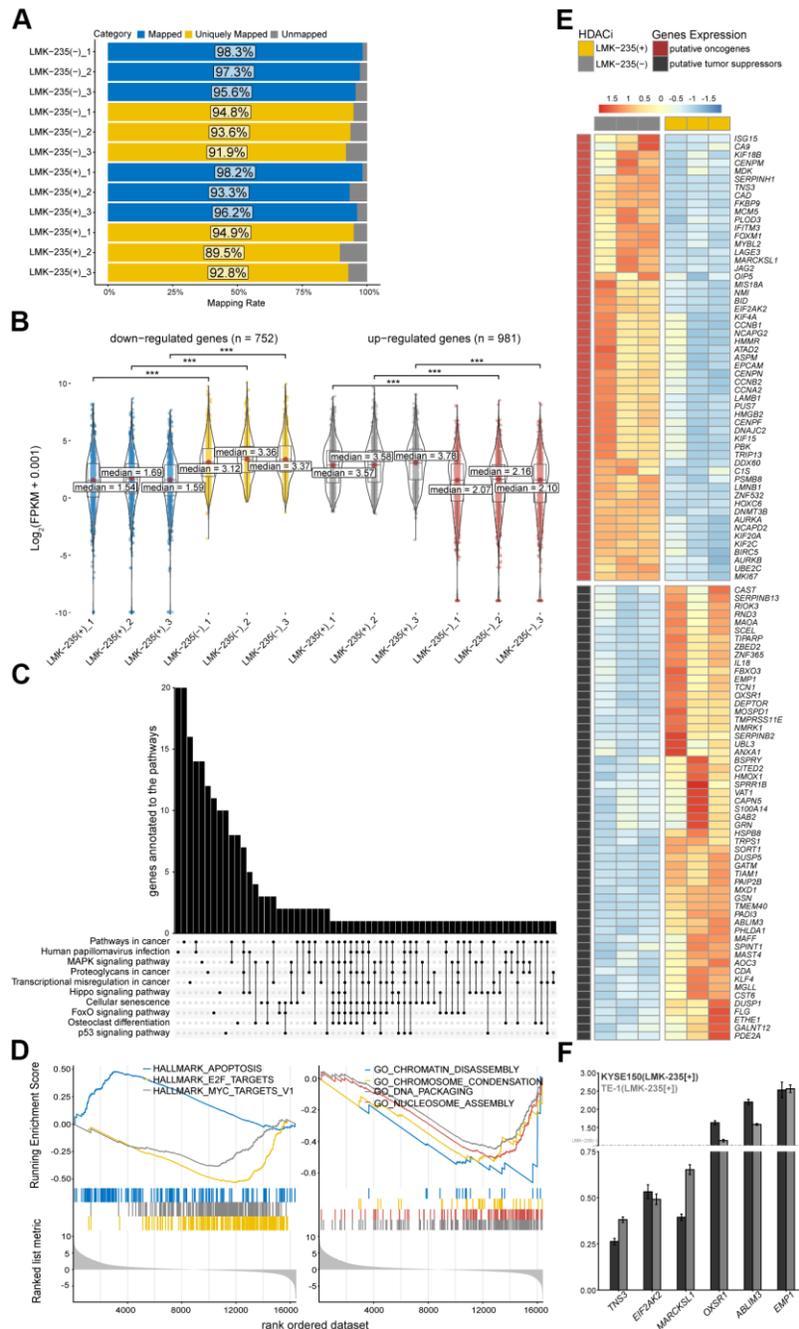
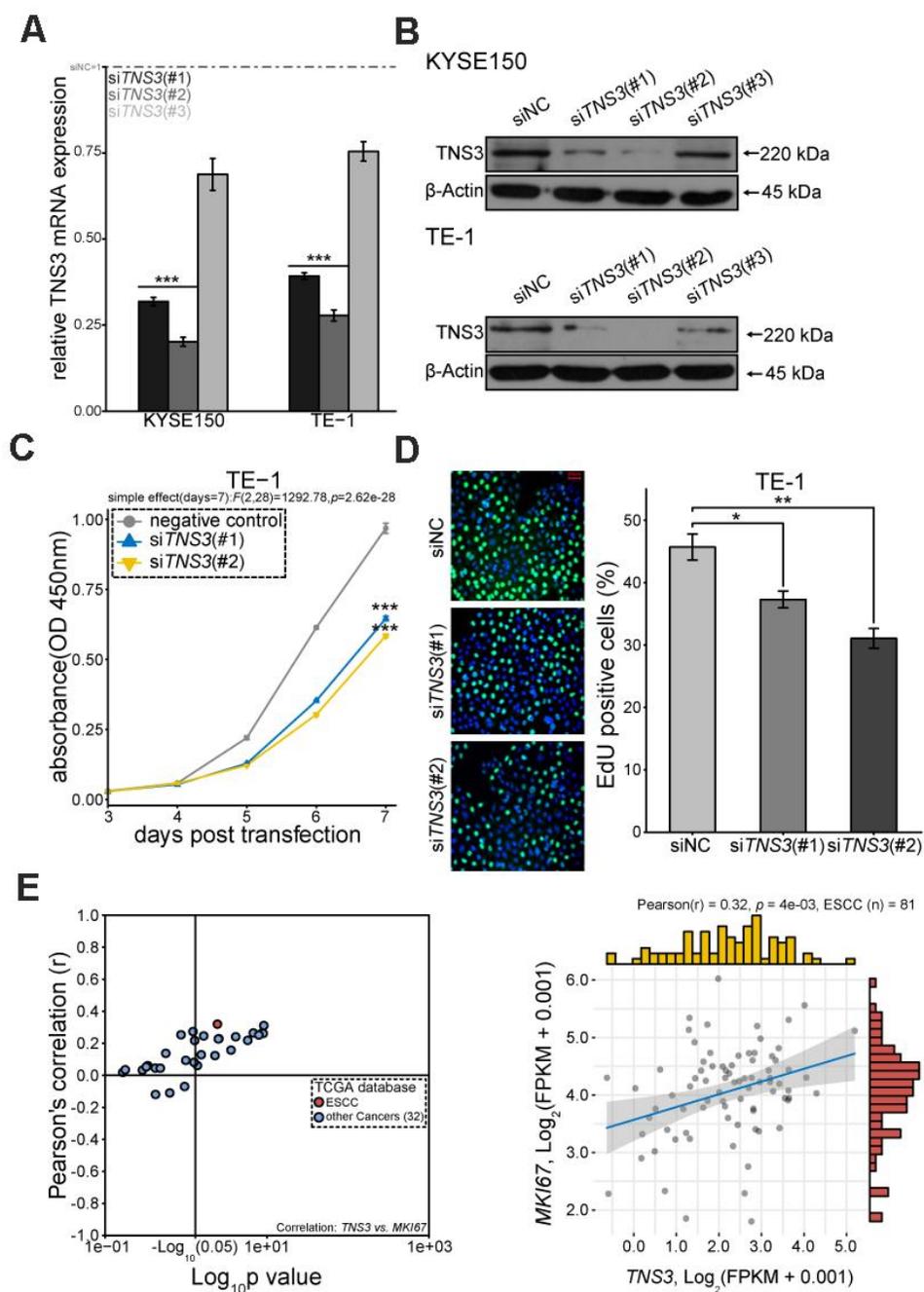


