

High Variability and Rapid Evolution of a Nanovirus

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Supplementary information:

Figures: 2

Tables: 5

Sequences as text files in fasta format.

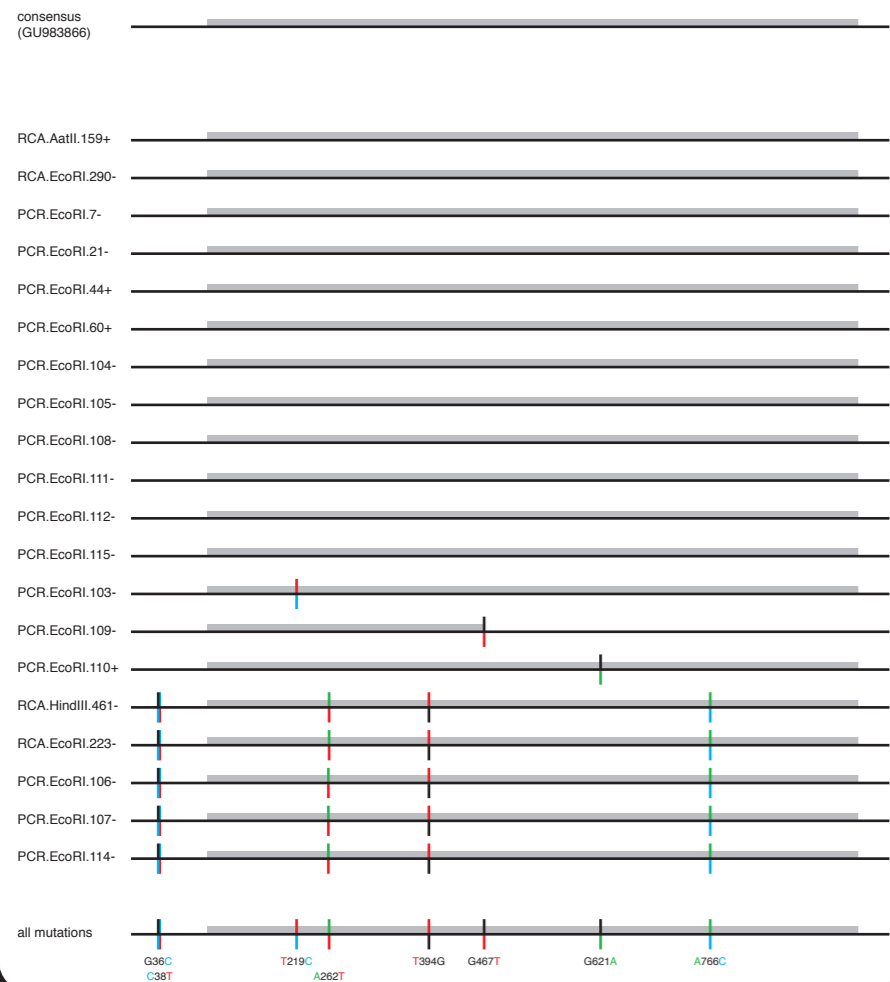
The following mutations were introduced for cloning purposes or overlap the primer sequences. The C51T change in DNA-R had occurred in the agrobacterium plasmid used to establish the ISV-T1 population. These sequence changes were not taken into account for the analyses:

Genome component	FBNSV-[ET:Hol] isolate	Clone no.	Mutation	Reason
DNA-R	1997	PCR.EcoRI.108-	G535T	Overlaps the primer Hol-R-EcoRI-dir
DNA-R	ISV-T1	All clones	C51T	Present in pBin19 DNA-R dim plasmid
DNA-U4	JKI-2000	All PCR.XbaI clones	C480T	XbaI site created for cloning reasons
DNA-U4	JKI-2000	PCR.XbaI.33+	T460G	Overlaps the primer Hol-U4-XbaI-rev

Supplementary Figure S1. Compilation of all cloned and sequenced FBNSV DNAs.

