



Cancer Genomics: Chapter 3. Cancer Transcriptome Sequencing and Analysis

Ryan D. Morin, Stephen B. Montgomery

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Identifying gene expression changes in cancer provides opportunities to identify biomarkers that can be informative in regard to risk and in the choice of treatment options. In recent years, advances in sequencing have provided not only a quantitative measure of gene expression, but the resolution of diverse species of RNA, alternative transcripts and allele-specific expression. As well, such data have revealed novel sequences such as those from pathogens, mutations resulting in amino acid differences and fusion transcripts resulting from translocations and other structural alterations, each of which can inform the development of novel treatment strategies or potential preventive measures. In this chapter, we will discuss how transcriptome sequencing is conducted and analyzed and provide examples that illustrate its utility in studying cancer samples.

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