## Supplementary Material

## 1 VOLCANO PLOTS OF ALL DATASETS:

PaCa and Normal


Figure (S1) Volcano plot of DEGs for E-GEOD-15471 dataset The red dots in upper left corner of graph represents underexpressed genes with p-value less than $0.05\left(-\log _{10} P\right.$ value greater than 1.3) and fold change less than -1 . Red dots in the upper right corner of graph represents overexpressed genes with p-value less than $0.05\left(-\log _{10} P\right.$ value greater than 1.3) and fold change greater than 1 . The overall 1665 DEGs retrieved from dataset E-GEOD-15471 full filling $\log _{2} F C$ and p-value criteria, out of which 1466 genes were overexpressed while 199 genes were underexpressed. The list of DEGs with $\log _{2} F C$ values is provided in Supplementary Table 1.

PaCa and Normal


Figure (S2) Volcano plot of DEGs for dataset E-GEOD-28735 After p-value and $\log 2 \mathrm{FC}$ threshold filtering 364 DEGs were identified, with 227 overexpressed and 137 underexpressed genes. The list of DEGs along with $\log _{2} F C$ values is provided in Supplementary Table 1.

PaCa and Normal


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 $\log _{2} F C$ values is provided in Supplementary Table 1.

PaCa and Normal


Figure (S4) Volcano plot of DEGs for dataset E-GEOD-62452 The total 274 DEGs obtained (174 overexpressed and 100 underexpressed), The list of DEGs along with the $\log _{2} F C$ values is provided in Supplementary Table 1.

## PaCa and Normal



Figure (S5) Volcano plot of DEGs for dataset E-GEOD-18670For E-GEOD-18670 total number of DEGs obtained after differential expression analysis were 1164, with 798 overexpressed and 366 underexpressed genes, The lists of DEGs with their $\log _{2} F C$ 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 upregulated and 980 down-regulated). The list of DEGs with the $\log _{2} F C$ 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 $\log _{2} F C$ 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 ( $\beta$ ) from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 20 was determined on the basis of scale independence plot. (b) Gene tree (dendogram) along with final modules with module colors. Total 7 modules were formed on $\beta$ 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) $\beta$ value from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 9 was determined on the basis of scale independence plot. (b) Gene tree (dendogram) along with final modules with module colors. Total 7 modules were formed on $\beta$ 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) $\beta$ value from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 10 was determined on the basis of scale independence plot. (b) Gene tree (dendogram) 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) $\beta$ value from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 16 was determined on the basis of scale independence plot. (b) Gene tree (dendogram) 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.
(a)

(c)

(e)

(b)

(d)

(g)


Figure (S12) Plots of Data E-GEOD-18670 (a) $\beta$ value from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 16 was determined on the basis of scale independence plot. (b) Gene tree (dendogram) 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) $\beta$ value from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 12 was determined on the basis of scale independence. (b) Gene tree (dendogram) 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) $\beta$ value from 2 to 20 was evaluated to obtain scale-free network on $R^{2} \geq 0.8$. The $\beta$ of 12 was determined on the basis of scale independence plot. (b) Gene tree (dendogram) 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.

