عنوان مقاله:

Integration of Transcriptome and Proteome Datasets for Finding Novel Biomarkers in Acute Lymphoblastic Leukemia

محل انتشار:

چهارمین کنفرانس زیست شناسی سامانه های ایران (سال: 1400)

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خلاصه مقاله:

Acute lymphoblastic leukemia (ALL) is characterized by abnormal proliferation, differentiation, and accumulation of lymphoid precursor cells in bone marrow. The etiology of ALL is largely unknown in most cases and it makes our understanding of the disease so complicated. Understanding the biological mechanism behind the disease and finding disease-related biomarkers is a critical issue since the cure rate among patients needs to improve. In this regard, we firstly collected deregulated proteomics and transcriptomics data in ALL from public databases. Then, the listed gene-related miRNAs and transcription factors (TFs) were identified as two main gene regulators. Moreover, the regulatory sub-network of the miRNA-TF-gene was constructed and the most important genes and TFs were identified including CCND۲, TP۵۳, ALDOA, GATA۶, NFIC, YY۱, and TPM۳. Besides, the GO-ontology of the collected gene list was determined using the DAVID bioinformatics tool. Among the enrichments, cell cycle, cell division, gluconeogenesis, and apoptosis were identified as the most significant processes. This work will provide some significant genes and TFs and pathways associated with the ALL pathology.

کلمات کلیدی:

Regulatory network, miRNA, Transcription Factor, Proteomics, Transcriptomics, Acute Lymphoblastic Leukemia

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