N7-methylguanosine

N7-methylguanosine (m7G) modification signature has recently emerged as a crucial regulator of tumor progression and treatment in cancer. However, there is limited information available on the genomic profile of low-grade gliomas (LGGs) related to m7G methylation modification genes' function in tumorigenesis and progression.

Maimaiti et al. employed bioinformatics methods to characterize m7G modifications in individuals with LGG from The Chinese Glioma Genome Atlas (CGGA) and The Cancer Genome Atlas (TCGA). They used gene set enrichment analysis (GSEA), single sample GSEA (ssGSEA), CIBERSORT algorithm, ESTIMATE algorithm, and TIDE to evaluate the association between m7G modification patterns, tumor microenvironment (TME) cell infiltration properties, and immune infiltration markers. The m7G scoring scheme using principal component analysis (PCA) was employed to investigate the m7G modification patterns quantitatively. We examined the m7G modification hub genes' expression levels in normal samples, refractory epilepsy samples, and LGG samples using immunohistochemistry, western-blotting, and qRT-PCR. Our findings revealed that individuals with LGG could be categorized into two groups based on m7G scores (high and low) according to the properties of m7G. Moreover, we observed that high m7G score was associated with significant clinical benefit and prolonged survival duration in the anti-PD-1 cohort, while low m7G score was associated with improved prognostic outcomes and increased likelihood of complete or partial response in the anti-PD-L1 cohort. Different m7G subtypes also showed varying Tumor Mutational Burden (TMB) and immune profiles and might have distinct responses to immunotherapy. Furthermore, we identified five potential genetic markers that were highly correlated with the m7G score signature index. These findings provide insight into the features and classification associated with m7G methylation modifications and may aid in improving the clinical outcome of LGG [1)]

The goal of a study was to examine the expression patterns of 31 critical regulators linked with m7G RNA methylation and their prognostic significance in gliomas. To begin, we systematically analyzed patient clinical and prognostic data and mRNA gene expression data from The Cancer Genome Atlas (TCGA) and the Gene Expression Omnibus (GEO) databases. We found that 17 key regulators of m7G RNA methylation showed significantly higher expression levels in gliomas. We then divided the sample into two subgroups by consensus clustering. Cluster 2 had a poorer prognosis than cluster 1 and was associated with a higher histological grade. In addition, cluster 2 was significantly enriched for cancer-related pathways. Based on this discovery, we developed a risk model involving three m7G methylation regulators. Patients were divided into high-risk and low-risk groups based on risk scores. Overall survival (OS) was significantly lower in the high-risk group than in the low-risk group. Further analysis showed that the risk score was an independent prognostic factor for gliomas [2)]

1)
Maimaiti A, Feng Z, Liu Y, Turhon M, Xie Z, Baihetiyaer Y, Wang X, Kasimu M, Jiang L, Wang Y, Wang Z, Pei Y. N7-methylguanosin regulators-mediated methylation modification patterns and characterization of the immune microenvironment in lower-grade glioma. Eur J Med Res. 2023 Mar 30;28(1):144. doi: 10.1186/s40001-023-01108-4. PMID: 36998056.
2)
Chen Z, Zhang Z, Ding W, Zhang JH, Tan ZL, Mei YR, He W, Wang XJ. Expression and Potential Biomarkers of Regulators for M7G RNA Modification in Gliomas. Front Neurol. 2022 May 9;13:886246. doi: 10.3389/fneur.2022.886246. PMID: 35614925; PMCID: PMC9124973.