

Supp. 1 Virus detection reports for six data

Figure S1. HPV-18 contigs from SRR031636

Reference	Length	Read_cov(%)	#(Contig_cov%)	Depth
M20325	3135	2324(74.1)	19(62.5)	0.6(8.5)

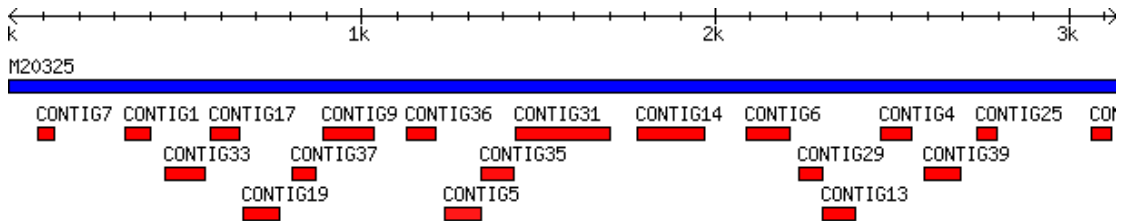


Figure S2. HBV contigs from SRR039620

Reference	Length	Read_cov(%)	#(Contig_cov%)	Depth
JQ688404	3215	1756(54.6)	7(13.3)	0.2(6.0)

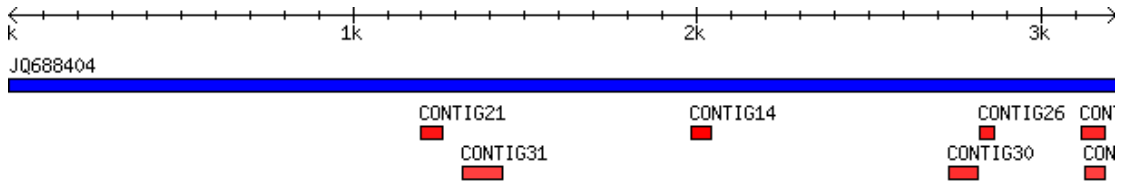


Figure S3. HCV contigs from SRR039622

Reference	Length	Read_cov(%)	#(Contig_cov%)	Depth
D85516	9535	1032(10.8)	1(0.5)	0.0(1.8)

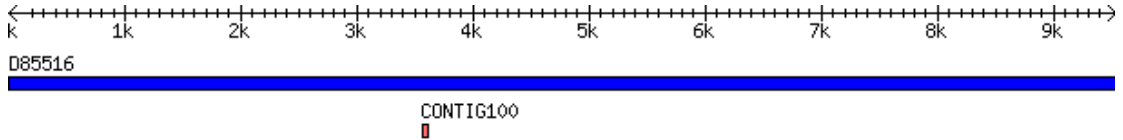


Figure S4. HIV-1 contigs from SRR941591

Reference	Length	Read_cov(%)	#(Contig_cov%)	Depth
M19921	14825	5831(39.3)	53(32.6)	3.5(210.1)

