



**Figure S5: Transcriptome traits in distinct m6Ascore of validation cohorts**

(a-b) KEGG analysis of differentially expressed genes (DEG) presented higher immune cell activation in low m6Ascore (a) and higher carcinogenic pathway in high m6Ascore (b) in GSE22153. (c-d) KEGG analysis of differentially expressed genes (DEG) presented higher inflammatory activation in low m6Ascore (c) and higher carcinogenic pathway in high m6Ascore (d) in GSE54467. (e-f) KEGG analysis of differentially expressed genes (DEG) presented higher immune cell activation in low m6Ascore (e) and higher active RNA modification and transcription in high m6Ascore (f) in GSE65904. (g) UMAP plot shows clustering based on aggregated gene expression profiles of T cells. A total of 20 groups were automatically clustered. Different clusters of cells are shown in different colors. (h) The expression of canonical marker genes in different clusters of T cells.