Genome components are shown in a linear fashion as scaled line drawings with ORF sequences represented as grey bars. Members of the three populations FBNSV-[ET:Hol;1997], FBNSV-[ET:Hol;JKI-2000] and FBNSV-[ET:Hol;ISV-T1] are framed. FBNSV-[ET:Hol;JKI-1998/99] and FBNSV-[ET:Hol;IPO-1998/99] consensus sequences are also framed. FBNSV-[ET:Hol;IPO-1998/99] refers to two sequences published by Franz *et al.*, (28). The first line within each frame represents the respective consensus sequence. Clone designations contain, from left to right, information about the respective amplification method (RCA or PCR), the restriction endonuclease site used for cloning, the clone number, and the relative orientation of the insert; (+): viral strand and *lac* promoter of the plasmid have same polarity, (-): viral strand and *lac* promoter of the plasmid have opposite polarity. Framed names indicate the clones of the FBNSV-[ET:Hol;JKI-2000] population that served to establish the FBNSV-[ET:Hol;ISV-T1] population. Base changes are indicated by bi-coloured vertical lines: the upper part of the vertical line denotes the nucleotide present in the FBNSV-[ET:Hol;1997] consensus sequence and the bottom part the allele. Nucleotides are colour-coded as in Applied Biosystems BigDye terminator sequencing; A: green; T: red; C: blue; G: black. Mutations that were completely fixed in the FBNSV-[ET:Hol;JKI-2000] population are shown in bold italics, mutations found in the majority of cases (> 50% and < 100%) are shown in bold. Deletions (Δ) or recombinant sequences are represented by blank or magenta sections of the scaled lines, respectively. Insertions are marked by a +. Altered ORF sequences due to frameshifts are shown as tawny bars. A summary of all sequence alterations within each population is shown below the individual clones (“all mutations”). In case of the FBNSV-[ET:Hol;JKI-2000] population, mutations clearly identified by directly sequencing of RCA products are shown below the “all mutations” line, and the relative proportion of the respective alleles is indicated by proportionally coloured bars.

