

COMPUTATIONAL PREDICTION AND IDENTIFICATION OF miRNAs IN ssRNA VIRUSES

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ABSTRACT:

MiRNAs are conserved endogenous small non-coding RNA molecules play a very important role in post-transcriptional regulation of gene by binding to mRNA. miRNAs have been identified in plants, animals, invertebrates and even in viruses. Recent studies have proved that as like DNA viruses even cytoplasmic RNA viruses encodes miRNA by noncanonical pathway. To find the miRNAs encoded by both (+) ssRNA and (-) ssRNA viruses, we used computational tool VMir to screen the complete genomes of selected RNA viruses. The predicted precursor miRNA hairpin structures obtained from VMir were further analyzed in miPred to identify real and pseudo miRNA. The real miRNAs analyzed in blastx program to exclude protein coding sequences and then finally identified mature miRNAs by using matureBayes. In our studies we analyzed 45 viral genomes, finally we observed that more miRNAs encoded by (-) ssRNA than the (+) ssRNA.

Keywords: *miRNAs, ssRNA viruses and computational tool.*

[I] INTRODUCTION:

MicroRNAs (miRNAs) are the class of small RNA molecules (22-25nt), single stranded conserved endogenous non-coding, which regulate the gene expression by binding to mRNA [1].

miRNA first observed in *C. elegans* [26]. miRNAs have been identified in plants [34, 28], vertebrates [25, 23, 22, 27, and 40], invertebrates [46, 43] and even in viruses. DNA viruses families such as herpesvirus, polyomavirus and

adenovirus have been identified to produce viral miRNAs [24, 2, 18, and 33]. Recent review has explained that, the expression and function of 12 miRNAs encoded by Kaposi's Sarcoma-associated Herpesvirus [17]. miRNA encoded by herpesvirus uses noncanonical mechanism [3]. These viruses have role to regulate their cellular transcriptome [36, 19, 5], replication cycles [22, 21] and also to produce small RNA product such as endogenous miRNA [39, 30]. Recent

studies have shown that RNA viruses such as influenza A virus can produce functional endogenous miRNA [44]. Noncanonical pathway is involved in cytoplasmic processes which encode functional miRNA [38, 35, 37]. Viruses encoding miRNA have been identified by cloning method [6, 7, 31,32, 5], microarray analysis [33]and by computational prediction [41, 9, 13]. In this report we used computational approach to predict miRNAs in the ssRNA viruses.

[II] MATERIALS AND METHODS:

2.1. Dataset Preparation:

There is 1037 RNA viruses, in which 860 are (+)ssRNA, 174 are(-)ssRNA, and 3 are unassigned ssRNA viruses out of this, we selected 10 viruses in both (+)ssRNA and (-)ssRNA viruses on the basis of criteria's: RNA viruses which is most commonly infect in human as a host and also recently updated in National Center for Biotechnology Information (NCBI). The selected viruses genomes were obtained from NCBI (www.ncbi.nlm.nih.gov/genome), sequences were stored in fastA format and used for further analysis.

2.2. Prediction of miRNAs encoded by ssRNA viruses:

The selected viral genomes which are stored in fastA file was scanned by using VMir Analyzer version 10[42]and visualized the hairpin-like structures of precursors miRNA candidates by using VMir Viewer[42].All resulted precursors miRNA candidates were analyzed in Blastx to identify the protein coding sequences and excluded them, the remaining sequences were analyzed in miPred program [21]to identify the real and pseudo candidates. The finally obtained precursors miRNA candidates are further analyzed to exclude the repeated sequences and then identify the mature miRNA candidates by using matureBayes[16].**[Figure 1]** shows a flowchart of ssRNA viruses prediction.

[III] RESULTS:

First we selected the list of ssRNA viruses based on the criteria's explained in dataset preparation. The preferred viruses in positive-strand viruses are *Dengue virus 1, 2, 3 and 4, Chikungunya, Encephalomyocarditis, Human enterovirus A, B, C and D, Murray Valley encephalitis, Human coronavirus, Human rhinovirus 14 and 89, Hepatitis A, B, C, delta and E, West Nile and Yellow fever virus*. And in negative-strand viruses are *Hendra, Human parainfluenza virus 1, 2, 3, 4a and 5, Measles, Mumps, Vesicular stomatitis Indiana virus, Rabies, Chandipura, Duvenhage, Human respiratory syncytial virus and Ebola virus-Sudan ebolavirus, Cote d'Ivoire ebolavirus, Reston ebolavirus and Bundibugyo ebolavirus*.

All this viral genomes are downloaded in fastA format retrieved from NCBI and each sequence was processed individually by scanning the viral genomes by VMir Analyzer [42]. The VMir Analyzer took 4hrs 20mins to display all possible pre-miRNAs hairpin structures in both direct and reverse orientation for all the viral genomes. The results of each viral genomes sequence were further filtered by using VMir Viewer [42]. The filter values for "minimal score" and "window counts" were set to the parameters of 100 and 35 respectively [42]. After the completion of all the viral genomes of both (+)ssRNA and (-)ssRNA prediction, the recorded pre-miRNAs hairpin structures were analyzed in Blastx program to identify the protein coding and non coding protein sequences, the non coding protein sequences are remained. Further analysis were carried out to the obtained viral hairpins to distinguish real from pseudo pre-miRNAs sequences by using miPred [21](<http://www.bioinf.seu.edu.cn/miRNA/>), a hybrid feature which consists of local contiguous structure sequence composition, minimum free energy (MFE) of the secondary structures were predicted by Vienna RNA software [20]and P-value of randomization test is used, which also decides whether it's a pre-miRNA hairpin like

sequences or not. Triplet-SVM-classifier which also classified real or pseudo precursor pre-miRNA [45] the prediction accuracy was 10% greater than the triplet-SVM classifier [21]. The [Table-1] shows the final predicted number list of each virus after analyzing in blastx and mipred. In both ssRNA viruses no predicted pre-miRNA sequences have been identified. The repetitive sequences are excluded. The finally obtained pre-miRNA candidates in all the ssRNA viruses were further investigated to identify the mature miRNA by using MatureBayes (<http://mirna.imbb.forth.gr/MatureBayes.html>). MatureBayes is a computational method that incorporates a Naive Bayes classifier to identify mature miRNA candidates based on sequence and secondary structure information of their miRNA precursors [16]. Naive Bayes is a simple probabilistic classifier which is based on the application of the Bayesian theorem with strong (naive) independence assumptions [16]. [Table-2] shows the pre-miRNA sequences and mature miRNA sequences predicted of each virus.

[IV] DISCUSSION:

In this study, we used computational prediction tool VMir, represents a low stringency prediction method for the identification of miRNA in viral genome of approximately 2MB in size [42]. VMir performs the analysis by sliding a 500-nt window, the program use RNAfold to perform a structure by MFE [42], by using this program we analyzed ssRNA viruses that encoded endogenous miRNA. The predicted precursor miRNAs hairpin-like structures obtained from VMir, further filtered in blastx and miPred program to obtained real precursor miRNAs candidates in the ssRNA viruses.

