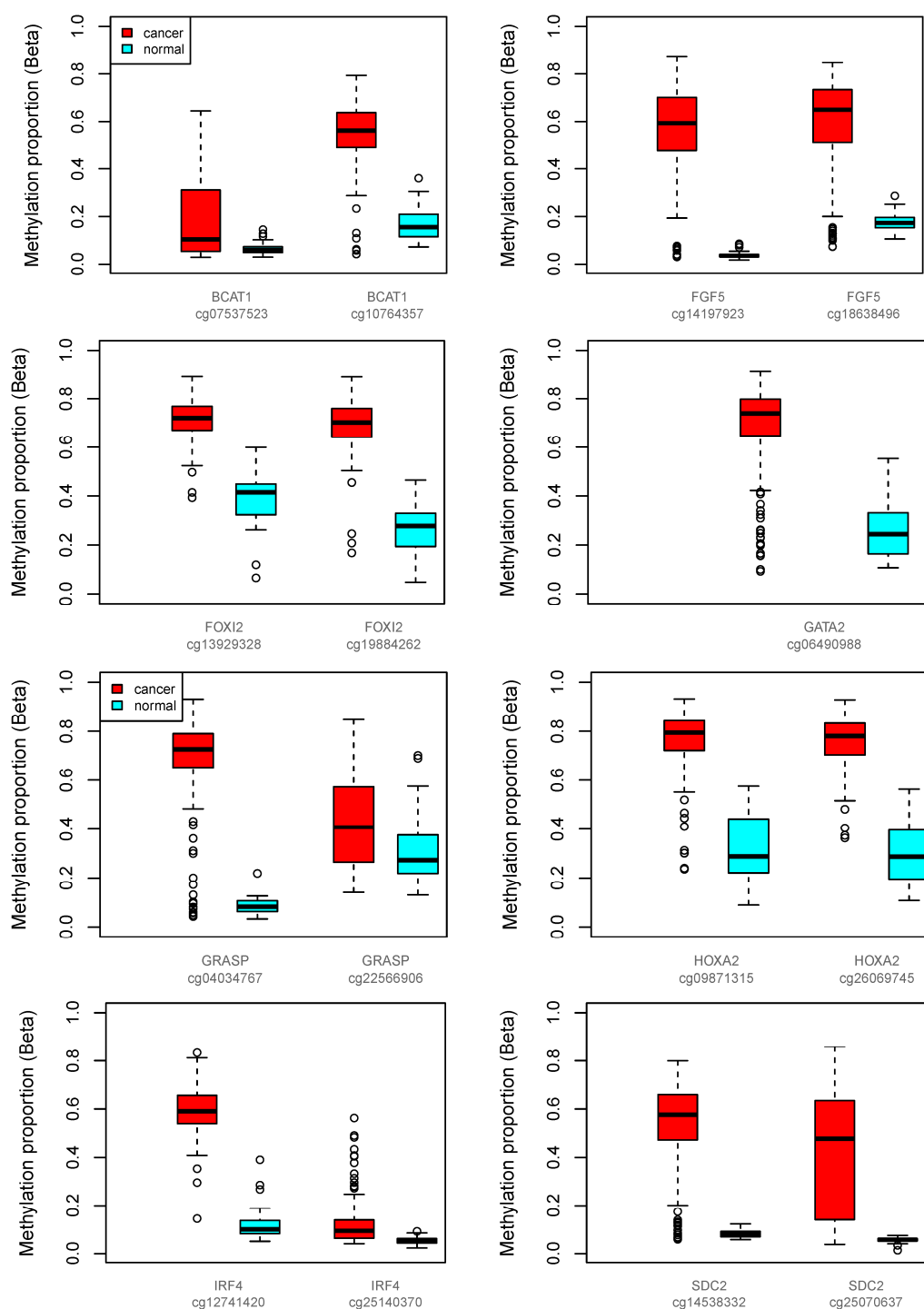


Supplementary Materials: Evaluation of Methylation Biomarkers for Detection of Circulating Tumor DNA with Application to Colorectal Cancer

