HIC2

HIC ZBTB transcriptional repressor 2 (HIC2) is a hypermethylated gene that plays an important functional role in cardiac development. However, the actual role of HIC2 in glioma progression remains unclear. This study aimed to investigate the function of HIC2 and whether it could be a prognostic biomarker in glioma.

Methods: The DNA methylation and mRNA expression profiles of HIC2 were downloaded from public databases. The prognostic prediction ability and mechanism research of HIC2 were evaluated.

Results: We found that HIC2 was hypermethylated and expressed at low levels in glioma samples. Hypermethylation and low expression of HIC2 predicted poor prognosis. Multivariate Cox regression analysis suggested that HIC2 was an independent prognostic factor for gliomas. Co-IP assays demonstrated that HIC2 interacts with RNF44, and dual-luciferase reporter assays and ChIP assays revealed that HIC2 transcriptionally inhibits PTPRN2 expression.

The findings suggest that HIC2 represents a tumor suppressor gene and prognostic biomarker for glioma progression and that overexpression of HIC2 inhibits the glioma proliferation in vitro and in vivo by interacting with RNF44 and PTPRN2 1).

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Luo F, Liao Y, Cao E, Yang Y, Tang K, Zhou D, Zhou D, Cai H. Hypermethylation of HIC2 is a potential prognostic biomarker and tumor suppressor of glioma based on bioinformatics analysis and experiments. CNS Neurosci Ther. 2023 Jan 17. doi: 10.1111/cns.14093. Epub ahead of print. PMID: 36650953.