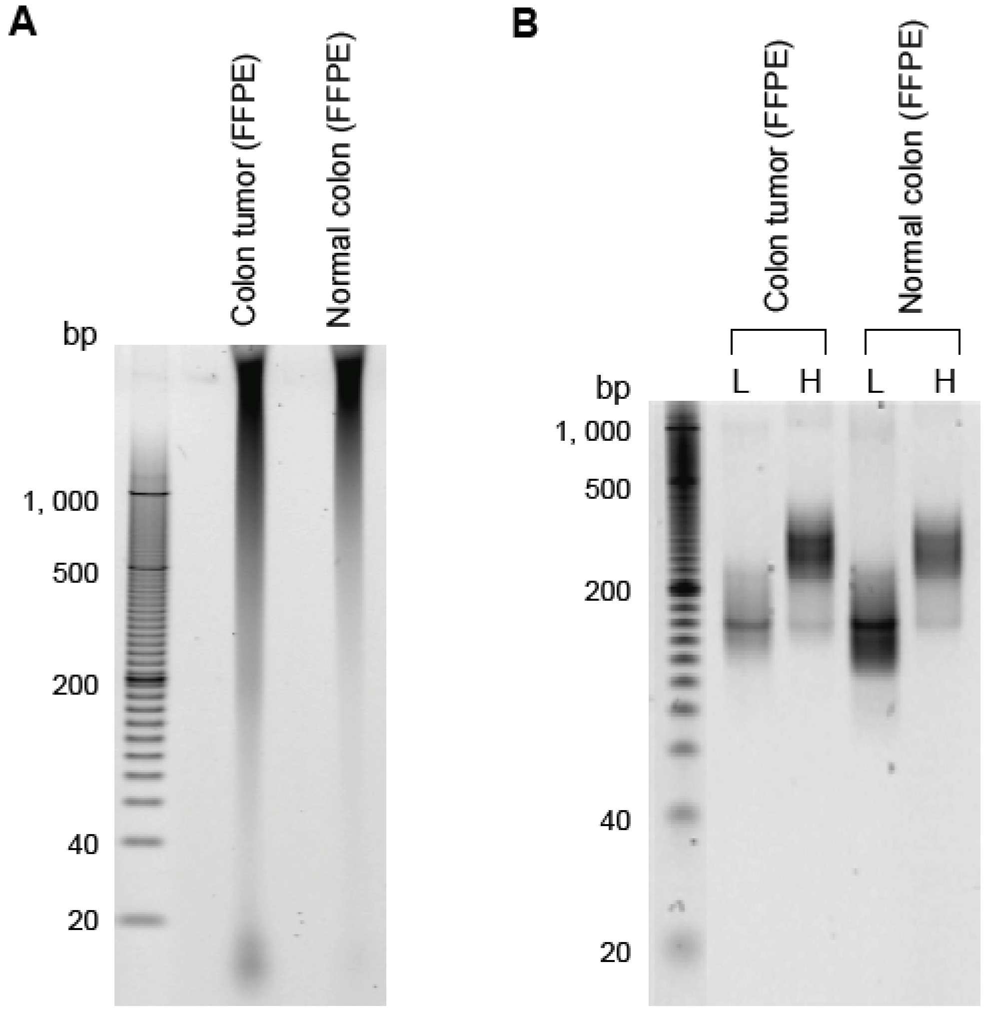
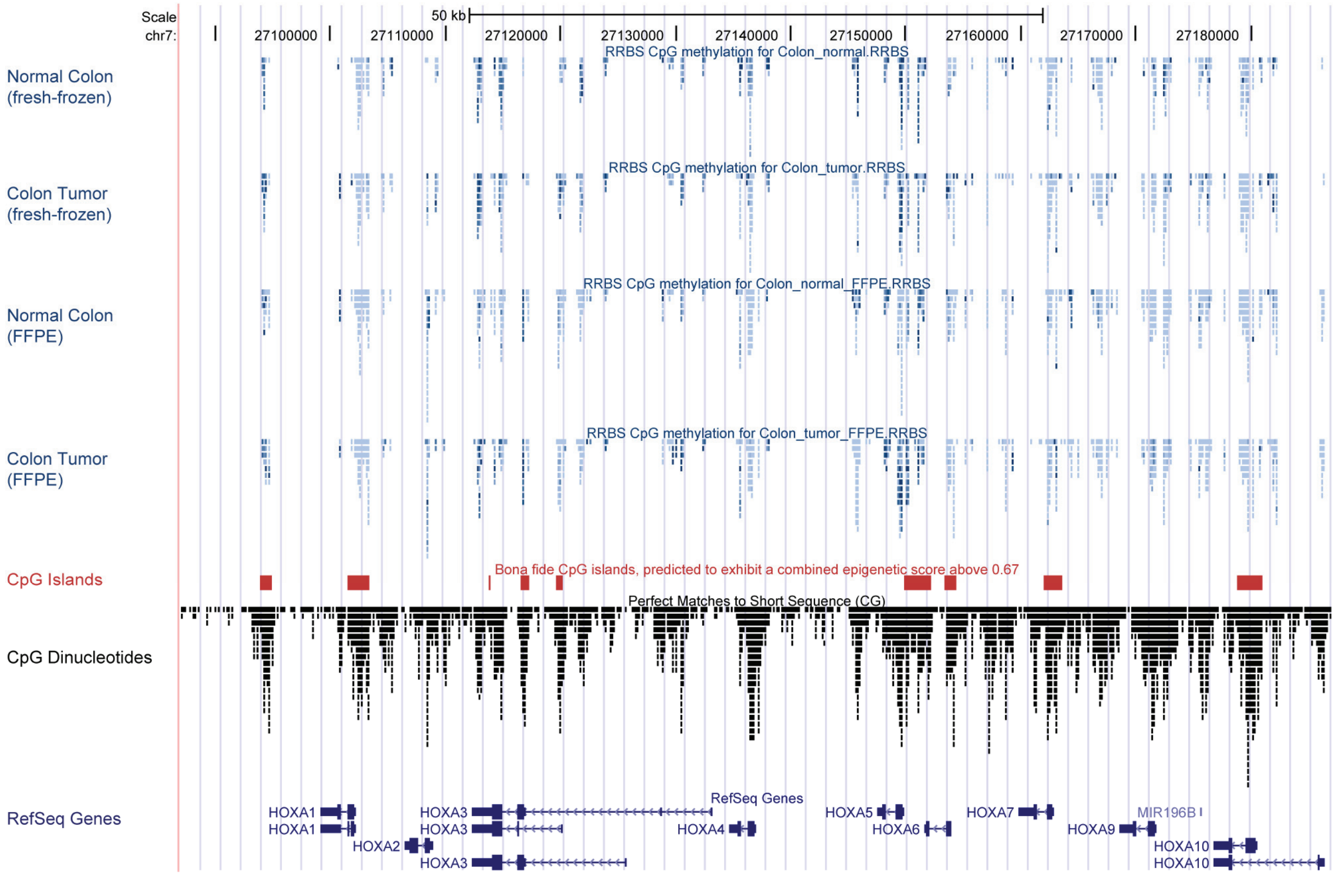
Supplementary Figure 1. Library generation from FFPE samples



