

Table S1. Number of sequenced reads, mapped reads, and covered CpGs

	total reads	mapped reads	%mapped	CpGs covered
colon normal HIGH MethylCap-seq	8,611,562	5,884,046	68.3	NA
colon tumor HIGH MethylCap-seq	8,093,347	5,648,639	69.8	NA
colon normal HIGH MethylCap-BS-seq	25,019,403	12,263,052	49.0	4,608,717
colon tumor HIGH MethylCap-BS-seq	20,637,230	11,514,170	55.8	4,266,794
HCT116 MethylCap LOW	8,391,253	5,649,714	67.3	NA
HCT116 MethylCap MEDIUM	7,238,849	4,810,256	66.5	NA
HCT116 MethylCap HIGH	8,410,985	5,088,619	60.5	NA
HCT116 H3K27me3 ChIP-seq	14,292,629	11,356,014	79.5	NA
HCT116 H3K27me3 ChIP-BS-seq	79,361,626	53,319,494	67.2	7,404,348
HCT116 H3K4me3 ChIP-seq	24,340,182	19,494,155	80.1	NA
HCT116 RNAseq	30,326,735	20,700,636	68.3	NA
mouse ES V6.5 H3K27me3 ChIP-seq	100,485,300	74,612,214	74.25	NA
mouse ES V6.5 H3K27me3 ChIP-BS-seq	118,130,215	67,493,142	57.1	6,889,510
mouse ES Dnmt TKO H3K27me3 ChIP-seq	99,556,666	62,365,980	62.64	NA
mouse ES Dnmt TKO H3K27me3 ChIP-BS-seq	120,490,814	58,632,732	48.7	7,255,564
mouse ES E14 MethylCap MEDIUM	13,286,203	10,414,439	78.39	NA
mouse ES E14 MethylCap HIGH	15,410,526	7,476,739	48.52	NA