Table S1. Sequencing information.

	Group	Sample number	Raw reads (pair-end, million, means ± s.d.)	Uniquely mapped reads (million, means ± s.d.)	Bisulfite conversion rates (%, means ± s.d.)
Validation experiments	FMG, WBCs, HePG2, Hela and dilution experiments	30	7.9 ± 2.8	3.2 ± 1.2	98.86 ± 0.19
T(HCC)	tissue	27	6.3 ± 2.3	2.1 ± 1.0	98.80 ± 0.18
T(Aj)	tissue	27	6.7 ± 3.0	2.2 ± 0.8	98.63 ± 0.47
T(NL)	tissue	3	5.3 ± 0.8	2.8 ± 0.3	98.90 ± 0.16
P(HCC)	plasma (training)	27	8.8 ± 2.7	3.3 ± 1.0	98.60 ± 0.37
P(Ci)	plasma (training)	17	7.8 ± 1.4	2.9 ± 0.6	98.51 ± 0.34
P(N)	plasma (training)	28	8.4 ± 2.6	3.0 ± 0.9	98.65 ± 0.44
P(HCC)	plasma (testing)	9	7.5 ± 2.5	2.7 ± 0.9	98.49 ± 0.11
P(N)	plasma (testing)	10	8.9 ± 2.6	4.5 ± 1.9	98.51 ± 0.13

Note: T(HCC), T(Aj) and T(NL) represent HCC tissues, adjacent noncancerous tissues and normal liver tissues, respectively. P(HCC), P(Ci) and P(N) represent plasma samples obtained from HCC patients, cirrhosis patients and normal individuals, respectively. The bisulfite conversion rates were assessed by lambda DNA as spike-in.