Original Article

Bioinformatic Evaluations for Locating the microRNA Suppressing PI3K/AKT Pathway and Analysis in Prostate Cancer Cell Lines

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Abstract

Objective: Prostate cancer is the fifth most common cancer. In 2012, it was the second leading cause of cancer death for men worldwide. The PI3K/AKT pathway plays an essential role in pathogenesis of prostate cancer; the key role of this pathway in cancer progression makes it an attractive target for prostate cancer therapy. MicroRNAs (miRNAs) that regulate gene expression have a special ability to simultaneously control multiple genes and pathways which make them candidates for therapeutics. This study aims to determine miRNAs which target the PI3K/AKT pathway and evaluate them in prostate cancer cell lines.

Methods: In order to determine an effective miRNA for the PI3K/AKT pathway, we assessed six genes from this pathway which have been proposed as drug targets in ten different prediction algorithms. Next, the candidate miRNAs were analyzed in expression profile and pathway analysis databases. Expression of candidate miRNAs in control and prostate cancer cell lines were subsequently evaluated.

Results: According to bioinformatics, the miR-29 family could target the most genes from this list. Other bioinformatic estimates confirmed these results. The miR-29 family showed significant downregulation in prostate cancer cell lines LNCAP, PC3 and DU-145 compared to control samples.

Conclusion: These results propose the possibility of using the miR-29 family to inhibit the PI3K/AKT pathway in prostate cancer.

Keywords: Prostate Cancer, PI3K/AKT Pathway, Bioinformatics Prediction, miR-29 Family

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PI3K/AKT

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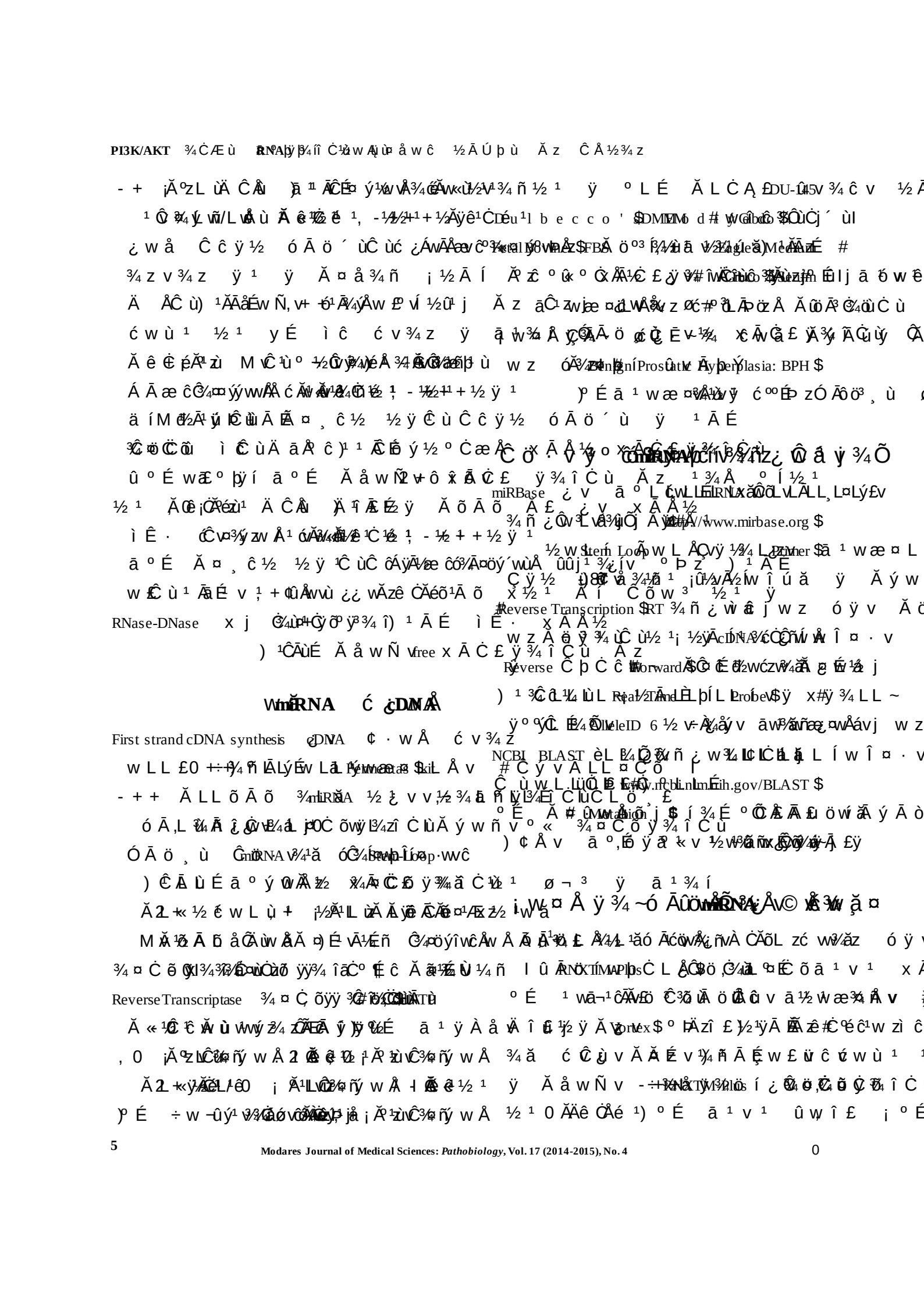
PC3 LNCAP

