CellMethy: Identification of a focal concordantly methylated pattern of CpGs revealed wide differences between normal and cancer tissues

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Supplementary data

Supplementary Figure 1. Evaluation of CMRs number between random and concordant methylation pattern. Length of windows from 2 to 10 CpGs (A) - (I). Red represents concordant methylation simulation data with different coverage, and black represents random methylation data.

Supplementary Figure 2. Evaluation of cumulative probability distribution of CG number in CMRs between random and concordant methylation pattern. Length of windows from 2 to 10 CpGs (A) - (I). Red represents concordant methylation simulation data with different coverage, and black represents random methylation data.

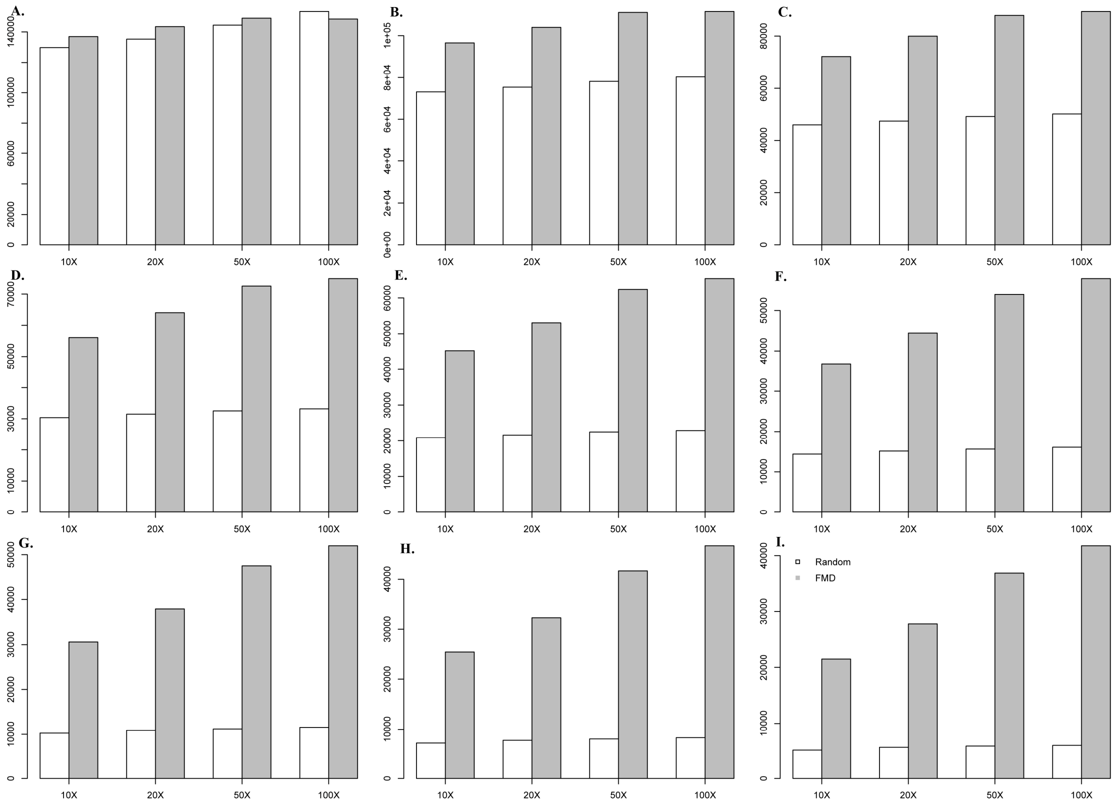
Supplementary Figure 3. Evaluation of probability density distribution of CM fraction between random and concordant methylation pattern. Length of windows from 2 to 10 CpGs (A) - (I). Red represents concordant methylation simulation data with different coverage, and black represents random methylation data.

Supplementary Figure 4. Relationship between average methylation levels and CM fractions in each cancer. Each point is a CMR, the black line is the fitted curve of the cancer and gray is the average fitted curve of all normal tissues/cells.

Supplementary Figure 5. Differences in CM fraction between breast cancer and normal cell line from genome wide BS-Seq data. (A) Box plot of CM fractions and average methylation levels between breast cancer and normal. * represents p value of Wilcoxon test less than 0.01. (B) Differential degree of CM fractions and average methylation between breast cancer and normal in eight genome regions.