In our analyses we took 45 viral genomes which includes both (+)ssRNA and (-)ssRNA viruses. Out of 45 viruses, 26 viral genomes encodes miRNAs, 12 from (+)ssRNA and 14 from (-)ssRNA viruses and remaining 19 viruses

doesn't encode miRNAs. More interestingly, among the 19 viruses, 15 viruses from (+)ssRNA and remaining 4 from (-)ssRNA. This observation strongly explains that more miRNAs encoded by (-)ssRNA than the (+)ssRNA [refer Table-1].

Viruses depend upon the infection of the host cell, that they infect the molecular machinery of the cell. Some of the possible interactions are: viral miRNA target the viral genes, host miRNAs target viral genes or viral miRNA target viral genes [10]. Other studies also shown that, virus encoded miRNA inhibits the viral replication [2] and promote host cell survival [12]. Epstein-Barr virus LMP1 induces cellular microRNA [8]. RNA viruses gene expression regulated by the miRNA pathway [11]. Viral miRNAs target both viral and cellular messenger RNA [14]. Host miRNAs act as antiviral activity against the viruses [4]. In plants and invertebrate's the antiviral immunity directed by miRNA [15]. Upcoming data have shown that viral miRNA have a particular role in regulating the transition from latent to lytic replication cycle and act as antiviral responses. There is a possibility that viral miRNA may act as a suppressor of its genes by preventing the replication. Recent review explains possible antiviral therapy against viral diseases [29]. In our studies, this is a first report predicting the possible viral miRNA of the above ssRNA viruses. The prediction of viral miRNAs by using computational tools may be further conformed by northern blotting. Further, experiential design is needed to prevent diseases caused by ssRNA viruses using antiviral properties.

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Figures and Tables:

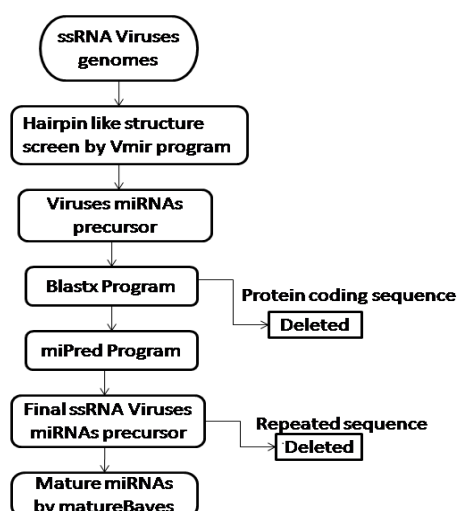


Figure 1. Flowchart explains the Predicted procedure of miRNA in ssRNA Viruses.

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ssRNA positive-strand viruses Names	Total	Predicted miRNAs	ssRNA negative-strand viruses Names	Total	Predicted miRNAs
Dengue virus 1 NC_001477.1	7	2	Hendra virus NC_001906.3	16	2
Dengue virus 2 NC_001474.2	13	2	Human parainfluenza virus 1 NC_003461.1	18	1
Dengue virus 3 NC_001475.2	10	2	Human parainfluenza virus 2 NC_003443.1	22	2
Dengue virus 4 NC_002640.1	12	Nil	Human parainfluenza virus 3 NC_001796.2	15	Nil
Chikungunya virus NC_004162.2	11	1	Human parainfluenza virus 4a NC_021928.1	18	3
Encephalomyocarditis virus NC_001479.1	7	Nil	Parainfluenza virus 5 NC_006430.1	17	1
Human enterovirus A NC_001612.1	7	Nil	Measles virus NC_001498.1	15	1
Human enterovirus B NC_001472.1	6	Nil	Mumps virus NC_002200.1	16	1
Human enterovirus C/Poliovirus NC_002058.3	3	Nil	Vesicular stomatitis Indiana virus NC_001560.1	15	Nil
Human enterovirus D NC_001430.1	6	Nil	Rabies virus NC_001542.1	11	Nil
Murray Valley encephalitis NC_000943.1	13	3	Chandipura virus NC_020805.1	8	Nil
Human coronavirus 229E NC_002645.1	98	1	Duvenhage virus NC_020810.1	12	2
Human rhinovirus 14 NC_001490.1	10	Nil	Ebola virus NC_002549.1	18	6
Human rhinovirus 89 NC_001617.1	13	Nil	Sudan ebolavirus NC_006432.1	27	7
Hepatitis A virus NC_001489.1	11	Nil	Cote d'Ivoire ebolavirus NC_014372.1	26	10
Hepatitis B virus NC_003977.1	3	Nil	Reston ebolavirus NC_004161.1	27	5
Hepatitis C virus genotype 1 NC_004102.1	35	2	Bundibugyo ebolavirus NC_014373.1	30	15
Hepatitis C virus genotype 2 NC_009823.1	32	2	Human respiratory syncytial virus NC_001781.1	17	3
Hepatitis C virus genotype 3 NC_009824.1	30	Nil			
Hepatitis C virus genotype 4 NC_009825.1	32	1			
Hepatitis C virus genotype 5 NC_009826.1	29	Nil			
Hepatitis C virus genotype 6 NC_009827.1	24	Nil			
Hepatitis delta virus NC_001653.2	3	Nil			
Hepatitis E virus NC_001434.1	10	Nil			
West Nile virus 1 NC_001563.2	12	2			
West Nile virus 2 NC_009942.1	16	2			
Yellow fever virus NC_002031.1	13	1			

Table-1: The predicted numbers of pre-miRNA sequences, the total column number explains the predicted pre-miRNA sequences by using VMir and Predicted miRNAs column explain the result after analyzed in blastx and miPred.

