Homology Directed Repair (HDR) scoring for individual *BRCA2* variants

Step1: Each variant was evaluated in a minimum of two experiments.

Step 2: GFP positive cell counts per 1 x 106 cells evaluated by flow cytometry were calculated for each experiment (variant, wildtype positive controls, p.D2723H negative controls and empty vector).

Step 3: A ratio of GFP cell counts for each individual experimental measurement for each variant relative to the average counts for empty vector was estimated.

Step 4: Ratios were converted to natural log (ln) and individual ln ratios for each variant were averaged to account for the non-linearity of the HDR assay.

Step 5: The average ln ratio for the p.D2723H negative control was subtracted from the averaged ln ratio of each variant to remove background effects.

Step 6: Ln ratios were divided by the average ln ratio for the wildtype positive control and multiplied by Ln5.

Step 7: The antilog of the resulting value yielded a final value scaled for 1 to 5 for each variant evaluated.