

Figure (S2) **Volcano plot of DEGs for dataset E-GEOD-28735** After p-value and log2FC threshold filtering 364 DEGs were identified, with 227 overexpressed and 137 underexpressed genes. The list of DEGs along with \log_2FC values is provided in Supplementary Table 1.

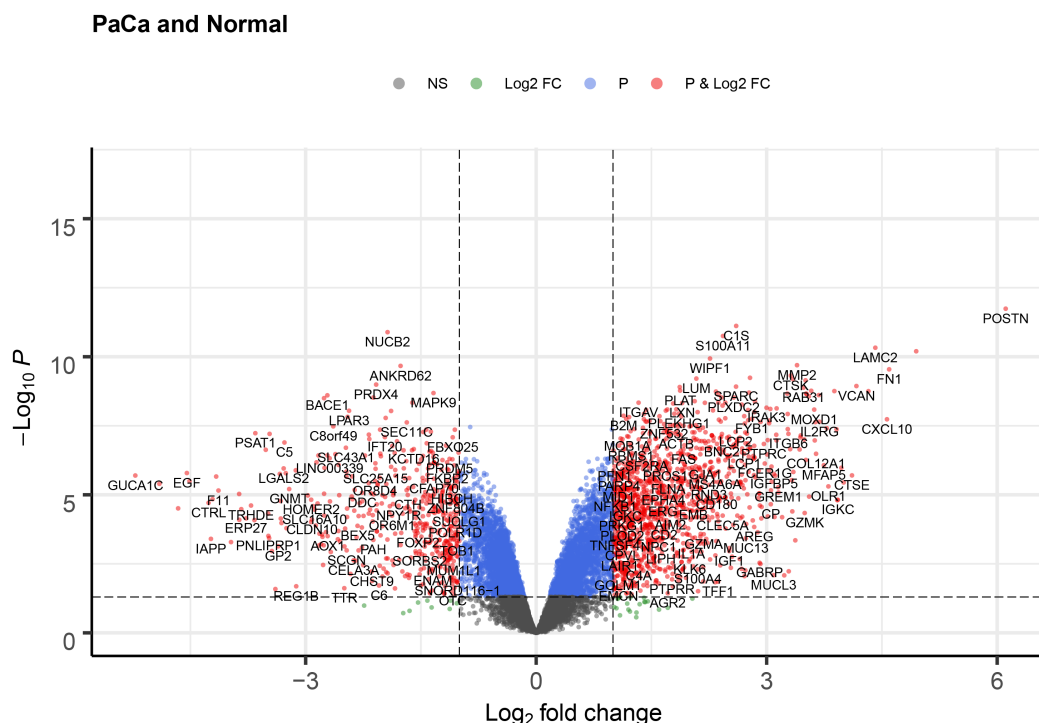


Figure (S3) **Volcano plot of DEGs for dataset E-GEOD-41368** The overall 1688 significant DEGs were retrieved, out of which 1222 overexpressed and 466 were underexpressed genes. The list of DEGs along with $\log_2 FC$ values is provided in Supplementary Table 1.



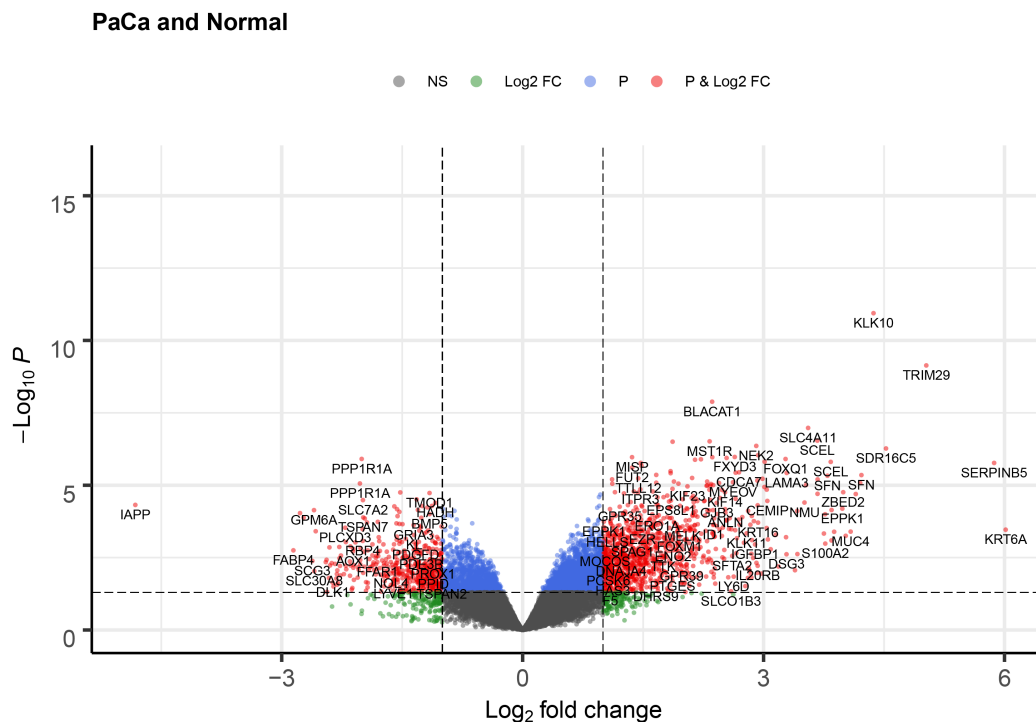


Figure (S5) Volcano plot of DEGs for dataset E-GEOD-18670 For E-GEOD-18670 total number of DEGs obtained after differential expression analysis were 1164, with 798 overexpressed and 366 under-expressed genes, The lists of DEGs with their \log_2FC values are provided in Supplementary Table 1.