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ssRNA positive-strand viruses Names	Pre-miRNA	Duplex	Mature 5' stem sequence	Mature 3' stem sequence
Dengue virus 1 NC_001477.1	>MR111 AGAACCGUUGAUUCAACAG CACCAUCCAUUUUUUGGCG UUCUGUGCCUGGAAUGAUGC UGUAGAGACAGCAGGAUCU	Position 6 (5' stem):UGUUGAUUCAACAG CACCAUUC Position 52 (3' stem):AAUGAUGCUGUAGA GACAGCAG	Position 12:UUCAACAGCACCAUCCAU UUU	Position 52:AAUGAUGCUGUAGAGACAG CAG
	>MD95 AGAUCUGCUGUCUCUACAG CAUCAUCCAGGCACAGAAC GCCAAAAAUGGAAUGGUGC UGUUGAAUCAACAGGUUCU	Position 6 (5' stem):UGCUGUCUCUACAG CAUCAUUC Position 52 (3' stem):AAUGGUGCUGUUGA AUAACAG	Position 18:AGCAUCAUCCAGGCACAG AAC	Position 52:AAUGGUGCUGUUGAAUCA CAG
Dengue virus 2 NC_001474.2	>MR116 AGAACCGUUGAUUCAACAG CACCAUCCAUUUUUGGCG UUCUGUGCCUGGAAUGAUGC UGAGGAGACAGCAGGAUCU	Position 6 (5' stem):UGUUGAUUCAACAG CACCAUUC Position 52 (3' stem):AAUGAUGCUGAGGA GACAGCAG	Position 12:UUCAACAGCACCAUCCAU UUU	Position 52:AAUGAUGCUGAGGAGACAG CAG
	>MD104 AGAUCUGCUGUCUCCUCAG CAUCAUCCAGGCACAGAAC GCCAAAAAUGGAAUGGUGC UGUUGAAUCAACAGGUUCU	Position 6 (5' stem):UGCUGUCUCCUCAG CAUCAUUC Position 52 (3' stem):AAUGGUGCUGUUGA AUAACAG	Position 6:UGCUGUCUCCUCAGCAUCAU UC	Position 52:AAUGGUGCUGUUGAAUCA CAG
Dengue virus 3 NC_001475.2	>MD69 ACUAAUGAUCUUGUUGACAG GUGGAGCAAUGCUUUUCUUG AUUUCAGGUAAGGGAUUGG AAAGACUCAAUAGGACUCA UUUGU	Position 33 (5' stem):UUUCUUGAUUACAG GUAAGGGG Position 46 (3' stem):GGUAAAGGGAUUG GAAAGACUU	Position 33:UUUCUUGAUUACAGGUA GGG	Position 49:AAAGGGAUUGGAAAGACU CAA
	>MR137 AGAACCGUUGAUUCAACAG CACCAUCCAUUUUUGGCG UUCUGUGCCUGGAAUGAUGC UGAGGAGACAGCAGGAUCU	Position 6 (5' stem):UGUUGAUUCAACAG CACCAUUC Position 52 (3' stem):AAUGAUGCUGAGGA GACAGCAG	Position 12:UUCAACAGCACCAUCCAU UUU	Position 52:AAUGAUGCUGAGGAGACAG CAG
Dengue virus 4 NC_002640.1	Nil			
Chikungunya virus NC_004162.2	>MR104 UGUUUAGGUACUACUGUCG GCUUCUGCAAAUAGGUAGC UGUAGUGCGUACCUAUUUUA	Position 2 (5' stem):UUUAGGUACUACU GUCGGCUU Position 36 (3' stem):UAGCUGUAGUGCGU ACCUAUUU	Position 8:UACUUACUGUCGGCUUCUGC AA	Position 36:UAGCUGUAGUGCGUACCU UUU
Encephalomyocar ditis virus NC_001479.1	Nil			
Human enterovirus A NC_001612.1	Nil			
Human enterovirus B NC_001472.1	Nil			
Human enterovirus C / Poliovirus NC_002058.3	Nil			
Human enterovirus D NC_001430.1	Nil			
Murray Valley encephalitis NC_000943.1	> MR129 GGAAUAGAGCAGAAGAUUCUC CUAGUCUUUCCCAGGUGUC AAUAUGCUGUUGUUGAUGC UUUUGAGAGUGGGUCUCCU CUAACUCUAGUCC	Position 20 (5' stem):CUAGUCUUUCCCA GGUGUCA Position 53 (3' stem):UUGAUGC UUUGAG AGUGGGGU	Position 38:UCAAU AUGCUGUUGUUUGA UGC	Position 53:UUGAUGC UUUGAGAGUGG GGU
	>MD127 AGAUCUUCUGCUCU AUUCCA ACAUCAGUCACAAGGCACCG AGCGCCGAACACUGUGACUG AUGGGGGAGAAGACCACAGG AUCU	Position 18 (5' stem):CAACAUCAGUCACA AGGCACCG Position 45 (3' stem):CGAACACUGUGACU GAUGGGGG	Position 11:UCUAUCCAACAUCAGUCA CAA	Position 45:CGAACACUGUGACUGAUGG GGG

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	>MR124 ACACGGGCUUCAUCUCCA GUUGGCAGGGACUCCUCU CGAGACGGUUCUGGGAGG UCCAACCGUGGAGAAUC CUUUGGU	Position 17 (5' stem):AUUGUUGGCAGG CUCUCUU Position 49 (3' stem):UCUGGGAGGCU CAACCGUG	Position 14:UCCAUUGUUGGCAGG CCU	Position 49:UCUGGGAGGCUUCCA GUG
Human coronavirus 229E NC_002645.1	>MD205 UGUCUUAAUUAUUUCAG CUGUAAGUUCUACAUAU UGCGUUUUGAGCGUUA GUCAAAUUGCAAUUUU AUGUUAGAAGUUACAGA CA	Position 25 (5' stem):AGUUCUACAUA UUGCGUU Position 65 (3' stem):AUUGCAAUAUU AAUGUUA	Position 25 :AGUUCUACAUAUUUGCG UU	Position 64:AAUGCAAUAUUUUAA GUA
Human rhinovirus 14 NC_001490.1	Nil			
Human rhinovirus 89 NC_001617.1	Nil			
Hepatitis A virus NC_001489.1	Nil			
Hepatitis B virus NC_003977.1	Nil			
Hepatitis C virus genotype 1 NC_004102.1	>MD85 ACAGCAGAGGGCGCGG AAGGUUGCGAGAGGGUC CCCCUUCUAUGGCCAGC UCGGCCAGCCAGCUGU	Position 13 (5' stem):CCGGGAGAAGG GCGAGAGG Position 44 (3' stem):UUCUAUGGCCA CCUCGGCC	Position 12:GCGGGAGAAGGUUG GAG	Position 44:UUCUAUGGCCAGCUC GCC
	>MR85 GACAGCUGGCGGCGGAG GCUGGCCAUAAGAAGGG ACCCUCUCGCCAACCUC CGGCCGCCUCUGCUUU	Position 2 (5' stem):CAGCUGGCGGCG AGGAGCUG Position 55 (3' stem):UUCUCCGGCCGC UCUGCUGU	Position 29:AGAAGGGGUGACCC GCC	Position 55:UUCUCCGGCCGCCUC GU
Hepatitis C virus genotype 2 NC_009823.1	>MD87 GGAGCUUGGAGAUCCAG UGGAGCCUGAGCAGGUA CCCCAACCCCCCAGGGG GGGGUGGCAGCUCGGC GGACUCGGGUCCUGGUC CUUGCUCC	Position 43 (5' stem):CAACCCCCCCCC GGGGGGG Position 59 (3' stem):GGGGGUGGCAG CCCCGCUC	Position 43:CAACCCCCCCCCAGG GG	Position 63:GGUGGCAGCUCGGC GAC
	>MR86 AGACCAGGACCCGAGUC AGCCGGGAGCUGCCACCC CCUUGGGGGGGGUUGGG CUCUACCUGCUCAGGCU GGUCUGGAUCU	Position 17 (5' stem):CCGAGCCGGGAG GCCACCC Position 53 (3' stem):GUUGGGGCUCU UGCUCAGG	Position 36:CCCCCUGGGGGGGG UGG	Position 53:GUUGGGGCUCUACC AGG
Hepatitis C virus genotype 3 NC_009824.1	Nil			
Hepatitis C virus genotype 4 NC_009825.1	>MD82 CUGACAGACCAUCACAU AACGGCGAAUUGCGGCG GGAGAUUGGCUCGAGGG CGACCCUCGCUAGCUAG CUCGGCAGUCAGCUUUC CCCUCUUCUCAG	Position 49 (5' stem):CUCGAGGGUCAC CCCUCGU Position 64 (3' stem):CCUCGCUAGCU UCCUGGC	Position 49:CUCGAGGGUCACGAC GCU	Position 68:GCUAGCUAGUCCUC AGU
Hepatitis C virus genotype 5 NC_009826.1	Nil			
Hepatitis C virus genotype 6 NC_009827.1	Nil			
Hepatitis delta virus NC_001653.2	Nil			
Hepatitis E virus NC_001434.1	Nil			
West Nile virus 1 NC_001563.2	>MD102 GGAUCUUCUGCUCUGCAC CCAGCCACACGGCAGUG GCCGACAUAGGUGGUGG GUGCUAGAACACAGGAUC	Position 4 (5' stem):CUUCUGCUCUGC AACGAC Position 54 (3' stem):CUGGUGGUCUAG ACACAGGA	Position 8:UGCUCUGCACAACCAG AC	Position 54:CUGGUGGUCUAGAACA GGA
	>MR110 GAUCCUGUGUUCUAGCAC CCAGCCACCUAUGUCGGC ACUGUGCCUGUGGCGGU GUGCAGAGCAGAAGAUC	Position 7 (5' stem):UGUUCUAGCAC CAGCCAC Position 49 (3' stem):UGUGGCGGUUG GUG	Position 37:CGCACUGGCGUGG GCU	Position 49:UGUGGCGGUUGGUG CAG

