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 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 TGFβ signaling pathway molecules and SNAI2 expression. A. The Pearson correlation coefficient between EPYC and TGFB1 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 TGFB3 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.