PaCa and Normal

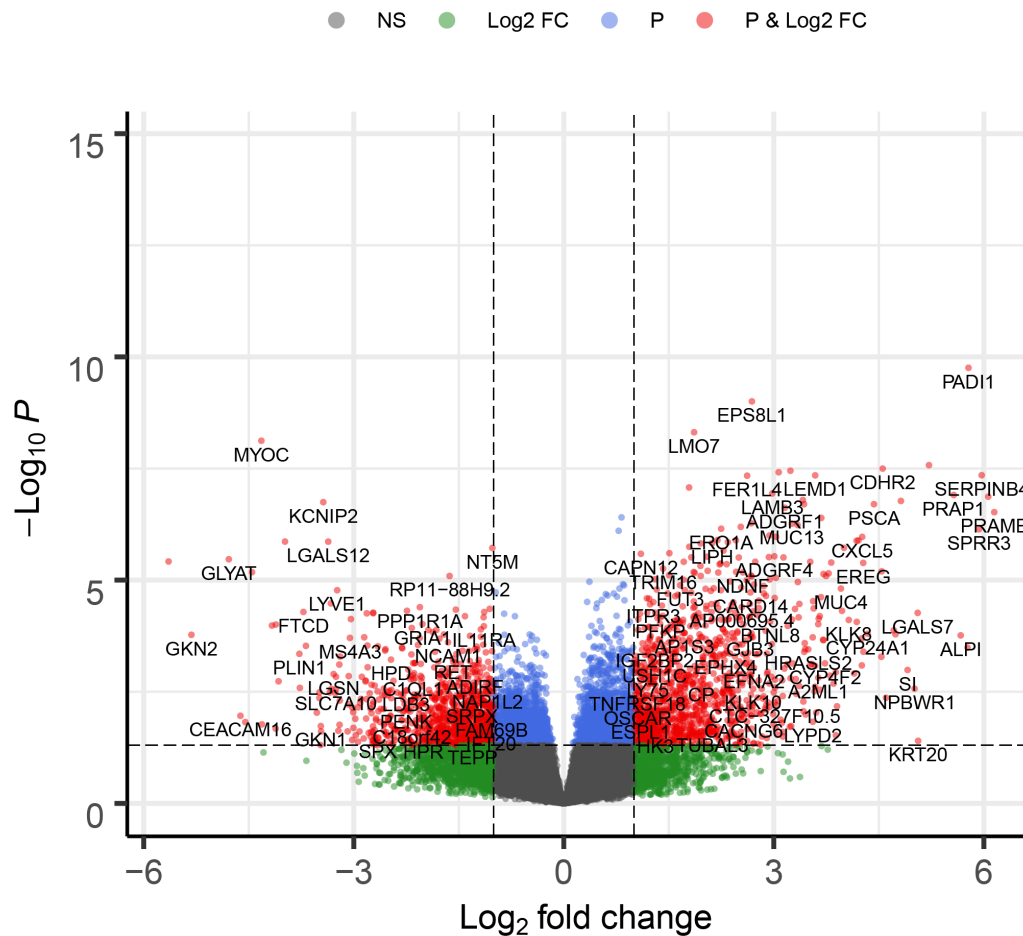


Figure (S6) **Volcano plot of DEGs for dataset GSE119794** Total of 2174 DEGs were retrieved (1194 up-regulated and 980 down-regulated). The list of DEGs with the $\log_2 FC$ values is provided in Supplementary Table 1.

