



**S22 Fig. Additional information about the classification model**

(A) Schematic of the exact best cut-off distribution influenced by different parameters, assuming no ties. The number of neutral ( $n_{\text{neutral}}$ ) and pathogenic ( $n_{\text{pathogenic}}$ ) variants influence the exact best cut-off distribution only if the number of values per mutant ( $n_{\text{mutant}}$ ) is above 1. The number of values in the WT reference ( $n_{\text{BRCA1}}$ ) does not influence the exact best cut-off distribution in the standard method, only in the standard with reference and MWW methods.

(B) Schematic of the approximate best cut-off distribution influenced by the number of bootstraps performed. Importantly, a single bootstrap ( $n_{\text{bootstrap}} = 1$ ) does not lead to the experimental best cut-off, except if  $n_{\text{best exact}} = 1$ .

(C) Accuracy of the probability and quantile systems of classification. The schematic illustration is valid, using either the exact or approximate best cut-off distribution.

(D) Correcting factor  $f_{\text{cor}}$  used in the probability system of classification, depending on the parameter  $a$  (see the S1 Text).  $f_{\text{cor}} = (n_{\text{neutral}} + n_{\text{pathogenic}}) / (n_{\text{neutral}} + n_{\text{pathogenic}} + a)$ . The framed value ( $a = 2$ ) was the value used in S13-S15 Tables.