

**Supplementary information, Table S3** Summary of shotgun bisulfite sequencing (BS-seq).

		genome depths	BS-conversion rate	#CG (5x)	CG(5x) covered	Average methylation level (ML <sub>BS</sub> )
<b>Patient 1</b>	Normal	21	99.24%	26.86 M	95.25%	75.3%
	ccRCC	25	99.07%	26.97M	95.64%	70.8%
<b>Patient 2</b>	Normal	23	99.69%	26.95M	95.55%	72.9%
	ccRCC	25	99.71%	27.11 M	96.07%	71.1%

Paired-reads were mapped uniquely to the reference genome (HG19, USCS) by Bismark. #CpG (5x): total number of CpG sites mapped at least five reads. Covered: proportion of mapped CpG sites over total CpG sites in genome. "M" means million.