Supplementary Figure 4. Variation of FGA values versus GAP-ploidy for HER2-amplified and HER2-negative breast cancers. GAP-ploidy estimates were binned in 0.1 bins represented by tick marks on the x-axis. Bins contain different number of samples. For each bin a box plot is displayed for LOH-FGA (top), CNN-AI-FGA (center), and CN-FGA (bottom) for (A) 99 HER2-amplified cases, (B) 96 HER2-negative basal-like cases, (C) 88 HER2-negative luminal A cases, (D) 90 HER2-negative luminal B cases, and (E) 34 HER2-negative normal-like cases.
B

LOH-FGA versus binned GAP-ploidy for 96 basal-like cases

CNN-FGA versus binned GAP-ploidy for 96 basal-like cases

CN-FGA versus binned GAP-ploidy for 96 basal-like cases
LOH-FGA versus binned GAP-ploidy for 88 Luminal A cases

CNN-FGA versus binned GAP-ploidy for 88 Luminal A cases

CN-FGA versus binned GAP-ploidy for 88 Luminal A cases
LOH-FGA versus binned GAP-ploidy for 90 Luminal B cases

CNN-FGA versus binned GAP-ploidy for 90 Luminal B cases

CN-FGA versus binned GAP-ploidy for 90 Luminal B cases
E

LOH-FGA versus binned GAP-ploidy for 34 Normal-like cases

CNN-FGA versus binned GAP-ploidy for 34 Normal-like cases

CN-FGA versus binned GAP-ploidy for 34 Normal-like cases