Supplementary Information for:

Regions of Focal DNA Hypermethylation and Long-Range Hypomethylation in Colorectal Cancer Coincide with Nuclear Lamina-associated Domains

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Abbreviations: hESCs (human Embryonic Stem Cells), iPSCs (induced Pluripotent Stem Cells), MR (Methylation-Resistant), MP (Methylation-Prone), ML (Methylation Loss), PMD (Partially Methylated Domain), LAD (Lamina-Associated Domain), CGI (CpG Island), TSS (Transcription Start Site), base pair (bp), kilobase (kb), megabase (Mb)

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Supplementary Note:

Bisulfite-seq library construction and bisulfite conversion

DNA libraries from each tissue sample were prepared using a customized DNA sample preparation protocol. Sample genomic DNA (5 µg) was fragmented using a S2 ultrasonicator (Covaris, Woburn, MA). Sizing of 50-100 ng fragmented DNA was performed using an Experion automated electrophoresis system and Experion 1K DNA Analysis kit (Bio-Rad, Hercules, CA) to confirm the correct average size and size range expected for each application. Fragmented DNA was repaired to blunt ends using the END-It kit (Epicentre Biotechnologies, Madison, WI). The end-repaired DNA was purified and recovered using a Qiagen MinElute PCR purification column. Addition of an 'A' base to the 3' end of blunt DNA was then accomplished using Klenow exo (3'- >5' exonuclease minus) (New England Biolabs, Ipswich, MA). The A-tailed DNA was then purified using the Qiagen MinElute PCR purification columns. Adapters with a 3' 'T' overhang were ligated to the end-modified DNA (see below).

For whole genome bisulfite sequencing, modified Illumina paired-end (PE) adapters were used in which cytosine bases in the adapter are replaced with 5-methylcytosine bases (Integrated DNA Technologies, Coralville, IA) to prevent conversion of the adapter sequence during bisulfite treatment. Double stranded annealed adapters were prepared by annealing and then ligated to the end-repaired DNA samples using ultrapure, rapid T4 ligase (Enzymatics, Beverly, MA) and purified on a Qiagen PCR purification column.

DNA libraries were bisulfite converted with the Zymo EZ DNA Methylation kit (Zymo Research, Orange, CA) according to the manufacturer's specifications. We then performed a series of MethyLight-based, quality control steps to ensure complete

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bisulfite conversion as described in the report from Campan and colleagues (PMID: 18987824). Specifically, each bisulfite-converted DNA sample was subject to four MethyLight assays to measure bisulfite conversion completeness and the amount of bisulfite converted DNA from each sample.

Quantitative PCR (qPCR) was performed on a fraction (1 ul) of the Adapterligated library using primers from Illumina (PE 1.0/2.0), master mix (Applied Biosystems 2X SYBR Green) and a serial dilution curve of PhiX library DNA as a standard using an ABI 7900HT real-time PCR machine (Applied Biosystems, Foster City, CA). Based on the amplification curve from the qPCR, the optimal cycle number was determined for each library as plateau cycle, where the reaction exits the linear phase of amplification, minus 3 cycles. Amplification of the Adapter-ligated library was performed using Pfu Cx Turbo Taq Polymerase (Stratagene, Carlsbad, CA) according to manufacturers instructions and Illumina primers (PE 1.0/2.0). A total of 30% of the bisulfite converted adapter-ligated library was added to a total of 450 ul of reaction mix, vortexed repeatedly, then divided into 9 separate wells (50uL each) for thermal cycling. Following PCR the 9 wells are pooled and PCR products are purified using a QIAquick PCR Purification kit (Qiagen, Valencia, CA). Size fractionation and removal of adapter dimers was performed using 10% TBE acrylamide gels and a 25bp ladder size standard (Invitrogen, Carlsbad, CA). An acrylamide gel slice containing the target library (typically 200-300bp) was excised from the gel, crushed and sheared to break up the acrylamide, soaked in a Tris/Ammonium Acetate buffer (10mM/2.5mM) and precipitated with Cluster density was estimated using qPCR with both PhiX library serial ethanol. dilutions and other libraries previously run with known cluster density. Amplified library DNA was denatured with NaOH prior to cluster generation. The denatured DNA was diluted to a 4pM concentration.

Illumina Genome Analyzer cluster generation and sequencing.

Attachment of the adapted DNA to the flow cell for Genome Analyzer sequencing was performed on an Illumina Cluster Station fluidics device. We use the Illumina Cluster Generation Kit to prepare each flow cell for sequencing. The protocol was performed for Amplification/Linearization/Blocking on one day and the flow cell is stored in a 50ml conical tube in storage buffer at 4°C for up to two weeks prior to sequencing. Single-end DNA sequencing (76 bp reads) of the bisulfite-converted DNA libraries from the colon tumor and normal adjacent tissues was performed using the Illumina Genome Analyzer IIx as described in ¹.

Gene expression assay (Illumina HumanRef-8 v3.0 Expression BeadChip)

All expression data are available at the NCBI Gene Expression Omnibus (http://www.ncbi.nlm.nih.gov/geo/) under accession number GSE25070. Total RNA from 25 normal pairs of colorectal tumor and non-tumor adjacent tissue samples was isolated using the TRIZOL® Reagent (Invitrogen, Burlington, ON) according to the manufacturer's protocol. The concentrations of RNA samples were measured using the NanoDrop 8000 (Thermo Fisher Scientific Inc., Waltham, MA). The quality of the RNA samples was assessed using the Experion RNA StdSens analysis kit (Bio-Rad, Hercules, CA). Expression analysis was performed using the Illumina Ref-8 wholegenome expression BeadChip (HumanRef-8 v3.0, 24,526 transcripts) (Illumina). Briefly,

RNA samples were processed using the Illumina TotalPrep RNA Amplification Kit (Illumina). Total RNA (500ng) from each sample was subject to reverse transcription with an oligo(dT) primer bearing a T7 promoter. The cDNA then underwent second strand synthesis and purification. Biotinylated cRNA was then generated from the double-stranded cDNA template through *in vitro* transcription with T7 RNA polymerase. The biotinylated cRNA (750ng) from each patient was then hybridized to the BeadChips. The hybridized chips were stained and scanned using the Illumina HD BeadArray scanner (Illumina). Scanned image and bead-level data processing were performed using the BeadStudio 3.0.1 software (Illumina). The summarized data for each bead type were then processed using the *lumi* package in Bioconductor. The data were log_2 transformed and normalized using Robust Spline Normalization (RSN) as implemented in the *lumi* package.

CpH methylation

Recent reports have identified significant DNA methylation occurring in mammalian cells at non-CpG cytosine (CpH) contexts, especially CpA ¹⁻³. We found that nuclear DNA had slightly greater CpH retention than mitochondrial DNA (0.65% retention vs. 0.25%), suggesting that there is indeed some low level methylation of nuclear CpH DNA. Bisulfite-seq reports of ES and iPSs have indicated that a significant fraction of CpHs are methylated in more than 25% of reads. When we searched for CpHs with >15 reads and at least 25% methylation, we found almost no difference between the normal tumor and colon, and both were at frequencies of approximately 0.1%, a level much more

consistent with that of somatic cell lines than hESCs or iPSCs, which generally had frequencies around 1% (Supplemental Figures S4-S5).

Bisulfite-seq identification of focal methylation elements: Methylation-Prone (MP),

Methylation-Resistant (MR), and Methylation Loss (ML)

Unmethylated regions (UMRs) were identified by scanning all windows of at least 10 individual cytosines contained within CpG dinucleotides (each CpG dinucleotide contains two, one on each strand). Only those covered by at least 3 cytosine or thymine reads were counted, and each CpG dinucleotide was assigned a weighting factor defined as the span (in base pairs) between the next CpG dinucleotide upstream and the next CpG dinucleotide downstream. A weighted average was calculated for each window, and those with an average methylation of less than 5% in both tumor and adjacent normal tissue were categorized as methylation resistant (MR). Those with less than 5% in the adjacent normal tissue and greater than 35% in the tumor were characterized as methylation prone (MR), and those with greater than 35% in the adjacent normal tissue and less than 5% in the tumor as methylation loss (ML). Two or more overlapping UMRs of a single class were merged into one. For "clustered" UMR loci, all UMRs of a single class within 500 bp of one another were merged into one.

Homer de novo motif searches

De novo Motif discovery was performed using HOMER (script v2.6 (10-22-10)), an algorithm previously described⁴. Briefly, MR, MP and ML genomic sequences were extracted using Galaxy⁵ and were divided into 'target' and 'background' sets for each

application of the algorithm (HOMER perl script 'findMotifs.pl'). When MP or MR were classified as 'target', known CpG Islands (CGI) overlapping domains were used for each application. Motifs of length 6, 7, 8, 10, 11, and 12 bp were identified separately for enrichment in 'target' compared to 'background' set using the cumulative hypergeometric distribution to score enrichment. To increase sensitivity of the method, up to two mismatches were allowed in each oligonucleotide sequence and distributions of CpG content in 'target' and 'background' sequences were selectively weighted to equalize the distributions of CpG content in both sets. To identify de novo motifs enriched in MP, 'target' was CGI overlapping MP and 'background' was CGI overlapping MR. To identify de novo motifs enriched in MR, 'target' was CGI overlapping MR and 'background' was CGI overlapping MP. To identify de novo motifs enriched in ML, 'target' was ML and 'background' was MR. Raw outputs from HOMER can be found in Supplementary Materials and Methods. HOMER perl script 'annotatePeaks.pl'4 and R software plus 'ggplot2' package6 were used to generate genomic distribution of each identified motifs.

Bisulfite-seq identification of Partially Methylated Domains (PMDs) in tumor and IMR90

Partially methylated domains were identified by scanning all windows of at least 10 kb and containing at least 10 individual cytosines contained within CpG dinucleotides (each CpG dinucleotide contains two, one on each strand). Only those covered by at least 3 cytosine or thymine reads were counted, and each CpG dinucleotide was assigned a weighting factor defined as the span (in base pairs) between the next CpG dinucleotide

upstream and the next CpG dinucleotide downstream. A weighted average was calculated for each window, and those with an average methylation between 20-60% were categorized as partially methylated. All overlapping partially methylated windows were collapsed into a single partially methylated domain (PMD), and those of less than 100 kb in length were discarded.

External data: ENCODE ChIP-seq

ChIP-seq data was downloaded from the UCSC ENCODE portal. (http://genome.ucsc.edu/ENCODE). Peaks defined for transcription factor binding clusters were highly specific, but peaks for histone modifications were overly broad so we used only the top 30% of peaks for a given mark, based on the average signal value in the ENCODE peaks files (supplemental fig X).

External data: Hi-C chromatin conformation capture data (GM12678 lymphoblastoid cells)

We used HiC compartments from GM06990 lymphoblastoid cells taken from⁷ (GEO #GSE18199). We downloaded 100 kb bin values based on the first principal component (eigenvector), and removed chromosomes 2 and 10 as the article supplement indicated that those two chromosomes did not follow the A/B compartment structure of the others. We identified compartment boundaries using the definition of two adjacent 100kb windows with negative values, followed by two adjacent windows with positive values (yielding 1,095 boundaries total, see Supplemental Data File).

External data: Replication Timing (BJ Fibroblasts)

We downloaded replication timing data from the supplemental materials of ref⁸. Based on a personal communication with the author Scott Hansen, we calculated the ratio of cells dividing at the late (S4 and G2) time points vs. the early (G1 and S1) timepoints for each locus in the genome, and identified those regions with a late:early log2-ratio of greater than 1.5. This cutoff was chosen based on a bimodal distribution of ratios, with a clear peak of early-replicating with values below -1.5, and a clear peak of late-replicating with values above 1.5 (data not shown). We merged any matching positions within 2 kb, and selected those regions larger than 100 kb as late replicating domains (yielding 1,029 late-replicating regions, see Supplemental data file).

Supplementary Table 1. Bisulfite-seq samples

													CpGs covered by	y CpGs covered by	Per cent CpGs
					Total uniquely			CpH retention	CpG retention	CpH retention	CpG retention		at least 5 non-	at least 10 non-	filtered out as
		PCR		Unique mapped	mapped	Avg	Genome	(nuclear	(nuclear	(mitochondrial	(mitochondrial	CpGs covered b	y duplicate reads	duplicate reads	possible genetic
Sample	ID	cycles	GAIIx	reads	sequence (Gb)	coverage	covered	genome)	genome)	genome)	genome)	at least 1 read	(either strand)	(either strand)	variants
Normal colon mucosa	OTB14838N	5	Single end 75bp	1,205,774,297	86.7	32.22	94.11%	0.61%	73.14%	0.25%	0.25%	87.17%	81.33%	75.74%	2.4%
Colon tumor	OTB14838T	7	Single end 75bp	1,050,881,599	75.8	28.13	94.25%	0.65%	61.98%	0.26%	0.27%	87.09%	79.43%	72.31%	3.8%

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Supplementary Table 2. Bisulfite-seq sample details

