

Figure S1. Single cell sequencing analysis of TAGLN expression in different tissues. The experimental data downloaded from The Human Protein Atlas database (<https://www.proteinatlas.org>). The results of single cell sequencing showed the expression level of TAGLN in various tissue structures and cell types of esophageal. TAGLN, transgelin; nTPM, normalized transcripts per million; UMAP, uniform manifold approximation and projection.

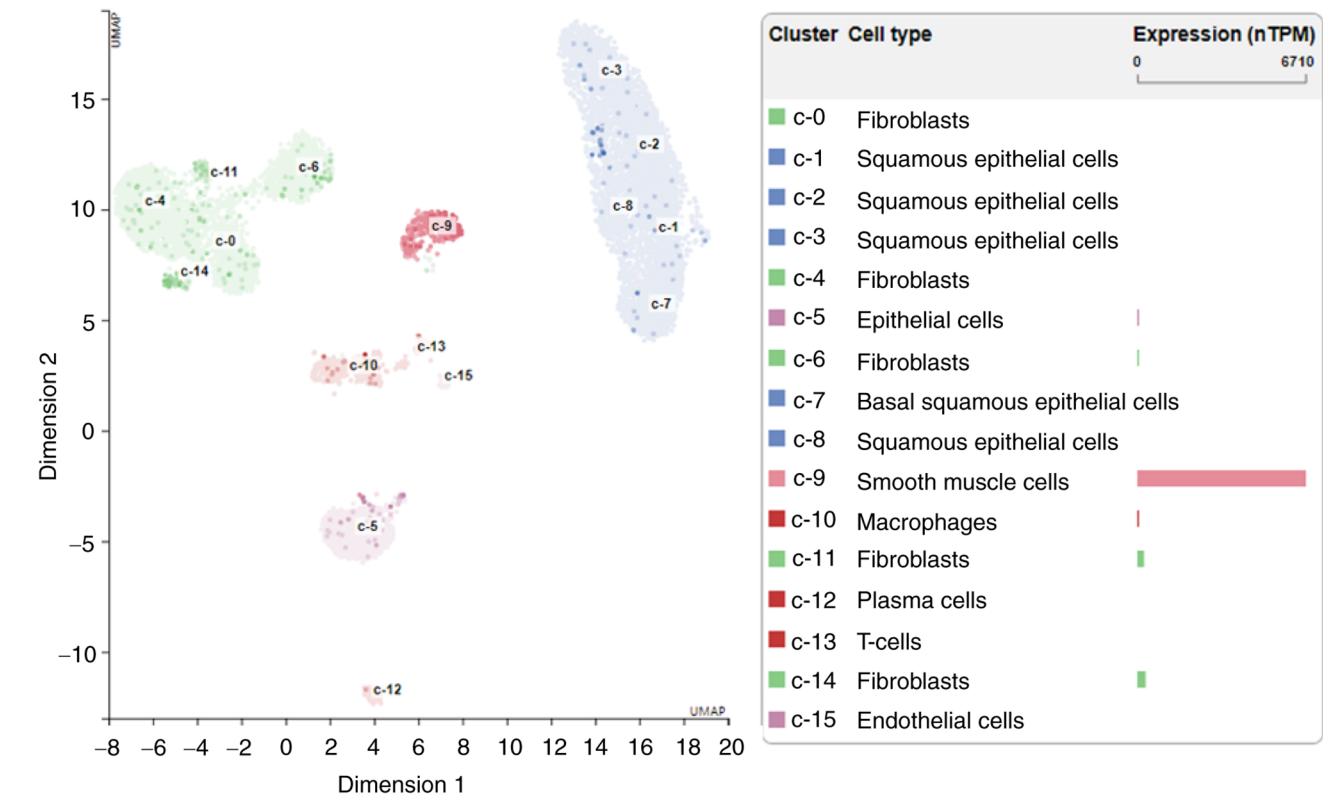


Figure S2. Wound healing assay of TAGLN overexpressing cells. A wound healing assay used to examine the effects TAGLN overexpression in Eca-109 and KYSE-150 cells and were subsequently measured at 0, 12, 24 and 36 h to assess the degree of cell migration ability. NC, negative control; TAGLN, transgelin.

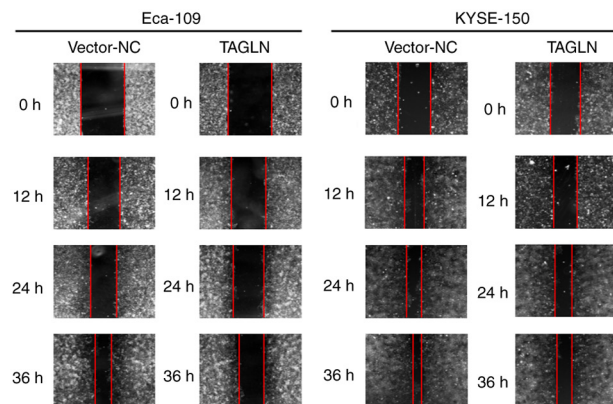


Figure S3. Sequencing analysis results of esophageal carcinoma cells in control group and TAGLN overexpression group. (A) Violin expression profile analysis of sequencing data from three NC groups and three TAGLN overexpression groups. The results show the overall distribution of each group of data. (B) Heat map showing correlation analysis results of sequencing data in the three NC groups and the three TAGLN overexpression groups. The results showed that there were differences in gene expression between the TAGLN group and the NC group, which can be used for GO, KEGG and PPI analysis. NC, negative control; TAGLN, transgelin.

