Supplementary Material and Methods

Plasmid construction. The reporter pFRT-IRES-HIV was derived from pDual-HIV(-1) (1) that contains the Rluc and Fluc coding sequences separated by HIV-1 frameshift region. Replacement of the frameshift region by the 5'UTR of HIV-1 was made in several steps. First, the AflII restriction site located near the T7 sequence of pDual-HIV(-1) was deleted to facilitate subsequent cloning. A PCR fragment was amplified using the ΔAflII-SpeI(+) and ΔAflII-HindIII(-) primers, which were inserted in the SpeI and HindIII sites of pDual-HIV(-1) to produce pDual-HIV(-1)ΔAflII. Next, the beginning of the HIV-1 5'UTR contained in pTAR (2) was amplified by PCR using the TAR-Kpn-uag(+) and TAR-Kpn(-) primers and cloned in the KpnI restriction site of pDual-HIV(-1)ΔAflII located between Rluc and Fluc coding sequences. This PCR introduced three stop codons to terminate the Rluc coding sequence. The rest of the 5'UTR was amplified directly from a proviral molecular clone of HIV-1 group M subtype B (pLAI) (4). The initiation codon for Fluc expression is located within the 5'UTR IRES and the context of the AUG encompassing 30 nt from the Gag sequence was included. A peptide linker (GGGGSGGGGS) was inserted by PCR immediately upstream of the Fluc coding sequence. The first half of the linker was inserted using PCR amplification on pLAI with the 5'UTR-AflII(+) and 5'UTR-BamHI(-) primers and the second half of the linker with the 5'UTR(+) and Linker-BamHI(-) primers. The linker was cloned in the AflII and BamHI restriction sites of pDual-HIV(-1)ΔAflII-TAR to generate pDual-IRES-HIV. This last step removed the frameshift region originally present in pDual-HIV(-1). Finally, we cut the fragment containing the Rluc coding sequence, the 5'UTR region of HIV-1 RNA and the Fluc coding sequence, using PmeI and ApaI restriction sites. This fragment was inserted into pcDNA5FRT (Invitrogen) previously linearized with SciI and ApaI to produce pFRT-IRES-HIV. Prior to this last cloning step, the KpnI and BamHI restriction sites from pcDNA5FRT were eliminated to facilitate subsequent cloning of mutant IRESes. To this end, an oligonucleotide cassette formed by the K7ΔKpnIΔBamHI(+) and K7ΔKpnIΔBamHI(-) primers was inserted in the HindIII and EcoRV restriction sites of pcDNA5FRT. The different mutants of HIV-1 IRES were made by PCR amplification with four primers. The external primers were Ext-KpnI(+) et Ext-BamHI(-). The details for all the primers used can be found in Supplementary Table 1. The resulting PCR products were cloned in the KpnI and BamHI restriction sites of pFRT-dual-IRES-HIV.

Supplementary Table I:
Names and Sequences of the Oligonucleotide Primers Used in this Study

Primer Name	Primer Sequence
ΔAflII-SpeI(+)	5′GACCCGGGGTACCAAGCTTGAGTTTAAACGCTAGCCAGC′3
ΔAflII-HindIII(-)	5′GCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGG′3
TAR-Kpn-uag(+)	5′GCGTTTAAACTTAAGCTTGGTACCCTAGGGTCTCTCTGGTTAGACCAG′3
TAR-Kpn (-)	5′CGAGCTCGGTACCAAGCTTTATTGAGGC′3
5′UTR-AflII(+)	5′GGCTAACTAGGGAACCCACTGCTTAAGCCTCAATAAAGCTTGCC′3
5′UTR-BamHI(-)	5′AAAAAAGGATCCGCTTCCGCCTCCGCCGGTGGCTCTAGCGCTCCCCCCGCTTAATACT GACGCTCTCGCACCCATCTCTCTCCC′3
Linker-BamHI(-)	5′TTTTTTGGATCCTGCTTCCGCCTCCGCCGCTTCCGCCTCCGCCGGTGGCTCTAGCGCT CCC′3
K7ΔKpnIΔBamHI(+)	5′AGCTTGGTAGCGAGCTCGCATCCACTAGTCCAGTGTGGTGGAATTCTGCAGAT′3
K7ΔKpnIΔBamHI(-)	5′ATCTGCAGAATTCCACCACACTGGACTAGTGGATGCGAGCTCGCTACCA′3
Ext-KpnI(+)	5′GAGCTTCGTGGAGAGAGTGCTG′3
Ext-BamHI(-)	5′CGTCTTCTTGGATCCTGGTGCTTCCGCCTC′3
M1-Δloop202-217(+)	5′GCCCGAACAGGGACTTCCAGAGGAGCTCTCTCGACGC′3
M1-Δloop202-217(-)	5′GAGAGAGCTCCTCTGGAAGTCCCTGTTCGGGCGCC′3
M2-ΔSL134-178(+)	5′GCCCGTCTGTTGTGTGACTCTGGTAACAGTGGCGCCCGAACAGGG′3
M2-ΔSL134-178(-)	5′CCCTGTTCGGGCGCCACTGTTACCAGAGTCACACAACAGACGGGC′3
M3-stem134(+)	5′CCCTTTTAGTCAGTGTGGAAACCGGGATCCAGTGGCGCCCGAACAGGG′3
M3-stem134(-)	5′CCCTGTTCGGGCGCCACTGGATCCCGGTTTCCACACTGACTAAAAGGG′3
M4-stem143(+)	5′GATCCCTCAGACCCTTTTAAGGAGACTTCAAAATCTCTAGCAGTGGCGCCCG′3
M4-stem143(-)	5′CCACTGCTAGAGATTTTCCACACTCCTTAAAAGGGTCTGAGGGATCTCTAGTTACC′3
M5-stem143bot(+)	5′GATCCCTCAGACCCTTTTAGTCAGACTTCAAAATCTCTAGCAGTGGCGCCCG′3
M5-stem143bot (-)	5′CCACTGCTAGAGATTTTGAAGTCTGACTAAAAGGGTCTGAGGGATCTCTAGTTACC′3
M6-stem143up(+)	5′GATCCCTCAGACCCTTTTAAGGAGTGTGGAAAATCTCTAGCAGTGGCGCCCG′3
M6-stem143up(-)	5′CCACTGCTAGAGATTTTCCACACTCCTTAAAAGGGTCTGAGGGATCTCTAGTTACC′3
M7-Δloop151(+)	5′CTAGAGATCCCTCAGAAGTCAGTGTGGAAAATCTCTCTAGC′3
M7-Δloop151(-)	5′GATTTTCCACACTGACTTCTGAGGGATCTCTAGTTACC′3
M8-loop151(+)	5′CTAGAGATCCCTCAGAGGGAAAAAGTCAGTGTGGAAAATCTCTAGC′3
M8-loop151(-)	5′GATTTTCCACACTGACTTTTTCCCTCTGAGGGATCTCTAGTTACCAG′3
M9-AAA-CCC(+)	5′CCCTTTTAGTCAGTGTGGCCCATCTCTAGCAGTGGCGCC′3
M9-AAA-CCC(-)	5′GGCGCCACTGCTAGAGATGGGCCACACTGACTAAAAGGG′3
M10-AAA-GGG(+)	5′CCCTTTTAGTCAGTGTGGGGGATCTCTAGCAGTGGCGCC′3

