

# MeRIP-Seq: A method for the detection and characterization of N6-methyladenosine (m6A) in RNA

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## Technology description

The inventors have described a technique for the detection and characterization of modified bases such as m6A in RNA transcriptomes using sequencing and algorithmic analysis.

# **Technology Overview**

m6A is a widespread, reversible modification that is commonly observed in evolutionarily conserved regions, and is enriched near the stop codon. It was recently discovered that FTO, a gene that regulates fat mass and obesity, is also capable of demethylating m6A. This suggests that RNA base modifications may display epigenetic properties, and that misregulation of pathways involving adenosine methylation may affect physiological processes in human. Hence, the identification and characterization of modified bases in RNA may lead to a better understanding of biological pathways. While several techniques exist for analyzing modifications in DNA bases, such methods are not available for the successful analysis of RNA transcriptomes. The inventors have disclosed a method that specifically enables them to enrich RNA fragments that contain m6A modification by separating them with an antibody specific for m6A (affinity enrichment strategy), and then characterizing these fragments by next generation sequencing and a sophisticated computational algorithmic analysis.

#### Additional Information

 $\cdot$  Comprehensive Analysis of mRNA Methylation Reveals Enrichment in 3' UTRs and Near Stop Codons . Meyer K.D., et. al., Cell 2012.

#### Application area

- · Detection and characterization of m6A modification in RNA
- · Identification of altered patterns of m6A distribution across different tissues for the diagnosis of specific associated disease states.
- · Determining the effect of therapy for specific associated disease states by analyzing the changes in m6A distribution patterns before and after treatment
- · Kits for the easy detection and characterization of m6A in RNA.

#### Advantages

- · This method is highly amenable to high throughput detection studies
- · This technique can be used to analyze RNA modifications from all major organisms
- · With the availability of specific antibodies, this method can be used to detect most types of modified bases

## Institution

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