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# Characterization of m6A modification patterns and their prognostic implications across various cancer types

Yebin Ryu[1,2], Eunhyong Chang[1,2], and Joon-Yong An[1,2,3,*]

[1] *Department of Integrated Biomedical and Life Science, Korea University*
[2] *L-HOPE Program for Community-Based Total Learning Health Systems, Korea University*
[3] *School of Biosystem and Biomedical Science, College of Health Science, Korea University*
**Corresponding author: joonan30@korea.ac.kr*

N6-methyladenosine (m6A) is the most prevalent internal modification found in the messenger RNA of eukaryotic cells. Growing evidence indicates that m6A RNA methylation significantly affects RNA metabolism, and disruptions in m6A modification and its associated components—writers, erasers, and readers—are commonly observed across various cancer types. Despite this, the clinical implications of m6A interactive genes on these cancers and their prognostic relationships remain largely undefined. In this study, we characterized m6A modification patterns across 10 different cancer types by analyzing the expression of 25 m6A regulatory genes. Our results revealed distinct m6A subtypes in 6 out of the 10 cancer types, with the expression of m6A readers IGF2BP family emerging as key determinants of subtype differentiation. Subtypes with elevated IGF2BP expression were characterized by enhanced cell cycle activity and reduced immune response. Furthermore, we conducted integrative proteomic and phosphoproteomic analyses, identifying distinct transcription factor and kinase activity among the subtypes. Our findings suggest potential strategies for targeting m6A regulators as a therapeutic approach and underscore the prognostic significance of m6A-related subtypes in cancer.