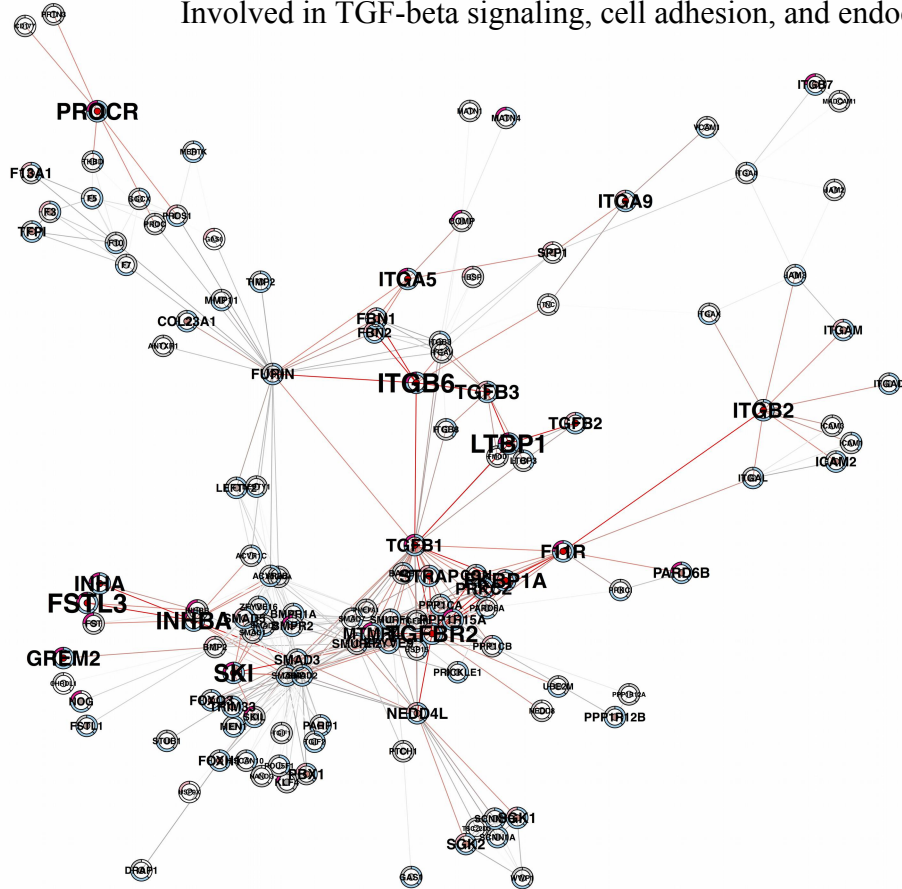


A) Module 1 (N = 130; p < 0.01):

Built around *TGFB1*, *ITGB2*, *INHBA*, *ITGA5*, *TGFB3*, *ITGB6*, *TGFB2*, *FKBP1A*, and *F11R*

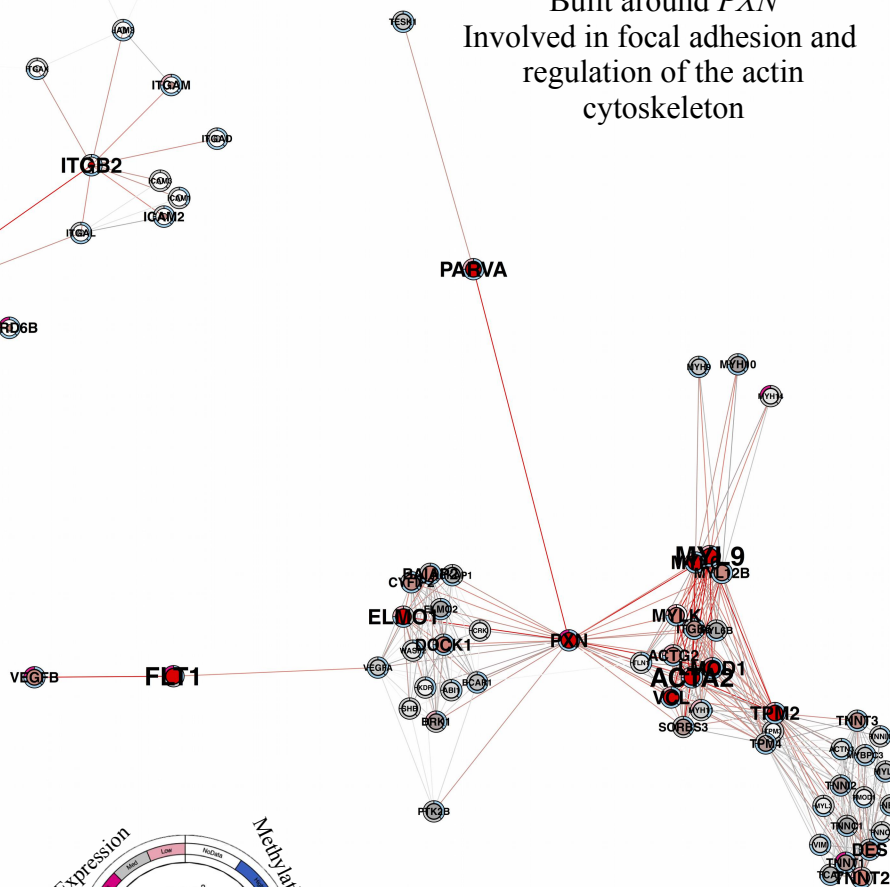
Involved in TGF-beta signaling, cell adhesion, and endocytosis



