Supplementary Materials

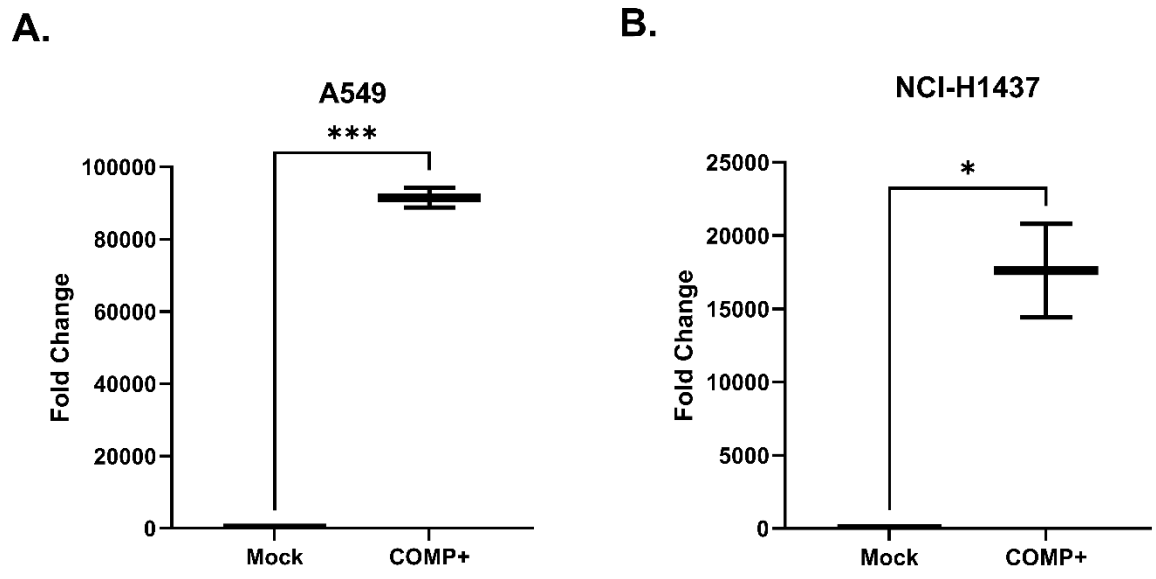


Figure S1. Q-PCR analysis of COMP mRNA expression in COMP-overexpressed and mock-transduced NSCLC cells. (A) COMP mRNA expression of mock-transduced and COMP-transduced A549 cells. (B) COMP mRNA expression of mock-transduced and COMP-transduced NCI-H1437 cells. Statistical analysis done by unpaired t-test. Error bars represent Min and Max (*$p<0.05$, ***$p<0.001$).

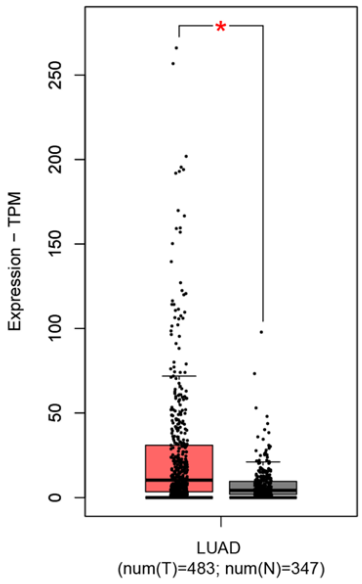


Figure S2. TCGA database analysis for COMP expression in lung adenocarcinoma. (A) RNA-seq data from the TCGA shows COMP expression is higher in lung adenocarcinoma (LUAD) tumor (T) tissue (n=483) compared to normal lung (N) tissue (n=347) (*p<0.05). Figure made using the GEPIA2 online tool [24].