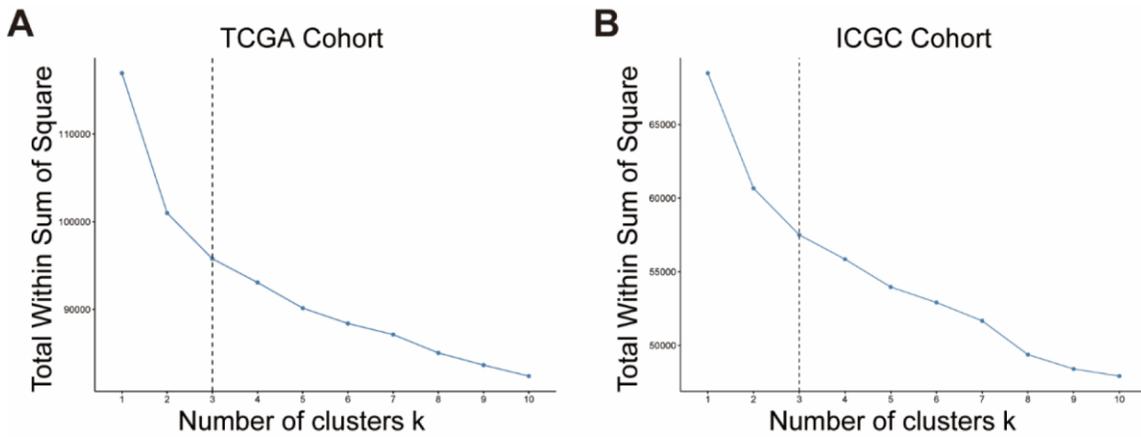
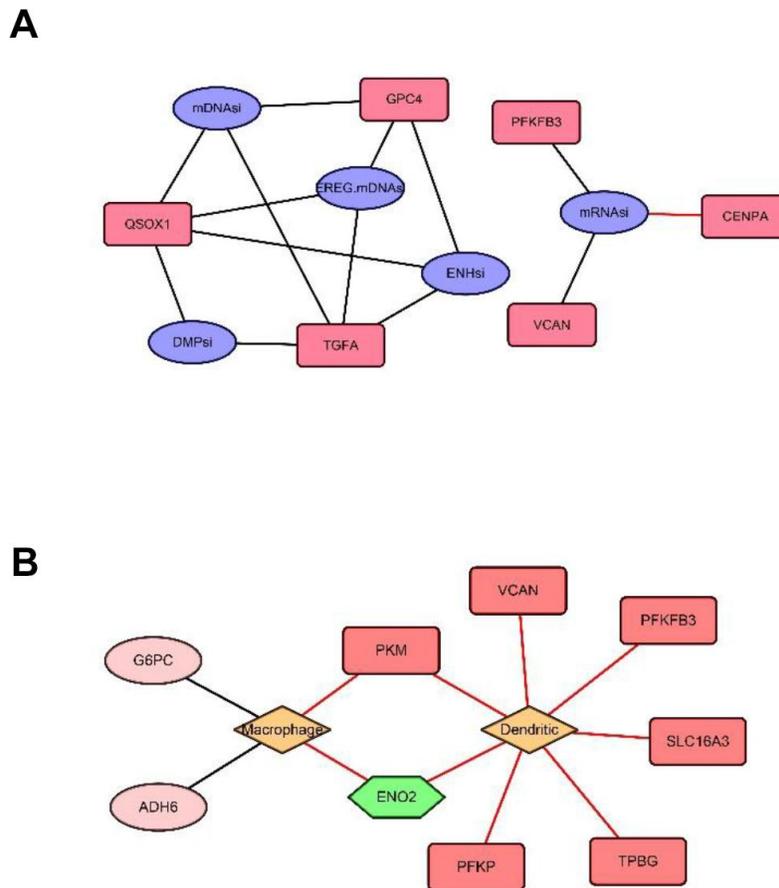


