Visualisation and functional analysis of single-nucleotide modifications in mRNAs using the RNAModR package

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1 Introduction

Following is a typical workflow for visualising and analysing single-nucleotide modifications:

1. Construction of a custom transcriptome.

2. Mapping of genome alignment-based single-nucleotide modifications to transcript coordinates.

3. Visualisation of basic metrics, e.g. distribution of sites across different transcript sections.

4. Enrichment analyses of single-nucleotide modifications.