

Table S1. The panel of 91 breast cancer-related genes.

Gene							
<i>AKT1</i>	<i>CCND1</i>	<i>ESR1</i>	<i>HNF1A</i>	<i>MAP2K4</i>	<i>NF2</i>	<i>PTPN11</i>	<i>TBX3</i>
<i>ALK</i>	<i>CCND2</i>	<i>EZH2</i>	<i>HRAS</i>	<i>MAP3K1</i>	<i>NFE2L2</i>	<i>RAF1</i>	<i>TERT</i>
<i>APC</i>	<i>CCND3</i>	<i>FBXW7</i>	<i>IDH1</i>	<i>MAPK1</i>	<i>NOTCH1</i>	<i>RB1</i>	<i>TP53</i>
<i>AR</i>	<i>CCNE1</i>	<i>FGFR1</i>	<i>IDH2</i>	<i>MAPK3</i>	<i>NPM1</i>	<i>RET</i>	<i>TSC1</i>
<i>ARAF</i>	<i>CDH1</i>	<i>FGFR2</i>	<i>IGF1R</i>	<i>MDM2</i>	<i>NRAS</i>	<i>RHEB</i>	<i>TSC2</i>
<i>ARID1A</i>	<i>CDK4</i>	<i>FGFR3</i>	<i>JAK2</i>	<i>MET</i>	<i>NTRK1</i>	<i>RHOA</i>	<i>VHL</i>
<i>ARID1B</i>	<i>CDK6</i>	<i>FOXA1</i>	<i>JAK3</i>	<i>MLH1</i>	<i>NTRK3</i>	<i>RIT1</i>	<i>ZNF21</i>
<i>ATM</i>	<i>CDKN2A</i>	<i>GATA3</i>	<i>KIT</i>	<i>MPL</i>	<i>PDGFRA</i>	<i>ROS1</i>	
<i>BRAF</i>	<i>CTNNB1</i>	<i>GNA11</i>	<i>KMT2C</i>	<i>MTOR</i>	<i>PIK3CA</i>	<i>SMAD4</i>	
<i>BRCA1</i>	<i>DDR2</i>	<i>GNAQ</i>	<i>KRAS</i>	<i>MYC</i>	<i>PIK3R1</i>	<i>SMO</i>	
<i>BRCA2</i>	<i>EGFR</i>	<i>GNAS</i>	<i>MAP2K1</i>	<i>NCOR1</i>	<i>PTCH1</i>	<i>SOS</i>	
<i>CBFB</i>	<i>ERBB2</i>	<i>GRB2</i>	<i>MAP2K2</i>	<i>NF1</i>	<i>PTEN</i>	<i>STK11</i>	

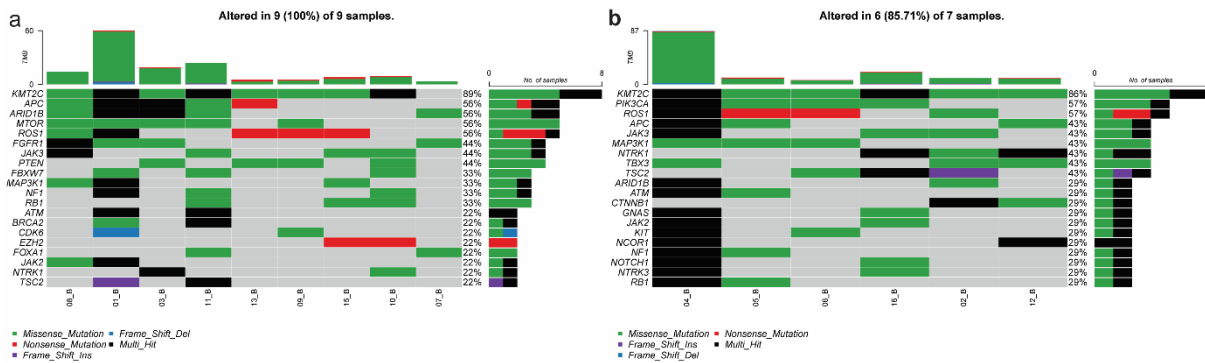


Figure S1. The top 20 most frequently mutated genes in blood samples collected at baseline for individual patients with IBC (a) or non-IBC (b). IBC: inflammatory breast cancer.

