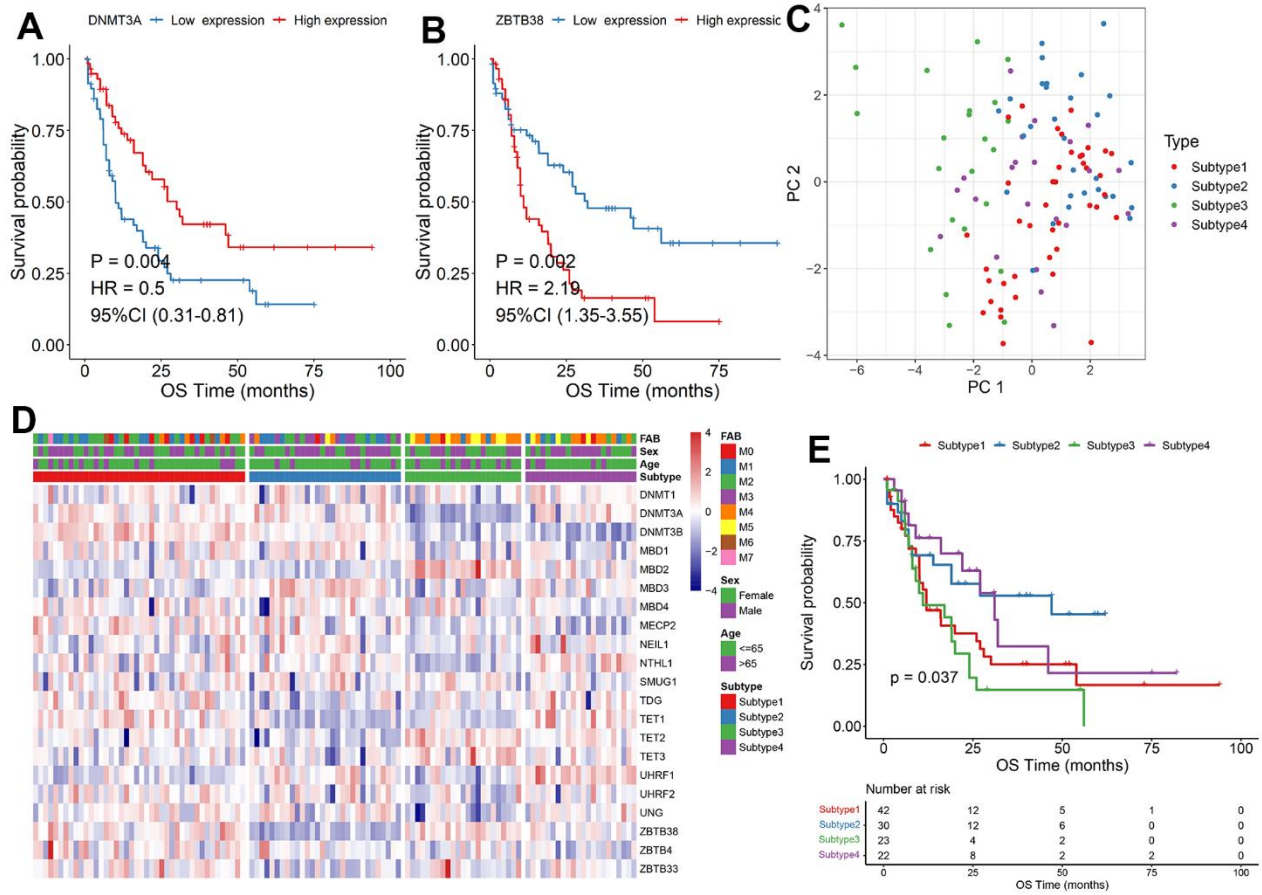
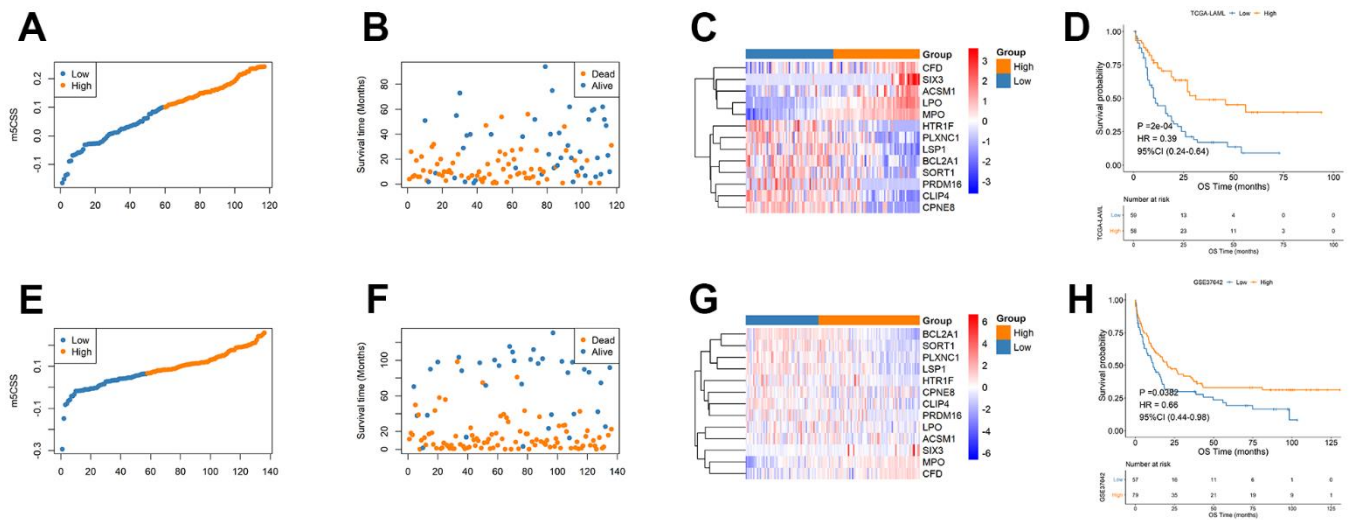


