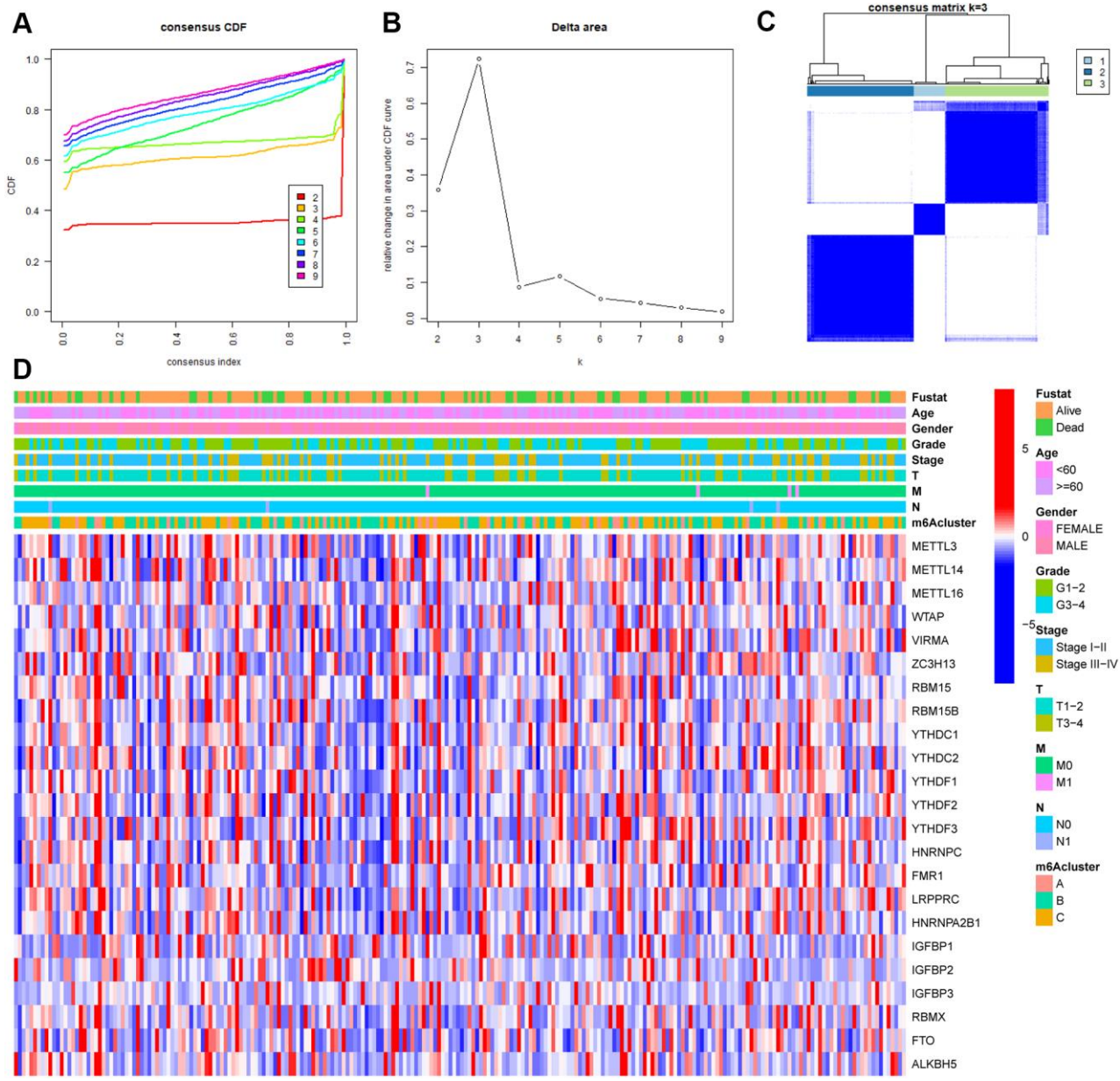
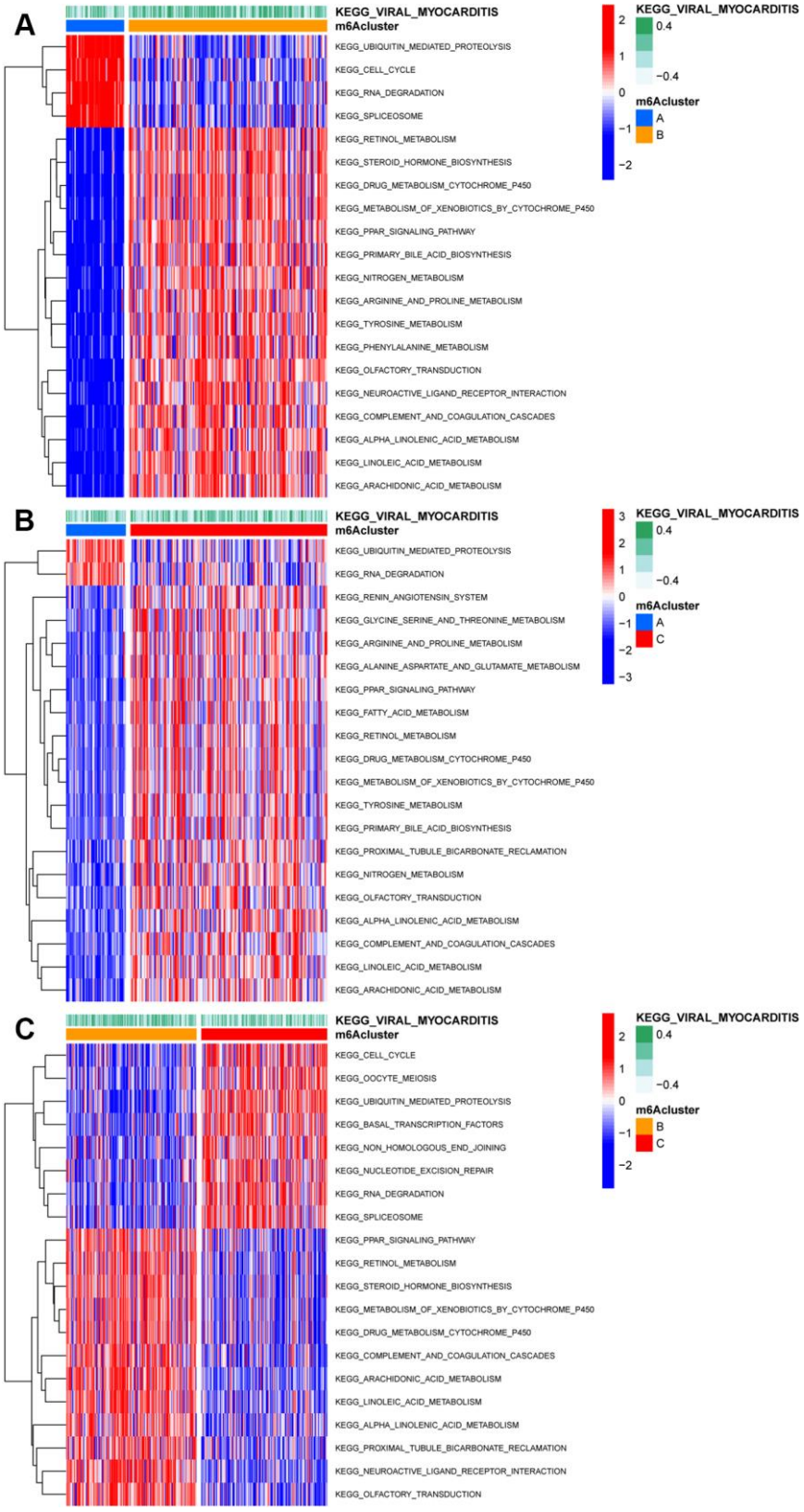
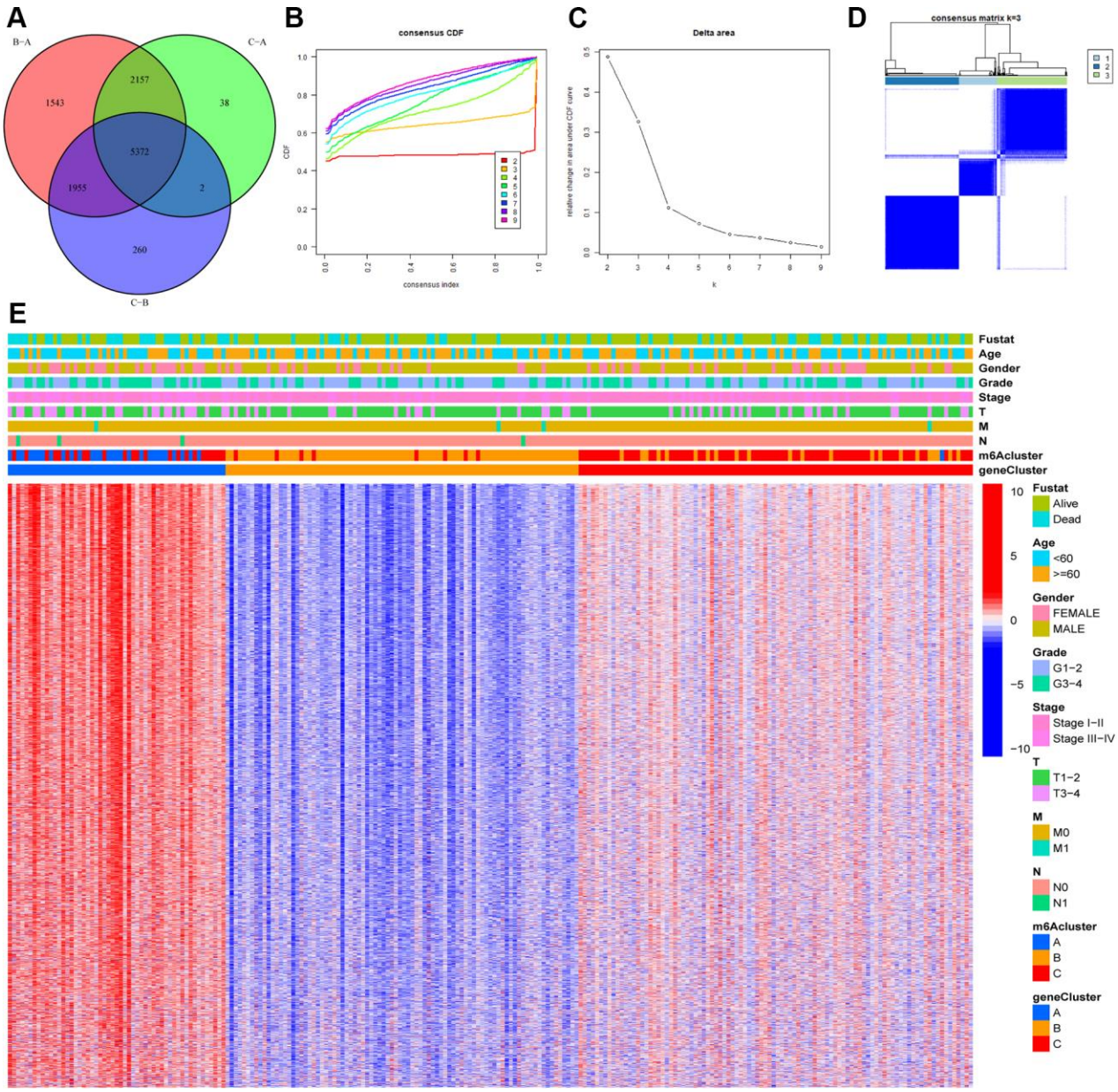
## SUPPLEMENTARY FIGURES



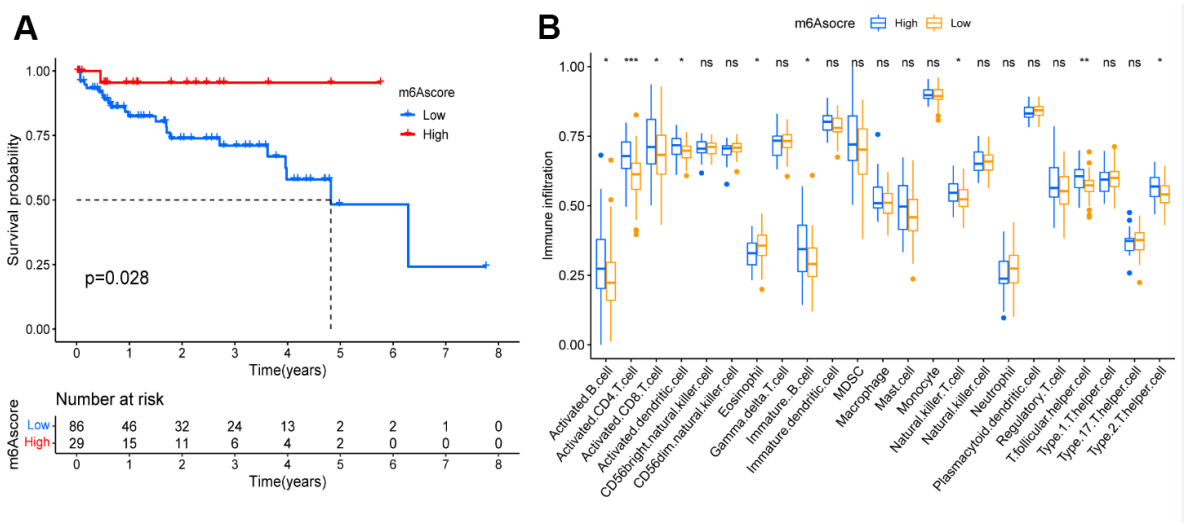

**Supplementary Figure 1. Consensus clustering of m6A regulators.** (**A**) Consensus among clusters with number k of each category. (**B**) Delta area curves for consistent clustering, representing the relative change in area under the cumulative distribution function (CDF) curve for each category number k versus k-1. The horizontal axis represents the number of categories k and the vertical axis represents the relative change in area under the CDF curve. (**C**) The