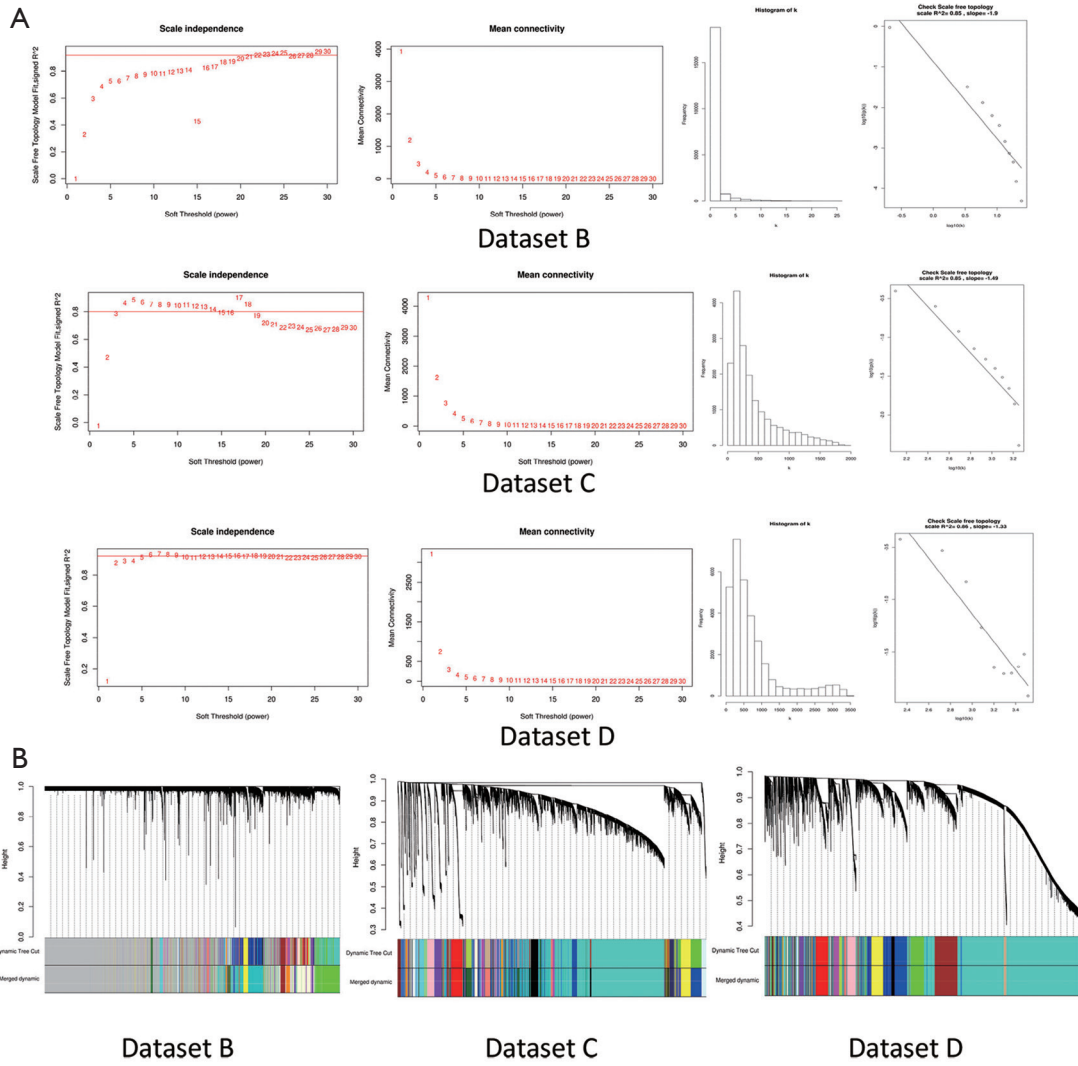
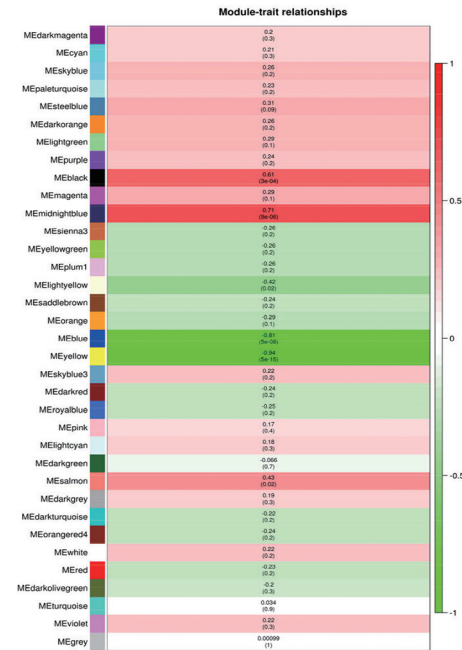
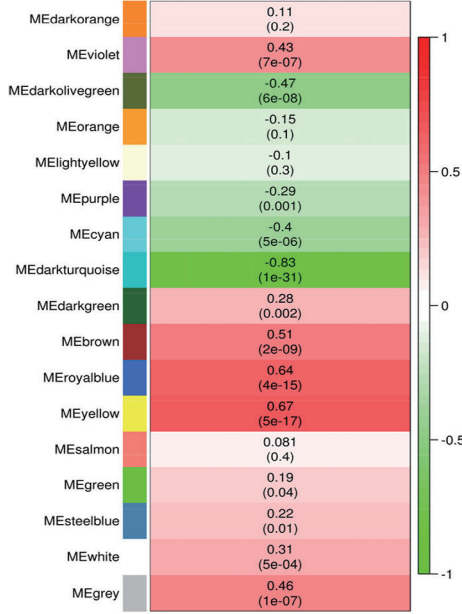


