





Supplementary Figure S1. Mean number of genomic alterations. A. *BRCA1*, *BRCA2*, BRCAX, and sporadic breast cancer. Significant differences (p -value<0.05 in U-Mann Whitney Test) are shown when comparing *BRCA1*- versus *BRCA2*-associated breast cancer (\pm), *BRCA1* versus BRCAX (§), or *BRCA1* versus sporadic tumors (#). B. Samples divided according to their estrogen receptor status. Φ means significant differences (p -value<0.05 in U-Mann Whitney Test). C. Tumors divided according to BRCA mutation, and further divided according to ER status. Significant differences (p -value<0.05 in U-Mann Whitney Test) are shown when comparing ER-negative vs ER-positive *BRCA1* tumors (\mathcal{K}), ER-negative vs ER-positive BRCAX tumors (*), and ER-negative vs ER-positive sporadic cancer (\mathcal{H}).

Supplementary Figure S2. Overall genomic aberration frequencies in *BRCA1*, *BRCA2*, BRCAX and sporadic breast cancer samples subdivided by ER status. The frequency of gains is shown in red and the frequency of losses in green.