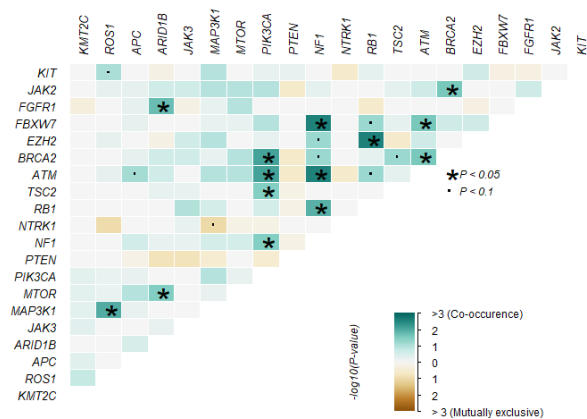


Figure S2. Co-occurrence and mutual exclusivity of mutated genes detected in baseline blood samples. Matrix depicting the degrees of co-occurrence (green scale) and mutual exclusivity (orange scale) of all possible pairwise combinations of any two mutated genes across a dataset of 20 analyzed genes.

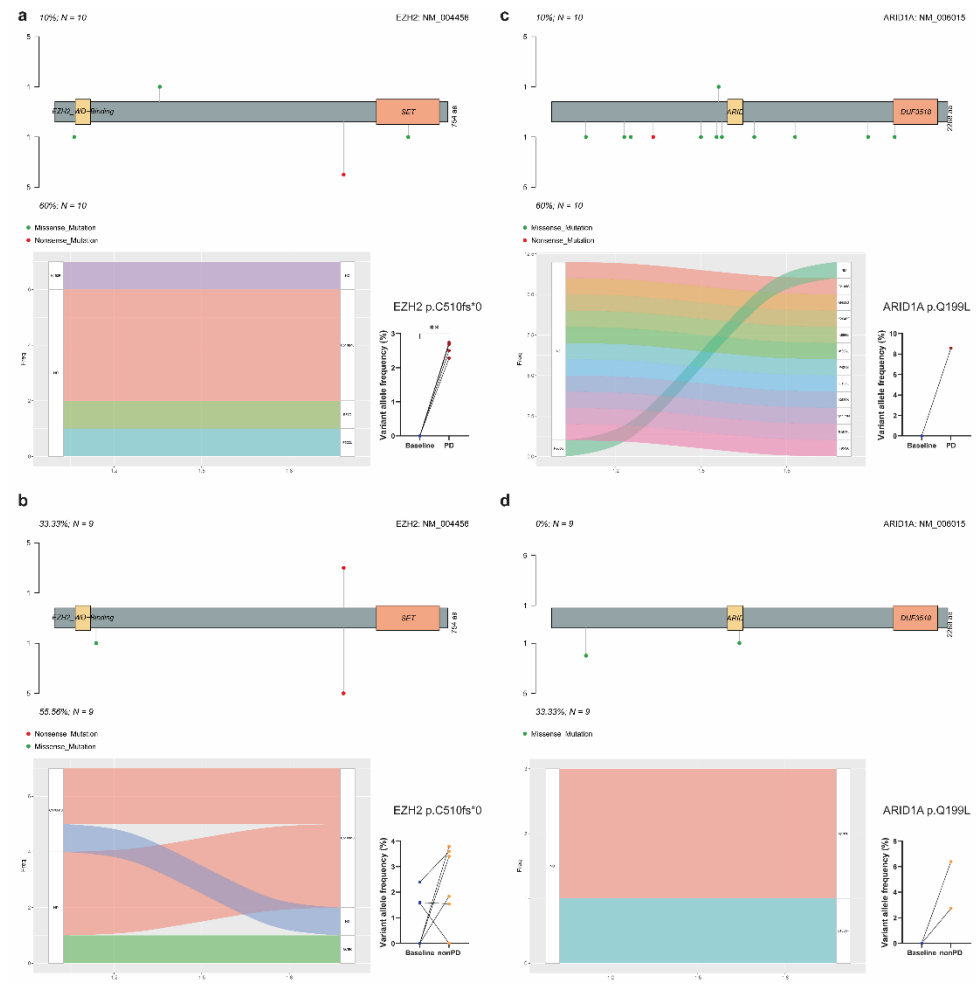


Figure S3. Changes in individual mutations in genes involved in epigenetic regulation and changes in variant allele frequency of a given mutation from baseline to follow-up as determined by analyzing paired samples. (a) and (b) show the changes in *EZH2* mutations in baseline-PD pairs or baseline-nonPD pairs. (c) and (d) show the changes in *ARID1A* mutations in baseline-PD pairs or baseline-nonPD pairs. PD: progressive disease; ND: not detected. ** represents $P < 0.01$.