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		CAGAGCAG		
West Nile virus 2 NC_009942.1	>MR112 AGAUCUGUGUUCUCGCACC ACCAGCCACCAUUGUCGGCG CACUGUGCCGUGUGGCUGGU UGUGCAGAGCAGAAGAUCU	Position 8 (5' stem):UGUUCUCGCACCAC CAGCCACC Position 50 (3' stem):UGUGGCUGGUUGUG CAGAGCAG	Position 5:CUGUGUUCUCGCACCACCA CC	Position 50:UGUGGCUGGUUGUCAGAG CAG
	>MD120 AGAUCUUCUGCUCUGCACA CCAGCCACACGGCACAGUGC GCCGACAAUGGUGGCUGGUG GUGCGAGAACACAGGAUCU	Position 4 (5' stem):CUUCUGCUCUGCAC AACCAGCC Position 54 (3' stem):CUGGUGGUGCGAGA ACACAGGA	Position 8:UGCUCUGCACAACCAGCCAC AC	Position 54:CUGGUGGUGCGAGAACA GGA
Yellow fever virus NC_002031.1	>MR120 AGUGUUUUGUGUUUGUCAU CCAAAGGUCUGCUUUAUCUU GAGCAAUCUGCUCACAGA CCUCUGGAGGAAAAGCAGAG AACCACU	Position 12 (5' stem):UUUGUCAUCCAAAG GUCUGCUU Position 55 (3' stem):ACAGACCUCUGGAG GAAAAGCA	Position 39:UGAGCAAACUGUCUCACA GAC	Position 55:ACAGACCUCUGGAGGAAA GCA

ssRNA negative-strand viruses Names	Pre-miRNA	Duplex	Mature 5'stem sequence	Mature 3'stem sequence
Hendra virus NC_001906.3	>MR195 CCGAACAAGGGUAAAGAGAGAU CGUUAUUAAAGUUUUUCUAAUA ACUGAUCUAUGUAGACUUGUUC GG	Position 24 (5' stem) : UUAUUAAAGUUUUUCUAAUAAC Position 39 (3' stem) : UAAUAACUGAUCUAUGUAGACU	Position 24 : UUAUUAAAGUUUUUCU UAAUAAC	Position 43 : AACUGAUCUAUGUA GACUUGUU
	>MD189 CCGAACAAGUCUACAUAGAUA GUUUAUUAAAGAAAACUAAUAA CGAUCUCUCUUUACCCUUGUUC GG	Position 6 (5' stem) : AAGUCUACAUAGAUCAGUUAAU Position 41 (3' stem) : UAACGAUCUCUCUUUACCCUUG	Position 24 : UAUUAAAGAAAACUU AAUAACG	Position 41 : UAACGAUCUCUCUU UACCCUUG
Human parainfluenza virus 1 NC_003461.1	>MD131 GAUCUUAUAUCUUCUCAUCUUU AUUAUCUAAUUUGUUUAAAGAG AUGAGUUAAACAAGUAAGAAU C	Position 4 (5' stem) : UUUAUCUUCUCAUCUUUAAUA Position 42 (3' stem) : AGAUGAGUUAAACAAGUAAGAA	Position 4 : UUUAUCUUCUCAUC UUUAUA	Position 42 : AGAUGAGUUAAACA GAUAAGAA
Human parainfluenza virus 2 NC_003443.1	>MR70 GCAAUCAGCAAUCCCACGACAA CCAAAGUAAUCACUGAUAGUAU UAAUGCUAUGCACUAGUGAA UAAAGUGUCUUGGCUGCCUGG CUUGAUUAGC	Position 4 (5' stem) : UCAGCAAUCCCACGACAAACAA Position 73 (3' stem) : UCUUGGCUGUCCUGGCUUGAUU	Position 43 : UUAUUGCUAUUGCAC UUAGUGA	Position 73 : UCUUGGCUGUCCUG GCUUGAUU
	>MR36 GGGGUUUGGACUAUGAUUUUGG GAUCUGUCUGAGAGGGCAAGCUU UCGGACCUAGAUUUUCUCUAUU GUGUCCUUUAAAUUUUACUUA CUUC	Position 9 (5' stem) : ACUAUGAUUUUGGGAUCUGUCU Position 50 (3' stem) : CUAGAUUUUCUCUAUUGUGUCC	Position 26 : UGUCUGAGAGGGCAAG CUUUCGG	Position 50 : CUAGAUUUUCUCUA UUGUGUCC
	Nil			
Human parainfluenza virus 4a NC_021928.1	>MR184 UUUAAUCUGAUUAAUAAUAG CCUAGGGAAUUCUUUGAUUAG GAUAUCUUGCAUGAUUAAUUC AUAAUCAUUAAA	Position 12 (5' stem) : AUAAUAAUAGCCUAGGGAAUUC Position 44 (3' stem) : GAUAUCUUGCAUGAUUAAUUC	Position 28 : GAAUUCUUUGAUU GGUAUUC	Position 44 : GAUAUCUUGCAUGA UUAAUUC
	>MR18 GGAAUUAGAAUUUAGUAGCC UGAACGAUUGAGUGACCUGAAU GCAACCGUUCAGCCUACGUAG UUUUUCU	Position 5 (5' stem) : UAGAAAUUUAGUAGCCUGAAC Position 48 (3' stem) : CCGUUCAGCCUACGUAGUUU	Position 10 : AUUAUAGUAGCCUGA ACGAUUG	Position 48 : CCGUUCAGCCUAC GUAGUUU
	>MR17 AUCAUAGUGAUUAGAUUCUUGU AUGCUGUCUUGCAUCAUGAUU	Position 2 (5' stem) : CAUAGUGAUUAGAUUCUUGUAU Position 34 (3' stem) :	Position 21 : UAUGCUGUCUUGCAU CAAUGAU	Position 34 : AUCAAUGAUUGGUC AGUUGUGA

