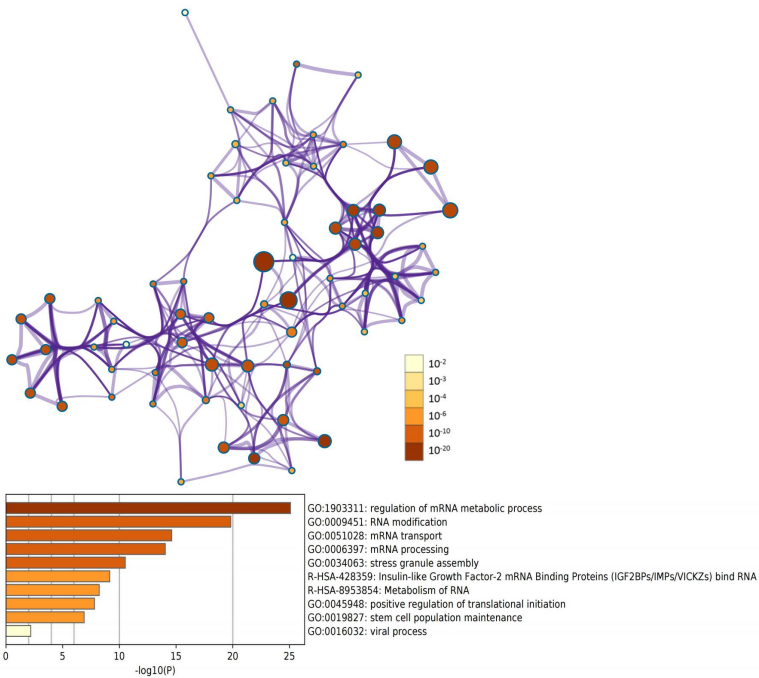
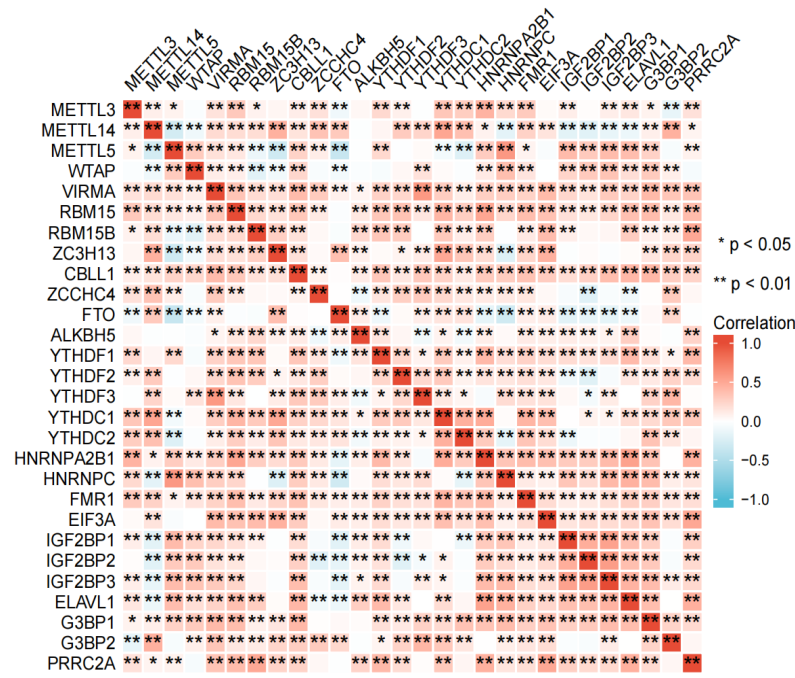
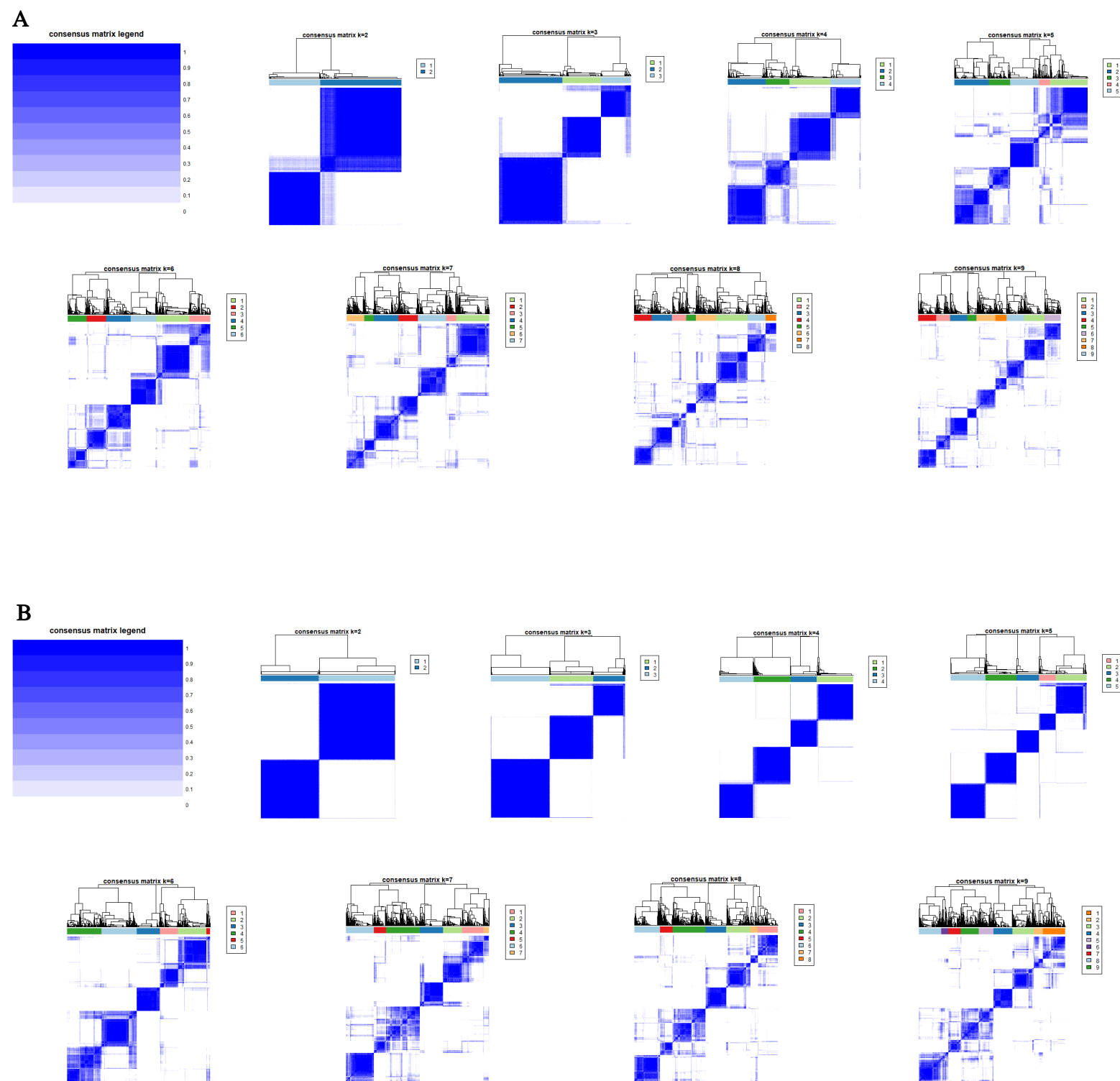
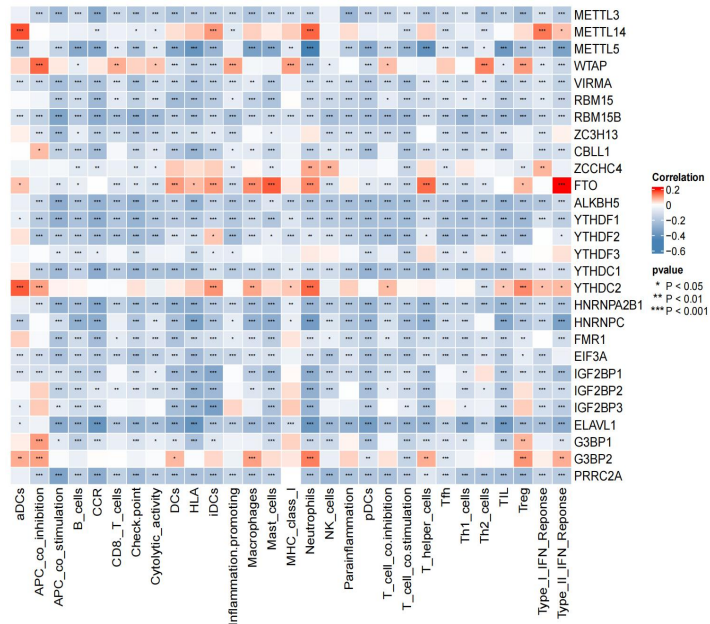
