

ABERRANT DNA METHYLATION OF RUN DOMAIN CONTAINING 3B IN  
LYMPHOID MALIGNANCIES

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ABSTRACT

Heritable changes to DNA conformation can have significant impacts on gene expression without altering the DNA sequence. The RUN domain containing 3B gene (*RUNDC3B*) has been shown to be differentially expressed in cancer types such as, acute lymphoblastic leukemia. This differential expression has been linked to methylation of the gene. Combined bisulfite restriction analysis and methylation specific PCR were used to determine the methylation status of five regions spanning a CpG island (CGI) in the promoter region of *RUNDC3B*. This analysis was completed in cell lines from lymphoid malignancies, myeloid malignancies, various solid tumor cancers, and healthy lymphoid cell lines. To determine the effect of aberrant DNA methylation on *RUNDC3B* expression, real-time PCR was utilized. The lymphoid malignancies were found to have more prominent methylation and express *RUNDC3B* at lower levels than other malignant and healthy lymphoid cell lines. Sequence analysis of the CGI in the *RUNDC3B* promoter (*RUNDC3B* CGI) was performed to support the importance of this region as a regulatory element in several species. In this project we have extended our understanding of aberrant *RUNDC3B* CGI methylation to include cell lines representing 15 malignancies. Our data suggest that methylation located in the *RUNDC3B* CGI may serve as a biomarker for lymphoid malignancies. Additionally, the results provide the basis for continued analysis of the role of *RUNDC3B* repression in the pathogenesis of lymphoid malignancies.