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	GGUCAGUUGUGAU	AUCAAUGAUUGGUCAGUUGUGA		
Parainfluenza virus 5 NC_006430.1	>MR67 GAAGGUUACAAACAGAAAGAAG AUGAAUAGGAAGCAGAAUUA GGUUUCCUGCUCUCCUUGUAGC UUUCU	Position 2 (5' stem) : AGGUUACAAACAGAAAGAAGAU Position 47 (3' stem) : UUCCUGCUCUCCUUGUAGCUUU	Position 31 : AAGCAGAUAAUUAGG UUCCUG	Position 47 : UUCCUGCUCUCCU GUAGCUUU
Measles virus NC_001498.1	>MD54 UGCGGGAGUUGUCCUGGCAGGU GCGGCCUAGGCGUUGCCACAG CUGCUCAGAAACAGCCGGCA	Position 6 (5' stem) : AGUUGUCCUGGCAGGUGCGGCC Position 39 (3' stem) : CACAGCUGCUCAGAAACAGCC	Position 6 : AGUUGUCCUGGCAGG UGCGGCC	Position 39 : CACAGCUCAGAA UAACAGCC
Mumps virus NC_002200.1	>MR22 GCUUGCCCGAAAGAAACACGA UCAAGAUAAUUGUGUGAUGCU CGUAGAACUAAUUCUUCCGGG CCUAGU	Position 23 (5' stem) : CAAGAUAAUUGUGUGAUGCUC Position 36 (3' stem) : UCGAUGCUCGUAAGAACUAAUUC	Position 23 : CAAGAUAAUUGUGUC GAUGCUC	Position 39 : AUGCUCGUAAGAACU AAUUCUUU
Vesicular stomatitis Indiana virus NC_001560.1	Nil			
Rabies virus NC_001542.1	Nil			
Chandipura virus NC_020805.1	Nil			
Duvnenge virus NC_020810.1	>MD56 GAGUGAGAGGCCCGAUGAUGCU UGAGGAUGUCCAGAUUGAACA UUCUUUAUGAUUUACCUCAUCA CUU	Position 5 (5' stem) : AGAGGCCCGAUGAUGCUUGAGG Position 43 (3' stem) : AUUCUUUAUGAUUUACCUCAUC	Position 28 : UGUCCAGAUUGAUA AUUCUUU	Position 43 : AUUCUUUAUGAUUU ACCUCAUC
	>MR58 UGUGGACUCCAGCAUGCUGAAA AAUGAUCGCUCAAGGAGGGGU GUUAAUUUUUUUUUUUUUUUU CUAUUCUCUUUGUGAUGUUUU UUUCAUGAGCACGCAUCCAUA	Position 20 (5' stem) : AAAUGAUCGCUCAAGGAGGG Position 69 (3' stem) : UUCCUUUUUGUGAUGUUUUUUU	Position 21 : AAAUGAUCGCUCAAA GGAGGGG	Position 69 : UUCCUUUUUGUGAU GUUUUUUU
Ebola virus NC_002549.1	>MD39 GAUGAAGAUUAAAGAAAACCUA CCUCGGCUGAGAGAGUUUUU UCAUUAACCUUCAUC	Position 3 (5' stem) : GAAGAUUAAAGAAAACCUACCU Position 35 (3' stem) : AGUGUUUUUCAUUAACCUUCA	Position 7 : AUUAAAGAAAACCUA CCUCGGC	Position 35 : AGUGUUUUUCAU AACCUUCA
	>MR63 GCUCAACGUUACAAGAUGAAG GUUAAUGAAAAACACUCUCUC AGCCGAGGUAGGUUUUUUUAA UCUUAUCACUUUUGGUUUGG U	Position 17 (5' stem) : UGAAGGUUAAUGAAAAACACU Position 52 (3' stem) : UAGGUUUUUUUAAUCUUAUC	Position 17 : UGAAGGUUAAUGAAA AAACACU	Position 52 : UAGGUUUUUUUAA UCUUAUC
	>MD77 UUCUAAUCUUUUAAACUCACA GUUAAUCAUAAACAAGGUUUGA CAUCAAUUCUAGUUAUCUCUUUG AGAAUGAUAAACUUGAUGAAGA UUAAGAA	Position 15 (5' stem) : ACUCACAGUUAUUAUAAACAA Position 60 (3' stem) : UCUUUGAGAAUGAUAAACUUGA	Position 39 : UUUGACAUAUUAUCU GUUAUCU	Position 60 : UCUUUGAGAAUGAU AAACUUGA
	>MD92 CCGGAUUUGCUAAACUAAUGAU GAAGAUUAAUGCGGAGGUCUGA UAAGAAUAAACCUUAAUUAUCA GAUUAGGCCCAAGAGGCAUUC UUAUCUCCUUUUAGCAAAGUA CUAUUUCAGG	Position 9 (5' stem) : CUAAACUAAUGAUGAAGAUUAA Position 84 (3' stem) : AUUCUUAUCUCCUUUUAGCAA	Position 26 : AUUAAUGCGGAGGUC UGAUAAG	Position 84 : AUUCUUAUCUCCU UUUAGCAA
	>MR128 CCUGAAAUAGUACUUUGCUAAA AGGAGAUAGAAGAUUGCCUUG GGGCCUAAUCUGAAUAAUAAAG UUUAAUUCUUAUCAGACCUCG AUUAAUCUUAUCUUAAGUUUA GCAUUUCGG	Position 13 (5' stem) : UUUGCUGAAAGGAGAUAGAA Position 90 (3' stem) : UAAUCUUAUCUUAAGUUUAGC	Position 13 : UUUGCUGAAAGGAGA UGAAGAA	Position 95 : UUAUCUUAAGUUU AGCAUUC
	>MR131 AGCCAUGGUUUUUUCUCAGGUC UUGCUGGUGUCUGGAGUAUCA	Position 19 (5' stem) : GUCUUGCUUGGUGUCUGGAGUA Position 55 (3' stem) :	Position 37 : AGUAUCAAUUUUUG UUGUCUA	Position 55 : UCUAGACACUCUCA GUUCAACC

