PCOS is arguably the most common endocrinopathy of reproductive-aged women, characterized by ovulatory dysfunction and hyperandrogenism. It has a highly enigmatic pathophysiology and manifestation. Transcriptome profiling proffers a valuable approach to identify the candidate genes and pathways involved in complex diseases. Our aim was to portray the differential gene expression in peripheral blood of PCOS and normal women. Peripheral blood samples were collected from 4 control women and 4 PCOS patients (according to Rotterdam criteria). Total RNA was extracted and the array hybridisation was performed on Illumina Human HT-12 V4 platform. Data were analyzed using GeneSpring and Ingenuity Pathways Analysis. Microarray results were positively validated using RT-PCR. To further delineate molecular characteristics of PCOS, we constructed an "integrative network" combining mRNA and upstream transcription factors. Gene ontology associated with the network was studied using DAVID 7.0. Gene expression analysis identified 1092 significantly differentially expressed genes. The integrative TF-mRNA network generated demonstrated that the entries were extensively interconnected with PCOS hallmarks. To further identify important network clusters we dissected the integrative network by using a Cytoscape plug-in, clusterMaker. This analysis resulted in 4 nonorphan network clusters including (ATF6, GFI1, HOXA5, STAT3, STAT5B, STAT6, and USF1). The major biological functions associated with the network profile were cytokine signaling, inflammatory pathways, IGF-1 signaling, Toll like receptor signaling, oxidative stress, EPO signaling, angiogenesis, cardiac hypertrophy, insulin signaling and apoptosis. Through this approach we identified important pathway clusters involved in PCOS etiology and therapeutic interventions based on these clusters can enable better management of PCOS.