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Analysis of fusion gene expression in prostate tumors by using single-end reads

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ABSTRACT. Fusion gene expression, a kind of chromosome rearrangement mode, has been strongly linked to prostate cancer diagnosis and prognosis as well as to the Gleason score and the American Joint Committee on Cancer stage assessment. In combination with traditional methods for locating fusion genes and scoring their association with cancer cell growth, proliferation, and invasion through the basement membrane, the emerging high-throughput sequencing technologies offer a panorama of fusion genes in a genome and facilitate the discovery of new fusion modes. We describe here a method for using single-end reads to analyze fusion gene expression in prostate tumors. We obtained the fusion gene expression profiling of prostate tumors, clustered them into several biological pathways, highlighted three "rediscovered" fusion genes (*TMPRSS2-ERG*, *KLK2*, and *KLK3*) and proved the reliability of our method.

Key words: Fusion gene; Prostate cancer; Single-end reads

