

An Extended Signal Involved in Eukaryotic ≥ 1 Frameshifting Operates through Modification of the E Site Trna

Michaël Bekaert and Jean-Pierre Rousset

Text File of the HMM Profile to be Used with the HMMER Package

HMMER2.0 [2.3.2]
 NAME virus.step2
 DESC Enhanced viral -1 frameshift site HMM
 LENG 17
 ALPH Nucleic
 RF no
 CS no
 MAP yes
 COM hmmbuild -f virus.enhance.hmm virus.enhance.st
 COM hmmscalibrate --seed 0 virus.enhance.hmm
 NSEQ 72
 DATE Wed Apr 7 13:26:53 2004
 CKSUM 5754
 GA 6.8 6.8
 TC 6.8 6.8
 NC 6.7 6.7
 XT -9967 -1 -1000 -1000 -9967 -1 -9967 -1
 NULT -1 -9967
 NULE 0 0 0 0
 EVD -7.780109 0.644326
 HMM A C G T

```

m→m m→i m→d i→m i→i d→m d→d b→m m→e
-20 * -6208
1 537 840 -1859 -1046 10
- 0 0 0 0
- -47 -11402 -12444 -894 -1115 -701 -1378 -1020 -5002
2 18 -2078 826 -33 11
- 0 0 0 0
- -48 -11402 -12444 -894 -1115 -701 -1378 -5020 -4955
3 18 -2597 829 63 12
- 0 0 0 0
- -50 -11405 -12447 -894 -1115 -701 -1378 -5020 -4909
4 524 -2597 372 141 13
- 0 0 0 0
- -51 -11405 -12447 -894 -1115 -701 -1378 -5020 -4859
5 1274 -2169 -4248 385 14
- 0 0 0 0
- -53 -11408 -12450 -894 -1115 -701 -1378 -5020 -4809
6 1274 -2169 -4248 385 15
- 0 0 0 0
- -55 -11410 -12452 -894 -1115 -701 -1378 -5020 -4757
7 1274 -2169 -4248 385 16
- 0 0 0 0
- -57 -11412 -12454 -894 -1115 -701 -1378 -5020 -4702
8 -737 1223 -4248 18 17
- 0 0 0 0
- -60 -11415 -12457 -894 -1115 -701 -1378 -5020 -4647
9 -1838 -2123 614 971 18
- 0 0 0 0
- -62 -11416 -12458 -894 -1115 -701 -1378 -5020 -4587
10 140 -967 1142 -2480 19
- 0 0 0 0
- -65 -11420 -12462 -894 -1115 -701 -1378 -5020 -4527
11 -447 434 824 -2788 20
- 348 -873 -345 479
- -6587 -83 -12465 -3 -9085 -701 -1378 -5020 -4462
12 714 -1884 -407 417 22
- 0 0 0 0
- -71 -11425 -12468 -894 -1115 -701 -1378 -5020 -4395
13 -121 -1045 1144 -1371 23
    
```

```

- 0 0 0 0
- -75 -11430 -12472 -894 -1115 -701 -1378 -5020 -4326
14 16 -198 960 -2543 24
- 0 0 0 0
- -79 -11433 -12475 -894 -1115 -701 -1378 -5020 -4252
15 -2212 264 1156 -1494 25
- 0 0 0 0
- -83 -11437 -12479 -894 -1115 -701 -1378 -5020 -4174
16 -1760 168 1163 -1546 26
- 0 0 0 0
- -88 -11443 -12485 -894 -1115 -701 -1378 -5020 -4092
17 -1488 295 1048 -1516 27
- * * * *
- * * * * * * * -5020 0
    
```

