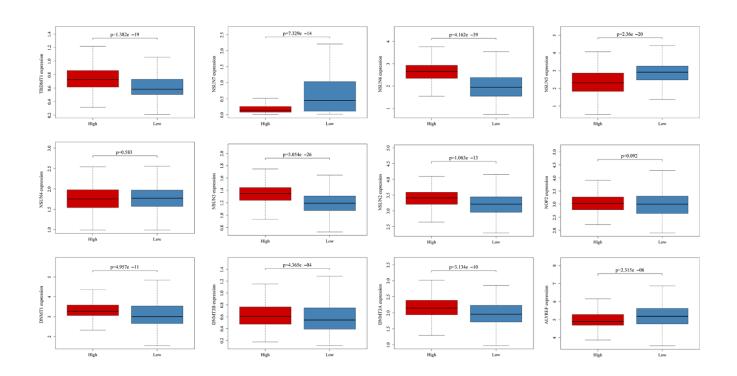
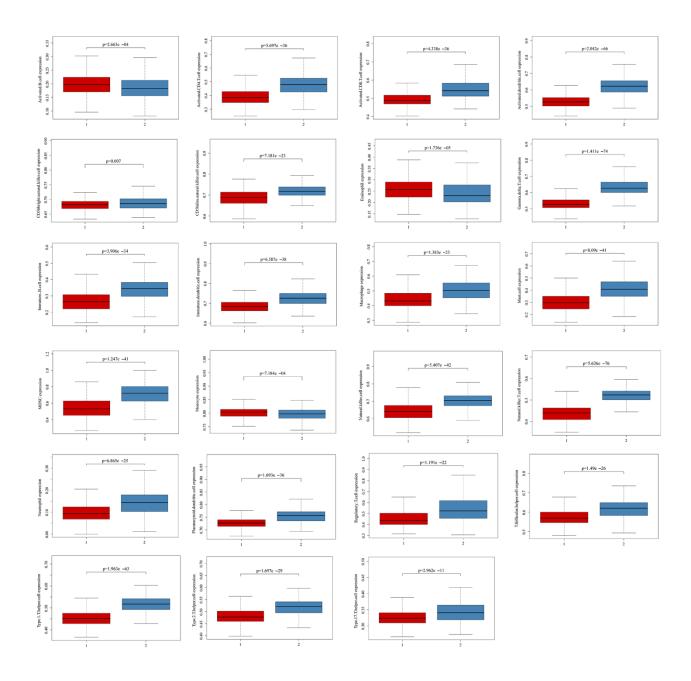
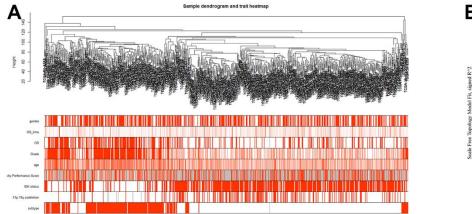
SUPPLEMENTARY FIGURES

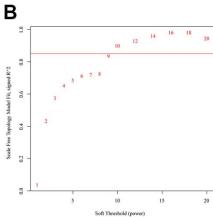


Supplementary Figure 1. Association between writer/reader gene expression and eraser gene expression.



Supplementary Figure 2. The differences of separate immune infiltration cells in m5c subclusters.





Supplementary Figure 3. The construction of a gene co-expression network. (A) The clusters were based on the transcriptome data from TCGA. The color intensity represented the clinical phenotypes. (B) Soft-thresholding power analysis was used to construct the scale-free fit index of network topology.