The gel in **Panel A** illustrates the size distribution of genomic DNA extracted from the two FFPE samples. Purified genomic DNA (75 ng) was run on a 4-20% Criterion precast gel (Bio-Rad) and stained with SYBR green. **Panel B** shows gel electrophoresis of high (H) and low (L) fragment libraries generated from the FFPE colon tumor and matched normal samples.

Supplementary Figure 2. DNA methylation in fresh-frozen and FFPE colon samples



This UCSC Genome Browser screenshot displays the distribution of DNA methylation in the *HOXA* cluster, which is one of the more CpG-rich regions in the human genome. Data is shown for the two fresh-frozen and the two FFPE colon samples, which are in good agreement with each other although they originate from different patients. Each dot corresponds to the methylation level at a single CpG, and dark blue dots indicate higher methylation levels than light blue dots. For Infinium, the methylation levels at single CpGs are shown as percentage values. The exact genomic region shown is chr7:27,087,000-27,187,000 (hg18).

Supplementary Table 1. Pairwise correlation of DNA methylation among the patient samples

	Normal Colon (fresh-frozen)	Colon tumor (fresh-frozen)	Normal Colon (FFPE)	Colon tumor (FFPE)	Whole blood (healthy)	Whole blood (colon cancer)
Normal Colon (fresh-frozen)	1.00	0.92	0.88	0.80	0.91	0.90
Colon tumor (fresh-frozen)	0.92	1.00	0.84	0.87	0.82	0.81
Normal Colon (FFPE)	0.88	0.84	1.00	0.85	0.87	0.87
Colon tumor (FFPE)	0.80	0.87	0.85	1.00	0.77	0.74
Whole blood (healthy)	0.91	0.82	0.87	0.77	1.00	0.96
Whole blood (colon cancer)	0.90	0.81	0.87	0.74	0.96	1.00

All values are pairwise Pearson correlation coefficients, calculated for the mean DNA methylation levels of all CpGs with at least 25-fold sequencing coverage in both samples. The two pairs of colon tumor and matched normal tissue were collected from different patients.