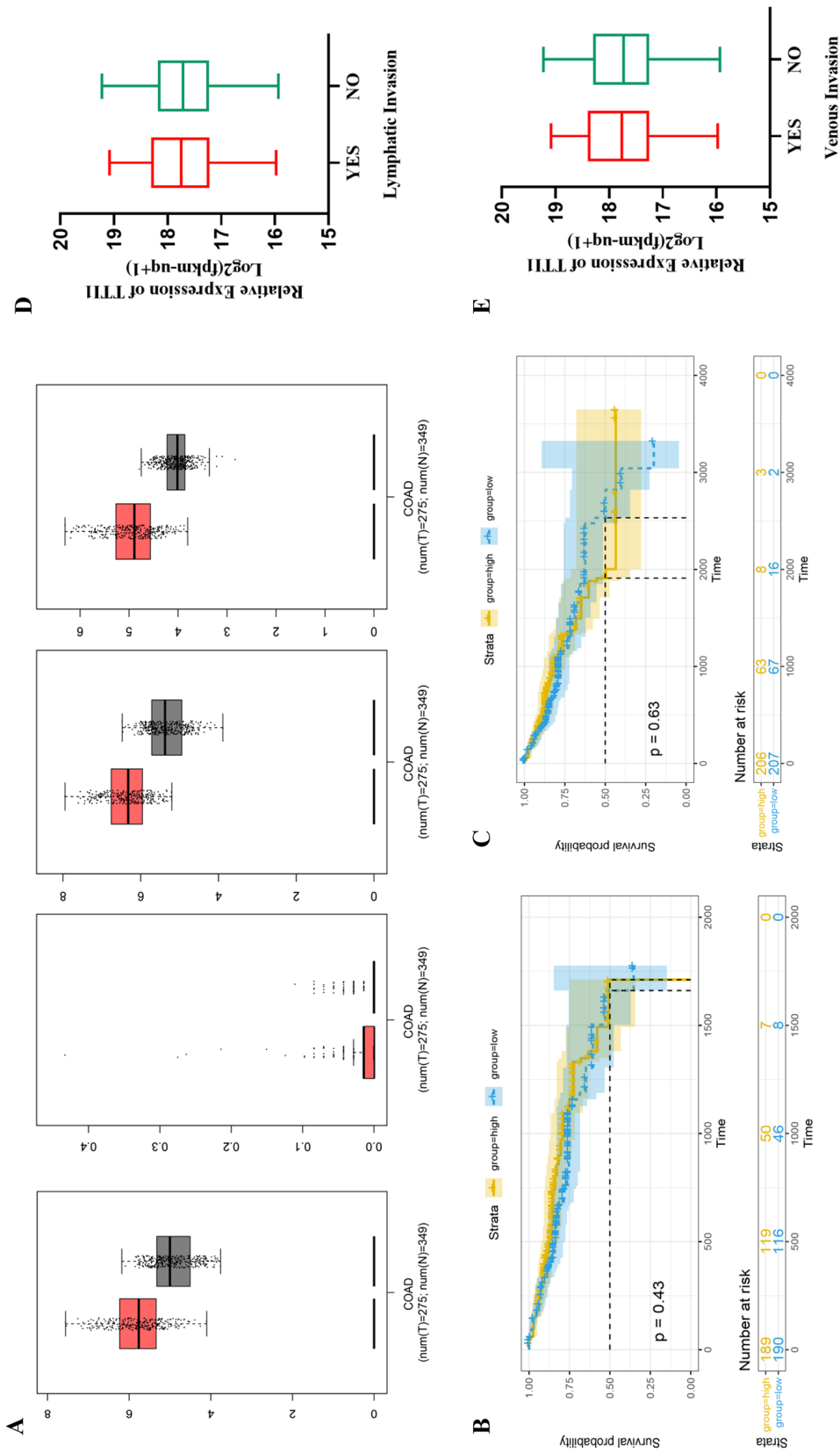


**Figure S1** GO analysis of DEGs and construction of WCGNA in R. (A) Top 20 GO analysis of up-regulated DEGs. (B) Top 20 GO analysis of down-regulated DEGs. (C) sample clustering of normal mucosa. (D) Scale-free fit index and the mean connectivity analysis for soft-thresholding power of normal samples. (E) The scale-free fit index and the mean connectivity analysis for soft-thresholding power of tumor samples. GO, Gene Ontology; DEG, differentially expressed gene; WCGNA, weighted gene co-expression network analysis.



**Figure S2** Expression of hub genes and clinical traits of TTH1. (A) The mRNA level of STAU, DPML1, CTNBB1 and GID8 in COAD patients from GEPIA. (B) Five-year survival curve of CRC patients. (C) Ten-year survival curve of CRC patients. (D) Correlation between TTH1 and lymphatic invasion ( $P>0.05$ ). (E) Correlation between TTH1 and venous invasion ( $P>0.05$ ). COAD, colon adenocarcinoma; GEPIA, Gene Expression Profiling Interactive Analysis; CRC, colorectal cancer.