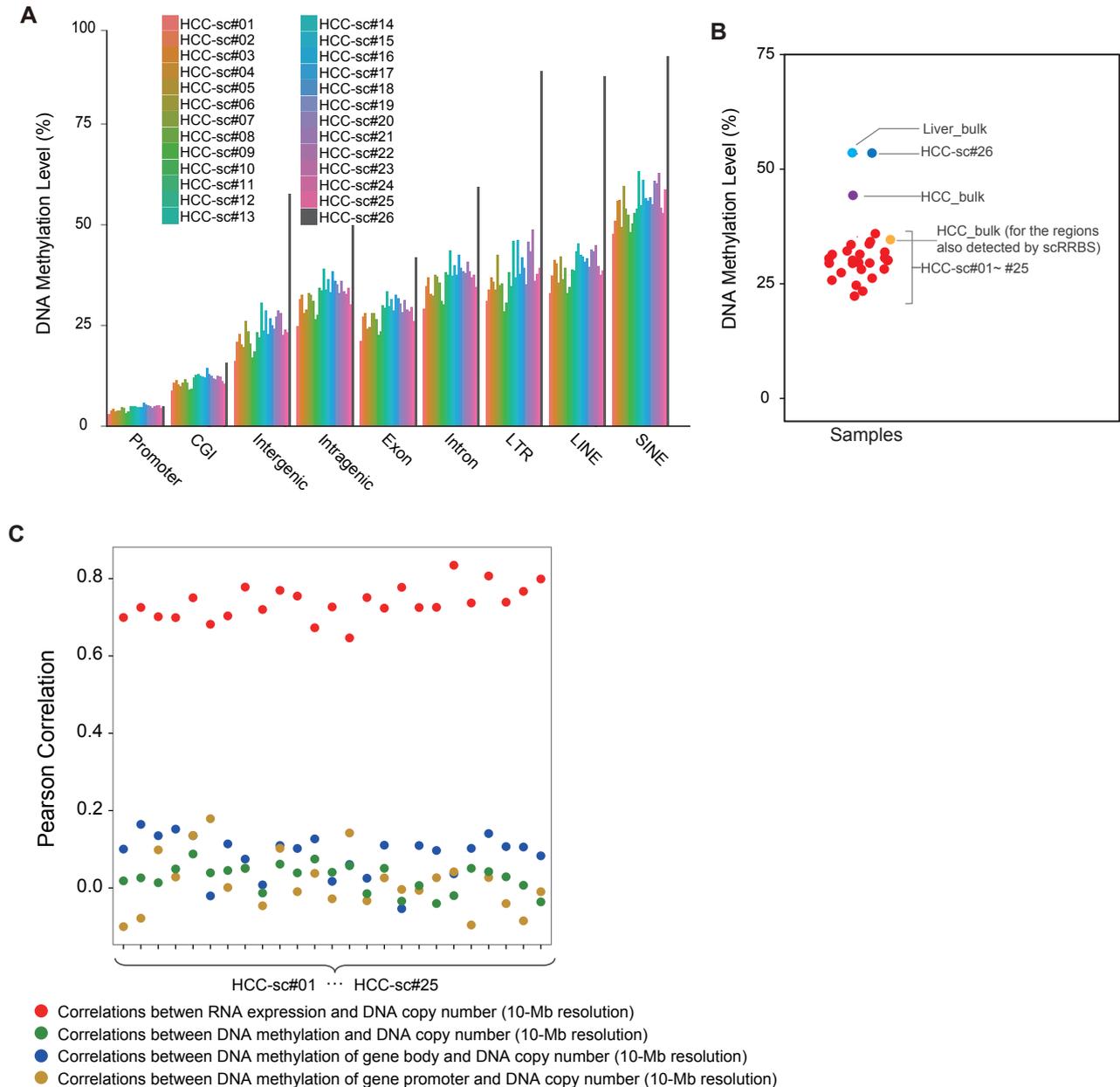


## Supplementary Figure 7



### Supplementary information, Figure S7. DNA methylome of single HCC cells.

- (A)** The average DNA methylation levels of CpG sites in different genomic regions as determined from HCC scTrio-seq data. The HCC-sc#26 cell which shows much higher DNA methylation level was likely a normal cell in HCC tissue.
- (B)** The global methylation levels of all the single HCC cells as well as HCC bulk and liver bulk samples. The HCC\_bulk (for the regions also detected by scRRBS) represents the DNA methylation of HCC\_bulk cells, the calculation for which only includes regions that are also detected in HCC scTrio-seq data.
- (C)** Pearson correlation coefficient values between digital DNA copy number values and gene expression (and DNA methylation) in each HCC cells.