



The Identification of Sub-pathways in Juvenile Idiopathic Arthritis by Integrating Expression Profiles between lncRNA-mRNA and Pathway Topologies

Wen-Hua Wang¹, Bin Wang², Jian Song¹, Hai-Yue Yu¹, Tao Wu¹ and Rong-Bin Li^{1*}

¹*Department of Rheumatism, The First Hospital of Qiqihar, Qiqihar 161005, China*

²*Department of Emergency, The First Hospital of Qiqihar, Qiqihar 161005, China*

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ABSTRACT Juvenile Idiopathic Arthritis (JIA) is a systemic disorder with autoimmune chronic joint inflammation. The pathogenic mechanisms of JIA are still unclear. It has been reported that lncRNA can regulate the mRNA by competitively binding to miRNAs. Analysis of pathway underlying certain disease is a valuable strategy for exploring the functional roles of these transcripts. Therefore, identification of competitively regulated subpathways can not only contribute to understand the occurrence and development of diseases, but also further help to gain the functional roles of lncRNAs. In this work, an effective method was proposed to identify the subpathways that competitively regulated by lncRNAs in JIA, which integrated the lncRNA-mRNA expression profile and pathway topologies. Eventually, based on the expression profile of JIA, 38 subpathways involved in 31 complete pathways were confirmed. Some key lncRNAs associated with JIA may be detected by identification of lncRNA competitively regulated subpathways.