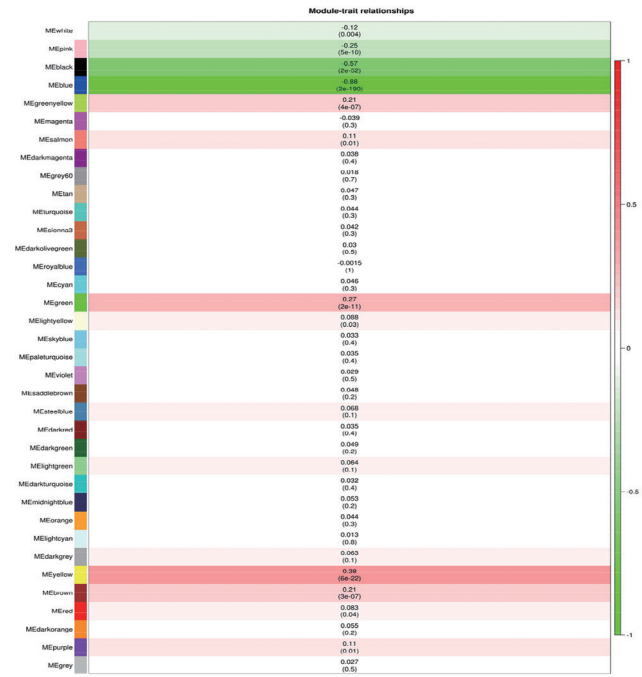
Figure S1 Survival curves of the 12-gene signature. Twelve genes were identified to have significant associations with the three-year survival of LUAD patients. LUAD, lung adenocarcinoma.