Supplementary Figure 6. Flowchart of simulation data.

Supplementary Table 1. Identification of CMRs based on genome wide BS-Seq data of breast cancer.



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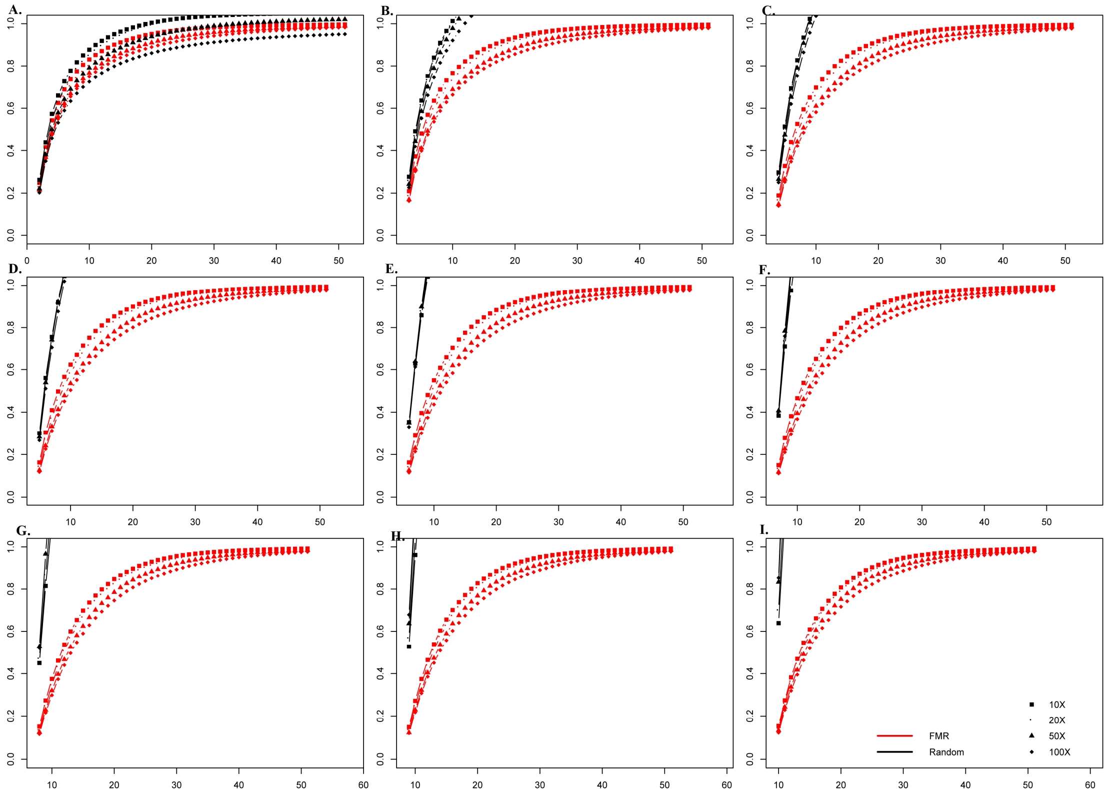
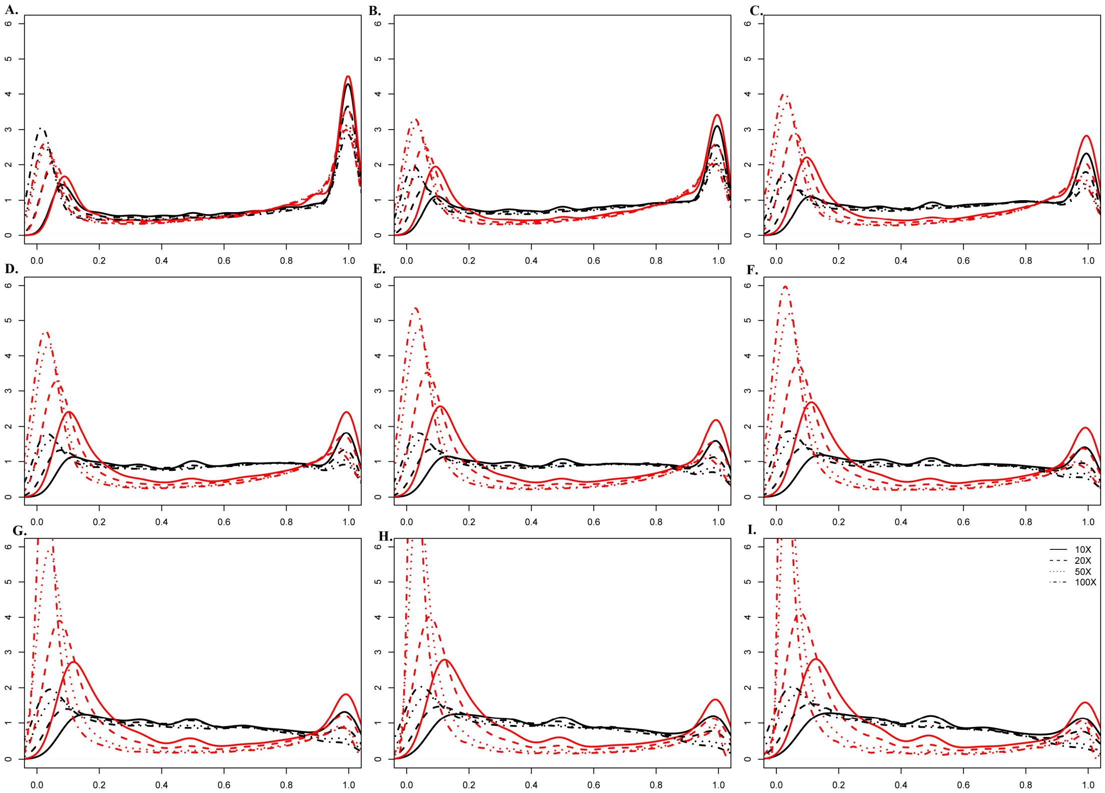