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	AUAAUUUGUUGUCUAGACACUC UCAGUUAACCUUGAAACCUUG CGCU	UCUAGACACUCUCAGUUAACCC		
Sudan ebolavirus NC_006432.1	>MR49 UUCUGAGUCCUAAAUUUGUUU AAAUGAGAUGAAGGUAAAGAAA AAGAUUUUCCUGAGAAAUC CUCUUUUUCUAAUCUUAUCA AUUUUAAUUUGCUCGGGGG	Position 27 (5' stem) : AGAUGAAGGUAAAGAAAAAGAU Position 63 (3' stem) : UCCUCUUUUUCUAAUCUUA	Position 27 : AGAUGAAGGUAAAGAA AAAAGAU	Position 62 : AUCCUCUUUUUCU UAAUCUUC
	>MD51 CCCGAGCAAAUAAAUGAUG AAGAUUAGAAAAAGAGGGAU UUCACAGGAAAAUCUUUUUC UUACCUCAUCUCAUUUAAACA AAUUUAGG	Position 15 (5' stem) : AUUGAUGAAGAUUAAAGAAAAAG Position 59 (3' stem) : UUUUUUCUUACCUUCUCUCAU	Position 22 : AAGAUUAGAAAAAG AGGGAU	Position 59 : UUUUUUCUUACCU CAUCUCAU
	>MR113 GAUGAAAAUUGGCAGAGCAAGG UGUUUGGAUUGAAGUCAUCU GGAACCUUCUCAUUAAUUUCA UC	Position 4 (5' stem) : AAAAUUGGCAGAGCAAGGUGUU Position 43 (3' stem) : UGGAACCUUCUCAUUAAUUUC	Position 6 : AAUUGGCAGAGCAAG GUGUUUG	Position 43 : UGGAACCUUCUCAU UAAUUUC
	>MR112 GACUGUAUUAAUAGUACGUGU AGGACUACCUAUACCUAAGAC UAUACUAUAUC	Position 3 (5' stem) : UGUAUUAAUAGUACGUGUAGG Position 32 (3' stem) : UAUACCUAAGACUAUAUCA	Position 16 : ACGUGUAGGACUACC CUAUACC	Position 32 : UAUACCUAAGACUA UACUAUCA
	>MD112 GAUGAAAAUAAUGAGAAGGUU CCAAGAUUGACUCAAUCCAAA CACCUUGCUCUGCCAAUUUCA UC	Position 2 (5' stem) : UGAAAAUAAUGAGAAGGUUCC Position 45 (3' stem) : ACCUUGCUCUGCCAAUUUCAU	Position 28 : UUGACUCAAUCCAA ACACCUU	Position 45 : ACCUUGCUCUGCCA AUUUUCAU
	>MD121 GGUCUAGAUUUAAUAGAAC GAGGAAGAUUAAAGAAAAAGUCC AUAAUGCUGGGGAGGCAUCCU UGCCACCAUAGGACUUUUCAA UUCUCUAAUUUUAUGAUGGCUA CCC	Position 36 (5' stem) : AAAAGUCCAAUAGCUGGGGAG Position 65 (3' stem) : UUGCCACCAUAGGACUUUUCAA	Position 35 : AAAAGUCCAAUAG CUGGGGA	Position 65 : UUGCCACCAUAGGA CUUUUCA
Cote d'Ivoire ebolavirus NC_014372.1	>MR62 CCUAUCAUCAUGUGUUGCGCC GGGCGCCUCCUACCGGUGUU UGGGACUGCCAUGCGUUGAUGU CUGAAGGUGAGGGAGGAUGGGA CCGCACGUGUCUUUGACUGGG	Position 14 (5' stem) : UUGUCGCGGGGCGCCUCCUCA Position 70 (3' stem) : AGGUGAGGGAGGAUGGGACCGC	Position 28 : CUCCUCACCGGUGU UUGGGAC	Position 70 : AGGUGAGGGAGGAU GGGACCGC
	>MR66 GAUGAAGUUUAAAGAAUAGCU CCUUGCAACUGAAGGAGGCUUU UUCUAAUCUUAUC	Position 2 (5' stem) : UGAAGUUUAAAGAAUAGCUCC Position 36 (3' stem) : GAGGCUUUUCUAAUCUUAUC	Position 16 : UUAGCUCCUUGCAAC UGAAGGA	Position 36 : GAGGCUUUUCUUA AUCUUAUC
	>MR83 GGGUGGGAGUGAAGCGGGGAG AGAUAGACGGUUUGAGCUGAUU UGCUGGGGUUGGUAUCGAGUU GGGGAAUUUUGCUGGCGUUGG UGGGAUUGCGGGAGGGGUUGAU CAGCUUAGACUUGGGGUCUGUG UUGCUCUGGCUUGAUGUUCU UGCUCU	Position 23 (5' stem) : GAUAGACGGUUUGAGCUGAUUU Position 109 (3' stem) : UCAGCUUAGACUUGGGGUCUGU	Position 23 : GAUAGACGGUUUGAG CUGAUUU	Position 135 : CUCCUGGCUUGAUG UUCUUUGC
	>MD48 GCUUAUAUUAAAGAAAAAGAACU UGAUGAAGAUUAAAGGCAACCAG UGGUGCUAUCUUAUCUCUUUG AUUUGAGUCUUAAGU	Position 11 (5' stem) : GAAAAAGAACUUGAUGAAGAUU Position 47 (3' stem) : UGCUAUCUUAUCUCUUUGAUU	Position 39 : ACCAGUGGUGCUAUC UUAUCU	Position 47 : UGCUAUCUUAUCU CUUUGAUU
	>MR109 UGUAUUUGUGGUCCUAGCAUAA AAUUUAUUGAGUUAUCCAGUUC UUUCAAUCCCCAGGAAUUUUG UGAGGUCCUUAUCAUAAAUA CA	Position 14 (5' stem) : UAGCAUAAAAUUUUAUUGAGUUA Position 49 (3' stem) : AAUCCCCAGGAAUUUUGUGAGG	Position 14 : UAGCAUAAAAUUUUAU UGAGUUA	Position 49 : AAUCCCCAGGAAUU UUGUGAGG

