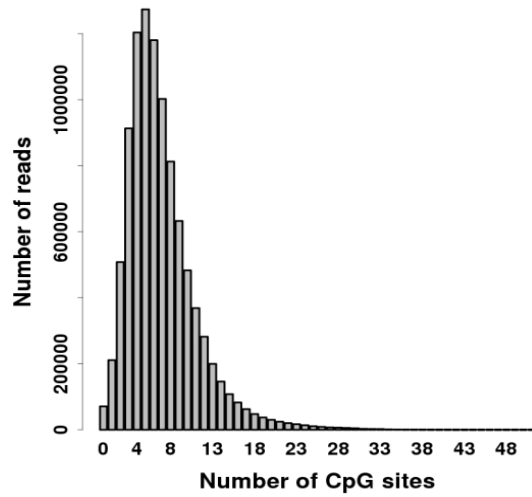
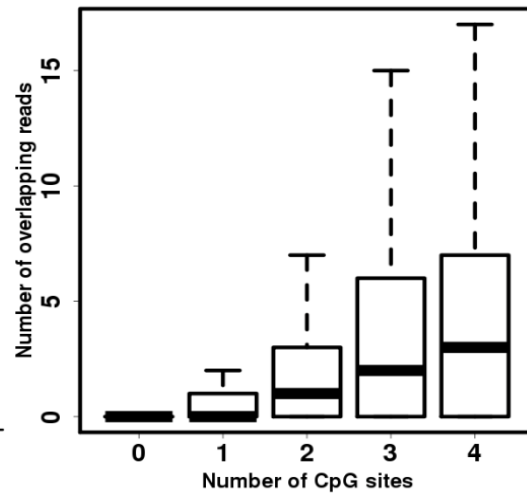


