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Identification of key genes and construction of microRNA-mRNA regulatory networks in non-small cell lung cancer

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Highlights

- We aimed to explore the of microRNA-mRNA regulatory networks for NSCLC
- A total of 160 differentially expressed microRNAs were identified
- CCND1 gene was determined as the potential biomarkers for NSCLC

Abstract

Non-small cell lung cancer (NSCLC) is the most common type of lung tumor. Deregulation of microRNA may be involved in the occurrence of NSCLC and we aimed to find the potential prognostic biomarkers for NSCLC. The microRNA microarray expression profiles were downloaded from GEO dataset and then generated by applying robust multi-array average (RMA). The normalized data was analyzed with a Bioconductor package linear model for microarray data and an independent dataset was used to inspect the results. Then, the differentially expressed genes were identified using the limma package. Besides, in order to investigate the

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