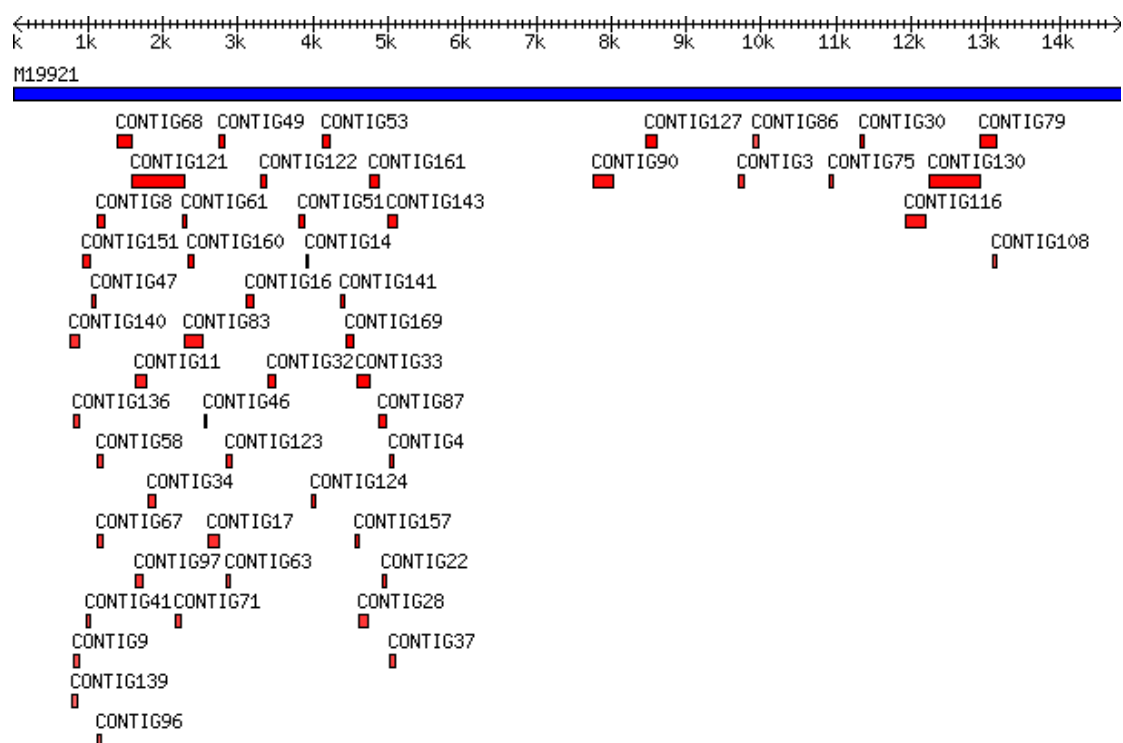


Figure S5. SMRV contigs from SRR1563017

Reference	Length	Read_cov(%)	#(Contig_cov%)	Depth
M23385	8785	8732(99.4)	1(76.9)	318.0(494.5)

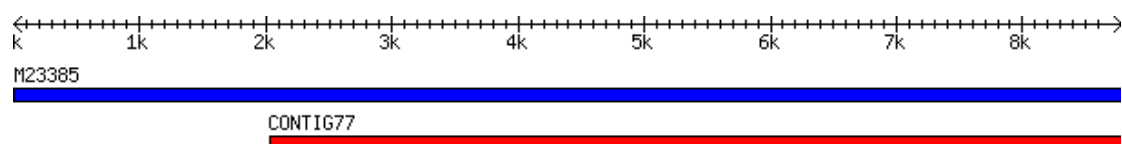


Figure S6. EBV contigs from SRR1563063

Reference	Length	Read_cov(%)	#(Contig_cov%)	Depth
M80517	184113	37898(20.6)	34(1.4)	1.2(52.8)