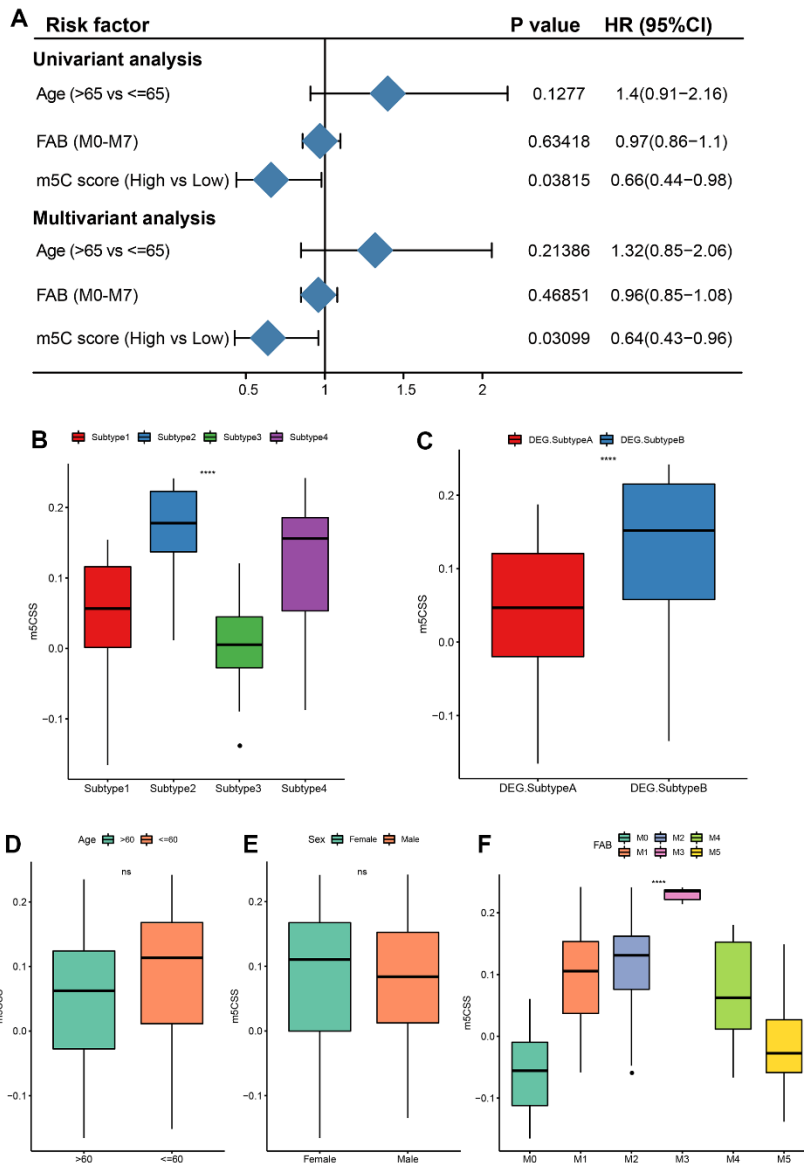
**SUPPLEMENTARY FIGURES**



**Supplementary Figure 1. m5C gene prognostic correlation and clustering analysis. (A) KM curves of DNMT3A and (B) ZBTB38, (C) principal component analysis of Subtype 1-4, (D) m5C gene expression distribution in Subtype 1-4, (E) KM curves of Subtype 1-4.**



**Supplementary Figure 2. The m5CSS gene characteristics of training and validation set.** In training set, (A) the m5CSS distribution, (B) survival time of different samples, (C) expression of model genes, (D) survival analysis of high and low m5CSS group; in validation set, (E) m5CSS distribution, (F) survival time of different samples, (G) expression of model genes, (H) survival analysis of high and low m5CSS group.



**Supplementary Figure 3. Distribution of m5C score for clinical characteristics samples and m5C subtypes.** (A) Univariable cox analysis in validation set, (B) m5C score difference between m5C subtypes, (C) m5C score difference between DEG subtypes, (D–F) m5C score distribution of different clinical characteristics samples (Age, Sex and FAB, respectively).