



Altered DNA Methylations May Contribute to Rheumatoid Arthritis

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ABSTRACT The purpose of this paper was to investigate roles of altered DNA methylations in rheumatoid arthritis (RA). To achieve this goal, firstly, DNA methylation data were recruited from the ArrayExpress database. Secondly, differentially methylated genes (DMGs) across RA patients and normals were detected based on *t*-test. Thirdly, hierarchical clustering analysis was performed to evaluate DMGs between RA patients and normal controls. Ultimately, functional enrichment analyses were conducted on DMGs to investigate significant biological functions in RA patients. A total of 45 DMGs (covering 50 CpGs) were obtained. Importantly, the DMGs could well classify RA patients and controls (accuracy = 0.9942), with well feasibility and confidence. Besides, the researchers identified 15 significant gene ontology (GO) terms and 10 significant pathways, respectively. In summary, the DMGs and their functional gene sets, which might shed new lights on the molecular mechanism of RA and provide potential biomarkers for prevention of this disease.