Supplementary Table 2. Summary of enrichment analysis of genomic features

Dataset*	Total No. windows	No. feature windows	Empirical frequency	p-value**
CpG islands				
Hg18	60,614,574	486,744	0.008	
Colon cancer data				
P001	26,133	19,119	0.732	$<2.23 \times 10^{-308}$
P010	470	226	0.481	$<2.23 \times 10^{-308}$
P011	56,819	40,753	0.717	$<2.23 \times 10^{-308}$
P110	377	36	0.096	5.09×10^{-81}
P101	103	64	0.621	$<2.23 \times 10^{-308}$
P100	873	61	0.070	1.85×10^{-93}
CTCF binding sites				
Hg18	60,614,574	2,177,551	0.036	
Colon cancer data				
P001	26,133	7,626	0.292	$<2.23 \times 10^{-308}$
P010	470	92	0.196	1.15×10^{-77}
P011	56,819	9,264	0.163	$<2.23 \times 10^{-308}$
P110	377	44	0.117	1.75×10^{-17}
P101	103	7	0.068	4.03×10^{-2}
P100	873	84	0.096	5.20×10^{-22}
Repetitive elements				
Hg18	60,614,574	38,192,602	0.630	
Colon cancer data				
P001	26,133	3,533	0.135	1
P010	470	64	0.136	1
P011	56,819	5,918	0.104	1
P110	377	105	0.279	1
P101	103	27	0.262	1
P100	873	384	0.440	1

*****The colon cancer data is categorized by differential methylation patterns; Hypermethylated in CIMP only (P001), Hypermethylated in non-CIMP only (P010), Hypermethylated in all tumors (P011), Hypomethylated in CIMP only (P110), Hypomethylated in non-CIMP only (P101), and Hypomethylated in all tumors (P100).

******P values were obtained by testing the hypothesis that the frequency of genomic features in the colon cancer dataset was greater than the genome average for the same feature.

Supplementary Table 6. Clinical details of tumor samples

Sample	MSI	*BRAF*	*KRAS*	CIMP markers	Stage	Site	Differentiation
T1	Stable	WT	MUT	0/5	4	Distal	Poor
T2	Stable	WT	MUT	0/5	3	Distal	Moderate
T3	Stable	WT	MUT	0/5	2	Distal	Moderate
T4	Unstable	MUT	WT	5/5	2	Proximal	Moderate
T5	Unstable	MUT	WT	5/5	2	Proximal	Moderate
T6	Unstable	MUT	WT	5/5	2	Proximal	Moderate