

Figure S1. miR-155 is associated with poor prognosis. TCGA datasets revealed that patients with ESCC with low expression of miR-155 exhibited superior overall survival compared with patients with high expression of miR-155 (P=0.0096).

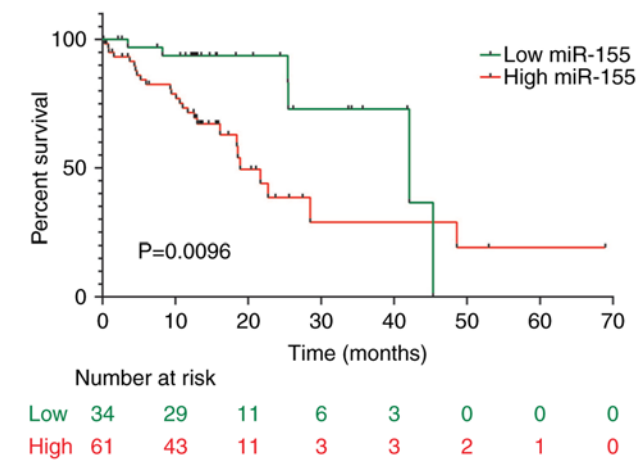


Figure S2. MAP3K10 effect on the migration, invasion and proliferation of ESCC cells. (A and B) The wound healing assay of ESCC cells treated with si-MAP3K10 or GFP-tagged MAP3K10 was measured at 0 and 22 h. The relative migration rate was then calculated and plotted. (C and D) The cell invasion activity was determined via Boyden chamber Transwell assay. The mean  $\pm$  standard deviation of five randomly selected fields were determined and plotted. (E) The proliferation of the cells was evaluated by CCK-8 following transfection with the indicated siRNA and overexpression constructs on 24, 48, 72 and 96 h, respectively. ESCC, esophageal squamous cell carcinoma; CCK-8; Cell Counting Kit-8. \* $P < 0.05$ .

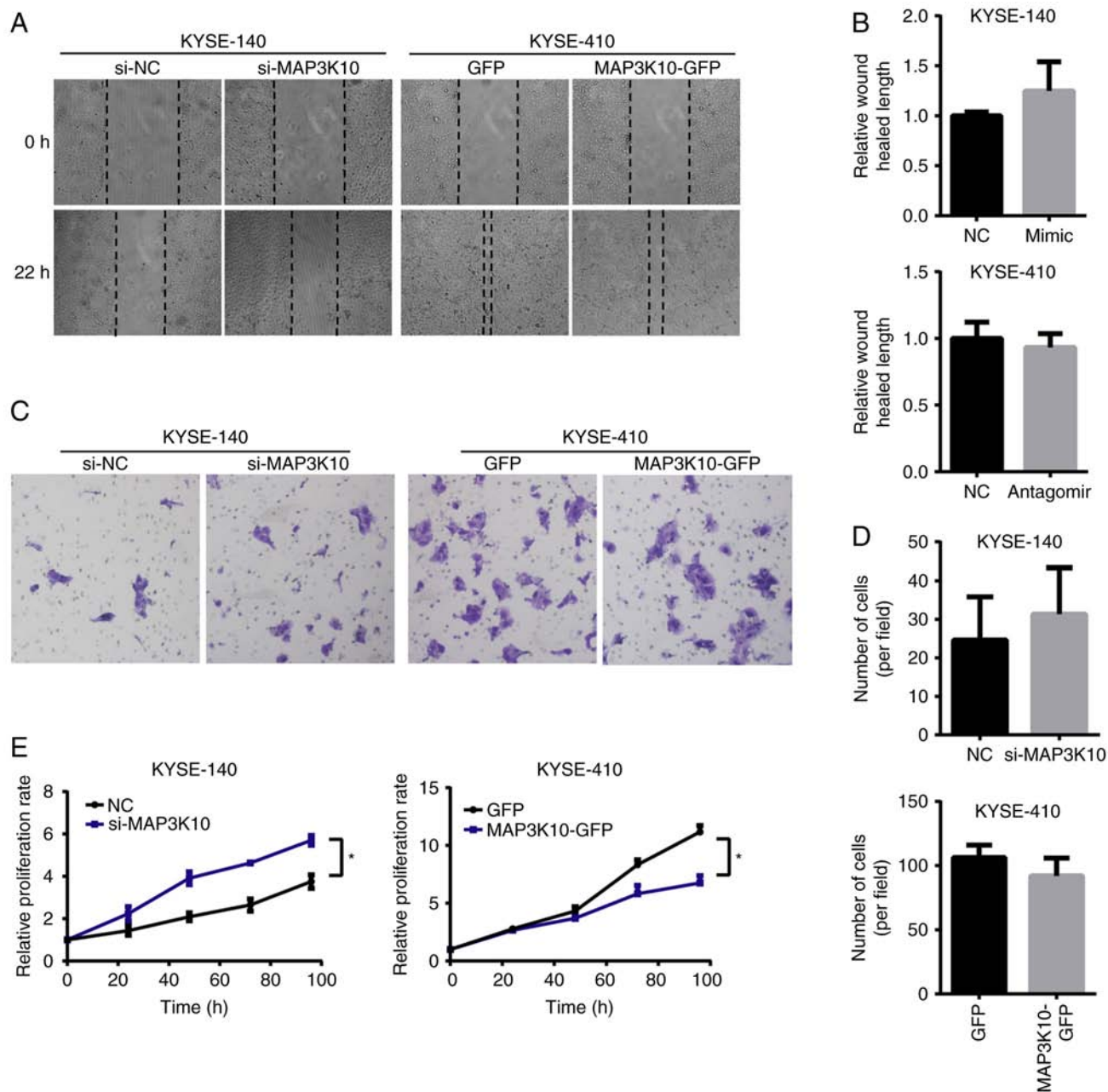


Figure S3. Expression of MAP3K10 in esophageal cancer. A mRNA expression analysis through the Oncomine database and gene microarray data analysis indicated that (A) MAP3K10 was slightly downregulated in esophageal squamous cell carcinoma samples compared with the paired normal tissue adjacent to the tumor ( $P=0.991$ ). (B) MAP3K10 was significantly upregulated in esophageal adenocarcinoma tissues than in adjacent non-tumor tissues.  $**P<0.001$ . ESCC, esophageal squamous cell carcinoma; EAC, esophageal adenocarcinoma.

