

This study was carried out using publicly available data, The Cancer Genome Atlas (TCGA). The patient diagnostic tissue histology slides were downloaded from The Cancer Genome Atlas (TCGA) breast cancer (TCGA-BRCA) cohort. TCGA-BRCA microbiome, transcriptome, and clinical data, including PAM50-based molecular subtypes, were downloaded from the cBioPortal (<https://www.cbioportal.org/>). We followed the regulation policy of public data.