Hybrid miRWalk miRDB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					hsa-miR-29b-3p						
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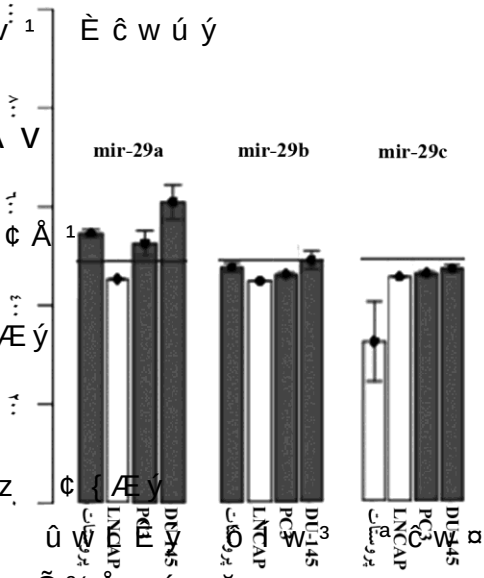

Real Time cÿDNA À**miR**Å©lv¾¸¤Åv

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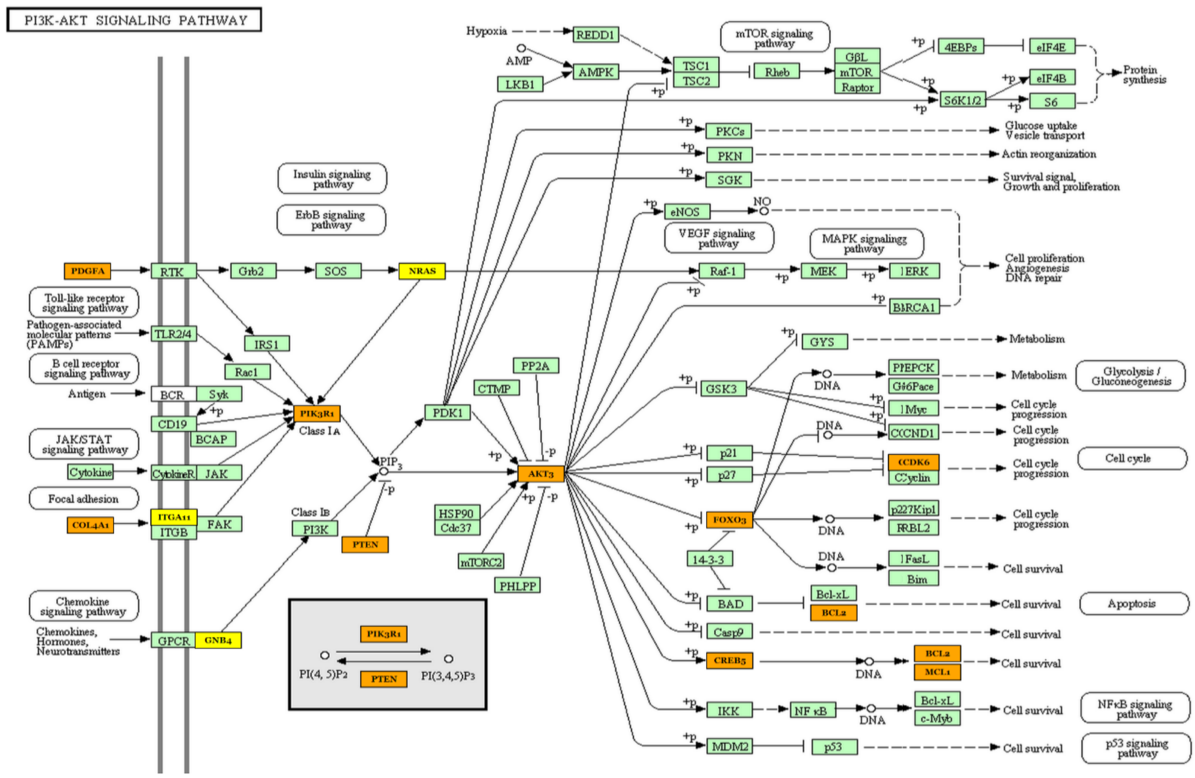

miR-29c-3p miR-29b-3p miR-29a-3p
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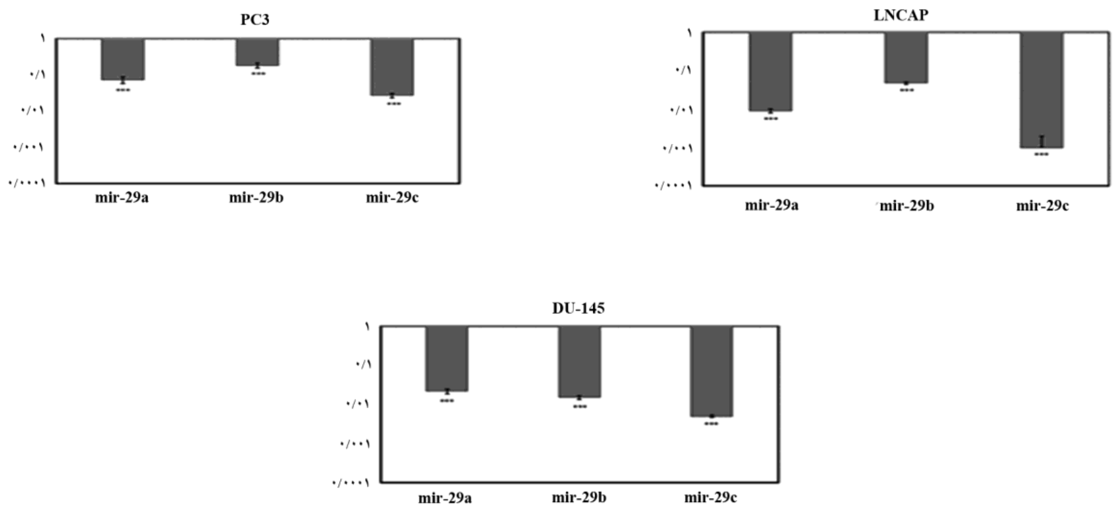

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