PaCa and Normal

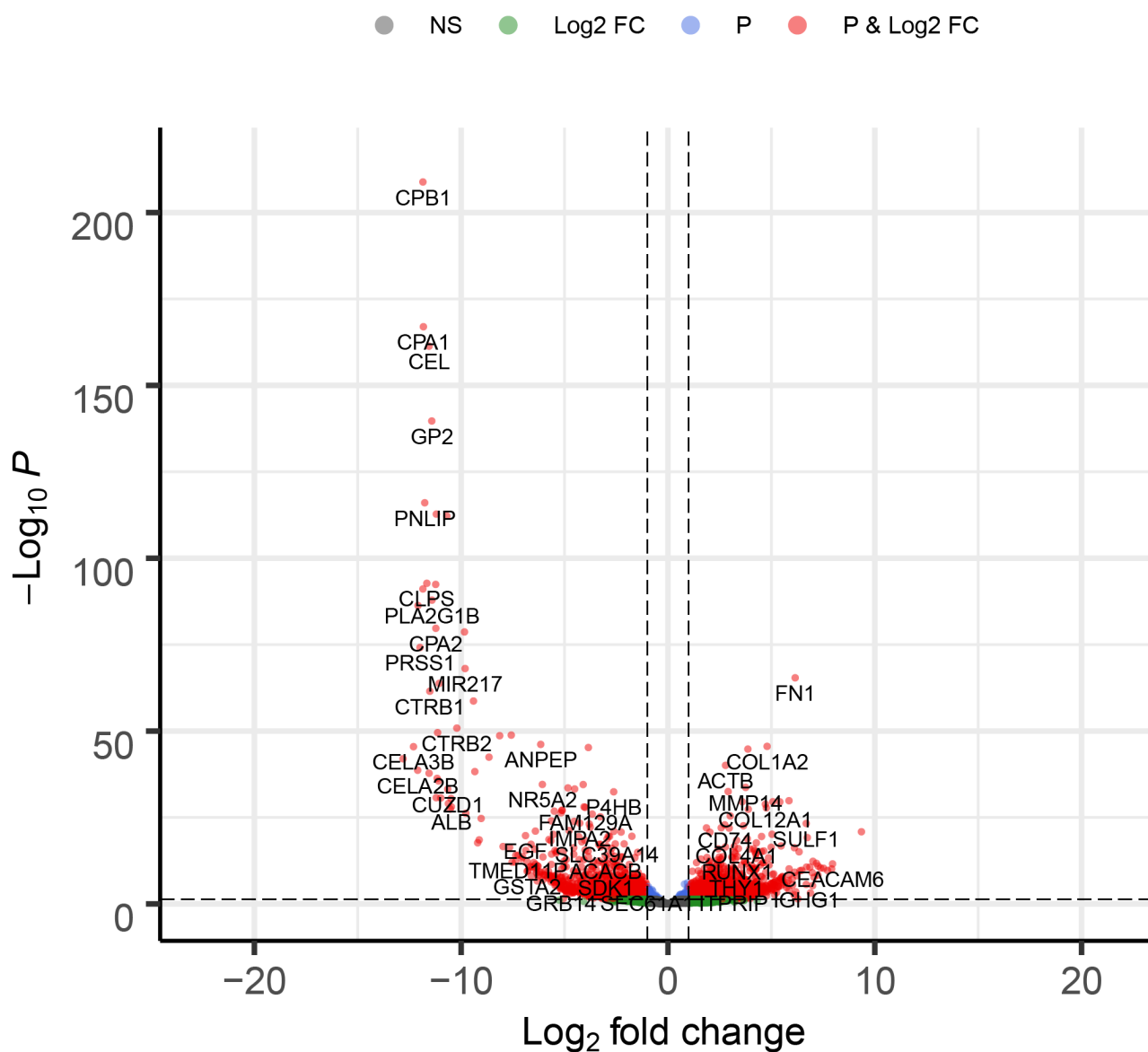


Figure (S7) **Volcano plot of DEGs for dataset E-GEOD-3494** Total 3804 DEGs identified, out of which 2193 gene were up-regulated and 1611 genes were down-regulated. The list of DEGs with the $\log_2 FC$ values is provided in Supplementary Table 1.