Supp. 2 Read distribution on six virus genomes

Figure S7. HPV-18 reads distribution in SRR031636

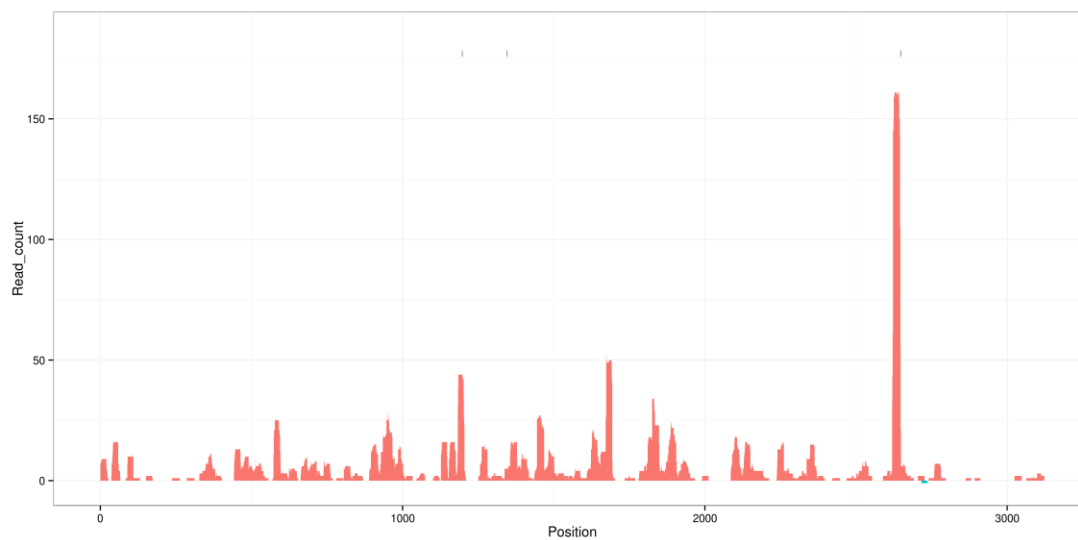


Figure S8. HBV reads distribution in SRR039620

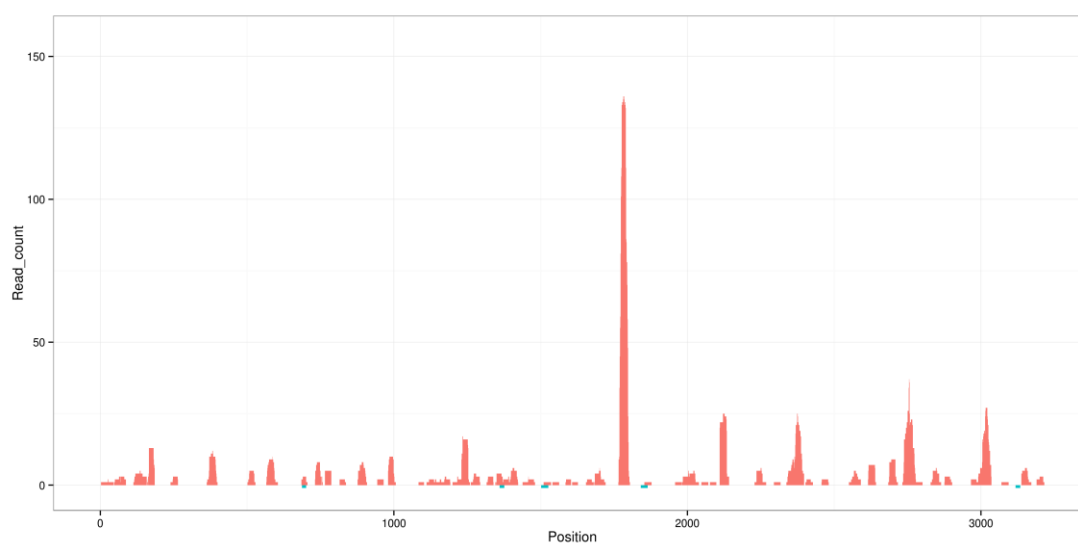


Figure S9. HCV reads distribution in SRR039622

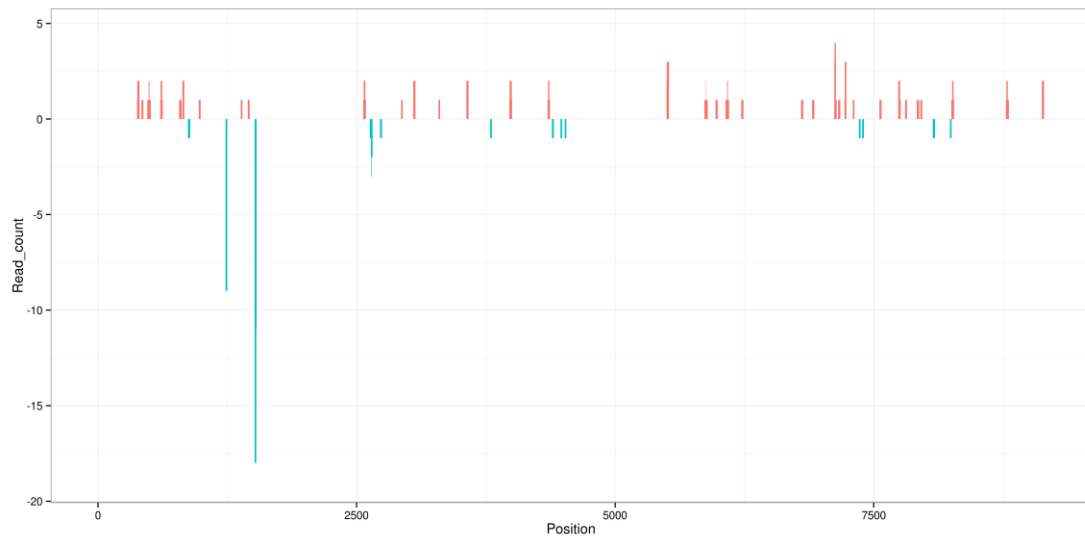


Figure S10. HIV-1 reads distribution in SRR941591

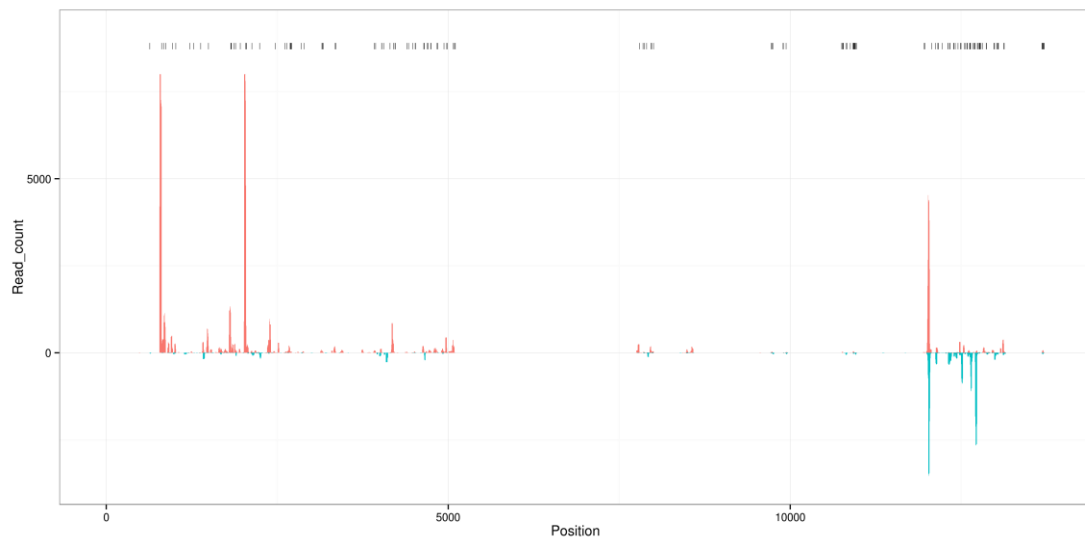


