

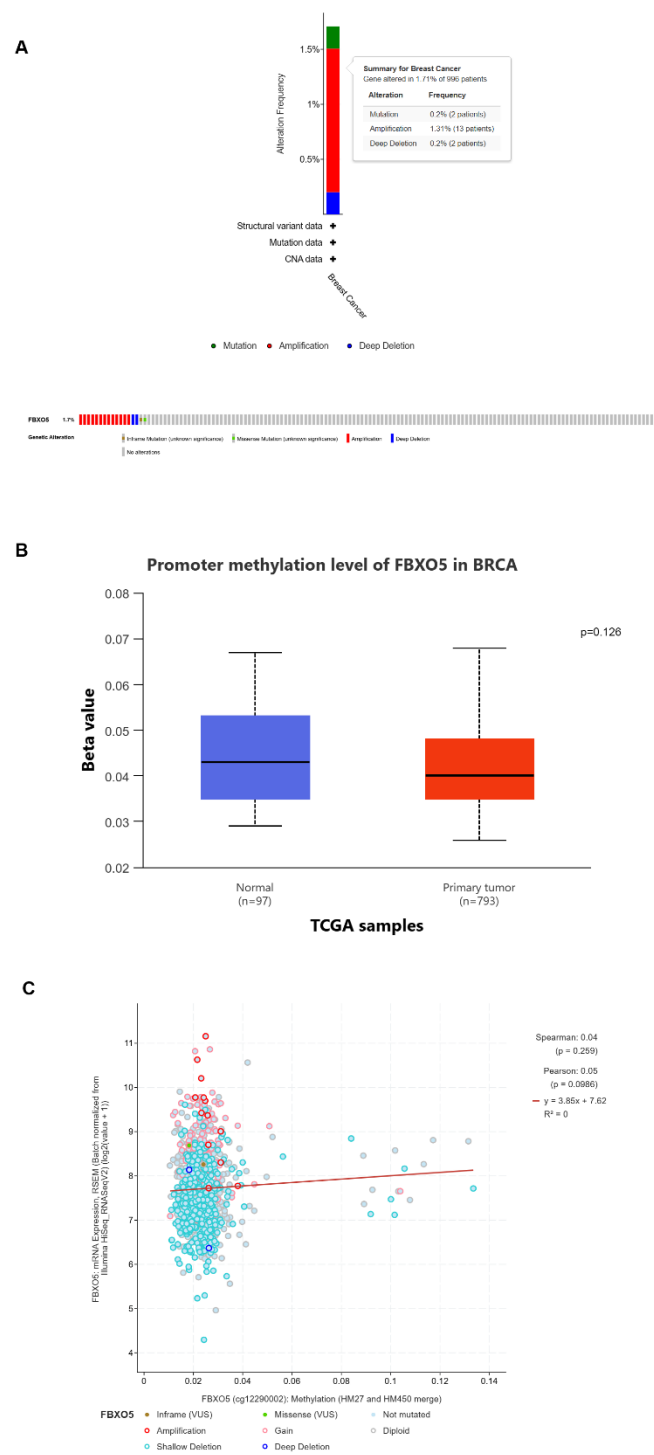


Fig. S1 FBXO5 genomic alterations and methylation status in TCGA BC cohort. **A** Frequencies of FBXO5 genomic alterations, including amplification, missense mutation, and deep deletion, in 996 BC samples, with a total alteration frequency of 1.71%. **B** Comparison of FBXO5 methylation levels between breast cancer tissues and normal tissues ($p = 0.126$). **C** Scatter plot showing correlation between FBXO5 methylation and mRNA expression (Spearman $r = 0.04$, $p = 0.259$; Pearson $r = 0.05$, $p = 0.0986$).