Normal Colon I	ncluding Di	apricates							High-con	idence C	pGs						High-confidence C	JUS
		Cytosine	Minimum converted							Total C/T		Jnique bases	Unique bases with at least		Jnique bases with at least			Unique ba
		maximum	CpHs for 5'		total genomic		CpGs removed	CpGs retained	Unique bases			vith at least 5		with at least 5 1			Unique bases	with at lea
		oppisite	CpG maximum conversion	total uniquely	coordinates	total sequence	5' conversion	5' conversion	covered (both		Total C r	eads (single-		reads (double- (Mean Per cent	covered (both Total C/T	otal C reads (sing
hrom	minMapQ	strand non-G	next base non-G filter	mapped reads		(bp)	filter	filter			sequence (bp)				stranded)	methylation	strands) sequence (bp) s	
hr1 hr2	3		0.101		211,260,609 226.185.997	7,031,554,208 7,563,554,712		64,942,250 63.804.488	3,870,875	59,892,578 59,778,945	43,093,105 44,576,932	3,306,768	2,616,016 2,596,842	3,711,576	3,485,912	71.19% 73.81%	79,939,278 1,303,055,382	7,439,216 68,714, 8.664.095 71.550.
1r2 1r3	3		0.101	1 105,049,371 1 86,695,031	187.499.838	6.242.037.408	5,510,420 4,221,470	47.953.236	3,727,898 2.830.916	44.701.386	33.360.036	3,227,640 2.441.877	1.957.583	3,592,105 2.726.158	3,402,780	73.81%	82,936,553 1,361,875,019 68.192.899 1.113.397.015	7.228.723 58.790
nr4	3		0.101	1 80,033,031	179 589 443			47,933,230	2,530,910	39 344 815	29 290 370	2.165.013	1,717,004	2,720,130	2,376,774	74.22%	62 671 877 989 047 918	7,228,723 58,730,
nr5	3		0.101	1 77,258,879	168,214,522			43,695,917	2,584,242	40,896,990	29,996,714	2,233,203	1,790,576	2,489,399	2,357,194	73.16%	60,790,971 988,588,905	6,506,959 52,313
ır6	3	0.101	0.101	1 74,162,466	159,991,399	5,326,983,568	3,902,141	44,225,908	2,553,557	41,350,886	30,467,734	2,204,846	1,768,450	2,460,361	2,327,991	73.32%	57,786,847 945,178,618	6,265,843 49,585
ır7	3		0.101	1 65,779,667	145,713,284	4,720,866,136		42,805,651	2,618,936	39,985,279	29,738,451	2,228,060	1,757,112	2,505,312	2,349,544	73.56%	53,349,894 852,090,136	5,421,948 45,494
nr8	3		0.101	1 63,431,077		4,567,037,544		38,445,236	2,267,074	36,078,962	26,795,919	1,968,736	1,579,681	2,190,453	2,076,673	73.52%	49,988,505 818,866,215	5,214,684 43,203,
nr9 nr10	3		0.101	1 48,702,816 1 58,707,349	106,140,129	3,506,602,752 4,221,358,568		32,153,883 40,890,421	1,984,975 2.334.717	30,243,086 38 354 884	22,107,900 28,488,153	1,692,709	1,335,463	1,898,646	1,781,566	71.84% 73.23%	39,775,169 645,307,789 46,690,092 780,612,140	3,812,255 34,187, 4,562,697 40,552
hr11	3		0.101	1 58,707,349 1 57,945,386	125,587,643	4,221,358,568	3,509,072	37,139,524		34,897,778	25,023,153	1.945.287	1,540,477	2,252,765	2,136,201	73.23%	45,690,092 /80,612,140 47,464,763 771,090,097	4,562,697 40,552, 4,367,904 40,877,
hr12	3		0.101	1 57,545,360	125,548,987	4,172,007,732	3,112,032	36,543,217	2,229,246	34,393,717	24,993,506	1,910,618	1,516,747	2,141,979	2,016,230	72.38%	46,506,429 748,890,079	4,582,362 39,923
r13	3		0.101	1 41,622,010	92,492,888	2,996,784,720		23,911,747		22,376,386	16,739,596	1,223,298	981,309	1,364,609	1,293,853	74.47%	32,566,589 519,677,265	3,744,646 27,862
r14	3	0.101	0.101	1 38,790,772	84,532,488	2,792,935,584	2,087,383	24,582,847	1,496,336	23,120,958	16,783,432	1,283,523	1,017,156	1,437,709	1,353,467	71.92%	31,420,691 508,215,112	3,103,098 27,044
r15	3		0.101	1 35,495,619	75,213,041	2,555,684,568	2,029,717	24,238,826	1,445,317	22,826,010	16,724,475	1,240,848	993,090	1,385,813	1,303,723	72.50%	28,651,367 477,881,244	2,685,195 24,782,
nr16	3		0.101	1 34,592,508	72,753,681	2,490,660,576		30,086,603		28,534,640	20,718,259	1,579,438	1,237,132	1,769,143	1,653,468	70.88%	29,020,356 482,819,319	2,357,998 25,200,
nr17	3		0.101	1 32,819,358	72,618,925	2,362,993,776	2,337,374	29,618,564	1,952,328	28,285,594	19,818,996	1,644,477	1,269,056	1,860,254	1,725,811	68.75%	29,335,234 465,344,584	2,188,699 25,183,
nr18 nr19	3		0.101	1 34,017,588 1 22,657,201	72,157,224 52,787,824	2,447,431,328	1,842,766	21,100,558 25.767.641	1,199,901 1.825.884	19,662,924	14,694,330 16.341.251	1,045,196 1,507,308	846,509 1.113.594	1,160,287 1,735,909	1,100,745	74.09% 65.67%	26,231,819 437,111,882 22,165,814 330,322,260	2,841,862 22,694, 1,332,069 18,636
nr20	3		0.101	1 22,657,201	57.625.600	2.028.663.792	1,994,708	21,566,664	1,025,004	20,426,355	14.541.883	1,307,308	898,797	1,735,909	1,171,470	69.92%	22,165,814 550,522,260 23.079.957 393.871.618	1,532,069 18,636,
nr21	3		0.101	1 15.496.466	32,918,345	1.115.745.552	969.028	11.316.216	660.845	10.568.765	7.871.080	574.592	459,444	638.221	604.112	73.64%	12.130.273 201.443.831	1,273,137 10,453
hr22	3		0.101	1 14,677,365	32,145,863	1,056,770,280		14,952,889	978,172	14,295,616	10,227,355	831,912	648,310	934,173	869,725	69.91%	13,666,922 219,074,773	876,882 11,863,
hrX	3		0.101	1 29,939,501	134,872,696	2,155,644,072	1,408,482	15,613,808	1,870,589	14,690,490	10,913,577	1,281,091	682,888	1,707,934	1,415,232	73.95%	46,581,686 379,239,566	2,471,664 31,263
hrY	3			1 3,222,428	13,954,655	232,014,816	191,238	1,760,858	166,159	1,522,248	1,132,641	108,101	58,028	145,428	118,687	75.07%	4,584,657 40,966,047	243,640 2,893,
nrM	3	0 0.101	0.101	1 993,674	16,239	71,544,528	235,873	1,856,826	783	2,040,971	5,030	702	697	757	753	0.25%	5,694 9,636,871	24,149 5,
clear genome totals				1,205,774,297	2,689,674,204	86,662,586,928	66,628,785	779,534,827	47,928,333	730,720,965	534,438,848	40,794,617	32,024,889	45,955,550	43,060,865		995,528,642 ##########	96,341,085 846,646,
			Summaries:	Mean reads per position co	worod (both et	rande)	32.22		Mean reads per CpG (each stra	ad)	15.25		High confidenc	e CpGs in sample		47,928,333		
			Julillanes.	Total bp covered in he18 (f		ranusj	2.858.034.764		Total CoGs in reference	iuj	56.328.604			ossible sequence		2.4%		
				Percentage of hg18 covere			94.1%		Total reference CpGs covered:		49.101.921		creene with pi	ossibie sequence	variant	2.470		
									Percent of reference covered (read including	87.17%							
									Percent of reference covered (81.58%							
				Mean CpH retention (nucle			0.61%		Percent of reference covered (.0 reads includi	76.45%			hylation (nuclear		73.14%		
				Mean CpH retention (mitor	chondrial geno	me)	0.25%					,	меан сро шес	hylation (mitoch	ondrial genor	0.25%		
Iormal Colon E	xcluding D	uplicates		mean CpH retention (mito	chondrial geno	me)	0.25%		High-con	fidence C	pGs		меан сро тес	hylation (mitoch	ondrial genor	0.25%	High-confidence C	oHs
Jormal Colon E	xcluding D		Minimum	Mean CpH retention (mitor	chondrial geno	me)	0.25%		· ·		•		Unique bases		Jnique bases	0.23%	High-confidence C	
Normal Colon E	xcluding D	Cytosine	converted			me)		Co Co sobole and		Total C/T		Jnique bases	Unique bases with at least	Unique bases v	Jnique bases with at least	0.2370		Unique ba
Normal Colon E	xcluding D	Cytosine maximum			total genomic		CpGs removed	CpGs retained	Unique bases	Total C/T sequence,			Unique bases with at least 10 reads		Unique bases with at least LO reads	Mean Per cent	Unique bases	
	excluding D	Cytosine	converted CpHs for 5'		total genomic coordinates		CpGs removed		Unique bases covered (both	Total C/T sequence,		Unique bases vith at least 5 : eads (single-	Unique bases with at least 10 reads (single-	Unique bases v with at least 5 1 reads (double- (Unique bases with at least LO reads		Unique bases covered (both Total C/T	Unique ba: with at lea
hrom	J	Cytosine maximum oppisite strand non-G	converted CpHs for 5' CpG maximum conversion	total uniquely	total genomic coordinates covered	total sequence	CpGs removed 5' conversion filter	5' conversion filter 55,693,355	Unique bases covered (both strands) 3,866,815	Total C/T sequence, single- stranded (bp) 52,470,518	Total C rsequence (bp) s	Jnique bases vith at least 5 : eads (single-tranded) : 3,275,861	Unique bases with at least 10 reads (single-	Unique bases v with at least 5 1 reads (double- (stranded) s 3,699,062	Unique bases with at least LO reads double-	Mean Per cent	Unique bases covered (both Total C/T	Unique ba with at lea otal C reads (sing
Normal Colon E	minMapQ 3 3	Cytosine maximum oppisite strand non-G 0 0.101	converted CpHs for 5' CpG maximum conversion next base non-G filter 0.101 0.101	total uniquely mapped reads 1 85,980,455 1 92,354,415	total genomic coordinates covered 211,125,778 226,073,954	total sequence (bp) 6,190,592,760 6,649,517,808	CpGs removed 5' conversion filter 0 4,649,722 3 4,781,114	5' conversion filter 55,693,355 55,643,376	Unique bases covered (both strands) 3,866,815 3,724,585	Fotal C/T sequence, single- stranded (bp) 52,470,518 52,203,162	Total C r sequence (bp) s 37,741,984 38,857,422	Jnique bases vith at least 5 : eads (single-tranded) : 3,275,861 3,200,320	Unique bases with at least 10 reads (single- stranded) 2,520,319 2,508,179	Unique bases v with at least 5 1 reads (double- (stranded) 3,699,062 3,581,679	Unique bases with at least 10 reads double- stranded) 3,453,680 3,375,051	Mean Per cent methylation 71.21% 73.83%	Unique bases covered (both Total C/T strands) sequence (bp) 9 79,869,127 1,146,913,356 82,872,455 1,199,399,834	Unique ba: with at lea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147, 7,648,002 70,982
orom ir1 ir2 ir3	minMapQ 3 3 3	Cytosine maximum oppisite strand non-G 0.1010 0.0101	converted CpHs for 5' CpG maximum next base non-G filter 0.101 0.101 0.101	total uniquely mapped reads 1 85,880,455 1 92,358,414 1 76,507,611	total genomic coordinates covered 211,125,778 226,073,954 187,434,938	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,543,888	CpGs removed 5' conversion filter 4,649,722 4,781,114 3,995,082	5' conversion filter 55,693,355 55,643,376 42,161,386	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807	Total C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776	Total C r sequence (bp) s 37,741,984 38,857,422 29,335,324	Jnique bases vith at least 5 : eads (single-tranded) : 3,275,861 3,200,320 2,420,764	Unique bases with at least 10 reads (single- stranded) 2,520,319 2,508,179 1,890,313	Unique bases v with at least 5 1 reads (double- (stranded) 3,699,062 3,581,679 2,717,924	Jnique bases with at least 10 reads double- stranded) 3,453,680 3,375,051 2,557,428	Mean Per cent methylation 71.21% 73.83% 74.31%	Unique bases covered (both Total C/T 1 strands) sequence (bp) s 79,869,127 1,146,913,356 82,872,455 1,199,399,834 68,146,685 983,985,353	Unique ba: with at lea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147, 7,648,002 70,982, 6,403,392 58,328,
nrom nr1 nr2 nr3 nr4	minMapQ 3 3 3 3	Cytosine maximum oppisite strand non-G 0.101 0 0.101 0 0.101 0 0.101 0 0.101 0 0.101	converted CpHs for 5' CpG maximum next base non-G filter 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 70,885,161	total genomic coordinates covered 211,125,778 226,073,954 187,434,938 179,506,091	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,543,888 5,082,131,592	CpGs removed 5' conversion filter 0 4,649,722 3 4,781,114 8 3,695,082 2 3,351,407	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807 2,525,383	Total C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261	Total C sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701	Jnique bases with at least 5 : eads (single-tranded) : 3,275,861 3,200,320 2,420,764 2,145,817	Unique bases with at least 10 reads (single- stranded) 2,520,319 2,588,179 1,695,845	Unique bases with at least 5 1 reads (double- (stranded) s 3,699,062 3,581,679 24 2,423,815	Jnique bases with at least 10 reads (double- stranded) 3,453,680 3,375,051 2,557,428 2,275,993	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24%	Unique bases covered (both Total C/T T strands) sequence (bp) s 79,869,127 1,146,913,356 82,872,455 1,199,399,834 68,146,685 983,985,353 62,623,587 874,467,075	Unique ba- with at lea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147, 7,648,002 70,982, 6,403,392 58,328, 6,428,509 52,834,
orom r1 r2 r3 r4 r5	minMapQ 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0.101 0	Converted CpHs for 5'	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 68,214,627	total genomic coordinates covered 211,125,778 226,073,954 187,434,938 179,506,091 168,139,838	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,543,888 5,082,131,592 4,911,453,144	CpGs removed 5' conversion filter 0 4,649,722 3 4,781,114 8 3,695,082 2 3,351,407 1 3,359,784	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263	Unique bases covered (both strands) 3,866,815 3,724,85 2,828,807 2,525,383 2,582,199	Total C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496	Total C r sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290	Jnique bases vith at least 5 : eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972	Unique bases with at least 10 reads (single-stranded) 2,508,179 1,890,313 1,655,845 1,729,437	Unique bases v with at least 5 1 reads (double- (stranded) s 3,699,062 3,581,679 2,717,924 2,423,815 2,482,327	Unique bases with at least 10 reads (double- stranded) 3,453,680 3,375,051 2,557,428 2,275,993 2,337,913	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19%	Unique bases covered (both Total C/T strands) sequence (bp) : 79,869,127 1,46,913,356 82,872,455 1,199,399,834 68,146,685 995,985,353 62,623,587 874,467,075 60,747,312 874,037,407	Unique ba: with at lea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147, 7,648,002 70,982, 6,403,392 58,328, 6,428,509 52,834, 5,768,257 51,898
nrom nr1	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0 0.101	converted CpHs for 5' CpG maximum next base non-G filter 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 70,885,161	total genomic coordinates covered 211,125,778 226,073,954 187,434,938 179,506,091	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,543,888 5,082,131,592	CpGs removed 5' conversion filter 1 4,649,722 4,781,114 8 3,695,082 2 3,351,407 3,359,784 6 3,319,038	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807 2,525,383 2,582,159 2,551,533	Total C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261	Total C sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701	Jnique bases with at least 5 : eads (single-tranded) : 3,275,861 3,200,320 2,420,764 2,145,817	Unique bases with at least 10 reads (single- stranded) 2,520,319 2,588,179 1,695,845	Unique bases with at least 5 1 reads (double- (stranded) s 3,699,062 3,581,679 24 2,423,815	Jnique bases with at least 10 reads (double- stranded) 3,453,680 3,375,051 2,557,428 2,275,993	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24%	Unique bases covered (both Total C/T T strands) sequence (bp) s 79,869,127 1,146,913,356 82,872,455 1,199,399,834 68,146,685 983,985,353 62,623,587 874,467,075	Unique ba- with at lea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147, 7,648,002 70,982, 6,403,392 58,328, 6,428,509 52,834,
nrom 1r1 1r2 1r3 1r4 1r5 1r6	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0 0.101	Converted Converted Cpth for 5' CpG maximum Conversion next base non-G filter 0.101	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 70,585,161 1 68,214,627 1 64,741,748	total genomic coordinates covered 211,125,778 226,073,954 187,434,938 179,506,091 168,139,838 159,932,089	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,543,888 5,082,131,592 4,911,453,144	CpGs removed 5' conversion filter 1 4,649,722 4,781,114 8 3,695,082 2 3,351,407 3,359,784 6 3,319,038	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263	Unique bases covered (both strands) 3,866,455 2,828,807 2,525,333 2,582,159 2,551,533 2,616,552 2,264,996	Total C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496 35,622,893	Total C r sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793	Jnique bases vith at least 5 : eads (single-tranded) : 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,185,937	Unique bases with at least 10 reads (single- stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,707,776	Unique bases v with at least 5 1 reads (double- (stranded) s 3,699,062 3,581,679 2,717,924 2,423,815 2,482,327 2,453,155	Jnique bases with at least LO reads double- stranded) 3,453,680 3,375,051 2,557,428 2,275,993 2,337,913 2,308,725	Mean Per cent methylation 71.21% 73.83% 74.31% 73.19% 73.34%	Unique bases covered (both Total C/T strands) sequence (bp) ; 79,869,127 1,46,591,356 82,872,455 1,199,398,346 68,146,685 983,885,356 62,623,598 7874,67,075 60,747,312 874,037,405 57,746,902 826,721,957	Unique bas with at lea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147, 7,648,002 70,982, 6,403,392 58,328, 6,428,509 52,834, 5,768,257 51,898, 5,516,154 49,186
rom 11 12 13 14 15 16 17 17	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0 0.101	Converted CpHs for 5'	total uniquely mapped reads 1 85,880,455 1 76,507,611 1 70,585,161 1 68,214,627 1 64,741,748 1 57,809,071	total genomic coordinates covered 211,125,778 226,073,954 187,434,938 179,506,091 168,139,838 159,932,089 145,633,704	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,543,888 5,082,131,453,144 4,661,405,856 4,162,253,112	CpGs removed 5' conversion filter 4,649,722 4,781,114 3,695,082 3,351,407 4,3,359,784 3,319,038 6,319,038	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648 37,337,576	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807 2,525,333 2,582,159 2,551,533 2,616,552	Total C/T iequence, ingle- itranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496 35,622,893 35,108,929	Total C r sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945	Jnique bases vith at least 5 : eads (single-tranded) : 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,185,937 2,206,872	Unique bases with at least 10 reads (single- stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,729,437 1,707,776	Unique bases v with at least 5 1 reads (double- stranded) s 3,699,062 3,581,679 2,717,924 2,423,815 2,482,327 2,453,155 2,496,906	Jnique bases with at least 10 reads double-stranded) 3,453,680 3,375,051 2,557,482 2,275,993 2,337,912 2,308,722 2,327,107	Mean Per cent methylation 73.83% 74.31% 74.24% 73.19% 73.34% 73.58%	Unique bases covered (both Total C/T strands) sequence (bp) 1 79,869,127 1,146,913,356 82,872,455 1,199,934 68,146,685 983,985,353 62,623,587 874,467,075 60,747,312 874,467,075 53,304,520 751,223,973 53,304,520 751,223,973	Unique bawith at lea requence (bp) strander) 6,548,785 68,147,7,648,002 70,982 6,403,392 58,328,6,428,509 52,834,5,768,257 51,888,5516,154 49,186,4788,523 45,098,
rom r1 r2 r3 r4 r5 r6 r7 r8 r9	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0 0.101	converted chairs for 'S' converted chairs for 'S' conversion next base non-G filter 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 85,804,5414 1 76,507,611 1 70,585,161 1 68,214,627 1 64,741,748 1 57,900,071 1 55,964,454 1 42,911,927 1 51,234,303	total genomic coordinates covered 211,125,778 226,073,954 187,434,938 159,932,089 145,633,704 136,313,188 106,042,601 106,042,601	total sequence (bp) 6,190,592,760 6,649,517,808 5,082,543,592 4,911,453,44 4,661,405,856 4,162,253,112 4,029,440,688 3,089,658,746	CpGs removed 5' conversion filter 4,649,722 4,781,114 3,595,082 2,3351,407 3,359,707 4,3359,707 6,3	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648 37,337,576 33,830,771 28,329,125 35,031,302	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807 2,525,383 2,582,159 2,551,533 2,616,552 2,264,996 1,982,899 2,332,921	rotal C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496 35,622,893 35,108,929 31,762,707 26,681,819 32,974,031	Total C r sequence (bp) s 37,741,984 838,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945 23,565,128 19,476,148 24,397,233	Jnique bases vith at least 5 eads (single-tranded)	Unique bases with at least 10 reads (single- stranded) 2,520,319 1,890,313 1,655,845 1,729,437 1,707,776 1,691,402 1,525,562 1,286,845	Unique bases v with at least 5 1 reads (double- (stranded) 2,717,924 2,423,815 2,482,327 2,433,155 2,496,906 2,184,601 1,892,627 2,246,728	Jnique bases with at least 10 reads double- tranded) 3,453,68(3,375,051 2,275,992 2,337,913 2,327,100 2,060,037 1,765,445 2,119,900	Mean Per cent methylation 71.21% 73.63% 74.31% 74.22% 73.19% 73.58% 73.54% 71.86% 73.25%	Unique bases covered (both Total C/T 1 starads, 59, 127 1,46,513,356 22,872,455 1,199,399,834 68,146,685 983,885,33 26,623,587 874,467,075 60,747,312 874,037,467 57,746,902 826,721,957 53,304,520 751,223,93 49,952,165 773,863,63 39,735,179 569,817,76 46,654,320 685,036,195	Unique ba with at lea equence (bp) stranded) 6,548,785 68,147,7,648,002 70,982 6,403,392 58,328,6428,509 52,834 4,788,523 45,008 4,614,402 42,868 3,363,268 33,907,399,44,3 40,240
rom r1 r2 r3 r4 r5 r6 r7 r8 r9 r10	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0.101 0 0.101	converted (Pist for 5') CpG maximum convertion next base non-6 filter () 0.101 () 0.	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 68,214,627 1 64,741,748 1 57,809,071 1 55,964,454 1 42,911,927 1 51,234,303 1 51,054,235	total genomic coordinates covered 226,073,954 187,434,938 1168,139,838 145,633,704 136,312,138 106,042,601 123,527,820	total sequence (bp) 6,190,592,760 6,649,517,808 5,508,2131,592 4,911,453,144 4,661,405,864 4,162,253,112 4,029,440,888 3,089,658,744 3,688,869,816 3,675,904,905	CpGs removed 5' conversion filter 4,649,722 4,4649,722 3,351,407 4 3,359,784 3,319,038 2,360,499 2,26,053 2,360,499 6 2,942,041 2,727,249	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648 37,337,576 33,830,771 28,329,125 35,031,302 32,699,549	Unique bases covered (both strands) 3,866,815 3,724,958 2,828,807 2,525,838 2,581,159 2,551,533 2,616,552 2,264,996 1,982,899 2,332,921 2,258,884	rotal C/T sequence, single- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,622,893 35,108,929 31,762,707 26,681,819 32,974,031 30,762,355	Total C r sequence (bp s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945 23,565,128 19,476,148 24,397,233 22,030,622	Unique bases vith at least 5: eads (single-tranded) 3,275,861 3,200,320 4,20,764 2,145,817 2,13,972 2,06,872 1,952,481 1,677,259 2,016,020 1,928,483 1,928,483 1,928,483	Unique bases with at least 10 reads (single-stranded) 2,520,319 2,508,179 1,890,313 1,702,776 1,691,402 1,525,62 1,286,845 1,588,284 1,484,391 1,484,391	Unique bases v with at least 5 reads (double- (stranded) s 3,699,062 3,581,679 2,717,924 2,423,815 2,482,327 2,453,155 2,496,906 2,128,601 1,892,627 2,246,728 2,170,979	Jnique bases with at least to reads double-tranded) 3,453,681 3,375,051 2,257,428 2,277,993 2,337,913 2,308,725 2,327,107 2,060,033 1,765,445 2,119,904 2,033,708 1,000	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.54% 71.66% 73.25% 70.74%	Unique bases cowered (both Total C/T 1 strands) sequence (bp) 1 79,869,127 1,146,913,656 82,872,455 1,199,399,834 68,146,685 983,935,33 62,623,587 874,467,075 60,747,312 874,037,07 57,746,902 826,721,957 53,304,520 751,221,93 49,952,165 723,885,336 39,785,779 569,817,579 569,817,179 46,654,320 685,036,195 47,429,148 680,956,195	Unique ba with at lea cads (sing at least
rrom 11 12 13 14 15 15 16 17 18 19 10 10 10 11 11 11 11	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0.101 0 0.101	converted	total uniquely mapped reads 1 85,980,455 1 92,354,414 1 76,507,611 1 79,585,161 1 68,214,6,27 1 64,741,748 1 57,809,071 1 55,964,454 1 42,911,927 1 51,234,303 1 51,054,235 1 50,786,765	total genomic coordinates covered 211,125,78 187,43,938 159,932,089 145,633,70 116,813,218 106,042,601 123,527,820 125,438,967	total sequence (bp) 6,190,592,760 6,649,517,808 5,082,131,592 4,911,453,144 4,661,405,856 4,162,253,112 4,029,440,688 3,089,658,744 3,688,869,874 3,688,869,874	CpGs removed 5' conversion filter 4,469,722 (4,649,722 (4,649,722 (4,649,722 (4,649,722 (4,649,724	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648 37,337,576 33,830,771 28,329,125 35,031,302 32,699,549 32,203,169	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807 2,555,383 2,582,159 2,551,533 2,616,552 2,264,996 1,982,899 2,332,921 2,258,884 2,227,631	Total C/T sequence, ingle- stranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496 35,622,893 35,108,929 31,762,707 26,681,819 32,974,031 30,323,950 30,323,950	Total C r sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945 23,565,128 19,476,148 24,397,233 22,030,622 22,015,087	Inique bases to that a least 5 and (single-tranded) 3,275,861 3,200,320 4,420,764 1,45,817 2,13,972 2,185,937 2,206,872 1,677,299 1,677,299 1,677,289 1,878,483 1,878,485 1,87	Unique bases with at least 10 reads single-stranded) 2,520,319 2,508,179 1,890,313 1,707,776 1,691,402 1,525,562 1,286,843 1,128,433 1,1484,391 1,461,906	Unique bases v with at least 5 reads (double- stranded) as 3,599,062 3,581,679 2,717,942 2,423,815 2,482,327 2,485,315 2,496,906 2,184,601 1,892,627 2,246,728 2,170,979 2,155,362	Unique bases with at least 10 reads double-stranded) 3,455,865 3,375,051 2,557,428 2,275,999 2,337,913 2,060,037 1,765,448 2,119,904 2,033,708 1,997,975	Mean Per cent methylation 71.21% 73.83% 74.13% 74.24% 73.19% 73.58% 73.58% 73.54% 73.55% 70.74% 72.39%	Unique bases covered (both Total C/T strands)	Unique bawith at tea vith at tea fotal C reads (sing equence (bp) stranded) 6,548,785 68,147,70,992, 6,403,392 58,328, 5,768,257 51,898, 5,768,257 51,898, 4,788,523 45,098, 4,734,402 42,868, 3,363,268 33,907, 3,394,413 40,240, 3,857,582 40,549, 4,054,946 39,592,
rom 11 12 13 14 15 16 17 18 19 10 10 11 11 11 11 11 11	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0.101 0	Converted Converted Converted Converted Convertion Conversion Convers	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 62,214,627 1 64,741,748 1 57,809,071 1 55,964,454 1 42,911,927 1 51,224,303 1 51,054,235 1 50,786,765 1 36,811,037	total genomic coordinates covered 211,125,778 226,073,954 179,956,091 168,139,838 179,956,091 145,633,704 136,313,218 106,042,601 123,527,820 7125,501,918 92,462,370	total sequence (bp) 6,190,592,760 6,649,517,800 5,508,243,888 5,508,243,888 4,61,405,864 4,61,405,864 4,61,405,864 4,62,244,068 3,689,565,744 3,688,869,816 3,675,904,92 3,656,647,080	CpGs removed 5' conversion filter 4,498,722 4,781,114 3,695,082 3,351,407 1,335,978 1,335,980 2,260,633 1,250,603 1,2727,246 1,2727,246 1,2772,473 1,2775,753 1,278,733	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648 37,337,576 33,830,771 28,329,125 35,031,302 32,699,549 32,203,169 21,051,801	Unique bases covered (both strands) 3,866,815 3,724,958 2,828,807 2,525,838 2,616,552 2,264,996 1,982,899 2,332,921 2,255,884 2,227,631 1,412,183	Total C/T requence, single-tranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496 35,622,893 31,762,707 26,681,819 26,764,031 30,762,355 30,323,950 19,707,113	Total C sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945 23,565,128 19,476,148 24,397,233 22,030,622 22,015,087 14,731,177	Jnique bases with at least 5 eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,06,872 1,952,481 1,677,259 2,016,020 1,928,483 1,892,935 1,213,218	Unique bases with at least 10 reads (single-stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,707,776 1,691,402 1,525,562 1,286,845 1,588,284 1,464,391 1,461,906 948,177 948,177	Unique bases v with at least 5 reads (double- f strander) 3,699,062 3,699,062 2,717,924 2,423,815 2,482,327 2,483,155 2,496,906 2,184,601 1,892,627 2,246,728 2,170,979 2,135,362	Jnique bases with at least 10 reads double- stranded) 3,453,680 3,375,051 2,557,428 2,337,915 2,308,725 2,327,107 2,060,037 1,765,445 2,119,900 2,033,708 1,979,797 4,128,404	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.54% 71.86% 73.25% 70.74% 72.39% 74.49%	Unique bases covered (both Total C/T strands) sequence (bp) 1 79,869,127 1,146,913,66 82,872,455 1,199,399,834 68,146,685 983,895,336 62,232,587 874,467,075 60,747,312 874,074,7312 874,074,7312 874,074,527 53,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 74,429,148 680,954,304 46,473,424 662,402,420 32,544,637 460,624,637 460,	Unique ba with at lea cotal C reads (single ba with at lea cotal C reads (single based bas
rom 11 12 23 33 34 45 55 67 77 89 91 111 112 113	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0 0.101	Converted Conv	total uniquely mapped reads 1 85,980,455 1 92,254,414 1 76,307,611 1 70,585,161 1 68,214,6,27 1 64,741,748 1 42,911,927 1 51,234,303 1 51,054,235 1 50,786,765 1 36,811,037	total genomic coordinates cowered 211,125,778 226,073,954 179,506,091 168,139,833 159,932,089 4136,313,218 106,042,601 123,527,820 125,438,967 125,501,918 92,462,370	total sequence (bp) 6.190.592,760 6.649.517,808 5.508,243,1529 4.911,453,144 4,661,405,856 4,162,253,112 4,029,440,683 3,688,869,316 3,685,664,709 2,650,394,664	CpGs removed 5' conversion filter 4,649,722 4,781,114 3,595,082 3,351,407 3,359,784 6,3183,980 2,2826,033 2,260,499 2,727,249 1,277,249 1,1832,142 1,1842,142 1,1842,	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,042,648 37,337,576 33,830,771 28,329,125 35,031,302 32,699,549 32,203,169 21,653,837	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,907 2,555,383 2,616,552 2,264,996 1,982,899 2,332,921 2,258,884 2,227,631 1,412,188 1,495,170	rotal C/T requence, ingle-tranded (bp) 52,470,518 52,203,162 39,343,776 35,622,893 31,762,707 26,681,819 30,762,355 30,323,950 19,707,113 20,384,419 20,38	Total C sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945 23,565,128 19,476,148 24,397,233 22,030,622 22,015,087 14,773,177 14,775,320	Jnique bases vith at least 5 cads (single- tranded) 3,275,861 3,275,861 2,145,817 2,213,972 2,185,937 2,2185,937 2,016,020 1,928,481 1,677,259 2,016,020 1,928,483 1,213,966 1,927,956 1,213,218 4,823,955 1,213,218 4,271,966	Unique bases with at least 10 reads (10 reads (15 reads	Unique bases with at least 5 reads (double, stranded) 5 3,699,662 3,581,679 2,717,924 2,423,815 2,445,327 2,453,155 2,456,906 2,184,601 1,892,627 2,170,979 2,155,362 1,360,996 1,433,253 1,433,253	Jnique bases with at least 10 reads double-tranded) 3,453,68(3,375,051 2,557,428 2,275,99 2,337,915 2,308,725 2,327,107 2,060,037 1,765,448 2,119,904 2,033,708 1,997,974 1,284,041 1,344,825	Mean Per cent methylation 71.21% 73.83% 74.13% 74.24% 73.19% 73.58% 73.58% 73.55% 70.74% 72.39% 74.49% 71.94%	Unique bases covered (both Total C/T stemarks) 52,872,455 1,194,591,356 82,872,455 1,194,591,399,834 68,146,685 983,885,335 26,623,587 874,467,075 60,747,312 874,637,465,902 282,721,957 53,304,520 751,223,193 49,952,165 723,686,336 39,735,179 569,817,7429,148 680,954,320 680,954,320 646,473,424 6626,420 232,544,637 460,659,643 240 680,954,313,396,432 449,468,881	Urique ba with at lea total C reads (in the control of the control
rom r1 r2 r3 r4 r5 r6 r7	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G 0 0.101	Converted Converted Converted Converted Convertion Conversion Convers	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 62,214,627 1 64,741,748 1 57,809,071 1 55,964,454 1 42,911,927 1 51,224,303 1 51,054,235 1 50,786,765 1 36,811,037	total genomic coordinates covered 211,125,778 226,073,954 179,956,091 168,139,838 179,956,091 145,633,704 136,313,218 106,042,601 123,527,820 7125,501,918 92,462,370	total sequence (bp) 6,190,592,760 6,649,517,800 5,508,243,888 5,508,243,888 4,61,405,864 4,61,405,864 4,61,405,864 4,62,244,068 3,689,565,744 3,688,869,816 3,675,904,92 3,656,647,080	CpGs removed 5' conversion filter 4,498,722 4,781,114 3,695,082 3,351,407 1,335,978 1,335,980 2,260,633 1,250,603 1,2727,246 1,2727,246 1,2772,473 1,2775,753 1,278,733	5' conversion filter 55,693,355 55,643,376 42,161,386 37,120,365 38,441,263 38,022,648 37,337,576 33,830,771 28,329,125 35,031,302 32,699,549 32,203,169 21,051,801	Unique bases covered (both strands) 3,866,815 3,724,958 2,828,807 2,525,838 2,616,552 2,264,996 1,982,899 2,332,921 2,255,884 2,227,631 1,412,183	Total C/T requence, single-tranded (bp) 52,470,518 52,203,162 39,343,776 34,499,261 35,997,496 35,622,893 31,762,707 26,681,819 26,764,031 30,762,355 30,323,950 19,707,113	Total C sequence (bp) s 37,741,984 38,857,422 29,335,324 25,688,701 26,391,290 26,190,793 26,069,945 23,565,128 19,476,148 24,397,233 22,030,622 22,015,087 14,731,177	Jnique bases with at least 5 eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,06,872 1,952,481 1,677,259 2,016,020 1,928,483 1,892,935 1,213,218	Unique bases with at least 10 reads (single-stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,707,776 1,691,402 1,525,562 1,286,845 1,588,284 1,464,391 1,461,906 948,177 948,177	Unique bases v with at least 5 reads (double- f strander) 3,699,062 3,699,062 2,717,924 2,423,815 2,482,327 2,483,155 2,496,906 2,184,601 1,892,627 2,246,728 2,170,979 2,135,362	Jnique bases with at least 10 reads double- stranded) 3,453,680 3,375,051 2,557,428 2,337,915 2,308,725 2,327,107 2,060,037 1,765,445 2,119,900 2,033,708 1,979,797 4,128,404	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.54% 71.86% 73.25% 70.74% 72.39% 74.49%	Unique bases covered (both Total C/T strands) sequence (bp) 1 79,869,127 1,146,913,66 82,872,455 1,199,399,834 68,146,685 983,895,336 62,232,587 874,467,075 60,747,312 874,074,7312 874,074,7312 874,074,527 53,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 751,213,304,520 74,429,148 680,954,304 46,473,424 662,402,420 32,544,637 460,624,637 460,	Unique ha with at lea with at lea could be counted by 3 randed by
rom 11 12 13 14 15 16 17 17 17 18 19 10 111 112 113 114	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite command on Grand on Gr	Converted Converted Converted Converted Converted Convertion Conversion Conversi	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 62,214,627 1 64,741,748 1 57,809,071 1 55,964,454 1 57,809,071 1 51,234,303 1 51,054,235 1 50,786,765 1 36,811,037 1 34,426,172 1 31,175,259 1 30,180,257 1 30,180,257 1 28,943,009	total genomic coordinates covered 211,125,778 226,073,954 187,43,938 116,932,089 145,633,704 123,527,820 125,438,967 125,501,918 92,462,370 84,491,577 75,162,006 72,686,680 72,573,782	total sequence (bp) 6,649,517,808 5,082,131,592 4,911,453,140,5856 4,911,453,140,5856 4,162,253,112 4,029,440,688 3,675,904,920 3,656,647,080 2,650,394,664 2,465,724,384 2,244,618,86 2,244,618,86 2,244,618,86 2,244,618,86	CpGs removed 5' conversion filter 4,649,722 4,781,114 5,3695,082 1,3353,746 1,319,038 1,2926,033 1,283,996 1,2942,041 1,774,756 1,1774,756 1,1774,756 1,1774,976 1,1774,976 1,1774,976 1,774,977 1,7754,976 1,774,977 1,	S conversion filter 55,693,355 5,693,355 5,693,375 642,161,386 37,120,365 38,442,263 38,022,648 37,337,576 33,383,071 28,329,125 32,203,169 32,203,203,203,200,200,200,200,200,200,2	Unique bases covered (both strands) 3,866,815 2,828,807 2,525,838 2,582,159 2,551,533 2,616,552 2,264,996 1,982,899 2,332,921 2,225,838 4,227,631 1,442,188 1,495,170 1,443,868 1,845,185	Fotal C/T equence, ingle-tranded (bp) 52.470,518 52.203,162 53.934,376 35,997,496 35,622,893 35,108,929 31,762,707 26,661,819 30,762,355 30,323,990 19,707,113 20,045,844,192 20,384,419 20,045,844 24,692,126 55,038,815	Total C sequence (bp) 9 37.741.984 38.857.422 93.35.322 42.5688.701 65.991.290 65.190.793 65.069.945 23.565.128 19.476.148 24.397.233 22.030.622 22.015.087 14.731.177 14.775.320 17.835.632 17.501.269	Inique bases with at least 5 cads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,06,872 1,952,481 1,677,259 2,016,000 1,928,483 1,892,935 1,213,218 1,271,966 1,229,631 1,564,257 1,627,579	Unique bases with at least 10 reads (10 reads	Unique bases v with at least 5 ! reads (double: stranded) s 3.599,0c2 3,581,679 2,717,924 2,472,815 2,485,315 2,485,315 2,486,218 4,601 1,892,67 2,246,728 2,170,979 2,135,362 1,360,966 1,433,253 1,361,361,361,361,361,361,361,361,361,36	Jnique bases with at least 10 reads double-tranded) 3,453,680 3,375,051 2,557,425 2,275,993 2,327,107 2,060,033 7,07 2,060,033 7,07 1,284,041 1,341,823 1,291,755 1,637,114 1,707,498	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.54% 71.86% 73.25% 70.74% 72.39% 74.49% 71.94% 72.52% 70.90% 68.77%	Unique bases cowered (both Total C/T strands) sequence (bp) : 78,869,127 1,146,913,66 82,877,455 1,199,399,834 68,146,685 989,839,33 62,623,587 874,467,075 60,747,312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,7312 874,074,174,174,174,174,174,174,174,174,174,1	Unique ha with at lea with at lea with at lea cotal C reads (both 2014) and the cotal C reads (both 2014) an
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rom 1 1 2 3 3 4 4 5 5 6 7 8 9 9 10 11 11 12 13 13 14 15 15 16 17 18 19 20 21 21 22 X X M	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G oppis	Converted CPG maximum converted CPG maximum conversion CPG maximum conversi	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 70,585,161 1 68,214,627 1 64,741,748 1 55,964,454 1 42,911,927 1 51,234,330 1 51,054,235 1 30,786,765 1 36,811,037 1 34,246,172 1 31,175,229 1 30,180,257 1 28,943,009 1 29,660,782 1 19,675,967 1 24,751,241 1 13,422,119 1 12,494,075 1 27,797,534 1 2,674,881 1 31,783 2 1,060,597,100 Mean reads per position cr Total bp covered in hg18 (total genomic coordinates covered 211,125,778 226,073,954 179,906,091 168,139,838 159,932,089 145,633,904 136,313,218 106,042,601 123,927,820 125,439,967 125,501,918 92,462,377 75,162,006 72,573,789 72,150,349 52,752,677 73,902,885 32,118,388 134,821,922 13,921,829 13,921,922 2,688,302,305	total sequence (bp) 6.190,592,760 6.649,517,808 5.082,131,592 4,911,453,144 4,651,405,856 4,162,253,112 4,102,440,688 3,089,658,740,492 2,652,934,664 2,652,934,664 2,244,616,648 2,244,616,648 2,244,616,648 2,172,973,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,	CpGs removed 5' conversion filter 4,469,722 4,781,114 5,369,082 1,3,359,784 1,3359,784 1,3,359,784 1,2,366,499 1,2,727,249 1,177,350 1,177,326 1,1	S' conversion filter 155,693,355 55,693,376 55,693,376 55,693,376 37,120,365 38,022,648 37,337,576 33,830,771 23,339,725 35,031,302 32,699,599 32,203,169	Unique bases covered (both strands) 3,868,815 3,724,585 2,828,807 2,552,383 2,552,159 2,551,533 2,616,525 2,616,996 1,982,899 2,332,921 2,258,884 2,227,651 1,412,183 1,495,170 1,443,886 1,861,385 1,1990,975 1,824,133 1,1890,302 660,308 977,172 1,869,322 1,665,610 666 Mean reads per CpG (each strand CpGs in reference	Total C/T equence, ingle-tranded by tranded	Total C sequence (bp) s 377.41.984 38.857.422 93.355.344 25.688.701 26.391.290 27.355.318 19.476.148 22.355.128 19.476.148 22.355.128 19.476.148 22.355.128 19.476.148 22.355.128 19.475.328 22.015.087 14.775.320 14.755.32	Jnique bases vith at least 5 eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,185,937 2,2185,937 2,165,2481 1,677,259 2,016,020 1,928,483 1,271,966 1,229,631 1,271,966 1,229,631 1,271,966 1,229,631 1,108,634 569,652 824,009 1,259,235 105,985 651 40,417,553	Unique bases with at least 10 reads (single-stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,729,437 1,707,776 1,691,402 1,525,562 1,588,284 1,484,391 2,900,635 958,386 6,177,900,635 1,693,245 1,217,143 869,303 443,206 622,670 626,825 52,987 627 30,837,718	Unique bases v with at least 5 i reads (double: stranded) s 3,581,679 2,717,924 2,423,815 2,485,315 2,485,315 2,485,315 2,485,315 2,170,979 2,486,728 2,170,979 2,486,728 2,170,979 1,135,362 1,175,175,175,175,175,175,175,175,175,17	Jnique bases with at least 10 reads double-tranded) 3,453,863,875,051 2,557,428 2,275,999 2,337,911 2,308,752 2,175,999 2,032,709 2,060,037 2,060,037 1,765,448 2,119,900 2,033,709 1,284,044 1,1707,498 1,082,599 1,571,488 2,186,807 1,162,751 1,162	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.35% 73.55% 70.74% 72.39% 74.25% 70.00% 68.77% 71.94% 72.55% 70.00% 68.77% 74.11% 65.68% 69.94% 73.67% 69.92% 73.98% 75.14% 0.30%	Unique bases covered (both Total C/T strands) seguence (bp) s 75 and 67 strands) seguence (bp) s 75 and 75	Unique bawith at lea with at lea cotal C reads (including land) and lea cotal C reads (including land) at le
om 1 2 3 4 5 6 6 7 7 8 9 9 101 111 112 113 113 114 115 115 117 118 119 120 121 121 121 131 144 155 167 17 188 199 190 190 190 190 190 190 190 190 190	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G oppis	Converted CPG maximum converted CPG maximum conversion CPG maximum conversi	total uniquely mapped reads 1 85,980,455 1 92,354,414 1 76,507,611 1 63,214,627 1 64,741,748 1 57,809,071 1 55,964,455 1 42,911,927 1 51,234,303 1 51,054,235 1 36,811,037 1 34,246,172 1 31,175,259 1 30,180,257 1 28,434,009 1 29,660,782 1 19,675,967 1 24,751,241 1 13,432,119 1 12,049,075 1 27,979,534 1 2,647,881 1 31,783 1 1,060,597,104 Mean reads per position cc	total genomic coordinates covered 211,125,778 226,073,954 179,906,091 168,139,838 159,932,089 145,633,904 136,313,218 106,042,601 123,927,820 125,439,967 125,501,918 92,462,377 75,162,006 72,573,789 72,150,349 52,752,677 73,902,885 32,118,388 134,821,922 13,921,829 13,921,922 2,688,302,305	total sequence (bp) 6.190,592,760 6.649,517,808 5.082,131,592 4,911,453,144 4,651,405,856 4,162,253,112 4,102,440,688 3,089,658,740,492 2,652,934,664 2,652,934,664 2,244,616,648 2,244,616,648 2,244,616,648 2,172,973,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,	CpGs removed 5' conversion filter 4,649,722 4,781,114 5,3695,082 5,353,1407 6,319,038 2,2926,033 1,383,987 6,2942,041 1,774,56 2,074,907 1,775,420	S' conversion filter 155,693,355 55,693,376 55,693,376 55,693,376 37,120,365 38,022,648 37,337,576 33,830,771 23,339,725 35,031,302 32,699,599 32,203,169	Unique bases covered (both strands) 3,866,815 3,724,585 2,828,807 2,525,838 2,582,159 2,551,533 2,616,552 2,264,996 1,982,899 2,332,921 2,258,884 2,227,631 1,412,183 1,495,170 1,443,868 1,845,185 1,950,581 1,199,075 1,824,133 1,280,302 660,308 977,172 1,869,328 16,5,610 696	Total C/T requence, imple to tal C/T requence, imple transfer of the total C/T requence, imple transfer of the total C/T requence, transfer of the total C/T requence of the t	Total C sequence (bp) sequence (bp) s7,741.98 438,857.422 93,335,344 25,688.701 65,391.290 65,190.793 65,069.945 23,565,128 93,476,5148 24,397,233 22,203,622 22,015,087 41,4731,177 14,775,320 41,4731,177 14,775,320 61,676,676 12,795,258 6,873,117 9,054,728 913,207 64,378,578 913,207 64,378,578 913,207 64,378,578 913,207 61,378 913,207 61,378 91	Jnique bases vith at least 5 eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,185,937 2,2185,937 2,165,2481 1,677,259 2,016,020 1,928,483 1,271,966 1,229,631 1,271,966 1,229,631 1,271,966 1,229,631 1,108,634 569,652 824,009 1,259,235 105,985 651 40,417,553	Unique bases with at least 10 reads (single-stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,729,437 1,707,776 1,691,402 1,525,562 1,588,284 1,484,391 2,900,635 958,386 6,177,900,635 1,693,245 1,217,143 869,303 443,206 622,670 626,825 52,987 627 30,837,718	Unique bases with at least 5 i reads (double, creads (double, creads (double, creads (double, creads (double, creads)), creads (double, creads), creads, cread	Jnique bases with at least 10 reads double-tranded) 3,453,863,875,051 2,557,428 2,275,999 2,337,911 2,308,752 2,175,999 2,032,709 2,060,037 2,060,037 1,765,448 2,119,900 2,033,709 1,284,044 1,1707,498 1,082,599 1,571,488 2,186,807 1,162,751 1,162	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.54% 71.86% 73.25% 70.74% 72.39% 74.49% 71.94% 72.52% 70.90% 68.77% 74.11% 65.68% 69.94% 73.67% 69.92% 75.14% 0.30%	Unique bases covered (both Total C/T strands) seguence (bp) s 75 and 67 strands) seguence (bp) s 75 and 75	Unique bawith at lea with at lea cotal C reads (including land) and lea cotal C reads (including land) at le
rom 11 12 12 13 14 14 15 16 17 18 19 19 11 11 11 11 11 11 11 11 11 11 11	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G oppis	Converted CPG maximum converted CPG maximum conversion CPG maximum conversi	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 70,585,161 1 68,214,627 1 64,741,748 1 55,964,454 1 42,911,927 1 51,234,330 1 51,054,235 1 30,786,765 1 36,811,037 1 34,246,172 1 31,175,229 1 30,180,257 1 28,943,009 1 29,660,782 1 19,675,967 1 24,751,241 1 13,422,119 1 12,494,075 1 27,797,534 1 2,674,881 1 31,783 2 1,060,597,100 Mean reads per position cr Total bp covered in hg18 (total genomic coordinates covered 211,125,778 226,073,954 179,906,091 168,139,838 159,932,089 145,633,904 136,313,218 106,042,601 123,927,820 125,439,967 125,501,918 92,462,377 75,162,006 72,573,789 72,150,349 52,752,677 73,902,885 32,118,388 134,821,922 13,921,829 13,921,922 2,688,302,305	total sequence (bp) 6.190,592,760 6.649,517,808 5.082,131,592 4,911,453,144 4,651,405,856 4,162,253,112 4,102,440,688 3,089,658,740,492 2,652,934,664 2,652,934,664 2,244,616,648 2,244,616,648 2,244,616,648 2,172,973,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,	CpGs removed 5' conversion filter 4,469,722 4,781,114 5,369,082 1,3,359,784 1,3359,784 1,3,359,784 1,2,366,499 1,2,727,249 1,177,350 1,177,326 1,1	S' conversion filter 155,693,355 55,693,376 55,693,376 55,693,376 37,120,365 38,022,648 37,337,576 33,830,771 23,339,725 35,031,302 32,699,599 32,203,169	Unique bases covered (both strands) 3,868,815 3,724,585 2,828,807 2,552,383 2,552,159 2,551,533 2,616,525 2,616,996 1,982,899 2,332,921 2,258,884 2,227,651 1,412,183 1,495,170 1,443,886 1,861,385 1,1990,975 1,824,133 1,1890,302 660,308 977,172 1,869,322 1,665,610 666 Mean reads per CpG (each strand CpGs in reference	Total C/T requence, ingle-tranded by tranded	Total C sequence (bp) s 377.41.984 38.857.422 93.355.344 25.688.701 26.391.290 27.355.318 19.476.148 22.355.128 19.476.148 22.355.128 19.476.148 22.355.128 19.476.148 22.355.128 19.475.328 22.015.087 14.775.320 14.755.32	Jnique bases vith at least 5 eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,185,937 2,2185,937 2,165,2481 1,677,259 2,016,020 1,928,483 1,271,966 1,229,631 1,271,966 1,229,631 1,271,966 1,229,631 1,108,634 569,652 824,009 1,259,235 105,985 651 40,417,553	Unique bases with at least 10 reads (single-stranded) 2,520,319 2,508,179 1,890,313 1,655,845 1,729,437 1,707,776 1,691,402 1,525,562 1,588,284 1,484,391 2,900,635 958,386 6,177,900,635 1,693,245 1,217,143 869,303 443,206 622,670 626,825 52,987 627 30,837,718	Unique bases v with at least 5 i reads (double: stranded) s 3,581,679 2,717,924 2,423,815 2,485,315 2,485,315 2,485,315 2,485,315 2,170,979 2,486,728 2,170,979 2,486,728 2,170,979 1,135,362 1,175,175,175,175,175,175,175,175,175,17	Jnique bases with at least 10 reads double-tranded) 3,453,863,875,051 2,557,428 2,275,999 2,337,911 2,308,752 2,175,999 2,032,709 2,060,037 2,060,037 1,765,448 2,119,900 2,033,709 1,284,044 1,1707,498 1,082,599 1,571,488 2,186,807 1,162,751 1,162	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.35% 73.55% 70.74% 72.39% 74.25% 70.00% 68.77% 71.94% 72.55% 70.00% 68.77% 74.11% 65.68% 69.94% 73.67% 69.92% 73.98% 75.14% 0.30%	Unique bases covered (both Total C/T strands) seguence (bp) s 75 and 67 strands) seguence (bp) s 75 and 75	Unique bawith at lea cotal Crass (1987) 18 (19
rom 11 12 12 13 14 15 15 16 17 17 18 19 19 11 11 11 11 11 11 11 11 11 11 11	minMapQ 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Cytosine maximum oppisite strand non-G oppis	Converted CPG maximum converted CPG maximum conversion CPG maximum conversi	total uniquely mapped reads 1 85,880,455 1 92,354,414 1 76,507,611 1 70,585,161 1 68,214,627 1 64,741,748 1 55,964,454 1 42,911,927 1 51,234,330 1 51,054,235 1 30,786,765 1 36,811,037 1 34,246,172 1 31,175,229 1 30,180,257 1 28,943,009 1 29,660,782 1 19,675,967 1 24,751,241 1 13,422,119 1 12,494,075 1 27,797,534 1 2,674,881 1 31,783 2 1,060,597,100 Mean reads per position cr Total bp covered in hg18 (total genomic coordinates covered 211,125,778 226,073,954 179,506,001 168,139,838 159,932,089 118,63139,838 159,932,089 1125,927,820 1125,927,820 125,501,918 92,462,370 84,491,577 57,5162,006 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,686,680 72,572,677 57,607,057 23,902,888 32,118,388 13,182,922 13,921,689 15,282 2,688,302,305 covered (both strom UCSC) dd	total sequence (bp) 6.190,592,760 6.649,517,808 5.082,131,592 4,911,453,144 4,651,405,856 4,162,253,112 4,102,440,688 3,089,658,740,492 2,652,934,664 2,652,934,664 2,244,616,648 2,244,616,648 2,244,616,648 2,172,973,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,974,504 2,172,	CpGs removed 5' conversion filter 4,469,722 4,781,114 5,369,082 1,3,359,784 1,3359,784 1,3,359,784 1,2,366,499 1,2,727,249 1,177,350 1,177,326 1,1	S' conversion filter 55,691,325 55,643,376 42,161,386 37,120,365 38,441,263 38,8022,484 37,337,576 33,830,777 33,830,777 32,293,159 32,293,169	Unique bases covered (both strands) 3,666,815 3,724,585 2,828,807 2,552,382 2,561,532 2,616,532 2,616,532 2,616,536 1,982,899 2,332,921 2,258,844 2,227,651 1,412,183 1,495,170 1,443,868 1,846,185 1,1950,581 1,1950,751 1,824,133 1,886,382 1,663,380 977,172 1,869,322 1,663,186 47,886,080 Mean reads per CpG (each stratotal cpGs in reference Crotal reference Cortal (Cacheron Cortal CpGs in reference Cortal referenc	Total C/T requence, imple to tal C/T requence, imple transfer to tal C/T requence, imple transfer to tal C/T requence, imple transfer to tal C/T requence, transfer to tal C/T requence to	Total C sequence (bp) sequence (bp) squence	Jnique bases vith at least 5 eads (single-tranded) 3,275,861 3,200,320 2,420,764 2,145,817 2,213,972 2,185,937 2,185,937 2,185,937 1,952,481 1,577,259 2,016,020 1,928,483 1,892,935 1,156,4257 1,036,814 1,279,631 1,564,257 1,036,814 4,59,652 824,009 1,259,235 105,985 105,985 105,985	Unique bases with at least 10 reads sixingle- stranded) 2,520,319 2,508,179 2,508,179 1,890,313 1,655,845 1,729,437 1,707,776 1,691,402 1,525,562 1,588,284 1,189,335 1,1461,906 948,177 980,635 958,386 1,189,324 1,217,143 869,030 443,206 622,670 626,825 52,987 627 30,837,718 High-confidence recent with percent ref cytical strands of the confidence of th	Unique bases v with at least 5 i reads (double: stranded) s 3,581,679 2,717,924 2,423,815 2,485,315 2,485,315 2,485,315 2,485,315 2,170,979 2,486,728 2,170,979 2,486,728 2,170,979 1,135,362 1,175,175,175,175,175,175,175,175,175,17	Jnique bases with at least 10 reads double-tranded) 3,453,68(3,375,051 2,275,992 2,275,992 2,337,911 2,308,725 2,337,911 1,765,445 2,119,904 2,033,708 1,997,974 1,341,822 1,162,255 1,637,114 1,341,822 1,162,255 1,571,48	Mean Per cent methylation 71.21% 73.83% 74.31% 74.24% 73.19% 73.35% 73.55% 70.74% 72.39% 74.25% 70.00% 68.77% 71.94% 72.55% 70.00% 68.77% 74.11% 65.68% 69.94% 73.67% 69.92% 73.98% 75.14% 0.30%	Unique bases covered (both Total C/T strands) seguence (bp) s 75 and 67 strands) seguence (bp) s 75 and 75	Unique bawith at lea cotal Crass (1987) 18 (19