M10-AAA-GGG(-)	5’GGCGCCACTGCTAGAGATCCCCCACACTGACTAAAAGGG’3
M11-AAA-UUU(+)	5’CCCTTTTAGTCAGTGTGGTTTATCTCTAGCAGTGGCGCC’3
M11-AAA-UUU(-)	5’GGCGCCACTGCTAGAGATAAACCACACTGACTAAAAGGG’3
M12-BMH(+)	5’GAGCTCTCTCGACGCACCCCTCGGCTTGCTGAAGCGC’3
M12-BMH (-)	5’GCTTCAGCAAGCCGAGGGGTGCGTCGAGAGAGCTCCTC’3
M13-BMH(+)	5’GCACGGCAAGAGGCGAGTCCAGGCGACTGGTGAGTACG’3
M13-BMH (-)	5’CGTACTCACCAGTCGCCTGGACTCGCCTCTTGCCGTGC’3
M14-BMH(+)	5’GGGAGGCGACTGGTGAGTCGCCTAAAATTTTGACTAGCGGAGGCTAG’3
M14-BMH(-)	5’CTAGCCTCCGCTAGTCAAAATTTTAGGCGACTCACCAGTCGCCTCCC’3
M15-LDI(+)	5’CGAGGGGAGGCGACTGGTGCGCACCCAAAAATTTTGACTAGC’3
M15-LDI(-)	5’GCTAGTCAAAATTTTTGGGTGCGCACCAGTCGCCTCCCCTCG’3
M16-LDI(+)	5’CGACTGGTGAGTACGCCATCCTTTTTGACTAGCGGAGGC’3
M16-LDI(-)	5’GCCTCCGCTAGTCAAAAAGGATGGCGTACTCACCAGTCG’3
M17-LDI(+)	5’GGTGAGTACGCCAAAAATTTTTTCTAGCGGAGGCTAGAAGGAGAG’3
M17-LDI(-)	5’CTCTCCTTCTAGCCTCCGCTAGAAAAAATTTTTGGCGTACTCACC’3

Supplementary Results

The 134-178 stem-loop, the 202-217 region and the four-nt bulge in the DIS hairpin, but not the A stretch in loop I, are highly conserved among natural variants of HIV-1 group M subtype B. The 5'UTR region of HIV-1 is the most conserved region in the HIV-1 genome (3). The HIV-1 5'UTR region used in this study originates from pLAI. We examined the conservation of the different regions which we found to influence the 5'UTR IRES activity among group M subtype B natural variants. These regions of pLAI were aligned with the corresponding regions of HIV-1 group M subtype B variants available in the HIV sequence database of the Los Alamos National Laboratory available at the following URL : http://www.hiv.lanl.gov/. When the 134-178 stem-loop (IRENE) from pLAI was aligned with the corresponding region of 97 available variants, we found that it is highly conserved (Supp. Fig. 1A). Most of the differences are located in the upper 7-pyrimidine loop, which did not influence the 5'UTR IRES activity. Twenty-one variants have mutations in the upper stem, but only five of these mutations disrupt a base-pair. The 3A bulge is conserved in all these variants except three. When nt 200-219 of pLAI were aligned with the corresponding region of 129 available variants (Supp. Fig. 1B), this unstructured region was also found to be highly conserved except for the four nt at the 3' end. When nt 236-246 of pLAI were aligned with the corresponding region of 142 available variants, we observed that the four-nt bulge at the beginning of the DIS hairpin (Supp. Fig. 1C) is highly conserved since only four variants differ from pLAI. Finally, nt 301-305 of pLAI, a stretch of five A in the beginning of loop I, were aligned with the corresponding region of 149 available variants (Supp. Fig. 1D). The five A are conserved in 60 variants. However, 62 variants have deletions and/or mutations in this region. Therefore, while the 301-305 segment shows some variability, IRENE, the 202-217 region and the 239-242 bulge are highly conserved.

Supplementary Figure Legends

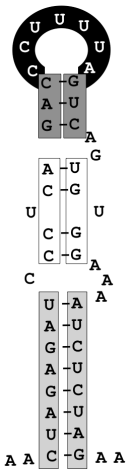
Supplementary FIGURE 1

(A) Sequence alignment of the 134-178 stem-loop. These sequences originated from pLAI and the corresponding regions of HIV-1 group M subtype B variants retrieved from HIV-1 database from Los Alamos National Laboratory. Lines indicate identical bases, R represents A or G; Y represents C or U; B represents C, G or U; N represents any nt. When the region of interest of a variant is identical to pLAI, its name is in bold. (B) Sequence alignment of the unstructured 202-217 segment. (C) Sequence alignment of the four-nt bulge in the DIS hairpin (nt 239-242). (D) Sequence alignment of the beginning of loop I (nt 302-305). In (B), (C) and (D), the region of interest is in gray.

Supplementary References

1. Dulude, D., Berchiche, Y.A., Gendron, K., Brakier-Gingras, L. and Heveker, N. (2006) Decreasing the frameshift efficiency translates into an equivalent reduction of the replication of the human immunodeficiency virus type 1. *Virology*, **345**, 127-136.
2. Gendron, K., Charbonneau, J., Dulude, D., Heveker, N., Ferbeyre, G. and Brakier-Gingras, L. (2008) The presence of the TAR RNA structure alters the programmed -1 ribosomal frameshift efficiency of the human immunodeficiency virus type 1 (HIV-1) by modifying the rate of translation initiation. *Nucleic Acids Res*, **36**, 30-40.
3. Berkhout, B. (1996) Structure and function of the human immunodeficiency virus leader RNA. *Prog Nucleic Acid Res Mol Biol*, **54**, 1-34.
4. Peden, K., Emerman, M. and Montagnier, L. (1991) Changes in growth properties on passage in tissue culture of viruses derived from infectious molecular clones of HIV-1LAI, HIV-1MAL, and HIV-1ELI. *Virology*, **185**, 661-672.