B) Module 2 (N = 55; p < 0.01):

Built around *PXN*

Involved in focal adhesion and regulation of the actin cytoskeleton

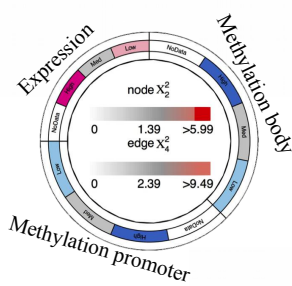
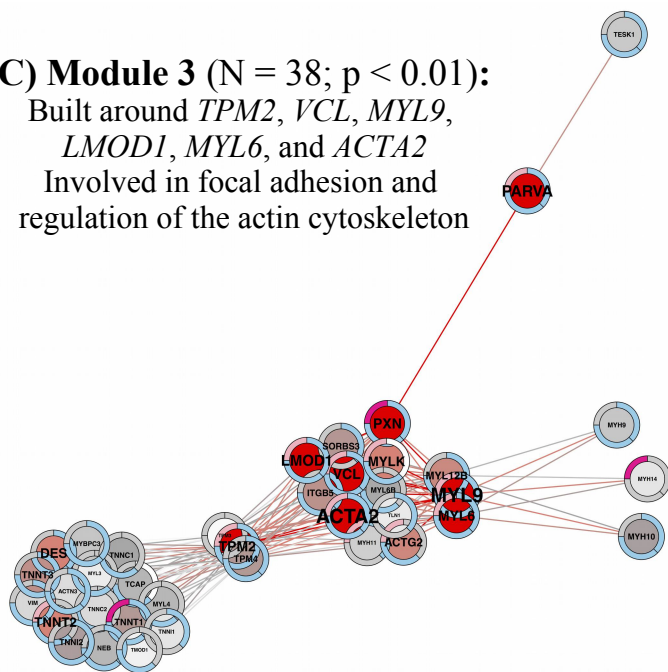


C) Module 3 (N = 38; p < 0.01):

Built around *TPM2*, *VCL*, *MYL9*,

LMOD1, *MYL6*, and *ACTA2*

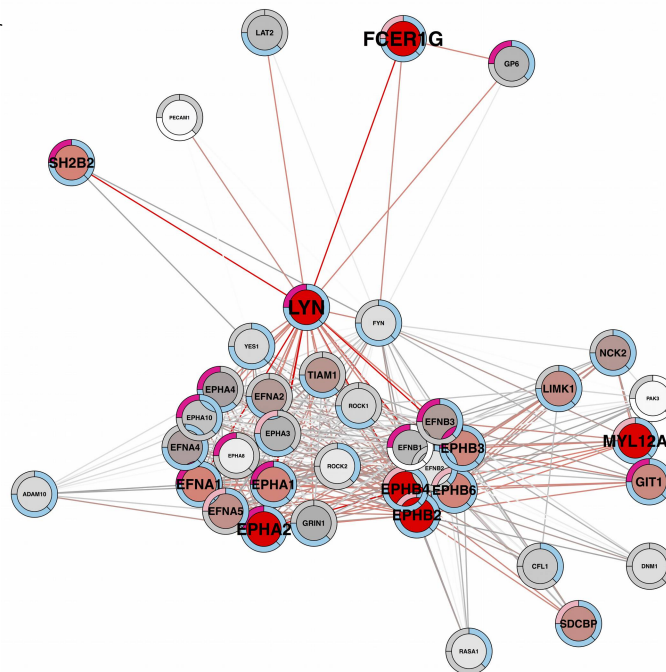
Involved in focal adhesion and regulation of the actin cytoskeleton



D) Module 4 (N = 39; p < 0.01):

