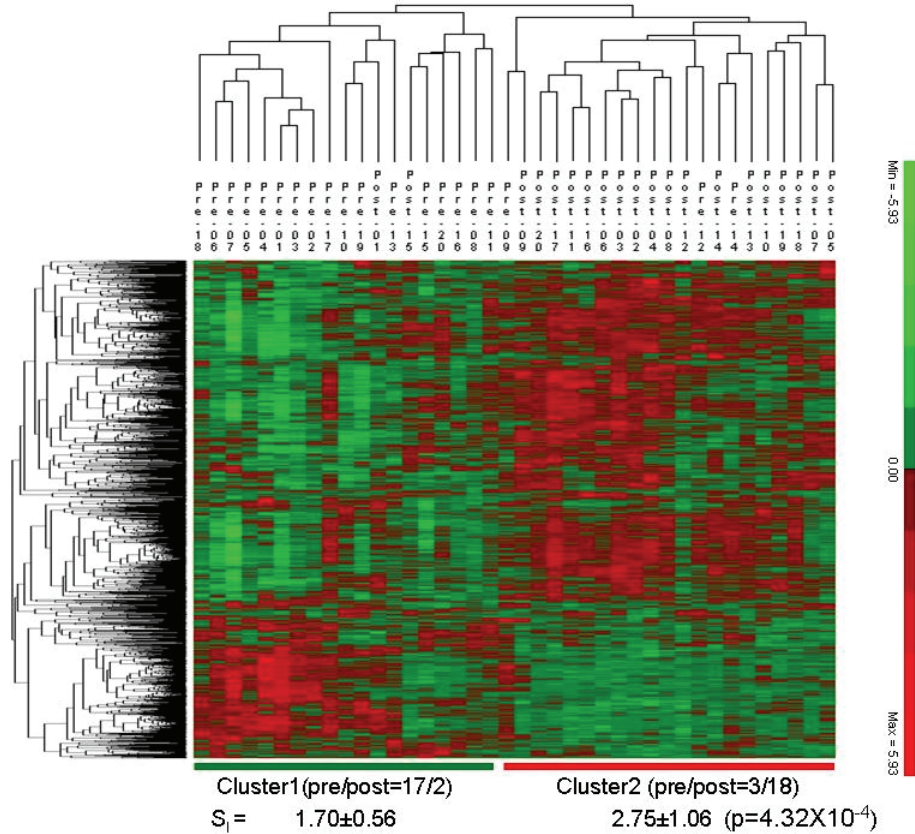
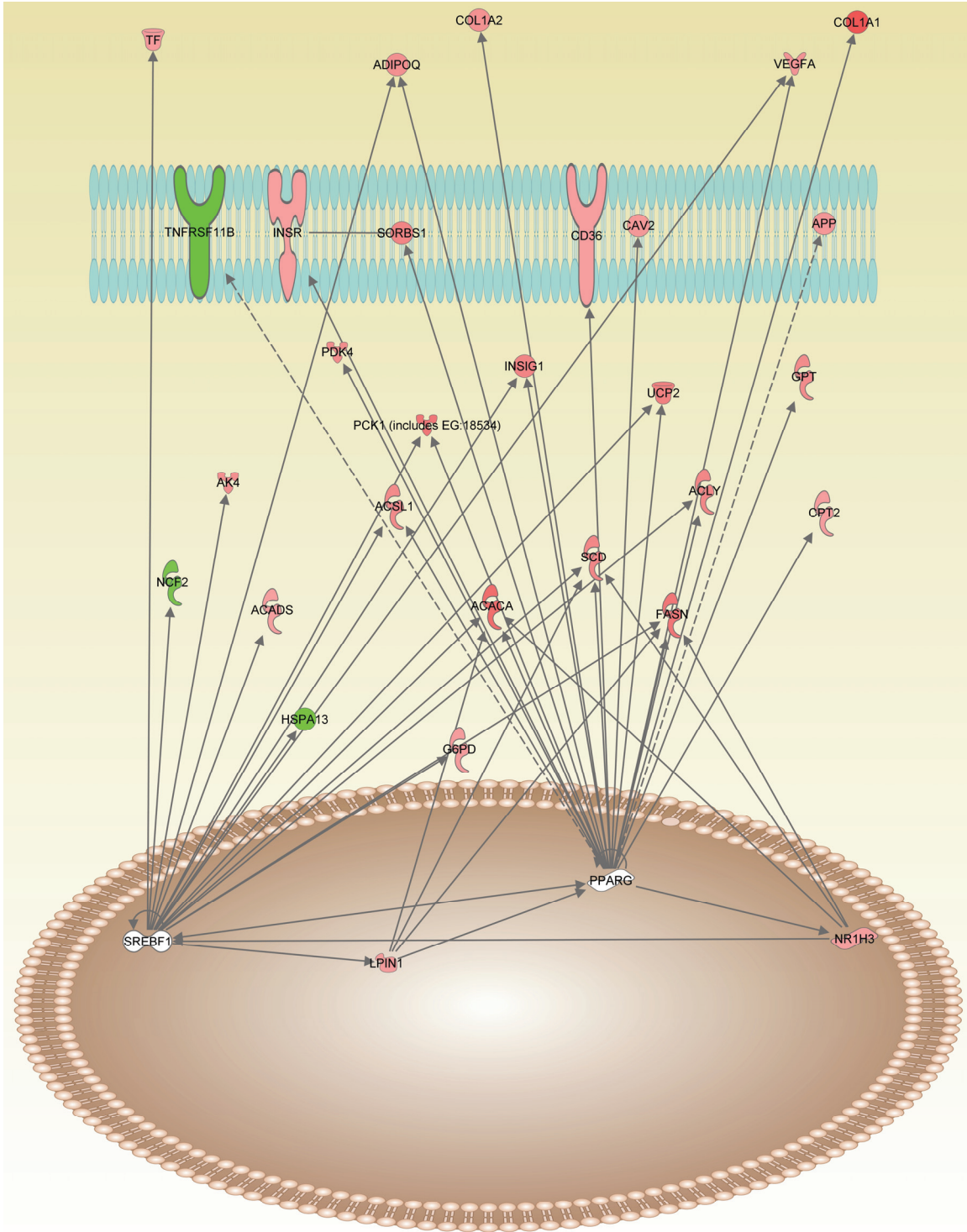