consistency clustering was applied to obtain a colored heat map of the consistency matrix corresponding to k=3. The color gradient indicates the consistency values between 0 and 1, with white representing 0 and dark blue representing 1. (**D**) A heatmap annotated with survival status (Fustat), age, gender, Stage, Grade, TNM staging and m6A methylation modification patterns (m6Acluster).



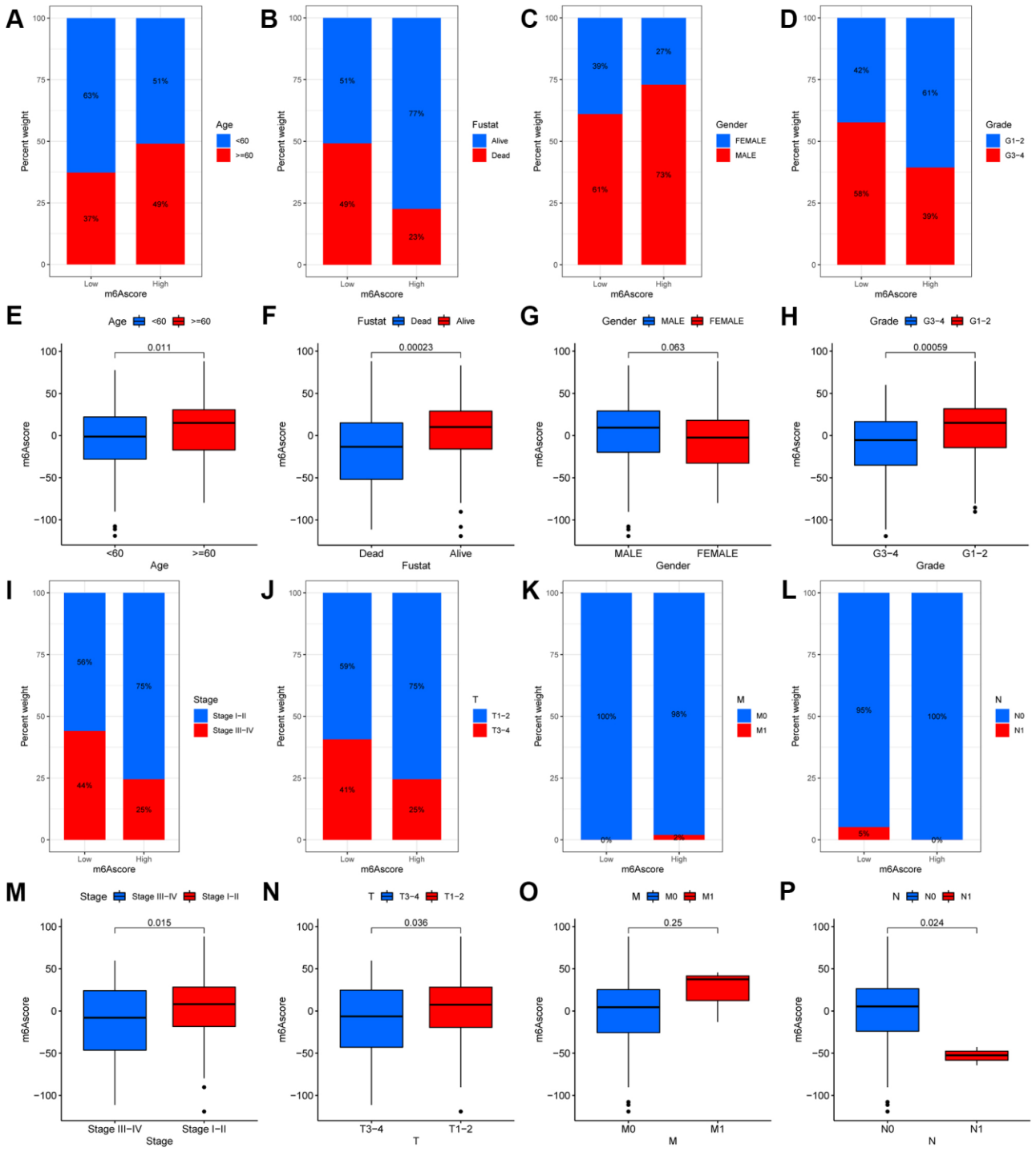

**Supplementary Figure 2. Biological pathway of m6A methylation modification pattern.** In the heatmap, red represents the activated pathway and blue represents the inhibited pathway. (**A**) m6Acluster A and m6Acluster B. (**B**) m6Acluster A and m6Acluster C. (**C**) m6Acluster B and m6Acluster C.



