



## **Abnormal DNA Methylations Associated with Allergic Asthma Children**

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**ABSTRACT** The purpose of this paper was to investigate abnormal DNA methylations in the progression of children with allergic asthma, and to reveal molecular mechanism underlying this disease. To achieve this goal, firstly, DNA methylation data for allergic asthma children were prepared from Gene Expression Omnibus (GEO) database. Secondly, differentially methylated genes were identified between allergic asthma and healthy subjects utilizing *t*-test. Subsequently, Gene Ontology (GO) and pathway enrichment analyses were conducted for differentially methylated genes using the Database for Annotation, Visualization and Integrated Discovery (DAVID) tool. Ultimately, the protein-protein interaction network (PPIN) for differentially methylated genes of allergic asthma children was constructed, following by hub genes identification. As a result, total 3 hub differentially hyper-methylated genes and 7 hub differentially hypo-methylated genes were obtained for allergic asthma. The findings might provide potential targets for allergic asthma diagnosis and treatment, and shed new lights on revealing molecular mechanism underlying this disease.