MicroRNAs are non-coding, short RNAs which regulate the gene expression in cells either by cleaving the target mRNAs or by suppressing the target protein synthesis. Differentially expressed microRNAs effect the normal gene expression and cause diseases such as cancer. MicroRNA expression profiling is possible due to microarray technology. There is a need for development of a computational technique to determine the biological pathways altered by the differentially expressed microRNAs so that the effective study of any type of cancer can be conducted easily whenever required. In this research, a microRNA dataset, consisting of normal and lung cancer data, is analyzed. The microRNA data are normalized and the microRNAs that are differentially expressed in the lung cancer microarray than in the normal lung microarray are obtained using statistical method called T-test. Only those microRNAs with p-values less than 0.01 are considered here for more preciseness. The samples of differentially expressed microRNAs are classified using KNN classifier for five categories of microRNAs: top 5, 10, 20, 40 and 50 microRNAs with 50 randomly generated test cases for each category. The classification was 81% accurate on average for five categories of top microRNAs. The results also indicated that the lung cancer samples can be classified using a small panel of 5 microRNAs with over 85% classification accuracy which means the lung cancer sample and normal lung sample are significantly distinct. The microRNA names made available in our dataset file are very specific names whereas predicted target list are available for more generic microRNA names. 15 unique microRNA names: hsa-mir-21, hsa-mir-210, hsa-mir-30d, hsa-mir-205, hsa-mir-30a, hsa-mir-191, hsa-mir-203, hsa-mir-24, hsa-mir-20, hsa-mir-214, hsa-mir-216, hsa-mir-29b, hsa-mir-30b, hsa-mir-215 and hsa-mir-218, were obtained by processing the top 50 differentially expressed microRNAs. 3103 predicted mRNA targets of those differentially expressed microRNAs are identified from online resource. The up-regulated and down-regulated microRNAs are identified and their targets are stored separately. The molecular functions associated with the predicted targets of both types of microRNAs are retrieved from Gene Ontology Consortium and are represented using GO IDs in directed acyclic graphs. Also, the GO IDs for the human’s entire GeneIDs are retrieved by processing files made available by European Bioinformatics Institute (EBI) through its Gene Ontology Annotation (GOA) project. They are also represented in a direct acyclic graph. The entire GeneID-GOID set of human as well as the GeneID-GOID sets of the predicted targets of both the up-regulated and down-regulated microRNAs are further processed. Fisher’s Exact Test was employed for conducting significance test to find those functional groups which are prominently affected by the differentially expressed microRNAs. The results show that the differentially expressed microRNAs could potentially change the expression of mRNAs and therefore modify the related cellular processes. Significance testing identified 213 molecular function groups which are exhibiting strong association with the differentially expressed microRNAs and hence with the lung cancer disease, and are potentially on the biological pathways altered by these differentially expressed microRNAs.