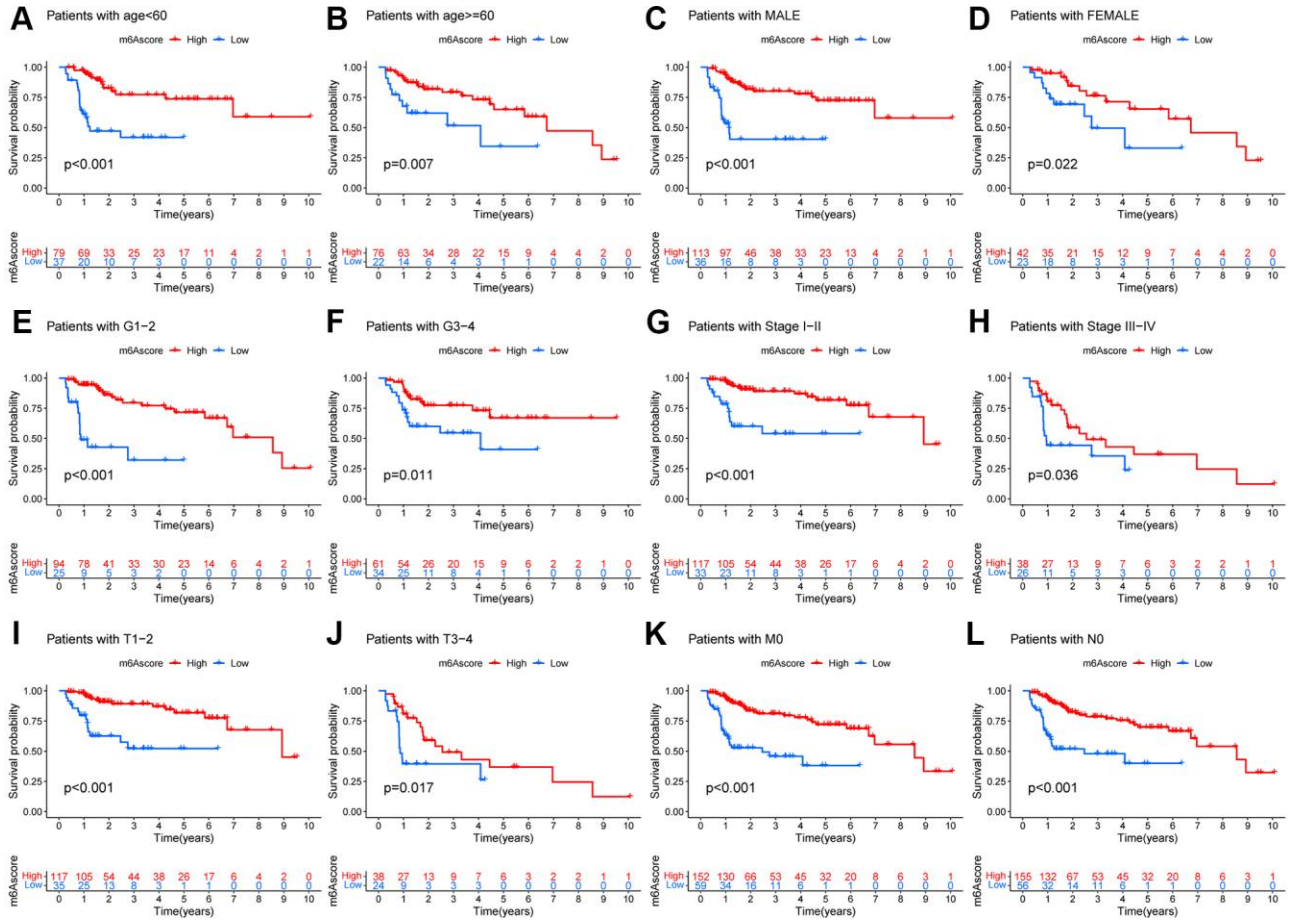

**Supplementary Figure 3. Consensus clustering of differentially expressed genes (DEGs) for the m6A modification patterns.** (**A**) 5372 m6A modification patterns related genes shown in Venn diagram. (**B**) Consensus among clusters with number k of each category. (**C**) Delta area curves for consistent clustering, representing the relative change in area under the cumulative distribution function (CDF) curve for each category number k versus k-1. The horizontal axis represents the number of categories k and the vertical axis