Supplementary Fig. 1

A

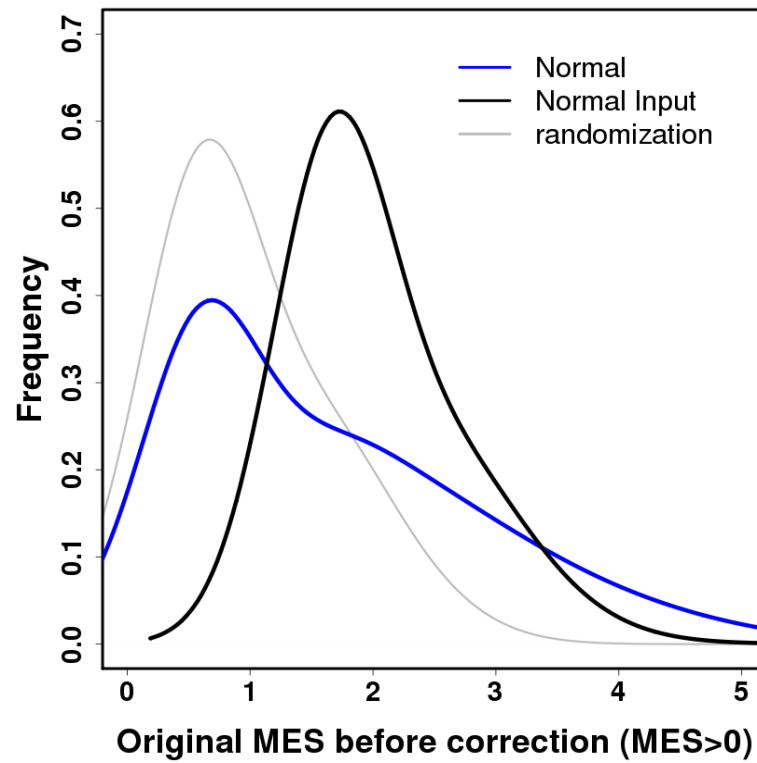


B



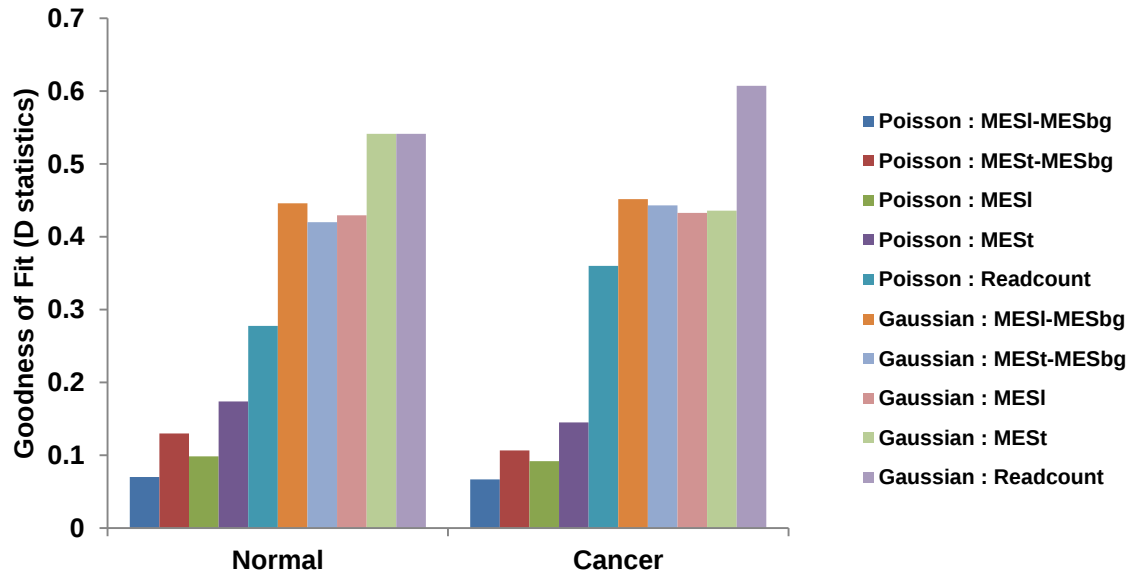
Sensitivity of the MIRA technique. Shown is the number of solexa reads containing CpG sites in their sequence (200bp) (A) and overlapping reads for 50bp genomic intervals containing 0 ~ 4 CpG sites in their sequence (B).

Supplementary Fig. 2



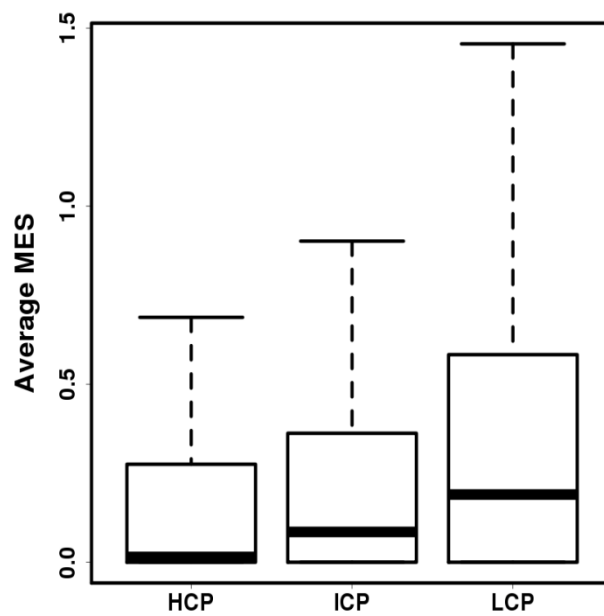
The distribution of MESs from MIRA-seq, input and randomized methylome of normal (permutation of MIRA reads along the chromosome). The original MES values before correction for sequencing bias were used for comparison.

