



Category: Cancer Genomics

Comparative Study of Transcriptomic profiling and Functional enrichment in Ovarian Cancer Cell lines

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Abstract

High-throughput cDNA sequencing (RNA-seq) has emerged as a sophisticated tool for transcriptomic studies, especially for identifying differentially expressed genes (DEGs) and measuring the transcripts between different sample groups or conditions. There are several pipelines and tools available for performing the task, but still there is no general consent for the protocol to be used for the analysis. In this comparative study, transcriptomic profiling of Ovarian cancer cell lines data sets were carried out by using two different pipelines- 'Tuxedo' protocol (Tophat, Cufflinks-Cuffdiff, Cummerbund) and 'new Tuxedo' protocol (HISAT, StringTie, Desq2) were used for estimating the transcript abundancies and for analysing differential expression. 'New Tuxedo' protocol was found to be fast and efficient than 'Tuxedo' protocol and the run time on an 8 GB RAM PC was ~ 2 hr and ~ 6 days, respectively. A total of 613 and 371 DEGs were obtained by using 'Tuxedo' and 'New Tuxedo' pipeline, respectively. Functional profiling was performed, by a comparative study of high throughput functional enrichment tools (clueGO, DAVID, EnRichr, FunRich, gProfiler, GSEA, PANTHER and webGestalt) to get the functions and pathways of most enriched genes involved in ovarian cancer cell lines. The common biological pathways and Gene Ontology (GO) terms were extracted with common genes from all the tools to get most enriched genes with the GO functional terms. Thus, the characterization of biological pathway and GO processes (Biological processes and Molecular Function) of most enriched gene sets involved in ovarian cancer cell lines were obtained.

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