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Profiling the expression of LncRNAs involved in colorectal cancer progression in search for suitable diagnostic biomarkers

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Abstract

Backgrounds: Colorectal cancer (CRC) is among the most lethal cancers in both women and men, worldwide. This high mortality rate can be prevented by early diagnosis and thus more efficient treatment strategies. To that end, introducing more effective and clinically relevant biomarkers would be very important. Recent comprehensive transcriptome studies highlighted the importance of differentially expressed LncRNAs (DELs) in the tumorigenesis pathways of CRC. In this study, we aimed to construct networks of co-expressed genes (modules) involved in CRC in search for novel LncRNAs that can serve as diagnostic biomarkers.

Materials and Methods: This project has been carried out using public RNA-seq data sets of NCBI (bio project: PRJEB27536). Data from 62 samples (tumor and adjacent normal tissue) in fastq file format were retrieved from SRA. Differential expression analysis was performed by DESeq2 package in R and by utilizing WGCNA algorithm. Genes that exhibit a similar expression pattern were classified into a number of modules.

Results: We found 251 upregulated and 192 downregulated LncRNAs in our analysis of CRC samples. WGCNA clustered all the genes into 20 distinct modules. Our gene of interest, *APOBEC3A* (LFC = -3.2) was highly co-expressed with these novel DELs: RP11-638I2.6, RP11-109D20.2 and RP11-342H21.2.

Conclusion: Our results revealed many unannotated LncRNAs that might be crucial in progress and/or prognosis of colorectal cancer. We speculate that RP11-638I2.6, RP11-109D20.2 and RP11-342H21.2 may have key roles in biological pathways related to RNA editing due to their tight association with APOBEC3A. Further functional analysis is required for clarifying the potential roles of these candidate LncRNAs as potential diagnostic markers or druggable targets in CRC.

Keywords: Colorectal cancer, Diagnostic biomarkers, Transcriptome analysis, Differential expression, Long non-coding RNAs