A) The 134-178 stem-loop (IRENE)



	pLAI	C.UAGAGAU	C	CC	U	CA	GAC	CCUUUUA	GUC	AG	UG	U	GG	AAA	A.UCUCUAG
B.FR.83.HXB2_LAI_IIIB_BRU.K03455	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.AU.86.MBC200.AF042100	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.AU.87.MBC925.AF042101	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.AU.x.1181.AF538302	-.-------	-	--	-	--	---	-------	U--	C-	--	-	A-	---	-.-------
B.AU.x.C24.AF538304	-.-------	-	--	-	--	---	-------	---	--	--	-	--	-G-	-.-------
B.AU.x.C42.AF538305	-.-------	-	--	-	--	---	-AA----	---	--	--	-	--	---	-.-------
B.AU.x.C76.AF538306	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.AU.x.C92.AF538307	-.-------	-	--	-	--	---	-------	---	--	--	-	--	-G-	-.-------
B.BR.02.02BR011.DQ358809	-.-------	-	--	-	--	---	-A---A-	---	--	--	-	--	---	-.-------
B.BR.02.02BR013.DQ358810	AC-------	-	--	-	--	---	-Δ-----	---	--	--	-	--	---	-A-------
B.BR.03.BREPM1023.EF637057	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.BR.03.BREPM1038.EF637048	-.-------	-	--	-	--	---	-A--C--	---	--	--	-	--	---	-.-------
B.BR.04.BREPM1066.FJ195090	-.-------	-	--	-	--	---	AΔC----	---	--	--	-	--	---	-.-------
B.BR.04.BREPM1070.FJ195086	-.-----U-	-	-U	-	--	---	-U-A--G	U--	--	-U	G	--	---	U.---U-GC
B.BR.05.BREPM1081.FJ195091	-.-------	-	--	-	--	---	A------	A--	C-	--	-	--	---	-.-------
B.BR.05.BREPM1093.FJ195089	-.-------	-	--	-	--	---	A------	---	--	--	-	--	---	-.-------
B.CA.96.WC10C_4.AY314056	-.-------	-	--	-	--	---	U------	---	--	--	-	--	---	-.-------
B.CN.02.02HNsc11.DQ007903	-.-------	-	--	-	--	-A	---A---	---	--	--	-	--	---	-.-------
B.CN.05.05CNHB_hp3.DQ990880	-.-------	-	--	-	--	---	--Δ----	--U	U-	--	-	--	---	-.-------
B.CU.99.Cu19.AY586542	-.-------	-	--	-	--	---	-U-C---	---	--	--	-	--	---	-.-------
B.CU.99.Cu43.AY586543	-.-------	-	--	-	--	---	-U-C---	---	--	--	-	--	---	-.-------
B.DE.86.D31.U43096	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.DE.86.HAN.U43141	-.-------	-	--	-	--	-U	-------	---	--	--	-	--	---	-.-------
B.ES.05.ES.EU786672	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.ES.06.ES.EU786676	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.ES.06.ES.EU786677	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.ES.07.ES.EU786678	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.ES.07.ES.EU786679	-.-------	-	--	-	--	---	A-AGC--	---	--	--	-	--	--U	-.-------
B.ES.07.ES.EU786680	-.-------	-	--	-	--	---	-AA----	---	C-	--	-	--	---	-.-------
B.ES.89.U61.DQ854716	-UAGAGAUC	-	-U	-	--	---	-AA----	---	--	--	-	-A	---	-.-------
B.GA.88.OYI.M26727	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.GB.83.CAM1.D10112	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.GB.86.GB8.AJ271445	-.-------	-	--	-	--	---	-------	---	--	--	-	A-	---	-.-------
B.GB.x.MANC.U23487	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.IU.05.SG1.DQ672623	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.JP.00.DR2508.AB289588	-.-------	-	--	-	--	---	-CUGG--	---	--	--	-	A-	---	-.-------
B.JP.01.DR388.AB289590	-.-------	-	--	-	--	---	-A---A-	---	--	--	-	--	---	-.-------
B.JP.04.04JPDR6075B.AB221125	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.JP.04.DR6089.AB286955	-.-------	-	--	-	--	---	-A---A-	---	--	--	-	--	---	-.-------
B.JP.05.DR6538.AB287363	-.-------	-	--	C	--	---	-------	---	--	--	-	--	---	-.-------
B.JP.05.DR6737.AB287364	-.-------	-	--	-	--	---	-A-----	---	C-	--	-	--	---	-.-------
B.JP.05.DR7060.AB287366	-.-------	-	--	-	--	---	AU--G--	---	--	--	-	--	---	-.-------
B.JP.05.DR7065.AB287368	-.-------	-	--	-	--	-U	AUC----	---	C-	--	-	--	---	-A-------
B.JP.99.DR1348.AB287370	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.KR.04.04KMH5.DQ295193	-.-------	-	--	-	--	---	-AA----	---	--	--	-	--	---	-.-------
B.KR.04.04LHS6.AY839827	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.KR.04.04LSK7.DQ295192	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.KR.04.04WK7_HIV_1_wk.DQ295194	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.KR.05.05CSR3.DQ837381	-.-------	-	--	-	--	---	AA-----	---	--	--	-	--	---	-.-------
B.NL.00.671_00U36.AY423387	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.NL.86.3202A21.U34604	-.-------	-	--	-	--	---	-------	---	--	--	A	--	---	-.-------
B.NL.96.H434_42_A1.AY970948	-.-------	-	--	-	--	---	-------	---	--	-A	-	--	---	-.-------
B.RU.04.04RU128005.AY682547	-.-------	-	--	-	--	---	-------	---	--	--	-	R-	---	-.-------
B.RU.04.04RU129005.AY751406	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.UW.94.UWCYS.AF086817	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.US.00.14294_1.DQ853436	-.-------	-	--	-	--	-U	-------	--U	--	C-	-	A-	---	-.-------
B.US.00.ES1_20.EF363123	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.04.ES10_53.EF363127	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.04.ES4_24.EF363124	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.04.ES8_43.EF363126	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.US.83.5018_83.AY835777	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.83.5157_83.AY835781	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.83.RF.M17451	-.-------	-	--	-	--	---	-UC----	---	--	--	-	--	---	-.-------
B.US.83.SF2.K02007	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-A-------
B.US.84.5019_84.AY835779	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.84.MNCG.M17449	-.-------	-	--	-	--	-U	-------	-G-	--	--	-	--	---	-.-------
B.US.84.NY5CG.M38431	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.84.SF33.AY352275	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.85.5077_85.AY835769	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.85.Ba_L.AB221005	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.86.5084_86.AY835775	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.86.5096_86.AY835749	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.86.5127_86.AY835774	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.86.AD87.AF004394	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.86.YU_2.M93258	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.87.5113_87.AY835758	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.87.BC.L02317	-.-------	-	--	-	--	U--	-------	---	--	--	-	--	---	-.-------
B.US.88.5160_88.AY835763	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.88.WR27.AF286365	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.89.P896.U39362	-.-------	-	--	-	--	---	-A-CC--	--U	--	--	-	A-	---	-.-------
B.US.90.WCIPR.U69591	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.90.WEAU160.U21135	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.US.91.5048_91.AY835761	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.91.DH12_3.AF069140	-.-------	-	--	-	--	---	-A-----	---	--	--	-	--	---	-.-------
B.US.93.WCD32P0793.DQ487188	-.-------	-	--	-	--	---	-AΔΔ-A-	---	--	--	-	--	---	-.-------
B.US.93.WCM32P0793.DQ487190	-.-------	-	--	-	--	---	--ΔΔ---	---	--	--	-	--	---	-.-------
B.US.94.5082_94.AY835773	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.95.5073_95.AY835768	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.96.5155_96.AY835753	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.97.ARES2.AB078005	-.-------	-	--	-	--	---	--Δ----	---	--	--	-	--	---	-.-------
B.US.98.15384_1.DQ853463	-.-------	-	--	-	--	---	-------	--U	--	C-	-	A-	---	-.-------
B.US.98.98USHVTN1925c1.AY560107	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.98.98USHVTN3605c9.AY560108	-.-------	-	--	-	--	---	-------	---	--	--	-	--	---	-.-------
B.US.98.98USHVTN8229c6.AY560109	-.-------	-	--	-	--	---	-Δ-----	---	--	-A	-	A-	---	-A-------
B.US.98.98USHVTN941c1.AY560110	-.-------	-	--	-	--	---	-A-----	---	--	-A	-	--	---	-.-------
B.US.98.WC3_0498_4.EF175212	-.-------	-	--	-	--	---	U------	---	--	--	-	-A	---	-.-------
B.ZA.03.03ZAPS045MB2.DQ396398	-.-------	-	--	-	--	---	-U--AA-	---	--	-A	G	AA	---	Δ.-------