Supplementary Figure 2. Evaluation of cumulative probability distribution of CG number in CMRs between random and concordant methylation pattern. Length of windows from 2 to 10 CpGs (A) - (I). Red represents concordant methylation simulation data with different coverage, and black represents random methylation data.



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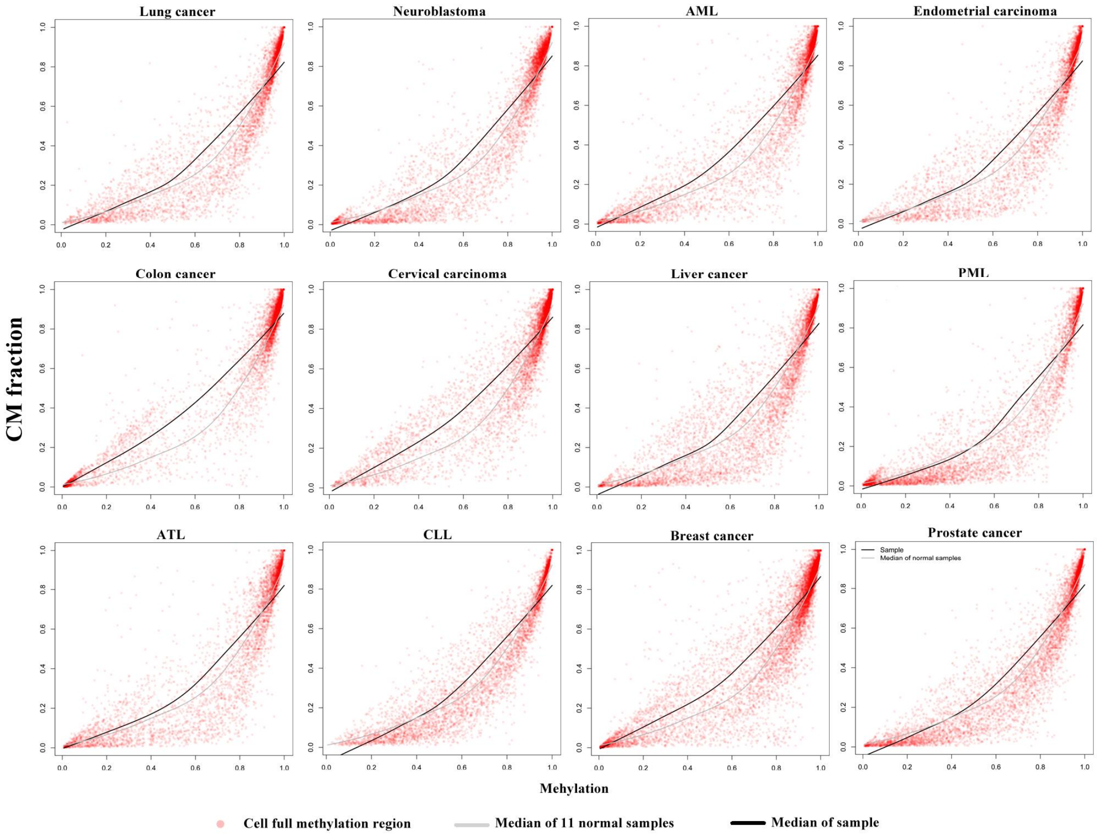

