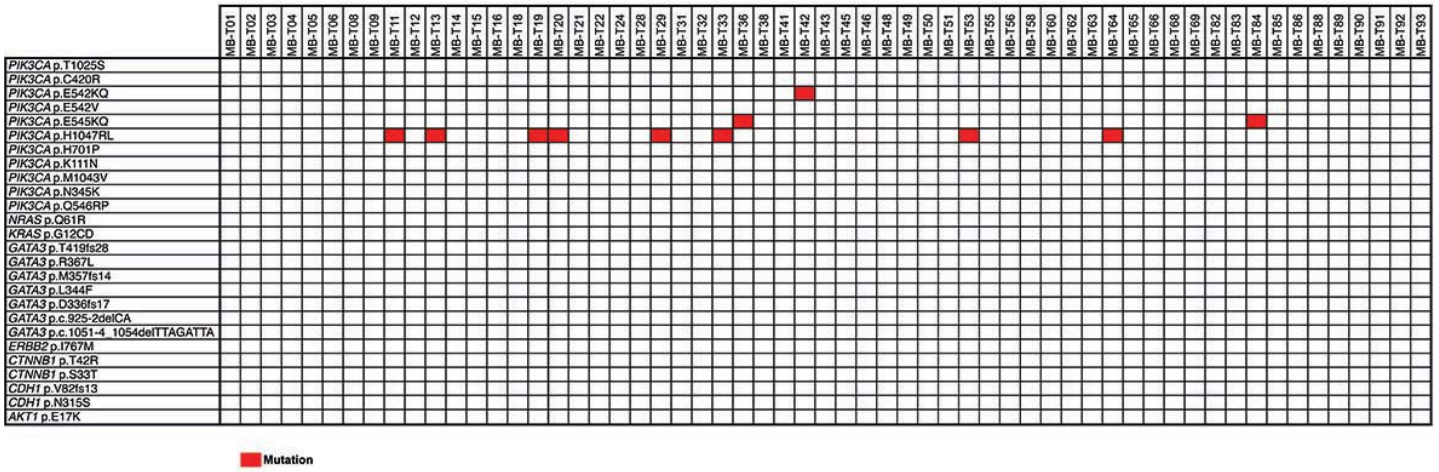
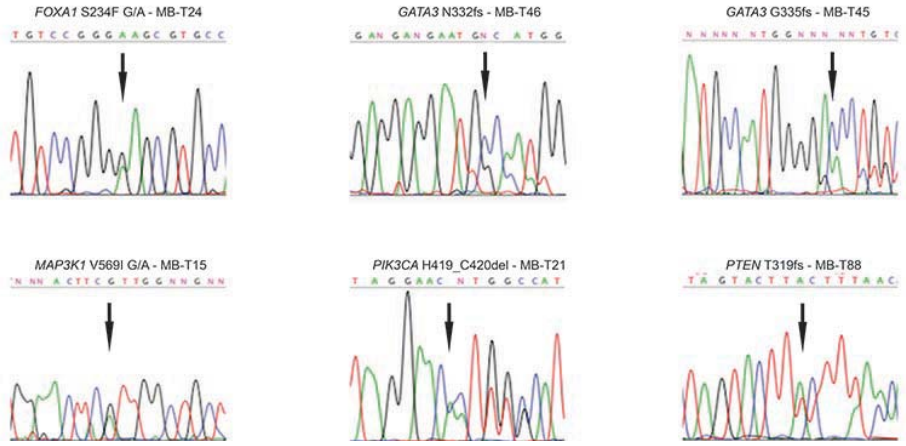
Supplementary Figure S1