Table S1. Viruses Identified by the HMM Profile Sought and Manually Examined

Virus Name	E Value	GenBank	Slippery Region (5' to 3')	Locus
dsRNA virus				
Totiviridae				
<i>Giardiavirus</i>				
<i>Giardia lamblia virus</i>	0.15	NC_003555	CCUGCGCCAU CCCUUUA UCCGAUCGUG	2841
<i>Trichomonas vaginalis virus 3</i>	0.24	NC_004034	GCGCGUAUCA GGGCCCU CGCUUGCAGG	2450
<i>Trichomonas vaginalis virus II</i>	0.42	NC_003873	CUGCCUACCA GGGCCCC AGCUUCGCGC	2382
<i>Totivirus</i>				
<i>Saccharomyces cerevisiae virus L-A</i>	0.27	NC_003745	GUACUCAGCA GGGUUUA GGAGUGGUAG	1964
<i>Saccharomyces cerevisiae virus L-BC</i>	0.10	NC_001641	CUGAGAAGUU GGAAUUU CGUGUAGCAG	1973
<i>Helminthosporium victoriae virus 190S</i>	0.24	NC_003607	CUGAUCGGGC CGAGGGA CAAUGAGUGA	2602
Retrovirus				
Retroviridae				
<i>Alpharetrovirus</i>				
<i>Avian leukosis virus</i>	0.061	NC_001408	UCCGCUUGAC AAAUUUA UAGGGAGGGC	2475
<i>Rous sarcoma virus</i>	0.03	NC_001407	UCCGCUUGAC AAAUUUA UAGGGAGGGC	2482
<i>Deltaretrovirus</i>				
<i>Bovine leukemia virus</i>	0.057	NC_001414	CCCUCAAAUC AAAAAAC UAAUAGAGGG	1596*
<i>Human T-lymphotropic virus 1</i>	0.13	NC_001436	UCCACACCC AAAAAAC UCCAUAGGGG	1718*
<i>Human T-lymphotropic virus 2</i>	0.15	NC_001488	CUACUGAGGA AAAAAAC UCCUUAAGGG	2087*
<i>Primate T-lymphotropic virus 3</i>	0.096	NC_003323	UCCGGGAGCA AAAAAAC UCCUCAGGGG	2001*
<i>Simian T-lymphotropic virus 1</i>	0.12	NC_000858	UCCACACCC AAAAAAC UCCAUAGGGG	2067*
<i>Simian T-lymphotropic virus 2</i>	0.15	NC_001815	CCACCGAGGA AAAAAAC UCCUGGGGG	2033*
<i>Lentivirus</i>				
<i>Bovine immunodeficiency virus</i>	0.032	NC_001413	ACUGCAGGUC AAAAAAC GGGAAGUGCU	1635
<i>Caprine arthritis-encephalitis virus</i>	0.0013	NC_001463	GAAAACAGCA GGGAAAC GGGAGGAGGG	1810
<i>Equine infectious anemia virus</i>	0.012	NC_001450	GAAGUGUUC AAAAAAC GGGAGCAAGG	1787
<i>Feline immunodeficiency virus</i>	0.00098	NC_001482	GAAAGAAUUC GGGAAAC UGGAAGGCGG	1884
<i>Human immunodeficiency virus 1</i>	0.022	NC_001802	GACAGGCUAA UUUUUUA GGGAAGAUCU	1637
<i>Human immunodeficiency virus 2</i>	0.02	NC_001722	GACAGGCAGG UUUUUUA GGGUUGGGCC	2401
<i>Jembrana disease virus</i>	0.011	NC_001654	ACUGCAAAUC AAAAAAC GGGAGGCGCU	1441
<i>Ovine lentivirus</i>	0.0064	NC_001511	CAUCACAGCA GGGAAAC AGCAGGAGGG	1812
<i>Simian immunodeficiency virus</i>	0.017	NC_001549	GACAGGCAAA UUUUUUA GGGUUUGGCC	2198
<i>Simian immunodeficiency virus 2</i>	0.024	NC_004455	AGAUGGUGAA UUUUUUA GGGAAUACCC	2056
<i>Simian-Human immunodeficiency virus</i>	0.017	NC_001870	GACAGGCGGG UUUUUUA GGCCUUGGUC	1840
<i>Visna virus</i>	0.0092	NC_001452	AGAAACAGCA GGGAAAC AACAGGAGGG	1769
ssRNA+ virus				
Astroviridae				
<i>Avastrovirus</i>				
<i>Avian nephritis virus</i>	0.099	NC_003790	UUUGUAAGUC AAAAAAC UAAUUGACCC	3025
<i>Turkey astrovirus</i>	0.05	NC_002470	CUACGUGUUC AAAAAAC UAGAUAGUCA	3307