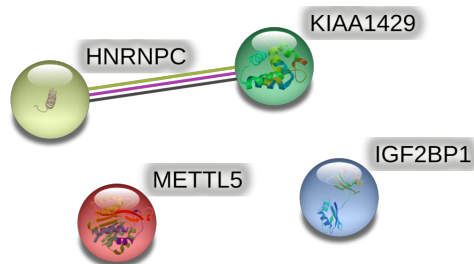
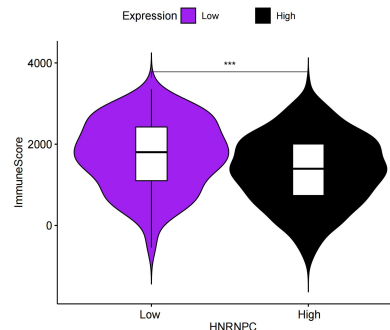
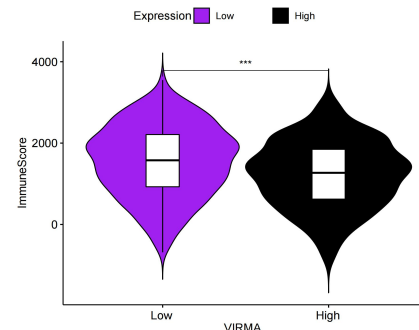


