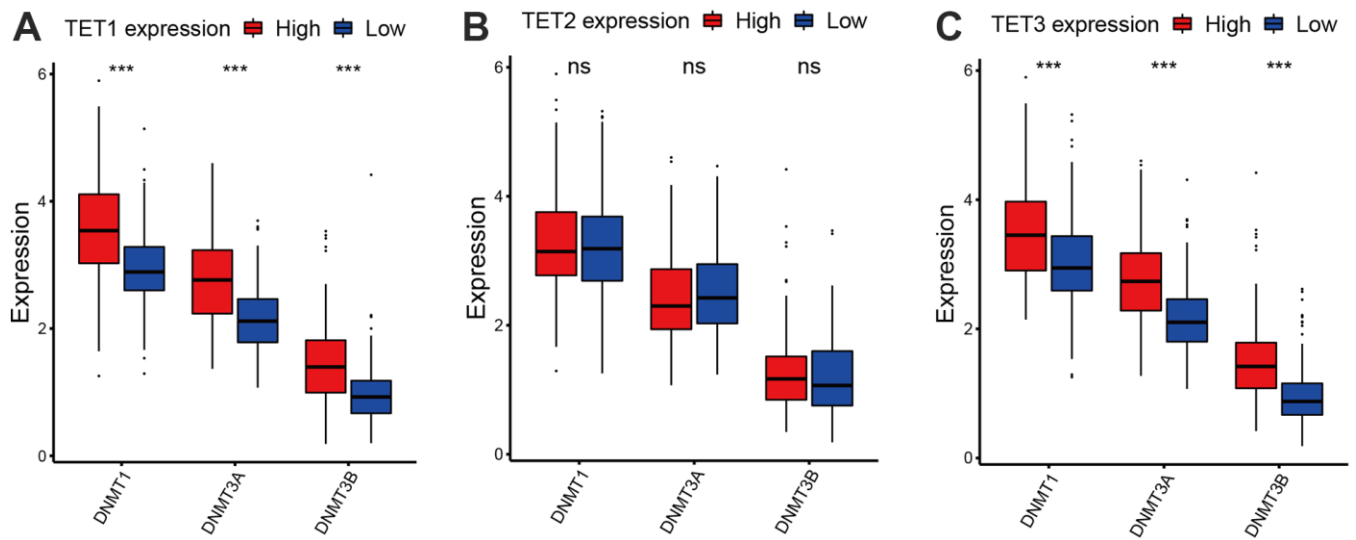
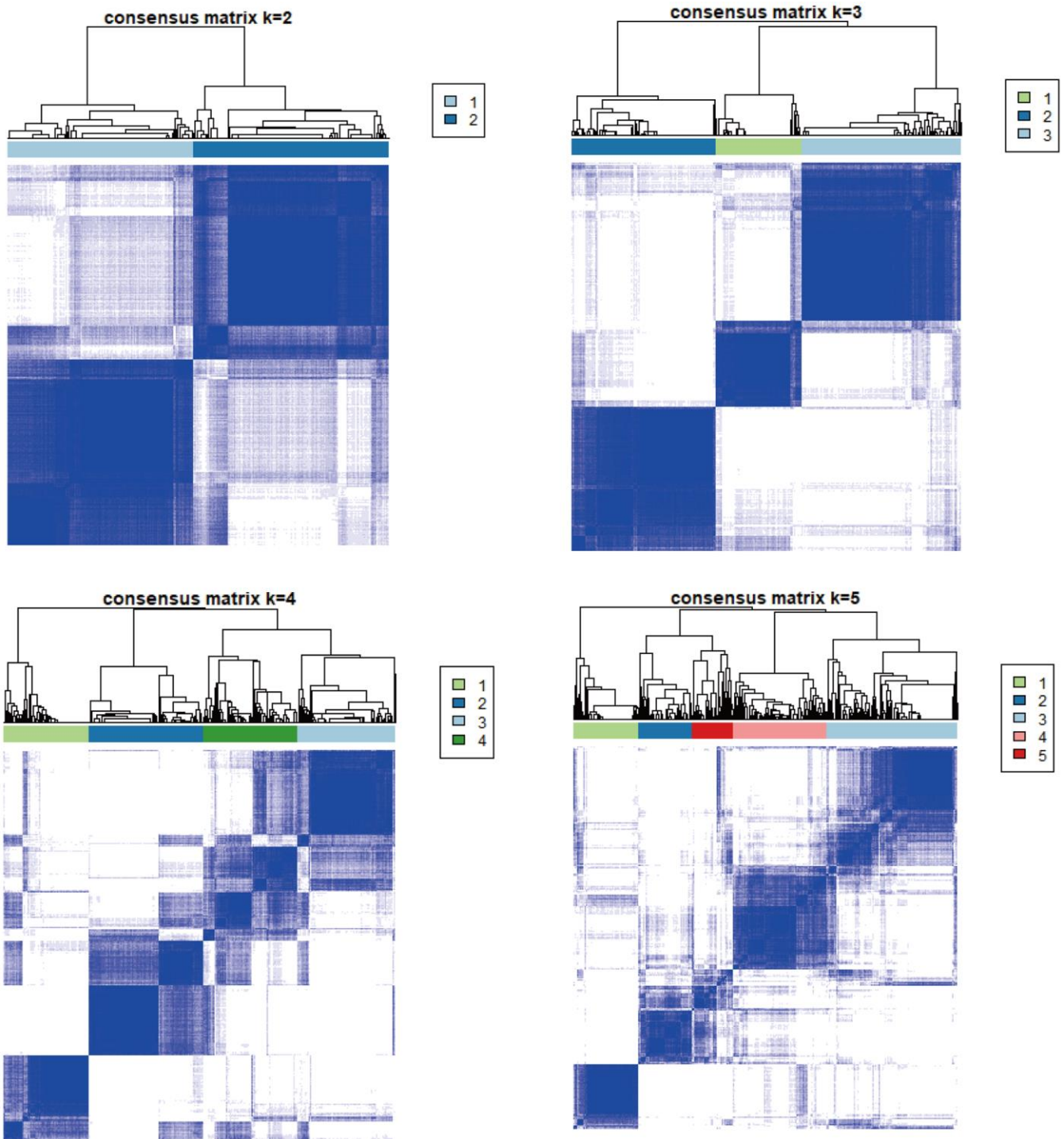