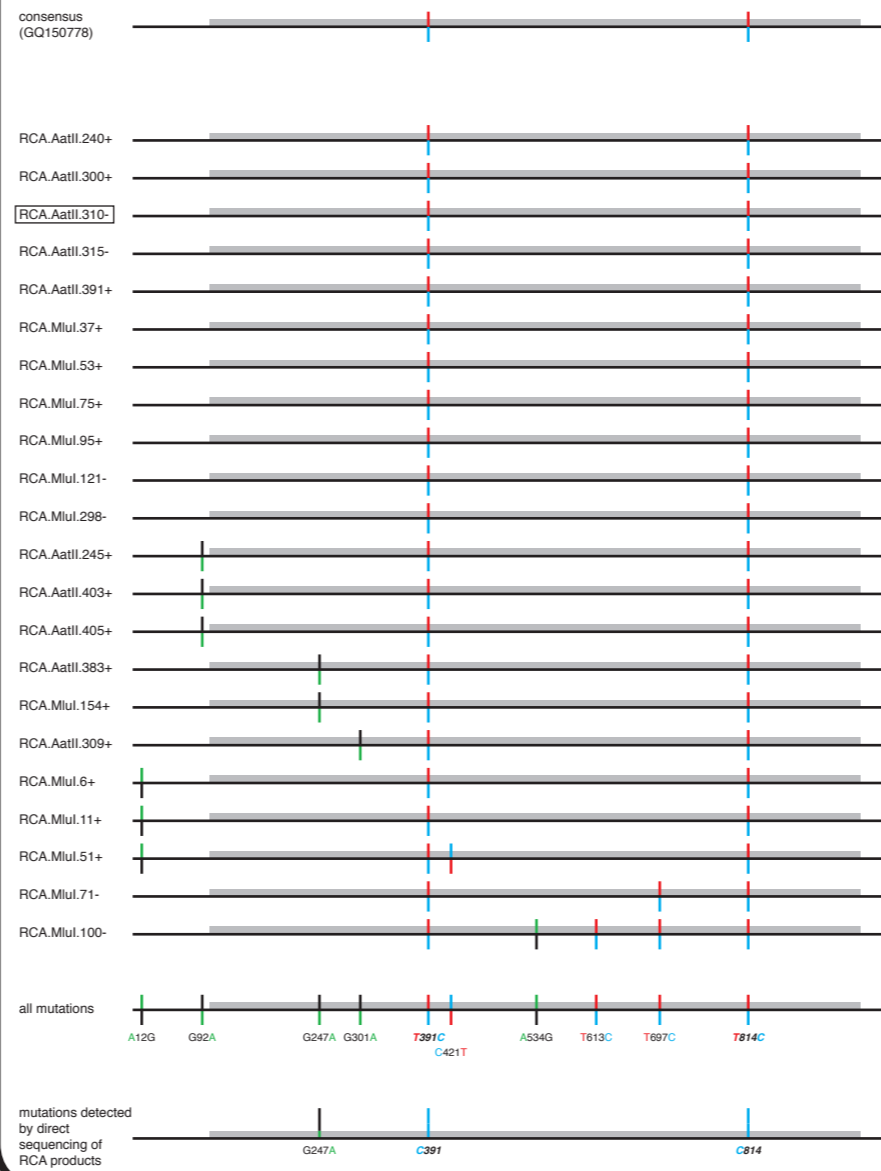
FBNSV-[ET:HoI;1997] DNA-R



FBNSV-[ET:HoI;JKI-1998/99] DNA-R

