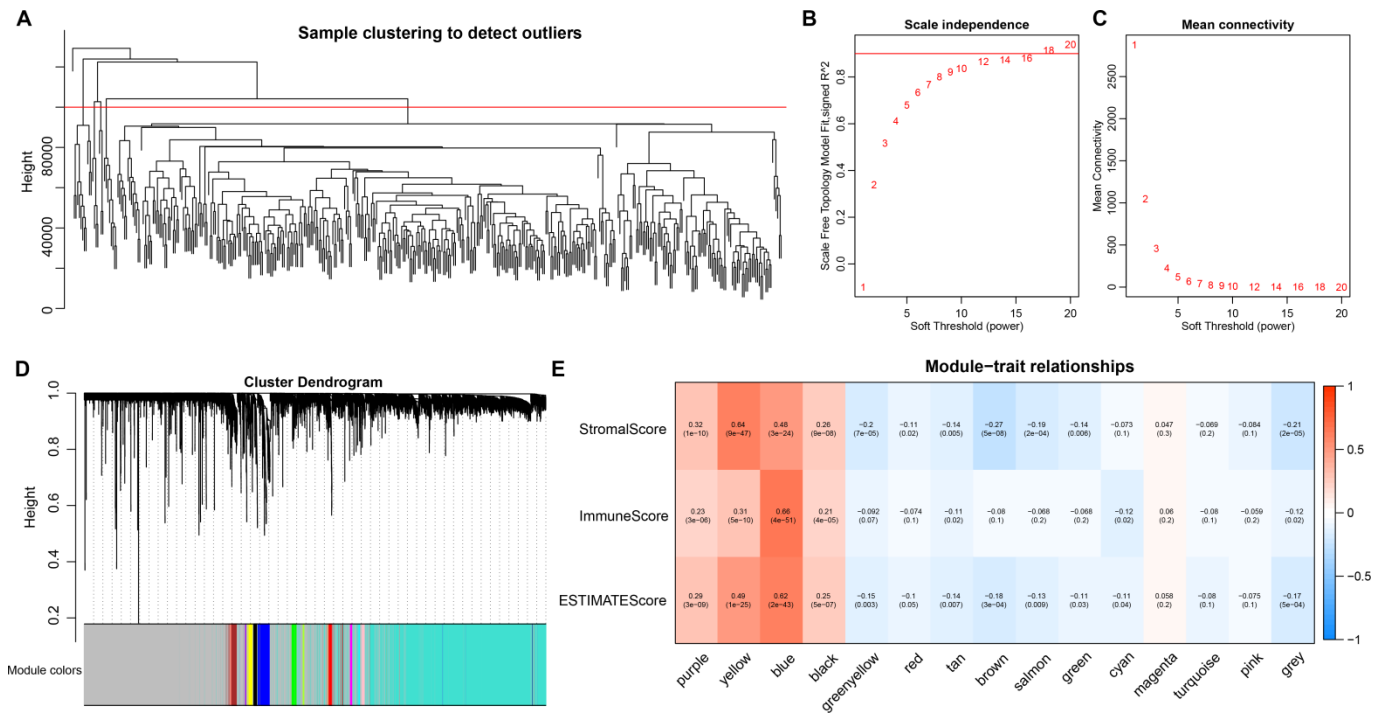


**SUPPLEMENTARY FIGURE**



**Supplementary Figure.** (A) Clustering analysis of all samples. 396 samples finally obtained after deleting outliers with height larger than 100000. (B, C) Analysis of network topology for various soft-thresholding powers to ensure it being scale-free network. (D) Results of gene dendrogram and module colors. 15 modules were obtained. (E) Module-trait relationship between the 15 modules eigenvectors and the three immune scores.