ABSTRACT

Prostate cancer (PC) is a heterogeneous disease that has a slow progression compared to other types of cancers, where the severity of prostate cancer commonly increases along the age of each individual. PC is still considered as a global disease and its development is affected by racial differences. African-American (AA) men are proven to be more susceptible to PC compared to European-American. Currently, lncRNA is widely identified as biomarkers that is suitable for cancers, including PC. In this study, the RNA-Sequencing analysis such as RNA-Alignment using STAR, Differential expression analysis, and the network analysis were run in order to search for the potential lncRNA(s) that might able to be developed as a biomarker for racial differences in PC. There were top 10 lncRNA(s) found, 7 of which were lncRNA(s) that had not been detected in context of PC but had been previously detected in other organs includes, *LINC01001, AC098617.1, AC005863.1, CALML3–AS1, LINC01087, AC064834.1*, and *LINC00958,* where it was found that LINC01001 had the most interaction with a total of 30 target genes. Meanwhile, the rest of the lncRNA(s) found were *LINC00261, F11–AS1* and *PCA3* which had been previously detected in PC and other body parts. Therefore, it was known that there were lncRNA(s) useful for further development as biomarkers for racial differences in PC patients of AA descent. However, further in vitro analysis validation is still needed to ensure the validity of these top 10 identified lncRNA(s) as PC biomarkers, especially in the context of racial differences.

Keywords: Differential Expression analysis, Long non-coding RNA (lncRNA), Prostate Cancer, Racial Differences, RNA-Sequencing.