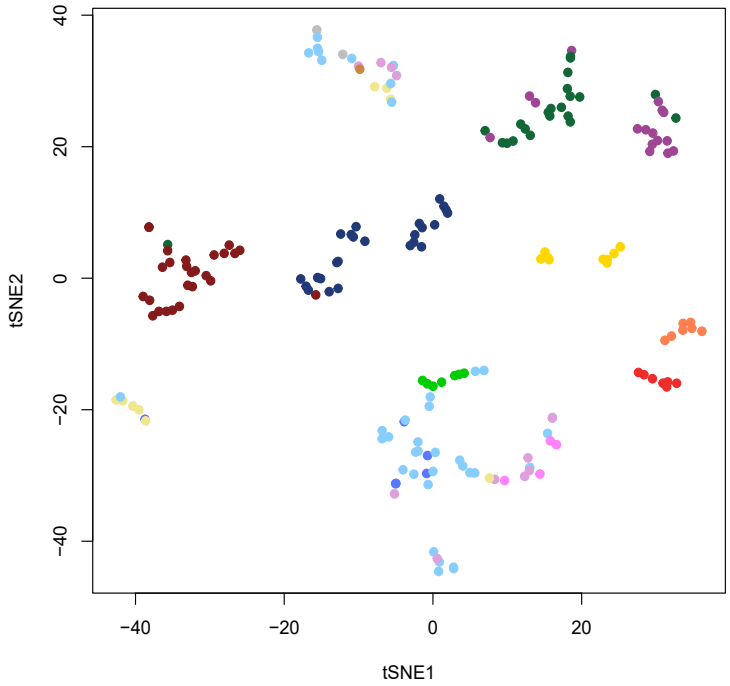

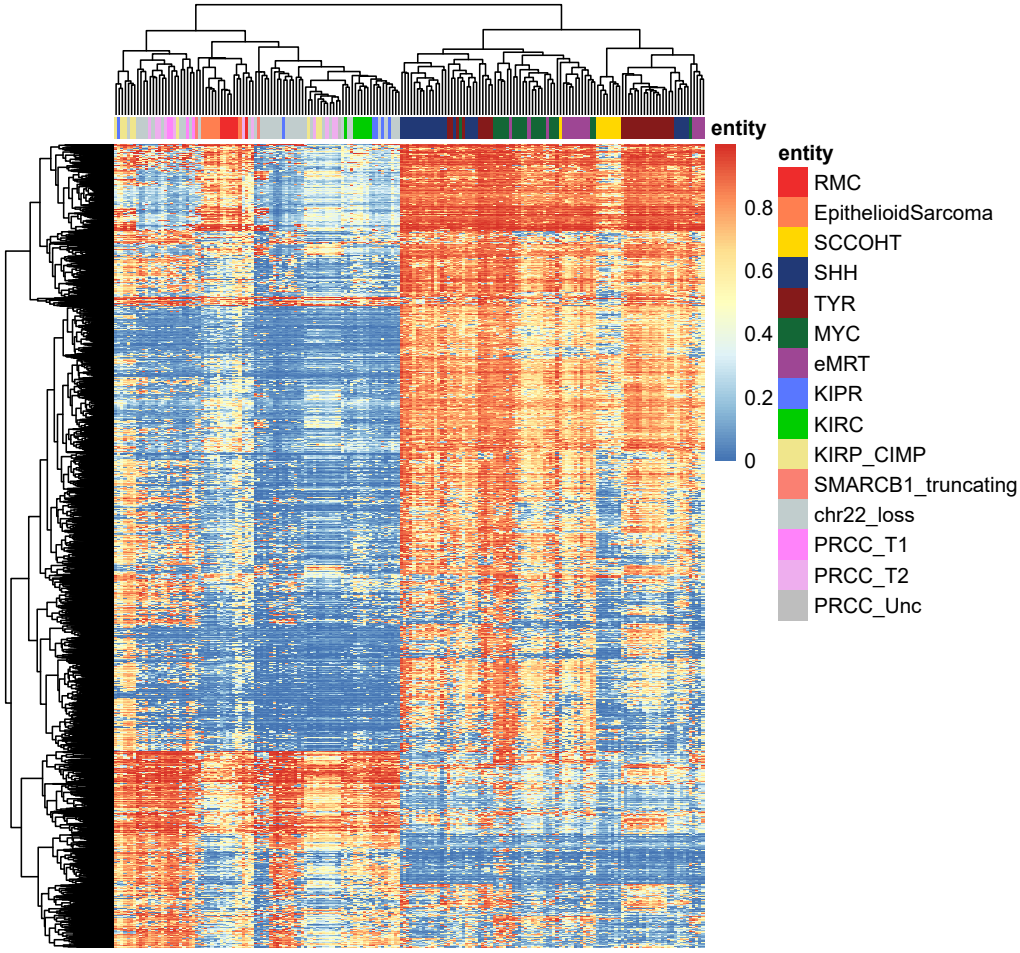

Supplementary figure S2: Unsupervised tSNE analysis based on DNA methylation profiles and unsupervised hierarchical clustering based on the 5000 most variably methylated genes.