AJ749894

FBNSV-[ET:HoI;JKI-2000] DNA-R



FBNSV-[ET:HoI;ISV-T1] DNA-R

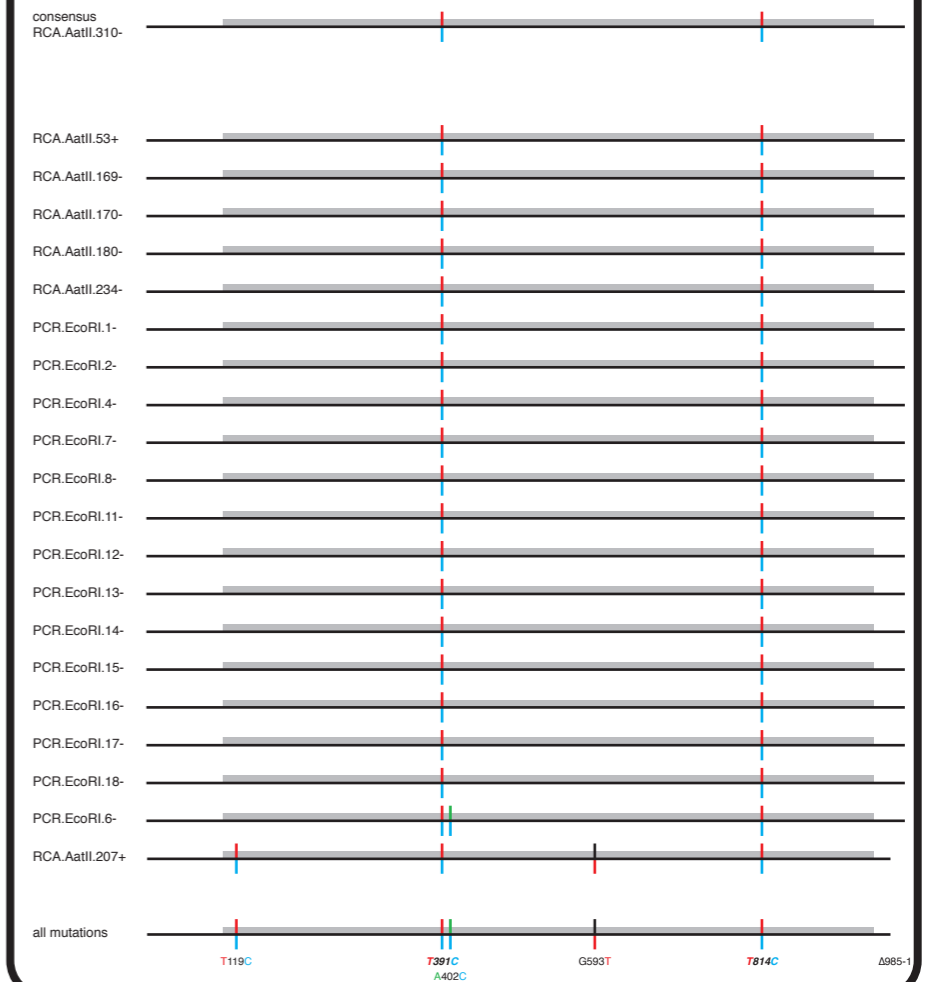
