

A # of pathogenic or likely pathogenic variants in each TP53 codon

S4 Fig. The distribution of altered codon in *BRCA*1 and *TP53* gene without hotspot (A) The bar graph shows the number of pathogenic or likely pathogenic variants in each *TP53* codon. *TP53* R175H (5.6%) and *TP53* R248Q/W (7.9%) were observed in three (4.8%) and two (3.2%) cases among 62 patients, respectively. *TP53* K132R, I195T, Y220C, and R306* variants were observed in three patients (4.8%). (B) The bar graph shows the number of pathogenic or likely pathogenic variants in each *BRCA1* codon. *BRCA1* Y130Ter variants were observed in three patients (3/22, 13.6%).