

Supplementary information, Table S6 The overlaps between aberrant 5hmC and 5mC changes at single nucleotide resolution during tumorigenesis.

		hypo-5mC	hyper-5mC	hypo-5mC_{BS}	hyper-5mC_{BS}
Patient 1	hypo-5hmC	20,658 (<i>p</i> = 1)	211,519 (<i>p</i> = 4.05E-67)	63,124 (<i>p</i> = 1)	39,975 (<i>p</i> = 1)
	hyper-5hmC	9,285 (<i>p</i> = 1)	2,733 (<i>p</i> = 1)	2,389 (<i>p</i> = 1)	5,215 (<i>p</i> = 1)
Patient 2	hypo-5hmC	9,516 (<i>p</i> = 1)	230,341 (<i>p</i> = 0)	41,492 (<i>p</i> = 1)	16,463 (<i>p</i> = 1)
	hyper-5hmC	74,908 (<i>p</i> = 1)	1,738 (<i>p</i> = 1)	3,976 (<i>p</i> = 1)	5,005 (<i>p</i> = 1)

Hypo and hyper represent 5hmC level for the tumor tissue is lower or higher than that in normal tissue, respectively. Hypo-5mC_{BS} and hyper-5mC_{BS} are calculated by BS-seq data. *P* value for the number of the overlapped sites was calculated using a custom script based on BEDTools fisher.