Figure S11. SMRV reads distribution in SRR1563017

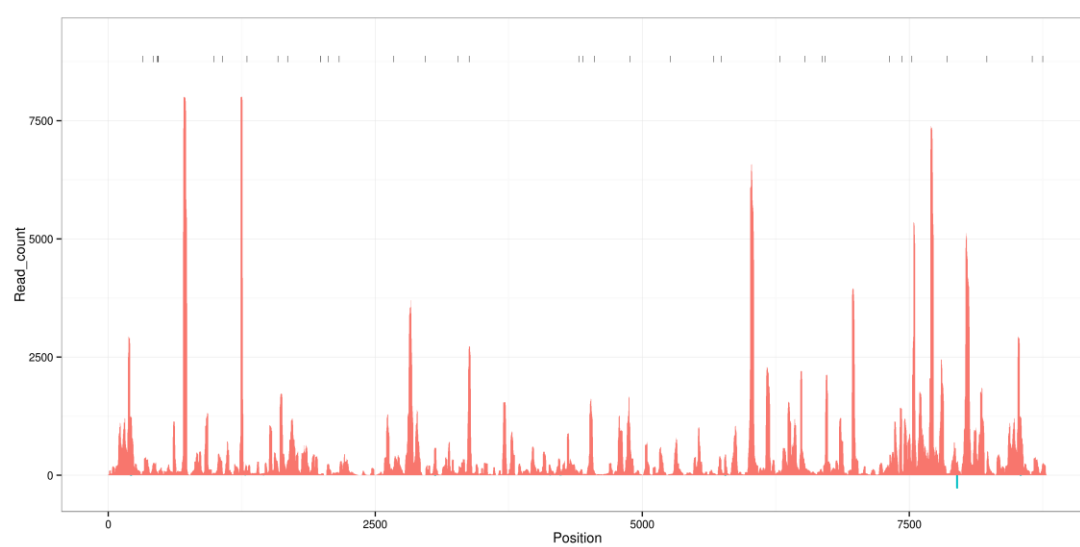
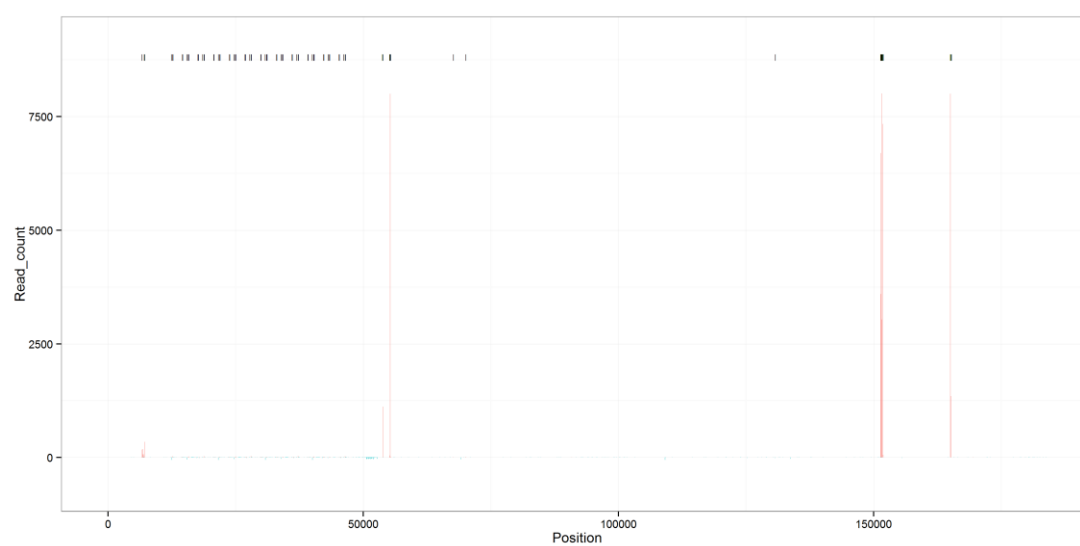


Figure S12. EBV reads distribution in SRR1563063



Supp. 3 Four miRNAs from seven duplexes

1. The first mature miRNA:

```
=====miRNA=====
CCCCGGGCCTGAAGAGGTTGAC
TTGGGGCCCGGACTTCTCCAAC

Query: 1-22 rlcY-miR-rL1-1-3p: 1-22 score: 101 evaluate: 0.004
UserSeq          1 ccccgggcccggaagagguugac 22
                  | |||||
rlcY-miR-rL1-1-3p 1 cuccggggcccggaagagguugac 22
```

2. The second mature miRNA:

```
=====miRNA=====
TCTTAGTGGAAGTGACGTGCTG
CCAGAATCACCTTCACTGCACG

Query: 1-20 eby-miR-BART1-5p: 1-20 score: 100 evaluate: 0.004
UserSeq          1 ucuuaguggaagugacgugc 20
                  |||||
eby-miR-BART1-5p 1 ucuuaguggaagugacgugc 20
```