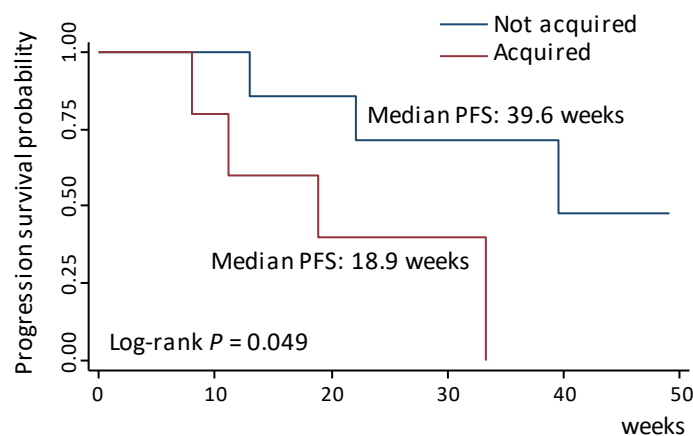


Figure S4. Kaplan-Meier curve showing survival difference between patients who acquired or did not acquire *CCNE1* mutations. PD status was determined by the first imaging test after treatment initiation. PD: progressive disease.

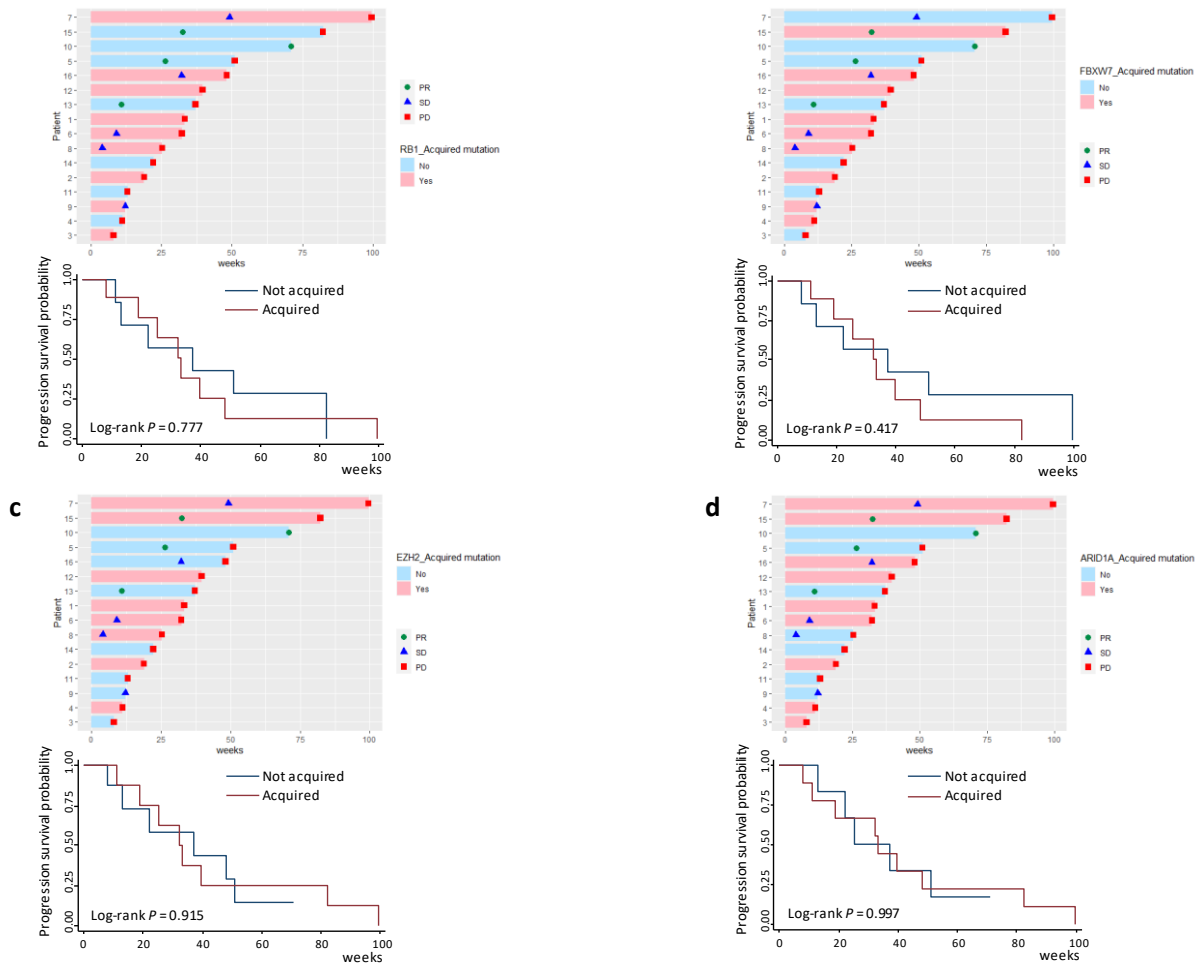


Figure S5. RECIST responses during follow-up for individual patients and survival difference between patients who acquired or did not acquire mutations in genes *RB1* (a), *FBXW7* (b), *EZH2* (c), and *ARID1A* (d). RECIST: the Response Evaluation Criteria in Solid Tumors; PD: progressive disease; PR: partial response; SD: stable disease.