A**B**

Supplementary figure 1. Functional enrichment and co-expression analysis of 28 m6A regulators in NSCLC. **(A)** Biological functional enrichment of 28 m6A regulators by metascape enrichment. The darker the strip color, the more significant the enrichment. **(B)** Co-expression relationships among 28 m6A regulators in the TCGA dataset in NSCLC. Blue indicates positive correlation, red indicates negative correlation, and the size of the semicircle area indicates the degree of correlation. *: p value < 0.05; **: p value < 0.01.



Supplementary figure 2. Results of unsupervised clustering. **(A)** Unsupervised clustering results for 28 m6A moderators. **(B)** Unsupervised clustering results of co-DGEs in three m6A modification patterns.

A**B****C****D****E**

Supplementary figure 3. Distribution of immune cells and immune functions in three m6A modification patterns and analysis of the immunomodulatory role of *VIRMA* and *HNRNPC* in NSCLC. **(A)** Heatmap of ESTIMATE scoring and immune cell and function in three m6A modification patterns. The yellow colour in the heatmap represents samples with high expression and the purple colour represents samples with low expression. **(B)** Pearson correlation analysis of 28 m6A regulators with immune cells and function. **(C)** *METTL5*, *HNRNPC*, *IGF2BP1* and *VIRMA* protein interactions analysis network. Interaction score > 0.70 was considered as a correlation between the two proteins. Immunoscore of *HNRNPC* **(D)** and *VIRMA* **(E)** in high and low expression groups in NSCLC. *: p value < 0.05; **: p value < 0.01; ***: p value < 0.001.