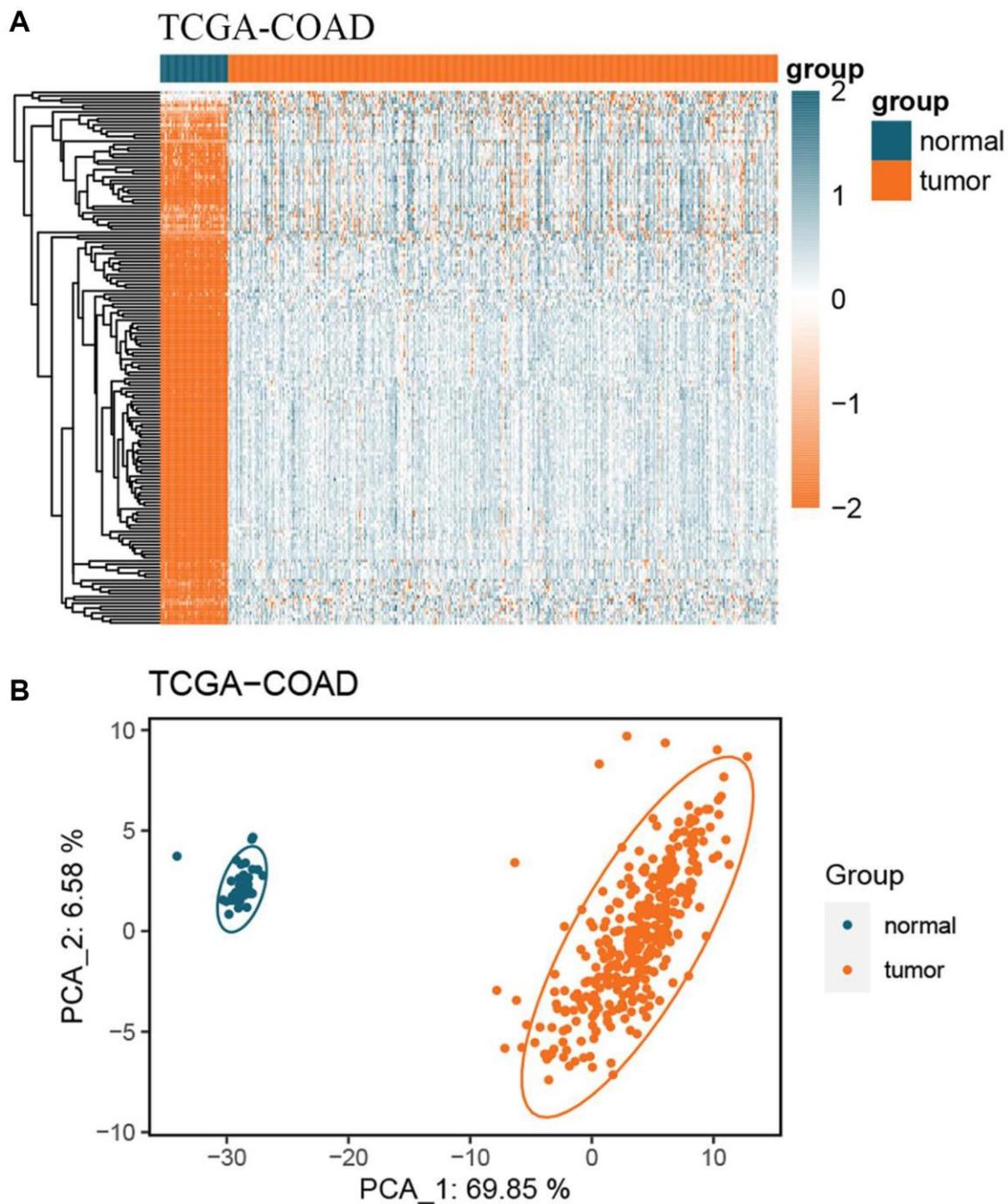
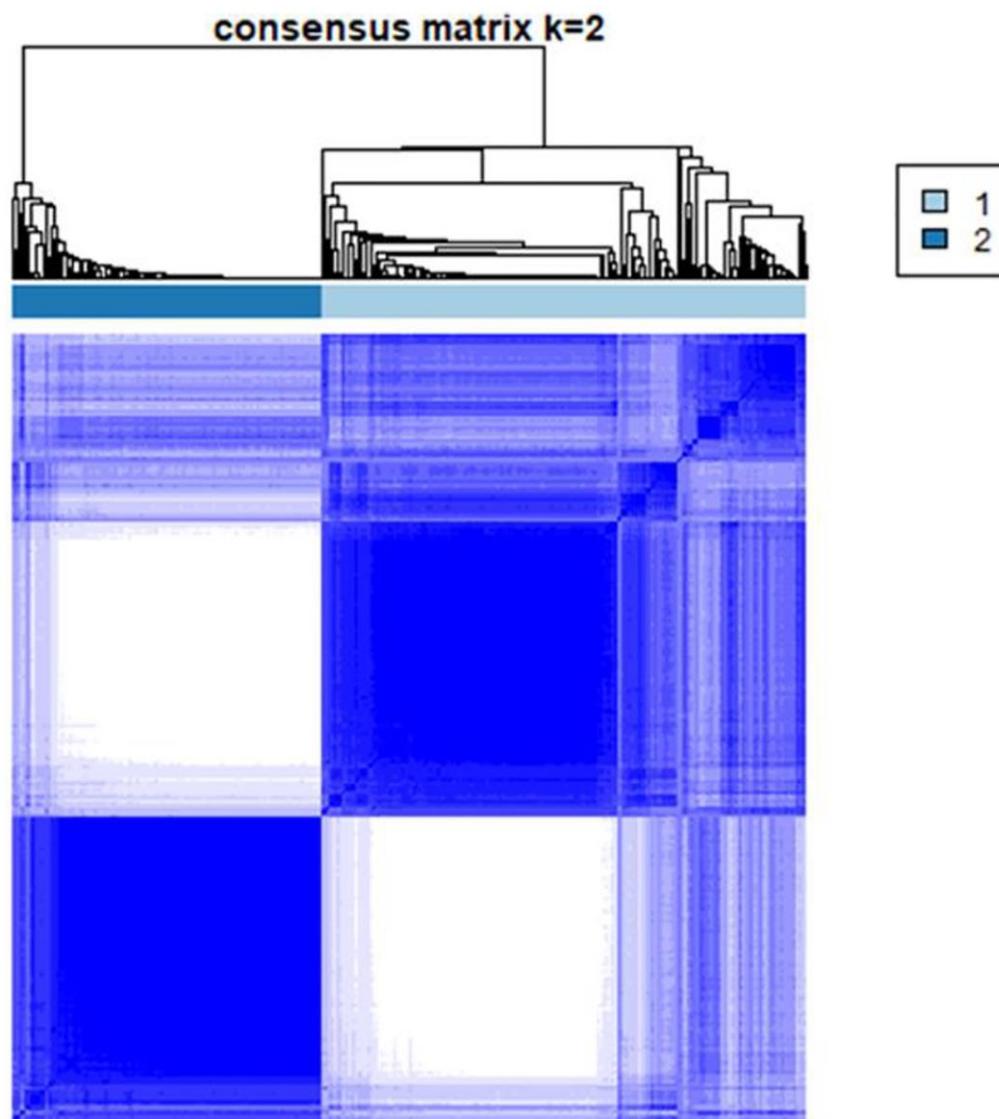


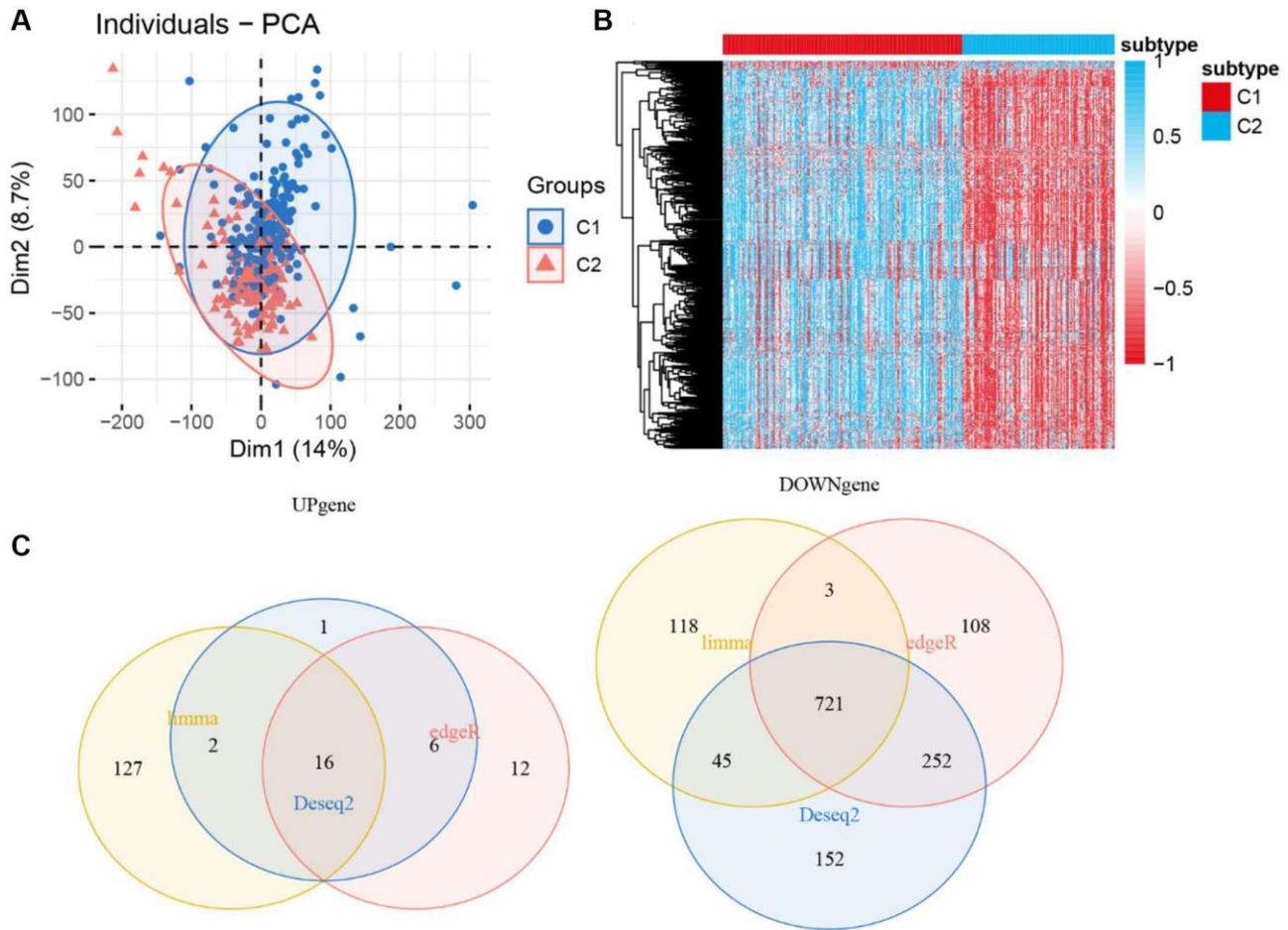
SUPPLEMENTARY FIGURES



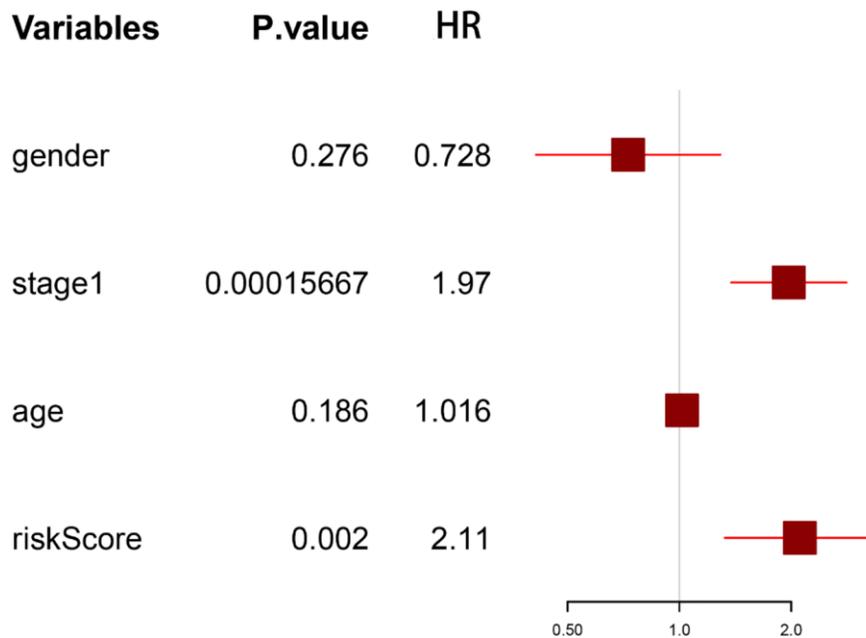
Supplementary Figure 1. Expression analysis of GMRGs in the TCGA-COAD