Supplementary Fig. 3



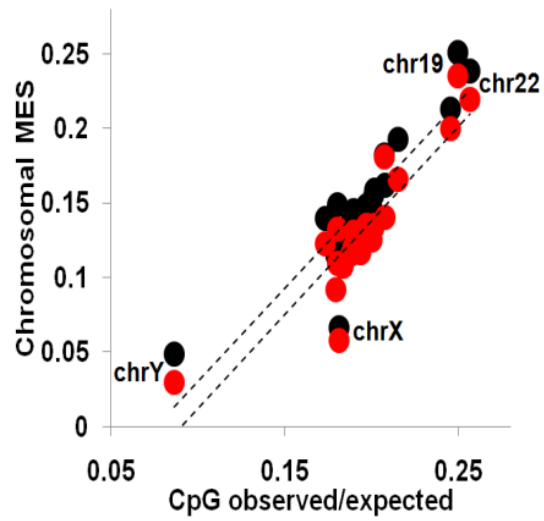
Goodness of fit was tested for two basic normalized MESs (MEST and MESI), two background normalized MESs (MEST-MESbg and MESI-MESbg), and raw readcounts against the Poisson and Gaussian model. The D statistic is from the Kolmogorov-Smirnov test. **MEST**; MES normalized by total readcount, **MESI**; MES normalized by local readcount, **MESbg**; MES of input sequencing

Supplementary Fig. 4



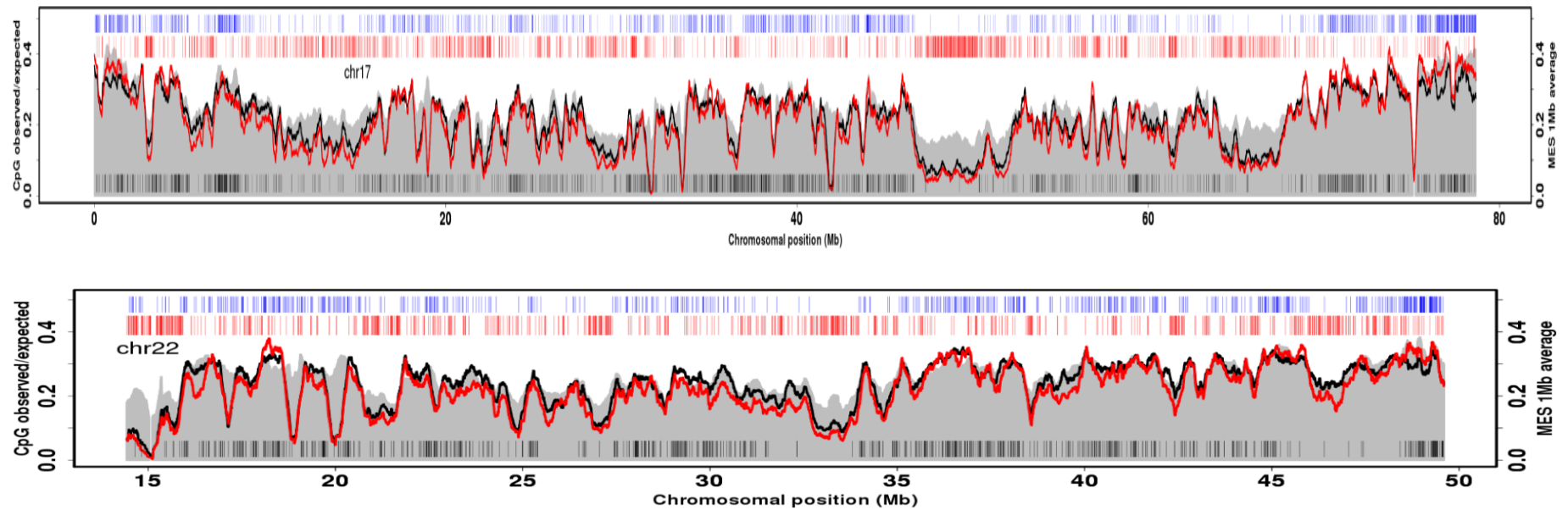
Average MES pattern of human promoters which were subgrouped into high, intermediate, and low CpG density promoters (HCP, ICP, and LCP, respectively).