<i>Mamastrovirus</i>					
<i>Human astrovirus</i>	0.072	NC_001943	ACAAGGCCCC AAAAAAC UACAAAGGGC	2845	
<i>Mink astrovirus</i>	0.019	NC_004579	AGCAGAAGCC AAAAAAC GGGAAGAGGG	2621	
<i>Ovine astrovirus</i>	0.091	NC_002469	UCCAGCAGCC AAAAAAC UCCAAAGGGG	2535	
Luteoviridae					
<i>Enamovirus</i>					
<i>Pea enation mosaic virus-1</i>	0.086	NC_003629	CCAGACGCUC GGGAAAC GGAUUUUCC	2035	
<i>Luteovirus</i>					
<i>Barley yellow dwarf virus - GAV</i>	0.14	NC_004666	UUGACUCUGU GGGUUUU UAGAGGGGCU	1159	
<i>Barley yellow dwarf virus - MAV</i>	0.16	NC_003680	UUGACUCUGU GGGUUUU AGAGGGGCU	1122	
<i>Barley yellow dwarf virus - PAS</i>	0.061	NC_002160	UUGACUCUGU GGGUUUU UAGAGGGGCU	1158	
<i>Bean leafroll virus</i>	0.098	NC_003369	UCACCUCAUC GGUUUUU UAGAGGGGCU	1282	
<i>Soybean dwarf virus</i>	0.1	NC_003056	UAAACGCUGA GGGUUUU UAGAGGGGCU	1226	
<i>Polerovirus</i>					
<i>Beet chlorosis virus</i>	0.1	NC_002766	CACAUCUGCC GGGAAAU GGACUGAGCG	1587	
<i>Beet mild yellowing virus</i>	0.16	NC_003491	CCGGAACAAC CGGAAAC GCAAGCACCC	1591	
<i>Beet western yellows virus</i>	0.073	NC_004756	CCAAGAGCUC GGGAAAC GGGAGAGCGG	1481	
<i>Cereal yellow dwarf virus - RPS</i>	0.055	NC_002198	CCGGAAGGUC GGGAAAC GCCAAGGCGG	1602	
<i>Cereal yellow dwarf virus - RPV</i>	0.018	NC_004751	AAGACGAGUC GGGAAAC GGGAAGGCGG	1699	
<i>Cucurbit aphid-borne yellows virus</i>	0.014	NC_003688	AAUACGAGUC GGGAAAC GGGCAGGCGG	1488	
<i>Potato leafroll virus</i>	0.066	NC_001747	CAAACAAGCC GGGAAAU GGGCAAGCGG	1774	
<i>Turnip yellows virus</i>	0.071	NC_003743	AAGAUCUGUC GGGAAAC GGAGUGCGCG	1559	
Unassigned Luteoviridae					
<i>Sugarcane yellow leaf virus</i>	0.099	NC_000874	CUCCAGACCA GGGAAAU GAGCCAAGUG	1759	
Nidovirales/Arteriviridae					
<i>Arterivirus</i>					
<i>Equine arteritis virus</i>	0.017	NC_002532	CAGUGAAUCA GUUAAAC UGAGAGCGCC	5405	
<i>Lactate dehydrogenase-elevating virus</i>	0.015	NC_002534	AGGCAUCGGC UUUAAAC UGCUGCCAC	6836	
<i>Porcine reproductive and respiratory syndrome virus</i>	0.013	NC_001961	AGGAGCAGUG UUUAAAC UGCUGCCGC	7695	
<i>Simian hemorrhagic fever virus</i>	0.015	NC_003092	CAUCUGAAGC UUUAAAC UGCUAACCGC	6521	
Nidovirales/Coronaviridae					
<i>Coronavirus</i>					
<i>Avian infectious bronchitis virus</i>	0.0016	NC_001451	AUAAGAAUUA UUUAAAC GGGUACGGGG	12354	
<i>Bovine coronavirus</i>	0.0013	NC_003045	AUACUAAUUU UUUAAAC GGGUUCGGGG	13341	
<i>Human coronavirus 229E</i>	0.006	NC_002645	AUAACAGUUA UUUAAAC GAGUCCGGGG	12520	
<i>Human coronavirus OC43</i>	0.0019	NC_005147	ATACUAAUUU UUUAAAC GGGUUCGGGG	13341	
<i>Murine hepatitis virus</i>	0.0011	NC_001846	ACACGAACUU UUUAAAC GGGUUCGGGG	13601	
<i>Porcine epidemic diarrhea virus</i>	0.0045	NC_003436	AUAUGGCUUA UUUAAAC GAGUACGGGG	12620	
<i>SARS coronavirus</i>	0.0037	NC_004718	CAUCAACGUU UUUAAAC GGGUUUGCGG	13398	
<i>Transmissible gastroenteritis virus</i>	0.007	NC_002306	AUCAAGUUA UUUAAAC GAGUGCGGGG	12338	
Tombusviridae					

