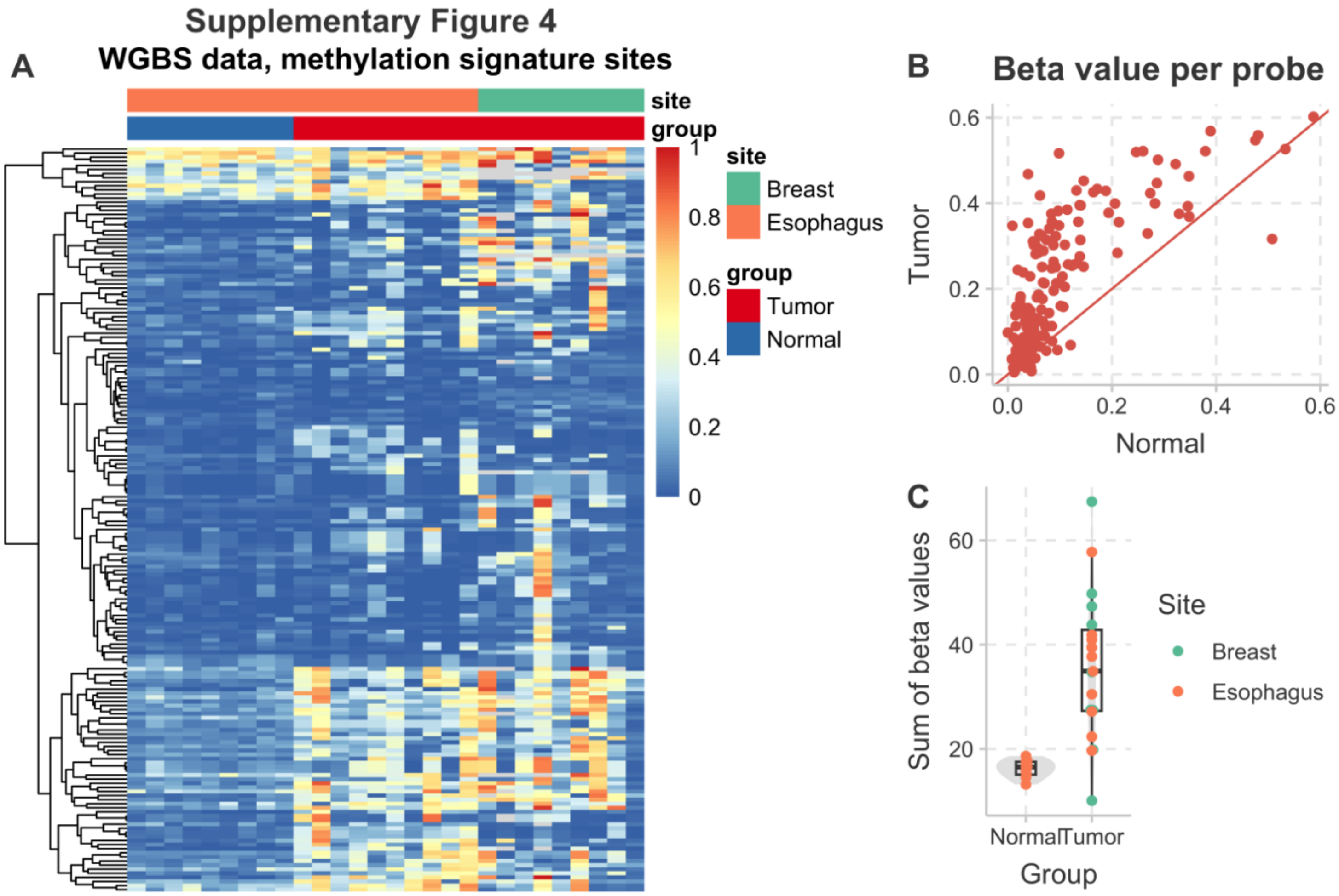

Supplementary Figure 4. Validation of the 200 CpG signature using publicly available WGBS data. A 200 CpG signature was generated using 450K array data from TCGA PanCanAtlas. We validated this signature in publicly available data from WGBS of esophageal squamous cell carcinoma and adjacent normal tissue (GSE149608), as well as breast cancers (GSE186747). (A) A heatmap of methylation beta values of our signature sites demonstrates that the methylation signature demonstrated hypermethylation in both esophageal and breast cancers relative to adjacent normal esophageal tissue. (B) A scatter plot of mean beta values, with one point for each signature window is shown. This confirms that any differentially methylated windows were generally hypermethylated in tumor relative to normal. (C) Methylation signature scores were computed by summing the beta values across all sites for each sample. This verified that tumors demonstrated higher scores than adjacent normal tissue.