2 WGCNA SOFT THRESHOLDS AND FINAL MODULES OF ALL DATASETS:

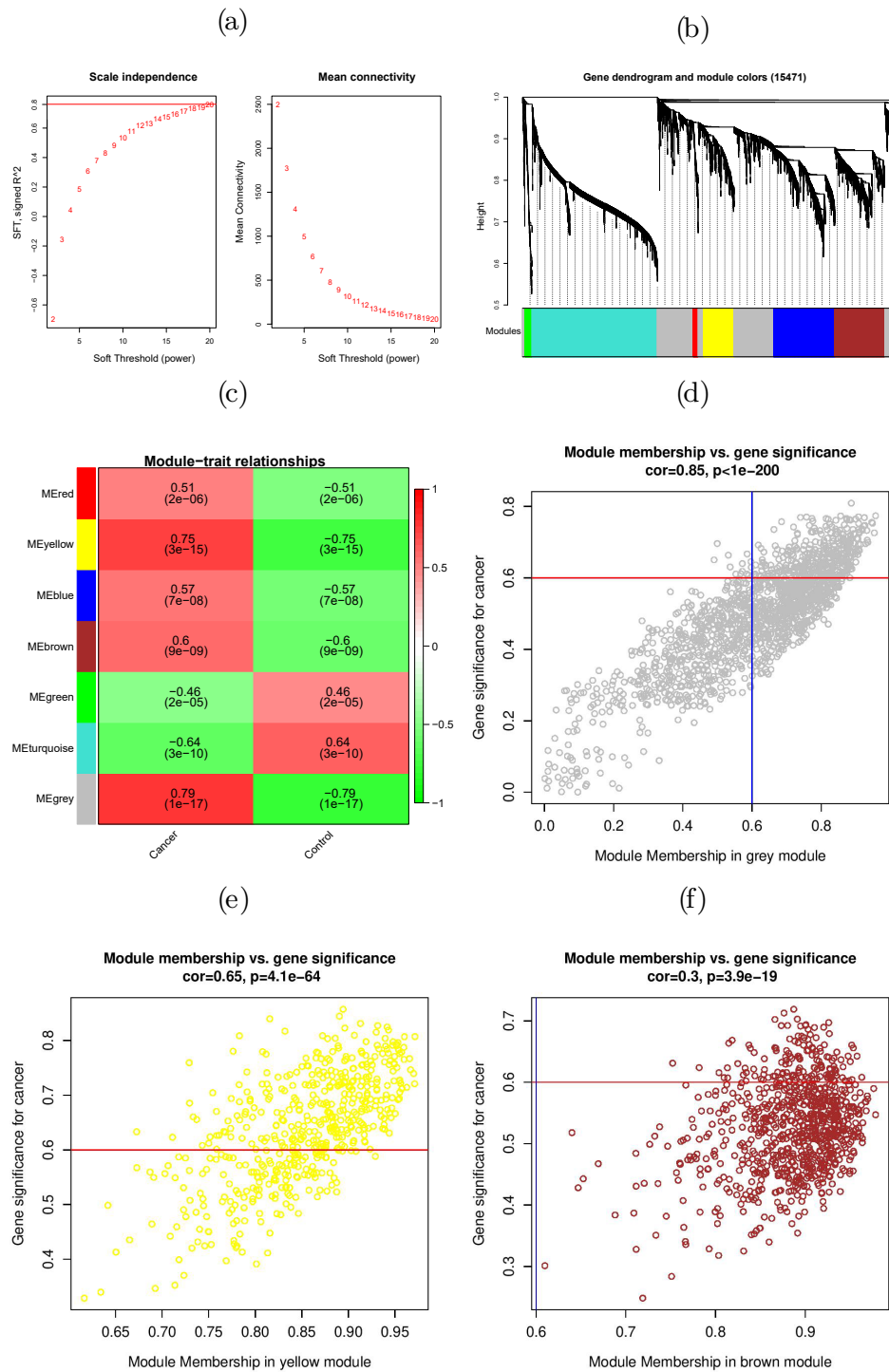


Figure (S8) Plots of Dataset E-GEOD-15471 (a) Scale Free Topology (SFT) model fitting construct scale-free network. Soft threshold value (β) from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 20 was determined on the basis of scale independence plot. (b) Gene tree (dendrogram) along with final modules with module colors. Total 7 modules were formed on β value of 20. (c) Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. (d) Scatter plot for module membership vs. gene significance for PC in the grey module. Hub genes with significance for cancer and Module membership > 0.6 were selected for further analysis. (e) Scatter plot for module membership vs. gene significance for PC in the yellow module. (f) Scatter plot for module membership vs. gene significance for PC in the brown module.