C **Module-trait relationships**



Dataset B



Dataset C

Dataset D

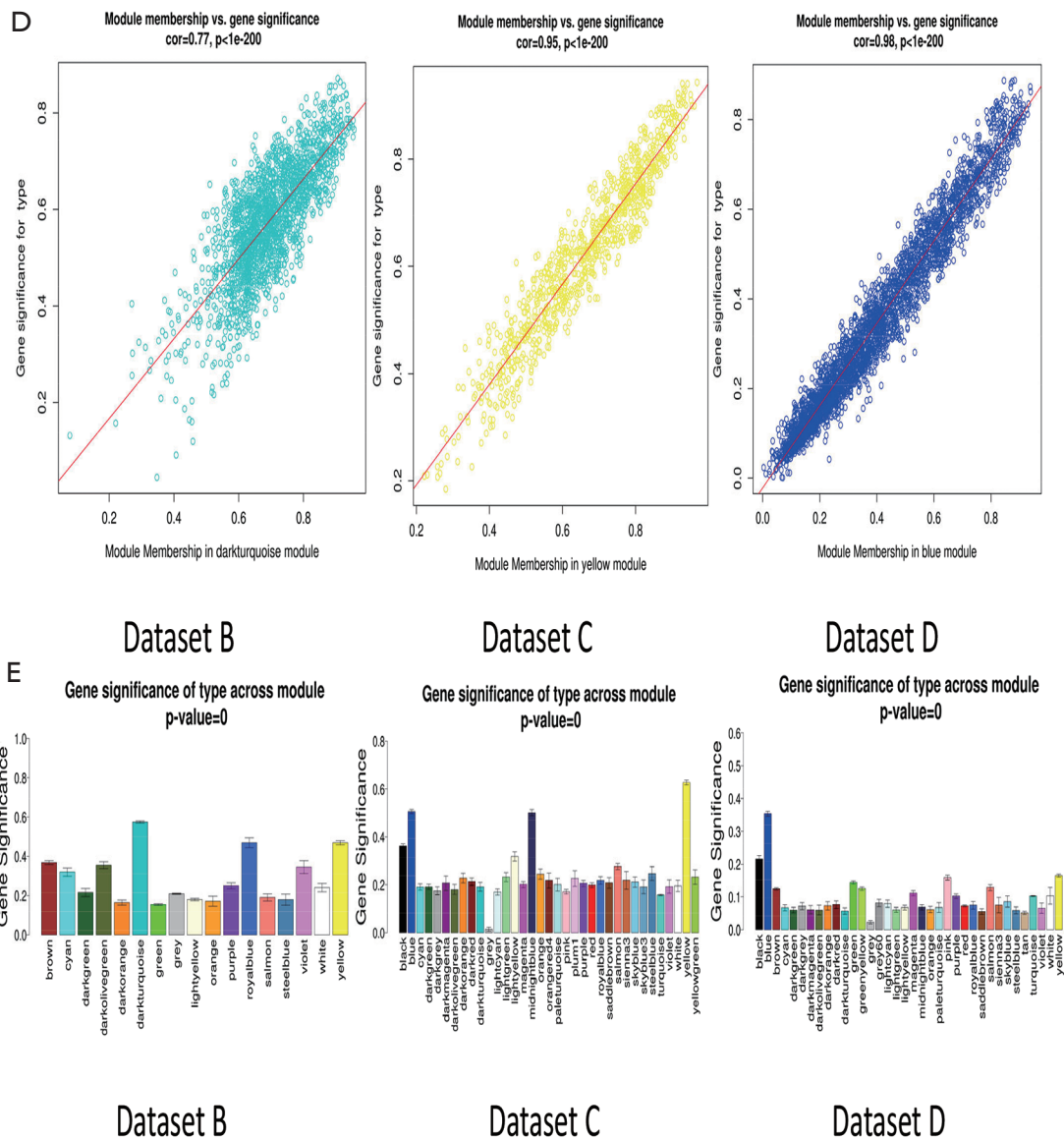


Figure S2 Coexpression network analysis by WGCNA. WGCNA results of dataset B, C and D are shown in this figure. (A) Network topology for various soft-threshold powers and the testing of the properties of the scale-free network were analyzed. (B) LUAD-specific coexpression modules were analyzed. Each short vertical line corresponds to one gene. Each branch represents one expression module of highly interconnected groups of genes. Below the dendrogram, each group of genes has been given one color, which indicates its module assignment. Gray suggests that the genes were outside all modules. (C) The associations between modules and LUAD were analyzed. (D) The associations between the most significant module membership and LUAD were analyzed. (E) The mean significance across modules was analyzed. WGCNA, weighted gene coexpression network analysis. LUAD, lung adenocarcinoma.