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Reston ebolavirus NC_004161.1	>MD85 GAUGAAGAUUAAUUGCAGAUGUC UAAAGGAUAAAACUCCAUGCA UCAGUGUUAAAUUGGGCUCUG UAGAAAUCUUAUC	Position 14 (5' stem) : CAGAUGUCUAAAGGAUAAAACAC Position 48 (3' stem) : UGUUAAAUUGGGCUCUGUAGA	Position 17 : AUGUCUAAAGGAUAA ACACUCC	Position 48 : UGUUAAAUUGGGC UCUGUAGA
	>MR156 UCAAUAGUUAGUAAUCUUAUCA AAAGUCUAAGGUGCAGCUUAAAG GAUCACAAGUUAGCAUUUUGAU GAGUUGAGUUAAUAGCGAGAG AACUAUUGA	Position 21 (5' stem) : AAAAGUCUAAGGUGCAGCUUAA Position 52 (3' stem) : GUUAGCAUUUUGAUGAGUUGAG	Position 16 : UUAUCAAAAAGUCUAA GGUGCAG	Position 52 : GUUAGCAUUUUGAU GAGUUGAG
	>MR158 GGUAGAAUGAACUUGAUUAUCU UGAGGGAUCUAAACUCGUUAA CAUGAUUGGGUAAUUGUGUAUU AAUGGUGAACCCCAUCUAUCUA AUGGGCAGUGUUCUUAUCCUCA UGUCAAAAGACAAUCAUC	Position 36 (5' stem) : GCUGUUAACAUGAUUGGGUAAU Position 73 (3' stem) : AACCCCAUCUAUCUAAUGGGCA	Position 36 : GCUGUUAACAUGAUU GGUAAU	Position 73 : AACCCCAUCUAUCU AAUGGGCA
	>MD97 UAGCUAUAGCUUGAGGAAGAUU AAGAAAAAGUGUCUGUGGGGUC UUUCGUGUAGAAGGGCACACA GCCAUAAUUCUCCUCUUAUA CAACAUGGCUA	Position 19 (5' stem) : AUUAAAGAAAAAGUGUCUGUGGG Position 60 (3' stem) : CACACAGCCAUAUUCUCCUC	Position 21 : UAAGAAAAAGUGUCU GUGGGGU	Position 60 : CACACAGCCAUAU UCUCCUC
	>MD105 GGUCUGAGGAAGAUUAGAAAA AGGCCUCGUGUUCACUUGGUUG CCGUAAGUAUCCUGUGGUUU UUUCUACCUAACUCCUCAUGC C	Position 6 (5' stem) : AGGAAGAUUAAAGAAAAAGGCCU Position 62 (3' stem) : UUUUUUUCUACCUAACUCCUC	Position 4 : UGAGGAAGAUUAAAGA AAAAGGC	Position 62 : UUUUUUUCUACCUA ACUCCUC
	>MD43 AUGUAAAUAUAACAAGUGAUGA AGAUUAGAAAAACCAGUCGGU AUUUCCAGACUUGGCAUUUCU UAUCUUAUCUUAUAAAGUGAG AUUUUUUAUCAU	Position 19 (5' stem) : UGAAGAUUAAAGAAAAACCAGUC Position 54 (3' stem) : CUUGGCAUUUCUUAUCUUAUC	Position 19 : UGAAGAUUAAAGAAAA ACCAGUC	Position 54 : CUUGGCAUUUCUUA UCUUAUC
	>MR38 GAUGAAGAUUAAAGAAUGCCAAG UCUGGAAAAUACCGACUGGUUU UUCUUAUCUUAUC	Position 2 (5' stem) : UGAAGAUUAAAGAAUGCCAAGUC Position 36 (3' stem) : ACUGGUUUUUCUUAUCUUAUC	Position 2 : UGAAGAUUAAAGAAUG CCAAGUC	Position 36 : ACUGGUUUUUCUUA AUCUUAUC
	>MR48 UGCUUGGUUUAGUUUUGACUGG GUUGAACUUCUCUUCUGGUUAC UGCAGAUAGUAGAAGCUCGCGC GGGUUCUCAAGGAAUUCUGCA	Position 18 (5' stem) : CUGGGUUGAACUUCUUCUGG Position 49 (3' stem) : AUAGUAGAAGCUCGCGGGGUU	Position 15 : UGACUGGGUUGAACU UCUCUUC	Position 49 : AUAGUAGAAGCUC GCCGGGUU
	>MD89 GAUGAAGAUUAAUUGCGGAGGA AUCAGGAAUUAACUUUAGUUC CUAAAGGCCUCGUCGGAUUCU CAUC	Position 4 (5' stem) : AAGAUUAAUUGCGGAGGAAUCA Position 45 (3' stem) : UUAAGGCCUCGUCGGAUUCU	Position 28 : AAUUAACUUUAGUU CCUUAAG	Position 45 : UUAAGGCCUCGUCC GAUUCUUC
Bundibugyo ebolavirus NC_014373.1	>MR127 ACAAAAGAUGAAGAUCUUGAA CAGAGUCUAAACUGGAACGUUUA AAUCACAAAUAUGUGUCCUUG GACAUUCGUAAUAAUCUUAUC ACUUGU	Position 20 (5' stem) : AACAGAGUCUAAACUGGAACGUU Position 55 (3' stem) : UGUGUCCUUGGACUUCUGCAU	Position 23 : AGAGUCUAAACUGGAA CGUUUAA	Position 55 : UGUGUCCUUGGAC AUCUGCAU
	>MR77 GCUGCAUUGGGCUUGCGAUGGU UGAGUUACUUCCGGAACUAAU UUCUGGACAGCAGCUUGCUAAU GGGUCUAUUGCUGC	Position 9 (5' stem) : GGCUUGCGAUGGUUGAGUUACU Position 50 (3' stem) : ACAGCAGCUUGCUAUUGGGUCU	Position 13 : UGCGAUGGUUGAGUU ACUUCC	Position 50 : ACAGCAGCUUGCUA UUGGGUCU
	>MR59 UGAGAACAUAUAAAGGCUAGAGG ACAUUGGUUAAUUUUAUUCUUA CAGUAGGUUGCAUUGGAAUUGA GAUCGGGUCCUGAUUGGCCUU GCGUUCUCA	Position 21 (5' stem) : GACAUUGGUUAAUUUUAUUCUUA Position 54 (3' stem) : CAUUGGAAUUGAGAUCCGGUCC	Position 8 : UUAAGGCUAGAGGA CAUUGGU	Position 54 : CAUUGGAAUUGAGA UCGGGUCC

