Supplementary

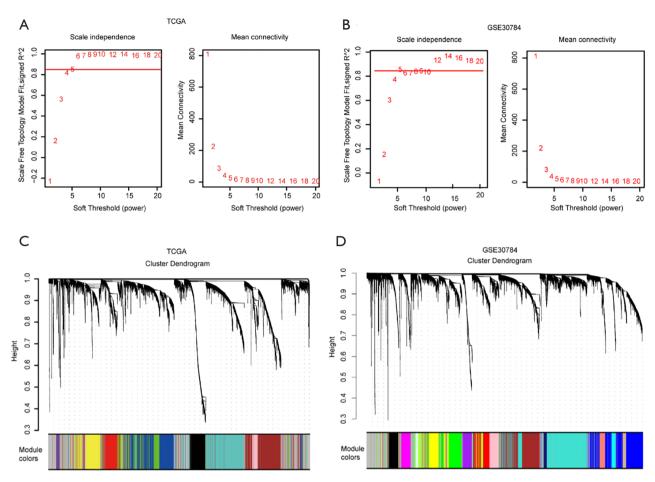


Figure S1 Construction of the weighted gene co-expression network in TCGA-OSCC dataset and GSE30784 dataset. (A,B) Analysis of the scale free fit index and the mean connectivity for various soft threshold power. (C,D) Hierarchical clustering tree developed by gene dissimilarity based on topological overlap. TCGA, The Cancer Genome Atlas; OSCC, oral squamous cell carcinoma.