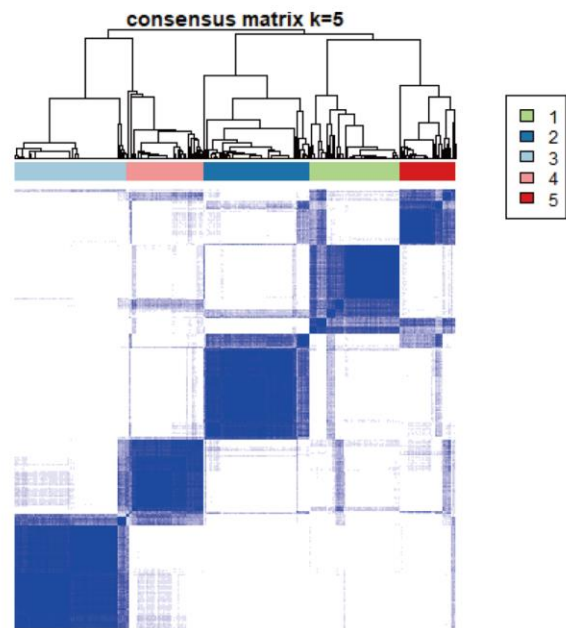
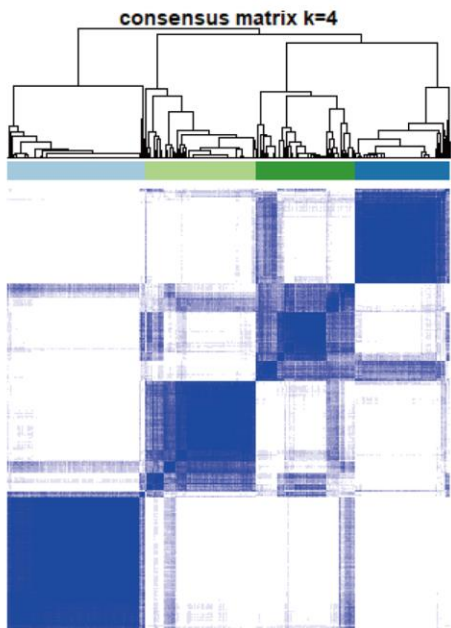
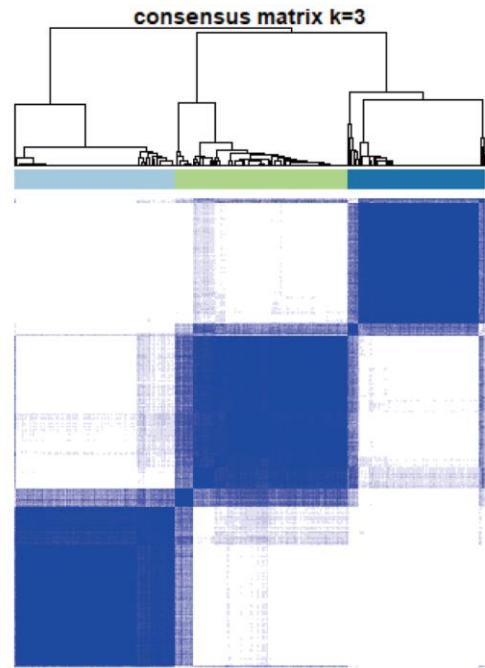
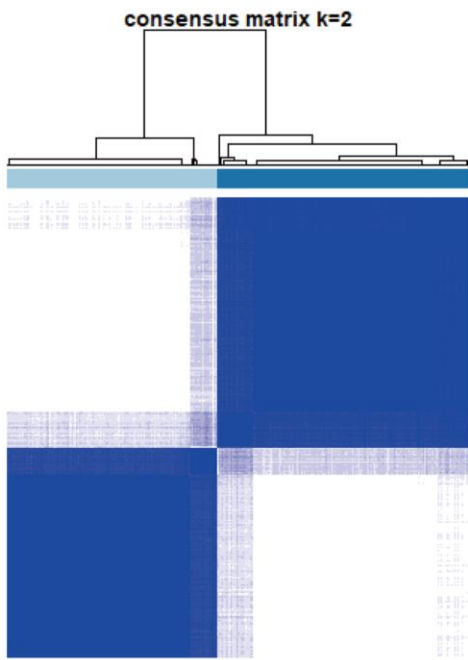
SUPPLEMENTARY FIGURES



