



Figure S6: Pooled analysis of 30 *BRCA1* variants in the N-terminal domain encoding region.

(A) 30 variants including known benign (8) and known pathogenic (7) controls were transfected for RMCE in parallel, selected and passaged with and without 4-OHT to switch off endogenous *Brca1* by Cre-ERT2. Ten days after 4-OHT induction of Cre activity (D10), samples of switched and non-switched cells were harvested for DNA, PCR amplification of the human *BRCA1* region containing the variants, and high-throughput sequence analysis. (B) As for A, but with cells cultured in the presence of 5 nM olaparib upon 4-OHT treatment. (C) Results from the olaparib sensitivity assay for the same variants as in A and B using individually transfected pools of cells (Tables S1, S2). *: Variant c.441G>C may affect mRNA splicing.