B) The 202-217 segment

pLAI	UU	GAAAG	.	CGAAAG	GGAA	AC
B.FR.83.HXB2_LAI_IIIB_BRU.K03455	C-	-----	.	------	----	--
B.AU.86.MBC200.AF042100	--	-----	.	------	-A--	--
B.AU.87.MBC925.AF042101	--	-U---	.	------	A---	--
B.AU.95.MBCC54.AF042103	--	-----	.	------	A---	--
B.AU.96.MBCD36.AF042105	--	-----	.	------	----	--
B.AU.x.1181.AF538302	--	-----	.	------	A---	--
B.AU.x.C24.AF538304	--	-----	.	------	A---	--
B.AU.x.C42.AF538305	CG	-----	.	------	AA--	--
B.AU.x.C76.AF538306	--	-----	.	------	A---	--
B.AU.x.C92.AF538307	--	-----	.	------	A---	--
B.BR.02.02BR008.DQ358808	CU	-----	.	U-----	UAG-	--
B.BR.02.02BR011.DQ358809	--	-----	.	------	UA-G	--
B.BR.02.02BR013.DQ358810	UA	-----	.	------	UAG-	C-
B.BR.03.BREPM1023.EF637057	C-	-----	.	------	-AG-	--
B.BR.03.BREPM1024.EF637056	--	-----	.	------	UAG-	--
B.BR.03.BREPM1027.EF637054	--	-----	.	------	UA--	--
B.BR.03.BREPM1033.EF637050	-C	-----	.	------	UAG-	--
B.BR.03.BREPM1038.EF637048	--	-----	.	------	UA-C	G-
B.BR.03.BREPM1040.EF637047	-A	----A	.	------	UAG-	--
B.BR.03.BREPM2012.EF637046	--	-----	.	------	UA--	G-
B.BR.04.BREPM1066.FJ195090	-C	----A	.	------	UAG-	--
B.BR.04.BREPM1070.FJ195086	--	----A	.	G----U	AAG-	--
B.BR.05.BREPM1081.FJ195091	--	----A	.	------	UA--	--
B.BR.05.BREPM1084.FJ195088	--	--G--	.	------	UAG-	--
B.BR.05.BREPM1093.FJ195089	C-	-----	.	------	UAG-	--
B.CA.96.WC10C_4.AY314056	--	-----	.	------	A---	--
B.CN.01.CNHN24.AY180905	-A	-----	.	------	U--G	--
B.CN.02.02HNsc11.DQ007903	C-	-----	.	------	U--G	--
B.CN.05.05CNHB_hp3.DQ990880	GC	-----	.	------	U--G	--
B.CN.x.RL42.U71182	--	-----	.	------	U--G	--
B.CU.99.Cu43.AY586543	--	-----	.	U-----	UAG-	--
B.DE.86.D31.U43096	--	-----	.	U-----	UA-G	--
B.DE.86.HAN.U43141	--	-----	.	------	UAG-	--
B.DK.01.CTL_016.EF514704	CG	-----	.	------	A---	--
B.DK.01.CTL_017.EF514705	--	-----	.	------	A---	--
B.DK.01.CTL_018.EF514706	--	-----	.	------	A---	--
B.DK.01.CTL_030.EF514708	GC	-----	.	------	UAG-	--
B.DK.01.CTL_033.EF514709	YU	A----	.	------	A---	--
B.DK.04.PMVL_012.EF514699	--	-----	.	------	A---	--
B.DK.04.PMVL_013.EF514700	--	-----	.	------	A---	--
B.DK.04.PMVL_018.EF514697	--	-----	.	------	A---	--
B.DK.04.PMVL_025.EF514702	--	-----	.	------	A---	--
B.DK.04.PMVL_027.EF514698	CU	-----	.	------	A---	--
B.DK.04.PMVL_039.EF514703	--	-----	.	U-----	A---	--
B.DK.04.PMVL_049.EF514701	--	-----	.	------	UAG-	--
B.ES.05.ES.EU786672	--	----A	.	------	A---	--
B.ES.06.ES.EU786675	CC	-----	.	------	UAG-	--
B.ES.06.ES.EU786676	--	-----	.	------	A---	--
B.ES.06.ES.EU786677	CC	-----	.	U-----	UUG-	--
B.ES.07.ES.EU786678	CG	-----	.	------	A---	--
B.ES.07.ES.EU786679	--	-----	.	------	----	--
B.ES.07.ES.EU786680	C-	-----	.	U-----	A-G-	--
B.ES.89.U61.DQ854716	--	-----	.	------	A---	--
B.GA.88.OYI.M26727	C-	U----	.	U-----	U-G-	--
B.GB.83.CAM1.D10112	--	----A	.	------	UAG-	--
B.GB.86.GB8.AJ271445	--	-----	.	U-----	UUG-	--
B.GB.x.MANC.U23487	C-	-----	.	------	UAG-	--
B.HK.x.HK003.FJ460500	C-	-----	.	------	A-Δ-	--
B.HK.x.HK004.FJ460501	C-	-----	.	------	A---	--
B.IT.05.SG1.DQ672623	C-	-----	.	------	A---	--
B.JP.00.DR2508.AB289588	C-	-----	.	------	UAG-	--
B.JP.01.DR388.AB289590	--	-----	.	------	UAG-	--
B.JP.04.04JPDR6075B.AB221125	GC	-----	.	------	UAG-	--
B.JP.04.DR6089.AB286955	--	-----	.	------	A---	--
