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Expression profile analysis reveals putative prostate cancer-related microRNAs

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ABSTRACT. Annotation of prostate cancer (PC) genomes provides a foundation for discoveries that can improve the understanding and treatment of the disease. Therefore, in the present study, we used the Student *t*-test to identify differentially expressed PC-related mRNAs and microRNAs (miRNAs). Then, we performed interrelated mapping of miRNA target genes between abnormally expressed mRNAs and miRNAs, and explored mRNA-target miRNA interrelated pairs to explain the biological functions of miRNA during the progression of PC, thus revealing the occurrence of miRNA-mediated PC. After Gene Set Functional Similarity analysis, we obtained 20 abnormal PC-related candidate miRNAs, including hsa-miR-26a, hsa-miR-152, hsa-miR-19a, hsa-miR-30c, hsa-miR-19b, and hsa-miR-146b-5p, among others. These results suggest that it may be possible to predict the clinical behavior of prostate cancer based on gene expression analysis.

Key words: miRNA; mRNA; Prostate cancer; Target gene; Gene set; Functional similarity