Supplementary Fig. 5



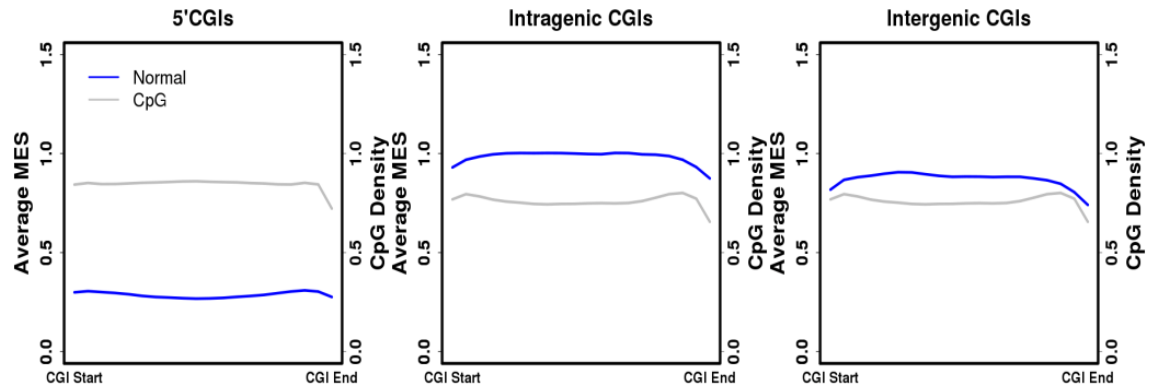
Chromosome-wide average MESs for normal (black circle) and cancerous (red circle) tissue.

Supplementary Fig. 6



Chromosomal distribution of the average MES (black (normal) and red (cancer) curve corresponding to the left axis) and the average CpG observed/expected ratio (gray shade corresponding to the left axis) in 1 Mb sliding windows. The positions of transcribed genes (black bars at the bottom) and those of long repeats (> 1kb; red bars on the top), CGIs (blue bars on the top) are compared in the context of DNA methylation and CpG density.