B.JP.05.DR6538.AB287363	--	-----	.	U-----	UAG-	--
B.JP.05.DR6737.AB287364	C-	----A	.	------	C-G-	--
B.JP.05.DR7060.AB287366	--	----A	.	------	UAG-	--
B.JP.05.DR7065.AB287368	C-	UG--A	G	------	U-G-	--
B.JP.99.DR1348.AB287370	--	-----	.	------	UA-G	--
B.KR.04.04KMH5.DQ295193	--	-----	.	------	UAG-	--
B.KR.04.04LHS6.AY839827	--	-----	.	------	U-GU	--
B.KR.04.04LSK7.DQ295192	--	-----	.	------	UAG-	--
B.KR.04.04WK7_HIV_1_wk.DQ295194	--	----A	.	------	UAG-	--
B.KR.05.05CSR3.DQ837381	--	-----	.	------	-A--	--
B.MM.99.mSTD101.AB097870	GC	-----	.	------	UA-G	--
B.NL.00.671_00T36.AY423387	--	---G-	.	ΔΔΔ---	UA--	--
B.NL.86.3202A21.U34604	GC	-----	.	------	A---	--
B.NL.96.H434_42_A1.AY970948	GC	-----	.	------	UAG-	--
B.RU.04.04RU128005.AY682547	YY	-----	.	------	A---	--
B.RU.04.04RU129005.AY751406	--	-----	.	U-----	----	--
B.RU.04.04RU139089.AY751407	--	-----	.	------	UAG-	--
B.RU.04.04RU139095.AY819715	--	-----	.	------	UAG-	--
B.TW.94.TWCYS.AF086817	C-	-----	.	-A----	A---	--
B.US.00.14294_1.DQ853436	GC	-----	.	------	UAG-	--
B.US.00.ES1_20.EF363123	--	-----	.	------	A---	--
B.US.04.ES10_53.EF363127	AC	-----	.	------	A---	--
B.US.04.ES4_24.EF363124	--	-----	.	------	----	--
B.US.04.ES8_43.EF363126	CG	-----	.	------	A---	--
B.US.83.5018_83.AY835777	--	-----	.	------	UA--	G-
B.US.83.5157_83.AY835781	--	-----	.	------	UA--	G-
B.US.83.RF.M17451	CA	-----	.	------	UAG-	--
B.US.83.SF2.K02007	GC	-----	.	------	UAG-	--
B.US.84.5019_84.AY835779	--	-----	.	------	UA--	G-
B.US.84.MNCG.M17449	--	-----	.	------	AA--	--
B.US.84.NY5CG.M38431	--	--G--	.	------	UA--	G-
B.US.84.SF33.AY352275	--	-----	.	U-----	UUΔ-	--
B.US.85.5077_85.AY835769	--	-----	.	------	UA--	G-
B.US.85.Ba_L.AB221005	--	-----	.	------	A---	--
B.US.86.5084_86.AY835775	--	-----	.	------	UA--	G-
B.US.86.5096_86.AY835749	--	-----	.	------	----	--
B.US.86.5127_86.AY835774	--	-----	.	------	UA--	G-
B.US.86.AD87.AF004394	--	-----	.	U-----	UAG-	--
B.US.86.YU_2.M93258	--	-----	.	------	-A--	--
B.US.87.5113_87.AY835758	--	-----	.	------	UA--	G-
B.US.87.BC.L02317	CG	-----	.	------	A---	--
B.US.88.5160_88.AY835763	--	-----	.	------	UA--	G-
B.US.88.WR27.AF286365	C-	A----	.	------	UAG-	--
B.US.89.P896.U39362	CG	-----	.	------	A---	--
B.US.90.US1.AY173952	C-	-----	.	------	A---	--
B.US.90.US2.AY173953	--	-----	.	------	----	--
B.US.90.US3.AY173954	-A	-----	.	------	UA--	--
B.US.90.US4.AY173955	CC	-----	.	------	UAG-	--
B.US.90.WCIPR.U69591	--	-----	.	------	----	--
B.US.90.WEAU160.U21135	CC	-----	.	------	----	--
B.US.91.5048_91.AY835761	--	-----	.	------	UA--	G-
B.US.91.DH12_3.AF069140	CG	-----	.	------	A---	--
B.US.93.WCD32P0793.DQ487188	C-	-----	.	U-----	A---	--
B.US.93.WCM32P0793.DQ487190	--	-----	.	------	-A--	--
B.US.94.5082_94.AY835773	--	-----	.	------	UA--	G-
B.US.95.5073_95.AY835768	--	-----	.	------	UA--	G-
B.US.96.5155_96.AY835753	--	-----	.	------	UA--	G-
B.US.97.ARES2.AB078005	--	-----	.	------	A---	--
B.US.98.15384_1.DQ853463	GC	-----	.	------	UA--	--
B.US.98.98USHVTN1925c1.AY560107	C-	-----	.	------	A---	--
B.US.98.98USHVTN3605c9.AY560108	--	-----	.	------	A---	--
B.US.98.98USHVTN8229c6.AY560109	AA	-UG-G	.	A-U-G-	U-Δ-	--
B.US.98.98USHVTN941c1.AY560110	CA	-----	.	------	UAG-	--
B.US.98.WC3_0498_4.EF175212	-C	-----	.	------	UAG-	--
B.ZA.03.03ZAPS045MB2.DQ396398	C-	-----	.	------	A---	--