Supplementary Table 2. Bisulfite-seq sample details (cont.)

				Cytosines	with am	biguous c	ontext					Possible	non-cyt	osines in s	ample ge	nome				
Unique bases		Unique bases		•			ı	Unique bases		Unique bases						Unique bases		Unique bases		
with at least	Unique bases	with at least				l	Jnique bases v	with at least	Unique bases v	with at least					Unique bases	with at least	Unique bases	with at least		
10 reads	with at least 5	10 reads		Unique bases		v	vith at least 5	10 reads	with at least 5 1	10 reads		Unique bases			with at least 5	10 reads	with at least 5	10 reads		
(single-	reads (double-	double-	Mean Per cent	covered (both	Total C/T	Total C r	eads (single- (single-	reads (double- ((double-	Mean Per cent	covered (both	Total C/T	Total C	reads (single-	(single-	reads (double	- (double-	Mean Per cent	cphConversio
stranded)	stranded)	stranded)	methylation	strands)	sequence (bp)	equence (bp) s	tranded) s	tranded)	stranded) s	stranded)	methylation	strands)	sequence (by) sequence (bp)	stranded)	stranded)	stranded)	stranded)	methylation	nPreFilter
53,675,646	78,284,077	75,352,670	0.67%	525,963	4,474,934	538,218	424,266	96,121	512,612	466,473	9.04%	344,32	3 5,430,98	5 283,939	277,468	209,690	336,001	1 299,05	7 5.58%	98.99%
56,056,924	81,378,446	78,479,617	0.75%	531,826	4,555,765	579,722	431,184	99,980	519,360	475,265	9.13%	359,01	5 5,770,40	2 313,147	292,546	222,809	351,348	315,53	1 5.59%	98.88%
45,944,674	66,992,738	64,604,572	0.77%	432,578	3,663,018	446,632	350,481	81,155	422,957	387,183	8.97%	298,63	4 4,708,84	18 250,062	243,369	185,496	292,420	262,85	1 5.49%	98.86%
40,825,999	61,459,219	59,007,245	0.87%	412,004	3,489,566	437,260	332,671	74,363	402,771	367,084	9.03%	295,08	5 4,667,41	2 244,198	239,279	179,949	288,479	5 258,60	9 5.41%	98.73%
40,827,251	59,658,992	57,498,126	0.78%	387,259	3,240,381	382,664	313,552	71,424	378,382	346,142	8.86%	263,97	4,105,28	7 214,117	215,308	163,644	258,425	5 232,20	8 5.46%	98.84%
38,561,897	56,709,917	54,613,830	0.79%	376,650	3,338,534	449,147	305,013	71,357	368,303	336,649	9.25%	262,49	2 4,250,90	9 242,220	213,673	162,294	256,941	1 230,52	2 5.64%	98.84%
35,217,218	52,096,507	49,914,285	0.74%	360,748	3,042,757	399,982	290,538	66,940	350,938	317,105	9.80%	240,67	2 3,665,45	6 215,012	192,953		234,624	4 208,28		98.89%
33,818,853	49,126,447	47,421,152	0.75%	320,986	2,709,710	331,589	260,963	60,559	314,311	288,365	9.16%	215,32	3,397,64	181,782	176,224	135,069	210,874	1 190,23	1 5.56%	98.88%
26,725,146	38,858,317	37,368,988	0.69%	264,072	2,244,627	281,122	213,327	49,178	256,788	233,139	9.45%	173,92	4 2,712,98	2 151,158	140,087	105,897	169,519	9 150,89	0 5.75%	98.95%
32,117,450	45,790,506	44,190,499	0.68%	304,016	2,764,664	401,423	247,566	61,459	296,847	271,704	9.83%	205,87	5 3,478,13	3 215,329	167,506	128,337	201,120	180,44	5 5.99%	98.97%
31,947,026	46,534,527	44,799,316	0.67%	312,448	2,622,110	316,205	252,647	58,415	305,151	278,069	9.14%	204,46	7 3,226,12	4 174,576	165,437	125,866	199,828	3 178,56	6 5.59%	98.99%
31,060,776	45,596,914	43,874,562	0.72%	308,336	2,563,609	310,892	248,505	56,337	300,896	274,077	9.30%	208,74	5 3,180,02	7 173,734	168,308	126,590	203,666	5 181,53	3 5.75%	98.92%
21,494,840	31,994,820	30,780,276	0.86%	210,075	1,737,722	207,720	170,164	37,358	205,688	187,782	9.00%	150,90	4 2,309,32	0 121,063	122,109	91,844	147,569	9 132,00	3 5.35%	98.75%
21,076,037	30,813,571	29,654,301	0.72%	206,614	1,723,800	209,847	166,963	38,291	201,698	183,651	9.36%	138,05	9 2,112,85	116,596	111,313	83,869	134,929	5 120,35	0 5.72%	98.92%
19,605,261	28,031,187	27,001,866	0.65%	186,922	1,600,367	206,383	150,773	36,343	181,755	165,079	9.65%	125,71	1,971,15	3 113,269	101,336	76,974	122,529	9 109,21	0 5.86%	99.00%
19,917,784	28,322,001	27,198,903	0.55%	204,501	1,857,493	285,952	165,853	41,929	198,603	179,349	11.11%	128,29	5 2,072,12	6 148,570	102,956	77,733	124,884	1 110,91	6 6.71%	99.12%
19,595,852	28,558,747	27,306,140	0.53%	214,059	1,780,576	231,455	171,392	39,569	207,466	185,869	10.40%	127,99	1,890,27	1 123,884	100,648	74,353	124,157	7 108,18	5 6.79%	99.15%
17,827,951	25,780,893	24,898,324	0.78%	167,564	1,516,876	222,011	136,042	32,079	164,030	150,381	9.42%	115,92	8 2,011,96	7 110,365	94,833	72,494	113,423	3 102,08	4 5.58%	98.86%
14,049,177	21,475,186	20,291,690	0.44%	181,282	1,528,407	211,832	143,197	31,026	175,128	154,228	11.39%	100,40	9 1,440,87	8 98,509	76,702	53,822	96,957	7 82,60	1 7.39%	99.27%
16,278,347	22,694,199	21,971,274	0.56%	150,187	1,324,337	174,663	122,836	30,877	146,878	134,823	9.98%	93,53	1,525,87	9 92,678	76,513	59,001	91,433	3 81,97	6 6.34%	99.11%
8,160,650	11,877,460	11,419,026	0.74%	83,465	816,904	131,995	67,742	17,047	81,289	73,976	10.68%	56,68	3 1,053,96	4 72,525	45,612	34,599	55,250	49,18	0 6.33%	98.89%
9,333,482	13,311,139	12,759,147	0.44%	99,882	842,111	114,986	80,575	19,442	96,762	86,967	11.00%	55,76	824,56	5 57,908	43,813	32,619	54,087	7 47,08	1 7.29%	99.26%
16,148,051	43,848,622	36,842,706	0.76%	400,449	2,565,065	120,496	295,951	19,386	385,875	308,858	4.83%	203,99	9 1,688,28	8 59,762	135,453	71,970	194,053	3 145,37	9 3.88%	98.85%
1,463,719	4,078,534	3,310,456	0.73%	42,132	391,477	66,146	30,671	3,932	39,619	31,074	6.42%	20,34	8 347,49	4 26,809	13,323	7,727	19,259	9 14,80	4 5.32%	98.99%
5,219	5,567	5,559	0.31%	61	5,621	20	50	34	60	59	0.90%	4	1 79,42	15 86	37	34	4:	1 4	0 0.14%	99.46%
651,730,011	973,272,966	930,558,971		6,684,018	56,394,810	7,058,342	5,372,872	1,194,567	6,514,107	5,883,288		4,390,16	0 67,842,92	9 3,801,208	3,516,765	2,627,386	4,281,767	7 3,792,49	7	

				Cytosin	es with an	nbiguous d	ontext					Possible	non-cyto	sines in s	ample ge	nome				
Unique bases		Unique bases		•		_		Unique bases	1	Unique bases						Unique bases		Unique bases		
with at least	Unique bases	with at least					Unique bases	with at least	Unique bases	with at least					Unique bases	with at least	Unique bases	with at least		
10 reads	with at least 5	10 reads		Unique base	5	,	with at least 5	10 reads	with at least 5	10 reads		Unique bases			with at least 5	10 reads	with at least 5	10 reads		
(single-	reads (double-	(double-	Mean Per cent	covered (bot	h Total C/T	Total C	eads (single-	(single-	reads (double-	double-	Mean Per cent	covered (both	Total C/T	Total C	reads (single-	(single-	reads (double	- (double-	Mean Per cent	cphConversio
stranded)	stranded)	stranded)	methylation	strands)	sequence (bp)	sequence (bp) :	tranded)	stranded)	stranded)	stranded)	methylation	strands)	sequence (bp)	sequence (bp)	stranded)	stranded)	stranded)	stranded)	methylation	nPreFilter
51,748,431	78,126,873	74,885,253	0.67%	545,7	3 4,328,047	468,834	440,414	88,949	532,258	483,106	8.73%	346,33	4,702,677	250,538	276,600	203,279	337,573	3 297,56	0 5.59%	98.99%
54,091,505	81,232,175	78,023,893	0.75%	553,04	3 4,432,961	496,415	448,694	92,818	540,319	493,200	8.81%	360,82	4,975,825	268,446	291,544	216,086	352,679	314,04	3 5.58%	98.88%
44,337,256	66,877,967	64,236,898	0.76%	449,2	3,595,298	395,083	364,134	75,233	439,468	401,078	8.64%	300,00	4,146,994	216,580	242,567	179,896	293,460	261,44	1 5.48%	98.86%
39,301,993	61,347,958	58,639,098	0.86%	427,2	5 3,394,428	383,589	344,862	68,612	417,867	379,647	8.73%	296,48	4,023,158	211,446	238,147	173,975	289,553	3 257,24	9 5.42%	98.73%
39,387,755	59,555,323	57,166,988	0.78%	402,44	3,201,796	344,831	326,051	66,354	393,400	358,939	8.54%	265,14	3,635,023	188,050	214,398	158,566	259,299	5 230,87	7 5.46%	98.84%
37,185,315	56,609,511	54,292,676	0.78%	391,39	9 3,144,668	361,506	317,008	66,353	382,847	348,990	8.94%	263,79	3,623,868	199,520	212,894	157,281	1 257,932	2 229,45	9 5.63%	98.84%
33,907,839	51,984,047	49,575,443	0.74%	374,2	8 2,975,299	355,076	301,439	61,978	364,237	328,126	9.48%	241,71	3,225,543	187,732	191,842	140,013	3 235,294	4 206,87	4 6.02%	98.89%
32,636,390	49,045,962	47,158,456	0.75%	333,4	0 2,674,554	299,542	271,257	56,320	326,681	298,828	8.86%	216,31	3,006,461	160,607	175,675	131,166	211,611	1 189,30	4 5.55%	98.88%
25,769,335	38,778,406	37,136,499	0.69%	273,9	3 2,188,570	247,655	221,437	45,465	266,612	241,436	9.11%	174,97	2,374,998	129,425	139,761	102,924	1 170,329	9 150,29	4 5.73%	98.96%
31,019,696	45,707,517	43,938,932	0.68%	315,8	5 2,583,241	310,851	257,236	56,960	308,625	281,732	9.45%	206,68	3 2,863,746	167,522	166,767	124,429	201,697	7 179,26	6 5.97%	98.97%
30,802,226	46,448,228	44,531,002	0.66%	324,8	4 2,588,468	285,744	262,733	54,302	317,421	288,498	8.83%	205,43	2,801,061	148,429	164,857	122,176	5 200,522	2 177,55	9 5.57%	98.99%
29,934,927	45,511,826	43,604,245	0.71%	320,2	2,527,924	280,130	258,151	51,933	312,671	283,899	8.99%	210,01	2,819,895	153,883	167,687	122,703	3 204,662	2 180,70	6 5.73%	98.92%
20,714,602	31,941,345	30,600,476	0.86%	218,6	2 1,725,108	187,637	177,144	34,693	214,192	195,009	8.67%	151,92	3 2,051,123	107,042	121,743	89,238	3 148,403	3 131,60	8 5.34%	98.75%
20,320,168	30,754,874	29,474,925	0.71%	214,6	9 1,706,025	190,601	173,604	35,598	209,708	190,481	9.04%	139,06	3 1,874,314	102,750	111,199	81,560	135,729	119,99	0 5.68%	98.92%
18,923,852	27,973,056	26,834,214	0.65%	194,0	7 1,568,834	184,160	156,693	33,678	188,871	171,157	9.31%	126,24	1,735,451	98,550	100,869	74,720	122,883	3 108,57	4 5.84%	99.00%
19,206,941	28,256,050	27,014,465	0.54%	211,59	2 1,749,220	234,396	171,580	38,594	205,591	185,302	10.71%	128,91	1,760,599	114,867	102,601	75,279	125,333	3 110,27	4 6.63%	99.12%
18,849,967	28,487,626	27,104,187	0.53%	221,6	8 1,750,132	208,937	177,496	36,466	214,916	192,016	10.06%	129,02	1,660,335	109,235	100,496	72,072	124,982	2 107,77	5 6.79%	99.16%
17,214,609	25,737,782	24,763,023	0.77%	174,2	7 1,403,611	161,952	141,662	29,738	170,715	156,120	9.09%	116,65	7 1,619,775	87,126	94,573	70,507	7 114,028	3 101,69	9 5.57%	98.85%
13,440,047	21,412,875	20,103,879	0.43%	187,0	6 1,434,522	181,119	147,668	28,187	180,779	158,647	11.05%	101,48	1,190,851	84,712	76,575	51,742	97,858	82,39	5 7.37%	99.28%
15,739,482	22,655,918	21,854,566	0.56%	156,0	1,287,414	153,346	127,728	28,778	152,589	139,814	9.64%	94,13	1,326,063	79,804	76,382	57,285	91,916	5 81,72	4 6.30%	99.12%
7,865,825	11,853,116	11,346,522	0.74%	86,43	6 741,789	104,294	70,165	15,848	84,257	76,427	10.38%	56,90	820,322	55,277	45,322	33,339	55,355	5 48,80	1 6.35%	98.89%
8,985,231	13,278,548	12,670,289	0.44%	103,4	5 829,057	104,772	83,528	18,061	100,336	90,057	10.66%	56,29	7 717,186	51,576	43,846	31,678	3 54,509	5 46,92	8 7.31%	99.27%
14,830,022	43,702,471	36,147,963	0.75%	411,4	3 2,584,389	114,990	303,993	15,879	396,542	314,626	4.72%	205,68	3 1,579,501	55,669	134,698	67,095	5 195,330	143,85	1 3.85%	98.85%
1,333,117	4,053,137	3,231,967	0.73%	42,8	0 302,877	29,427	31,097	3,215	40,388	31,328	6.19%	20,17	7 196,843	13,380	13,013	7,078	3 19,045	5 14,31	0 5.38%	98.93%
4,560	5,020	4,968	0.31%		370	0	22	7	32	30	0.00%	3	2,639	4	29	29	9 32	2 3	0.85%	99.43%
627.546.531	971.332.591	924 335 859		6.933.9	4 54.718.232	6.084.887	5,575,774	1.104.012	6.761.290	6.088.459		4.414.22	58.731.612	3.242.166	3,504,052	2.544.087	7 4.299.974	4 3.772.56	1	

Supplementary Table 2. Bisulfite-seq sample details (cont.)