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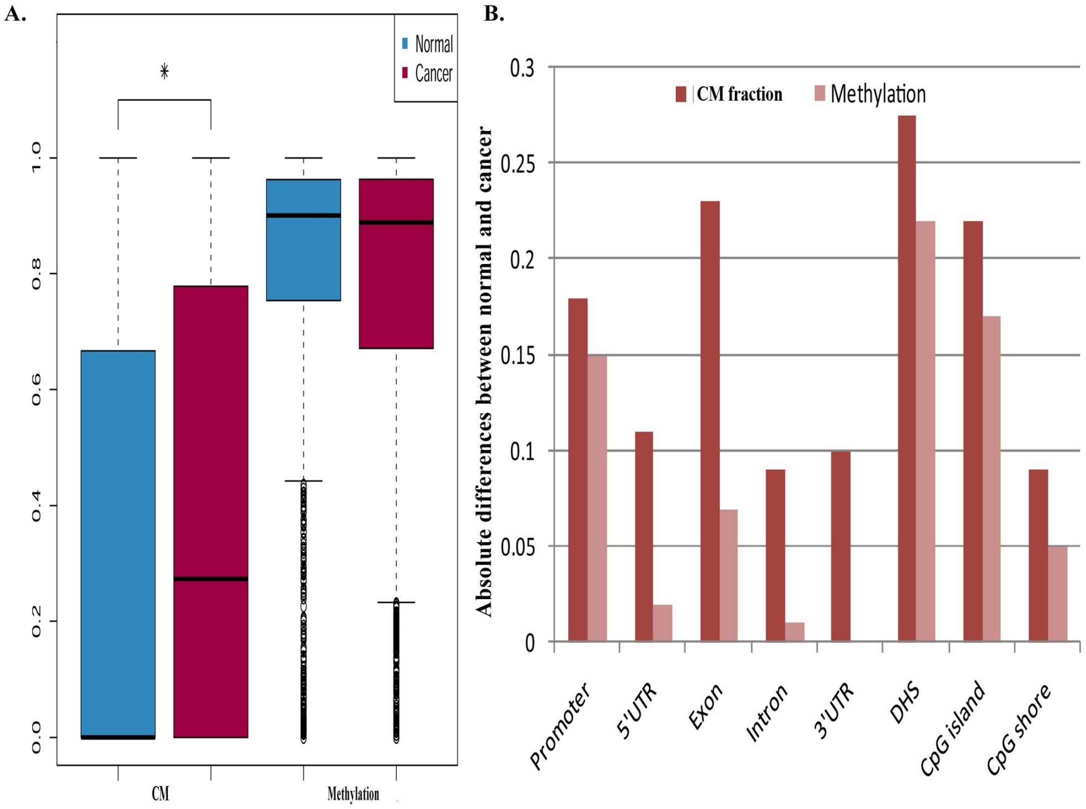

