

MAPPING GENOME-WIDE DNA METHYLATION PATTERNS IN GLIOMAS IN CONTEXT OF IDH GENE MUTATION STATUS AND REST TRANSCRIPTION FACTOR BINDING

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Methylation of DNA regulatory regions influence gene expression. Alterations of methylome play an important role in the glioma pathogenesis. Here we have identified differentially methylated sites in gliomas of different histopathological WHO grades (I,II,III and IV) or IDH gene mutation status (n = 21). We used bisulphite conversion and SeqCap Epi CpGiant Methylation panel with Illumina NGS sequencing. Additionally ChIPseq analysis for REST transcription factor was performed on chromatin isolated from freshly resected glioma tumors as well as from IDH mutated and paired isogenic WT cell line. For the same brain tumor samples RNA-seq was performed. We have detected differential pathways affected in IDH mutant and WT samples. We have also noted differential REST transcription factor binding to differentially methylated promoters. We believe that REST may be a mediator of IDH-related phenotype in human gliomas.

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