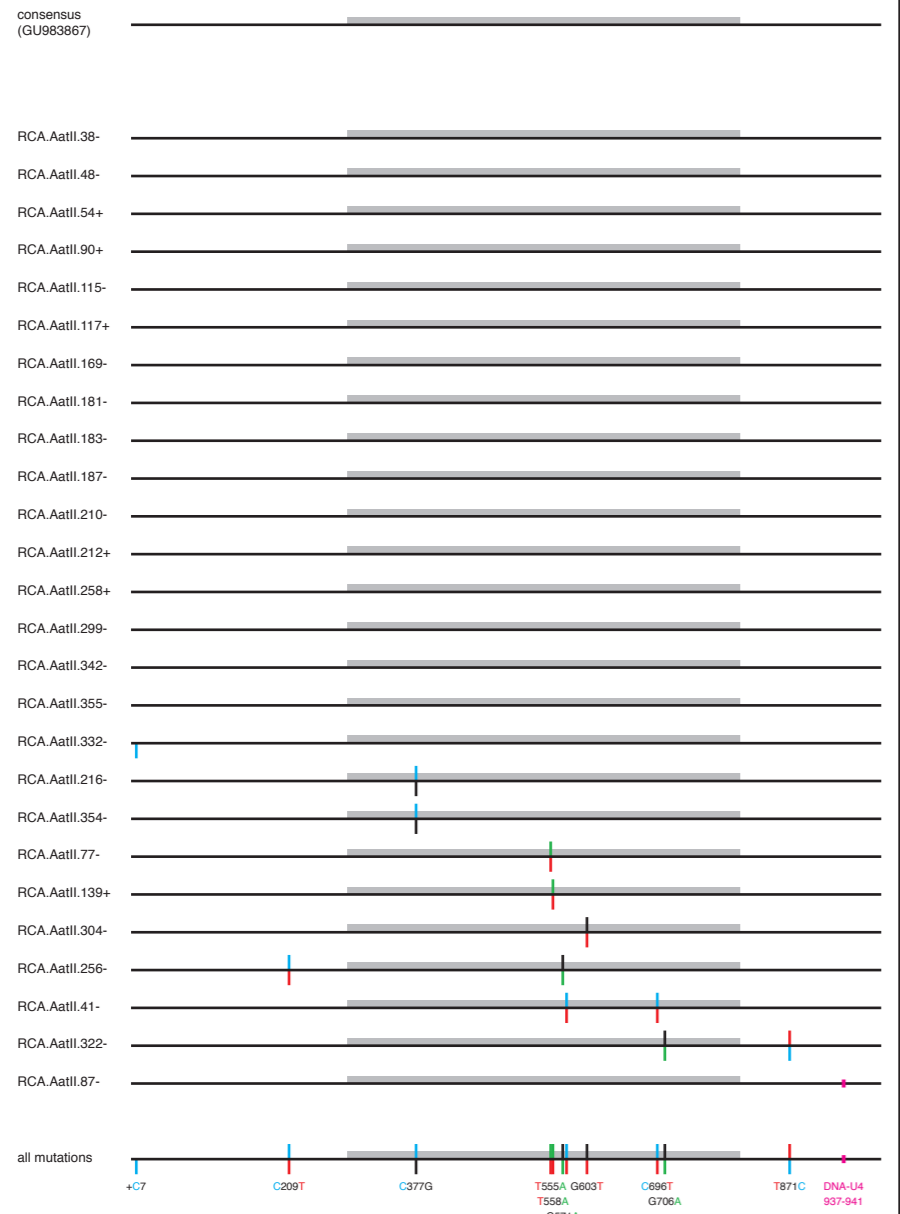
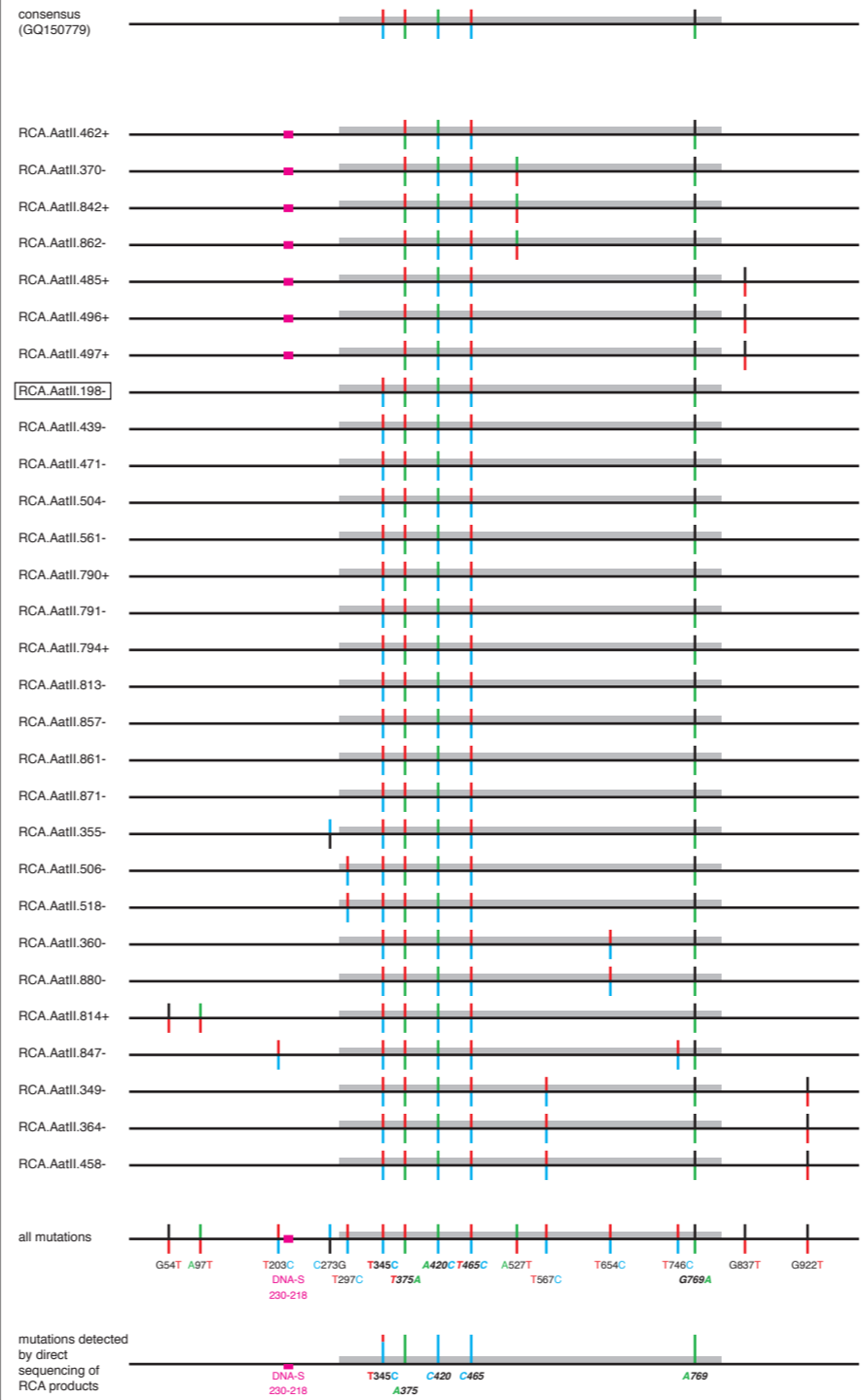


