

# MIR2911 is a potential inhibitor for Nipah virus



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## Supplementary tables

**Table S1.** Exact genomic coordinates, local target sequences, genomic annotations, and cross-lineage conservation of the 18 high-confidence MIR2911-binding sites in Nipah virus.

Site ID	Coordinates on gene	Local target sequence (5'-3')	MFE (kcal/mol)	Full seed match (2-8 nt)	Conserved in representative Bangladesh strains
Site 1	14089-14110	target 5' C    UU   U                    A 3' UCCU CCC UUCCUGGU AGGG GGG AGGGGGCCG miRNA 3' UC   C                    G 5'	-32.0 kcal/mol	Yes	No
Site 2	14905-14926	target 5' C                    U                    A 3' UUUCGG CCUG CUCCUGGU AGGGUC GGGC GGGGGCCG miRNA 3'                    A                    G 5'	-30.2 kcal/mol	Yes	Yes
Site 3	11242-11266	target 5' C    U   AU AUAA    A 3' UCC GCC U   CUCCGGCU GGG CGG A   GGGGCCGG miRNA 3' A    U   GC   G            5'	-29.5 kcal/mol	Yes	No
Site 4	5326-5350	target 5' U                    GUUGA            G 3' TCTTGCTCG   CUUCGGU AGGGUCGGGC   GGGGCCG miRNA 3'                    AG                    G 5'	-28.9 kcal/mol	Yes	No
Site 5	17557-17581	target 5' C                    CACU                    A 3' TTCTAGTTT   UUCCUCGGC AGGGUCGGG   AGGGGGCCG miRNA 3'                    C                    G 5'	-28.0 kcal/mol	Yes	Yes



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Table S1. Cont.

Site ID	Coordinates on gene	Local target sequence (5'-3')	MFE (kcal/mol)	Full seed match (2-8 nt)	Conserved in representative Bangladesh strains
Site 6	14648-14672	target 5' C UU A GAG U 3' U GGC UCG UCCUGGUC G UCG GGC GGGGGCCGG miRNA 3' A GG A 5'	-26.6 kcal/mol	Yes	No
Site 7	16040-16059	target 5' A AGA A 3' CCUGGU CCUUGGUC GGGUCG GGGGCCGG miRNA 3' A GGCAG 5'	-26.2 kcal/mol	Yes	No
Site 8	3428-3450	target 5' A AAUUU A 3' CCAGC CC UCUCUGGC GGUCG GG GGGGGCCG miRNA 3' AG CA G 5'	-26.2 kcal/mol	Yes	Yes
Site 9	1083-1109	target 5' U A AU GU U 3' UCCCG UCC GUU UUCUGGUC AGGGU GGG CAG GGGGCCGG miRNA 3' C 5'	-25.6 kcal/mol	Yes	Yes
Site 10	687-713	target 5' A GU A A 3' CU A GUU UCCCCUGGUC GG U CGG AGGGGGCCGG miRNA 3' A G GC 5'	-25.2 kcal/mol	Yes	No
Site 11	4413-4434	target 5' A AU A 3' UAGUCC GUUUUUUGGCU GUCGG CAGGGGGCCGG miRNA 3' AGG 5'	-25.1 kcal/mol	Yes	Yes
Site 12	6827-6851	target 5' A AUUUUU A 3' UCGGCC GUUUUUUGGU GGUCGG CAGGGGGCCG miRNA 3' AG G G 5'	-24.0 kcal/mol	Yes	Yes
Site 13	1415-1436	target 5' G G AG A 3' U CGGU GUU UCUUGGCC G GUCG CAG GGGGCCGG miRNA 3' A G GG 5'	-23.1 kcal/mol	Yes	No
Site 14	17018-17050	target 5' C A GGUGA GCUGA U 3' UCCAGC U CGU UUUUUGGCC GGGUCG G GCA GGGGGCCGG miRNA 3' A 5'	-22.8 kcal/mol	Yes	Yes
Site 15	3352-3374	target 5' A AAA AA G 3' UCUAG CU CUUUGGCU GGGUC GG GGGGCCGG miRNA 3' A G CAG 5'	-22.1 kcal/mol	Yes	Yes
Site 16	14516-14534	target 5' A UU A 3' CUC GCCU UCUUGGU GGG CGGG GGGGCCG miRNA 3' A U CAG G 5'	-22.0 kcal/mol	Yes	Yes
Site 17	14927-14945	target 5' A GUU A UU UG U 3' UCU G U GU UCCUUGGCU AGG C G CA GGGGGCCGG miRNA 3' GU GG 5'	-22.0 kcal/mol	Yes	Yes
Site 18	16377-16401	target 5' A G ACAU G U 3' U UAG U GUUCUUCGGUU G GUC G CAGGGGGCCGG miRNA 3' A G G G 5'	-21.2 kcal/mol	Yes	Yes

Representative genomes from the Malaysia and Bangladesh lineages used for comparison are listed here:  
Bangladesh lineage of Nipah virus (NiV-B): AY988601.1

**Table S2.** Mutant core sequences used in the reporter assays.

<b>Construct</b>	<b>Mutant core sequence introduced into the reporter insert (5'–3')</b>
MUT-NiV-target 1	AGGATTGGGTAAAGGGACCA
MUT-NiV-target 2	AAAGCCTGGACGAGGACCA
MUT-NiV-target 3	AGGTCGGATAATAAGAGGCCGA
MUT-NiV-target 4	AGAACCGAGCGTTGAGAAGCCA
MUT-NiV-target 5	AAGATCAAACACTAAGGAGCCG