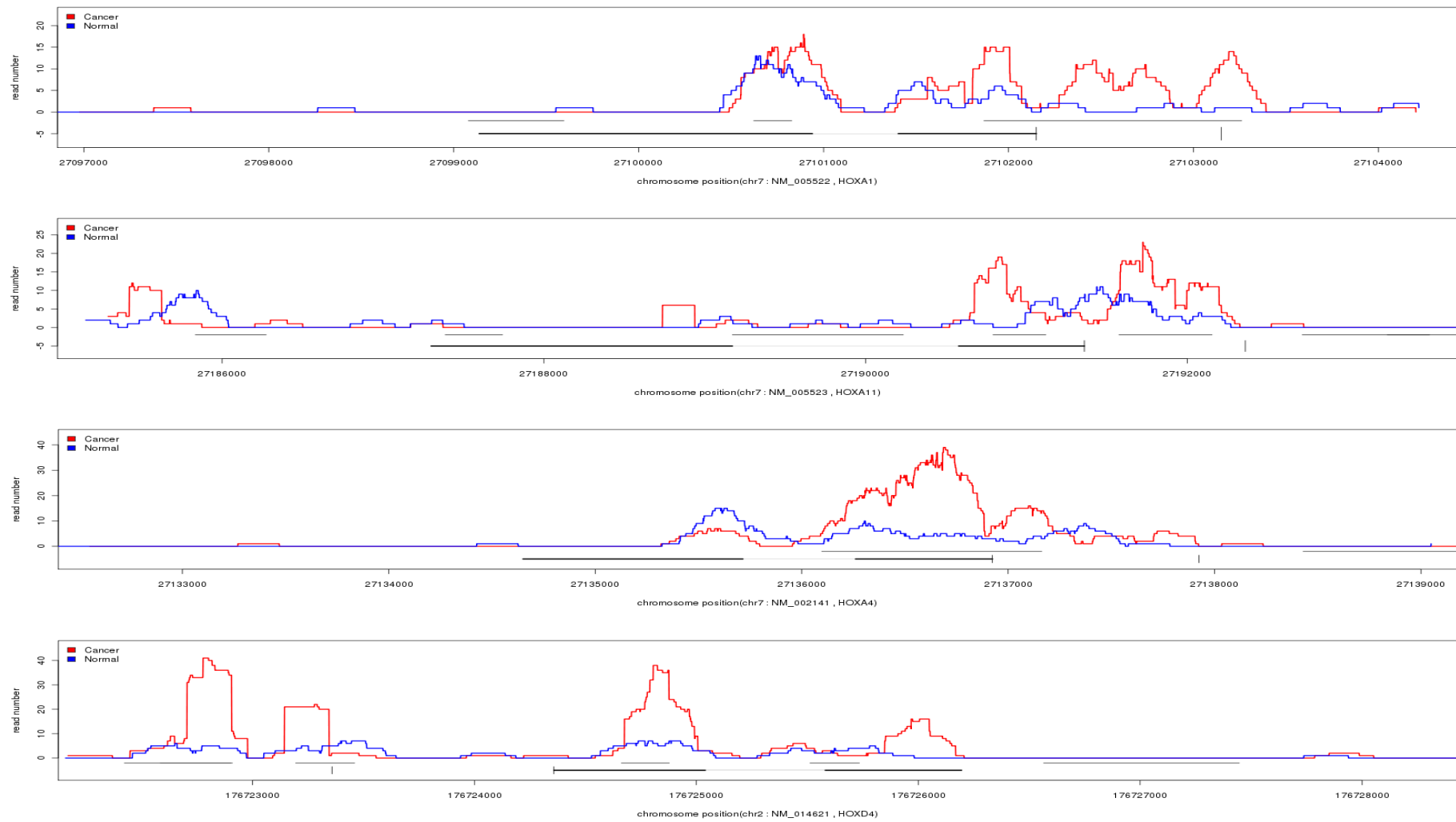
Supplementary Fig. 7

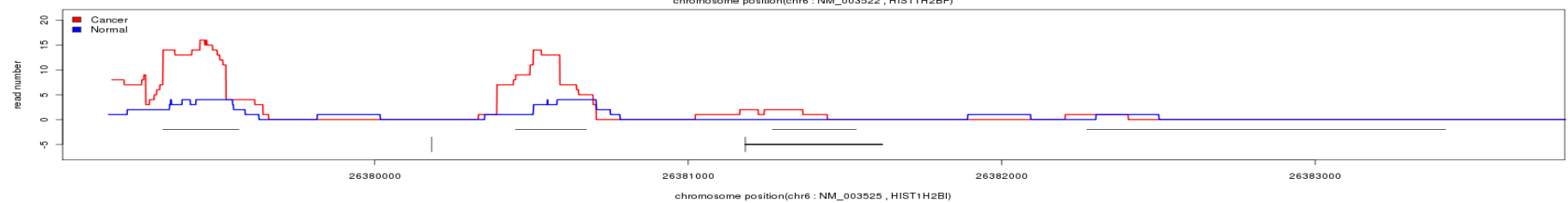
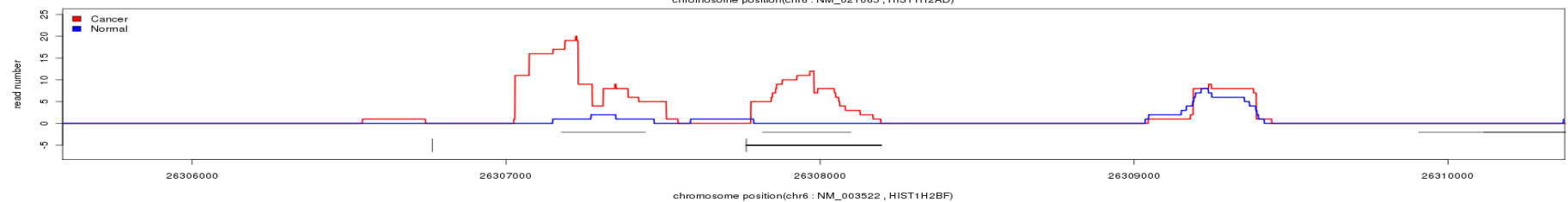
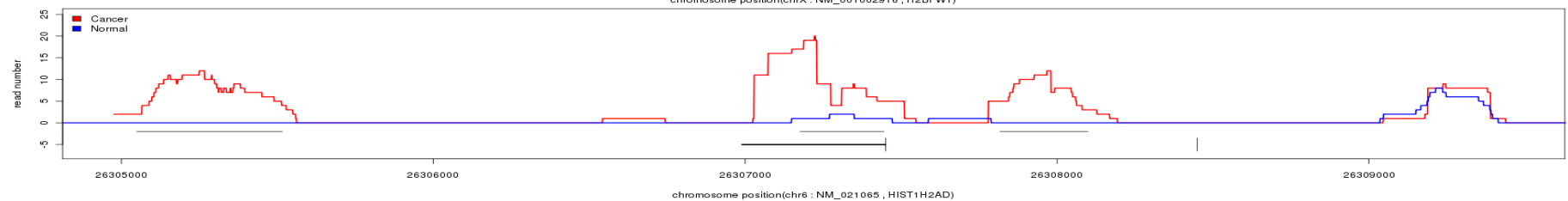
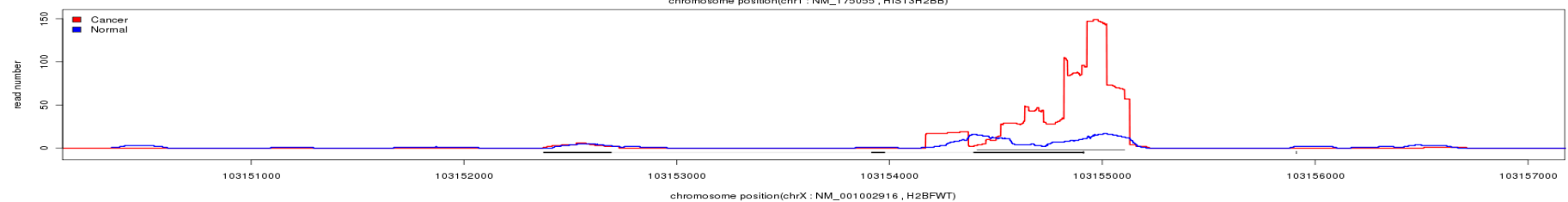
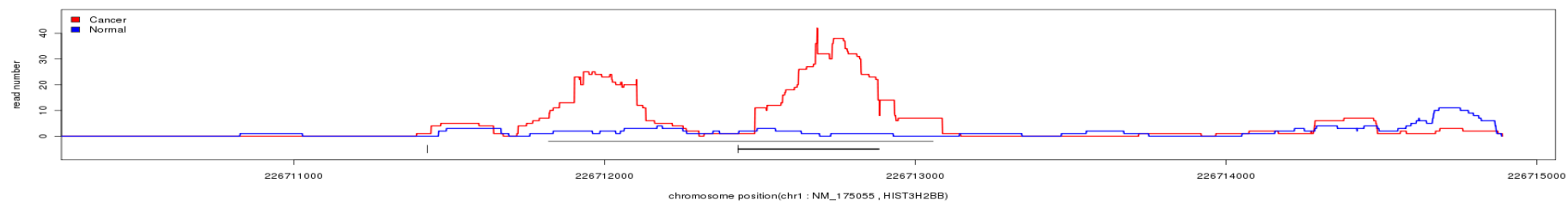


Average MES pattern of subgrouped CGIs (5'CGIs, intragenic CGIs and intergenic CGIs).

Each CGI was partitioned into 20 bins, and the average MES was obtained for each bin of all corresponding elements. Blue line; average MES of 5'CGIs in normal sample, Gray line; average CpG density in 5'CGIs region.