Supplementary Figures:

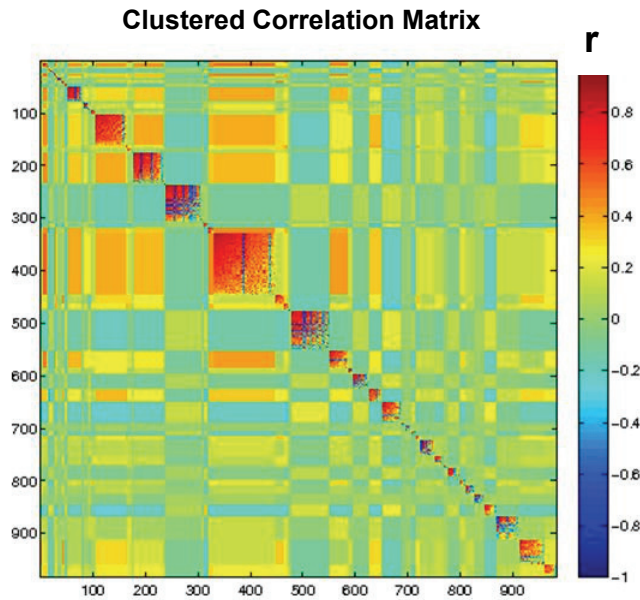
Supplementary figure-1: Unsupervised hierarchical clustering for transcripts differentially modulated in adipose tissue upon PPAR agonist treatment clustered pre and post treatment samples in two major groups. Intensity of red and green color in heat map indicates degree of high and low expression respectively. S_I , Insulin sensitivity from minimal model analyses of FSIGT data. Pre, pre treatment (N=20); Post, post treatment (N=20)



Supplementary figure-2: Genes modulated by transcription factor PPAR γ and SREBF1 and regulatory relationships among those genes based on IPA knowledgebase. Up-regulated (post/pre treatment) genes are red and down regulated genes are green. Only highly validated direct interactions based on IPA knowledge base are included.

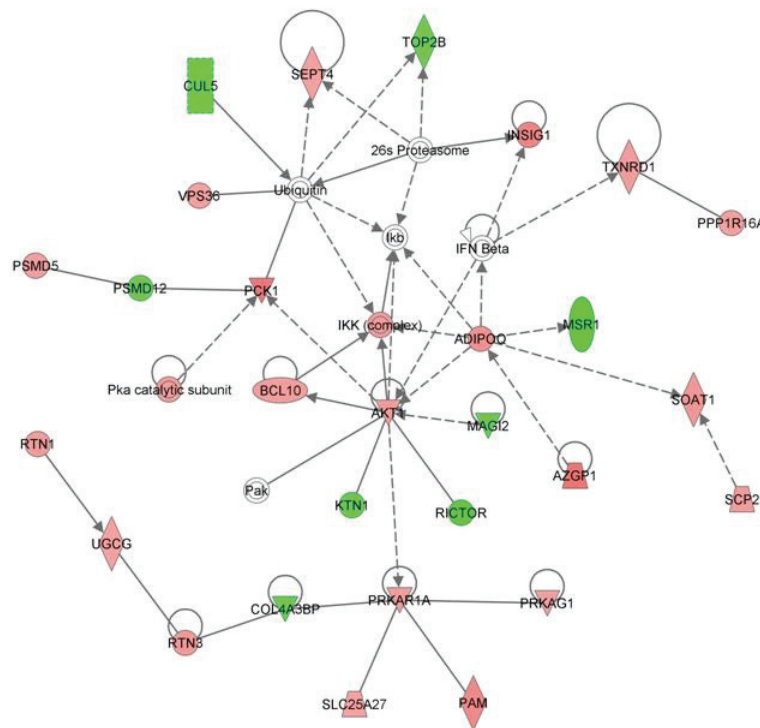


Supplementary figure-3: Modulated Modularity Clustering (MMC) analysis of PPAR agonist modulated transcripts in adipose tissue. The reordered matrix of pairwise genetic correlations between transcriptional profile of 983 genes are shown. From Upper left (module 1) to lower right (module 54, see supplementary table- 7), modules are ordered by decreasing average connectivity, defined as average absolute pairwise correlation within modules. r , spearman correlation coefficient.



Supplementary figure-4: Ingenuity knowledge based biological interaction networks among genes differentially expressed upon PPAR agonist treatment in adipose tissue of impaired glucose tolerant subjects. Selective networks involved in lipid metabolism are shown A) Network 4: score= 34 with 28 differentially expressed genes B) Network 14: score= 23 with 22 differentially expressed genes. Nodes of the interaction network containing up-regulated (post/pre treatment) genes are red and down regulated genes are green. Both direct and indirect interactions are included in the analysis. For this analysis genes differentially modulated by PPAR agonists were mapped to its corresponding gene object in Ingenuity pathway knowledge base. These focus genes were then used for generating biological networks. The software computes a score for each network according to the fit of the focus genes using Fisher's exact test. The score is derived from p-value and indicates likelihood of the focus genes in a network being found together due to random chance. A score of ≥ 2 have 99% confidence of not being generated by random chance alone (see supplementary table-8 for all networks).

A)



B)