<i>Dianthovirus</i>				
<i>Carnation ringspot virus RNA 1</i>	0.21	NC_003530	AAUCCUCUGA GGAUUUU UAAGUGCCCC	765
<i>Red clover necrotic mosaic virus RNA 1</i>	0.22	NC_003756	AAUCCUUGA GGAUUUU UAGCGGCC	831
<i>Sweet clover necrotic mosaic virus RNA 1</i>	0.18	NC_003806	AAUCCUUGA GGAUUUU UAGCGGCGG	828
<i>Sobemovirus</i>				
<i>Cocksfoot mottle virus</i>	0.12	NC_002618	CAAUCCGGCC UUUAAAC UACCAGCGGG	1640
<i>Subterranean clover mottle virus</i>	0.09	NC_004346	UGCUCGAGCA UUUAAAC UGCCAGCGGG	1852
<i>Turnip rosette virus</i>	0.092	NC_004553	CAGUGAGCUC UUUAAAC UGCCAGCGGG	1757
<i>Umbravirus</i>				
<i>Carrot mottle mimic virus</i>	0.17	NC_001726	CACCCAUCCG GGAUUUU UACUAGGGGA	1031
<i>Groundnut rosette virus</i>	0.12	NC_003603	CCGGGGCACA AAAUUUU UAGUUGGGGA	867
<i>Pea enation mosaic virus-2</i>	0.11	NC_003853	GGCGCGCGGC GGAUUUU UGGUAGGGGC	923
<i>Tobacco bushy top virus</i>	0.18	NC_004366	GUGGGCCCAA GGAUUUU UGCUAGGGGA	952
Unassigned				
<i>Acyrtosiphon pisum virus</i>	0.037	NC_003780	AAGGCUAUUC UUUAAAC UUCUAGCCCC	8154

Table S2.

A. Oligonucleotides Used for Viral Frameshifting Evaluations

Oligonucleotides	Sequences (5' to 3')
BChV.w	CTGTGCGGAAATGGACTGAGCGGGCGCGACCGCCAAACAACCGGCAC
BChV.c	GTGCCGGTTGTTTGGCGGTGCGCGCCGCTCAGTCCATTTCCCGACAG
BLV.w	AAATCAAAAACATAAGAGGGGGGACTTAGCGCCCCCAAACCGTA
BLV.c	TACGGTTTGGGGGGCGCTAAGTCCCCCTCTATTAGTTTTTTGATTT
BWYV.w	CTGTGCGGAAACGGAGTGCGCGGCACCGTCCGCGGAACAACCGG
BWYV.c	CCGTTTGTTCGCGGACGGTGCCGCGCACTCCGTTTCCCGACAG
BYDV-NY-RPV.w	GAGTCGGGAAACGGGAAGGCGCGGGCTCCGCGTAACAACCGC
BYDV-NY-RPV.c	GCGTTTGTACGGCGGACGCCGCGCCTTCCCGTTTCCCGACTC
CABYV.w	GAGTCGGGAAACGGGACGGCGGCGGCGACCGCCGAAACAACCGC
CABYV.c	GCGTTTGTTCGCGGTCGCGCGCGCCTGCCGTTTCCCGACTC
EIAV.w	GTTCCAAAAACGGGAAGCAAGGGGCTCAAGGGAGGCCCCAGAAACAACCTTCCC
EIAV.c	GGGAAAGTTTGTTCGTTGGGGCCTCCCTTGAGCCCTTGTCTCCCGTTTTTGAAC
FIV.w	AATTCGGGAAACTGGAAGGCGGGGCGAGCTGCAGCCCAATGAATCAATGCAGCA
FIV.c	TGCTGCATTTGATTCACTGGGGCTGCAGCTCGCCCGCCTTCCAGTTTCCCGAAT
HIV.w	CAGGCTAATTTTTAGGGAAGATCTGGCCTTCTACAAGGGAAGGCCAGGGAA
HIV.c	TTCCCTGGCCTTCCCTTGTAGGAAGGCCAGATCTTCCCTAAAAAATTAGCCTG
IBV.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTAAATAATTCTT
IBV.w	AAGAATTAATTAACGGGTACGGGGTAGCAGTGCAGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
L-A.w	CAGCAGGTTTAGGAGTGGTAGGCTTACGATGCCAGCTGTAATGCCTACCGGAGAACCTACAGCTGGCGCT GCCCA
L-A.c	TGGGCAGCGCCAGCTGTAGTTCTCCGGTAGGCATTACAGCTGGCATCGTAAGACCTACCACTCCTAAACCCT GCGT
L-BC.w	AAGTTGGATTTTTCTGTAGCAGCTTACGCGATACCAAGTTTGTGCGGCGCAATATGCCATCCTTACACCATCAG GAAC
L-BC.c	GTTCTGATGGTGTAAAGGATGGCATATTGCTGCCCGACAACTTGGTATCGCGTAAGCTGCTACACGAAAAATC CAACTT
LDV.w	TCTGCTTAAACTGTTGACCACCTCTGGCCTTGAACGCTGCTCTAGAGGTGGTGTACTGTGTCCAAGGACGCG GTC
LDV.c	GACCGGTCCTTGGACACAGTGACACCACCTTAGAGCAGCGTTCAAGGCCAGAGGTGGTCAACAGTTTAAAGC AGA
MMTV_gag/pro.w	AATTCAAAAACTTGTAAAGGGGCGAGTCCCTAGCCCGCTCAAAGGGGGAT
MMTV_gag/pro.c	ATCCCCCTTTGAGCGGGGCTAGGGGACTGCCCTTTACAAGTTTTTTGAATT
PEMV.w	CGCTCGGGAACCGATTATTCGGTTCGACTCCGGAGAAACAAGTCA
PEMV.c	TGACTTTGTTTCTCCGAGTCGACCGGAATAATCCGTTTCCCGAGCG
PLRV-S.w	AAGCCTTAAATGGGCAAGCGGCACCGTCCGCCAAAACAACCGG
PLRV-S.c	CCGTTTGTTCGCGGACGGTGCCGCTTCCCATTTAAAGGCTT
PLRV-W.w	AAGCCTTAAATGGGCGAGCGGCACCGCCCGCCAAAACAACCGG
PLRV-W.c	CCGTTTGTTCGCGGGCGGTGCCGCTCGCCATTTAAAGGCTT

