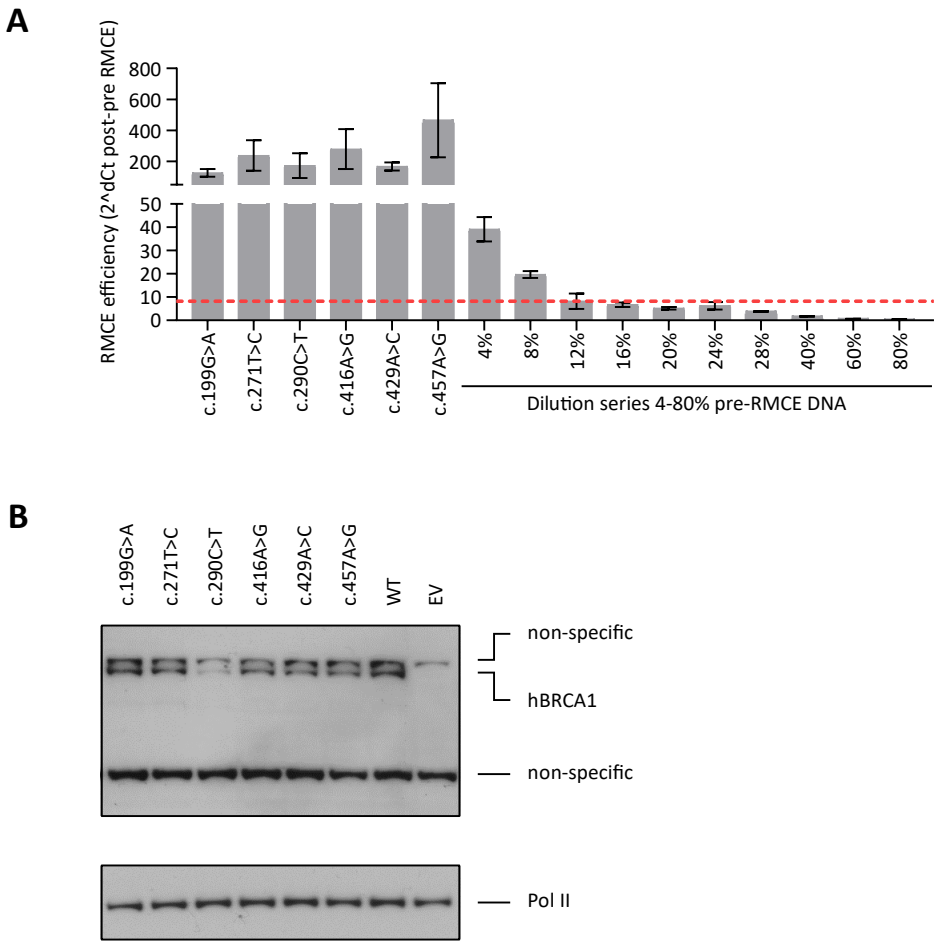

Figure S1: RMCE qPCR and Western blot analysis of human *BRCA1* complemented ES cells.
(A) Example of the quantitative PCRs on genomic DNA to verify RMCE efficiencies of *BRCA1* complemented ES cells. The percentage of cells without targeted integration of the human *BRCA1* sequence variant was estimated based on the delta Ct of quantitative PCRs for the *Rosa26* RMCE locus before and after RMCE. Each run included a standard curve of samples with different ratios of genomic DNA from cells before and after RMCE. Pools of ES cells with 12% or more non-recombined *Rosa26* loci (red dotted line) were excluded from functional analyses and replaced. Error bars indicate standard deviation. (B) Example of Western blot analysis of human *BRCA1* variants in pools of transfected ES cells. Expression of DNA-Directed RNA Polymerase II largest subunit (Pol II) was used as a loading control.