3. The third mature miRNA:

```
=====miRNA=====
TAGCCCCGCTATCCACTATGTC
GTATCGGGGCGATAGGTGATAC

Query: 1-22 eby-miR-BART1-3p: 1-22 score: 101 evaluate: 0.003
UserSeq          1 uagcccgccuauccacuauguc 22
                  |||| |||||
eby-miR-BART1-3p 1 uagcaccgcuauccacuauguc 22
```

4. The predicted miRNA:

```
=====miRNA=====
GCCGGGCGGCCGCGGTGGGTC
CGGCCC GCCGGCGCCACCCAG
```

Predicted miRNA precursor sequence, 90 bp, dG = -69.8 [Initially -69.3]

gccgggCGGCCGCGGTGGGTCGCTGGGCGGCTGCCCCGCTCCGGGTGGGGGGTGG
CCCCGCTGGGACCGCTGCGCCGCCGCCAGGT

15May03-09-11-36-1db38914b3 is the 2584933rd nucleic acid sequence folded on the RNA Institute mfold server.

- Sunday, May 03 09:11:38 EDT 2015 -

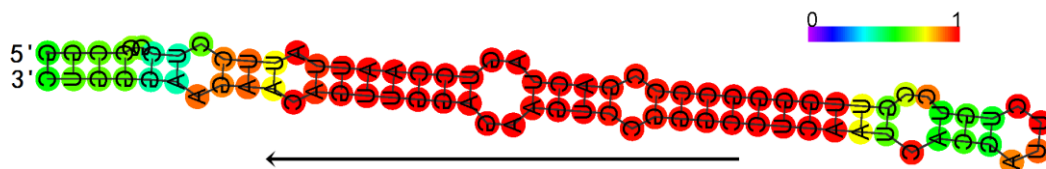
The repeated regions on the M80517 reference sequence.

```
>M80517:50578-50702
50578                               50623                               50702
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:50703-50827
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:50828-50952
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:50953-51077
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51078-51202
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51203-51327
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51328-51452
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51453-51577
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51578-51702
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51703-51827
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51828-51952
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:51953-52077
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCCGGGGGCAgcccgggcggccgcccgtgggtcCGCTGGGCCGCTGCCCCGCTCCGGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCG
>M80517:52078-52115
CCGCCAGGTCCTGGGGCAGCCGGGGTTCCTGGCGCTCC
```


Supp. 4 The predicted second structures of seven duplexes

1. The first mature miRNA:

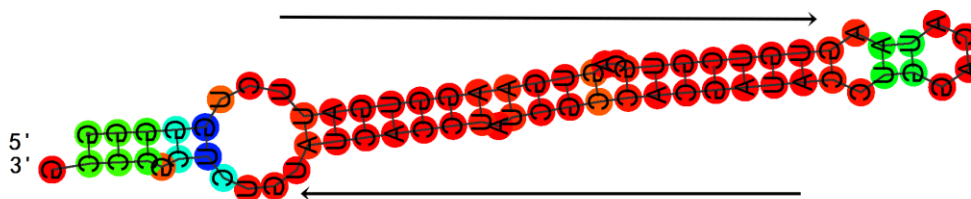
pre-miRNA	Length	C+G	MFE(-)	MFEI
rlcv-mir-rL1-1	85	49	37.70	0.91
GGCCGGCUCCUUAUUAACCUGAUCAGCCCCGGGGUUGCCUGUCU UAGCACUAAcuccgggccugaagagguugacAAGAAGGGUC				