Supplementary Fig. 8

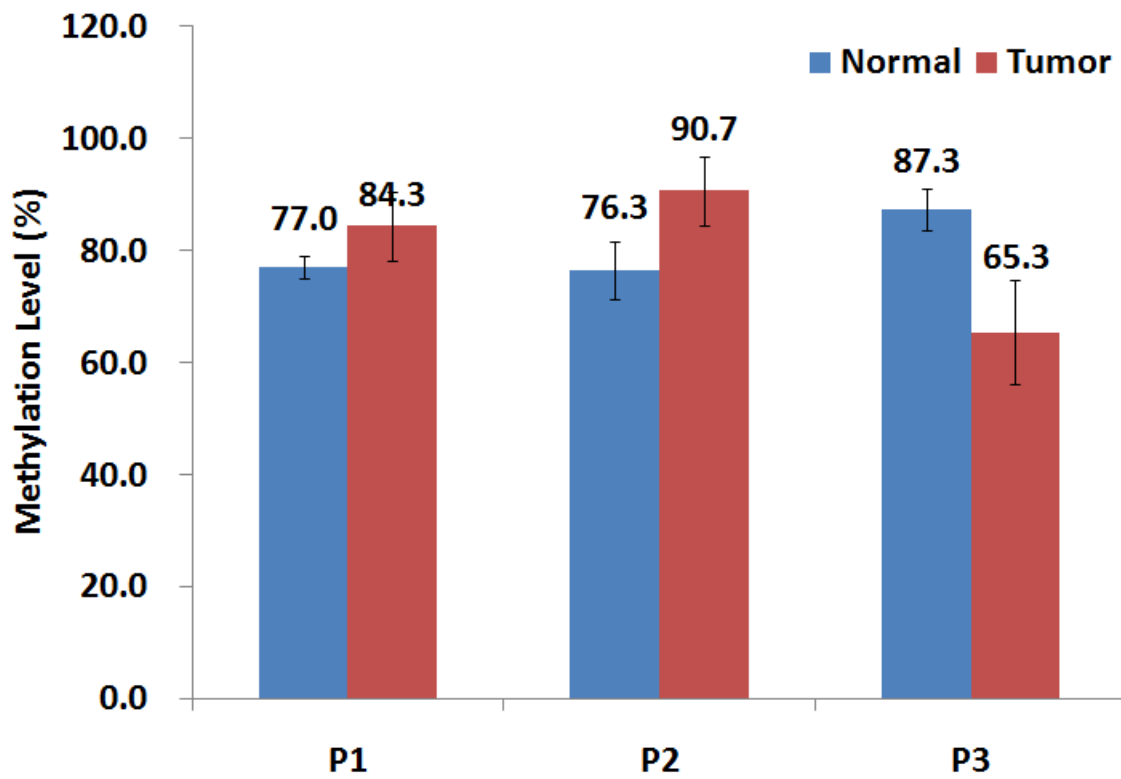






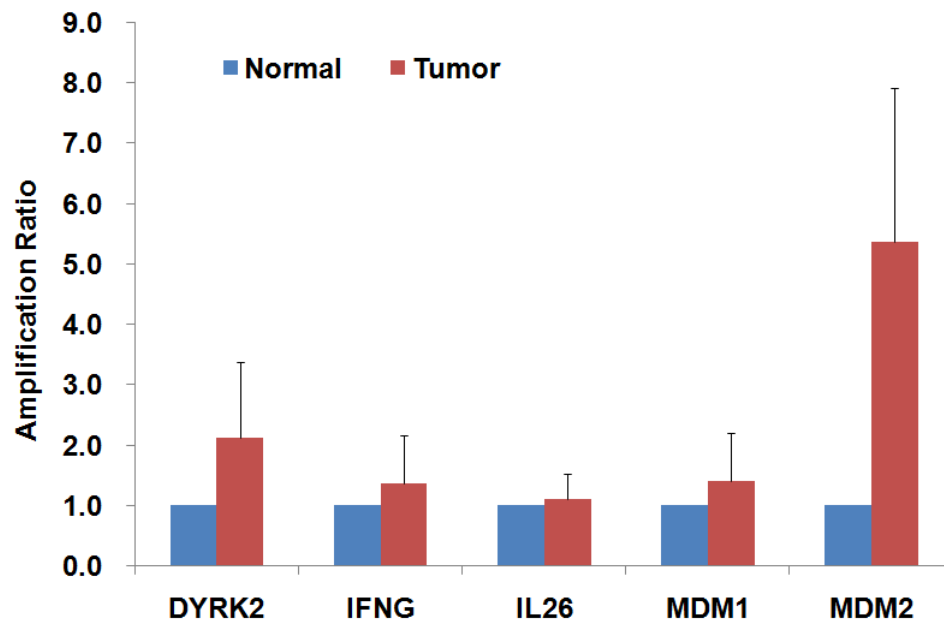
Plots of several genes with 5'CGIs hypermethylation. Red; cancer, blue; normal, gray; CG island, black; exon