C) The 4-nt 239-242 bulge

pLAI	C	.	GC	AGGA	..	CUCG
B.FR.83.HXB2_LAI_IIIB_BRU.K03455	-	.	--	----	..	----
B.AU.86.MBC200.AF042100	-	.	--	----	..	----
B.AU.87.MBC925.AF042101	-	.	--	----	..	----
B.AU.95.MBCC54.AF042103	-	.	--	----	..	----
B.AU.96.MBCC98.AF042104	-	.	--	----	..	----
B.AU.96.MBCD36.AF042105	-	.	--	----	..	----
B.AU.x.1181.AF538302	-	.	--	----	..	----
B.AU.x.2870718.AY857022	-	.	--	----	..	----
B.AU.x.C24.AF538304	-	.	--	----	..	----
B.AU.x.C42.AF538305	-	.	--	-A--	..	----
B.AU.x.C76.AF538306	-	.	--	----	..	---U
B.AU.x.C92.AF538307	-	.	--	----	..	----
B.AU.x.VH.AF146728	-	.	--	----	..	----
B.BR.02.02BR008.DQ358808	-	.	--	----	..	----
B.BR.02.02BR011.DQ358809	-	.	--	----	..	----
B.BR.02.02BR013.DQ358810	A	C	--	----	..	----
B.BR.03.BREPM1023.EF637057	-	.	--	----	..	----
B.BR.03.BREPM1024.EF637056	-	.	--	----	..	----
B.BR.03.BREPM1027.EF637054	-	.	--	----	..	----
B.BR.03.BREPM1028.EF637053	-	.	--	----	..	----
B.BR.03.BREPM1032.EF637051	-	.	--	----	..	----
B.BR.03.BREPM1033.EF637050	-	.	--	----	..	----
B.BR.03.BREPM1035.EF637049	-	.	--	----	..	----
B.BR.03.BREPM1038.EF637048	-	.	--	----	..	----
B.BR.03.BREPM1040.EF637047	-	.	--	----	..	----
B.BR.03.BREPM2012.EF637046	-	.	--	----	..	----
B.BR.04.BREPM1066.FJ195090	-	.	--	----	..	----
B.BR.04.BREPM1070.FJ195086	-	.	C-	----	..	--G-
B.BR.05.BREPM1081.FJ195091	-	.	--	----	..	----
B.BR.05.BREPM1084.FJ195088	-	.	--	----	..	----
B.BR.05.BREPM1093.FJ195089	-	.	--	----	..	----
B.CA.96.WC10C_4.AY314056	-	.	--	----	..	----
B.CN.01.CNHN24.AY180905	-	.	--	----	..	----
B.CN.02.02HNsc11.DQ007903	-	.	--	----	..	----
B.CN.05.05CNHB_hp3.DQ990880	-	.	--	----	..	----
B.CN.x.RL42.U71182	-	.	--	----	..	----
B.CU.99.Cu19.AY586542	-	.	--	----	..	----
B.CU.99.Cu43.AY586543	-	.	--	----	..	----
B.DE.86.D31.U43096	-	.	--	----	..	----
B.DE.86.HAN.U43141	-	.	--	----	..	----
B.DK.01.CTL_016.EF514704	-	.	--	----	..	----
B.DK.01.CTL_017.EF514705	-	.	--	----	..	----
B.DK.01.CTL_018.EF514706	-	.	--	----	..	----
B.DK.01.CTL_023.EF514707	-	.	--	----	..	----
B.DK.01.CTL_030.EF514708	-	.	--	----	..	----
B.DK.01.CTL_033.EF514709	-	.	--	----	..	----
B.DK.01.CTL_035.EF514710	.	.	--	----	..	----
B.DK.01.CTL_043.EF514712	-	.	--	----	..	----
B.DK.04.PMVL_012.EF514699	-	.	--	----	..	----
B.DK.04.PMVL_013.EF514700	-	.	--	----	..	----
B.DK.04.PMVL_018.EF514697	-	.	--	----	..	----
B.DK.04.PMVL_025.EF514702	-	.	--	----	..	----
B.DK.04.PMVL_027.EF514698	-	.	--	----	..	----
B.DK.04.PMVL_039.EF514703	.	.	-G	GBAU	GG	GGG-
DK.04.PMVL_049.EF514701	-	.	--	----	..	----
B.ES.05.ES.EU786672	-	.	--	----	..	----
B.ES.06.ES.EU786675	-	.	--	----	..	----
B.ES.06.ES.EU786676	-	.	--	----	..	----
B.ES.06.ES.EU786677	-	.	--	----	..	----
B.ES.07.ES.EU786678	-	.	--	----	..	----
B.ES.07.ES.EU786679	-	.	--	----	..	----
B.ES.07.ES.EU786680	-	.	--	----	..	----
B.ES.89.U61.DQ854716	-	.	--	----	..	----
B.GA.88.OYI.M26727	-	.	--	----	..	----
B.GB.83.CAM1.D10112	-	.	--	----	..	----
B.GB.86.GB8.AJ271445	-	.	--	-A-G	A.	----
B.GB.x.MANC.U23487	-	.	--	----	..	----
B.HK.x.HK003.FJ460500	-	.	--	----	..	----
B.HK.x.HK004.FJ460501	-	.	--	----	..	----
B.IN.x.11807.EF694037	-	.	--	----	..	----
B.IT.05.SG1.DQ672623	-	.	--	----	..	----
B.JP.00.DR2508.AB289588	-	.	--	----	..	----
B.JP.01.DR388.AB289590	-	.	--	----	..	----
B.JP.04.04JPDR6075B.AB221125	-	.	--	----	..	----
B.JP.04.DR6089.AB286955	-	.	--	----	..	----
B.JP.05.DR6538.AB287363	-	.	--	----	..	----
B.JP.05.DR6737.AB287364	-	.	--	----	..	----
B.JP.05.DR7060.AB287366	-	.	--	----	..	----
B.JP.05.DR7065.AB287368	-	.	--	----	..	----
B.JP.99.DR1348.AB287370	-	.	--	----	..	----
B.KR.04.04KMH5.DQ295193	-	.	--	----	..	----
B.KR.04.04LHS6.AY839827	-	.	--	----	..	----
B.KR.04.04LSK7.DQ295192	-	.	--	----	..	----
B.KR.04.04WK7_HIV_1_wk.DQ295194	-	.	--	----	..	----
B.KR.05.05CSR3.DQ837381	-	.	--	----	..	----
B.MM.99.mSTD101.AB097870	-	.	--	----	..	----
B.NL.00.671_00T36.AY423387	-	.	--	----	..	----
B.NL.86.3202A21.U34604	-	.	--	----	..	----
B.NL.96.H434_42_A1.AY970948	-	.	--	----	..	----
B.RU.04.04RU128005.AY682547	-	.	--	----	..	----
B.RU.04.04RU129005.AY751406	-	.	--	----	..	----
B.RU.04.04RU139089.AY751407	-	.	--	----	..	----
B.RU.04.04RU139095.AY819715	-	.	--	----	..	----
B.TH.90.BK132.AY173951	-	.	--	----	..	----
B.TW.94.TWCYS.AF086817	-	.	--	----	..	----
B.US.00.14294_1.DQ853436	-	.	--	----	..	----
B.US.00.ES1_20.EF363123	-	.	--	----	..	----
B.US.04.ES10_53.EF363127	-	.	--	----	..	----
B.US.04.ES4_24.EF363124	-	.	--	----	..	----
B.US.04.ES8_43.EF363126	-	.	--	----	..	----
B.US.83.5018_83.AY835777	-	.	--	----	..	----
B.US.83.5157_83.AY835781	-	.	--	----	..	----
B.US.83.RF.M17451	-	.	--	----	..	----
B.US.83.SF2.K02007	-	.	--	----	..	----
B.US.84.5019_84.AY835779	-	.	--	----	..	----
B.US.84.MNCG.M17449	-	.	--	----	..	----
B.US.84.NY5CG.M38431	-	.	--	----	..	----
B.US.84.SF33.AY352275	-	.	--	----	..	----
B.US.85.5077_85.AY835769	-	.	--	----	..	----
B.US.85.Ba_L.AB221005	-	.	--	----	..	----
B.US.86.5084_86.AY835775	-	.	--	----	..	----
B.US.86.5096_86.AY835749	-	.	--	----	..	----
B.US.86.5127_86.AY835774	-	.	--	----	..	----
B.US.86.AD87.AF004394	-	.	--	----	..	----
B.US.86.JRFL.U63632	-	.	--	----	..	----
B.US.86.YU_2.M93258	-	.	--	----	..	----
B.US.87.5113_87.AY835758	-	.	--	----	..	----
B.US.87.BC.L02317	-	.	--	----	..	----
B.US.88.5160_88.AY835763	-	.	--	----	..	----
B.US.88.WR27.AF286365	-	.	--	----	..	----
B.US.89.P896.U39362	-	.	--	----	..	----
B.US.90.US1.AY173952	-	.	--	----	..	----
B.US.90.US2.AY173953	-	.	--	----	..	----
B.US.90.US3.AY173954	-	.	--	----	..	----
B.US.90.US4.AY173955	-	.	--	----	..	----
B.US.90.WCIPR.U69591	-	.	--	----	..	----
B.US.90.WEAU160.U21135	-	.	--	----	..	----
B.US.91.5048_91.AY835761	-	.	--	----	..	----
B.US.91.DH12_3.AF069140	-	.	--	----	..	----
B.US.93.WCD32P0793.DQ487188	-	.	--	----	..	----
B.US.93.WCM32P0793.DQ487190	-	.	--	----	..	----
B.US.94.5082_94.AY835773	-	.	--	----	..	----
B.US.95.5073_95.AY835768	-	.	--	----	..	----
B.US.96.5155_96.AY835753	-	.	--	----	..	----
B.US.97.ARES2.AB078005	-	.	--	----	..	----
B.US.98.15384_1.DQ853463	-	.	--	----	..	----
B.US.98.98USHVTN1925c1.AY560107	-	.	--	----	..	----
B.US.98.98USHVTN3605c9.AY560108	-	.	--	----	..	----
B.US.98.98USHVTN8229c6.AY560109	-	.	--	-A-G	A.	----
B.US.98.98USHVTN941c1.AY560110	-	.	--	----	..	----
B.US.98.WC3_0498_4.EF175212	-	.	--	----	..	----
B.ZA.03.03ZAPS045MB2.DQ396398	-	.	--	----	..	----

