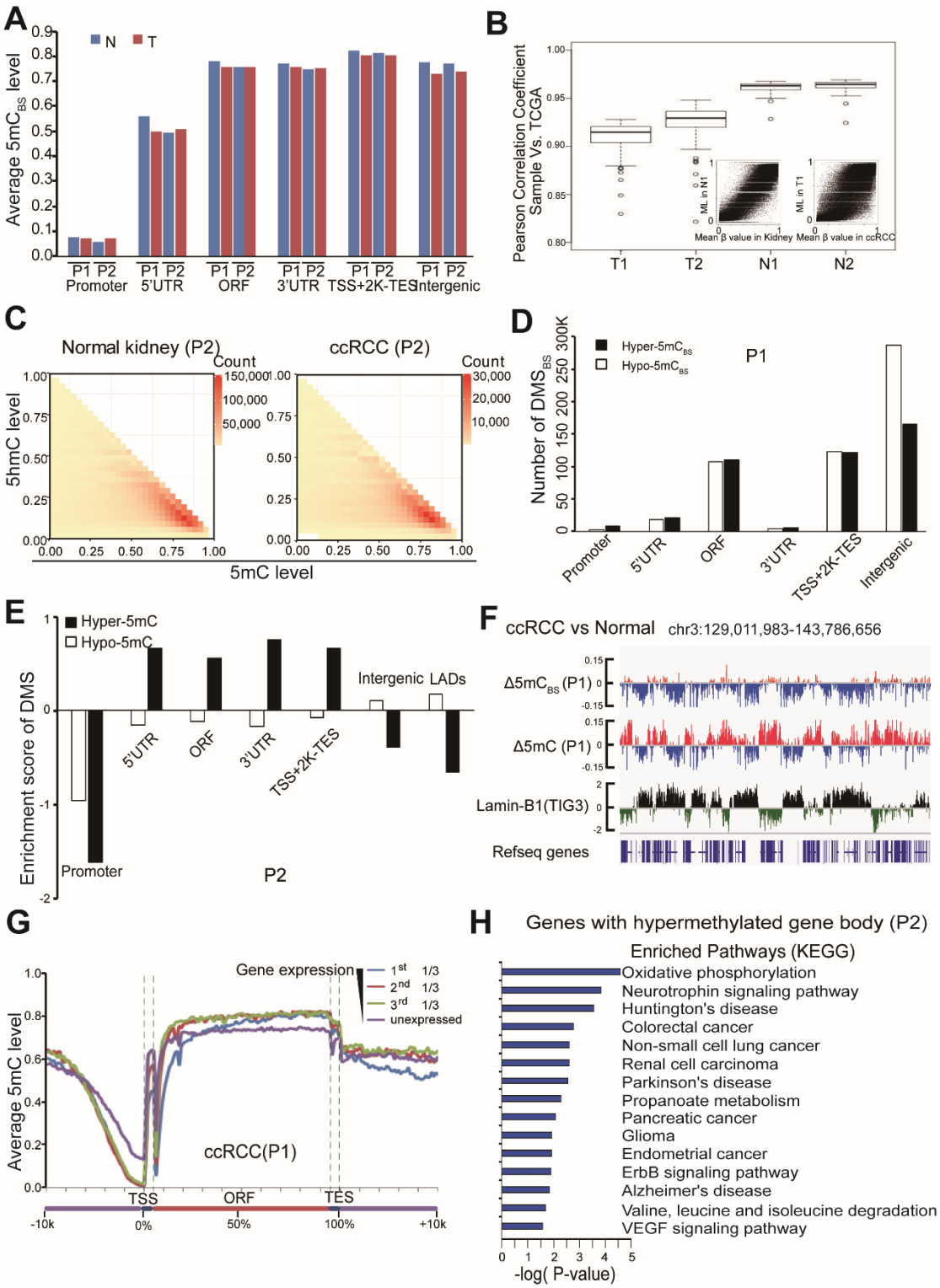

Supplementary information, Figure S3 Genome-wide single nucleotide resolution mapping of 5mC by combing BS-seq and TAB-seq method. **(A)** Global changes of average 5mC levels in different genomic elements for the tumor and matched normal tissues. $5mC_{BS}$ was estimated from BS-Seq (5hmC+5mC). **(B)** The box plot showed the distribution of Pearson correlation coefficients between our indicated sample and 160 samples from TCGA data. The 160 paired normal and tumor KIRC-HumanMethylation-450K data were downloaded from TCGA website. The dot plot represents the association between the methylation level of our sample and the mean β values of 160 indicated samples from TCGA. (**C**) Heatmap of estimated abundances of 5mC at 5hmC modified sites in tumor and matched normal tissue. The scale bar from yellow to red represents the number of 5mC/5hmC modified sites from low to high. X and Y axis showed the 5mC and 5hmC level of those modified sites, respectively. **(D)**

The distributions of the differentially methylated sites (DMS_{BS}) in different gene-associated genetic elements (promoter defined as ±500bp of TSS). $5mC_{BS}$ represents the 5mC level estimated from BS-seq data. **(E)** The enrichment scores of DMS in different genomic elements. LADs represent nuclear lamina-associated domains in TIG3 fibroblast cells. (**F**) A representative 15-Mb region on chromosome 3q showing substantial overlap between kidney tumor hypomethylated regions and LAD regions. Lamin-B1 track is from the UCSC annotation database. $5mC_{BS}$ represents the methylation level from BS-seq only. (**G**) The average 5mC level in ccRCC tissue throughout different gene-associated regions. Genes in the analyzed sample were divided into four groups according to gene expression level (FPKM value). **(H)** The KEGG pathways analyses with the genes that gain of methylation in gene body regions during tumorigenesis. P1 and P2 represent patient 1 and 2, respectively. T and N represent tumor and matched normal tissue, respectively.