Built around *MYL12A* and *EPHA2*

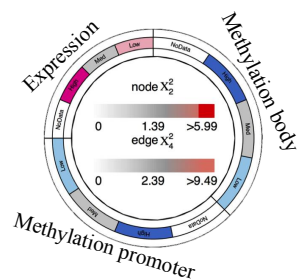
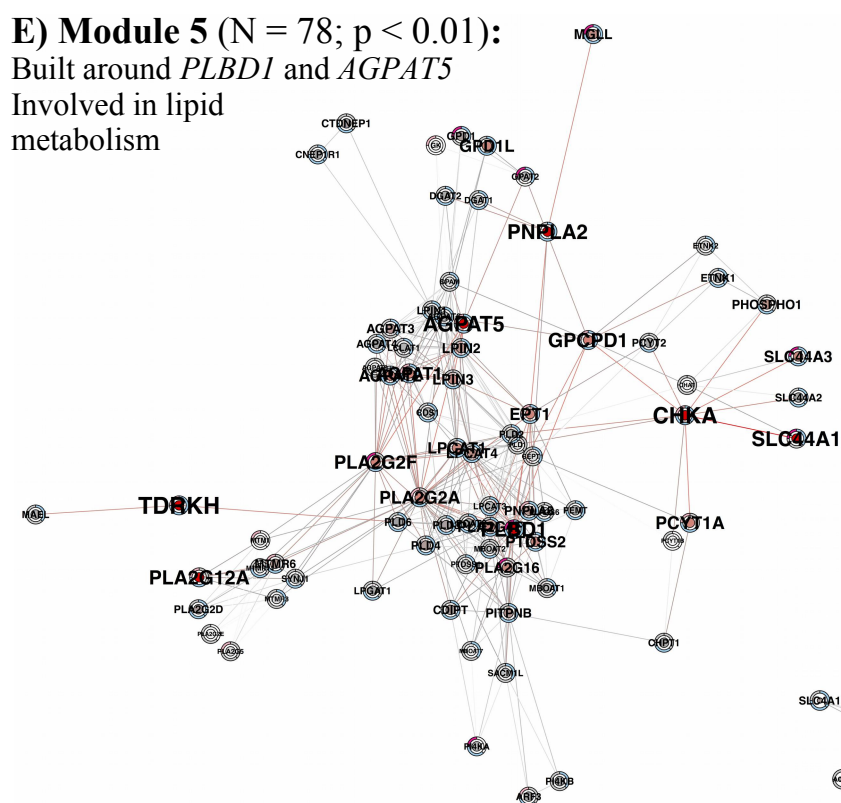
Involved in leukocyte transendothelial migration and the actin cytoskeleton



E) Module 5 (N = 78; p < 0.01):

Built around *PLBD1* and *AGPAT5*

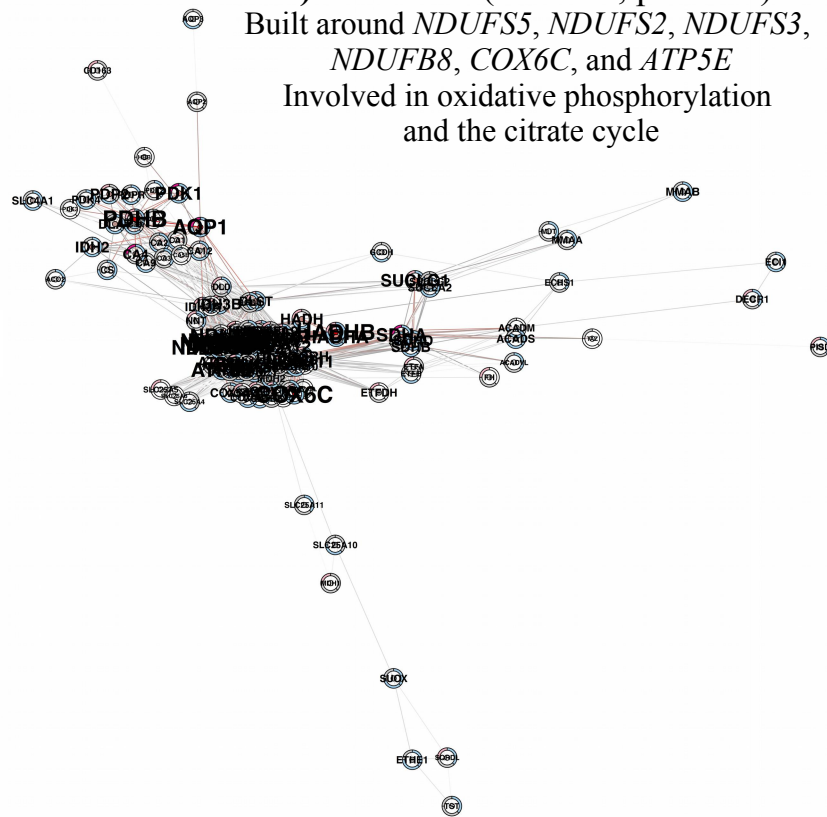
Involved in lipid metabolism



F) Module 7 (N = 144; p = 0.04):