on Tumor In	ncluding Du	uplicat	tes							High-conf	idence C	pGs						High-confidence	CpHs	
				Minimum										Jnique bases		Inique bases				
		Cytosii		converted CpHs for 5'							Total C/T		Inique bases vith at least 5 1		Unique bases w with at least 5 1			Unique bases		Unique
		oppisit		naximum conversion	total uniquely	total genomic		CpGs removed 5' conversion		Unique bases s covered (both s			eads (single- (with at least 5 1 reads (double- (d		Mean Per cent	covered (both Total C/T	Total C	with at reads (:
	minManΩ			ase non-G filter	manned reads		(hn)		iltor			sequence (bp) s					nethylation		p) sequence (b	
		30	0.101	0.101	1 81.614.082	211,399,502		4.308.633	50.244.185		45,131,842		3,004,064	2,069,117	3,576,970	3,222,871	62.50%	79,455,676 1,061,900,		
		30	0.101	0.101	1 93,973,585	226,591,412		4.781.793	54,664,409		50.660.599	31.823.635	3,107,078	2,352,909	3,529,624	3,306,554	63.58%	82.900.501 1.218.435.		
		30	0.101		1 78,360,386	187,799,393	5.664.593.572	3.717.945	41,614,016		38.395.351		2.357.467	1.787.908	2.680.282	2.510.203	63.25%	68.169.770 1.006.365.		
		30	0.101	0.101	1 75,150,675	179,943,698	5,431,779,468	3,565,638	37,949,496	2,501,115	34,916,336	21,250,250	2,106,739	1,600,678	2,396,906	2,247,660	62.16%	62,780,693 928,786,	92 7,124,8	65 53
		30	0.101	0.101	1 70,282,648	168,530,199	5,080,628,732		38,026,193		35,238,577		2,153,951	1,637,147	2,445,505	2,292,373	61.96%	60,792,652 899,326,		
		30	0.101	0.101	1 66,889,650	160,253,383	4,792,693,236	3,430,369	38,270,569	2,521,548	35,364,446	22,095,857	2,125,099	1,609,161	2,417,386	2,264,913	63.31%	57,765,159 852,445,	06 5,949,8	53 4
		30	0.101	0.101	1 58,435,236	145,928,194	4,204,763,652	3,130,837	36,156,111		33,265,563	20,869,020	2,117,158	1,545,769	2,449,952	2,258,395	63.70%	53,275,291 754,028,		
		30	0.101	0.101	1 54,753,748	136,550,681	3,958,352,980	2,820,518	32,185,624	2,235,745	29,912,877	18,400,652	1,880,320	1,404,514	2,147,778	2,008,621	62.40%	49,862,276 709,235,	49 4,733,3	88 4
		30	0.101		1 42,257,619	106,409,875	3,055,335,248	2,261,496	26,681,711		24,783,328	15,564,922	1,608,252	1,169,438	1,857,841	1,716,117	63.19%	39,729,359 559,689,		
		30	0.101	0.101	1 50,223,334	123,779,493	3,624,682,508	2,962,824	34,112,958		31,602,431	20,150,666	1,939,327	1,454,126	2,207,133	2,064,562	63.88%	46,599,031 669,265,		
		30	0.101	0.101	1 50,934,510	125,703,299	3,682,718,040	2,653,006	31,287,256		29,050,289	17,420,648	1,854,920	1,360,990	2,133,125	1,980,112	60.79%	47,408,055 677,865,		
		30	0.101	0.101	1 50,252,942	125,732,275	3,633,167,968	2,645,714	30,432,804		28,291,997	17,601,782	1,818,899	1,335,170	2,096,653	1,942,651	63.38%	46,426,021 654,198,		
		30	0.101	0.101	1 38,856,727	92,647,750	2,808,654,616	1,921,218	21,228,728		19,701,481	11,999,231	1,189,425	913,037	1,344,395 1,409,276	1,266,185	62.23%	32,599,118 484,484, 31.367.823 441.527.		
		30	0.101 0.101	0.101	1 33,694,527 1 29,206,355	84,665,011 75,302,002	2,436,155,620	1,760,009	20,454,280		19,025,188 18.094.905	11,612,156 11.414.208	1,224,765 1.171.151	898,009 857.287	1,409,276	1,307,594	62.10% 63.81%	31,367,823 441,527, 28.544.832 394.801.		
		30	0.101	0.101	1 29,206,355	75,302,002	2,111,994,376	1,642,574	23,540,929		22.034.736	13,957,092	1,171,151	1.026.659	1,352,437	1,248,642	63.81%	28,544,832 394,801,		
		30	0.101	0.101	1 25.112.365	72,622,511		1,761,412	22,200,028		20,876,733		1,472,648	1.007.547	1,722,303	1,572,000	62.58%	29,120,205 357,844.		
		30	0.101	0.101	1 30.207.064	72,051,716	2.181.136.208	1,597,776	18.041.167		16.666.061	10.327.394	1,005,618	765.743	1,138,907	1.070.011	63.01%	26,205,883 388,422.		
		30	0.101	0.101	1 16.508.610	52,761,330	1.171.867.876	1.451.883	18,529,565		17.113.019	10,655,986	1,333,583	797,544	1.664.290	1,442,740	62.02%	21,915,394 240,819.		
		30	0.101	0.101	1 22,997,195	57,677,280	1,663,335,072	1,392,591	17.186.725		16.073.301	9.742.617	1,052,084	766.177	1.208.745	1,121,331	61.25%	22,978.812 323.120.		
		30	0.101	0.101	1 13,452,782	32,981,512	970,145,120	801,755	9,291,111	-,,	8,556,444		545,659	401,053	624,377	582,121	63.63%	12,116,690 174,544,		
		30	0.101	0.101	1 10,906,288	32,177,040	789,252,388	847,579	11,137,694		10,498,688	6,644,642	764,242	514,195	904,591	818,702	63.14%	13,562,203 164,575,		
		30	0.101	0.101	1 26,183,187	135,071,481	1,892,751,928	1,201,964	13,189,882	1,836,146	12,246,521	7,362,730	1,138,648	493,083	1,639,850	1,249,843	61.22%	46,420,044 332,207,	18 2,262,4	90
		30	0.101	0.101	1 2,919,452	14,061,667	211,043,596	164,229	1,566,682		1,331,043	854,899	99,459	46,234	141,187	108,054	64.09%	4,612,726 37,703,		
		30	0.101	0.101	1 1,235,800	16,449	87,653,540	281,146	2,323,051		2,518,746	6,755	710	698	763	754	0.50%	5,855 13,234,	69 34,7	26
ome totals					1,050,881,599	2,693,703,851	75,771,870,852	56,135,811	647,438,468	47,213,781	598,831,756	371,158,370	38,580,430	27,813,495	44,890,613	41,222,653		993,491,504 ########	## 89,369,7	80 8
				Summaries:	Mean reads per position co	vered (both st	rands)	28.13		Mean reads per CpG (each stran	nd)	12.68		ligh-confidence	CpGs in sample		47,213,781			
					Total bp covered in hg18 (f	rom UCSC)		2,858,034,764		Total CpGs in reference		56,328,604	F	ercent with po	ssible sequence	variant	3.8%			
					Percentage of hg18 covere	d		94.3%		Total reference CpGs covered:		49,057,680								
										Percent of reference covered (1										
										Percent of reference covered (5										
								0.65%						Anan CnG moth	vlation (nuclear	genome)	61.98%			
					Mean CpH retention (nucle Mean CpH retention (mitoo		me)	0.26%		Percent of reference covered (1	o reads includ	73.18%			nylation (mitocho	ondrial genom	0.27%			
							me)			Percent of reference covered (1	o reads includ	73.18%				ondrial genom	0.27%			
) Tumor F	xcluding D	unlica	tes				me)									ondrial genom	0.27%	High-confidence	CnHs	
Tumor E	xcluding D	uplica	tes	Minimum			me)			High-conf					nylation (mitocho	ondrial genom	0.27%	High-confidence	СрНѕ	
Tumor E	xcluding D	Cytosii	ne	converted	Mean CpH retention (mitod	chondrial geno	me)	0.26%		High-conf	fidence C	p Gs	l Inique bases v	Jnique bases vith at least 1	uuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuuu	Unique bases	0.27%	<u> </u>	СрНѕ	
Tumor E	xcluding D	Cytosii	ne num	converted CpHs for 5'	Mean CpH retention (mitod	chondrial geno		0.26% CpGs removed		High-conf T Unique bases s	Fidence C	p Gs	lnique bases v	Jnique bases vith at least 1.0 reads	unique bases with at least 5 1	Inique bases vith at least 0 reads		Unique bases	•	with
Tumor E		Cytosii maxim oppisit	ne num te CpG n	converted CpHs for 5' naximum conversion	Mean CpH retention (mitod	chondrial geno	total sequence	0.26% CpGs removed (5' conversion)	conversion	High-conf T Unique bases s covered (both s	Fidence C Fotal C/T Requence, Lingle-	p Gs L V Total C	Inique bases v vith at least 5 1 eads (single- (Jnique bases vith at least 1.0 reads visingle-	Unique bases we with at least 5 1 reads (double-	Unique bases vith at least O reads double-	Mean Per cent	Unique bases covered (both Total C/T	Total C	wit
Tumor E	xcluding D	Cytosii maxim oppisit	ne num te CpG n I non-G next t	converted CpHs for 5' naximum conversion pase non-G filter	Mean CpH retention (mitod) total uniquely mapped reads	chondrial geno total genomic	total sequence (bp)	CpGs removed 5' conversion filter	conversion	High-conf Unique bases s covered (both s strands) s	Fidence C Fotal C/T requence, ringle- stranded (bp)	pGs L v Total C r, sequence (bp) s	Inique bases vith at least 5 1 eads (single- (tranded) s	Jnique bases vith at least 1.0 reads visingle-randed)	Unique bases wwith at least 5 1 reads (double- (cstranded) s	Unique bases with at least O reads double- tranded)	Mean Per cent nethylation	Unique bases covered (both Total C/T strands) sequence (Total C	wit rea op) stra
Tumor E	minMapQ	Cytosii maxim oppisit strand	ne num te CpG n non-G next t 0.101	converted CpHs for 5' naximum conversion pase non-G filter 0.101	Mean CpH retention (mitod total uniquely mapped reads 1 70,975,448	total genomic coordinates covered 211,263,806	total sequence (bp) 5,133,080,880	CpGs removed 5 conversion filter 3,648,862	conversion ilter 42,972,568	High-conf T Unique bases s covered (both s strands) s 3,788,141	fidence C Total C/T requence, ringle- tranded (bp) 39,870,425	Total C resequence (bp) s 24,631,906	Inique bases with at least 5 1 teats (single-(tranded) s 2,958,704	Jnique bases vith at least 1.0 reads visingle-1 single-1	Unique bases wwith at least 5 1 stranded) sr 3,561,857	Unique bases with at least O reads double- tranded) 3,172,941	Mean Per cent nethylation 62.51%	Unique bases covered (both Total C/T strands) sequence (79,370,902 939,972,	Total C p) sequence (b) 72 5,830,8	wit rea pp) stra 74
Tumor E	minMapQ	Cytosii maxim oppisit strand 30	ne num te CpG n non-G next t 0.101 0.101	converted CpHs for 5' naximum conversion pase non-G filter 0.101 0.101	total uniquely mapped reads 1 70,975,488 1 82,660,673	total genomic coordinates covered 211,263,806 226,476,113	total sequence (bp) 5,133,080,880 5,977,570,076	0.26% CpGs removed 5' conversion 1 filter 3,648,862 4,146,302	c' conversion ilter 42,972,568 47,830,228	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586	fidence C Total C/T requence, ringle- stranded (bp) 39,870,425 44,367,204	Total C rsequence (bp) s 24,631,906 27,823,029	Inique bases vith at least 5 1 eads (single- (tranded) s 2,958,704 3,070,717	Jnique bases vith at least 1,0 reads vitranded) s 1,937,249 2,231,039	Unique bases wwith at least 5 1 reads (double- (stranded) stranded) stranded) 3,561,857 3,517,907	Unique bases with at least 0 reads double- tranded) 3,172,941 3,271,847	Mean Per cent methylation 62.51% 63.59%	Unique bases covered (both Total C/T strands) sequence 79,370,902 939,972, 82,819,397 1,073,079,	Total C p) sequence (b) 72 5,830,8 96 7,205,8	wit rea op) stra 74
Tumor E	minMapQ	Cytosii maxim oppisii strand 30 30	ne num te CpG n non-G next t 0.101 0.101	converted CpHs for 5' conversion pase non-G filter 0.101 0.101	total uniquely mapped reads 1 70,975,448 1 82,660,673 1 69,138,284	total genomic coordinates covered 211,263,806 226,476,113 187,726,483	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008	0.26% CpGs removed 5' conversion filter 3,648,862 4,146,302 3,246,780	conversion ilter 42,972,568 47,830,228 36,653,677	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724	Fidence C Fotal C/T sequence, single- stranded (bp) 39,870,425 44,367,204 33,844,157	TpGs Total C rosequence (bp) s 24,631,906 27,823,029 20,999,727	Inique bases v vith at least 5 1 eads (single- tranded) s 2,958,704 3,070,717 2,330,080	Unique bases vith at least 1,00 reads vith at least 1,00 reads vith at least 2,1937,249 2,231,039 1,596,634	Unique bases w with at least 5 1 reads (double- (stranded) stranded) stranded) 2,671,907 2,671,192	Unique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,626	Mean Per cent methylation 62.51% 63.59% 63.26%	Unique bases covered (both Total C/T strands) sequence (79,370,902 939,972, 82,819,397 1,073,079, 68,109,123 888,764,	Total C p) sequence (b 72 5,830,8' 96 7,205,8' 91 6,090,1'	wit rea op) str 374 887
Tumor E	minMapQ	Cytosii maxim oppisii strand 30 30 30 30	ne num te CpG n non-G next t 0.101 0.101 0.101	converted CPHs for 5' naximum conversion nase non-G filter 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 82,666,673 1 69,138,284 1 66,089,418	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,778,177,208	0.26% CpGs removed 5' conversion filter 3,648,862 4,146,302 3,246,780 3,028,232	d' conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546	Total C/T requence, ingle- tranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690	TpGs Total C resequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666	Inique bases vith at least 5 1 eads (single- (tranded) s 2,958,704 3,070,717 2,330,080 2,081,664	Jnique bases vith at least 1,0 reads vitranded) 1,1,317,249 2,231,039 1,696,634 1,519,412	Unique bases with at least 5 1 reads (double- (stranded) s 3,561,857 3,517,907 2,671,192 2,388,598	Unique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,626 2,224,032	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18%	Unique bases covered (both Total C/T strands) sequence 79,370,902 939,972, 82,819,397 1,073,079, 68,109,123 888,764, 62,720,082 818,055,	Total C p) sequence (b 72 5,830,8 96 7,205,8 91 6,090,1 18 6,279,8	wit rea pp) str 374 887 .50
Tumor E	minMapQ	Cytosii maxim oppisii strand 30 30	ne num te CpG n non-G next t 0.101 0.101	converted CpHs for 5' conversion pase non-G filter 0.101 0.101	total uniquely mapped reads 1 70,975,448 1 82,660,673 1 69,138,284	total genomic coordinates covered 211,263,806 226,476,113 187,726,483	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008	0.26% CpGs removed 5' conversion filter 3,648,862 4,146,302 3,246,780	conversion ilter 42,972,568 47,830,228 36,653,677	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273	Fidence C Fotal C/T sequence, single- stranded (bp) 39,870,425 44,367,204 33,844,157	Total C rosequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 18,821,892	Inique bases v vith at least 5 1 eads (single- tranded) s 2,958,704 3,070,717 2,330,080	Unique bases vith at least 1,00 reads vith at least 1,00 reads vith at least 2,1937,249 2,231,039 1,596,634	Unique bases w with at least 5 1 reads (double- (stranded) stranded) stranded) 2,671,907 2,671,192	Unique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,626	Mean Per cent methylation 62.51% 63.59% 63.26%	Unique bases covered (both Total C/T strands) sequence (79,370,902 939,972, 82,819,397 1,073,079, 68,109,123 888,764,	Total C p) sequence (b) 72 5,830,8 96 7,205,8 91 6,090,1 18 6,279,8 46 5,510,7	wit rea pp) str. 374 887 .50 90
Tumor E	minMapQ	Cytosii maxim oppisit strand 30 30 30 30 30 30	ne num te CpG n non-G next t 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101	converted CPHs for 5' naximum conversion pase non-G filter 0.101 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,248 1 62,007,059 1 58,240,774	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 160,186,298	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,778,177,208 4,483,655,652 4,211,379,180	0.26% CpGs removed 5' conversion filter 3,648,862 4,146,302 3,246,780 3,028,232 2,955,761 2,887,049	' conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151	Fidence C Total C/T requence, ringle- stranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320 30,354,812	Total C r sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 18,821,892 18,886,517	Inique bases vith at least 5 1 eads (single- (tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156	Unique bases vith at least 1.0 reads single-tranded) 2,231,039 1,696,634 1,519,412 1,554,223 1,525,693	Unique bases with at least 5 1 reads (double) stranded) stranded) stranded) stranded, 2,488,598 2,437,744 2,409,117	Inique bases vith at least 0 or eads double-tranded) 3,172,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33%	Unique bases covered (both Total C/T strands). 939,972,993,973,079, 68,109,123,888,764, 62,720,082 818,055, 60,736,458 794,049, 57,712,657 743,459,	Total C p) sequence (b; 72 5,830,8' 96 7,205,8' 91 6,090,1' 18 6,279,8' 46 5,510,7' 83 5,215,1'	with real pp) str (74 is 87 is 50 is 90 is 44 is 42 is 64 is
Tumor E	minMapQ	Cytosii maxim oppisit strand 30 30 30 30 30 30 30 30	ne num te CpG n 0.101 0.101 0.101 0.101 0.101 0.101	converted CPHs for 5' conversion pase non-6 filter 0.101 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 92,956,481 1 62,000,009 1 66,089,148 1 62,000,059	total genomic coordinates covered 211,263,806 226,476,113 187,726,883 179,856,705 168,449,241	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,778,177,208 4,483,655,652	0.26% CpGs removed 5' conversion filter 3,648,862 4,146,302 3,246,780 3,028,232 2,955,761	' conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371	Fidence C Fotal C/T requence, ringle- tranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320	Total C r sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 18,821,892 18,886,517	Inique bases vith at least 5 1 eads (single- (tranded) 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324	Jnique bases vith at least 10.0 reads visingle-tranded) 1,937,249 2,231,039 1,696,634 1,519,412 1,554,223	Unique bases with at least 5 1 reads (double- (stranded) stranded) stranded) stranded, 2,351,907 2,671,192 2,388,598	Unique bases vith at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,626 2,248,332 2,268,539	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 61.98%	Unique bases covered (both Total C/T strands) sequence (79,370,902 939,972, 82,819,397 1,073,079, 68,109,123 888,764, 62,720,082 818,055, 60,736,458 794,052,	Total C p) sequence (b) 72 5,830,8 96 7,205,8 91 6,090,1 18 6,279,8 46 5,510,7 83 5,215,1 21 4,488,1	wi re pp) str 74 887 50 90 44 42
Γumor E	minMapQ	Cytosii maxim oppisii strand 30 30 30 30 30 30 30 30	ne num tee CpG n next t 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101	converted CPHs for 5' convesion lase non-G filter 0.101 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001 0.1001	total uniquely mapped reads 1 70,975,448 1 82,660,673 1 69,138,284 1 66,098,418 1 52,007,059 1 58,240,774 1 51,295,989	total genomic coordinates covered 211,263,806 226,476,113 179,856,705 168,449,241 160,186,298 145,839,672	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,778,177,208 4,483,655,652 4,211,379,180	0.26% CpGs removed 5' conversion filter 3,648,862 4,146,302 3,246,780 3,028,232 2,955,761 2,887,049 2,712,507	5' conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794	fidence C Total C/T sequence, single- 39,870,425 44,367,204 33,646,204 30,566,690 31,041,320 30,354,812 29,262,772	Total C v sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 18,821,892 18,886,517 18,355,856	Inique bases vith at least 5 1 eads (single- (tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156 2,088,837	Jnique bases with at least 10 or eads vingle-11,937,249 2,231,039 1,696,634 1,519,412 1,554,223 1,525,693 1,457,351	Unique bases with at least 5 1 reads (double- (stranded) s 3,561,857 3,517,907 2,671,192 2,388,598 2,437,744 2,409,117 2,440,147	Unique bases vith at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 2,229,241	Mean Per cent methylation 63.59% 63.26% 62.18% 61.98% 63.33% 63.71%	Unique bases covered (both Total C/T strands) sequence (79,370,902 939,972, 28,819,397 1,073,379, 68,109,123 888,764, 62,720,082 818,055, 60,736,458 794,062, 57,712,657 743,490, 53,217,513 665,077,	Total C p) sequence (b) 72 5,830,8' 95 7,205,8' 96 6,279,8' 46 5,510,7' 84 5,510,7' 82 4,488,1' 84 4,188,5'	wi res (74 (87 (50 (90 (44 (42 (70 (31)
Fumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30	ne num te CpG n next b 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101	converted CPHs for 5' convesion lase non-G filter 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,899 1 48,485,101	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,449,241 160,186,298 145,839,672 136,488,737	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,778,177,208 4,483,655,24 211,379,180 3,709,518,640	0.26% CpGs removed 5' conversion 1 filter 3,648,862 4,146,302 3,028,232 2,955,761 2,887,049 2,712,507 2,475,528	5' conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794	Fidence C Total C/T equence, ingle- stranded (bp) 39,870,425 44,367,204 33,844,157 33,041,320 30,354,812 29,262,772 26,456,889	Total C v v sequence (bp) s 24,631,906 27,823,029 18,616,666 18,821,892 18,886,517 18,355,856 16,281,827	Inique bases with at least 5 1 deads (single-(tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156 2,088,837 1,857,993	Jnique bases vith at least 10 reads vith at least 1, 1937, 249 2,231,039 1,696,634 1,519,412 1,554,223 1,525,693 1,457,351 1,329,593	Unique bases w with at least 5 1 reads (double- (stranded) s 3,561,857 3,517,907 2,671,192 2,388,598 2,437,744 2,409,117 2,440,147 2,140,868	Unique bases with at least 0 reads double- tranded) 3,172,941 2,483,626 2,224,032 2,268,539 2,240,861 2,229,241 1,986,950	Mean Per cent nethylation 62.51% 63.59% 62.26% 61.98% 63.33% 63.71% 62.41%	Unique bases covered (both Total C/T strands) sequence (79,37,90,29 393,972, 28,819,397 1,073,979, 68,109,123 888,764, 62,720,028 818,055, 60,736,458 794,062, 57,712,657 744,800, 53,217,513 665,072, 49,816,729 622,851,	Total C p) sequence (b) 72 5,830,8' 96 7,205,8' 991 6,090,1' 18 6,279,8' 46 5,510,7' 83 5,215,1' 24 4,488,1' 34 4,188,5' 82 3,110,2'	wi rei (74) (87) (50) (90) (44) (42) (70) (31)
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne num te CpG n next t 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101 0.101	converted CpHs for 5' conversion land make non-G filter 0.101 0.1001	total uniquely mapped reads 1 70,975,448 1 62,000,000 1 58,240,774 1 51,259,599 1 48,485,101 1 37,354,464	total genomic coordinates covered 211,263,806 226,476,113 179,856,705 168,49,241 160,186,288 145,839,672 136,488,737 106,305,755	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,478,177,208 4,4211,379,130 3,709,518,640 3,506,127,312 2,701,592,060	0.26% CpGs removed 5' conversion filter 3,648,652 4,146,302 3,246,780 3,028,232 2,955,761 2,887,049 2,712,507 2,475,528	5 conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119 23,652,944	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287	Fidence C Fotal C/T requence, single- tranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320 30,344,812 29,262,772 26,456,889 21,988,096	Total C rosequence (bp) s 24,631,905 27,823,029 20,999,727 18,615,666 18,821,892 18,885,517 18,355,856 16,281,827 13,808,166	inique bases v vith at least 5 j eads (single- (1,75,72,73,72,73,73,73,73,73,73,73,73,73,73,73,73,73,	Jnique bases with at least 10, 0 reads 1,937,249 2,231,039 1,596,634 1,525,633 1,457,351 1,329,593 1,101,904	Unique bases with at least 5 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	Inique bases with at least 0 reads double- 3.172,941 3.271,847 2.483,626 2.224,032 2.268,539 2.240,861 1,986,950 1,695,360	Mean Per cent methylation 62.51% 63.59% 62.26% 62.18% 63.33% 63.71% 62.41% 63.21%	Unique bases covered (both Total C/T strands) 79,370,902 939,972, 28,819,397 1,073,979, 68,109,123 888,764, 62,720,082 818,055, 60,736,458 794,062, 57,712,657 743,490, 53,217,513 665,072, 49,816,729 628,551, 39,679,902 49,556,8	Total C p) sequence (b) 72 5,830,8 91 6,090,1 18 6,279,8 46 5,510,7 83 5,215,1 21 4,488,1 34 4,188,5 82 3,110,2 66 3,607,1	wi re op) sti 374 887 50 90 444 42 70 31 18 65
Tumor E	minMapQ	Cytosii maxim oppisii strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne non-G next t 0.101	converted CPHS for S' naximum conversion sase non-G filter 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,989 1 48,485,101 1 37,354,464 1 43,319,371 1 44,487,582 1 44,487,582	total genomic coordinates covered 211,626,76,11 179,856,705 168,49,241 160,188,967,725 116,489,341 106,305,755 123,713,843 125,641,750	total sequence (bp) 5.133,080,880 5.975,750,707 4,999,343,008 4,778,177,208 4,483,655,65 4,211,379,180 3,709,518,804 3,506,127,312 2,172,43,93 3,249,218,804 3,249,218,804	0.26% CpGs removed 5' conversion ifilter 3,648,862 4,146,302 3,246,780 3,028,232 2,955,761 2,9887,049 2,712,507 2,475,528 1,987,871 2,425,2139 2,425,928 2,273,388	3 conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119 23,652,944 29,128,166 27,623,252 26,968,622	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165	Fidence C Total C/T requence, ingle- 198,870,425 43,367,240 33,844,157 30,566,690 33,344,157 26,456,889 27,085,266 27,085,266 25,666,157 25,072,150	Total C sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 18,821,832 18,886,517 18,335,855 16,281,827 13,908,166 17,129,884 15,403,536 15,609,839	Inique bases vith at least 5 1 acads (single- (tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156 2,088,837 1,857,993 1,587,320 1,916,618 1,831,844 1,795,230	Jinique bases vith at least 10 reads single 1,231,032 1,532,563 1,132,953 1,101,001 1,375,490 1,284,548	Unique bases with at least 5 1 stranded) s' 3,561,857 3,517,907 2,671,1907 2,438,598 2,437,744 2,409,117 2,440,147 2,140,168 1,850,813 2,200,154 2,125,913 2,208,138	Unique bases vith at least 0 reads to use of the bases vith at least 10 reads 1,721,41 3,721,847 2,483,626 2,224,032 2,268,539 2,240,861 1,986,950 1,095,360 2,042,631 1,957,109 1,919,050	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.89% 60.80% 63.39%	Unique bases covered (both Total C/T strands) sequence (79,370,902 939,972, 28,819,971 (073,079,96,61,09),123 888,764, 62,720,028 2818,055, 60,736,458 794,062, 57,712,657 744,490, 53,217,513 665,072, 49,816,729 622,851, 39,679,802 49,568, 46,552,820 588,472, 47,362,328 598,996, 64,382,145 579,983,215 579,983,	Total C p) sequence (b 72 5,830,8 91 6,090,1: 18 6,279,8 3 5,215,1: 21 4,488,1: 34 4,188,5: 82 3,110,2 66 3,607,1: 19 3,622,3: 97 3,778,4	wi re ip) str i74 i87 i50 i90 i44 i42 i70 i31 i18 i65 i60 i33
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne ne comment to the comme	converted CpHs for S' converted CpHs for S' conversion lase non-G filter 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,259,899 1 48,485,101 1 37,354,464 1 43,919,371 1 44,487,582 1 44,487,582 1 34,274,204	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 145,819,672 136,488,731 106,305,755 123,713,843	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,778,177,208 4,483,655,652 4,211,379,108 3,709,518,640 3,506,127,312 2,701,592,060 3,176,525,088	0.26% CpGs removed 15' conversion filter 3,648,65' 4,146,302 3,246,780 3,028,212 2,955,761 2,487,528 1,987,871 2,459,837 2,232,139	2 conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119 23,652,944 29,128,166 27,623,252	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,530,273 2,519,151 2,579,371 2,233,794 1,994,796 2,300,287 2,227,099 2,196,165 1,396,032	Fidence C Fotal C/T requence, ingle- tranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690 30,354,812 29,262,772 26,456,889 21,988,096 27,085,526 27,085,526	Total C v 24,631,906 22,631,906 27,823,907 20,999,727 18,616,666 18,821,892 15,886,517 13,388,651 16,281,827 13,388,651 15,281,827 15,383,66 17,129,894 15,403,536	inique bases v vith at least 5 1 example 1 2,958,704 (17,012) 1 2,330,080 (2,081,664 (2,129,324 (2,100,156 (2,088,837 (1,916,158 (1,916,158) (1,916,158) (1,916,158) (1,916,158) (1,916,158) (1,916,158) (1,916,158) (1,916,158)	Jnique bases with at least 1,0 reads 1,337,249 1,152,549 1,137,490 1,375,490 1,284,586 1,295,655 888,101	Unique bases with at least 5 1 stranded s 3,561,87 9.07 2,671,192 2,388,598 2,437,744 2,409,117 2,440,147 2,140,868 1,850,813 2,200,154 2,125,913 2,089,138	Inique bases with at least 0 reads double-tranded) 3,172,941 3,271,847 2,268,539 2,240,851 2,229,241 1,986,590 1,695,360 2,042,631 1,957,109	Mean Per cent methylation 62.51% 63.59% 62.18% 61.98% 63.33% 63.71% 62.41% 63.21% 63.89% 60.80%	Unique bases covered (both Total C/T strands) sequence (179,370,390,200,393,972,82,819,397 1,073,079,86,109,123 888,746,62,720,082 818,055,60,736,458 794,062,57,712,657 743,490,53,217,513 665,072,49,816,729 628,551,39,679,302 495,568,46,552,820 888,472,47,362,328 599,966,46,382,145 579,943,32,571,525 427,582,125 587,948,33,25,71,525 427,582,125 587,9483,	Total C p) sequence (b) 52 5,830,8 96 7,205,8 91 6,090,1 18 6,279,8 46 5,510,7 83 5,215,1 21 4,488,1 34 4,188,5 84 3,110,2 66 3,607,1 19 3,622,3 96 3,778,4	wi res (74 (87 (50 (90 (44 (42 (70 (31 (18 (65 (60 (33) (64
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne num te CpG n ext t 0.101	converted CPHs for 57 conversion assement GPHs for 57 conversion 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,989 1 48,485,101 1 47,354,446,748 1 44,925,937 1 44,487,582 1 44,472,487 1 44,475,582 1 34,274,204 1 30,100,434	total genomic coordinates covered 211,62,626,476,113 187,726,483 179,856,705 168,449,241 160,186,298 1106,305,755 123,713,843 125,641,750 125,647,633 92,616,285	total sequence (bp) 5.133,080,880 5,977,570,076 4,999,343,080 4,783,177,208 4,483,655,652 4,211,379,180 3,709,518,640 3,709,518,640 3,709,518,640 3,709,518,640 3,249,218,804 3,249,218,804 3,247,243,922 4,478,101,684 2,176,821,968	0.26% CpGs removed 5' conversion iffilter 3,648,862 4,146,302 3,246,780 3,028,232 2,955,761 2,887,049 2,475,528 1,987,871 2,322,139 2,459,837 2,322,139 1,576,258 1,579,049 1,576,258	conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119 29,128,166 27,623,252 26,968,622 18,687,866 18,298,173	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322	Fidence C Total C/T requence, ingle- tranded (bp) 39,870,425 44,367,204 33,844,157 30,354,812 29,262,772 26,456,889 27,085,526 27,085,526 27,085,526 17,341,667 17,302,766	Total C v sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 18,821,882 18,886,517 13,808,166 17,129,894 15,403,536 15,609,839 10,568,126 10,309,0758	Inique bases vith at least 5 1 deads (single-tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156 2,088,837 1,857,993 1,587,320 1,916,518 1,831,844 1,795,230 1,176,084 1,212,155	Jinique bases with at least 10 reads single- tranded 1,937,249 2,231,039 1,596,263 1,554,223 1,252,693 1,101,904 1,275,490 1,284,548 1,259,655 868,101 853,905	Unique bases w with at least 5. Unique bases w with at least 6. Signature 1. Line	Inique bases with at least 0 reads double- 1 randed 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 1,986,950 1,095,369 1,195,709 1,253,845 1,294,475 1,294,475 1,294,475 1,294,475 1,294,475 1,294,475 1,294,475 1,294,475	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.89% 60.80% 63.39% 62.25% 62.25%	Unique bases covered (both Total C/T strands) sequence (79,75,700,23 335,972, 28,189,397 1,073,079), 68,109,123 888,764, 62,720,082 818,055, 60,736,458 794,052, 57,712,557 744,490,55,127,7513 665,072, 49,816,729 622,551, 33,679,802 49,558, 46,552,202 588,472,47,362,238 598,996, 46,382,415 579,943, 32,571,525 427,582, 31,347,461 334,941,461 344,941,461	Total C pl) sequence (b) 72 5,830,8 96 7,205,8 91 6,090,1 18 6,279,8 46 5,510,7 21 4,488,1 34 4,188,5 34 4,188,2 3,110,2 66 3,607,1 19 3,622,3 97 3,778,4 91 3,244,2 91 2,559,0	wii re (74 / 1887 / 150 / 1990 / 144 / 142 / 170 / 131 / 118 / 165 / 166
Tumor E	minMapQ	Cytosii maxim oppisii strandi 30 30 30 30 30 30 30 30 30 30 30 30 30	ne num te CpG n next t 0.101	converted Copts for Converted Copts for Conversion Sea non-6 filter 0.101	total uniquely mapped reads 1 82,666,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,259,589 1 48,485,511 44,487,582 1 44,487,582 1 44,487,582 1 44,487,582 1 44,487,582 1 34,274,204 1 51,618,789	total genomic coordinates covered 211,263,80 226,476,113 187,726,483 179,856,705 169,499,241 160,186,298 145,839,672 136,488,731 106,305,755 125,641,750 125,641,750 125,641,750 125,642,848 84,625,607 75,261,456	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,008 4,483,655,652 4,211,379,189,210 3,709,518,640 3,709,518,640 3,701,592,060 3,176,525,008 3,217,243,932 2,478,101,682 2,478,101,682 2,478,101,682	0.26% CpGs removed: 5' conversion: filter 3,448,862 4,146,780 3,028,232 2,955,761 2,487,049 2,711,207 2,475,528 1,987,871 2,459,837 2,322,139 1,562,588 1,679,049 1,562,588	conversion ilter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119 23,652,944 29,128,166 27,623,252 26,968,622 18,687,866 18,298,173 17,431,305	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,530,273 2,531,151 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,472,138	Fidence C rotal C/T requence, ingle- tranded (bp) 33,870,425 44,367,204 33,844,157 30,566,690 31,041,320 30,354,812 29,262,772 56,455,889 21,988,096 27,085,525 25,666,157 25,072,150 17,341,667 17,202,760	Total C r sequence (bp) a 24,631,906 27,823,029 20,999,727 18,616,686,517 18,821,828 61,281,827 15,609,839 15,609,839 15,609,839 10,568,126 10,309,758 10,248,352 10,309,758 10,248,352 10,309,758 10,568,126 10,309,758	inique bases vith at least 5 1 sadd (single - tranded) s 2,958,704 3,070,717 2,330,060 4,129,324 4,100,156 2,088,837 1,516,518 1,831,844 1,795,230 1,176,084 1,212,155 1,159,524	Jinique bases with at least 1,0 reads single-tranded) 1,937,249 1,937,249 1,554,223 1,555,633 1,101,904 1,375,490 1,284,548 1,259,655 888,101 853,905 816,530 916	Unique bases with a least 51 reads (double- (stranded) s 3.561,857 3.517,907 2.188,598 2.437,744 2.409,117 2.140,868 1.2200,154 2.125,913 2.009,138 1.200,154 2.125,913 2.009,138 1.340,548 1.340,548 1.348,540 1.348,548 1.348,540 1.348,548 1.348,540 1.348,548 1.348,540 1.348,548 1.348,540 1.348,548 1.348,540 1.348,548 1.348,540 1.348,54	Inique bases vith at least 0 reads 10 uble- 13,172,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 2,29,241 1,986,950 1,695,360 2,042,631 1,957,109 1,919,050 1,253,845 1,254,475 1,254,475	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.89% 63.39% 63.39% 62.25% 62.11% 63.89% 62.25% 62.11%	Unique bases covered (both Total C/T strands) sequence (1973) 20 939,972, 82,819,397 1,073,079, 86,109,123 888,746, 62,720,082 818,055, 60,736,458 79,940,52,271,657 743,490, 53,217,513 665,072,49,816,729 628,551, 39,679,902 495,568, 46,552,820 588,472, 47,362,328 598,966, 43,882,145 579,943, 32,571,555 427,582, 31,347,461 394,941, 28,527,361 354,274, 381,381,381,381,381,381,381,381,381,381,	Total C 72 5,830,8 96 7,205,8; 96 7,205,8; 96 6,279,8; 18 6,279,8; 44,88,1 14 4,488,1 14 4,488,1 19 3,622,3; 19 3,728,4 69 3,244,24 86 2,599,0 86 2,091,3,78	wire re pp) str 774 887 550 990 444 42 770 631 118 665 660 333 664 007
「umor E	minMapQ.	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne num te CpG n ext to 0.101	converted 5 converted 5 converted 5 conversion control filter 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,99 1 48,485,101 1 47,354,446 1 43,191,371 1 44,475,582 1 34,274,00,434 1 30,100,434 1	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,499,241 160,186,298 115,839,672 136,488,737 160,305,755 123,713,843 125,641,750 125,679,633 92,616,285 84,625,607 75,261,456 72,771,688	total sequence (bp) 5.133,080,880 5.977,570,076 4.999,343,080 4.778,177,208 4.483,655,652 2.701,592,060 3,709,518,640 3,709,518,640 3,249,218,804 3,249,218,804 3,247,243,92 2,478,101,684 2,176,823,985 1,893,925,420	CpGs removed : 5' conversion ; filter 4,146,302 3,246,780 3,028,212 2,955,761 2,878,709 2,712,507 2,475,528 1,987,871 2,322,139 2,717,507 2,322,139 1,562,588 1,462,459 81,1662,459 1,6658,388 1,462,459	depth of the conversion of the	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810	fidence C fotal C/T equence, ingle- tranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320 29,262,772 56,456,889 27,085,526 27,085,526 27,085,526 25,666,157 25,072,130 17,341,667 17,020,766 16,224,940	Total C resequence (bp) s 24,631,906 27,823,029 20,999,727 18,355,856 618,821,892 13,808,166 15,403,536 15,609,839 10,568,126 10,309,758 10,234,352 12,191,908	Inique bases virth at least 5 1 adds (single-tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156 2,088,837 1,857,993 1,587,320 1,791,618 1,831,844 1,795,230 1,176,084 1,212,155 1,159,524 1,456,545	Jinique bases with at least 10 reads single- tranded 1, 1937,249 2,231,039 1,595,693 1,103,295 3,103,256,693 1,103,26,588 888,101 888,305 816,530 970,285	Unique base w with at least 5 1 2 3,561,857 3,561,857 3,561,857 2,437,744 2,409,117 2,440,147 2,409,117 2,440,147 2,409,118 1,340,540 1,155,913 1,340,227 1,40,881 1,340,447 2,140,881 1,340,447 2,140,881 1,340,447 2,140,881 1,340,447 2,140,881 1,340,447 2,140,881 1,340,447 2,140,847 2,1	Inique bases with at least 0 reads double- 1 read of 3,172,941 3,271,847 2,483,626 2,224,035 2,240,861 2,292,431 1,986,950 1,095,384 1,971,99,050 1,253,845 1,236,613 1,554,485 1,254,611 3,1554,611 3,1554,611	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.37% 63.21% 63.21% 63.21% 63.21% 63.89% 60.80% 62.25% 62.11% 63.82% 62.11% 63.82% 63.11%	Unique bases covered (both Total C/T strands) sequence (79,70,700,22 383,972, 28,181,9397 1,073,079), 68,109,123 888,764, 62,720,082 818,055, 60,736,458 794,052, 57,712,557 744,490,553,127,513 665,072, 49,816,729 622,551, 33,679,802 49,558, 46,552,202 588,472,247,362,238 598,996, 46,382,415 579,943, 32,571,525 427,582, 31,347,461 384,941,28,527,361 384,276, 28,862,191 347,621 38,482,191 347,621 384,941	Total C p) sequence (b) 72	wi re r
