Supplementary material:

Table 1: Algorithms used to predict antagomir targets

Software used	**Purpose**
Sfold	To determine the antagomir sequence
mfold	Designing the secondary structure of antagomirs

Table 2: List of putative antagomirs and their target sequence

Seq No.	Target Position	Target Sequence	Putative Antagomirs	Binding energy	GC Content
1	27- 46	UCAGGAGGCUCUCAAUGUGU	ACACATTGAGAGCCTCCTGA	-8.7	50.0%
2	1-20	AGGAAGCUUCUGGAGAUCCU	AGGATCTCCAGAAGCTTCCT	-11.3	50.0%
3	35- 54	GAUGUUUACCGUUUAAAUCC	GGATTTAAACGGTAAACATC	-4.6	35.0%
4	35- 54	CCCUUAGAUGCUAAGAUGGG	CCCATCTTAGCATCTAAGGG	-8.7	50.0%
5 a	34- 53	UGUGAGGUAUUUUAGUAACA	TGTTACTAAAATACCTCACA	-2.6	30.0%
5 b	35- 54	GUGAGGUAUUUUAGUAACAU	ATGTTACTAAAATACCTCAC	-2.6	30.0%
5 c	36- 55	UGAGGUAUUUUAGUAACAUC	GATGTTACTAAAATACCTCA	-2.6	30.0%
5 d	37- 56	GAGGUAUUUUAGUAACAUCA	TGATGTTACTAAAATACCTC	-2.6	30.0%
6 a	25- 44	GUCUAGUAUGUCUCAUCCCC	GGGGATGAGACATACTAGAC	-8.0	50.0%
6 b	33- 52	UGUCUCAUCCCCUACUAGAC	GTCTAGTAGGGGATGAGACA	-8.0	50.0%
7	79- 98	UGGGUUUGAAUAUCGACAGC	GCTGTCGATATTCAAACCCA	-12.2	45.0%
8 a	23- 42	UGGGAUUUGCUUCCUGUCAC	GTGACAGGAAGCAAATCCCA	-7.0	50.0%
8 b	24- 43	GGGAUUUGCUUCCUGUCACA	TGTGACAGGAAGCAAATCCC	-7.0	50.0%
9	31- 50	GGUAGCUUUUUGAGAUCUAC	GTAGATCTCAAAAAGCTACC	-0.8	40.0%
10 a	28- 47	UUGCCUUGUGGCAUGGAGUU	AACTCCATGCCACAAGGCAA	-4.4	50.0%
10 b	31- 50	CCUUGUGGCAUGGAGUUCAA	TTGAACTCCATGCCACAAGG	-4.4	50.0%
10 c	32- 51	CUUGUGGCAUGGAGUUCAAG	CTTGAACTCCATGCCACAAG	-4.4	50.0%
10 d	33- 52	UUGUGGCAUGGAGUUCAAGC	GCTTGAACTCCATGCCACAA	-4.4	50.0%
10 e	33- 52	UGUGGCAUGGAGUUCAAGCA	TGCTTGAACTCCATGCCACA	-4.4	50.0%
11 a	25- 44	UGGGCCUGGGUUUCUGAACA	TGTTCAGAAACCCAGGCCCA	-8.7	50.0%
11 b	27- 46	GGCCUGGGUUUCUGAACACA	TGTGTTCAGAAACCCAGGCC	-8.7	50.0%
12	29- 48	UCCUCUCAACAGUAGUCAGG	CCTGACTACTGTTGAGAGGA	-6.2	50.0%
13 a	50- 69	UAGAUAACUAAAUCGACAAC	GTTGTCGATTTAGTTATCTA	-1.4	30.0%
13 b	51- 70	AGAUAACUAAAUCGACAACA	TGTTGTCGATTTAGTTATCT	-1.4	30.0%
13 c	52- 71	GAUAACUAAAUCGACAACAA	TTGTTGTCGATTTAGTTATC	-1.4	30.0%
14 a	50- 69	GUUGUUGUCUUACUGCGCUC	GAGCGCAGTAAGACAACAAC	-9.9	50.0%
14 b	53- 72	GUUGUCUUACUGCGCUCAAC	GTTGAGCGCAGTAAGACAAC	-9.9	50.0%
14 c	56- 75	GUCUUACUGCGCUCAACAAC	GTTGTTGAGCGCAGTAAGAC	-9.9	50.0%
15 a	48- 67	UGUUGUUCUGAUGUACUACG	CGTAGTACATCAGAACAACA	-5.4	40.0%
15 b	49- 68	GUUGUUCUGAUGUACUACGA	TCGTAGTACATCAGAACAAC	-5.4	40.0%
15 c	50- 69	UUGUUCUGAUGUACUACGAC	GTCGTAGTACATCAGAACAA	-5.4	40.0%
15 d	51- 70	UGUUCUGAUGUACUACGACA	TGTCGTAGTACATCAGAACA	-5.4	40.0%
15 e	52- 71	GUUCUGAUGUACUACGACAA	TTGTCGTAGTACATCAGAAC	-5.4	40.0%
15 f	53- 72	UUCUGAUGUACUACGACAAC	GTTGTCGTAGTACATCAGAA	-5.4	40.0%
15 g	54- 73	UCUGAUGUACUACGACAACA	TGTTGTCGTAGTACATCAGA	-5.4	40.0%
16	91- 110	UGACAUAAACACUCCGCUCU	AGAGCGGAGTGTTTATGTCA	-11.5	45.0%
17 a	46- 65	UGUGUGGUAUCCGUAUAGUC	GACTATACGGATACCACACA	-6.8	45.0%
17 b	47- 66	GUGUGGUAUCCGUAUAGUCA	TGACTATACGGATACCACAC	-6.8	45.0%
17 c	48- 67	UGUGGUAUCCGUAUAGUCAC	GTGACTATACGGATACCACA	-6.8	45.0%
17 d	49- 68	GUGGUAUCCGUAUAGUCACA	TGTGACTATACGGATACCAC	-6.8	45.0%
17 e	50- 69	UGGUAUCCGUAUAGUCACAG	CTGTGACTATACGGATACCA	-6.8	45.0%
18	44- 63	UGUGAGCAAUAGUAAGGAAG	CTTCCTTACTATTGCTCACA	-10.3	40.0%
19	55- 74	GGUGAGUUUGGGAUUUGAAA	TTTCAAATCCCAAACTCACC	-10.1	40.0%
20 a	54- 73	UGGGUUGAACUGUGUGGACA	TGTCCACACAGTTCAACCCA	-6.8	50.0%
20 b	55- 74	GGGUUGAACUGUGUGGACAA	TTGTCCACACAGTTCAACCC	-6.8	50.0%
20 c	56- 75	GGUUGAACUGUGUGGACAAG	CTTGTCCACACAGTTCAACC	-6.8	50.0%
20 d	57- 76	GUUGAACUGUGUGGACAAGC	GCTTGTCCACACAGTTCAAC	-6.8	50.0%
20 e	59- 78	UGAACUGUGUGGACAAGCUC	GAGCTTGTCCACACAGTTCA	-6.8	50.0%
21	48- 67	UUUGGGCAGCUCAGGCAAAC	GTTTGCCTGAGCTGCCCAAA	-8.4	55.0%
22 a	43- 62	CACUGGUGAGGUAACAGGAU	ATCCTGTTACCTCACCAGTG	-12.9	50.0%
22 b	44- 63	ACUGGUGAGGUAACAGGAUC	GATCCTGTTACCTCACCAGT	-12.9	50.0%