

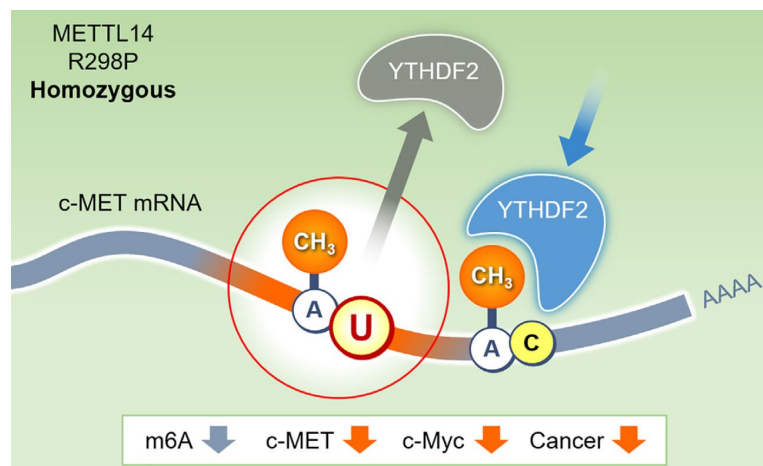
A cancer-associated METTL14 mutation induces aberrant m6A modification, affecting tumor growth

Keywords: RNA methylation, post-transcriptional modification, METTL14, cancer

Highlights

- A homozygous cancer-associated METTL14 mutation suppresses cancer cell proliferation
- Mutant METTL14 induces m6A modification at aberrant motifs
- Aberrant m6A modification affects the methylation efficiency at canonical sites
- Aberrant m6A modification destabilizes c-MET mRNA, reducing cell proliferation

The methyltransferase-like 3 (METTL3)-/METTL14-containing complex predominantly catalyzes N6-methyladenosine (m6A) modification, which affects mRNA stability. Although the METTL14 R298P mutation is found in multiple cancer types, its biological effects are not completely understood. The research group of Kotaro Miyake and Atsushi Kumanogoh (Graduate School of Medicine, Osaka University/ Immunopathology, IFRc) found that the cancer associated METTL14 R298P mutation not only reduces methylation efficacy at canonical sites but also induces m6A modification at aberrant motifs. Such aberrant modification alters the methylation pattern at the surrounding canonical sites, which affects mRNA stability and cancer cell proliferation.



Article

Journal: Cell Reports (June 23, 2023 online)

Title: A cancer-associated METTL14 mutation induces aberrant m6A modification, affecting tumor growth

Authors: Kotaro Miyake¹, Pedro Henrique Costa Cruz, Izumi Nagatomo, Yuki Kato, Daisuke Motooka, Shingo Satoh, Yuichi Adachi, Yoshito Takeda¹, Yukio Kawahara, Atsushi Kumanogoh* (*corresponding)

doi: 10.1016/j.celrep.2023.112688.