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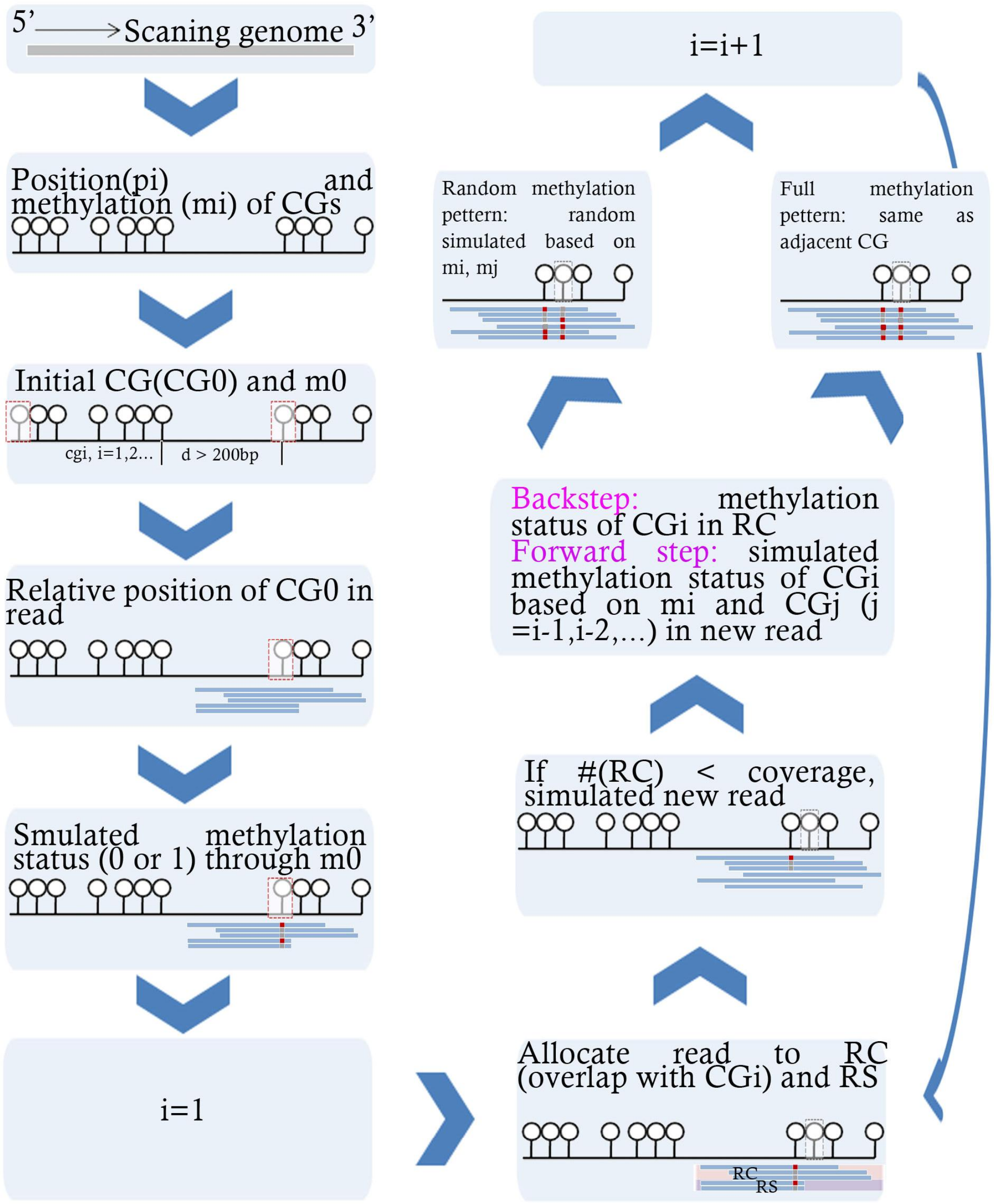
5’
Scaning genome
3’
Position(pi) and methylation (mi) of CGs
Initial CG(CG0) and m0
cgi, i=1,2…
d > 200bp
Relative position of CG0 in read
Smulated methylation status (0 or 1) through m0
i=1
Allocate read to RC (overlap with CGi) and RS
RC
RS
If #(RC) < coverage, simulated new read
Backstep: methylation status of CGi in RC
Forward step: simulated methylation status of CGi based on mi and CGj (j =i-1,i-2,…) in new read
Random methylation pettern: random simulated based on mi, mj
Full methylation pettern: same as adjacent CG
i=i+1

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Supplementary Table 1. Identification of CMRs based on genome wide BS-Seq data of breast cancer

Sample	NO	CG ± SD	length ± SD	FMC ± SD	Meth ± SD
Normal	835	5 ± 1	50.82 ± 29.18	0.60 ± 0.28	0.91 ± 0.16
Cancer	1093	6 ± 2	55.4 ± 35.55	0.67 ± 0.30	0.90 ± 0.21