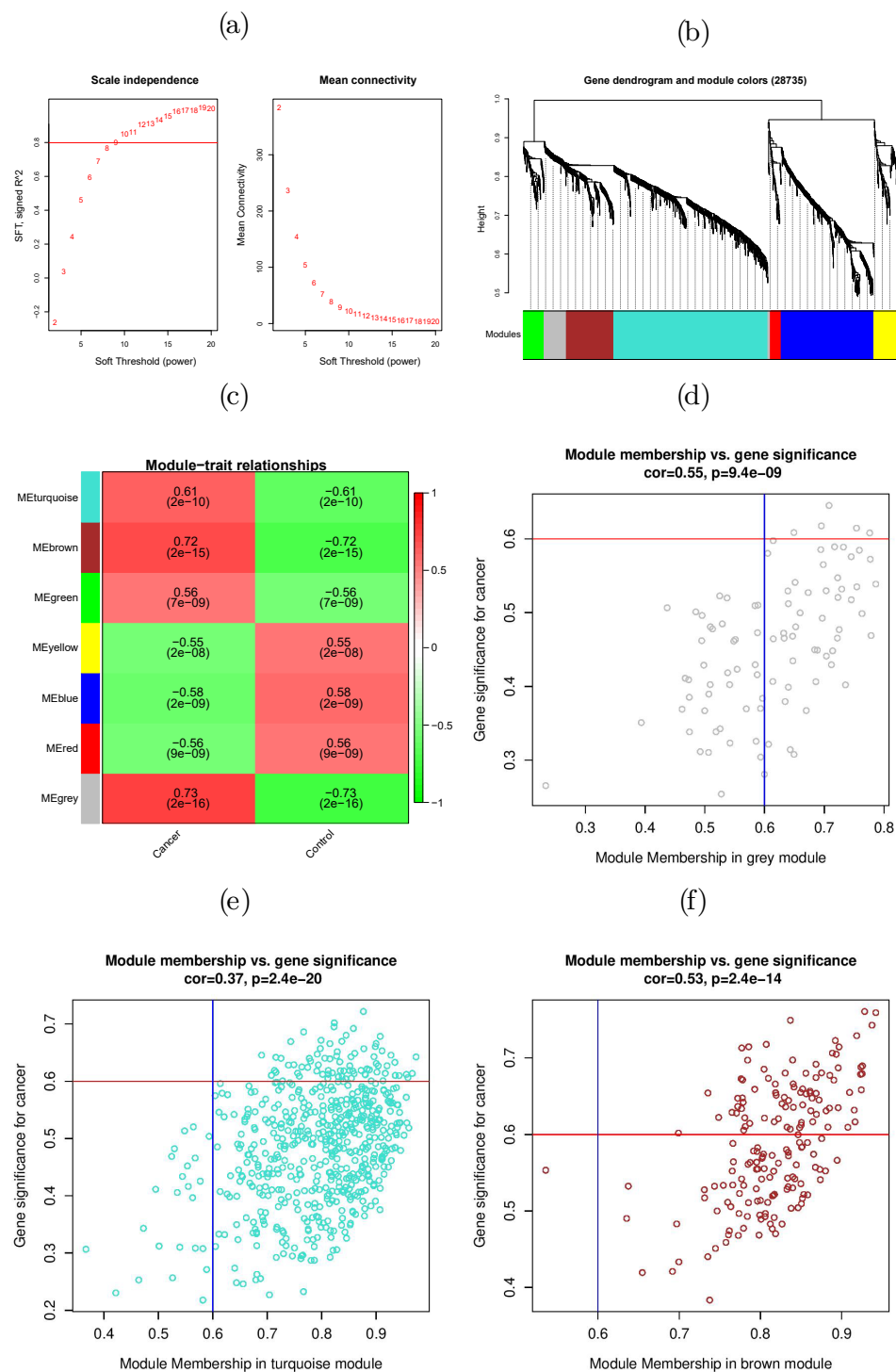


Figure (S9) Plots of Dataset E-GEOD-28735 **(a)** β value from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 9 was determined on the basis of scale independence plot. **(b)** Gene tree (dendrogram) along with final modules with module colors. Total 7 modules were formed on β of 9. **(c)** Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. **(d)** Scatter plot for module membership vs. gene significance for PC in the grey module. **(e)** Scatter plot for module membership vs. gene significance for PC in the turquoise module. **(f)** Scatter plot for module membership vs. gene significance for PC in the brown module.

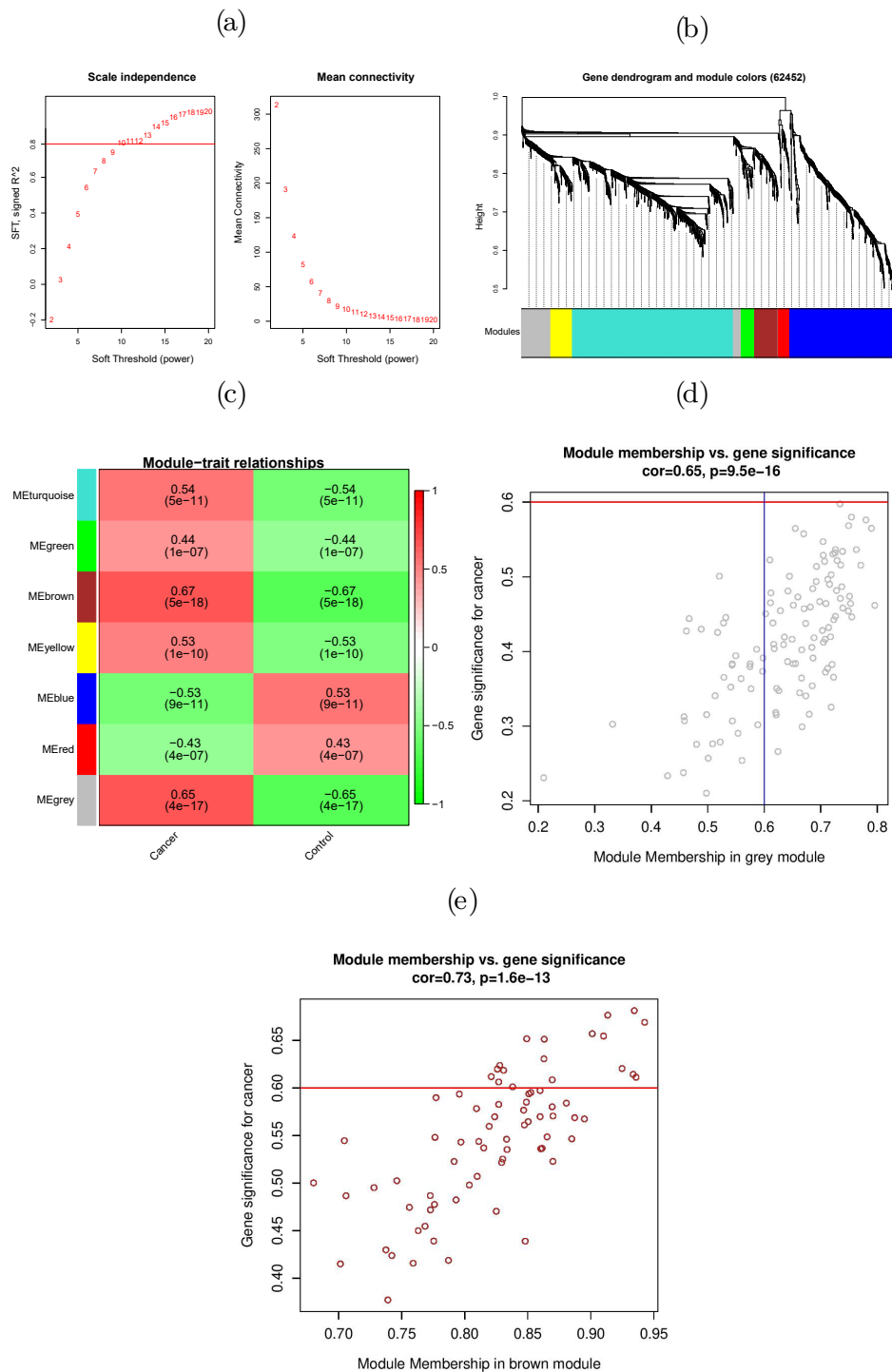


Figure (S10) Plots of Data E-GEOD-62452 (a) β value from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 10 was determined on the basis of scale independence plot. (b) Gene tree (dendrogram) along with final modules with module colors. Total 7 modules were formed on SFT of 10. (c) Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. (d) Scatter plot for module membership vs. gene significance for PC in the grey module. (e) Scatter plot for module membership vs. gene significance for PC in the brown module.