D) The stretch of A in loop I (nt 301-305)

pLAI	AAAAA	.....	.....	UUUUGA
B.FR.83.HXB2_LAI_IIIB_BRU.K03455	-----	.....	.....	------
B.AU.86.MBC200.AF042100	-----	A....	....U	------
B.AU.87.MBC925.AF042101	-----	A....	.....	------
B.AU.95.MBCC54.AF042103	----Δ	.....	....U	------
B.AU.96.MBCC98.AF042104	-----	.....	.....	------
B.AU.96.MBCD36.AF042105	-----	.....	.....	------
B.AU.x.1181.AF538302	----Δ	.....	...UU	------
B.AU.x.2870718.AY857022	G----	.....	.....	------
B.AU.x.8634991.AY857144	-----	AUAAA	...AA	------
B.AU.x.9125091.AY857165	----Δ	.....	....U	------
B.AU.x.C24.AF538304	---ΔΔ	.....	...UA	------
B.AU.x.C42.AF538305	-----	.....	.....	------
B.AU.x.C76.AF538306	-----	.....	.....	------
B.AU.x.C92.AF538307	-----	.....	.....	------
B.AU.x.VH.AF146728	-----	.....	.....	------
B.BR.02.02BR008.DQ358808	-ΔΔΔΔ	.....	...UU	------
B.BR.02.02BR011.DQ358809	---C-	UAAAA	.....	------
B.BR.02.02BR013.DQ358810	-----	UAAAA	.....	------
B.BR.03.BREPM1023.EF637057	----Δ	.....	....U	------
B.BR.03.BREPM1024.EF637056	-----	.....	.....	------
B.BR.03.BREPM1027.EF637054	--ΔΔΔ	.....	.....	------
B.BR.03.BREPM1028.EF637053	---ΔΔ	.....	.....	------
B.BR.03.BREPM1032.EF637051	-----	A....	....U	------
B.BR.03.BREPM1033.EF637050	-ΔΔΔΔ	.....	...UU	------
B.BR.03.BREPM1035.EF637049	--ΔΔΔ	.....	UUUUA	------
B.BR.03.BREPM1038.EF637048	---ΔΔ	.....	....U	------
B.BR.03.BREPM1040.EF637047	--ΔΔΔ	.....	....U	------
B.BR.03.BREPM2012.EF637046	-U---	A....	.....	------
B.BR.04.BREPM1066.FJ195090	U----	.....	.....	------
B.BR.04.BREPM1070.FJ195086	-----	.....	.....	------
B.BR.05.BREPM1081.FJ195091	-----	AUUAA	..AAA	------
B.BR.05.BREPM1084.FJ195088	-----	UAAAA	...UU	------
B.BR.05.BREPM1093.FJ195089	-----	.....	.....	------
B.BR.89.BZ167.AY173956	-U-ΔΔ	.....	....U	------
B.CA.96.WC10C_4.AY314056	---ΔΔ	.....	....U	------
B.CA.97.CANB3FULL.AY779553	-----	.....	.....	------
B.CA.x.HDM003V01.DQ322227	----Δ	.....	C	------
B.CN.01.CNHN24.AY180905	---ΔΔ	.....	...UU	------
B.CN.02.02HNsc11.DQ007903	-----	A....	...UU	--G---
B.CN.05.05CNHB_hp3.DQ990880	-ΔΔΔΔ	.....	...UU	------
B.CN.x.RL42.U71182	--ΔΔΔ	.....	.....	Δ-----
B.CU.99.Cu19.AY586542	----Δ	.....	....U	------
B.CU.99.Cu43.AY586543	----Δ	.....	....U	------
B.DE.86.D31.U43096	-----	.....	.....	------
B.DE.86.HAN.U43141	----Δ	.....	.....	------
B.DK.01.CTL_016.EF514704	G--ΔΔ	.....	...UU	-G----
B.DK.01.CTL_017.EF514705	G-U-Δ	.....	.....	------
B.DK.01.CTL_018.EF514706	--ΔΔΔ	.....	.....	------
B.DK.01.CTL_023.EF514707	-----	.....	.....	------
B.DK.01.CTL_030.EF514708	-----	.....	.....	------
B.DK.01.CTL_033.EF514709	--G-Δ	.....	....U	------
B.DK.01.CTL_035.EF514710	--ΔΔΔ	.....	....U	------
B.DK.01.CTL_041.EF514711	---ΔΔ	.....	....U	------
B.DK.01.CTL_043.EF514712	----Δ	.....	....U	------
B.DK.04.PMVL_012.EF514699	--U--	.....	.....	------
B.DK.04.PMVL_013.EF514700	---ΔΔ	.....	.....	C-----
B.DK.04.PMVL_018.EF514697	----Δ	.....	....U	------
B.DK.04.PMVL_025.EF514702	-U---	.....	.....	------
B.DK.04.PMVL_027.EF514698	C----	A....	....U	------
B.DK.04.PMVL_039.EF514703	----Δ	.....	...UU	------
B.DK.04.PMVL_049.EF514701	----Δ	.....	....U	------
B.ES.05.ES.EU786672	-----	.....	.....	------
B.ES.06.ES.EU786674	---ΔΔ	.....	...UU	------
B.ES.06.ES.EU786675	-U--Δ	.....	.....	------
B.ES.06.ES.EU786676	--ΔΔΔ	.....	.....	------
B.ES.06.ES.EU786677	----Δ	.....	.....	------
B.ES.07.ES.EU786678	G----	.....	.....	------
B.ES.07.ES.EU786679	-----	A....	...UU	------
B.ES.07.ES.EU786680	G----	.....	....U	------
B.ES.89.U61.DQ854716	----Δ	.....	.....	------
B.GA.88.OYI.M26727	-----	.....	....U	------
B.GB.83.CAM1.D10112	-ΔΔΔΔ	.....	.UUUA	------
B.GB.86.GB8.AJ271445	-----	.....	.....	------
B.GB.x.MANC.U23487	-----	.....	.....	------
