**Description about INPUT files**

**Input file name:** m6A\_modification\_seuence.csv(comma separated columns).

Description of this input file’s columns are as follows:

Column 1: Name of the transcript

Column 2: Sequence of m6A modification site

**Input file name:** mRNA\_3utr\_target\_sequence.txt

This file contains 3’UTR sequence of the target mRNAs in FASTA format.

**Description about OUTPUT files**

**mRNA\_3utr\_target\_sequence\_nr.txt:** This file contains 3’UTR sequence of the target mRNAs in FASTA format and it remove any newline in the sequence.

**m6A\_modification\_location\_for\_distance\_calculation.csv:** This file contains location of sequence of m6A modification site with respect to first nucleotide of the 3’UTR of the mRNA. This file will be used as input for distance calculation.

**m6A\_modification\_position\_\_gene\_not\_matched.csv:** This file contains the gene list which didn’t match to mRNAs used as input 3’UTR sequences

**m6A\_modification\_position\_not\_find.csv:** This file contains the sequence of m6A modification site which was not align in the target mRNA.

**m6A\_modification\_loaction.csv:** Combination of the other three output files

Description of the output files’ columns are as follows:

Column 1: Name of the transcript

Column 2: Sequence of m6A modification site

Column 3: Number of nucleotide(s) from start of the 3’UTR to nearest nucleotide of the sequence of m6A modification site.

Column 4: Number of nucleotides from start of the 3’UTR to middle most Adenine(A) of the sequence of m6A modification site.

Column 5: Number of nucleotide(s) from start of the 3’UTR to farthest nucleotide of the sequence of m6A modification site.

Column 6: Length of 3’UTR of the mRNA.