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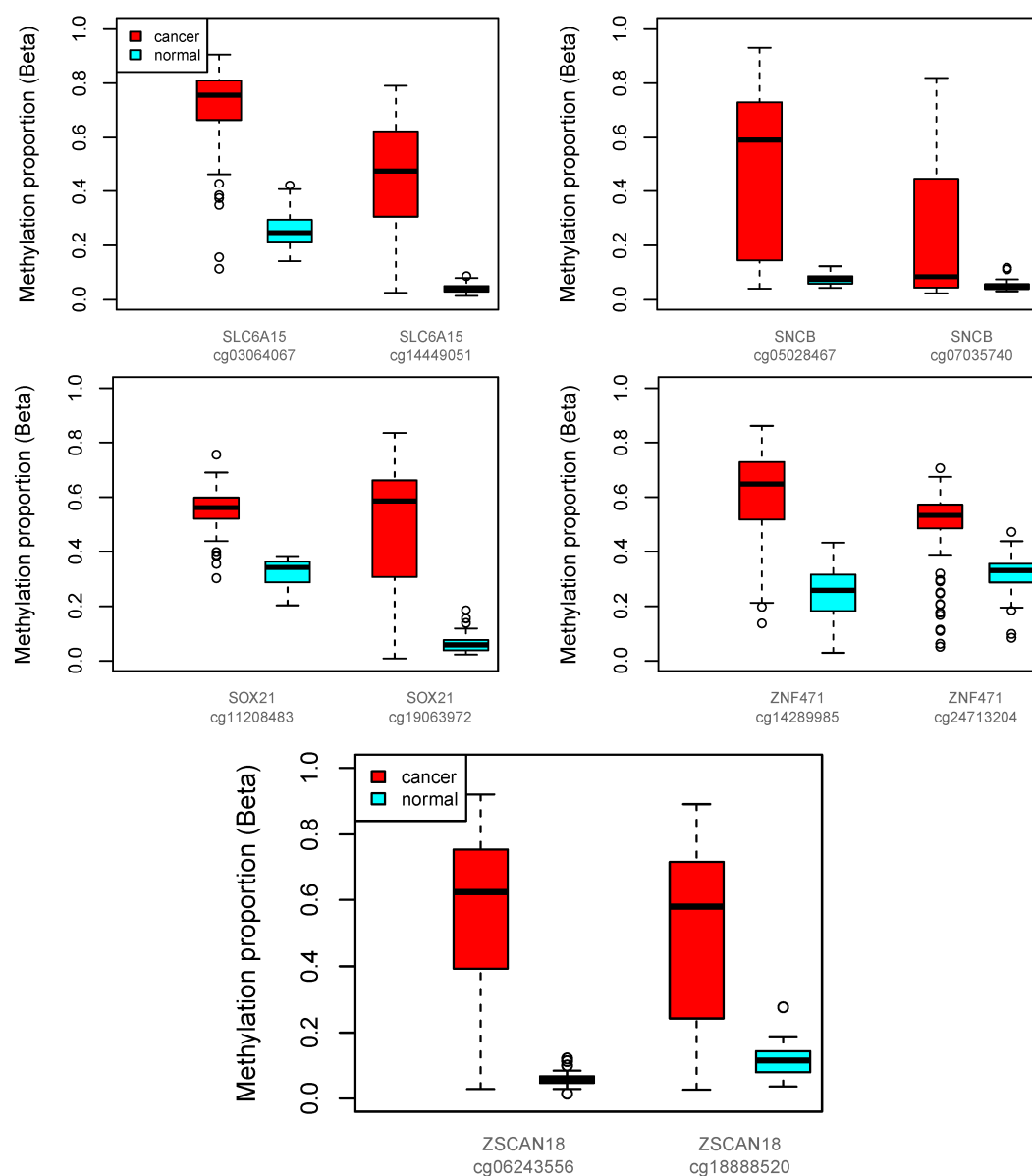


Figure S1. Methylation in cancer and normal subjects: TCGA array probe data. Box plots show ranges of methylation at individual probes on the Illumina Infinium Human Methylation27K bead array data from the Cancer Genome Atlas consortium. Red: colorectal cancer tissue samples, Blue: normal colorectal tissue. Plots are included for all genes where probes were within 800 bp of target regions and were used to guide design of conversion-specific amplicons.