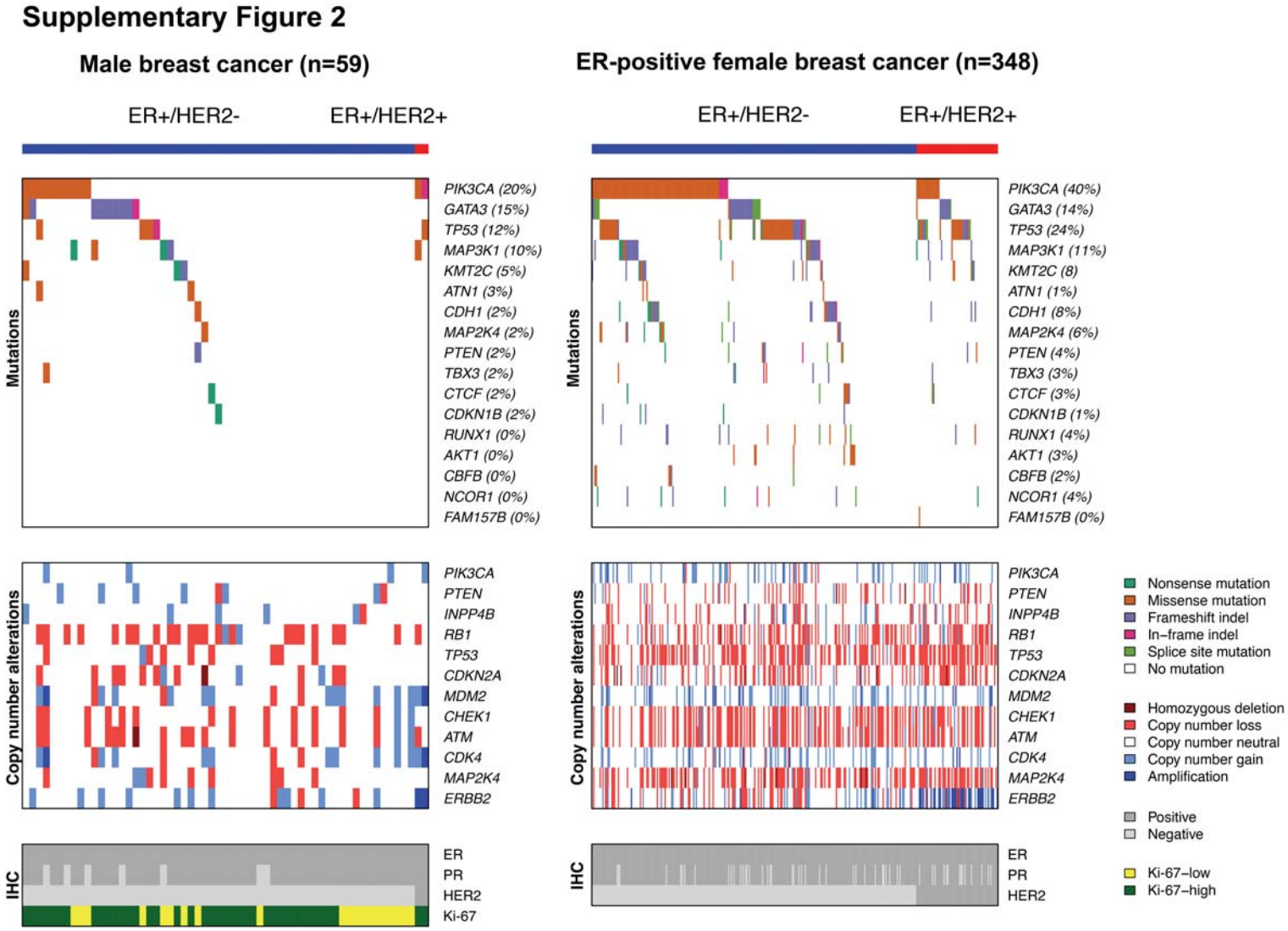
A



B

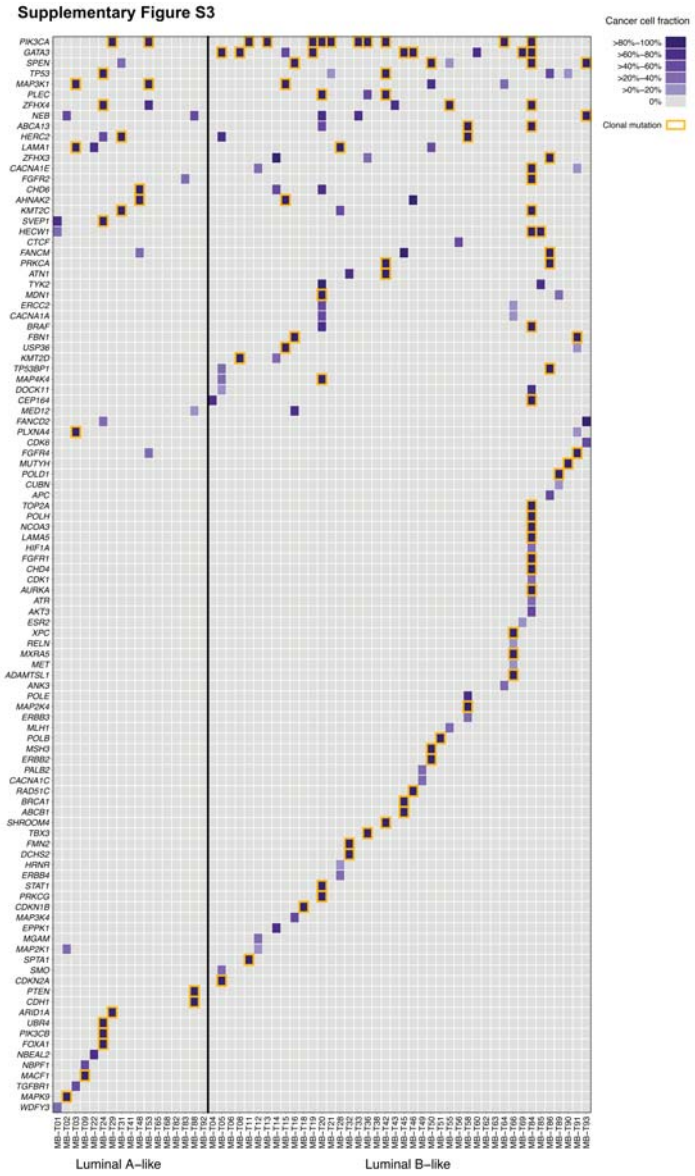


Supplementary Figure S1: Validation of mutations using Sequenom MassARRAY and Sanger sequencing.
(A) 26 hotspot mutations in *PIK3CA*, *GATA3*, *CTNNB1*, *KRAS*, *NRAS*, *CDH1, AKT1* and *ERBB2* were assessed in the 59 male breast cancers included in this study using Sequenom MassArray. Red boxes indicate the presence of a specific mutation. **(B)** Representative Sanger sequencing chromatograms of selected validated mutations. Black arrows indicate the presence of a mutation.



Supplementary Figure S2: Repertoires of mutations and copy number alterations in ER-positive/HER2-negative male breast cancer and ER+/HER2- female breast cancer.

Somatic mutations in the 241 genes, either recurrently mutated in female breast cancer (FBC) or related to DNA repair, included in the targeted capture massively parallel sequencing assay employed in this study. The results for ER-positive/HER2-negative male breast cancer (MaBC) and ER-positive/HER2-negative FBC are ordered from top to bottom in decreasing order of mutational frequency in MaBCs (Top). Patterns of copy number alterations in MaBCs and FBCs in selected genes (Middle). Expression of ER, PR, HER2 and Ki-67 (MaBC only) as defined by immunohistochemistry (IHC) in the samples analyzed. Sequencing and copy number data of the FBCs were retrieved from The Cancer Genome Atlas (13).



Supplementary Figure S3: Cancer cell fraction and clonality of non-synonymous mutations identified in male breast cancer subjected to targeted capture massively parallel sequencing.

All mutations identified in the 241 genes assessed by targeted capture massively parallel sequencing are shown in the 59 male breast cancers studied classified into luminal A-like and luminal B-like subtypes. Each column represents one sample; genes are reported in rows. The cancer cell fraction of each mutation is color-coded according to the legend. Clonal mutations are highlighted by an orange box.