Figure S1 A

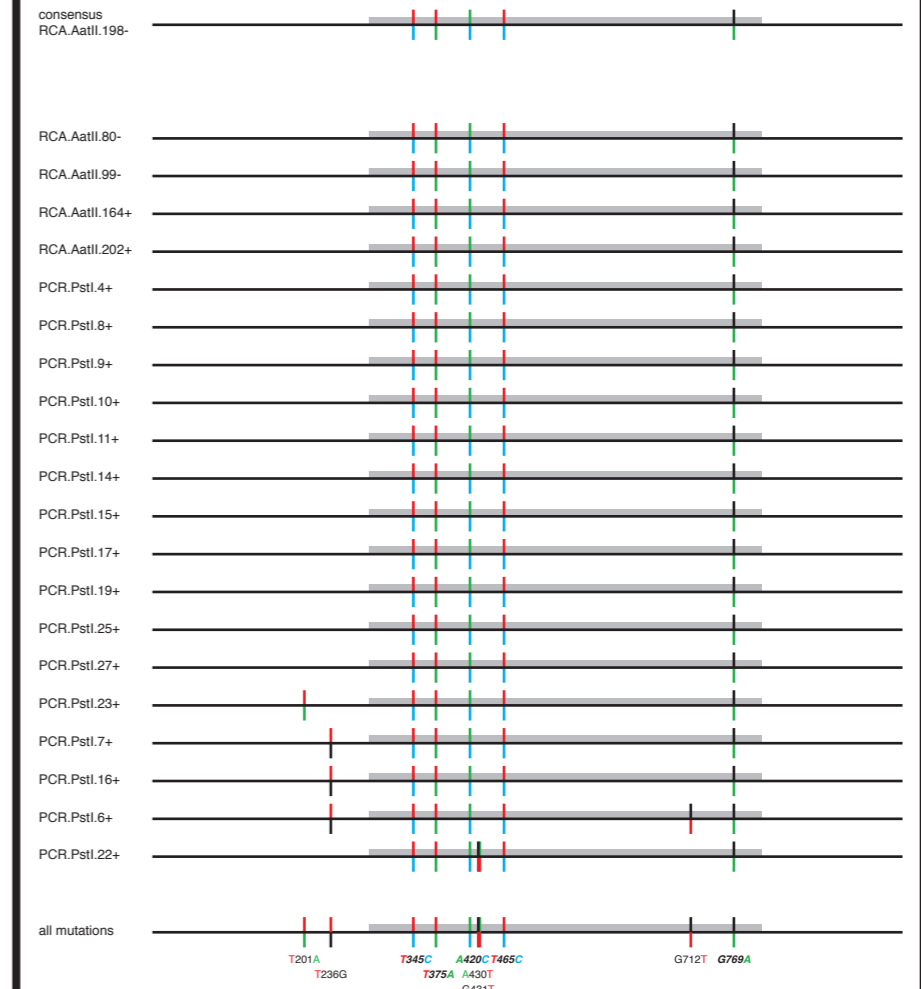
FBNSV-[ET:Hol;1997] DNA-S



FBNSV-[ET:Hol;JKI-2000] DNA-S



FBNSV-[ET:Hol;ISV-T1] DNA-S