Tumor E	minMapQ.	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne hum te CpG n ext t 0.101	converted Copts for Converted Copts for Conversion See non-6 filter 0.101 0.10	total uniquely mapped reads 1 2,05,75,76,75,75,75,75,75,75,75,75,75,75,75,75,75,	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,449,241 160,186,298 145,839,675 123,713,843 125,641,750 125,679,633 92,616,288 84,625,640 67,771,688	total sequence (bp) 5,977,570,076 4,979,343,080,880 4,778,177,080 4,437,851,772,08 4,433,655,652 4,211,379,180 3,709,518,640 3,506,127,312 2,748,101,680 3,217,243,932 2,478,101,680 2,176,821,956 1,788,682,828 1,768,82,828	0.26% CpGs removed: 5' conversion: filter: 4,448,862 4,146,302 3,246,780 3,028,232 2,955,761 2,495,837 2,271,507 2,475,528 1,979,799 1,562,588 1,462,499 1,562,588 3,1589,083 1,589,083 1,562,588 3,1589,083 1,562,588 3,1589,083 1,562,588 3,1589,083 1,589,080 1,589,080 1,589,080 1,589,080 1,589,080 1,589,080 1,589,08	depth of the conversion of the	High-conf Unique bases s covered (both s strands) s 3.788,141 3.678,586 2.795,724 2.498,546 2.590,273 2.519,151 2.579,371 2.233,794 1.954,796 2.300,287 2.227,099 2.196,165 1.396,032 1.475,322 1.422,158 1.813,810 1.913,425	fidence C Total C/T sequence, ingle- sequence, ingle- 33,870,425 43,367,435 30,366,690 33,844,157 30,366,690 30,354,812 29,262,772 26,456,889 27,085,526 27,085,526 27,085,526 17,020,760 16,224,940 19,402,205	Total C r sequence (ph) s 24,631,906 27,833,029 20,999,227 18,616,65,656 16,281,827 13,808,166 17,129,894 15,609,839 15,609,839 15,609,839 10,558,126 10,309,758 10,244,332 12,191,908 11,838,046 18	inique bases y vith at least 5 ; eads (single- (tranded) s 2.958, 704 3.070, 177 2.330,080 2.081,564 2.109,156 3.187,993 1,587,993 1,587,993 1,176,084 1,176,084 1,176,084 1,176,084 1,176,545 1,159,524 1,159,524 1,159,545	Jinique bases with at least 10, 0 reads 1, 10 reads 1,	Unique bases with a least 51 reads (double (strander) s. 3,561,857 3,517,907 2,140,868 1,200,154 2,400,117 2,140,868 1,200,154 2,125,913 2,089,138 1,171,7095 1,717,09	Unique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,240,382 2,268,539 2,240,861 2,29,241 1,986,950 1,695,360 2,042,631 1,957,109 1,919,084 1,233,845 1,234,475 1,236,485 1,236,485 1,236,485 1,598,883	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.99% 63.21% 63.21% 63.21% 63.11% 63.21% 63.11% 63.25% 63.11% 63.25% 63.11%	Unique bases covered (both Total C/T strands) strands) sequence (1) 32,819,397 1,073,079, 88,199,327 8,989,228,889,397 1,073,079, 88,199,328 88,764, 62,720,082 818,055, 60,736,458 79,940,25, 52,171,657 743,490, 53,217,513 665,072, 49,816,729 628,551, 39,679,902 495,568, 46,552,820 588,472, 47,362,328 598,996, 46,382,145 579,943, 32,571,552 427,582, 31,347,461 394,941, 28,527,361 354,276, 28,862,191 347,632, 29,102,7773 324,571, 20,102,7773 324,571, 20,102,7773 324,571, 20,102,7773 324,571, 20,102,7773 324,571, 20,102,7773 324,571, 20,102,7773 324,571, 20,102,7773 324,571,771,772,771,771,771,771,771,771,771,7	Total C p) sequence (b) P3 sequence (b) P4 7,205,8i P5 6,909,17,205,8i P5 6,709,18i P5 6,709,18i P5 7,205,8i P5 7,	wire respp) str 374 487 550 990 444 42 770 631 818 665 660 633 644 77 78 852
Tumor E	тіпМарQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne num te CpG n ext t 0.101	converted conver	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 66,089,418 1 62,007,059 1 58,240,774 1 51,295,989 1 48,485,101 1 44,925,937 1 44,487,582 1 34,274,204 1 30,100,434 1 26,184,799 1 24,681,383 1 22,737,907 1 26,617,914	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,499,241 160,186,298 1145,839,675 123,713,843 125,641,750 125,679,633 92,616,285 84,625,607 75,261,456 72,711,688 72,616,832 72,616,832	total sequence (bp) 5.133,080.880 5.977.570.076 4.999.343,080 4.778.177.208 4.438,655,652 4.211.379.180 3.709,518,640 3.709,518,640 3.249,218,804 3.249,218,804 3.249,218,804 3.247,243,92 2.478,101,684 2.176,821,965 1.893,925,420 1.798,526,420 1.978,526,420 1.978,526,420 1.974,803,925	CpGs removed : 5' conversion : filler : 3,648,862 4,146,302 3,246,780 3,028,212 2,955,761 2,887,099 2,712,507 2,475,528 1,987,871 2,322,139 2,177,388 1,462,459 8,31 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,586,988 1	2 conversion ilter 42,972,568 47,830,228 46,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,119 23,652,944 26,968,622 18,298,173 17,431,305 20,696,342 20,160,065	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278	fidence C fotal C/T equence, ingle- tranded (bp) 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320 20,345,812 25,666,157 27,085,526 27,085,526 27,085,526 27,085,526 17,341,667 17,020,760 16,224,940 19,402,205 18,967,107	Total C sequence (bp) s 24,631,906 27,833,029 20,999,727 18,355,836 18,812,892 13,808,166 15,403,536 15,609,839 10,568,126 10,390,758 10,234,352 12,191,908 11,838,044 9,033,953 11,838,044	inique bases v vith at least 5 1 eads (single- tranded) s 2,958,704 3,070,717 2,330,080 2,081,664 2,129,324 2,100,156 2,088,837 1,587,320 1,176,084 1,795,230 1,176,084 1,795,521 1,456,545 1,456,545 1,495,209 997,140	Jriique bases with at least 10, or eads 1, 231, 231, 231, 231, 231, 231, 231, 2	Unique bases w with at least 5 1 reads (double-(cstranded) s 3,561,857 3,561,857 2,437,744 2,409,117 2,440,147 2,409,118 1,340,247 1,40,868 1,850,813 2,200,514 2,125,913 2,089,138 1,340,227 1,40,868 1,850,813 1,340,270 1,405,818 1,348,540 1,755,913 1,405,270 1,755,261 1,136,311 1,136,3	Inique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,626 2,224,032 2,268,539 1,965,560 1,965,560 1,253,845 1,957,109 1,253,845 1,294,475 1,236,113 1,554,485 1,558,883 1,554,885 1,558,883	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.89% 60.80% 62.25% 62.11% 63.82% 63.11% 62.60% 63.03%	Unique bases covered (both Total C/T strands) sequence (79,707002) 393,972, 28,2819,397 1,073,079, 68,109,123 888,764, 62,720,082 818,055, 60,736,458 794,052, 57,712,557 744,490, 53,217,513 665,072, 49,816,729 622,551, 33,679,802 49,558, 46,552,202 588,472,47,362,228 598,996, 46,382,415,579,943, 32,571,525 427,582, 31,347,461 384,941,28,527,361 354,276, 28,862,919 347,623, 29,102,777 324,571, 26,194,865 342,589, 194,476,585 342,589, 194,476,589,476,5	Total C p) sequence (b) 72	wire re opp) str 74 (887 (850 (890 (890 (890 (890 (890 (890 (890 (89
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne hum te CpG n ext t 0.101	converted Conver	total uniquely mapped reads 1 70,975,448 1 66,938 284 1 66,938 284 1 66,938 418 1 66,934 1 1 43,919,371 1 44,487,582 1 44,487,582 1 34,274,204 1 30,100,438 1 22,273,907 1 24,681,333 1 22,273,907 1 26,617,934 1 1 26,617,934 1 1 14,925,192	total genomic coordinates covered 211, 263, 806 212, 6476, 131 187, 726, 483 179, 856, 705 168, 449, 241 160, 186, 289 113, 648, 737 125, 641, 750 125, 679, 633 22, 611, 285 84, 525, 607 72, 71, 688 72, 71, 688	total sequence (bp) 5,977,570,076 4,979,343,080,880 4,778,177,08 4,438,565,562 4,211,379,180 3,709,518,600 3,709,518,600 3,709,518,600 3,217,243,932 2,478,101,680 2,478,101,680 2,478,101,680 1,1645,2647,910 1,1645,2647,910	0.26% CpGs removed: 5' conversion iffilter 4,146,300 3,246,780 3,028,222 3,055,761 2,887,049 1,987,871 2,459,837 2,322,139 1,570,049 1,562,588 1,462,499 1,562,588 1,370,084	2 conversion liter 42,972,568 47,830,228 36,653,677 33,194,822 33,492,800 32,777,945 31,489,484 28,471,115 23,652,944 29,128,166 27,623,252 26,968,622 18,687,866 18,287,97 20,696,346 20,160,965 15,682,141	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,539,151 2,579,371 2,233,794 1,934,795 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278	fidence C Total C/T requence, ingle- ingle- 39,870,425 44,367,204 33,844,157 30,3566,590 31,041,320 30,354,812 25,262,772 25,072,150 17,341,667 17,020,760 19,402,205 18,967,707 14,575,033	Total C r sequence (b) is 24,631,906 27,823,029 20,999,227 18,861,892 118,886,517,129,894 15,403,536 15,609,839 10,588,126 10,398,758 10,024,535 21,191,908 11,383,046 9,039,939 9,613,444 9,039,953	inique bases y vith at least 5 leads (single- (tranded) s 2,958,704 3,070,717 2,330,080 2,081,6618 1,212,934 2,100,156,618 1,831,844 1,795,230 1,191,6618 1,131,084 1,212,155 1,159,524 1,456,545 1,492,209 997,140 1,313,94	Jinique bases with at least 10, 0 reads 11, 10, 10, 10, 10, 10, 10, 10, 10, 10,	Unique bases with a teast 51 reads (double- (strander) s. 3,561,857 3,561,857 2,671,192 2,388,561,177 2,140,868 1,200,154 2,125,913 2,009,138 1,200,154 2,175,177 2,177,95 1,177,95 1,177,95 1,178,311 1,158,311 1,158,311	Unique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,240,381 2,224,032 2,268,539 2,240,861 1,996,590 1,995,360 2,042,631 1,957,109 1,753,845 1,294,475 1,294,475 1,294,475 1,598,483 1,061,706	Mean Per cent methylation 62.51% 63.59% 62.18% 61.98% 63.33% 63.71% 62.41% 63.91% 63.90% 63.39% 62.25% 62.11% 63.82% 63.11% 63.60% 63.39% 62.25% 62.11% 63.60% 63.30% 63.03% 63.03% 63.03% 63.03% 63.03% 63.03% 63.03% 63.03%	Unique bases covered (both Total C/T strands) strands) sequence (1) 32,322,323,323,323,323,323,323,323,323,	Total C p) sequence (b) F32 5,830,819 F34 6,090,11 F35 6,279,81 F35 7,205,81 F35 7,	wires (74) str (74) str (74) str (74) str (75) s
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne num te CPG n ext t 0.101	converted conver	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,999 1 48,485,101 1 44,925,937 1 44,487,582 1 34,274,204 1 30,100,434 1 26,184,799 1 24,681,383 1 22,737,907 1 26,617,914 1 145,921,92	total genomic coordinates covered 211,263,806 212,6476,131 187,726,483 179,856,705 168,449,241 160,186,298 145,839,672 136,488,73 125,641,750 125,679,633 92,616,285 84,625,607 75,271,456 72,214,897 52,737,469 57,661,933	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,080 4,778,177,208 4,438,655,652 4,211,379,180 3,709,518,600 3,709,518,600 3,709,518,600 3,217,243,92 2,176,821,962 1,176,821 1,176,821	CpGs removed : 5' conversion : filter : 3,648,862 4,146,302 3,246,780 3,028,212 2,955,761 2,878,709 2,712,507 2,475,528 1,987,871 2,322,139 2,475,528 1,1658,388 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,582,423 1,562,588 1,582	2 conversion ilter 42,972,568 47,830,228 47,830,228 33,194,822 33,492,800 31,489,484 28,471,115 23,652,944 29,128,166 27,623,252 26,968,622 18,687,866 18,298,173 17,431,305 20,696,346 20,160,965 15,682,141 16,372,627	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278 1,782,259 1,259,892 1,259,892	Fidence C Total C/T requence, ingle- ingle- 19,870,425 44,367,204 33,844,157 30,566,690 31,041,320 30,354,812 29,262,772 26,456,889 21,988,096 27,985,25 25,666,157 25,412,67 17,341,667 17,202,760 16,224,940 19,402,205 18,967,107 14,575,033 15,493,454 14,437,926	Total C sequence (bp) s 24,631,906 27,833,029 20,999,727 18,355,856 18,872,892 13,808,166 15,408,353 15,509,839 10,568,126 10,390,758 10,234,352 12,191,908 11,838,044 9,039,593 9,613,434	inique bases vith at least 5 lads (single- (tranded) s. 2,558,704 3,070,171 2,330,080 2,100,156 2,088,837 1,587,320 1,176,084 1,795,230 1,176,084 1,413,13,924 1,456,545 1,492,209 997,140 1,313,924 1,042,835	Jinique bases with at least 10, or eads 1, 231, 231, 231, 231, 231, 231, 231, 2	Unique bases w with at least 5 1 2 3 3,561,857 3,561,857 3,561,857 2,409,117 2,440,147 2,409,117 2,440,147 2,409,117 2,440,147 2,140,848 1,850,813 2,200,154 2,125,913 2,089,138 1,340,227 1,405,881 1,348,540 1,156,587,01 1,136,311 1,658,701 1,136,311 1,658,701 1,205,889 1,136,227 1,405,228 1,405,	Inique bases with at least 0 reads double- tranded) 3,172,941 3,271,847 2,483,665 2,224,032 1,268,539 2,240,861 1,996,950 1,995,3601 1,995,3601 1,995,3601 1,253,845 1,254,611 1,554,485 1,598,883 1,061,706 1,418,704 1,111,371	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 63.21% 63.89% 60.80% 62.21% 63.82% 62.11% 63.82% 62.11% 63.82% 62.10% 63.00% 62.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.11% 63.00% 62.10% 62.10% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 63.00% 62.10% 62.10% 63.00% 62.1	Unique bases covered (both Total C/T strands) superact (superact 79,370,002 393,972,79,370,002 310,003,003,003,003,003,003,003,003,003,	Total C p) sequence (b) 720 5,830,89 7,205,83 91 6,090,11,11 81 6,279,81 81 6,279,81 81 6,279,81 81 6,279,81 81 6,279,81 81 6,381	wii rea pp) str 174 187 150 190 144 142 170 131 118 165 160 160 161 161 161 161 161 161 161 161
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne ne num te CpG m ext te CpG n	converted Converted Converted Converted Converted Converted Conversion Season-6 filter 0.101 0.1	total uniquely mapped reads: 1 70,975,448 1 82,666,673 1 66,089 418 1 82,666,673 1 66,089 418 1 84,865,101 1 37,354,464 1 43,191,371 1 44,487,582 1 34,274,204 1 30,100,434 1 26,184,183 1 24,861,383 1 22,737,907 1 26,617,934 1 14,925,192 1 12,01,102,484 1 11,492,192 1 12,01,102,484 1 11,492,192	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,449,241 160,186,298 179,856,705 123,713,843 125,641,750 125,679,633 92,616,285 84,625,406 72,771,688 72,716,688 72,771,688 72,716,689	total sequence (bp) 5,977,570,076 4,979,343,080,880 4,778,177,080 4,478,157,500,776 4,211,379,180 3,506,127,312 2,792,180 3,176,525,088 3,217,243,932 2,478,101,684 2,176,821,956 1,785,682,828 1,1645,2647,916 1,924,936 1,924,936 1,936	0.26% CpGs removed: 5' conversion: filter 4,146,302 3,246,780 3,028,222 2,955,761 2,857,049 1,957,971 2,475,528 1,957,979 1,552,588 1,679,049 1,562,588 1,679,049 1,562,588 1,770,084 1,462,499 1,562,588 1,370,084 1,462,493 1,253,423 1,240,374 701,747	2 conversion litter 42,972,568 47,830,228 47,830,228 47,830,228 47,830,228 47,830,228 47,830,228 47,812 47,812 47,912 47,623,277,945 47,623,2652,944 29,128,166 27,623,252 65,968,622 47,431,305 20,696,342 40,160,965 18,298,173 17,431,305 20,696,342 40,160,965 15,682,141 16,372,627 15,419,197 8,205,689	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,233,794 1,934,796 2,300,287 2,227,999 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278 1,782,259 1,259,892 650,716	fidence C Total C/T requence, ingle- ingle- 139,870,425 44,367,204 33,844,157 30,354,812 20,456,839 31,041,320 30,354,812 21,988,096 27,085,526 27,085,526 27,085,526 27,085,526 27,085,526 17,020,760 16,224,940 19,402,205 11,987,707 14,575,033 15,493,454 14,437,926 7,625,247	Total C r sequence (ph) s 24,631,906 27,823,029 20,999,227 18,616,658,585 16,281,827 15,808,656 17,129,894 15,403,536 15,609,839 10,0548,135 12,191,908 11,3838,468 9,039,538 43,875,538 44,903,993 93,613,444 8,755,338 4,800,098	inique bases y vith at least 5 leads (single- (tranded) s 2,958,704 3,070,177 2,330,080 2,081,6618 1,187,932 1,187,932 1,187,932 1,191,6618 1,187,932 1,191,6618 1,176,084 1,121,155 1,176,084 1,121,155 1,1492,209 997,140 1,131,942 1,142,835 540,899 997,140	Jinique bases with at least 10, or eads 1, o	Unique bases with a least 51 reads (double least strander) s 3,561,857 3,361,857 2,482,744 2,409,11 2,140,868 1,2200,154 2,125,913 2,089,138 1,200,154 2,177,179,179,179,179,179,179,179,179,179	Inique bases with at least 0 reads double- tranded) 3,772,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 2,022,21 1,986,950 1,919,050 1,919,050 1,919,050 1,238,485 1,294,475 1,236,485 1,294,475 1,258,485 1,294,475 1,258,485 1,294,475 1,296,475 1,298	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.39% 62.25% 62.11% 63.89% 62.25% 62.11% 63.20% 63.30% 63.30% 63.30% 63.30% 63.30% 63.30% 63.60% 63.60% 63.60% 63.65%	Unique bases covered (both Total C/T strands) Sequence (1) \$173,70,902 939,972, 82,819,397 1,073,079, 88,199,123 888,746, 62,720,082 818,055, 60,736,658 794,062, 57,712,657 743,490, 53,217,513 665,072, 49,816,729 628,551, 39,679,902 495,568, 46,552,820 588,472, 47,362,328 589,996, 46,382,145 579,943, 32,571,525 427,582, 31,347,461 394,941, 28,527,361 354,276, 28,862,191 347,632, 29,102,777 324,571, 26,194,865 342,589, 21,903,610 217,301, 22,969,066 290,095, 21,903,610 217,301, 22,969,066 290,095,	Total C p) sequence (b) 72 5,830,8 96 7,205,8 191 6,090,11 81 6,079,8 18 6,279,8 18 6,279,8 18 6,279,8 19 18 6,279,8 19 19 19 19 19 19 19 19 19 19 19 19 19 1	wii rea pp) str 174 187 1990 444 42 770 331 118 166 166 167 147 17.78 165 162 163 164 167 167 167 167 167 167 167 167 167 167
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne tum tee CpG n ext t 0.101	converted 5 converted 5 converted 5 conversion control filter 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,99 1 48,485,101 1 43,73,54,464 1 43,199,371 1 44,475,591 1 44,475,591 1 22,737,907 1 26,617,914 1 1 22,737,907 1 24,613,83 1 22,737,907 1 26,617,914 1 1 14,592,192 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 9,888,433	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,449,241 160,186,298 145,839,672 136,488,73 125,641,750 125,679,633 92,616,285 84,625,607 75,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,080 4,78,177,208 4,483,655,62 4,211,379,180 3,709,518,600 3,709,518,600 3,709,518,600 3,709,518,600 3,217,243,932 2,478,101,684 2,176,821,952 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,622,53,76 1,941,942,803,95 1,941,942,803,95 1,941,942,803,95 1,941,942,803,95 1,941,942,94 1,941,943,94 1,941,944,94 1,941,944,98 1,941,941,944,94 1,941,944,94 1,941,941,944,94 1,941,941,944,94 1,941,941,944,94 1,941,941,941,94 1,941,941,941,94 1,941,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,9	CpGs removed of Sconversion in the CpGs removed of Sconversion in the CpGs removed of April 24,46,302 a,246,780 a,287,2475,528 a,987,871 a,2475,528 a,987,871 a,2475,528 a,1987,871 a,2475,381 a,1679,049 a,1676,381 a,1679,049 a,1676,381 a,1676,	2 conversion litter 42,972,568 47,830,228 47,830,228 47,830,228 34,992,800 33,194,822 33,499,800 32,777,945 31,489,484 29,128,166 29,626,626 3	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278 1,782,259 1,259,892 650,716 958,347	Fidence C rotal C/T requence, ingle- ingle- 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320 30,354,812 29,262,772 25,6456,889 21,988,096 27,085,256 17,341,667 17,202,760 16,224,940 19,402,205 18,967,107 14,575,033 15,493,454 14,437,926 7,625,247 9,555,077 9,555,077	Total C sequence (bp) s 24,631,906 27,823,029 20,999,727 18,315,856 18,812,892 13,808,166 15,281,827 13,808,166 15,408,336 15,408,336 15,609,839 10,568,126 10,309,758 10,234,352 12,191,908 39,613,434 45,403,436 46,604,550	inique bases vith at least 5 i aeads (single- (tranded) s. 2,958,704 3,070,717 2,330,080 2,100,156 2,088,837 1,200,156 2,088,837 1,916,618 1,831,844 1,795,230 1,176,084 1,4795,230 1,176,084 1,476,545 1,492,209 997,140 1,313,924 1,042,835 540,899 755,605	Jinique bases with at least 10 or eads 1,00 reads 1,231,00 reads 1,231,00 reads 1,231,00 reads 1,231,00 reads 1,532,64 reads 1,532,64 reads 1,532,64 reads 1,532,64 reads 1,532,64 reads 1,532,65 reads 1	Unique bases w with at least 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Unique bases with at least 0 reads double-tranded) 1,3771,847 2,483,665 2,224,032 2,268,539 2,240,861 2,259,241 1,986,950 1,053,845 1,254,861 13 1,554,485 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,558,883 1,558,883 1,558,883 1,558,883 1,558,883 1,558,885 1,558,883 1,588,883 1,588	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 62.21% 63.39% 66.80% 63.39% 62.25% 62.11% 63.82% 62.11% 63.82% 62.11% 63.62% 62.16% 63.65% 63.65% 63.16%	Unique bases covered (both Total C/T strand) sequence (\$20,000,000,000,000,000,000,000,000,000,	Total C p) sequence (b) 72 5,830,89 7,205,83 91 6,090,11 81 6,079,81 81 6,279,81	wir rei ire
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne ne num te te CpG n ext te Cp	converted conver	total uniquely mapped reads 1 70,975,448 1 82,666,673 1 69,138,284 1 66,898 418 1 48,485,101 1 37,544,64 1 33,010,43 1 44,487,582 1 34,274,204 1 30,100,43 1 26,617,934 1 26,617,934 1 26,617,934 1 26,617,934 1 26,617,934 1 14,925,937 1 24,938,343 1 22,737,907 1 26,617,934 1 14,925,937 1 1 26,617,934 1 14,925,937 1 1 20,100,43 1 1 20,918,243 1 1 1,925,192 1 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 9,888,433 1 2,727,181 1 4,727,181 1 1 9,888,433 1 2,727,181 1 1 9,888,433 1 2 24,727,181 1 24,727,181 1 1 9,888,433 1 2 24,727,181 1 24,727,181 1 1 9,888,433 1 2 24,727,181 1 24,727,181 1 1 9,888,433 1 2 24,727,181 1 24,	total genomic coordinates covered 211, 263, 806 212, 6476, 113 187, 726, 483 179, 856, 705 158, 449, 241 150, 186, 289 145, 839, 672 130, 148, 737 125, 641, 750 125, 679, 633 29, 2616, 282 84, 525, 640 72, 77, 648 72, 77, 648 73, 748 748 748 748 748 748 748 748 748 748	total sequence (bp) 5,977,570,076 4,978,177,08 4,478,177,208 4,421,379,180 3,709,518,600 3,506,127,312 2,748,101,600 3,176,525,088 3,217,243,932 2,478,101,68 2,4	0.26% CpGs removed : 5' conversion : filter 4.146,300 3.246,780 3.028,222 9.955,761 2.887,009 1.967,827 1.967,827 1.967,827 1.967,827 1.967,838 1.370,084 1.462,439 1.580,838 1.370,084 1.253,423 1.240,374 761,747 761,370 1.124,838	2 conversion litter 42,972,568 47,830,228 47,830,228 47,830,228 47,830,228 47,830,228 47,831,492,800 32,777,945 13,489,484 29,162,3652,944 29,162,946,365 18,298,173 17,431,300 20,696,342 20,160,965 15,682,141 16,372,627 15,419,199 10,140,061 21,400,061	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,488,546 2,550,273 2,559,151 2,579,371 2,233,794 1,954,796 2,300,287 2,270,999 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278 1,782,259 1,259,882 650,347 1,836,475	fidence C fotal C/T requence, ingle- ingle- 39,870,425 44,367,204 33,844,157 30,556,569 31,041,320 30,354,812 26,476,889 27,085,526 27,085,526 27,085,526 27,020,760 13,401,677 17,020,760 16,224,940 19,402,205 18,967,107 14,575,035 15,493,454 14,437,926 7,625,247 9,556,075	Total C r sequence (b) a 24,631,906 72,7823,029 20,999,727 18,865,18,821,892 18,886,517 12,984 15,609,839 15,609,839 15,609,839 15,609,839 10,284,532 12,191,908 11,3830,468 49,039,593 96,634,560,634,880,098 6,045,530 6,045,530 6,045,530 6,931,382	Inique bases vith at least 5 cads (single- (tranded) s 2,958,704 3,070,717 2,330,080 2,100,156 618 1,107,107 1,107	Jinique bases with at least 1, 0, reads 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	Unique bases with a least 51 stranded) s 3,561,857 s 3,561,857 s 3,561,857 s 2,487,744 2,409,117 2,140,868 2,437,744 2,140,868 2,437,744 2,140,868 2,437,744 2,140,868 2,125,913 2,009,138 1,136,311 1,136,311 1,136,311 1,136,311 1,136,311 1,262,588 901,920 1,633,847 1,638,89 1,920 1,633,847 1,638,91 1,91 1,91 1,91 1,91 1,91 1,91 1,91	Inique bases with at least 0 reads double- tranded) 3,772,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 2,292,241 1,986,950 2,042,631 1,957,109 1,919,050 1,253,845 1,294,475 1,258,485 1,294,475 1,258,485 1,25	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.25% 62.25% 62.11% 63.60% 63.03% 62.00% 63.03% 62.00% 63.03% 62.00% 63.03% 63.0	Unique bases covered (both Total C/T strands) sequence (1) strands) sequence (2) strands) sequence (3) sequen	Total C p) sequence (b f2 5,830,8 6 7,205,8 6 1,909,1 18 6,279,8 6 6,510,7 18 6,627,8 18 6,279,8 18 6,279,8 19 3,178,2 11 4,488,1 19 3,622,3 110,2 10 3,244,2 10 91 3,254,2 10 1,798,1 10 3,71,798,1 1	wii rea (pp) str (74 174 174 174 174 174 174 174 174 174 1
Tumor E	minMapQ	Cytosis maxim oppisit strand 30 30 30 30 30 30 30 30 30 30 30 30 30	ne tum tee CpG n ext t 0.101	converted 5 converted 5 converted 5 conversion control filter 0.101	total uniquely mapped reads 1 82,660,673 1 69,138,284 1 62,007,059 1 58,240,774 1 51,295,99 1 48,485,101 1 43,73,54,464 1 43,199,371 1 44,475,591 1 44,475,591 1 22,737,907 1 26,617,914 1 1 22,737,907 1 24,613,83 1 22,737,907 1 26,617,914 1 1 14,592,192 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 1,482,492 1 1 9,888,433	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,449,241 160,186,298 145,839,672 136,488,73 125,641,750 125,679,633 92,616,285 84,625,607 75,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456 72,271,456	total sequence (bp) 5,133,080,880 5,977,570,076 4,999,343,080 4,78,177,208 4,483,655,62 4,211,379,180 3,709,518,600 3,709,518,600 3,709,518,600 3,709,518,600 3,217,243,932 2,478,101,684 2,176,821,952 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,219,52 1,768,622,53,76 1,941,942,803,95 1,941,942,803,95 1,941,942,803,95 1,941,942,803,95 1,941,942,94 1,941,943,94 1,941,944,94 1,941,944,98 1,941,941,944,94 1,941,944,94 1,941,941,944,94 1,941,941,944,94 1,941,941,944,94 1,941,941,941,94 1,941,941,941,94 1,941,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,941,94 1,941,9	CpGs removed of Sconversion in the CpGs removed of Sconversion in the CpGs removed of April 24,46,302 a,246,780 a,287,2475,528 a,987,871 a,2475,528 a,987,871 a,2475,528 a,1987,871 a,2475,381 a,1679,049 a,1676,381 a,1679,049 a,1676,381 a,1676,	2 conversion litter 42,972,568 47,830,228 47,830,228 47,830,228 34,992,800 33,194,822 33,499,800 32,777,945 31,489,484 29,128,166 29,626,626 3	High-conf Unique bases s covered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278 1,782,259 1,259,892 650,716 958,347 1,836,475	Fidence C rotal C/T requence, ingle- ingle- 39,870,425 44,367,204 33,844,157 30,566,690 31,041,320 30,354,812 29,262,772 25,6456,889 21,988,096 27,085,256 17,341,667 17,202,760 16,224,940 19,402,205 18,967,107 14,575,033 15,493,454 14,437,926 7,625,247 9,555,077 9,555,077	Total C sequence (bp) s 24,631,906 27,823,029 20,999,727 18,315,856 18,812,892 13,808,166 15,281,827 13,808,166 15,408,336 15,408,336 15,609,839 10,568,126 10,309,758 10,234,352 12,191,908 39,613,434 45,403,436 46,604,550	inique bases vith at least 5 i aeads (single- (tranded) s. 2,958,704 3,070,717 2,330,080 2,100,156 2,088,837 1,200,156 2,088,837 1,916,618 1,831,844 1,795,230 1,176,084 1,4795,230 1,176,084 1,476,545 1,492,209 997,140 1,313,924 1,042,835 540,899 755,605	Jinique bases with at least 10 or eads 1,00 reads 1,231,00 reads 1,231,00 reads 1,231,00 reads 1,231,00 reads 1,532,64 reads 1,532,64 reads 1,532,64 reads 1,532,64 reads 1,532,64 reads 1,532,65 reads 1	Unique bases w with at least 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Unique bases with at least 0 reads double-tranded) 1,3771,847 2,483,665 2,224,032 2,268,539 2,240,861 2,259,241 1,986,950 1,053,845 1,254,861 13 1,554,485 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,554,85 1,558,883 1,558,883 1,558,883 1,558,883 1,558,883 1,558,883 1,558,885 1,558,883 1,588,883 1,588	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 62.21% 63.39% 66.80% 63.39% 62.25% 62.11% 63.82% 62.11% 63.82% 62.11% 63.62% 62.16% 63.65% 63.65% 63.16%	Unique bases covered (both Total C/T strands) sequence (79,370002 393,972 C8,819,397 1,073,079,68,109,123 888,764,62,720,082 818,055,60,736,458 794,052,57,712,657 744,490,53,217,513 665,072,49,816,729 622,551,39,679,802 495,588,405,522,205 588,472,47,362,228 598,996,46,382,147,461 394,941,28,527,361 34,274,61 394,941,28,527,361 34,276,219,102,777 324,571,251 49,066 290,096,62 20,096,	Total C p) sequence (b) 27,205,8 266 7,205,8 267 7,205,8 268 6,090,1:1 218 6,279,8 26 5,510,7 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 22 3,110,2 26 63,607,1 21 99 3,622,3 27 3,778,4 69 3,244,2,9 27 2,354,0 20 956,6 27 2,354,0 20 956,6 27 1,479,8 28 640,0 20 966,6 20 97,378 4,99,8 20 98,6 20 99,6 20 966,6 20 97,9 20 98,6 20 99,9 20 96,6 20 96,6 20 99,9 20 96,6 20 99,9 20 96,6 20 99,9 20 99	with read only strain (174 strain 174 strain
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686,045,550 6,931,382 688,661 686,045,550 6,931,382 688,661 686,045,550 6,931,382 688,661 686,045,550 697,680 6	Inique bases vith at least 5 leads (single- (tranded) s 2-958,704 3,070,717 2,330,080 2,108,164 2,129,324 2,100,156 2,088,837 1,857,932 1,916,184 1,175,084 1,175,175,175 1,175,175 1,175,175 1,	Jinique bases with at least 1, 0, reads 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	Unique bases with a least 51 reads (double- (stranded) s 3,561,857 3,561,857 3,561,857 2,471,192 2,409,117 2,440,147 2,409,117 2,440,147 2,140,868 2,437,744 2,109,813 2,200,154 1,108,618 1,177,095 1,108,618 1,177,095 1,136,511	Dnique bases with at least 0 reads double-tranded) 3,172,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 2,292,241 1,986,950 2,042,631 1,957,109 1,919,050 1,253,845 1,294,475 1,256,113 1,554,485 1,294,475 1,256,113 1,554,485 1,294,475 1,294,475 1,294,475 1,294,475 1,294,475 1,296,113 1,554,485 1,294,475 1,296,113 1,554,485 1,294,475 1,296,113 1,554,485 1,298,113 1,298	Mean Per cent methylation 62.51% 63.59% 62.18% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.25% 62.25% 62.11% 63.62% 63.16% 64.16% 64.16% 64.16% 64.11% 64.11% 64.11%	Unique bases covered (both Total C/T strands) sequence (79,370002 393,972 C8,819,397 1,073,079,68,109,123 888,764,62,720,082 818,055,60,736,458 794,052,57,712,657 744,490,53,217,513 665,072,49,816,729 622,551,39,679,802 495,588,405,522,205 588,472,47,362,228 598,996,46,382,147,461 394,941,28,527,361 34,274,61 394,941,28,527,361 34,276,219,102,777 324,571,251 49,066 290,096,62 20,096,	Total C p) sequence (b) 27,205,8 266 7,205,8 267 7,205,8 268 6,090,1:1 218 6,279,8 26 5,510,7 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 22 3,110,2 26 63,607,1 21 99 3,622,3 27 3,778,4 69 3,244,2,9 27 2,354,0 20 956,6 27 2,354,0 20 956,6 27 1,479,8 28 640,0 20 966,6 20 97,378 4,99,8 20 98,6 20 99,6 20 966,6 20 97,9 20 98,6 20 99,9 20 96,6 20 96,6 20 99,9 20 96,6 20 99,9 20 96,6 20 99,9 20 99	with read with r
	minMapQ	Cytosin maxim oppisiti strand 3 30 30 30 30 30 30 30 30 30 30 30 30 3	ne ne numer te CpG n ext te CpG	converted conver	total uniquely mapped reads 1 7,0757-5,48 1 82,660,673 1 69,138,284 1 62,007,059 1 48,485,101 1 37,354,486 1 1 43,295,397 1 44,4725,397 1 44,4725,397 1 2 44,725,397 1 2 42,681,383 1 22,773,907 1 26,617,914 1 14,921,92 1 20,610,284 1 14,272,381 1 22,473,391 1 24,723,81 1 22,733,907 1 20,610,284 1 11,427,429 1 20,610,284 1 11,427,429 1 20,882,433 1 22,773,81 1 22,838,342 1 32,269 928,275,602 Mean reads per position cc Total bp covered in hg18 (F Percentage of hg18 covered to 18 18 covered to 18 1	total genomic coordinates covered (211, 263, 266 226, 476, 131 137, 264, 483 145, 289, 267 277, 264, 267 2777, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277, 267 277,	total sequence (bp) 5.977.570.076 4.799.345.088 4.778.177.263 4.778.177.263 4.778.177.263 4.778.177.263 4.778.177.263 5.766.127.317.263 5.766.127.317.263 5.766.127.317.263 5.766.127.317.263 5.766.127.317.263 5.766.128 5.766.12	CpGs removed of 5' conversion : fifting fiftin	2,000 (200 (200 (200 (200 (200 (200 (200	High-conf Unique bases sovered (both s strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,374 2,230,728 2,105,616 1,306,022 1,125,125 1,126	Fidence C Total C/T requence, ingle- ingle- 39,870,425 44,367,204 33,844,157 30,566,590 31,041,320 30,354,812 29,262,772 25,6456,839 12,988,996 21,988,98	Total C sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 118,821,892 13,808,1664 15,409,389 10,588,166 11,540,389 10,588,126 10,588,	inique bases vith at least 5 v	Jinique bases with at least 10 oreads 1,193,194,194,195,196,196,196,196,196,196,196,196,196,196	unique bases w with at least 5 in the standard s	Inique bases with at least 0 reads double-tranded) 3,172,941 3,271,847 2,483,626 2,224,032 2,268,539 2,240,861 2,292,241 1,986,950 2,042,631 1,957,109 1,919,050 1,538,485 1,294,475 1,236,113 1,554,485 1,294,475 1,236,113 1,554,485 1,294,475 1,294,475 1,298,131 1,554,485 1,294,475 1,298,133 1,061,706 1,418,704 1,111,371 1,577,205 809,017 1,218,136 105,392 67 40,731,519	Mean Per cent methylation 62.51% 63.59% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.39% 63.11% 62.25% 62.11% 63.89% 60.00% 63.39% 62.25% 62.11% 63.60% 63.60% 63.03% 62.02% 61.26% 63.16% 64.11% 0.14%	Unique bases covered (both Total C/T strands) sequence (79,370002 393,972 C8,819,397 1,073,079,68,109,123 888,764,62,720,082 818,055,60,736,458 794,052,57,712,657 744,490,53,217,513 665,072,49,816,729 622,551,39,679,802 495,588,405,522,205 588,472,47,362,228 598,996,46,382,147,461 394,941,28,527,361 34,274,61 394,941,28,527,361 34,276,219,102,777 324,571,251 49,066 290,096,62 20,096,	Total C p) sequence (b) 27,205,8 266 7,205,8 267 7,205,8 268 6,090,1:1 218 6,279,8 26 5,510,7 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 22 3,110,2 26 63,607,1 21 99 3,622,3 27 3,778,4 69 3,244,2,9 27 2,354,0 20 956,6 27 2,354,0 20 956,6 27 1,479,8 28 640,0 20 966,6 20 97,378 4,99,8 20 98,6 20 99,6 20 966,6 20 97,9 20 98,6 20 99,9 20 96,6 20 96,6 20 99,9 20 96,6 20 99,9 20 96,6 20 99,9 20 99	with read with r
enome totals	minMapQ	Cytosin maxim oppisiti strand 3 30 30 30 30 30 30 30 30 30 30 30 30 3	ne ne numer te CpG n ext te CpG	converted conver	total uniquely warming to mapped reads 1 82,660,673 1 69,138,284 1 66,089,418 1 62,007,059 1 58,240,774 1 51,259,599 1 48,485,101 1 37,354,464 1 43,919,371 1 44,4725,937 1 44,487,582 1 34,274,204 1 1 30,100,434 1 26,184,799 1 24,681,383 1 22,737,907 1 266,617,914 1 11,482,429 1 20,100,128 1 1,482,429 1 20,100,128 1 1,482,429 1 20,100,128 1 1,482,429 1 20,269 1 99,88,433 1 24,727,181 1 24,727,	total genomic coordinates covered 211,263,806 226,476,113 187,726,483 179,856,705 168,449,241 160,186,298 145,839,672 136,488,737 106,305,755 123,713,848 125,641,750 125,679,633 22,616,285 84,625,607 75,2761,685 27,2761,856 27,2761,85	total sequence (bp) 5,133,080,880 5,977,570,076 4,799,343,080,880 4,778,177,080 4,478,177,208 4,211,379,180 3,506,127,312 2,701,592,080 3,176,525,088 3,709,518,640 2,701,592,080 1,701,	CpGs removed : 5' conversion : filter 3,648,862 4,146,302 3,246,780 3,028,212 2,955,761 2,887,009 2,712,507 2,475,528 1,987,871 2,322,139 2,475,528 1,987,871 2,322,139 2,1562,588 1,462,459 1,562,588 1,462,459 1,562,588 1,462,459 1,240,374 701,747 701,747 701,747 701,747 701,747 6,204 48,720,932 48,720,932 48,720,932 48,720,932 48,720,932 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 2,858,034,764 48,720,932 49,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,720,932 40,7	2,000 (200 (200 (200 (200 (200 (200 (200	High-conf Unique bases sovered (both strands) strands) s 3,788,141 3,678,586 2,795,724 2,498,546 2,550,273 2,519,151 2,579,371 2,233,794 1,954,796 2,300,287 2,227,099 2,196,165 1,396,032 1,475,322 1,422,158 1,813,810 1,913,425 1,184,278 1,782,259 1,259,892 650,716 958,347 1,836,475 164,513 701 Mean reads per CpG (each strar Total CpGs in reference Total reference covered:	Fidence C Total C/T requence, ingle- ingle- 39,870,425 44,367,204 33,844,157 30,566,590 31,041,320 30,354,812 29,262,772 25,6456,839 12,988,996 21,988,98	Total C sequence (bp) s 24,631,906 27,823,029 20,999,727 18,616,666 118,821,892 13,808,1664 15,409,389 10,588,166 11,540,389 10,588,126 10,588,	inique bases vith at least 5 1 acads (single- (tranded) s. 2,958,704 3,070,717 2,330,080 2,100,156 2,088,837 1,210,156 2,088,837 1,587,320 1,176,084 1,795,230 1,176,084 1,712,155 1,159,524 1,492,209 997,140 1,313,924 1,042,835 540,899 755,605 1,117,348 97,445 656 38,110,200	Unique bases with at least 10, or eads 1, 231, 241, 241, 241, 241, 241, 241, 241, 24	Unique bases with a least 51 reads (double- (stranded) s 3,561,857 3,561,857 3,561,857 2,471,192 2,409,117 2,440,147 2,409,117 2,440,147 2,140,868 2,437,744 2,109,813 2,200,154 1,108,618 1,177,095 1,108,618 1,177,095 1,136,511	Inique bases with at least 0 reads to use of the country of the co	Mean Per cent methylation 62.51% 63.59% 62.18% 63.26% 62.18% 63.33% 63.71% 62.41% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.21% 63.25% 62.25% 62.11% 63.62% 63.16% 64.16% 64.16% 64.16% 64.11% 64.11% 64.11%	Unique bases covered (both Total C/T strands) sequence (79,370002 393,972 C8,819,397 1,073,079,68,109,123 888,764,62,720,082 818,055,60,736,458 794,052,57,712,657 744,490,53,217,513 665,072,49,816,729 622,551,39,679,802 495,588,405,522,205 588,472,47,362,228 598,996,46,382,147,461 394,941,28,527,361 34,274,61 394,941,28,527,361 34,276,219,102,777 324,571,251 49,066 290,096,62 20,096,	Total C p) sequence (b) 27,205,8 266 7,205,8 267 7,205,8 268 6,090,1:1 218 6,279,8 26 5,510,7 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 21 4,488,1 22 3,110,2 26 63,607,1 21 99 3,622,3 27 3,778,4 69 3,244,2,9 27 2,354,0 20 956,6 27 2,354,0 20 956,6 27 1,479,8 28 640,0 20 966,6 20 97,378 4,99,8 20 98,6 20 99,6 20 966,6 20 97,9 20 98,6 20 99,9 20 96,6 20 96,6 20 99,9 20 96,6 20 99,9 20 96,6 20 99,9 20 99	1774 6 8 1774 6