cohort. (A) PCA plot of GMRGs. (B) Heatmap of GMRGs. Abbreviations: GMRGs: gut microbes-related genes; PCA: principal component analysis.



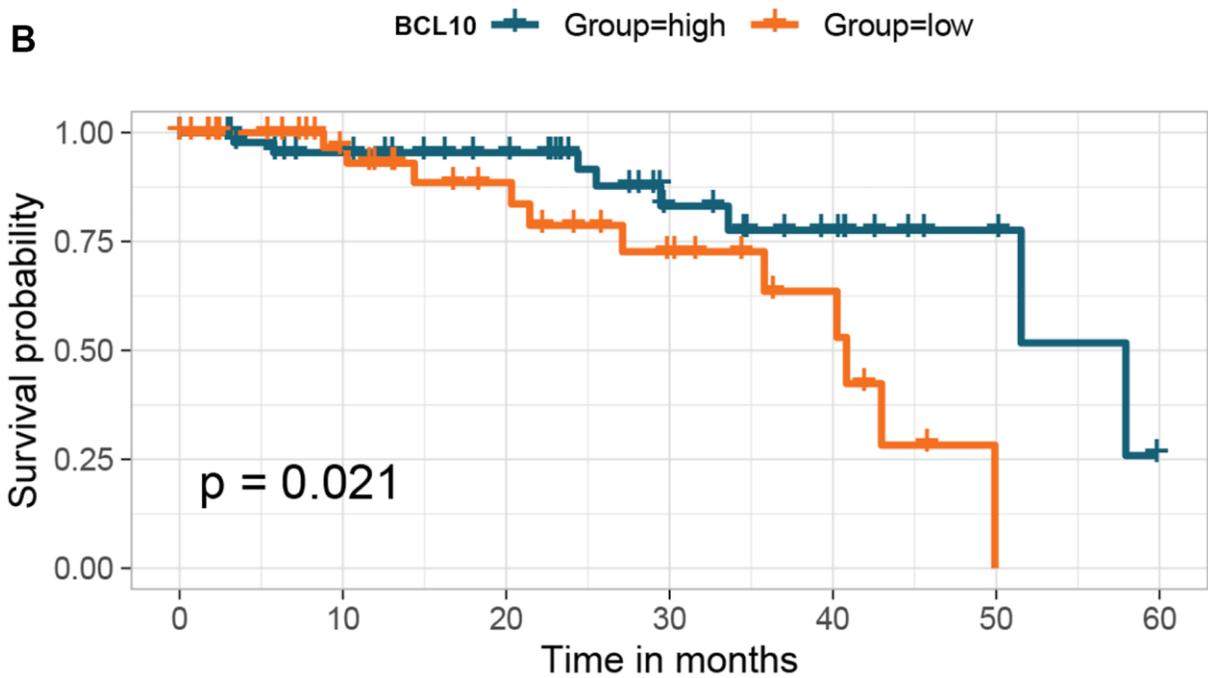
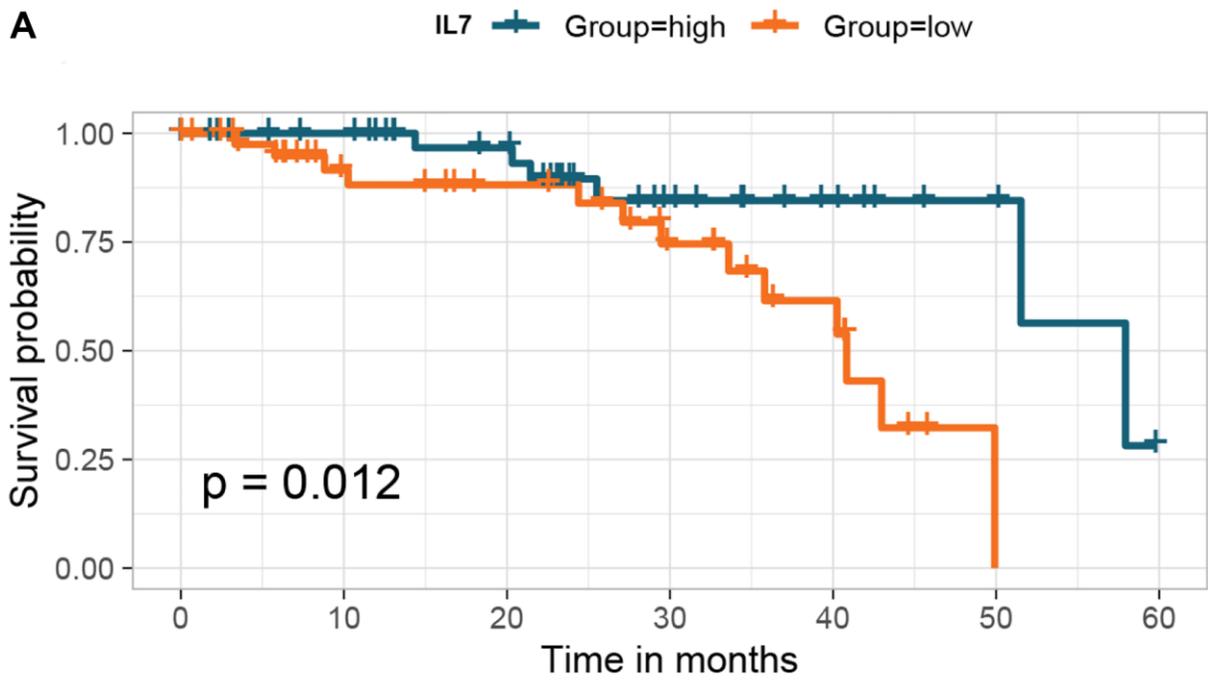
Supplementary Figure 2. Construction of GM molecular subtypes using TCGA-COAD samples. The two GM subtypes identified by the consensus clustering. Abbreviation: GM: gut microbes.



Supplementary Figure 3. DEGs between GM molecular subtypes. (A) PCA plot of DEGs. (B) Heatmap of DEGs. (C) Venn diagram of DEGs. Abbreviations: DEGs: differentially expressed genes; GM: gut microbes; PCA: principal component analysis.



Supplementary Figure 4. Clinical value of risk signature. Forest plot of clinical characteristics and risk scores.



Supplementary Figure 5. K-M survival analysis based on GMRBs expression in the GSE87211 cohort. (A) K-M survival analysis between high and low expression groups of IL7. **(B)** K-M survival analysis between high and low expression groups of BCL10. Abbreviations: K-M: Kaplan-Meier; GMRBs: gut microbes-related biomarkers.