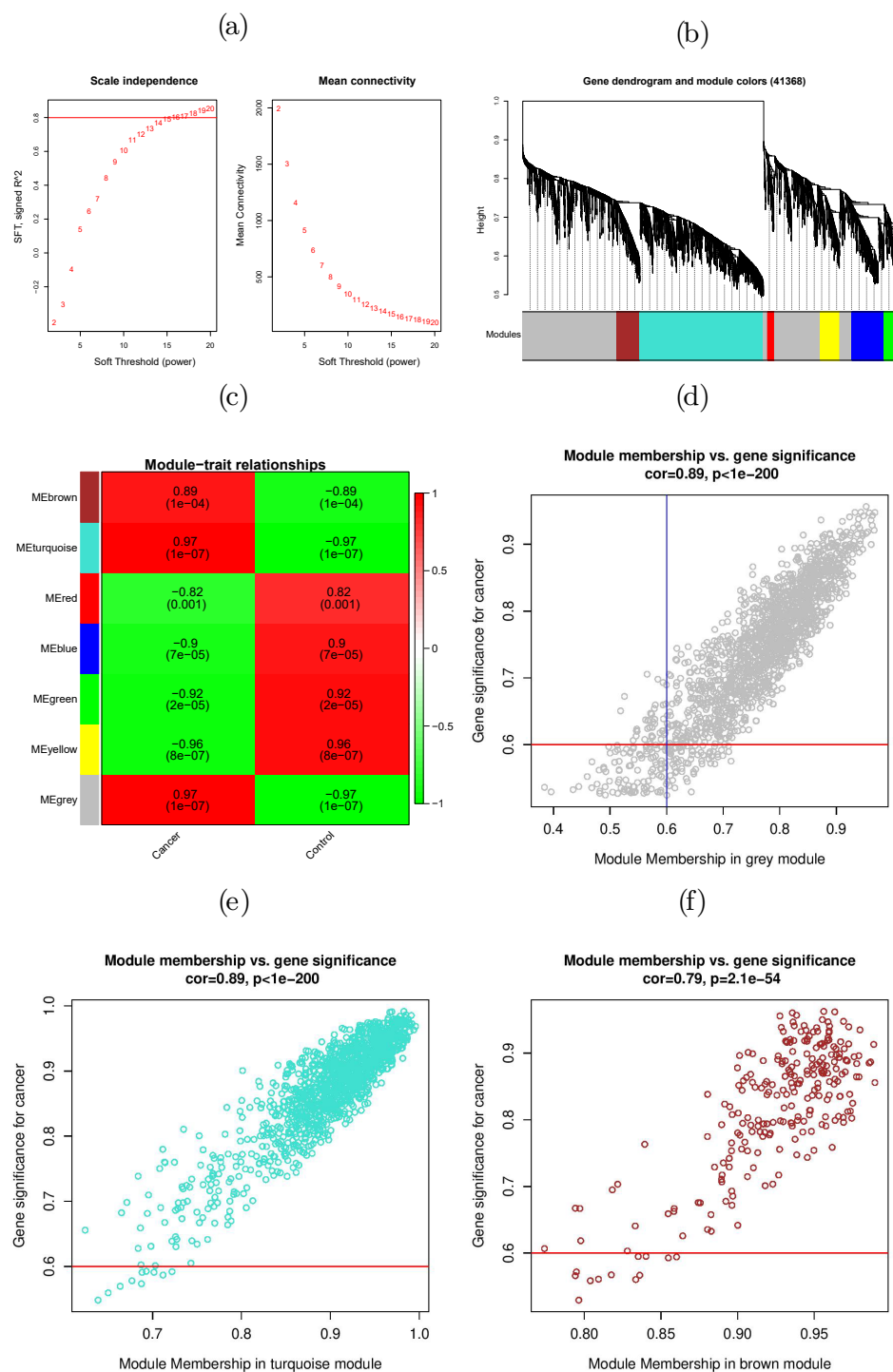


Figure (S11) Plots of E-GEOD-41368 (a) β value from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 16 was determined on the basis of scale independence plot. (b) Gene tree (dendrogram) along with final modules with module colors. Total 7 modules were formed on SFT of 16. (c) Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. (d) Scatter plot for module membership vs. gene significance for PC in the grey module. (e) Scatter plot for module membership vs. gene significance for PC in the turquoise module. (f) Scatter plot for module membership vs. gene significance for PC in the brown module.

