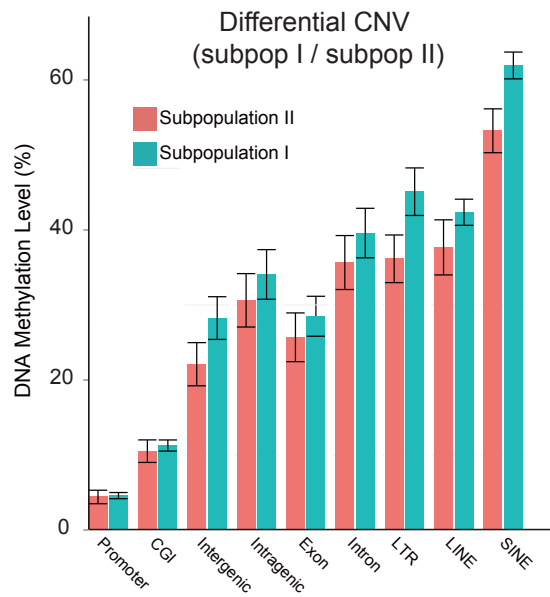
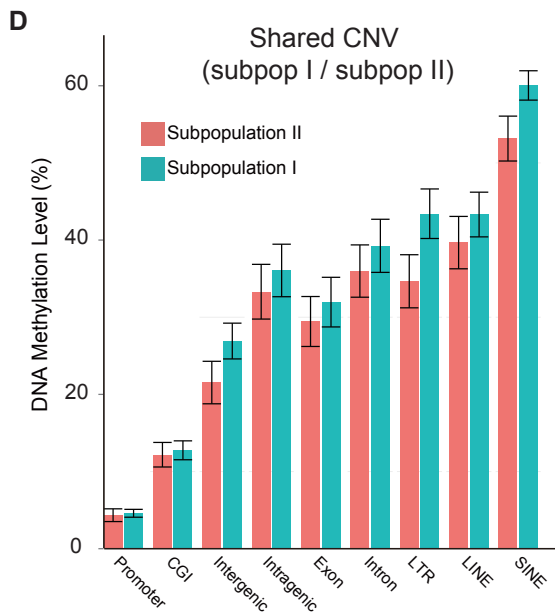
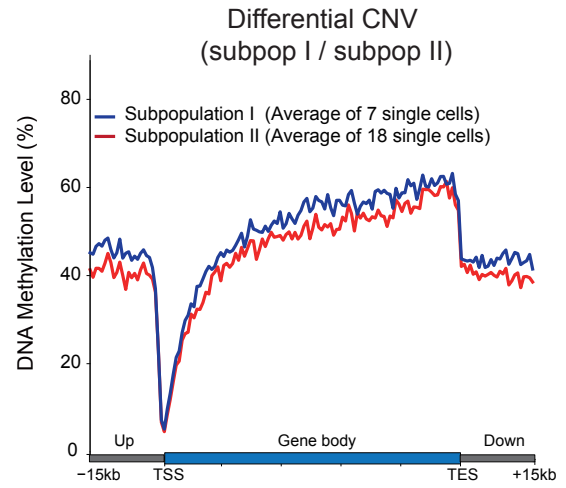
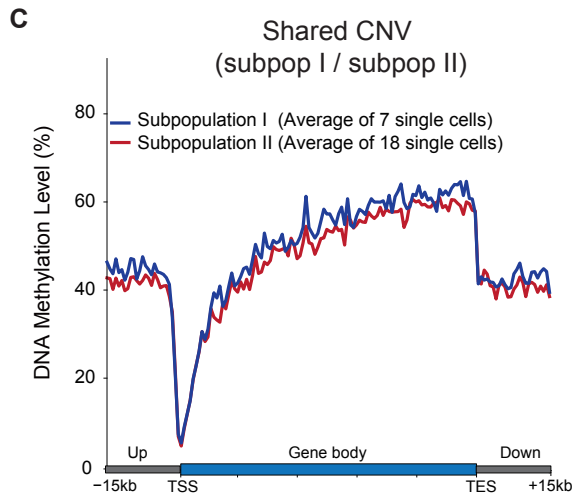
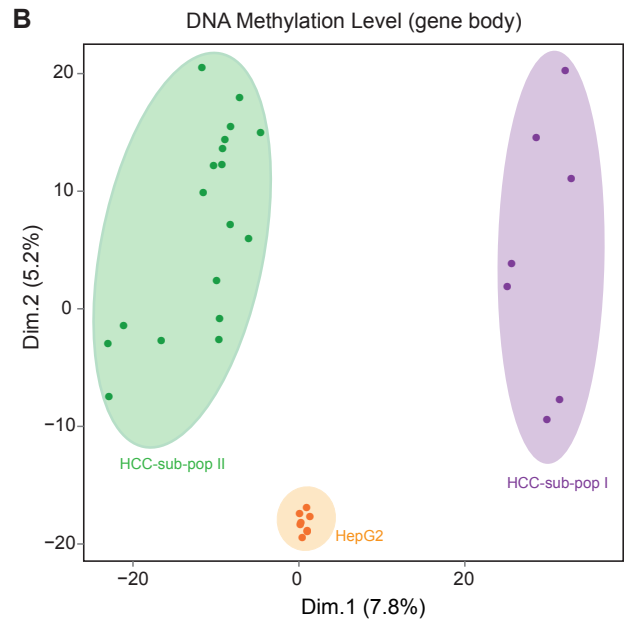
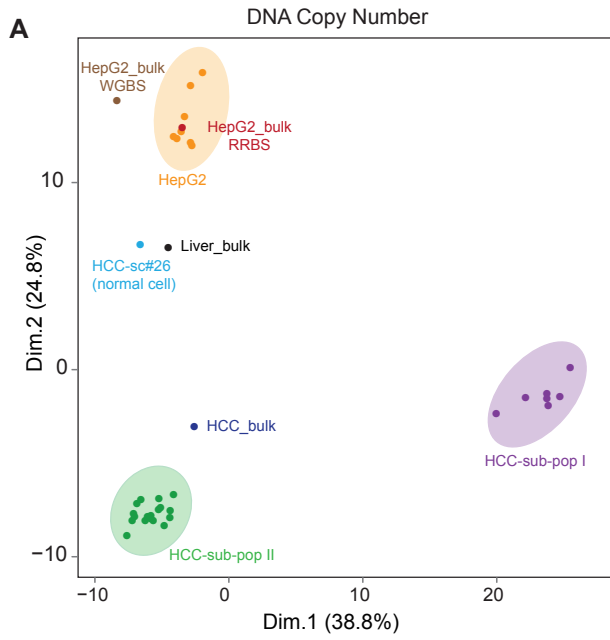


# Supplementary Figure 9



**Supplementary information, Figure S9. Differences between subpopulation I and subpopulation II HCC cells.**

- (A) Principal component analysis of HepG2 cells and HCC cells according to the DNA copy number values of each 10-Mb window.
- (B) Principal component analysis of HepG2 cells and HCC cells according to the gene body DNA methylation levels of each RefSeq gene.
- (C) The average DNA methylation levels from TSSs to TESs of all RefSeq genes and their 15-kb flanking regions in subpopulation I and subpopulation II in HCC cells. Left, the genes that are located in the shared CNV regions; right, the genes that are located in the differential CNV regions.
- (D) The average DNA methylation levels of different genomic regions in subpopulation I and subpopulation II in HCC cells. Left, the regions that are located in the shared CNV regions; right, the genes that are located in the differential CNV regions.