Supplementary information, Table S1 Summary of single-base 5hmC sequencing using TAB-seq.

	Patient 1		Patient 2	
	Normal	**ccRCC**	**Normal**	**ccRCC**
glucosylation protection rate	95.88%	95.58%	94.89%	95.33%
Bisulfite conversion rate	99.11%	99.20%	99.53%	99.51%
Tet oxidization rate	96.52%	95.35%	98.18%	97.95%
Mapped depth	33	34	35	30
#Cytosines covered > 5X	27.16M	27.12M	23.46M	22.01M
Average 5hmC level	7.07%	1.93%	6.96 %	1.52%
#5hmC modified sites	6,412,879	285,918	6,757,760	1,323,254
#hypo-5hmC sites (ccRCC vs. normal)	3,163,758		3,442,630	
#hyper-5hmC sites (ccRCC vs. normal)	222,824		659,608	

Both bisulfite conversion rate and oxidation rate by Tet was calculated by *M. SsI* treated spiked lambda DNA. Average 5hmC levels for all CG sites is calculated as C/(C+T), then corrected with the following formula: $5hmC\%_{corrected}=5hmC\%_{measured}/$protection rate of $5hmC-5mC_{BS-seq}*(1-$ Tet oxidization rate$_{5mC\ to\ 5caU/U})$. Hypo and hyper represent 5hmC level for the tumor tissue is lower or higher than that in normal tissue, respectively. "M" means million. # represents the number.