represents the relative change in area under the CDF curve. (**D**) The consistency clustering was applied to obtain a colored heat map of the consistency matrix corresponding to k=3. The color gradient indicates the consistency values between 0 and 1, with white representing 0 and dark blue representing 1. (**E**) A heatmap annotated with survival status (Fustat), age, gender, Stage, Grade, TNM staging, m6A methylation modification patterns (m6Acluster) and m6A modification genomic phenotypes (geneCluster).




**Supplementary Figure 4. Validation of the m6A-scoring signature in the GSE76427 cohort.** (**A**) The overall survival of m6A-scoring signature using Kaplan–Meier in Log-rank test. (**B**) Differences in immune cell infiltration of m6A-scoring signature (*, P < 0.05; **, P < 0.01; ***, P < 0.001; ns, no significant).




**Supplementary Figure 5. Clinical correlation analysis of the m6A-scoring signature with distinct clinical subgroups.** The percent weight of patients with distinct clinical subgroups in low or high m6A score groups (including patients with Age (**A**), survival status (Fustat) (**B**), Gender (**C**), Grade (**D**), Stage (**I**), T staging (**J**), M staging (**K**), N staging (**L**)). Differences in m6A-scoring signature among Age (**E**), Fustat (**F**), Gender (**G**), Grade (**H**), Stage (**M**), T staging (**N**), M staging (**O**), N staging (**P**), of which Age, Fustat, Grade, Stage, T staging, N staging were statistically significant.




**Supplementary Figure 6. The prognostic value of the m6A-scoring signature with distinct clinical subgroups using Kaplan–Meier in Log-rank test.** The patients with Age<60 (**A**), Age >60 (**B**), Male (**C**), Female (**D**), G1-2 (**E**), G3-4 (**F**), Stage I+II (**G**), Stage III+IV (**H**), T1+2 (**I**), T3+4 (**J**), M0 (**K**), N0 (**L**) were statistically significant, and the survival of patients in the high m6A score group is better than that in the low m6A score group.