SUPPLEMENTARY FIGURES



Supplementary Figure 1. The transcriptome of KYSE150 is regulated by LMK-235. (A) Mapping rate of RNA-seq. **(B)** Log₂(FPKM + 0.001) of genes distinctly regulated by LMK-235, including 752 down-regulated and 981 up-regulated genes. The significant criteria are set as FDR < 0.05 and Log₂|FC| > 1. **(C)** Top 10 KEGG pathways impacted by the treatment of LMK-235. **(D)** GSEA presents groups of genes regulated by LMK-235. The representative gene sets are displayed: Hallmark gene sets, left; Ontology gene sets, right. **(E)** Heatmaps of the genes (shown in Figure 2A), which are represented as transformed Z score of FPKM shown in each row. Labels are shown as the panels. **(F)** qRT-PCR analysis of the six growth-related genes in KYSE150 and TE-1 treated with LMK-235. Data are relative to vehicle control and normalized to *GAPDH*. Error bar denotes SEM of three replicates.



Supplementary Figure 2. *TNS3* serves as pro-proliferation factor in ESCC. (A) qRT-PCR analyses of *TNS3* expression in KYSE150 (left) and TE-1 (right) cells transfected with si*TNS3* (#1, #2, #3) and siNC for 48 hr. Data are relative to the negative control (siNC) and normalized to *GAPDH*. (B) *TNS3* immunoblots of WCE from KYSE150 (upper) and TE-1 (bottom) transfected as (A). β -actin is used as a loading control. (C) Proliferation curves of TE-1 transfected with si*TNS3* (#1, #2) and siNC for 48 hr. (D) EdU incorporation assay of TE-1 transfected as (C). Scale bar = 50 μ m. (E) Correlations between *TNS3* and *MKI67* in cancers based on TCGA database. (A, C, D). Error bar denotes SEM of three replicates.