عنوان مقاله:

Predicting a miRNA as potential biomarker in breast cancer diagnosis thorough bioinformatics analysis

محل انتشار:

چهارمین کنگره بین المللی و شانزدهمین کنگره ملی ژنتیک (سال: 1399)

تعداد صفحات اصل مقاله: 2

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خلاصه مقاله:

Background and Aim: Breast cancer (BC) is a heterogeneous and malignant neoplasm derived from breast tissue, and accounts for about ۱۶% of all cancers and ۲۲.۹% of invasive cancers in women. So, it is essential to identify potential molecular diagnostic markers and therapeutic targets for early detection, especially the invasive ones. Recent studies showed the great potential of small RNAs in the development of novel biomarkers and therapeutic targets. miRNAs are a new class of small non-coding regulatory RNAs that are involved in gene expression regulating at the post-transcriptional level and play regulatory roles in tumor initiation and progression.Methods: In this study in order to detect differentially smallRNAs, several studies such as GSE۹۳۷۴۰, GSE۱۰۸۲۹۱, and GSE۲۹۱۷۳ have been investigated to find candidate microRNAs which express differentially in breast tumors. MiARma-Seq tool version ۱.۷.۲ was used to align and quantify short RNAs based on HG۱۹ Human Genome Assembly. Also, miRdeep۲ tool was applied to find the small RNAs that have the potential characters to be miRNAs based on secondary structure prediction. This tool utilizes Cutadapt to trim RNA-seq reads and uses bowtie tool to align reads to HG۱۹ Human Genome Assembly.Results: Finally,we again used miARma-Seq pipeline to feature count and miRbaseV۱۹ annotation to quantify small RNAs and discard known miRNAs. We identified ۴۰۰ annotated and unannotated small RNAs. In the next step other databases including UCSC, mirBase, RNAfold, SRA, miPred and PHDcleav were used to clarify some characteristics such as conservation, expression status in tumor and non-tumor tissues, secondary structure and Dicer binding site for unannotated potential to wonder whether they can be miRNAs.Conclusion: In conclusion, we used GEO(gene expression omnibus) database and analyzed candidate small RNAs by bioinformatics tools to reveal that they can be a real precursor for miRNA. Also other characteristics such as differential expression, conservation, secondary structure have been survived to detect small RNA with the most significant score as miRNA biomarker for .early detection of breast cancer

کلمات کلیدی:

Breast cancer,Small RNA, Biomarker