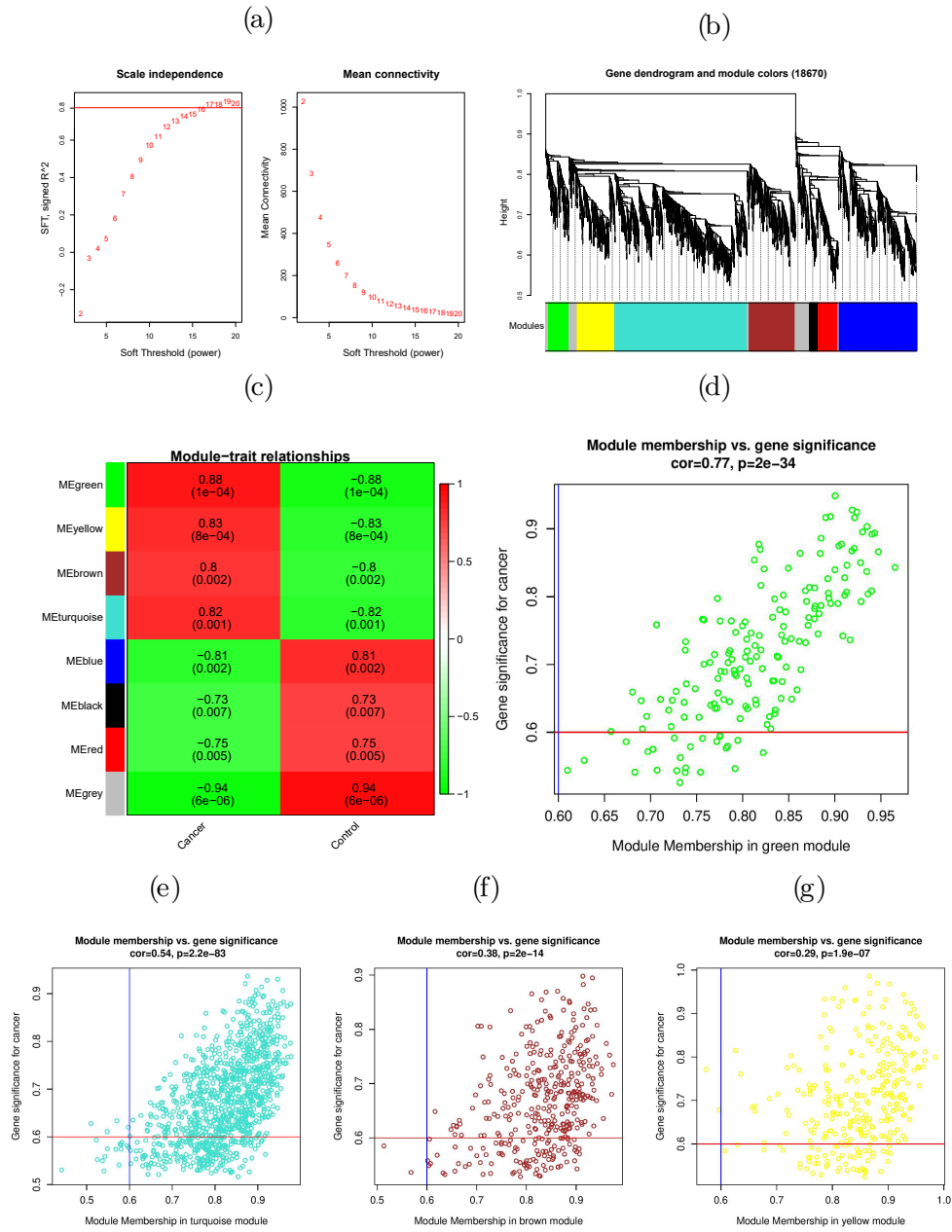


Figure (S12) Plots of Data E-GEOD-18670 (a) β value from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 16 was determined on the basis of scale independence plot. (b) Gene tree (dendrogram) along with final modules with module colors. Total 8 modules were formed on SFT of 16. (c) Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. (d) Scatter plot for module membership vs. gene significance for PC in the green module. (e) Scatter plot for module membership vs. gene significance for PC in the turquoise module. (f) Scatter plot for module membership vs. gene significance for PC in the brown module. (g) Scatter plot for module membership vs. gene significance for PC in the yellow module.