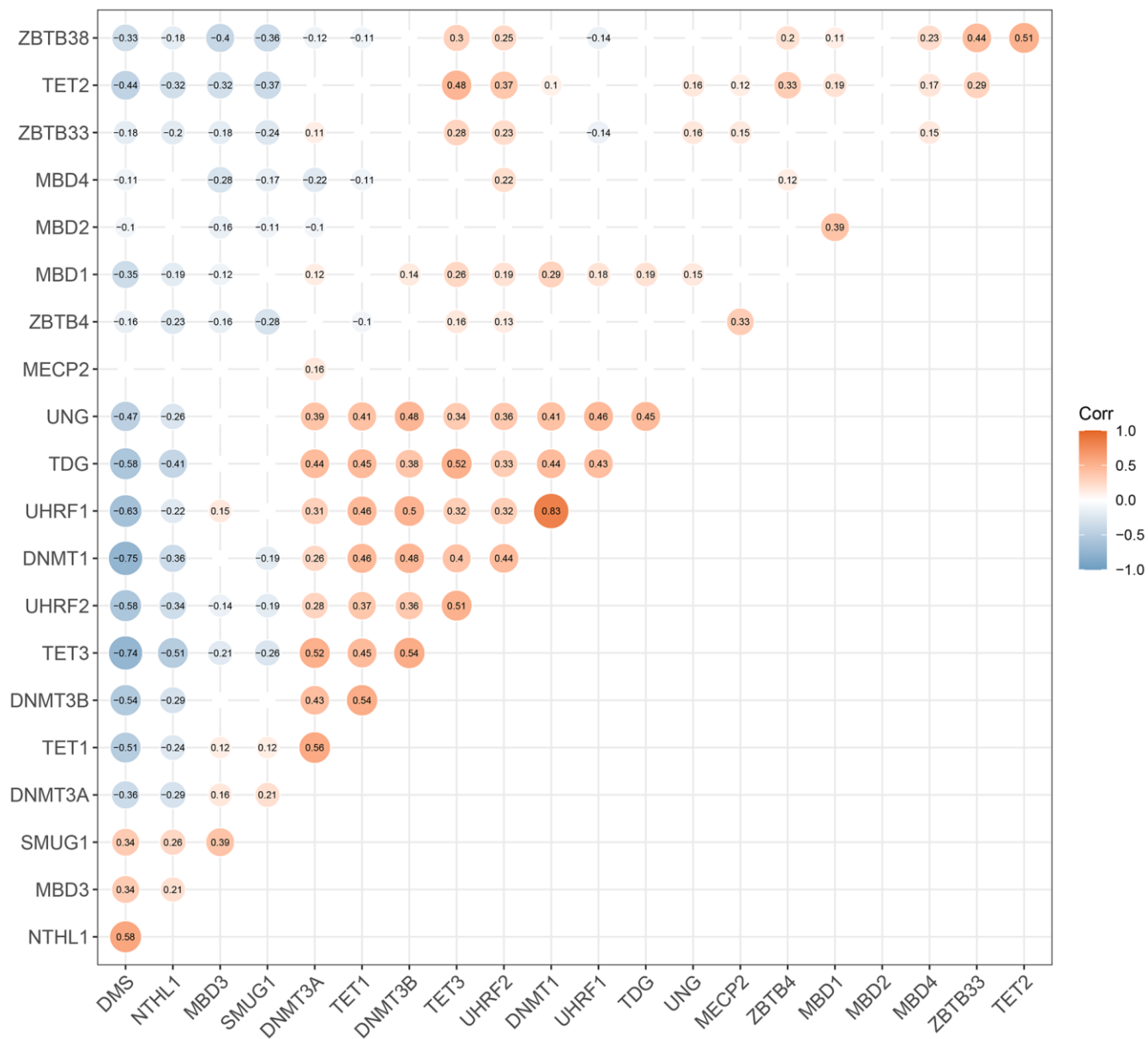
Supplementary Figure 1. Difference in writer gene expression between low and high eraser genes. (A) TET1. (B) TET2. (C) TET3. Data analyses were based on the TCGA-LIHC cohort.



Supplementary Figure 2. Consensus matrices of 20 DNA methylation regulators for k = 2, k=3, k=4 and k=5. Data analyses were based on the TCGA-LIHC cohort.



Supplementary Figure 3. Consensus matrices of 1037 overlapping differentially expressed genes for $k = 2$, $k=3$, $k=4$ and $k=5$. Data analyses were based on the TCGA-LIHC cohort.



Supplementary Figure 4. Correlation between DMS score and expression of 20 DNA methylation regulators. The numbers in the circles represented the correlation coefficients.