



## Significant Roles of Aberrant DNA Methylations in Colorectal Cancer

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**ABSTRACT** The aim of this study was to investigate aberrant DNA methylations in colorectal cancer (CRC). Based on DNA methylation data collected from the ArrayExpress, differentially methylated genes (DMGs) between CRC patients and normal controls were identified using *t*-test. Subsequently, the feasibility of these DMGs were determined using a hierarchical clustering analysis and significant biological functions and processes involved by these DMGs were assessed by functional enrichment analyses. Ultimately, a protein-protein interaction (PPI) network was constructed and the topological centrality analysis was applied to screen the hub DMGs for CRC. A total of 1,123 DMGs between CRC samples and normal samples were obtained. Moreover, the DMGs had a good classification performance with accuracy = 0.9935, which suggested the feasibility and confidence of these DMGs. 37 significant gene ontology (GO) terms and 31 significant pathways were gained for CRC patients. 7 hub DMGs were extracted from the sub-network of PPI network