Note: the mature miRNA is in lower case letters

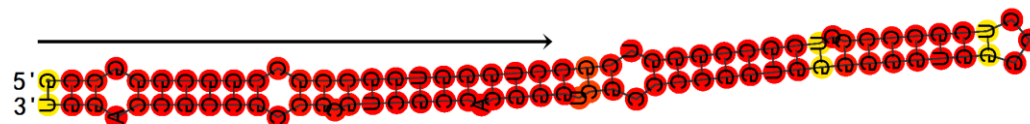
2. The second and third mature miRNA:

pre-miRNA	Length	C+G	MFE(-)	MFEI
ebv-mir-BART1	70	39	30.57	1.12
GGGGGucuuaguggaagugacgugcugUGAAUAC AGGUCCAuagcaccgcuauccacuaugucUCGCCCCG				



3. The predicted mature miRNA:

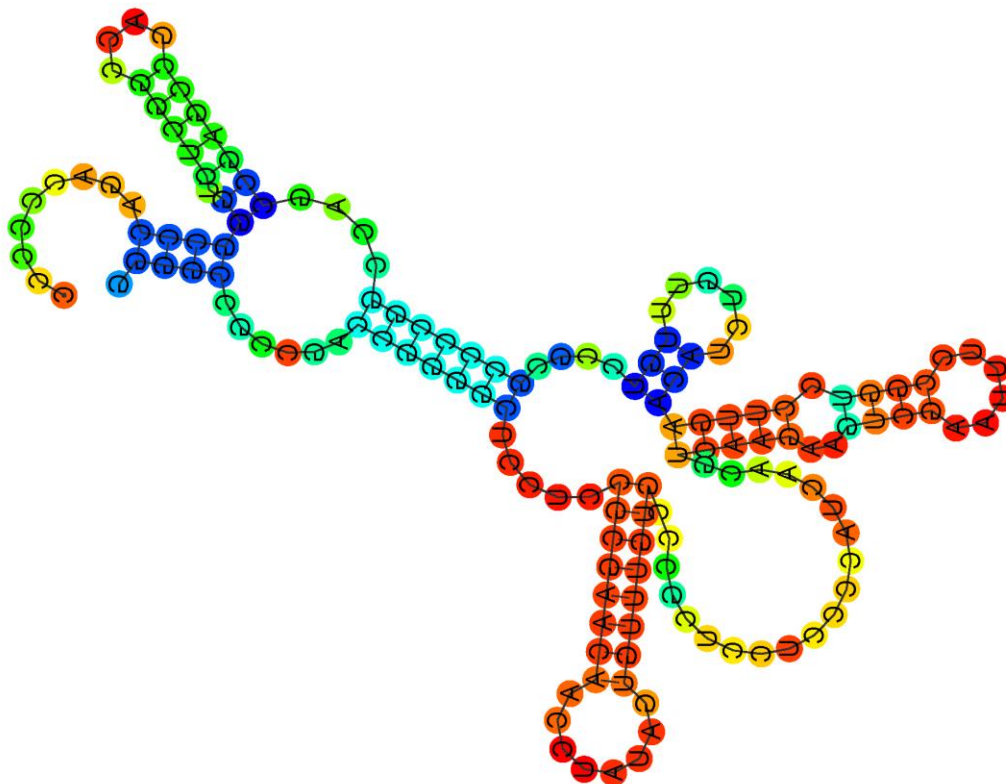
pre-miRNA	Length	C+G	MFE(-)	MFEI
new finding	90	77	69.46	1.00
gccggggcgccgcgggtgggtcCGCTGGGCGCTGCCCCGCTCC GGGTGGGGGGTGGCCCCGCTGGGCACCGCTGCGCCGCCGCCAGGT				



4. The unknown 1 and 2 duplexes:

Two duplexes	unknown	Length	C+G	MFE(-)	MFEI
NA		76	65	46.46	0.94

CCCCCcagaccggtctcggccagCCGAGCCGACCGGCCC CGCGCCTGGcgcctcctcggggccagccgcgCCGGGG
--



5. The unknown 3 duplex:

unknown duplex	Length	C+G	MFE(-)	MFEI
NA	80	39	10.4	0.33
ttgtctacaagtctctggccTTTAAGCTGAAGAACTGCAACTACCCCTCCTCGCCC GTGTTTGTGATATCCAACAACGG				

