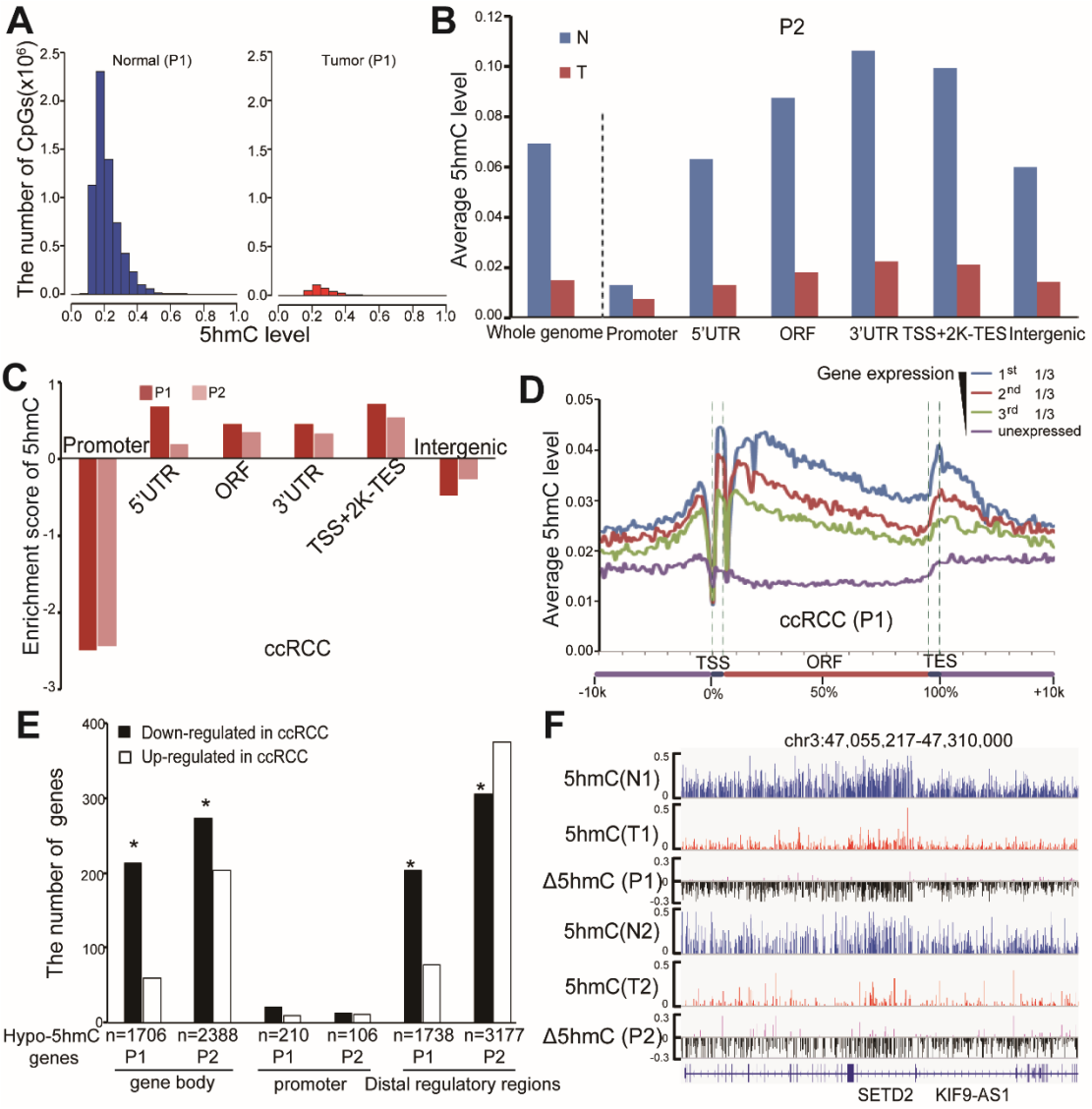

Supplementary information, Figure S2 Genome-wide dynamic patterns of 5hmC during kidney tumorigenesis. **(A)** The distribution of estimated abundances of 5hmC at called 5hmC modified CpG sites in the indicated samples from TAB-seq data. **(B)** Global changes of average 5hmC levels in different genomic elements were determined by TAB-seq (promoter defined as ±500bp of TSS). **(C)** The enrichment scores of hypo-5hmC sites in genomic elements. Score >0 were defined as enriched. **(D)** The average 5hmC levels in ccRCC tissue across different gene-associated regions. Genes in the analyzed sample were divided into four groups according to gene expression level (FPKM value). For each gene, from transcriptional start site (TSS) to transcriptional end site (TES) was divided into 100 bins, and 5'UTR and 3'UTR contributed 5 bins each, average 5hmC levels for each bin were calculated in the indicated samples. **(E)** The bar plot showed that the association between 5hmC changes and gene expression changes during tumorigenesis in gene body regions, promoter regions and distal regulatory regions (12-2K upstream to TSS). The significance of the overlapped numbers is calculated by Fisher's exact test. * represents $p < 0.001$. **(F)** Graphical representation of the dynamic 5hmC pattern during tumorigenesis at a 5hmC-enriched gene, *SETD2*. P1 and P2 represent patient 1 and 2, respectively. T and N represent tumor and matched normal tissue, respectively.