data from archival and baseline samples. \**p* < 0.05; \*\**p* < 0.01.

Connected dots represent two cases where on-trial progression samples were available. GSVA, gene set variation analysis; WT, wildtype.

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