

Supplementary Materials:

synZIKV H/PF/2013

#	Position	Sequences		Score
1	34-83	Original	ttcgagtttgaagcgaagctagcaacagtatcaacaggtTttatTTTgg	0,98
		Modified	Not modified due to RNA secondary structures	
2	905-954	Original	gcttttgggaagctcaacgagccaaaaagtcataacttgGtcatgatac	0,98
		Modified	gcttCtgggaagctcaacgagccaaaaagtcataacttgGtcatgatac	
3	1432-1481	Original	tcgttaatgacacaggacatgaaactgatgagaatagagcGaaggttgag	0,97
		Modified	tcgttaatgaTacaggacatgaaactgatgagaCagagcGaaggttgag	
4	1836-1885	Original	ggccacttgaatgtcgctgaaaatggataaacttagatTgaagggcgt	0,96
		Modified	ggccacCtgaatgtcgctgaaaatggaCaaacttagatTgaagggcgt	
5	2104-2153	Original	tggaacttgatccaccatttggggactcttacattgtcatAggagtcggg	0,86
		Modified	tggaactCgatccaccatttggggactcttacattgtcatAggagtcggg	
6	2205-2254	Original	gcatttgaagccactgtgagaggtgccaagagaatggcagTcttgggaga	0,94
		Modified	gcattCgaagccactgtgagaggtgccaagagGatggcagTcttgggaga	
7	2341-2390	Original	cattgttggaggaatgtcctggttctcacaattctcatTggaacgttg	0,99
		Modified	cattgttCggaggaatgtcctggttctcacaGattctcatTggaacgttg	
8	2560-2609	Original	acgttgaagcctggaggaccggtacaagtaccatcctgaCtccccctg	0,88
		Modified	acgtCgaagcctggaggaccggtacaagtaccatcctgaCtccccctg	

X exchanged nucleotides for CEP silencing X +1 nt of *in silico* predicted CEP (program output)

Figure S1: Results of *in silico* prediction of cryptic prokaryotic promoters in the MR766 sequence.

synZIKV MR766

#	Position	Sequences		Score
1	34-83	Original	ttcagagtttgaagcgagagctaacaacagtatcaacaggtTtaatttggga	0,98
		Modified	Not modified due to RNA secondary structures	
2	353-402	Original	aaatttaagaaagatccttgctgccatgttgagaataatcaAtgctaggaa	0,97
		Modified	aaatttaagaaagatccttgctgccatgttgagGataatcaAtgctaggaa	
3	692-741	Original	acttgggttgtgtacggaacctgtcatcataaaaaaggtgAagcacggcg	0,94
		Modified	acGtgggttgtgtacggaacctgtcatcaCaaaaaaggtgAagcacggcg	
4	781-830	Original	gaaattgcaaacgcggtcgagacttggctagaatcaagaGaatacacaa	0,97
		Modified	gaaattAcaaacgcggtcgagacttggctGgaatcaagaGaatacacaa	
5	904-953	Original	gcttttgggaagctcgacgagccaaaaagtcatatacttgGtcatgatac	0,97
		Modified	gcttttAggaagctcgacgagccaaaaagtcatTtacttgGtcatgatac	
6	1215-1263	Original	cctacctgacaagcaatcagacactcaatatgtttgcaaAagaacattg	0,96
		Modified	cctacctCgacaagcaatcagacactcaatatgtCtgcaaAagaacattg	
7	1657-1706	Original	tccacattggaacaacaaggaggcattagtgaattcaagGacgcccacg	0,94
		Modified	tccacaCtggacaacaacaaggaggcattagtgaGttcaagGacgcccacg	
8	1780-1829	Original	ggctgagatggatggtgcaaaggaaggctattctctggcCacttgaat	0,88
		Modified	ggctgagatggatggtgcaaaggaaggctGttctctggcCacttgaat	
9	2048-2097	Original	gtgattactgaaagcactgagaattcaagatgatgttggAgctcgacc	0,94
		Modified	gtgatCactgaaagcactgagaattcaagatgatgttggAgctcgacc	
10	2111-2160	Original	tcttacattgtcataggagttgggataagaaaatcaccAtcactggca	0,94
		Modified	tcttacatCgtcataggagttgggataagaaGatcaccAtcactggca	
11	2186-2235	Original	gcatttgaagccactgtgagaggcgctaagagaatggcagTcctggggga	0,95
		Modified	gcattCgaagccactgtgagaggcgctaagagGatggcagTcctggggga	
12	2541-2590	Original	acgttgaagcctggaggaccggtacaagtaccatcctgaCtcccctcgt	0,88
		Modified	acgtCgaagcctggaggaccggtacaagtaccatcctgaCtcccctcgt	

X exchanged nucleotides for CEP silencing **X** +1 nt of *in silico* predicted CEP (program output)

Figure S2: Results of *in silico* prediction of cryptic prokaryotic promoters in the H/PF/2013 sequence.

Table S1. Modified restriction sites in MR766 syn-sequence.

Position of restriction site	Original codon within site	Changed codon within site	Enzyme	Added/deleted	Comment
896	GCC	GCG	NruI	+	Methylated in dcm ⁺ / dam ⁺ bacteria
1748	GGA	GGC	NarI	+	None
3317	GGT	GGA	KpnI	-	One site remains
3845	CTG	CTA	NheI	-	One site remains
6387	AGG	CGG	XmaI	+	None
7769	GCT	GCG	AscI	+	None
8264	GGA	GGC	SpeI	-	One site remains

Table S2. Modified restriction sites in H/PF/2013 syn-sequence.

Position of restriction site	Original codon within site	Changed codon within site	Enzyme	Added/deleted	Comment
711	GGA	GGT	KpnI	+	None
747	TCT	TCC	XbaI	-	One site remains
2581	AGG	CGG	AgeI	+	None
2712	GAG	GAA	SacI	-	One site remains
3858	AGC	AGT	SphI	-	One site remains
4323	GCC	GCA	SacII	-	One site remains
5752	AGC	AGT	SacI	-	One site remains
7737	GAG	GAA	EcoRI	+	None
8520	AGG	AGA	BamHI	-	One site remains
9120	TTT	TTC	XbaI	-	One site remains