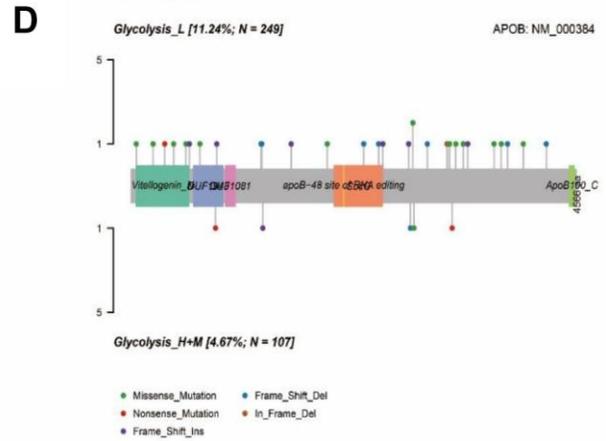
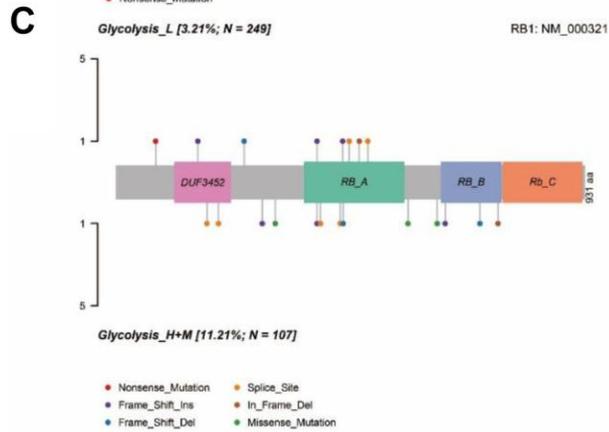
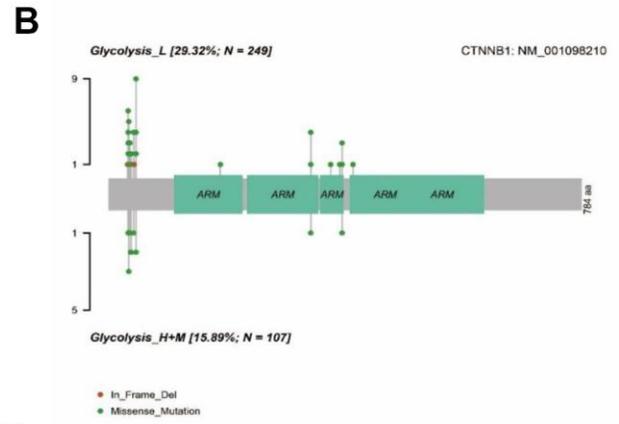
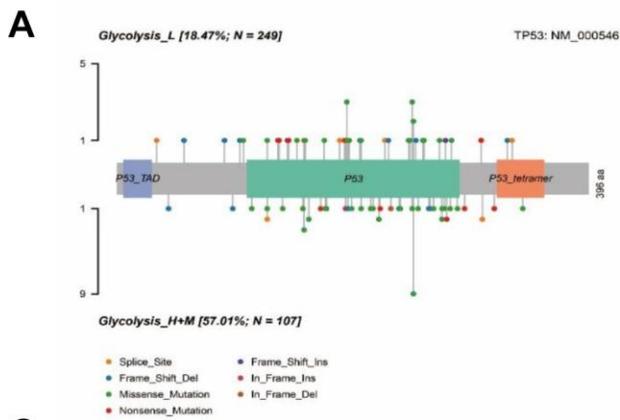
**SUPPLEMENTARY FIGURES**



**Supplementary Figure 1.** Elbow plot of TCGA (A) and ICGC (B) cohort. Vertical axis showed the total within sum of square, horizontal axis represented the number of clusters.



**Supplementary Figure 2.** (A) The regulatory network of stem cell indices and glycolysis-associated genes. (B) The regulatory network of macrophages, dendritic cells, and glycolysis-associated genes. Black edge for negative-regulated and red edge for positive-regulated.



**Supplementary Figure 3.** The lollipop plot of TP53 (A), CTNNB1 (B), RB1 (C), and APOB (D) showed each mutation with its location and accumulated burden of each gene.