Supplementary Table 2. Bisulfite-seq sample details (cont.)

				Cytosine	es with am	biguous c	ontext					Possible	non-cyt	osines in s	ample ge	nome				
Unique bases		Unique bases						Unique bases		Unique bases			•			Unique bases		Unique bases		
with at least	Unique bases	with at least				l	Inique bases	with at least	Unique bases	with at least					Unique bases	with at least	Unique bases	with at least		
10 reads	with at least 5	10 reads		Unique bases		v	vith at least 5	10 reads	with at least 5	10 reads		Unique bases			with at least 5	10 reads	with at least 5	10 reads		
(single-	reads (double-	(double-	Mean Per cent	covered (both	Total C/T	Total C r	eads (single-	(single-	reads (double-	(double-	Mean Per cent	covered (both	Total C/T	Total C	reads (single-	(single-	reads (double	- (double-	Mean Per cent	cphConversio
stranded)	stranded)	stranded)	methylation	strands)	sequence (bp)	sequence (bp) s	tranded)	stranded)	stranded) :	stranded)	methylation	strands)	sequence (b)) sequence (bp)	stranded)	stranded)	stranded)	stranded)	methylation	nPreFilter
46,490,825	77,300,669	72,775,588	0.68%	734,62	5,782,107	581,166	584,219	113,061	715,259	638,157	9.19%	570,23	5 7,743,0	1 317,916	459,436	327,027	556,171	1 488,27	0 4.69%	98.90%
53,561,480	81,185,086	77,996,188	0.75%	698,583	5,813,975	653,339	570,020	133,326	682,942	625,777	9.45%	578,07	1 8,756,9	0 366,133	483,499	366,973	566,762	2 512,52	3 4.62%	98.81%
44,262,253	66,852,315	64,273,703	0.77%	557,649	4,643,206	491,444	455,311	107,458	545,455	500,305	9.00%	476,09	4 7,171,2	7 289,929	399,214	303,919	467,127	7 423,24	8 4.45%	98.79%
40,397,567	61,512,220	59,100,534	0.86%	514,437	7 4,333,489	466,294	419,266	99,616	502,946	461,024	9.00%	459,51	5 7,113,14	6 280,200	384,976	292,729	450,479	5 408,98	7 4.41%	98.67%
39,480,860	59,563,002	57,262,448	0.78%	499,199	4,121,968	427,799	407,636	95,281	488,310	448,084	9.01%	422,83	6,338,3	.1 251,499	354,890	269,436	414,662	2 376,17	3 4.45%	98.77%
37,034,193	56,599,337	54,336,399	0.78%	487,673	3 4,215,822	499,138	398,027	93,960	477,290	437,653	9.43%	417,16	6,385,30	15 279,030	348,017	263,333	408,890	369,75	2 4.64%	98.77%
33,125,606	51,844,964	49,327,024	0.74%	475,415	3,876,669	446,567	383,637	86,503	462,571	417,498	10.07%	381,90	1 5,463,49	5 247,216	312,664	231,859	372,959	332,23	4 4.97%	98.81%
31,423,898	48,868,579	46,779,396	0.75%	430,954	3,494,284	369,464	350,660	78,438	422,187	386,134	9.23%	350,67	4 5,064,60	6 210,914	292,436	218,081	344,134	4 310,07	8 4.56%	98.82%
24,848,927	38,675,776	36,917,228	0.69%	354,189	2,871,379	323,808	286,231	62,606	344,649	312,456	9.94%	280,26	4,008,39	0 175,562	230,424	171,067	273,716	5 244,41	1 4.83%	98.88%
29,753,386	45,572,090	43,667,419	0.69%	413,882	3,575,521	465,222	337,441	79,349	404,514	369,656	10.10%	329,03	6 4,991,62	1 246,473	272,827	204,340	321,904	4 289,21	9 5.04%	98.91%
29,978,362	46,365,646	44,357,877	0.67%	417,483	3,404,711	361,405	339,361	76,594	408,118	372,049	9.37%	327,54	1 4,801,59	0 193,984	271,257	202,577	320,553	3 287,71	5 4.59%	98.91%
29,060,148	45,389,814	43,372,471	0.72%	408,462	3,287,878	358,744	330,011	72,768	398,708	362,474	9.64%	331,48	4,700,0	.6 200,080	272,803	202,301	324,094	4 289,71	0 4.82%	98.84%
21,202,483	32,004,515	30,822,047	0.86%	267,907	7 2,212,804	233,200	218,873	51,587	262,314	241,415	9.17%	237,45	3,578,4	6 142,476	199,729	151,708	232,885	5 211,81	2 4.45%	98.68%
19,672,607	30,678,310	29,328,954	0.72%	276,137	7 2,223,514	236,245	224,019	49,349	269,839	245,686	9.46%	222,99	1 3,155,91	132,777	183,849	136,383	218,389	9 195,39	4 4.70%	98.85%
17,681,235	27,818,344	26,496,702	0.66%	256,794	2,071,581	232,289	207,091	45,952	250,082	226,037	9.83%	203,09	9 2,811,0	.1 126,230	165,639	121,826	198,266	5 176,03	1 4.90%	98.94%
17,447,286	28,039,258	26,533,284	0.56%	290,48	2,394,683	320,423	234,633	50,804	282,600	253,431	11.42%	205,78	8 2,807,19	8 159,600	166,013	118,962	200,461	1 176,31	4 5.75%	99.06%
16,411,259	28,157,400	26,351,830	0.55%	310,857	7 2,365,589	281,941	246,681	45,977	301,706	267,218	11.03%	212,38	2,613,0	7 138,148	166,919	114,770	206,280	177,39	9 5.82%	99.09%
16,955,970	25,705,168	24,733,084	0.77%	221,160	1,910,081	223,891	180,890	42,668	216,445	199,108	9.58%	186,20	2,950,9	5 124,361	156,134	118,638	182,458	8 165,40	3 4.56%	98.80%
10,786,600	20,994,448	19,045,639	0.47%	269,647	7 1,985,109	260,225	208,214	32,711	260,631	223,020	12.35%	164,96	7 1,831,7	2 106,509	122,043	75,562	158,849	9 130,29	8 6.60%	99.21%
14,579,075	22,510,744	21,541,129	0.57%	212,685	1,752,161	205,471	173,395	38,958	208,137	189,831	10.31%	153,33	2,178,8	8 101,027	126,634	93,792	149,988	3 134,04	8 5.19%	99.05%
7,587,957	11,829,095	11,291,090	0.74%	113,669	1,019,499	137,866	92,457	21,838	110,926	101,024	10.92%	89,32	7 1,463,3	3 77,090	73,583	54,899	87,238	8 78,13	8 5.31%	98.82%
7,666,583	13,113,038	12,288,915	0.47%	149,929	1,141,967	141,019	119,747	22,542	145,518	129,467	11.60%	93,93	1,134,5	3 64,640	73,511	50,039	90,883	3 77,97	1 6.28%	99.21%
12,781,123	43,226,658	34,229,727	0.76%	498,572	3,125,980	168,428	362,068	22,504	478,972	368,751	5.60%	360,53	8 2,723,2	9 82,768	236,507	109,301	344,535	5 251,72	6 3.41%	98.79%
1,266,730	4,057,091	3,162,612	0.73%	51,330	434,158	62,397	36,960	4,574	48,262	36,771	6.77%	34,59			22,652	11,489	32,741	1 24,35	9 4.16%	98.95%
5,324	5,726	5,670	0.29%	72	22,014	42	62	48	71	66	0.34%	6	129,1	1 200	53	5	3 60	0 6	0 0.15%	99.50%
603,456,413	967.863.567	915,991,288		8,911,707	7 72,058,135	7,947,785	7,166,848	1,528,424	8,688,381	7,813,026		7,089,40	9 100,221,50	8 4,340,695	5,775,652	4,210,999	6,924,420	6,131,21	3	