B.HK.x.HK003.FJ460500	----Δ	.....	....U	------
B.HK.x.HK004.FJ460501	----Δ	.....	....U	------
B.IN.x.11807.EF694037	-----	.....	.....	------
B.IT.05.SG1.DQ672623	---ΔΔ	.....	...UU	------
B.JP.00.DR2508.AB289588	--ΔΔΔ	.....	....U	------
B.JP.01.DR388.AB289590	---ΔΔ	.....	C	------
B.JP.04.04JPDR6075B.AB221125	--ΔΔΔ	.....	....U	------
B.JP.04.DR6089.AB286955	G---Δ	.....	....U	------
B.JP.05.DR6538.AB287363	-----	A....	...UU	------
B.JP.05.DR6737.AB287364	---ΔΔ	.....	...UU	------
B.JP.05.DR7060.AB287366	-----	UAAAA	....U	------
B.JP.05.DR7065.AB287368	--ΔΔΔ	.....	...UU	------
B.JP.99.DR1348.AB287370	----Δ	.....	C	------
B.KR.04.04KMH5.DQ295193	----Δ	.....	....U	------
B.KR.04.04LHS6.AY839827	-ΔΔΔΔ	.....	.UUUU	G-----
B.KR.04.04LSK7.DQ295192	G--ΔΔ	.....	...UU	------
B.KR.04.04WK7_HIV_1_wk.DQ295194	-----	.....	...UU	------
B.KR.05.05CSR3.DQ837381	----Δ	.....	....U	------
B.MM.99.mSTD101.AB097870	-----	.....	.....	-C----
B.NL.00.671_00T36.AY423387	U----	A....	.....	------
B.NL.86.3202A21.U34604	-----	.....	....U	------
B.NL.96.H434_42_A1.AY970948	N----	A....	.....	------
B.RU.04.04RU128005.AY682547	-----	A....	.UUUU	------
B.RU.04.04RU129005.AY751406	-----	.....	.....	------
B.RU.04.04RU139089.AY751407	-----	UAAAA	....U	--C---
B.RU.04.04RU139095.AY819715	----Δ	.....	....U	------
B.TH.90.BK132.AY173951	-----	.....	.....	------
B.TW.94.TWCYS.AF086817	----Δ	.....	....U	------
B.US.00.14294_1.DQ853436	-U--Δ	.....	.....	------
B.US.00.ES1_20.EF363123	----Δ	.....	....U	------
B.US.04.ES10_53.EF363127	----Δ	.....	....U	------
B.US.04.ES4_24.EF363124	-----	.....	.....	------
B.US.04.ES8_43.EF363126	G---Δ	.....	....U	------
B.US.83.5018_83.AY835777	-----	.....	.....	------
B.US.83.5157_83.AY835781	-----	.....	.....	------
B.US.83.RF.M17451	G----	.....	.....	------
B.US.83.SF2.K02007	--ΔΔΔ	.....	....U	------
B.US.84.5019_84.AY835779	-----	.....	.....	------
B.US.84.MNCG.M17449	-----	.....	....U	-C----
B.US.84.NY5CG.M38431	-----	.....	.....	------
B.US.84.SF33.AY352275	-----	A....	.....	------
B.US.85.5077_85.AY835769	-----	.....	.....	------
B.US.85.Ba_L.AB221005	----Δ	.....	....U	------
B.US.86.5084_86.AY835775	-----	.....	.....	------
B.US.86.5096_86.AY835749	----Δ	.....	....U	------
B.US.86.5127_86.AY835774	-----	.....	.....	------
B.US.86.AD87.AF004394	-----	.....	.....	------
B.US.86.JRFL.U63632	-----	.....	.....	------
B.US.86.YU_2.M93258	-----	A....	....U	------
B.US.87.5113_87.AY835758	-----	.....	.....	------
B.US.87.BC.LO2317	-----	.....	.....	------
B.US.88.5160_88.AY835763	-----	.....	.....	------
B.US.88.WR27.AF286365	-U--Δ	.....	.....	------
B.US.89.P896.U39362	---ΔΔ	.....	...UU	------
B.US.90.US1.AY173952	-----	.....	.....	------
B.US.90.US2.AY173953	-----	.....	....U	------
B.US.90.US3.AY173954	----Δ	.....	.....	------
B.US.90.US4.AY173955	----Δ	.....	....U	------
B.US.90.WCIPR.U69591	-----	.....	.....	------
B.US.90.WEAU160.U21135	G---Δ	.....	.....	------
B.US.91.5048_91.AY835761	-----	.....	.....	------
B.US.91.DH12_3.AF069140	----Δ	.....	.....	------
B.US.93.WCD32P0793.DQ487188	----Δ	.....	....U	------
B.US.93.WCM32P0793.DQ487190	----Δ	.....	.....	------
B.US.94.5082_94.AY835773	-----	.....	.....	------
B.US.95.5073_95.AY835768	-----	.....	.....	------
B.US.96.5155_96.AY835753	----Δ	.....	....U	------
B.US.97.ARES2.AB078005	---C-	.....	.....	------
B.US.98.15384_1.DQ853463	-U--Δ	.....	.....	------
B.US.98.98USHVTN1925c1.AY560107	----Δ	.....	....U	------
B.US.98.98USHVTN3605c9.AY560108	----Δ	.....	....U	------
B.US.98.98USHVTN8229c6.AY560109	-----	.....	...UU	------
B.US.98.98USHVTN941c1.AY560110	----Δ	.....	....U	------
B.US.98.WC3_0498_4.EF175212	G----	.....	.....	------
B.ZA.03.03ZAPS045MB2.DQ396398	---ΔΔ	.....	....U	------