FBNSV-[ET:Hol;JKI-1998/99] DNA-S

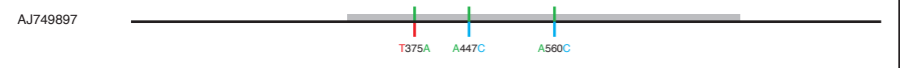
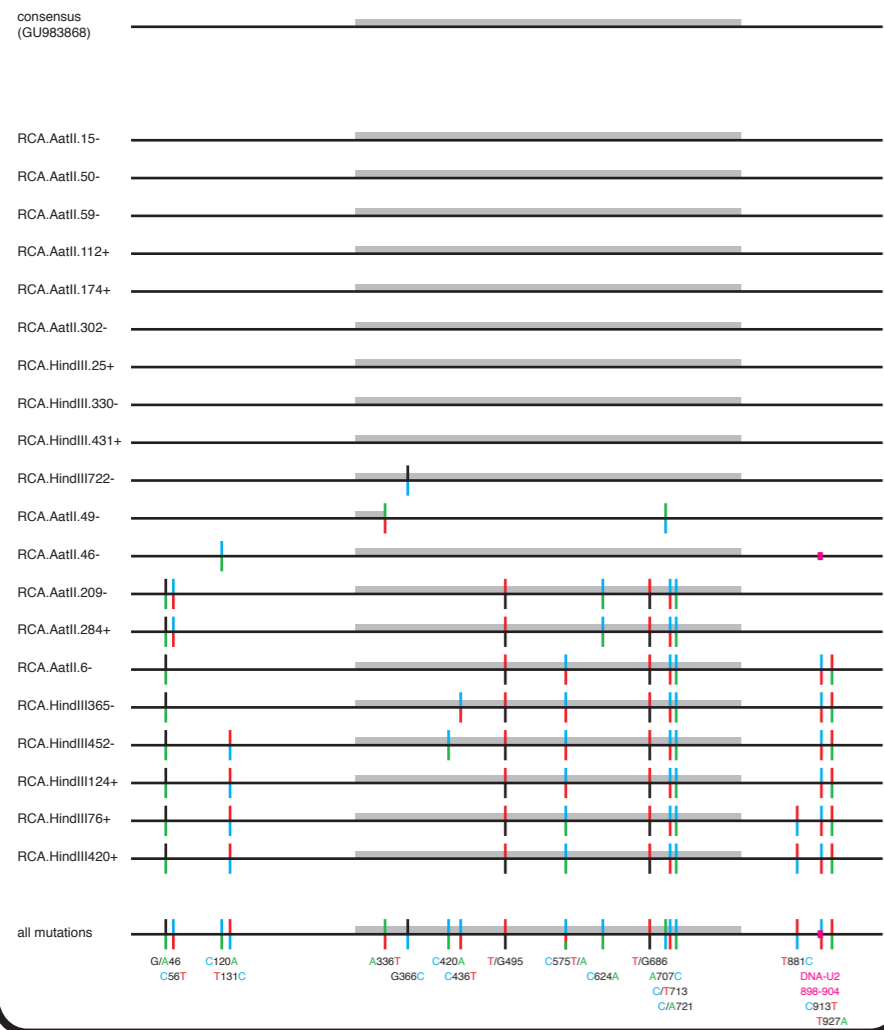
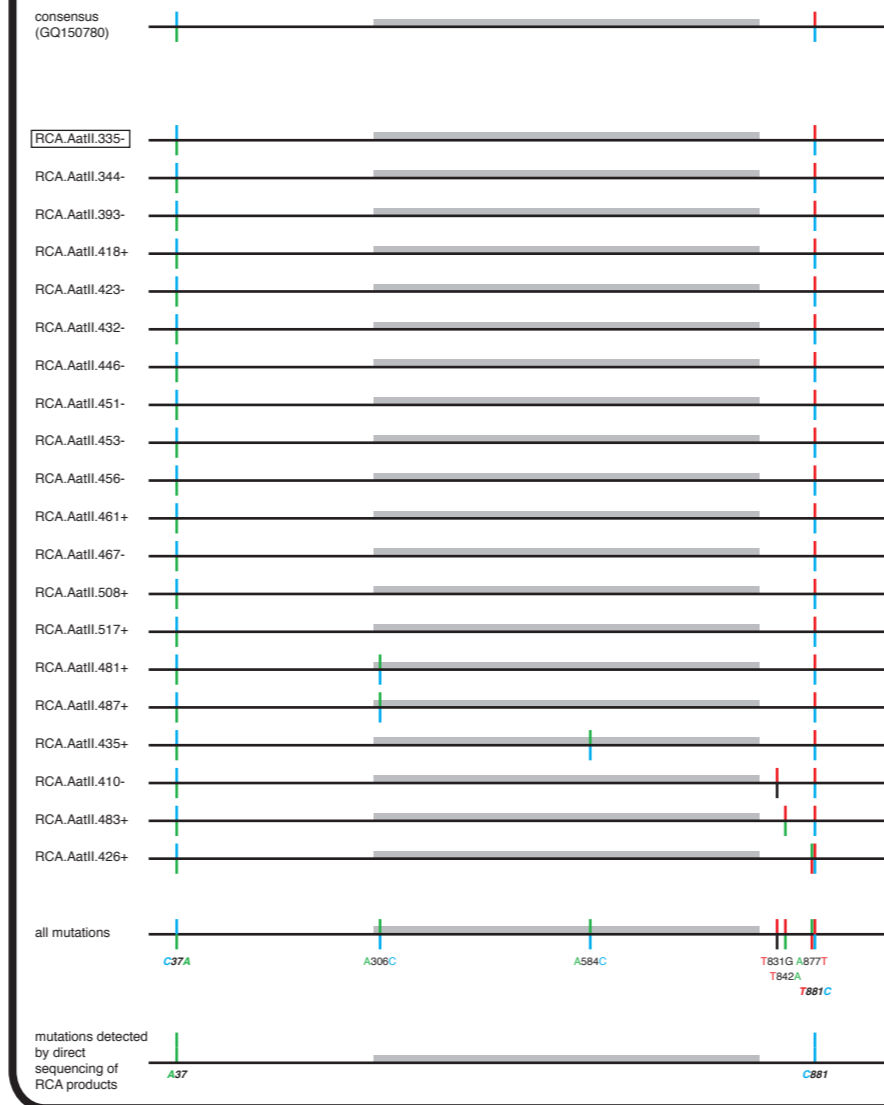


