

Supplementary Materials for

“Integrated analyses of m⁶A regulator-mediated methylation modification patterns and tumor microenvironment infiltration characterization in pan-cancer”

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Overview of Supplementary Materials:

Supplementary Figures

Supplementary Figure S1: Kaplan-Meier curves of patients in the low-RBM15 group and the high-RBM15 group in pan-cancer.

Supplementary Figure S2: Unsupervised clustering based on 20 m⁶A regulators. The consensus fraction matrix of all samples when k=2.

Supplementary Figure S3: Functional annotation for m⁶A phenotype-related using KEGG enrichment analysis.

Supplementary Figure S4: Unsupervised clustering based on 37 m⁶A phenotype-related genes. The consensus fraction matrix of all samples when k=2.

Supplementary Tables

Supplementary Table S1: Spearman correlation analysis of the 20 m⁶A modification regulators.

Supplementary Table S2: Samples clustering in pan-cancer.

Supplementary Table S3: Enrichment score of KEGG pathways in pan-cancer.

Supplementary Table S4: TME infiltration characteristics of samples in pan-cancer.

Supplementary Table S5: The correlation of m⁶A modification regulators and TME infiltration Characteristics.

Supplementary Table S6: The Univariate Cox regression analysis of 40 differential genes.

Supplementary Table S7: Functional annotation for m⁶A phenotype-related genes.

Supplementary Table S8: Gene signatures used in this study for marking biological processes.

Supplementary Table S9: The gene sets used in this work for marking 28 types immune infiltration cells.

Supplementary Figures

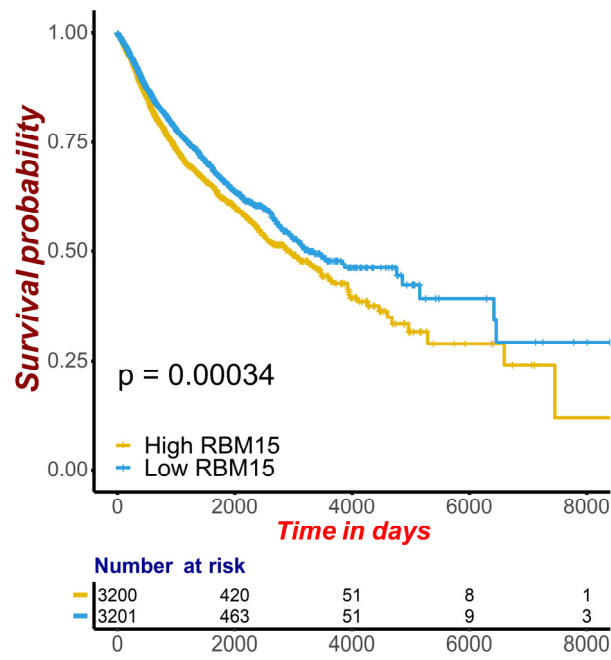


Figure S1. Kaplan-Meier curves of patients in the low-RBM15 group and the high- RBM15 group in pan-cancer. The X-axis shows survival time in days. The Y-axis shows the overall survival rate.

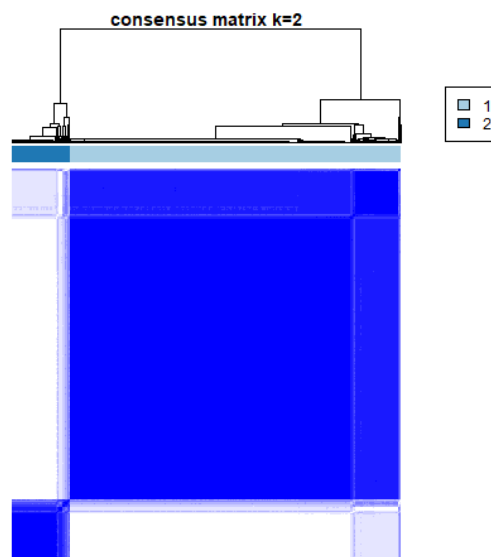


Figure S2. Unsupervised clustering based on 20 m⁶A regulators. The consensus fraction matrix of all samples when k=2.

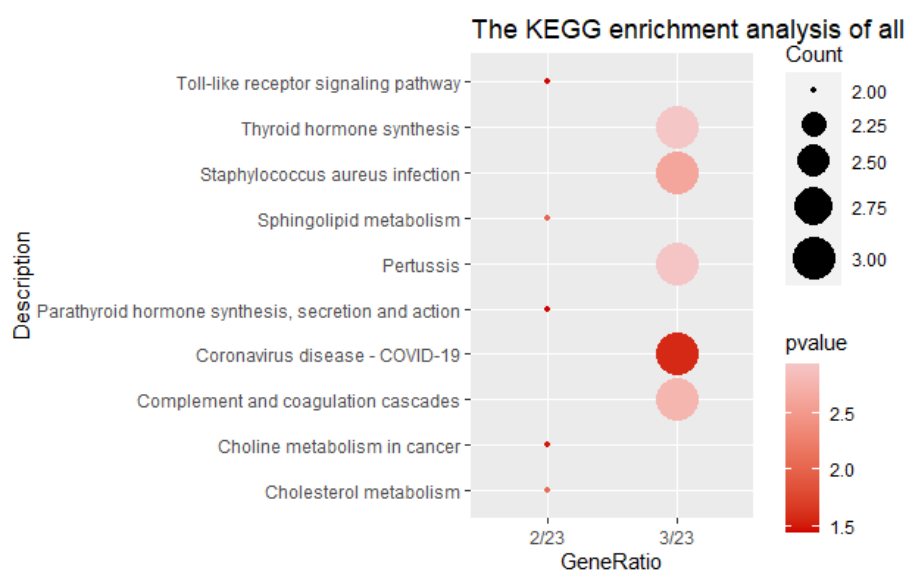


Figure S3. Functional annotation for m⁶A phenotype-related genes using KEGG enrichment analysis.

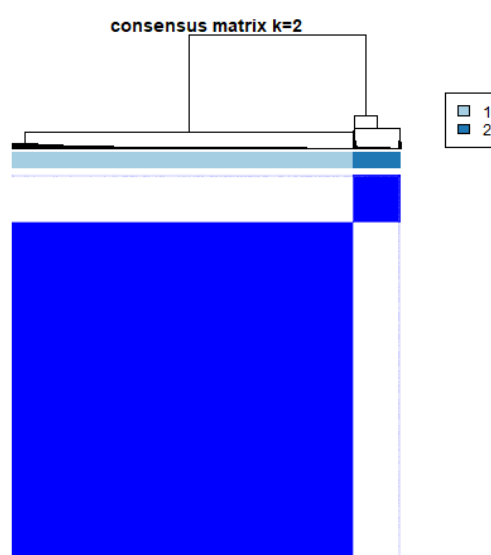


Figure S4. Unsupervised clustering based on 37 m⁶A phenotype-related genes. The consensus fraction matrix of all samples when k=2.