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>MD36 GUUCUCAAAAAUAACAAGUGAUG AAGAUUAAAGAAAAAGCAUCCUU UACUUGAGAGGAGCUAAUUCUU UAUACUUAUCUAAUCUUUAAG UAAGUUGAAC	Position 20 (5' stem) : UGAAGAUUAAAGAAAAAGCAUCC Position 55 (3' stem) : AGCUAAUUCUUUAUACUUAUC	Position 17 : UGAUGAAGAUUAAGA AAAAGCA	Position 55 : AGCUAAUUCUUUAU ACUUAUC
>MR74 AUGAAGGUCGGAUGGUUGGUUC GGUAGCCGGACGAAGGCCUGG GGGUCGUGUGGGCCGGCAGCC UCGGACUUAU	Position 7 (5' stem) : UCGGAUGGUUGGUUCGGUAGCC Position 49 (3' stem) : GUGUGGGCCGGCAGCCUCGGA	Position 12 : UGGUUGGUUCGGUAG CCGGACG	Position 49 : GUGUGGGCCGGGA GCCUCGGA
>MD154 GUAAUUUGAAGUUAAUUUAUG AUUAGUCUUUAUCUAAAAUA AUAGCUAAUACCAAGUAUACACA AGAAGUUUAUGAUUUUGUAUUA AAUUUAU	Position 19 (5' stem) : AUGAUUAGUCUUUAUCUAAAA Position 54 (3' stem) : CAAGUAUACACAAGAAGUUUAUG	Position 19 : AUGAUUAGUCUUUA ACUAAAA	Position 54 : CAAGUAUACACAAG AAGUUUAUG
>MR108 UAUUACAGUACAACUUAGUCA AGUCAUCUGGCUGUUCUAAAUA CCCUGAGAAUUAAUAAAGUUCU AGAUUUUUGAAGGUAAUUAGGA UUUUUAGAGGUAUCUUUUUG ACUUAAUAGUUGAUUUUUGCUG AAAUG	Position 31 (5' stem) : GCUGUUCUAAAUACCCUGAGAA Position 71 (3' stem) : UUUGAAGGUAAUUAGGAUUUAU	Position 35 : UUCUAAAUACCCUGA GAAUUA	Position 71 : UUUGAAGGUAAUUA GGAUUUAU
>MR147 UUGCUCUUUUUUAAAAGUCCU CCUUAAUUAUAGUGAUAAAGCUU AAAUUGAUAGACUUUUAAAAGG AGUAA	Position 4 (5' stem) : UCUUUUUUAAAAGUCCUCCUU Position 46 (3' stem) : AUUGAUAGACUUUUAAAAGGAG	Position 11 : UAAAAGUCCUCCUU AAUUUA	Position 46 : AUUGAUAGACUUUU AAAAGGAG
>MD87 UCAUUUUCUUAAUAAUUUUCU CUAAAUUACUGACUUAAUUAGC UUGUAUCAGAUAAUUCGAAA CCAAUUUAUCAUAAGGCAUAAU UUGUAUAAGUGAUUUAGGAUUU ACCCAGAAUGA	Position 21 (5' stem) : UCUAAAUUACUGACUUAAUUAG Position 83 (3' stem) : AUAAAUUUGUAUAAGUGAUUUAG	Position 21 : UCUAAAUUACUGACU UAAUUAG	Position 84 : UAAUUUGUAUAAGU GAUUUAGG
>MD19 CCUCCCAAGUUGUCAUUAAAGA AAAAAUUAUGAUGAAGAUUAA AACCUCUACAGAGCUUUUCU UCUACGCUUGGUAGG	Position 12 (5' stem) : GUCAUUAAAGAAAAAUUAUGA Position 49 (3' stem) : UCAUCAGAGCUUUUCUUCUAC	Position 18 : AAGAAAAAUUAUG AUGAAGA	Position 49 : UCAUCAGAGCUAUU UCUUCUAC
>MR60 GAUGAAGUAUAAAGAAUUAGCU CCUCUCAAGUAAAGGAUGCUUU UUCUUAUCUUAUC	Position 2 (5' stem) : UGAAGUAUAAAGAAUUAGCUCC Position 36 (3' stem) : GAUGCUUUUCUUAUCUUAUC	Position 7 : UAUAAAGAAUUAGCU CCUCUCA	Position 36 : GAUGCUUUUCUUA AUCUUAUC
>MR224 UAUAACUCAACAUUUAGGUAAG AAUUAAUCUAAUUUAUCCUAC UGUGAUGUCAUUUUAAUGCAUA AACCACAGUAAUUUUUCUUAU UGAUAGAGUAUAUG	Position 15 (5' stem) : AGGUAAGAAUUAAUCUUAUUUA Position 64 (3' stem) : UAAACCACAGUAAUUUUUCUUA	Position 7 : CAACAUUUAGGUAAG AAUUAAAC	Position 64 : UAAACCACAGUAAU UUUUUCUUA
>MD64 UGGAGGCAAUGGGUCCUGCCG GGAUCGGGAUCACGGGGUAAU AAUCGAGUUUAUAGCACUGCUG UGUAUUUGCAAAUUUCUACUCU AAUCUAGUCCGACUCUGUACCA GCAUAAUGGCCUCUA	Position 41 (5' stem) : AAUAAUCGAGUUUAUAGCACUG Position 64 (3' stem) : UGUGUAUUUGCAAAUUUCUACU	Position 41 : AAUAAUCGAGUUUAU AGCACUG	Position 98 : GACUCUGUACCAGC AUAAUGGC
>MR130 CUAAAUCACUUUAUACAAUUUAU GCCUUUAUGAUAAUUUGGUUUCG AUUUUAUCUGAUUACAAGCUAA UUUAGUCAGUAAUUUAGAGAAA UAUUUAUAAAGAUAAUUGAUUGUC GUAAGUAAUGAAUUUGAGAGUG AUGCUAG	Position 2 (5' stem) : AAAUCACUUUAUACAAUUUAUGC Position 116 (3' stem) : AAUGAAUUUGAGAGUGAUGCUA	Position 8 : CUUAUACAAUUUAUG CCUUAUG	Position 116 : AAUGAAUUUGAGAG UGAUGCUA

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	>MD34 GGGUAUGAUCGCGUAAAAAUA AGCUUCCAACAUAUUGAUACAC GAUCCAUAUCC	Position 2 (5' stem) : GUAUGAUCGCGUAAAAAUAAG Position 32 (3' stem) : AUAUUGAUACACGAUCCAUAUC	Position 3 : UAUGAUCGCGUAAAA AAUAAGC	Position 32 : AUAUUGAUACACGA UCCAUAUC
Human respiratory syncytial virus NC_001781.1	>MR55 UAUAAAUGGUUGUUGAGAUUGA UUGAACUCUAACUAAUGUCUAU UUACCCAUUUUUGGUUUUAU UUACCUAUUCGCACUCUAGGUC UAGCAGAUAGUGGCUGGUAGUG AUUUUGGAUUUUGAGUGGGAAU GGUUUGUGUGAUGAAGUGUGUA GUGUAGAUGUUCAUGAUGUUUG GAUAUAGUGUGUA	Position 37 (5' stem) : UGUCUAUUUACCCCAUAAUUUG Position 145 (3' stem) : AAGUGUGUAGUGUAGAUGUUA	Position 37 : UGUCUAUUUACCCCA UAUUUUG	Position 111 : UUUUGGAUUUUGAG UGGGAUUG
	>MR38 GAUUGAUGUCUGUUUUUAUUGAU GUUGUUGAUUGCUGAGUGAGUU GAUCACUGAUCAAAAUCAUCA AGUGACAGAUCAUUGUC	Position 14 (5' stem) : UUAUUGAUGUUGUUGAUUGCUG Position 48 (3' stem) : ACUGAUCAAAAUCAUCAAGUG	Position 31 : UGCUGAGUGAGUUGA UCACUGA	Position 48 : ACUGAUCAAAAAUC AUCAAGUG
	>MR182 GAAAAAAGUGUCAAAAAACUAA UGUCUCGUUGUGUUGUAAAUGC ACAUGUAUCAUUGUUAGUUUA GACUUUAUUC	Position 2 (5' stem) : AAAAAAGUGUCAAAAAACUAAUG Position 54 (3' stem) : UUGUUAGUUUUAGACUUUAUU	Position 7 : AGUGUCAAAAAACUAA UGUCUCG	Position 54 : UUGUUAGUUUUAGA CUUUUAUU

Table 2: The computational prediction of pre-miRNA sequences and mature miRNA sequences of each ssRNA viruses.