**Description about INPUT files**

**Input file name:** miRNA\_RBP\_binding\_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 miRNA target/RBP binding site

**Input file name:** miRNA\_RBP\_3utr\_target\_sequence.txt

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

**Description about OUTPUT files**

**miRNA\_RBP\_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.

**miRNA\_RBP\_binding\_location\_for\_distance\_calculation.csv:** This file contains location of target sequence of miRNAs or binding sequence of RBPs with respect to first nucleotide of the 3’UTR of the mRNA. This file will be used as input for distance calculation.

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

**miRNA\_RBP\_binding\_position\_not\_find.csv:** This file contains the target/binding sequence which was not align in the target mRNA.

**miRNA\_RBP\_binding\_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 miRNA target/RBP binding site

Column 3: Number of nucleotide(s) from start of the 3’UTR to nearest nucleotide of the target/binding sequence of miRNA/RBP.

Column 4: Number of nucleotides from start of the 3’UTR to middle most nucleotide of the target/binding sequence of miRNA/RBP.

Column 5: Number of nucleotide(s) from start of the 3’UTR to farthest nucleotide of the target/binding sequence of miRNA/RBP.

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