Sunitha et al. (2017) Can J Biotech, Volume 1, Special Issue, Page 63
https://doi.org/10.24870/cjb.2017-a50

Canadian Journal of Biotechnology

ISSN 2560-8304

Poster Presentation **OPEN ACCESS**

Category: Cancer Genomics

Identification of differentially expressed snoRNAs in Ovarian Cancer from RNA-Seq data

Sunitha P.[1], Jiffy John[1], Umesh P.[2], Sugunan V.S.[3], Oommen V. Oommen[4], Achuthsankar S. Nair[1] and P.R. Sudhakaran[1]

[1]Department of Computational Biology & Bioinformatics, University of Kerala, INDIA
[2]College of Engineering Aranmula, INDIA
[3]University College, Trivandrum, INDIA
[4]Kerala State Biodiversity Board, Trivandrum, INDIA

Presenting author: sunifeb12@gmail.com

Abstract

Non-coding RNAs (ncRNAs) are a large class of important regulatory molecules involved in many physiological and cellular processes. Small nucleolar RNAs (snoRNAs), a subset of the small ncRNAs, are molecules located in the cell nucleolus. Even though, they are one of the most ancient and evolutionary conserved ncRNAs, they are gaining more prominence and attention in the recent years only. The classical function of snoRNAs is to act as guide RNAs of rRNAs and nucleolytic processing of the rRNA transcripts. However several scientific evidences have indicated that other than the classical functions, they are involved in multiple functions such as metabolic stress regulation, modulation of alternative splicing, controlling cell behavior, etc. and the dysregulation of snoRNAs could contribute to carcinogenesis. Even though many independent works have been carried out, to examine the role of snoRNAs in several human diseases including cancer, specific projects to study the cumulative role of snoRNAs in a disease is limited. The advent of high throughput and deep sequencing technologies has opened up new avenues for carrying out such studies. This study focusses on the utilization of snoRNAs as potential biomarkers characteristic to ovarian cancer based on a RNA-Seq data. We have downloaded a transcriptome data, [PRJNA209481] from the NCBI BioProject, pertaining to human ovarian cancer cell lines. Downstream analysis was done by Tuxedo pipeline of RNA-Seq data analysis. The differential expression analysis by Cuffdiff threw a total of 847 differentially expressed genes, of which we found, 71 snoRNAs to be up regulated and 34 snoRNAs as down regulated. Many of the previously reported snoRNAs having a role in tumorigenesis in a variety of cancers are also seen to be dysregulated in this study. Further investigation is underway to analyze the effect of differentially expressed snoRNAs in ovarian cancer and their potential as biomarkers.

References

[1] Mannoor, K., Liao, J. and Jiang, F. (2012) Small nucleolar RNAs in cancer. *Biochim Biophys Acta* 1826: 121-128. https://doi.org/10.1016/j.bbcan.2012.03.005
[2] Thorenoor, N. and Slaby, O. (2015) Small nucleolar RNAs functioning and potential roles in cancer. *Tumour Biol* 36: 41-53. https://doi.org/10.1007/s13277-014-2818-8
[3] Mleczko, A. M. and Bąkowska-Żywicka, K. (2016) When small RNAs become smaller: emerging functions of snoRNAs and their derivatives. *Acta Biochim Pol* 63: 601-607. https://doi.org/10.18388/abp.2016_1330
[4] Trapnell, C., Roberts, A., Goff, L., Pertea, G., Kim, D., Kelley, D.R., Pimentel, H., Salzberg, S.L., Rinn, J.L. and Pachter, L. (2012) Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. *Nat Protoc* 7: 562-578. https://doi.org/10.1038/nprot.2012.016

Citation: Sunitha, P., John, J., Umesh, P., Sugunan, V.S., Oommen, O.V., Nair, A.S. and Sudhakaran, P.R. Identification of differentially expressed snoRNAs in Ovarian Cancer from RNA-Seq data [Abstract]. In: Abstracts of the NGBT conference; Oct 02-04, 2017; Bhubaneswar, Odisha, India: Can J biotech, Volume 1, Special Issue, Page 63. https://doi.org/10.24870/cjb.2017-a50