Figure S4 The median distribution of 5hmC is similar between cancer and control. (**A-Q**) shows the distribution of each feature category, respectively, for plasma cfDNA samples (upper panels) and tissue gDNA samples (lower panels). (**A**) Gene bodies, defined by gene start (GS) and end (GE) sites, were divided into 20 positional bins; (**B**) Regions flanking transcription start (TS) or end (TE) sites; (**C**) CpG islands; (**D**) DNase I hypersensitivity regions; (**E**) Formaldehyde-assisted isolation of regulatory elements; (**F**) Transcription factor binding peaks; (**G**) H2A.Z variant; (**H**) H3K27ac; (**I**) H3K27me3; (**J**) H3K36me3; (**K**) H3K4me1; (**L**) H3K4me2; (**M**) H3K4me3; (**N**) H3K79me2; (**O**) H3K9ac; (**P**) H3K9me1; (**Q**) H3K9me3; and (**R**) H4K20me1. In (C-R), equal-sized bins were centered at the feature center and extended to up- and down-stream.