Built around *NDUFS5*, *NDUFS2*, *NDUFS3*, *NDUFB8*, *COX6C*, and *ATP5E*

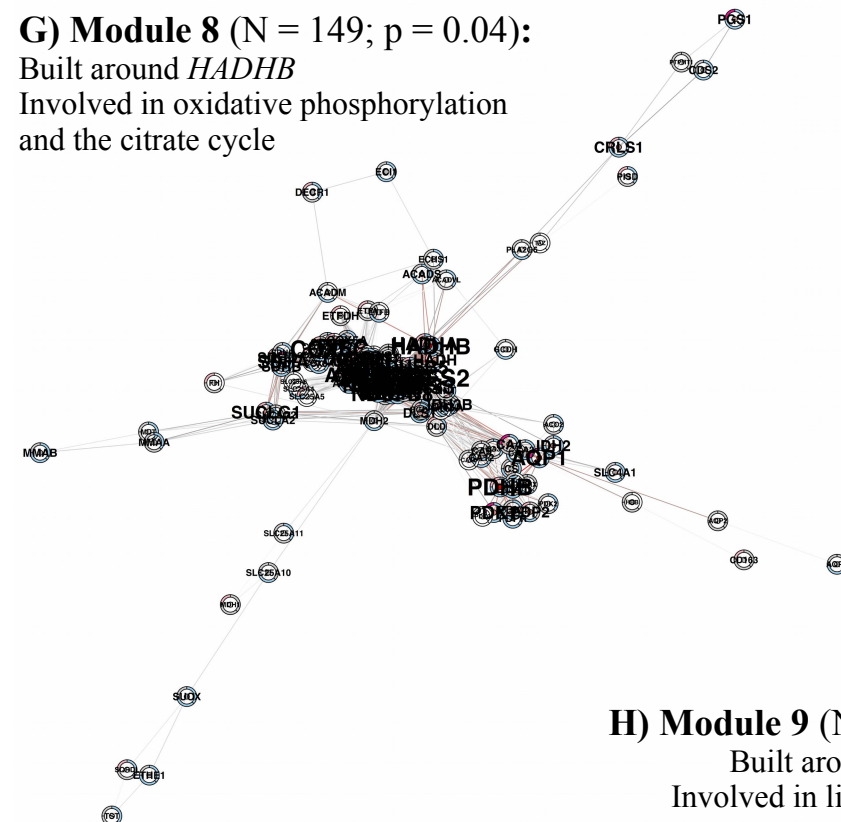
Involved in oxidative phosphorylation and the citrate cycle



G) Module 8 (N = 149; p = 0.04):

Built around *HADHB*

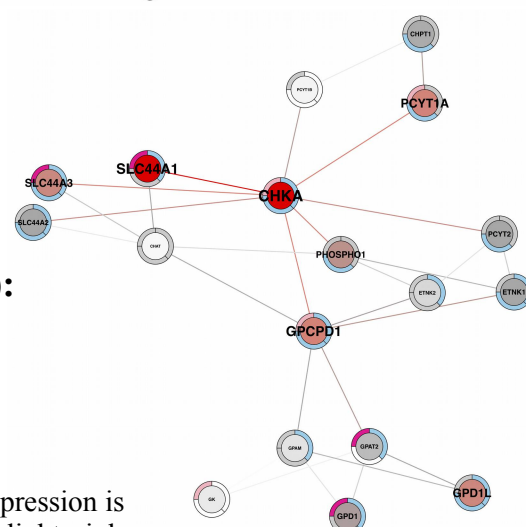
Involved in oxidative phosphorylation and the citrate cycle



H) Module 9 (N = 18; p = 0.05):

Built around *CHKA*

Involved in lipid metabolism



Supplementary Figure 4. Functional SMITE modules identified in cluster 2. Expression is shown on the top left edge of each gene circle (upregulated: dark pink, downregulated: light pink, grey: not significant, white: no data); scored promoter and body methylation are shown on the bottom left and top right of each circle, respectively (hypermethylated: dark blue, hypomethylated: light blue, grey: not significant, white: no data), compared to cluster 1. The symbol text sizes and center node colors are based on the total gene score (low (grey) to high (red)) and the edge colors are representative of the strength of the associations between the genes (low (grey) to high (red)). Cluster 2 module 6 is shown in Figure 3a.