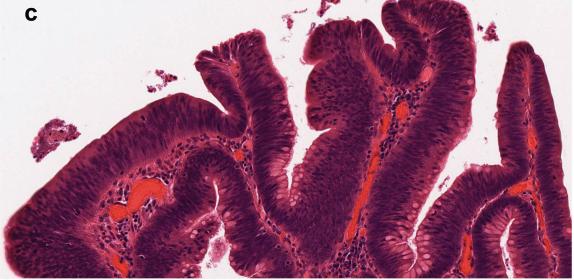
				Cytosines	with am	biguous c	ontext					Possible	non-cyto	sines in s	ample ge	nome				
Unique bases		Unique bases		-			l	Unique bases		Unique bases						Unique bases		Unique bases		
with at least	Unique bases						Jnique bases v		Unique bases N						Unique bases		Unique bases			
10 reads	with at least 5	10 reads		Unique bases		١	with at least 5 1	LO reads v	with at least 5 1	10 reads		Unique bases			with at least 5	10 reads	with at least 5	10 reads		
(single-	reads (double-	(double-	Mean Per cent	covered (both	Total C/T	Total C r	eads (single- (single- r	reads (double- (double-	Mean Per cent	covered (both	Total C/T	Total C	reads (single-	(single-	reads (double-	(double-	Mean Per cent	cphConversio
stranded)	stranded)	stranded)	methylation	strands)	sequence (bp)	sequence (bp) s	tranded) s	tranded) s		stranded)	methylation	strands)	sequence (bp)	sequence (bp)	stranded)	stranded)		stranded)	methylation	nPreFilter
43,832,073	77,098,986	72,046,972		759,318	5,584,794	530,996	602,330	96,030	739,597	656,392	8.87%	576,762			460,090	314,424	561,917	488,402		98.90%
50,914,402		77,435,723	0.75%	724,620	5,644,402	573,602	590,287	115,606	708,682	647,096	9.12%	584,35	7,682,050		484,794	355,276	572,401	513,262		98.82%
42,110,417	66,715,572	63,825,848	0.76%	579,408	4,533,349	438,249	472,503	93,410	566,911	518,204	8.65%	481,133	6,372,467	253,567	400,067	294,425	471,650	423,844		98.79%
38,419,034		58,679,219	0.85%	534,087	4,187,479	412,979	434,286	86,559	522,311	476,942		463,953	6,183,02	245,429	385,303	283,031	454,423	409,071		98.67%
37,569,441	59,440,216	56,862,833	0.77%	517,853	4,030,018	386,568	422,229	82,517	506,783	463,231	8.66%	427,456		224,117	355,792	261,149	418,861	376,860		98.78%
35,192,035		53,940,430	0.78%	506,349	3,957,149	405,847	412,504	81,658	495,683	452,715		421,769			348,852	255,047	413,040	370,214		98.77%
31,385,176		48,899,002	0.74%	491,760	3,769,214	402,658	395,943	74,419	478,631	429,946		385,897	4,855,530		312,814	223,335	376,435	332,191		98.81%
29,807,858		46,424,006	0.75%	447,583	3,438,078	338,409	363,546	67,940	438,638	399,394		354,524			293,067	210,638	347,561	310,454		98.82%
23,545,264		36,617,201	0.69%	366,539	2,798,234	291,867	295,770	53,911	356,989	322,440	9.60%	283,006			230,683	164,845	276,137	244,378		98.89%
28,225,865	45,470,498	43,337,118	0.68%	429,008	3,333,387	360,301	348,919	68,239	419,403	381,914	9.74%	333,220	4,223,860	194,726	273,753	197,610	325,756	289,994	5.01%	98.91%
28,428,928		44,013,147	0.67%	432,250	3,321,281	328,883	350,569	65,756	422,576	383,701	9.04%	331,20			271,872	195,829	323,833	288,160		98.92%
27,536,078		43,024,533	0.71%	423,393	3,224,150	326,299	341,592	62,781	413,463	374,339		335,448			273,606	195,251	327,667	290,343		98.85%
20,176,212		30,613,822	0.85%	278,721	2,174,388	213,094	227,302	44,751	272,956	250,294		239,664			199,739	146,537	234,863	211,799		98.68%
18,776,533		29,135,769	0.71%	284,795	2,182,579	217,990	230,812	42,871	278,360	252,629	9.15%	224,700		119,352	183,846	131,901	219,910	195,160		98.86%
16,898,041	27,767,564	26,322,557	0.66%	264,261	2,023,669	212,947	212,867	39,820	257,388	231,973	9.53%	204,483	2,532,422	112,897	165,564	117,813	199,415	175,693	4.87%	98.95%
16,615,177	27,982,265	26,333,873	0.56%	298,390	2,285,285	275,545	240,433	43,876	290,418	259,524	11.09%	207,084	2,473,253	129,441	165,732	114,463	201,564	175,812		99.06%
15,537,250	28,096,320	26,124,312	0.55%	318,904	2,316,657	260,982	252,326	38,911	309,573	273,158	10.71%	214,55	2,362,148	126,041	167,154	110,377	208,220	177,358	3 5.82%	99.09%
16,273,958	25,671,273	24,607,355	0.77%	228,556	1,792,094	184,459	186,632	37,406	223,740	205,354		187,259	2,477,002		156,013	115,085	183,371	165,053	4.60%	98.79%
10,088,895	20,939,255	18,812,819	0.47%	275,325	1,908,420	235,289	212,060	27,020	266,199	226,259	12.05%	166,93	1,597,853	96,701	122,218	71,960	160,566	130,152	6.65%	99.21%
13,944,800	22,478,019	21,415,248	0.57%	218,958	1,693,245	182,064	178,349	33,825	214,321	194,842	9.93%	154,827	1,947,674	91,025	126,980	90,916	151,322	134,241	5.20%	99.06%
7,256,918	11,807,485	11,219,862	0.74%	117,068	943,903	115,239	95,127	18,873	114,265	103,761	10.54%	89,859	1,194,669	61,228	73,439	53,088	87,646	77,908		98.82%
7,249,196	13,083,308	12,184,032	0.47%	153,520	1,119,939	131,541	122,382	19,108	149,066	132,224	11.27%	95,018	1,019,927	59,294	73,781	48,031	91,815	78,109	6.26%	99.22%
11,537,705	43,139,844	33,511,516	0.76%	510,180	3,116,348	160,489	369,071	16,160	490,125	373,155	5.49%	364,423	2,582,138	78,909	235,694	100,269	348,023	249,632	3.41%	98.79%
1,140,862	4,038,157	3,085,775	0.73%	52,079	352,156	31,466	37,296	3,551	48,978	36,887	6.59%	34,534			22,185	10,383	32,664	23,697	7 4.16%	98.89%
4,573	5,112	5,034	0.21%	37	576	3	24	8	33	30	1.22%	35	3,32	3	32	31	. 34	33	0.09%	99.64%
572.462.118	965.764.934	908.472.972		9.212.925	69.730.218	7.017.763	7.395.135	1.314.998	8.985.056	8.046.370		7.162.052	88.389.12	3.790.819	5.783.038	4.061.683	6 989 060	6.131.783	1	

Berman et al., 2011 Supplementary Figure 1

Colon tumor (OTB #B0068109)

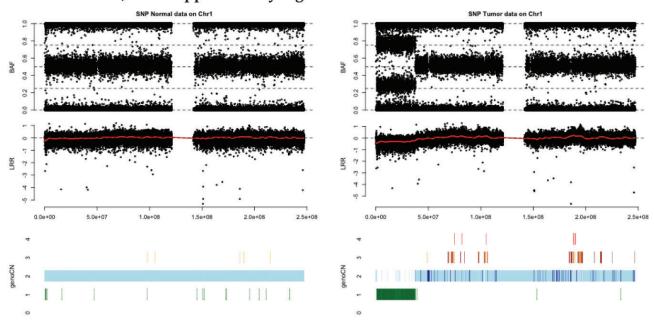
Colon mucosa (OTB #B0068110)

Colon mucosa (OTB #B0068110)



Supplementary figure 1: H&E histological stains show high tumor purity. Colon tumor (a,c) and normal colonic mucosa (b) images were taken directly from Ontario Tumor Bank. Tumor images show high content of transformed epithelial cells within sample, while colon mucosa primarily consists of normal epithelial nuclei.

Berman et al., 2011 Supplementary Figure 2



Supplementary Figure 2: Copy number alterations identified using the Infinium 1M SNP array. genoCNV9 plot showing chromosome 1, with a 100 Mbp deletion at the telomeric end of chr1p. Variant copy number calls (genoCN=0, 1, 3, 4) were used to compare Bisulfite-seq and the Infinium DNA methylation values in regions of altered copy number (Supplemental Figure 3).

Berman et al., 2011 Supplementary Figure 3 b Normal colon mucosa (n=21,713) **Colon tumor (n=18,923)** r=0.97 r=0.95 1 1 0.9 0.9 Infinium Beta Value Infinium Beta Value 0.8 8.0 0.7 0.7 0.6 0.6 0.5 0.5 0.4 0.4 0.3 0.3 0.2 0.2 0.1 0.1 0 0 0.5 Bisulfite-seq fraction methylated Bisulfite-seq fraction methylated d C 0.9 0.9 Infinium Beta Value Infinium Beta Value 0.8 0.8 0.7 0.7 0.6 0.6 0.5 0.5 0.4 0.4 0.3 0.3 0.2 0.2 0.1 0.1 0 0

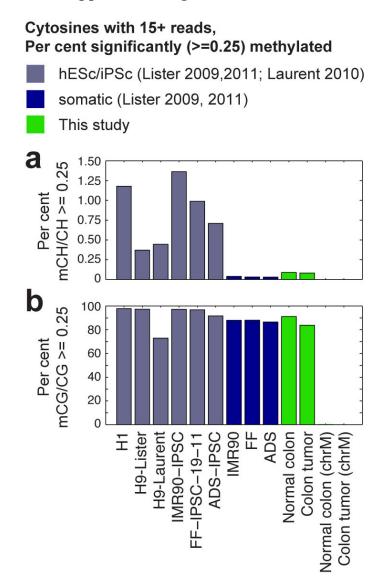
Supplementary Figure 3: Bisulfite-seq and Infinium methylation array give similar methylation levels, even in regions of altered copy number. Values are shown for 21,713 CpGs present on Infinium 27k array and with at least 5 reads on each strand of bisulfite-seq data for the normal colon mucosa (a,c), and 18,923 are shown for CpGs with at least 5 reads on each strand of bisulfite-seq data for the colon tumor (b,d). Top panels (a,b) are colored by feature density, while lower panels (c,d) are color-coded by copy number as determined using Infinium 1M SNP array (CN1, copy number loss, CN2 diploid copy number, CN3+ copy number gain).

Min 5 reads per strand

Bisulfite-seq fraction methylated

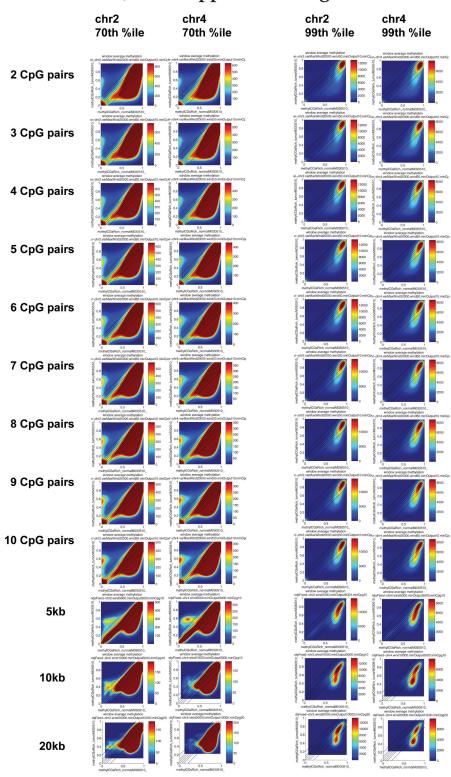
Bisulfite-seq fraction methylated

Berman et al., 2011 Supplemental Figure 4

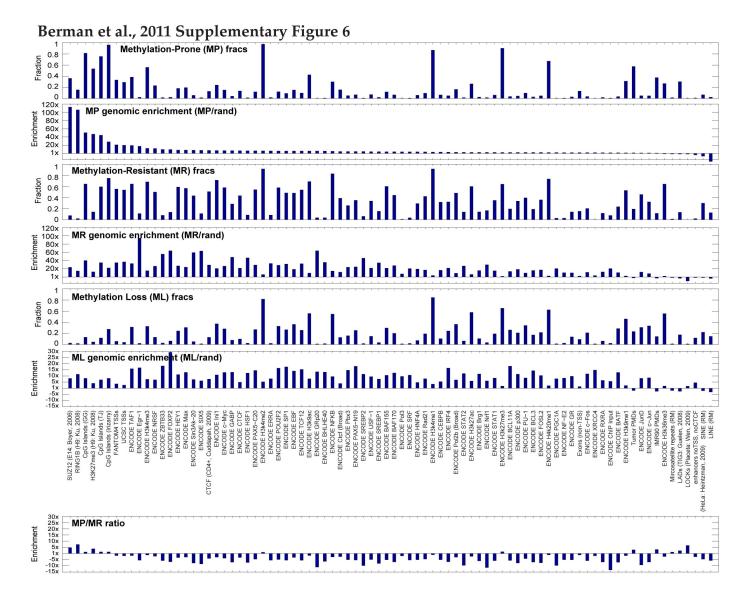


Supplementary Figure 4: Unlike hESCs, colon tumor and normal mucosa have extremely low levels of CpH methylation. Normal and colon methylomes (green) were compared to somatic (blue) and hESC/iPSC (gray) cell lines from ref2. Methylation levels were compared at cytosines with at least 15 uniquely positioned reads. Charts show the percentage of cytosines with at least 25% of reads methylated, for CpH (top) and CpG (bottom). For comparison, tumor and normal colon levels were also compared for the mitochondrial genome, which lacks methylation. While the tumor and normal samples do have about 0.1% of nuclear CpHs methylated, significantly more than the mitochondrial genome, this only represents about 30,000 individual CpHs. These levels are similar to those of somatic cell lines from ref2, and only about 10% of CpH levels in hESC/iPSC cells.

Berman et al., 2011 Supplemental Figure 5

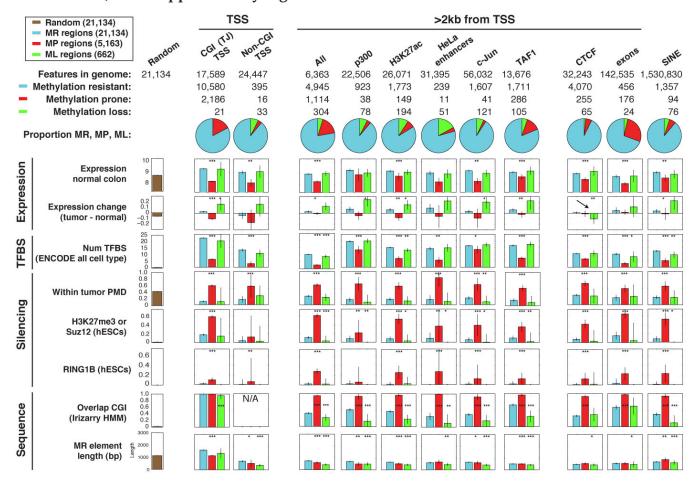


Supplementary Figure 5: The majority of the tumor and normal colon genomes are methylated. Small genomic windows reveal unmethylated regions in the normal colon, while large genomic windows reveal Partially Methylated Domains in the tumor. Moving averages of CpG methylation were taken for windows of varying sizes, and joint densities of tumor and normal averages were plotted as scatterclouds (each axis is split into 50 bins of 0.02 methylation units). For each window size, scatterclouds are shown for two different chromosomes (chr2 and chr4), and two different color scales – for the columns labeled "70th %ile", the darkest red corresponds to the 70th percentile of all 2,500 bin values, and likewise for the 99th percentile. In rows labeled 2-10 CpG pairs, variable window sizes with a minimum number of CpG dinucleotides were used. For rows labeled 5-20 kb, fixed window size were used.



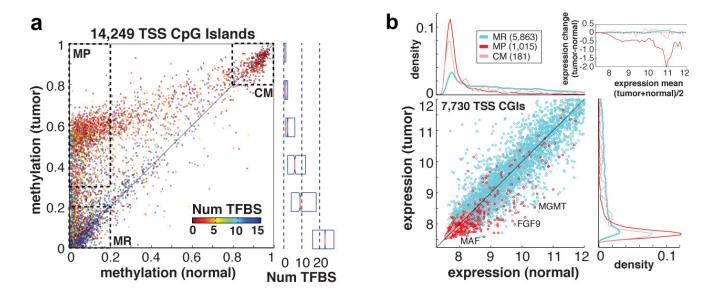
Supplementary Figure 6: Methylation-Resistant (MR) and Methylation Loss (ML) focal elements are enriched in similar sets of genomic features, distinct from those of Methylation-Prone (MP) elements. Comparison of each methylation class to ENCODE protein/DNA binding (ChIP-seq) data10 and other genomic features. "MP fracs" plot shows the absolute fraction of MP elements overlapping each feature, while "MP genomic enrichment" was determined by dividing this fraction by the average fraction within ten sets of size-matched, randomly generated genomic locations (shown as fold change). To reduce random variation for features with small numbers of items, a pseudocount of 5 was used to calculate each mean in the ratio. At bottom, the ratio between MP and MR elements is shown, also using a pseudocount of 5.

Berman et al., 2011 Supplementary Fig 7



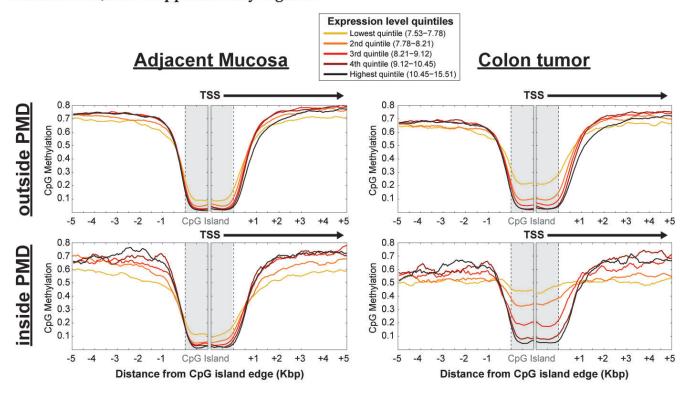
Supplementary Figure 7: Hypermethylated focal elements are more abundant at promoters than non-coding regulatory sequences, but all have low expression in normal colon, Polycomb Repressive Complex activity, and relative enrichment within PMDs. Sequence and expression properties are shown for selected classes of MP, MR, and ML elements that either overlap (left) or do not overlap (right) an annotated TSS (from either the UCSC knownGenes or FANTOM411 databases). Each plot shows mean values for the three methylation classes, along with 95% confidence intervals shown as error bars. MP and ML values were each compared to MR values using a two-sided Mann-Whitney U-test, and the significant outcomes were indicated by *(p<0.05), **(p<0.01), or ***(p<0.0001).

Berman et al., 2011 Supplementary Figure 8



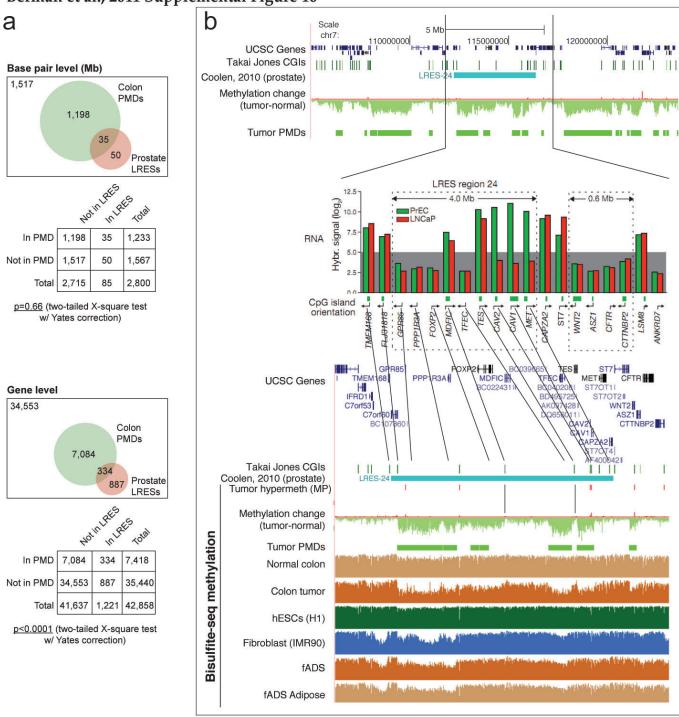
Supplementary Figure 8: Hypermethylated CpG Island promoters lack transcription factor binding across a number of cell types, and are predominantly unexpressed in normal colon, and are down-regulated in colon tumor. Mean DNA methylation values for 14,249 Takai-Jones CpG Islands overlapping a transcription start site (TSS) are shown for the colon tumor (y-axis) and the normal-adjacent sample (x-axis). CpG islands were categorized based on their DNA methylation levels - MR - DNA Methylation-Resistant, with methylation<0.2 for both normal and tumor tissues (n=10,631 loci), MP - DNA Methylation-Prone, with methylation levels <0.2 in the normal-adjacent tissue and >0.3 in the tumor sample (n=1,826 loci), CM - constitutively methylated, with methylation >0.8 in both samples (n=397 loci), and the remainder (n=1,395, labeled "misc") with intermediate methylation levels. Point color corresponds to the number of ENCODE ChIP-seq transcription factor binding sites (TFBS) from any cell type that overlap the CpG island promoter. b Mean log2-transformed microarray expression levels for two technical replicates of normal-adjacent colon and colon tumor RNA, showing all genes corresponding to a CpG Island TSSs from panel (a). Each axis shows the expression density plots for each of the three DNA methylation classes. The majority of MP and CM genes having low expression in both tissues. Inset (MA-plot) shows expression change in each methylation class as a function of mean expression in both tissues (using a moving average of 0.1 expression units).

Berman et al., 2011 Supplementary Figure 9



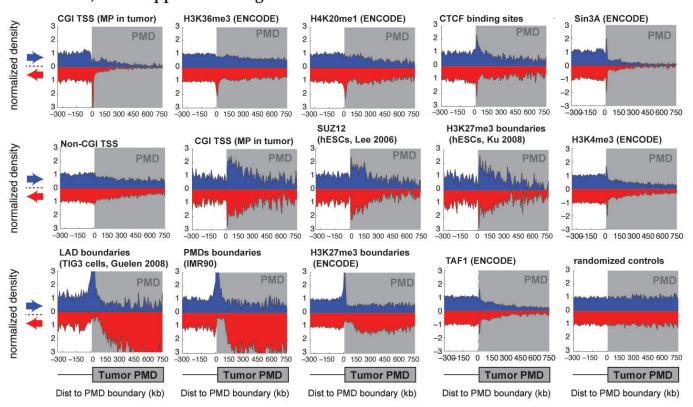
Supplementary Figure 9: Promoters for most genes with low expression become hypermethylated within tumor PMDs, but not the rest of the genome, and focal hypermethylation corresponds to regional hypomethylation both upstream and downstream of these PMD promoters. 7,153 CpG islands overlapping a promoter with valid microarray expression data were analyzed with respect to DNA methylation and expression. The top two plots show the 5,809 CGI-TSS located outside of tumor PMDs (Partially Methylated Domains from this study), and the bottom two plots show the 1,344 located inside of PMDs. In each plot, genes are stratified by expression level, and methylation levels are shown relative to the edges of the CpG island, with the left edge representing the 5' upstream region and the right edge representing the transcribed region. Methylation was averaged within sliding 150 bp windows in increments of 50 bp.

Berman et al., 2011 Supplemental Figure 10



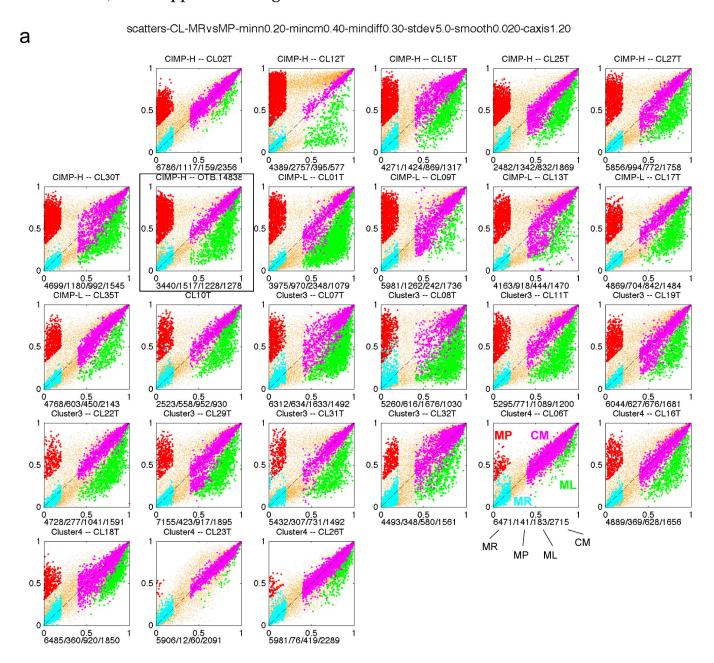
Supplementary Figure 10: Comparison to domains of Long Range Epigenetic Silencing from prostate cancer12 shows similarities and differences. 48 genomic regions from a previous study12 were compared to 2,850 tumor PMDs identified in the current study. a Overlap at the base pair level is close to random, while genes within Prostate LRESs are significantly enriched for tumor PMD genes (p<0.0001). b The region shown in Figure 3 of ref12 (LRES-24), with methylation tracks from the current study and prostate expression levels from Figure 3 of ref12. The top shows that LRES-24 is only one of several colon tumors within the larger genomic region. The bottom shows LRES-24 in greater detail, showing that a large segment in the center of it (from the MFDIC gene to the BC0396651 transcript) is not hypomethylated in the colon tumor. Because MFDIC does not appear to be silenced in LNCaP prostate cancer cells, this region is most likely not part of a true LRES, and is only included in LRES-24 due to the low resolution of the expression array used. Plots for the 7 examples included in ref12 show this to be the case for a number of LRESs, and are available as a Supplemental Document.

Berman et al., 2011 Supplemental Fig 11



Supplementary Figure 11: Partially Methylated Domain boundaries suggest a close relationship with nuclear lamina association and Polycomb silencing programs. Average genomic density of a number of annotation features is plotted for 10 kb bins relative to colon tumor PMD boundaries. Plots are oriented with regions outside the PMD to the left of the midpoint and regions inside the PMD to the right of the midpoint (shaded gray), as shown in the diagrams below each plot. Genomic density was normalized by dividing the value within each bin by the average density within bins lying outside of PMDs. Densities in blue indicate features oriented on the forward strand relative to the PMD boundary (i.e. pointing the same direction as the PMD boundary), and red indicate those oriented on the reverse strand (i.e. pointing the opposite direction).

