# A043 · Single-base mapping of m6A in lncRNAs reveals a distinct landscape linked to transposable elements and RNA processing

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N6-methyladenosine (m6A) is one of the most abundant internal modifications in eukaryotic RNAs. m6A have been extensively studied in mRNAs and shown to regulate multiple aspects of mRNA metabolism. Functional roles for m6A have been reported in several well-characterized lncRNAs, including MALAT1 and Xist. However, the transcriptome-wide m6A landscape and its potential roles in long non-coding RNAs (lncRNAs) remains poorly understood. To address this gap, we performed integrative multi-omics analysis to characterize its landscape in single-base resolution and potential roles in lncRNA processing. We identified a distinct m6A landscape in lncRNAs compared with mRNAs and found that m6A deposition was associated with transposable elements-derived sequence and structural features. Additionally, m6A deposition was negatively associated with lncRNA exon number, suggesting a potential inhibition between m6A deposition and lncRNA splicing. To investigate the underlying mechanism, we found that depletion of the exon junction complex (EJC) increased the number of m6A-containing internal exons, suggesting that EJC may inhibit m6A deposition during lncRNA splicing. Extending our analysis to 3′-end processing, we found that m6A was enriched near non-canonical cleavage sites of lncRNAs, suggesting an association between m6A and alternative cleavage and polyadenylation. Together, our findings define single-base-resolution m6A landscape in lncRNAs and link m6A to transposable elements and key aspects of lncRNA processing, including splicing and 3′-end formation. These results broaden our understanding of the epitranscriptomic landscape of lncRNAs and reveal potential roles for m6A in regulating lncRNA processing.

# Single-base mapping of m6A in lncRNAs reveals a distinct landscape linked to transposable elements and RNA processing

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**ABSTRACT**

N6-methyladenosine (m6A) is one of the most abundant internal modifications in eukaryotic RNAs. m6A have been extensively studied in mRNAs and shown to regulate multiple aspects of mRNA metabolism. Functional roles for m6A have been reported in several well-characterized lncRNAs, including *MALAT1* and *Xist*. However, the transcriptome-wide m6A landscape and its potential roles in long non-coding RNAs (lncRNAs) remains poorly understood. To address this gap, we performed integrative multi-omics analysis to characterize its landscape in single-base resolution and potential roles in lncRNA processing. We identified a distinct m6A landscape in lncRNAs compared with mRNAs and found that m6A deposition was associated with transposable elements-derived sequence and structural features. Additionally, m6A deposition was negatively associated with lncRNA exon number, suggesting a potential inhibition between m6A deposition and lncRNA splicing. To investigate the underlying mechanism, we found that depletion of the exon junction complex (EJC) increased the number of m6A-containing internal exons, suggesting that EJC may inhibit m6A deposition during lncRNA splicing. Extending our analysis to 3′-end processing, we found that m6A was enriched near non-canonical cleavage sites of lncRNAs, suggesting an association between m6A and alternative cleavage and polyadenylation. Together, our findings define single-base-resolution m6A landscape in lncRNAs and link m6A to transposable elements and key aspects of lncRNA processing, including splicing and 3′-end formation. These results broaden our understanding of the epitranscriptomic landscape of lncRNAs and reveal potential roles for m6A in regulating lncRNA processing.