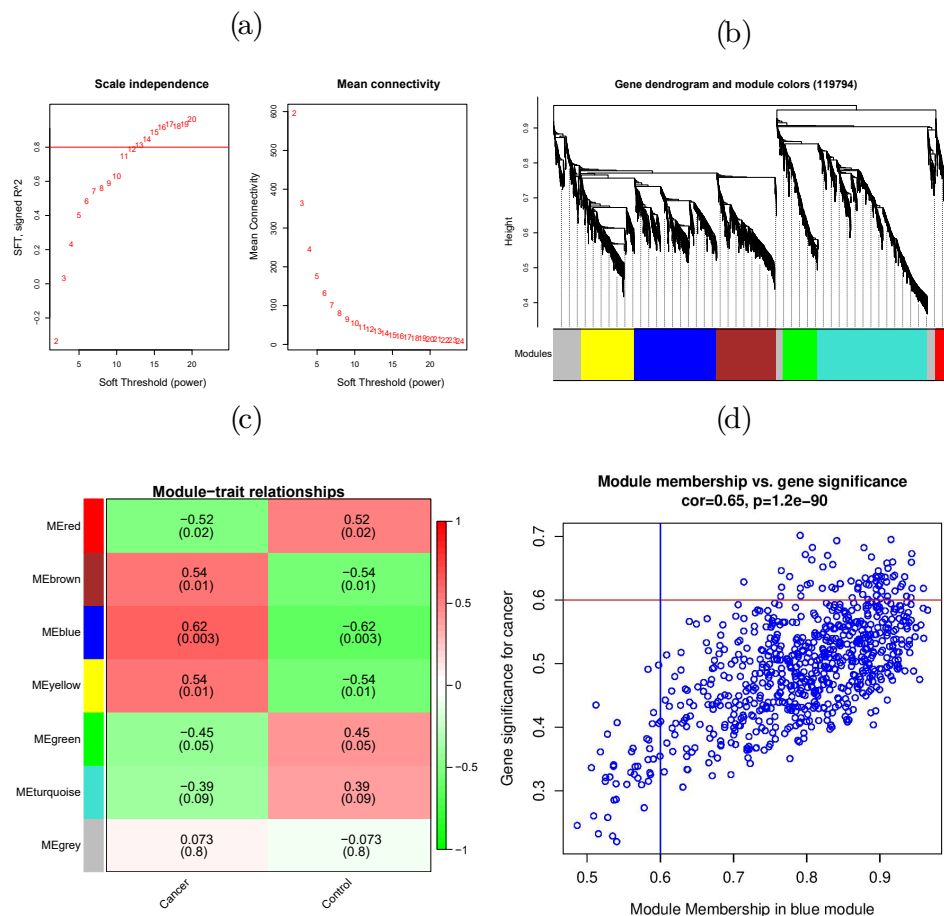


Figure (S13) Plots of Dataset GSE119794 (a) β value from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 12 was determined on the basis of scale independence. (b) Gene tree (dendrogram) along with final modules colors, Total 7 modules were formed on SFT of 12. (c) Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. (d) Scatter plot for module membership vs. gene significance for PC in the blue module.

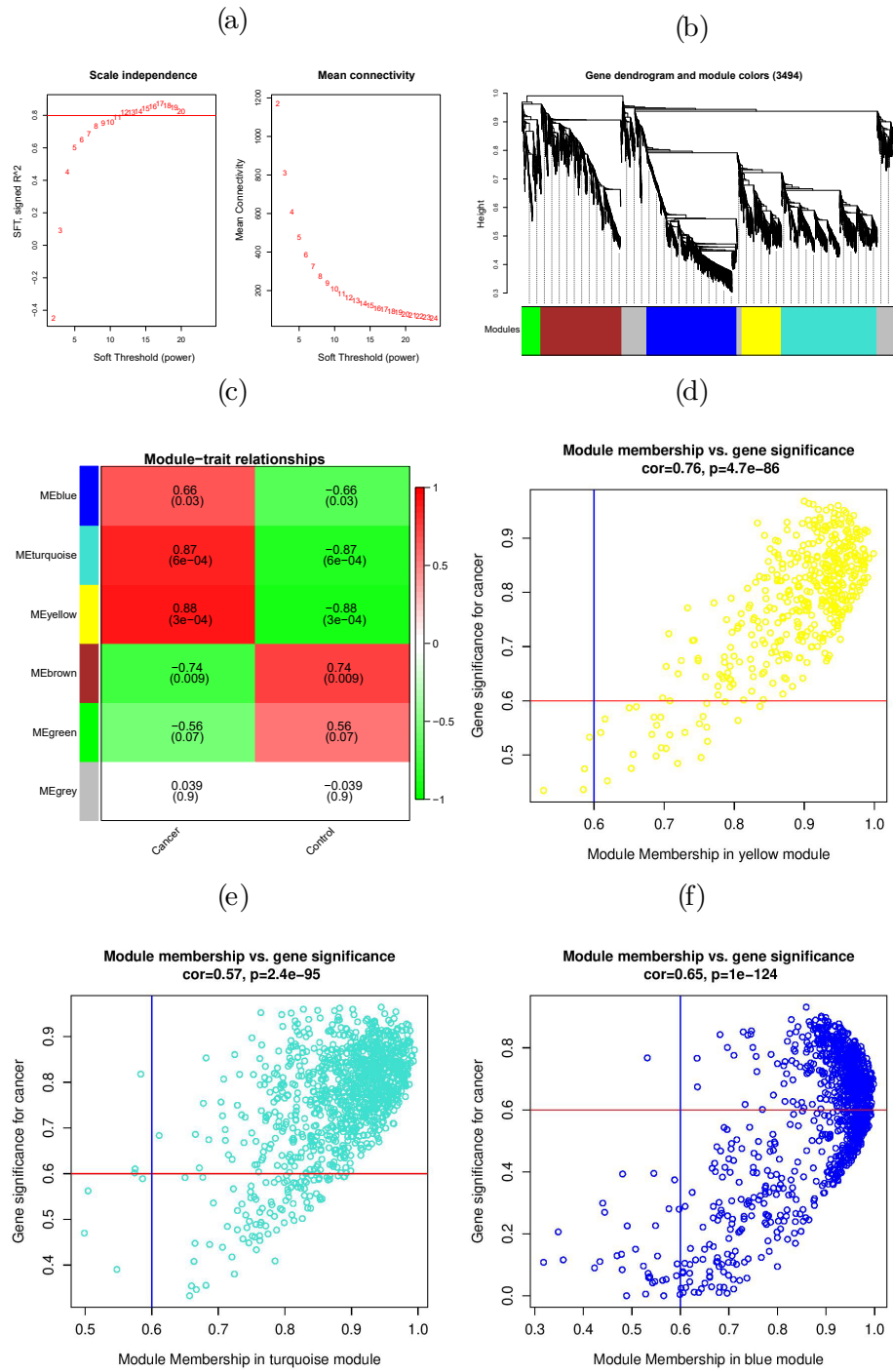


Figure (S14) Plots of Dataset E-MTAB-3494 (a) β value from 2 to 20 was evaluated to obtain scale-free network on $R^2 \geq 0.8$. The β of 12 was determined on the basis of scale independence plot. (b) Gene tree (dendrogram) along with final modules with module colors. Total 6 modules were formed on SFT of 12. (c) Modules correlation plot with pancreatic cancer and control, along with correlation values and p-values for all modules. (d) Scatter plot for module membership vs. gene significance for PC in the yellow module. (e) Scatter plot for module membership vs. gene significance for PC in the turquoise module. (f) Scatter plot for module membership vs. gene significance for PC in the blue module.