Berman et al., 2011 Supplemental Figure 12



Supplementary Figure 12: An independent validation set consisting of 25 colon and rectal tumors and matched normal mucosa shows that the extent of hypermethylation and hypomethylation are correlated within a tumor. Infinium HumanMethylation27k scatter plots are shown here for colon and rectal tumor/normal pairs used in Figure 6, along with the case used for bisulfite-seq (OTB.14838). They are ordered by methylation subtype from their original study13, "CIMP-H", "CIMP-L", "Cluster 3", and "Cluster 4". For each pair, four methylation categories (MR, MP, ML, CM) were identified as described in Methods, and array features within each category are shown in a particular color. The number of features in each category is shown below the scatter, as illustrated for "Cluster 4 – CL06T". OTB.14838 is outlined

Supplementary Figure 13 HOMER Results:

Methylation-Prone CGI promoters (MP-CGIs)

VS.

Methylation-Resistant CGI promoters (MR-CGIs)

Homer de novo Motif Results

Supplementary Figure 13: HOMER results for MP CGI promoters vs. MR CGI promoters

Known Motif Enrichment Results

Gene Ontology Enrichment Results

If Homer is having trouble matching a motif to a known motif, try copy/pasting the matrix file into STAMP More information on motif finding results: <u>HOMER</u> | <u>Description of Results</u> | <u>Tips</u>

Rank Motif		P-value	log P- pvalue	Best Match/Details	Motif File
l	ACACACACAC	1.267e- 113	2.600e+02	SeqBias: CA-repeat More Information Similar Motifs Found	motif file (matri
2	<u>AGAGAGAGAG</u>	7.799e- 80	1.822e+02	SeqBias: GA-repeat More Information Similar Motifs Found	motif file (matri
3	CCCCGC	6.427e- 58	1.317e+02	PB0164.1_Smad3_2 More Information Similar Motifs Found	motif file (matri
1	GCGCCC	9.425e- 55	1.244e+02	PB0052.1_Plagl1_1 More Information Similar Motifs Found	motif file (matr
5	CCTCCC	6.197e- 49	1.110e+02	PF0024.1_GGGAGGRR More Information Similar Motifs Found	motif file (matr
6	CTCCCC	6.154e- 48	1.087e+02	MA0079.2_SP1 More Information Similar Motifs Found	motif file (matr
7	CCCTCC	4.624e- 47	1.067e+02	PF0099.1_ATCMNTCCGY More Information Similar Motifs Found	motif file (matr
3	CCCGCG	9.644e- 44	9.905e+01	MA0399.1_SUT1 More Information Similar Motifs Found	motif file (matr
)	<u><u><u><u><u></u><u><u><u><u></u><u><u><u></u></u> <u><u><u></u></u> <u><u></u> <u></u> <u> </u> </u></u></u></u></u></u></u></u></u></u>	4.409e- 43	9.753e+01	SeqBias: GCW-triplet More Information Similar Motifs Found	motif file (matr
10	GCCGCC	7.393e- 42	- 9.471e+01	YY1/Promoter/Homer More Information Similar Motifs Found	motif file (matr
	<u>AGCCAGC</u>	2.503e-	_	PB0206.1_Zic2_2 More Information Similar	motif

				Motifs Found	(matrix)
12	CGGGGC	1.151e- 33	- 7.584e+01	Sp1/Promoter/Homer More Information Similar Motifs Found	motif file (matrix)
13	CAGCCC	3.673e- 30	- 6.778e+01	CN0218.1_LM218 More Information Similar Motifs Found	motif file (matrix)
14	CGCGCC	3.422e- 29	- 6.554e+01	PB0009.1_E2F3_1 More Information Similar Motifs Found	motif file (matrix)
15	GCTTTTTGCCCC	3.243e- 28		PPARE(DR1)/3T3L1- Pparg-ChIP-Seq/Homer More Information Similar Motifs Found	motif file (matrix)
16	CCGCCG	6.186e- 27	- 6.035e+01	MA0320.1_IME1 More Information Similar Motifs Found	motif file (matrix)
17	CTCCTTCTCC	2.267e- 20	- 4.523e+01	PB0203.1_Zfp691_2 More Information Similar Motifs Found	motif file (matrix)
18	GAGAGC	8.133e- 17	3.705e+01	MA0205.1_Trl More Information Similar Motifs Found	motif file (matrix)
19	CACCACCACCAC	1.338e- 16	3.655e+01	MA0073.1_RREB1 More Information Similar Motifs Found	motif file (matrix)
20	EGETGGEGA	4.627e- 16		GATA:SCL/Ter119-SCL- ChIP-Seq/Homer More Information Similar Motifs Found	motif file (matrix)
21	AGÇAGAŞ	5.860e- 14	3.047e+01	CN0146.1_LM146 More Information Similar Motifs Found	motif file (matrix)
Na 1 2re	Genetics Control of the Control of t	4.551e- 12	- 2.612e+01	CN0177.1_LM177 More Information Similar Motifs Found	motif file (matrix)

Supplementary Figure 14 HOMER Results:

Methylation-Resistant CGI promoters (MR-CGIs)

VS.

Methylation-Prone CGI promoters (MP-CGIs)

Homer de novo Motif Results

Supplementary Figure 14: HOMER results for MR CGI promoters vs. MP CGI promoters

Known Motif Enrichment Results Gene Ontology Enrichment Results

If Homer is having trouble matching a motif to a known motif, try copy/pasting the matrix file into STAMP More information on motif finding results: <u>HOMER</u> | <u>Description of Results</u> | <u>Tips</u>

Rank Motif		P-value	log P- pvalue	Best Match/Details	Motif File
	<u>AGGGGCGGGC</u>	3.504e- 285		Sp1/Promoter/Homer More Information Similar Motifs Found	motif file (matr
	GCGCATGCGCA	4.433e- 197	1	NRF1/MCF7-NRF1-ChIP-Seq/Homer More Information Similar Motifs Found	motif file (matr
	<u>atgacgtga</u>	7.761e- 193		PB0007.1_Bhlhb2_1 More Information Similar Motifs Found	motif file (matr
	\$\$CCGGAAGT	9.236e- 189	- 4.330e+02	GABPA/Jurkat-GABPa-ChIP- Seq/Homer More Information Similar Motifs Found	motif file (matr
	<u>ACCGGAAGTG</u>	2.773e- 175		PB0020.1_Gabpa_1 More Information Similar Motifs Found	motif file (matr
	SCAASATGGCG	1.472e- 135	1	YY1/Promoter/Homer <u>More Information</u> <u>Similar Motifs Found</u>	motif file (matr
	CGTAAC	2.107e- 122	1	MA0043.1_HLF More Information Similar Motifs Found	motif file (matr
	ZAACTA	8.647e- 117	1	PH0154.1_Prrx1 More Information Similar Motifs Found	motif file (matr
	<u><u><u><u><u>GATTGG</u></u></u></u></u>	1.690e- 113	1	NFY/Promoter/Homer <u>More Information</u> <u>Similar Motifs Found</u>	motif file (matr
0	TACCITA	5.878e- 105	1	PH0071.1_Hoxc6 More Information Similar Motifs Found	motif file (matr
1	≜ACTASA	2.200e- 99	1	GFY/Promoter/Homer <u>More Information</u> <u>Similar Motifs Found</u>	motif file (matr
2	TÇÇŢŞA	3.242e- 91	1	PB0161.1_Rxra_2 More Information Similar Motifs Found	motif

13	CASTAA	3.380e- 85		PB0016.1_Foxj1_1 More Information Similar Motifs Found	motif file (matrix)
14	ACSITA	1.810e- 82		PH0174.1_Vax1 More Information Similar Motifs Found	motif file (matrix)
15	ACTIAA	9.761e- 82		PH0117.1_Nkx3-1 More Information Similar Motifs Found	motif file (matrix)
16	<u>AAAAAAAAAA</u>	1.397e- 81		PB0182.1_Srf_2 More Information Similar Motifs Found	motif file (matrix)
17	<u>GTGASTCA</u>	7.416e- 77	- 1.753e+02	NFAT:AP1/Jurkat-NFATC1-ChIP- Seq/Homer More Information Similar Motifs Found	motif file (matrix)
18	<u>GTACTA</u>	8.895e- 70		PB0096.1_Zfp187_1 More Information Similar Motifs Found	motif file (matrix)
19	GITAAC	7.653e- 69		PB0109.1_Bbx_2 More Information Similar Motifs Found	motif file (matrix)
20	<u>AAÇÇŢŢA</u>	6.485e- 65		PB0109.1_Bbx_2 More Information Similar Motifs Found	motif file (matrix)
21	CCTGTAATCCCA	7.747e- 64		PH0137.1_Pitx1 More Information Similar Motifs Found	motif file (matrix)
22	TCAAAA	1.127e- 52		CN0230.1_LM230 More Information Similar Motifs Found	motif file (matrix)
23	AGTGCAGTGGCG	4.178e- 49	- 1.114e+02	PB0091.1_Zbtb3_1 More Information Similar Motifs Found	motif file (matrix)
Nature	Genetics the GENERAL GENETICS AND THE GE	3.107e- 45	- 1.025e+02	PF0151.1_RYAAAKNNNNNNTTGW More Information Similar Motifs Found	motif file (matrix)

Supplementary Figure 15 HOMER Results:

Methylation Loss elements (ML)

VS.

Methylation-Resistant elements (MR)

Homer de novo Motif Results results for ML CGI promoters

Supplementary Figure 15: HOMER results for ML CGI promoters vs. MR CGI promoters

Known Motif Enrichment Results
Gene Ontology Enrichment Results

If Homer is having trouble matching a motif to a known motif, try copy/pasting the matrix file into \underline{STAMP} More information on motif finding results: $\underline{HOMER} \mid \underline{Description\ of\ Results} \mid \underline{Tips}$

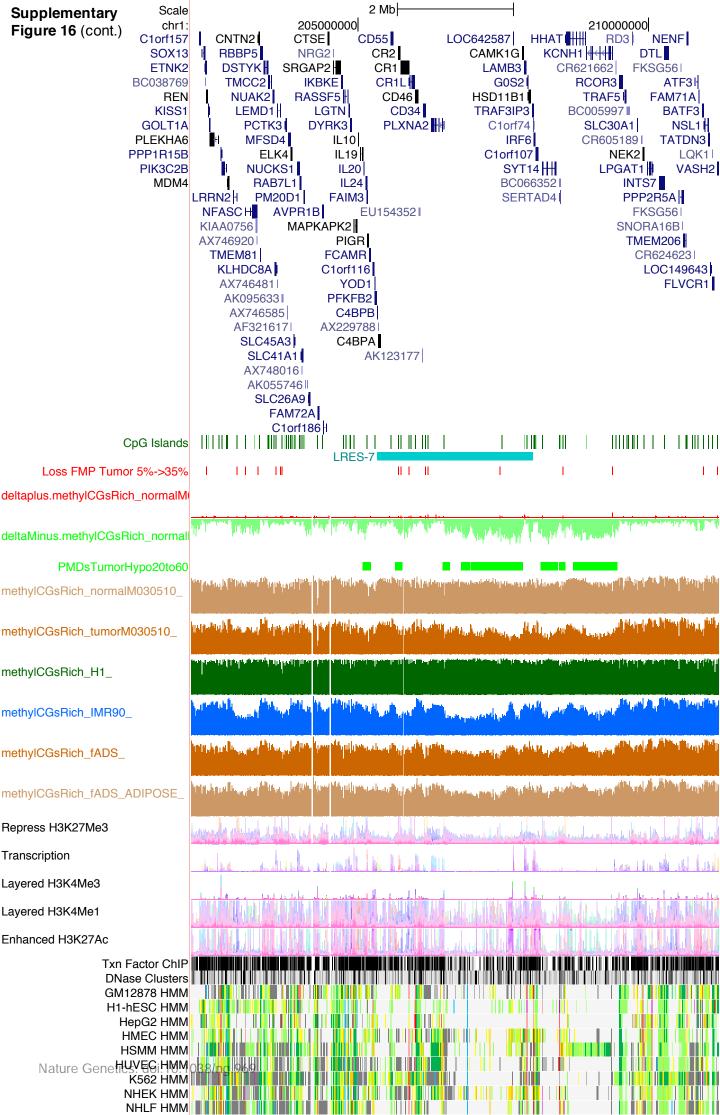
* - possible false positive

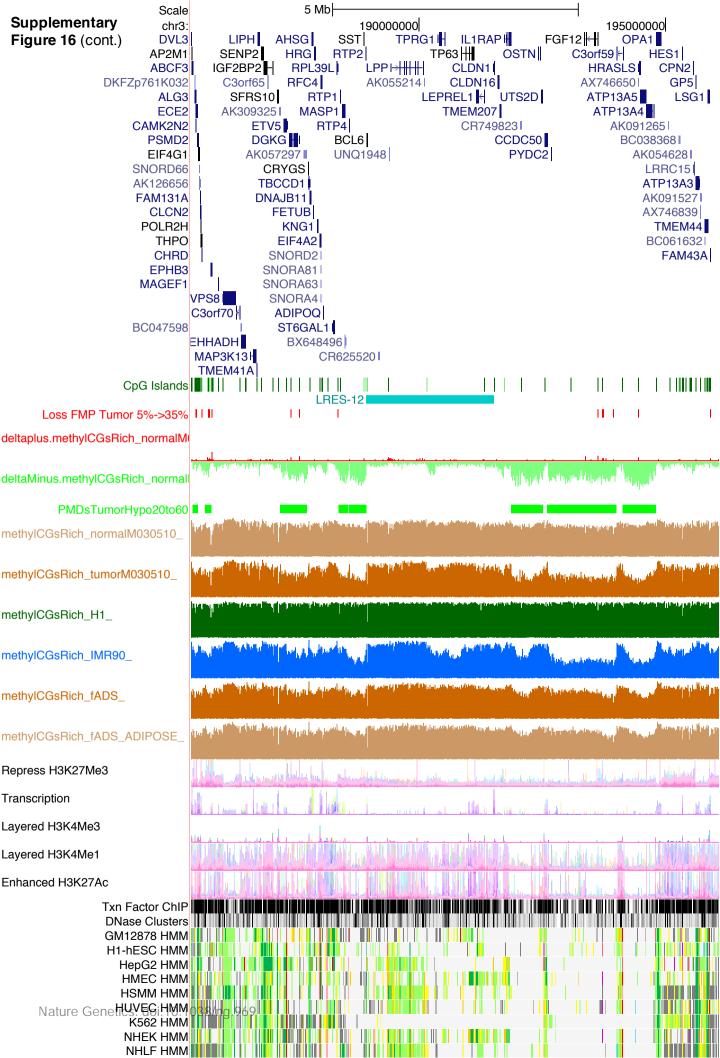
Rank	Motif	P-value	log P- pvalue	Best Match/Details	Motif File
1	<u>\$TGAŞTCAŞŞ</u>	2.025e- 86	- 1.973e+02	NFAT:AP1/Jurkat- NFATC1-ChIP- Seq/Homer More Information Similar Motifs Found	motif file (matrix
2	JATGASTCA	5.799e- 86	- 1.963e+02	MA0303.1_GCN4 More Information Similar Motifs Found	motif file (matrix
3	ATAQATAAA	1.575e- 47	- 1.078e+02	MA0345.1_NHP6A More Information Similar Motifs Found	motif file (matrix
4	AIIIII	2.177e- 41	- 9.363e+01	PB0116.1_Elf3_2 More Information Similar Motifs Found	motif file (matrix
5	AAATATA	6.933e- 38	- 8.556e+01	MA0386.1_TBP More Information Similar Motifs Found	motif file (matrix
6	AATCACA AATCACA	5.176e- 20	- 4.441e+01	PB0120.1_Foxj1_2 More Information Similar Motifs Found	motif file (matrix
7	<u>ATAGAAAŞ</u> A	3.888e- 19	- 4.239e+01	MA0346.1_NHP6B More Information Similar Motifs Found	motif file (matrix
8	ATARCAT	5.040e- 19	- 4.213e+01	PH0148.1_Pou3f3 More Information Similar Motifs Found	motif file (matrix
9	<u>GCCTGTAATCC</u>	5.822e- 17	- 3.738e+01	PH0139.1_Pitx3 More Information Similar Motifs Found	motif file (matrix
10	CCATAGGCACGC	9.258e-	-	PB0095.1_Zfp161_1 More Information	motif file
iture G	enetics: doi:10.1038/ng.969				

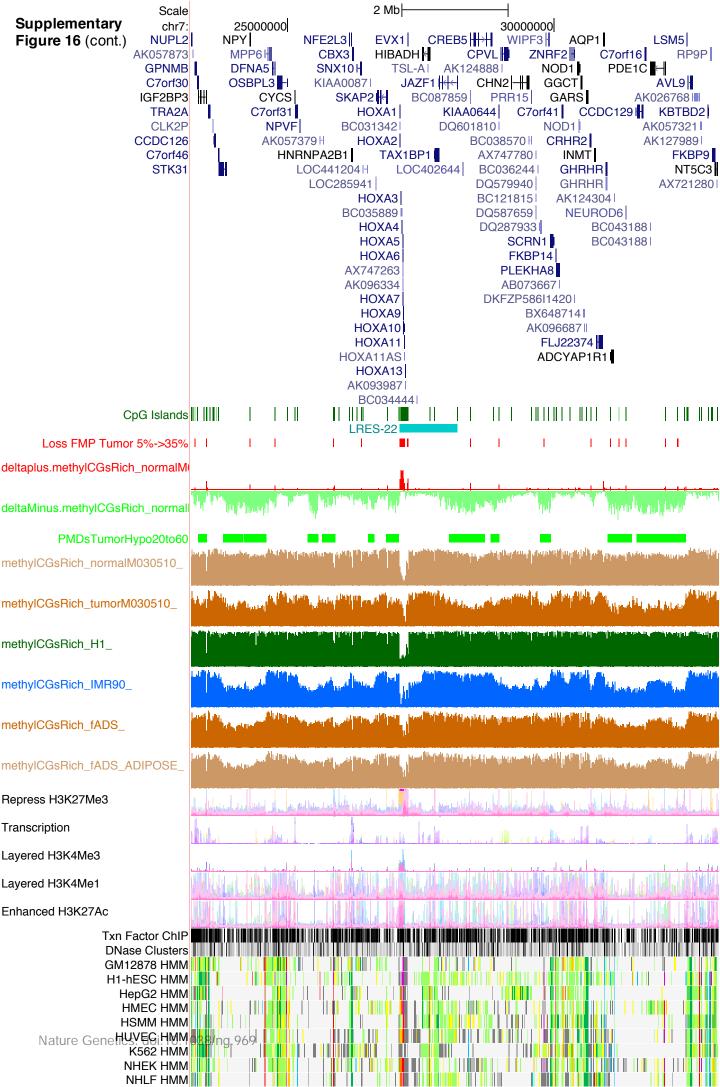
		16	3.462e+01	Similar Motifs Found	(matrix)
11	GCTGAGACAGGA	1.702e- 15	- 3.401e+01	CN0106.1_LM106 More Information Similar Motifs Found	motif file (matrix)
12	GCTCACTGSAA	1.098e- 14	- 3.214e+01	PB0091.1_Zbtb3_1 More Information Similar Motifs Found	motif file (matrix)
13	CACTTTGGGAGG	1.343e- 14	3.194e+01	MA0088.1_znf143 More Information Similar Motifs Found	motif file (matrix)
14	ASATGAA	1.655e- 14	3.173e+01	PB0028.1_Hbp1_1 More Information Similar Motifs Found	motif file (matrix)
15	<u> TAAAAAAG</u> TA	1.064e- 13	I	FOXA1:AR/LNCAP- AR-ChIP-Seq/Homer More Information Similar Motifs Found	motif file (matrix)
16 *	AIGEAT	4.097e- 10	- 2.162e+01	PH0148.1_Pou3f3 More Information Similar Motifs Found	motif file (matrix)
17 * Nature	Genetics: <u>dol</u> 10-009/4.949	4.762e- 10		RUNX(AML)/CD4+- PolII-ChIP- Seq/Homer <u>More Information</u> <u>Similar Motifs Found</u>	motif file (matrix)

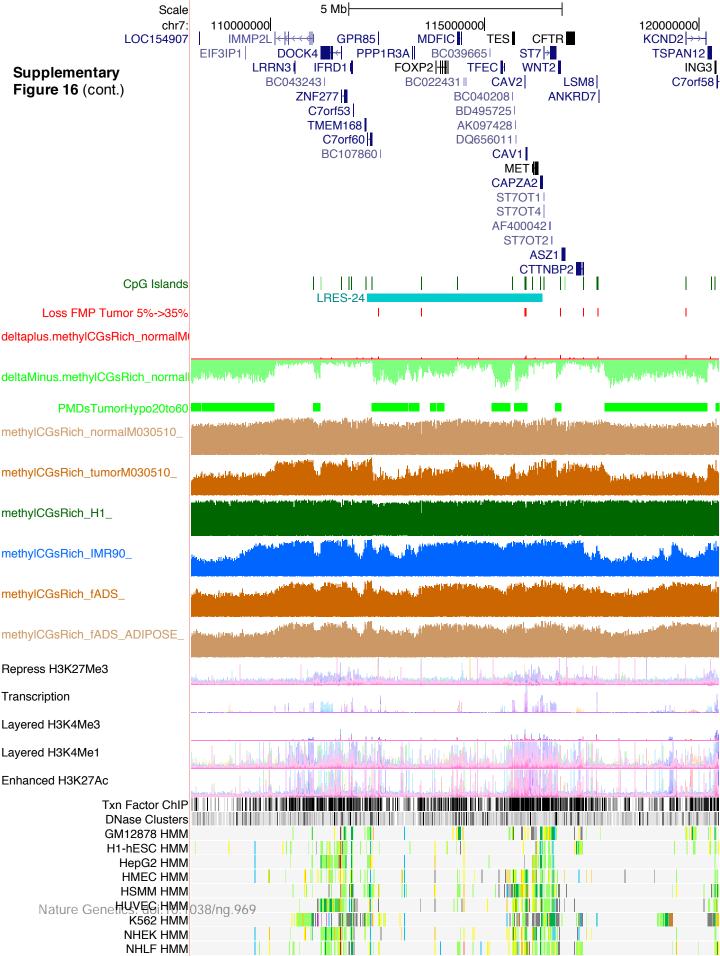
Supplementary Figure 16

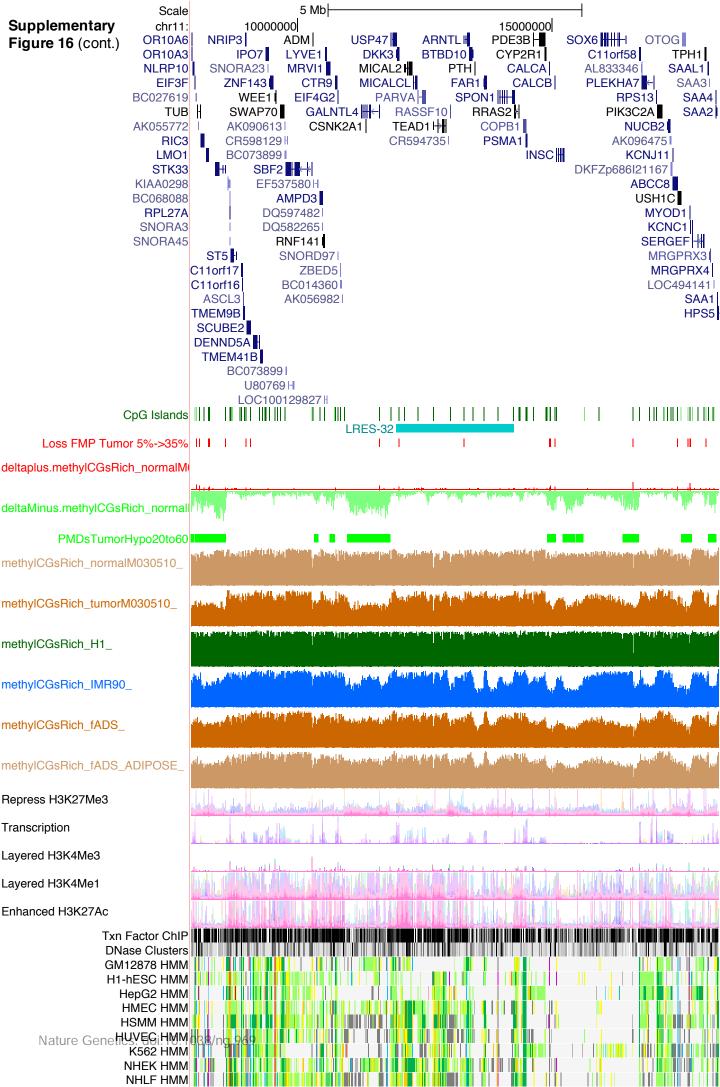
Methylation patterns around prostate cancer Long-Range Epigenetic Silencing (LRES) domains from Coolen, et. al. 2010¹²

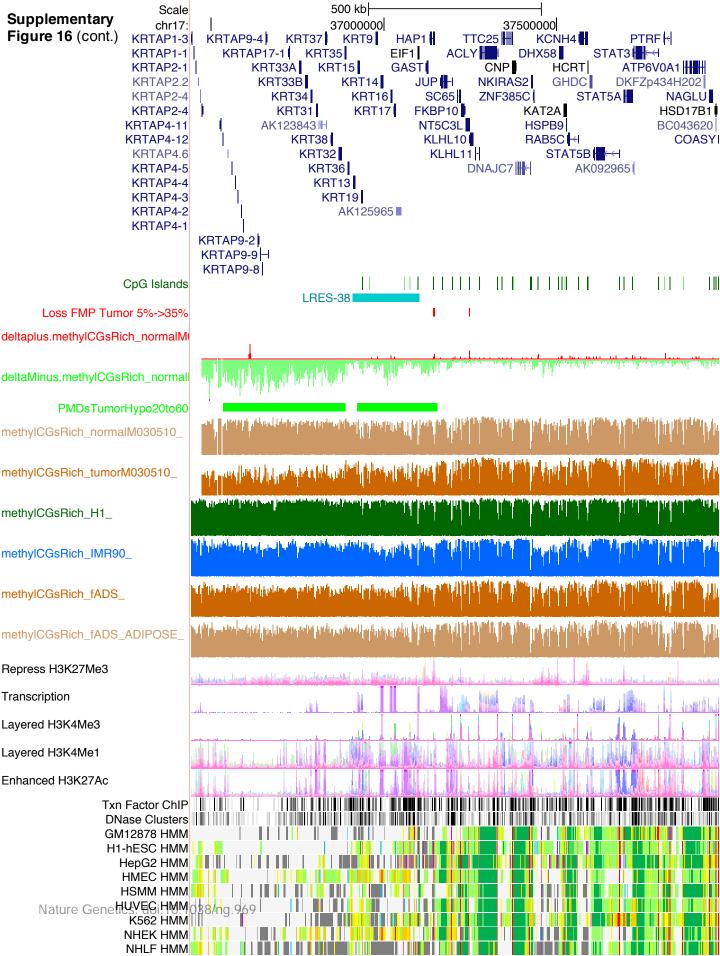


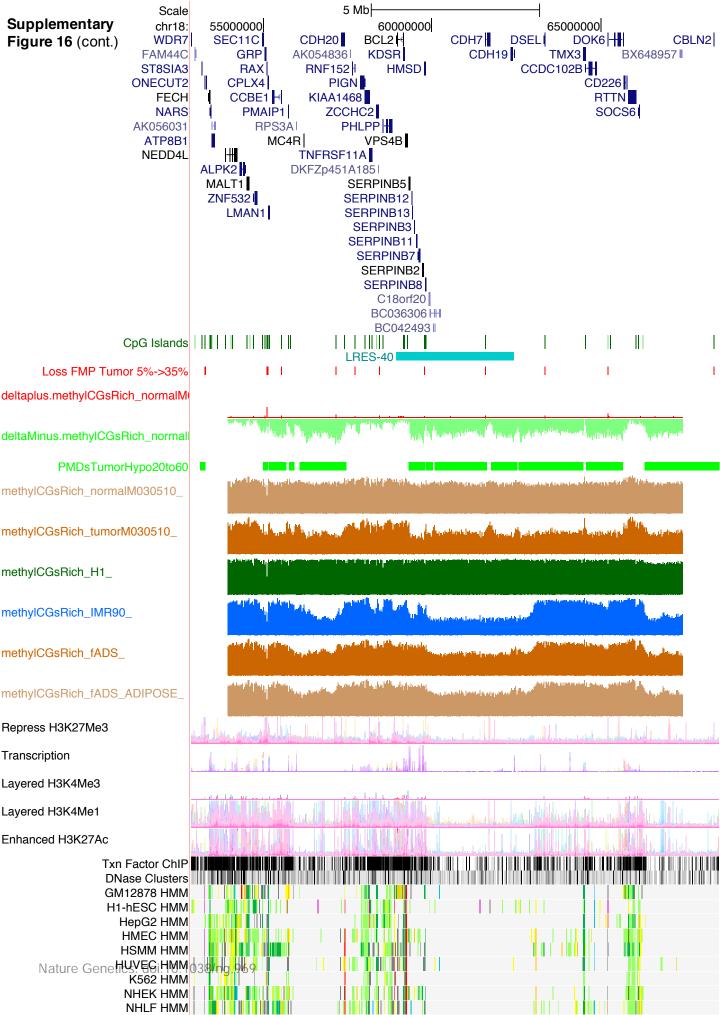












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