Supplementary Fig. 9



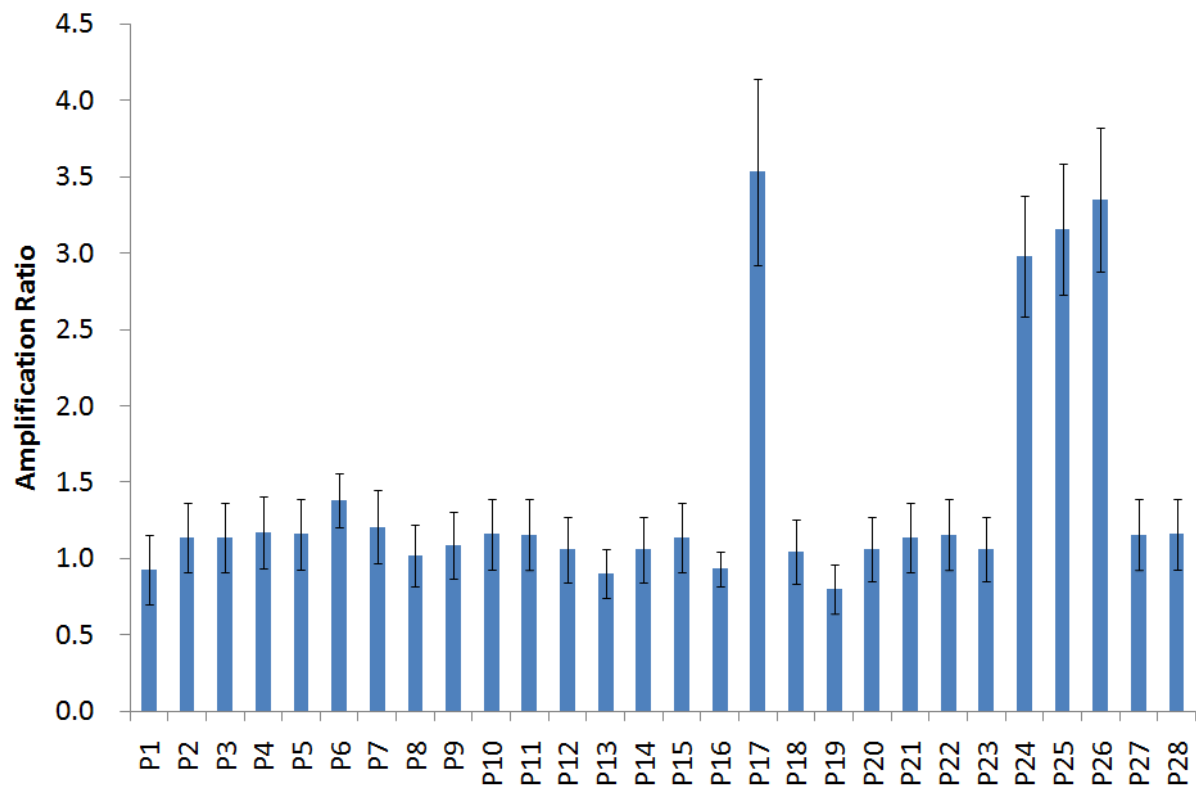
MDM2 methylation level of normal and cancerous tissue in three individual samples by pyrosequencing.

Supplementary Fig. 10



Amplification ratio of several genes (*DYRK2*, *IFNG*, *IL26*, *MDM1*, and *MDM2*) within chromosome 12q14 LRES region by real-time qPCR.

Supplementary Fig. 11



Amplification ratio of specific locus in an upstream region of *MDM2* by real-time qPCR.