PRRSV.w	CAGTGTTTAAACTGCTAGCCGCCAGCGGCTTGACCCCGTGTGGTCGCGGCGGCTTGGTTGTACTGAGACAGC GGTA
PRRSV.c	TACCGCTGTCTCAGTAACAACCAAGCCGCGCCGACCACAGCGGGTCAAGCCGCTGGCGGCTAGCAGT TTAAACACTG
PRRSV-LV.w	CAGTGTTTAAACTGTTAGCCGCCAGCGGCTTGACCCCGTGTGGCCGCGGCGGCCTAGTTGTACTGAAACGGC GGTA
PRRSV-LV.c	TACCGCCGTTTCAGTCAACAAGTACGCGCCGCGGCCACAGCGGGTCAAGCCGCTGGCGGCTAACAGT TTAAACACTG
SARS.w	ACGTTTTTAAACGGGTTTGCGGTGTAAAGTGCAGCCCTTACACCGTGCGGCACAGGCACTAGTACTGA TGTCGTCTACAGGGCT
SARS.c	AGCCCTGTAGACGACATCAGTACTAGTGCCTGTGCCGACAGTGTAAAGACGGGCTGCACTTACACCGCAA CCCGTTTTAAAAACGT
ScYLV.w	GACCAGGAAACGAGCCAAGTGGCGCCGACCCTTAAAAACACCGGA
ScYLV.c	UCCGGTGTTTTTAAGTGGTCGGCGCCACTTGGCTCGTTTCCCTGGTC
SRV1_gag/pro.w	CATCAGGAAACGACTGAGGGGCCAGCCCCAGGCCCGAAACAAGCTTATGGGGC
SRV1_gag/pro.c	GCCCCATAAGCTTGTTCGGGGCTGGGGCTGGCCCTCAGTCCGTTTCCCTGATG

B. Oligonucleotides Used for Dinucleotide Impact Evaluations

Oligonucleotides	Sequences (5c to 3c)
IBV.5.TA.0.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.TA.0.w	AAAGAATTATTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.AA.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.AA.w	AAGAATAATTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.AC.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.AC.w	AAGAATACTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.AG.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.AG.w	AAGAATAGTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.AT.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.AT.w	AAGAATATTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.CA.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.CA.w	AAGAATCATTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.CC.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.CC.w	AAGAATCCTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.CG.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.CG.w	AAGAATCGTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.CT.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.CT.w	AAGAATCTTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.GA.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.GA.w	AAGAATGATTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.GC.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.GC.w	AAGAATGCTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.GG.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.GG.w	AAGAATGGTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.GT.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.GT.w	AAGAATGTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.TA.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.TA.w	AAGAATTATTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.TC.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.TC.w	AAGAATCTTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.TG.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.TG.w	AAGAATTGTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT
IBV.5.TT.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTTTAAATAATTCTT
IBV.5.TT.w	AAGAATTTTTTAAACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT

C. Oligonucleotides Used for Mutant Heptamer Evaluations

Oligonucleotides	Sequences (5c to 3c)
IBV.aua.c	AAAGGCTCGCTTTGCAAGGGGTATCAGCCGAGCCTCACTGCTACCCCGTACCCGTATAAATAATTCTT
IBV.aua.w	AAGAATTATTTATACGGGTACGGGGTAGCAGTGAGGCTCGGCTGATACCCCTTGCAAAGCGAGCCTTT