

# Supporting Information

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**Table S1. Percentages of bins showing hypomethylation and CNA in the plasma of the 16 healthy subjects in the test group**

Case	Percentage of bins showing significant hypomethylation, %	Percentage of bins showing a CNA aberration, %
CTR101	0	0.52
CTR106	0.73	0.18
CTR107	0.15	0.11
CTR110	0.18	0.15
CTR111	0	0.11
CTR113	0	0.07
CTR114	0	0.04
CTR117	0.40	0.14
CTR118	0.37	1.08
CTR128	0.04	0.37
CTR129	0	0.04
CTR148	0	0.08
CTR149	0	0.11
CTR151	0.22	0.18
CTR97	0	0.67
CTR98	2.34	5.53

**Table S2. Serial analyses of plasma hypomethylation and CNAs for cases TBR34 and TBR36**

Case no.	Time point	Percentage of bins showing significant hypomethylation, %	Percentage of bins showing a CNA aberration, %
TBR34	Before surgery	64.3	57.0
	3 d after surgery	75.5	11.7
	2 mo after surgery	38.8	14.6
TBR36	Before surgery	98.7	25.3
	3 d after surgery	6.3	6.3
	3 mo after surgery	0	0.3
	6 mo after surgery	0.1	0.3
	12 mo after surgery	0	0.3

**Table S3. The mean coefficient of variation (CV) for measuring genome-wide methylation densities in the 16 healthy subjects in the reference group**

Class of CpGs	CV, %
All CpGs in the genome	1.9
Repeat elements*	0.9
CpG shores	1.8
CpG islands	6.2
Promoters	6.7
Within 1 kb downstream of transcription start sites	7.4

\*The annotated repeat elements were obtained from University of California, Santa Cruz, database (<http://genome.ucsc.edu>), including long interspersed nuclear element, long terminal repeats, satellite, short interspersed nuclear element, and simple repeats.

**Fig. S1.** Plasma methylation and copy number aberration (CNA) analyses for all studied subjects. The CNA z scores are shown in the inner ring. The green, red, and gray dots represent bins with chromosome gain, loss, and normal chromosome dosage, respectively. The methylation z scores using sequenced reads from one lane and 10 million reads are shown in the middle and outer rings, respectively. The red and gray dots represent bins with and without hypomethylation, respectively. The distance between two parallel lines represents a z-score difference of 5.

[Fig. S1](#)

**Fig. S2.** (A) CNAs detected in the tumor tissues and plasma of two hepatocellular carcinoma (HCC) patients, TBR34 and TBR36, using bisulfite (BS) and nonbisulfite converted (nBS) DNA. From inner to outer rings: tumor tissue (nBS), tumor tissue (BS), plasma (nBS), and plasma (BS). The chromosomal ideograms are arranged in a clockwise manner in the outermost ring. Each dot represents a 1-Mb bin. The green, red, and gray dots represent bins with chromosome gain, loss, and normal chromosome dosage, respectively. For tumor tissues, the distance between two lines represents one copy difference in chromosome dosage. For plasma, it represents a z-score difference of 5. (B) Scatter plots showing the correlation between the CNA z scores for plasma DNA sample with and without bisulfite treatment. A good positive correlation was observed between the two sets of results ( $r = 0.83$  and  $0.89$  for TBR34 and TBR36, respectively, Pearson correlation).

[Fig. S2](#)