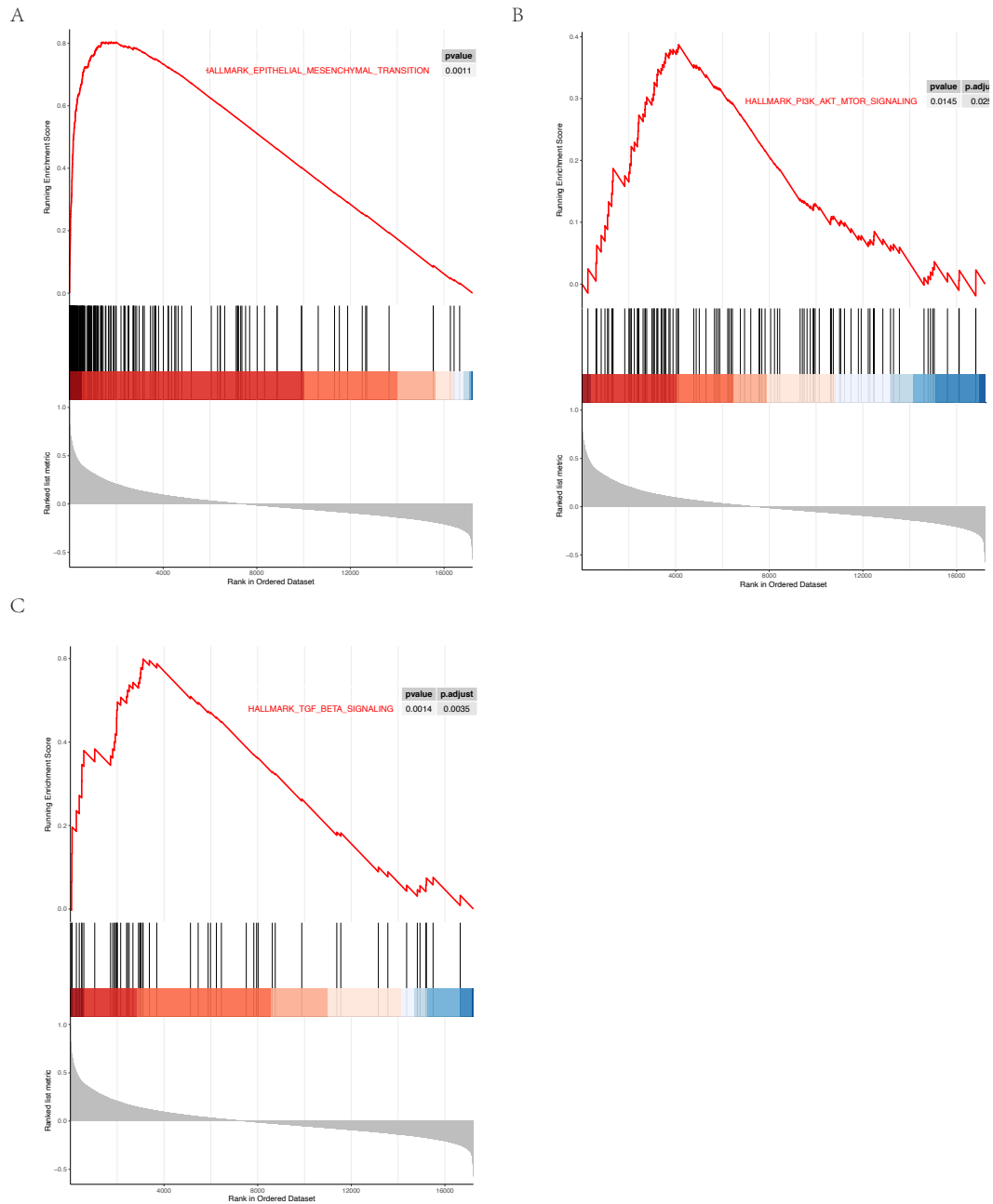


Supplementary Figure 1. Gene lists were sorted by correlation and ranked Gene Set Enrichment Analysis (GSEA) was performed. A. GSEA enrichment analysis shows that EPYC-related genes positively activate the EMT pathway; B. GSEA enrichment analysis shows that EPYC-related genes are significantly enriched in the PI3K/AKT signaling pathway and positively activate the pathway; C. GSEA enrichment Set analysis showed that EPYC-related genes were significantly enriched in the TGF- β signaling pathway and positively activated the pathway.



Supplementary Figure 2. EPYC has a strong correlation with TGF β signaling pathway molecules and SNAI2 expression. A. The Pearson correlation coefficient between EPYC and TGFBI is 0.389, $p < 0.001$; B. The Pearson correlation coefficient between EPYC and TGFBI is 0.506, $p < 0.001$; C. The Pearson correlation coefficient between EPYC and TGFBI3 is 0.445, $p < 0.001$; D. Pearson correlation coefficient between EPYC and TGFBR1 is 0.332, $p < 0.001$; E. Pearson correlation coefficient between EPYC and TGFBR2 is 0.391, $p < 0.001$; F. Pearson correlation coefficient between EPYC and TGFBR3 is -0.214, $p < 0.001$; G. The Pearson correlation coefficient between EPYC and SNAI2 is 0.607, $p < 0.001$.