Figure S1 B

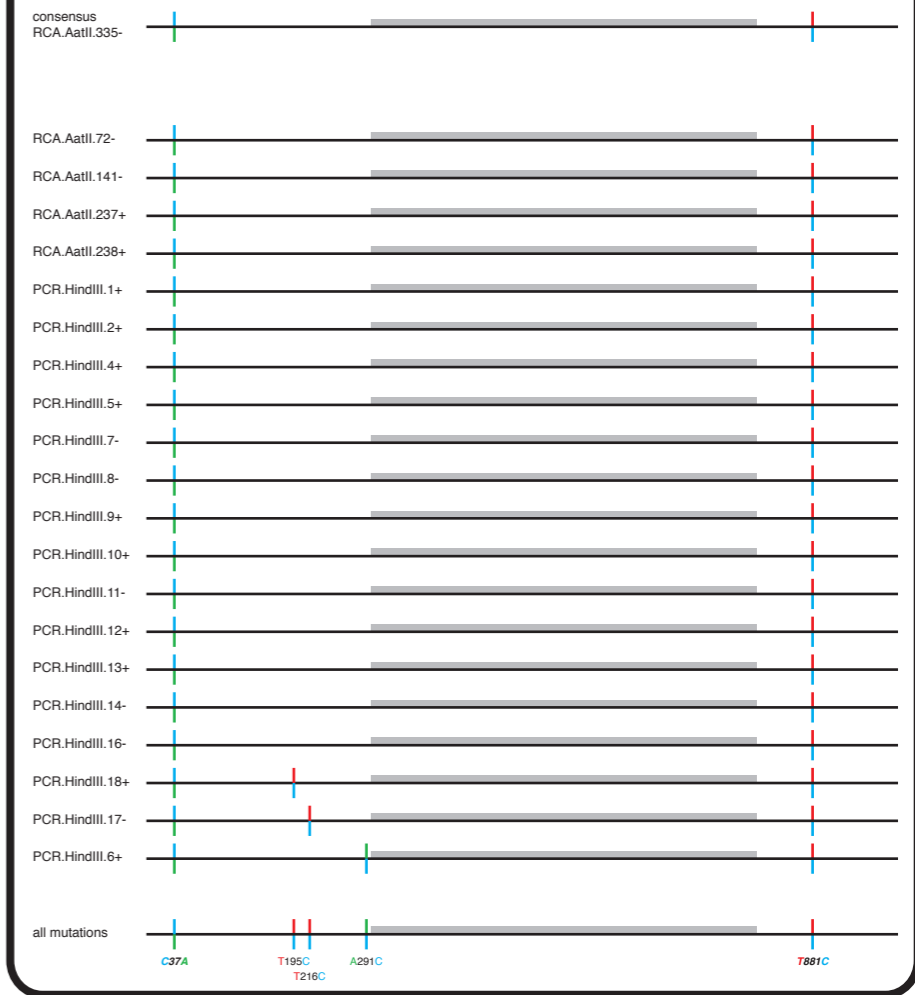
FBNSV-[ET:HoI;1997] DNA-C



FBNSV-[ET:HoI;JKI-2000] DNA-C



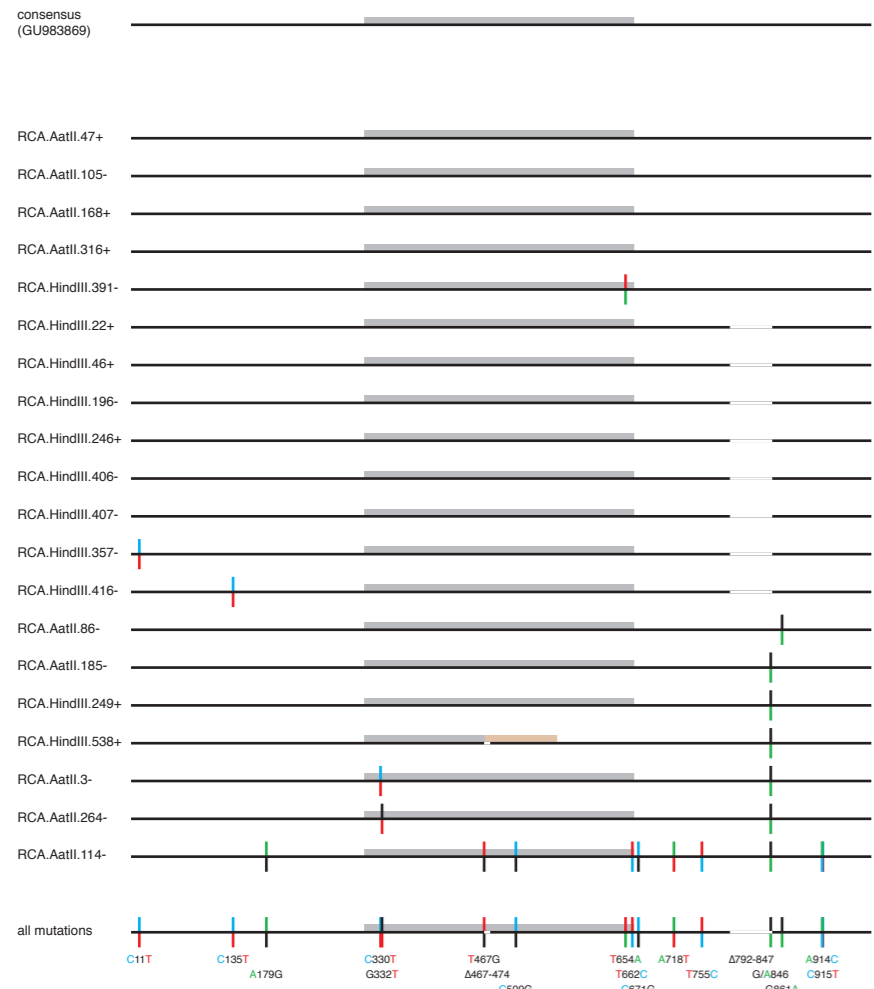
FBNSV-[ET:HoI;ISV-T1] DNA-C



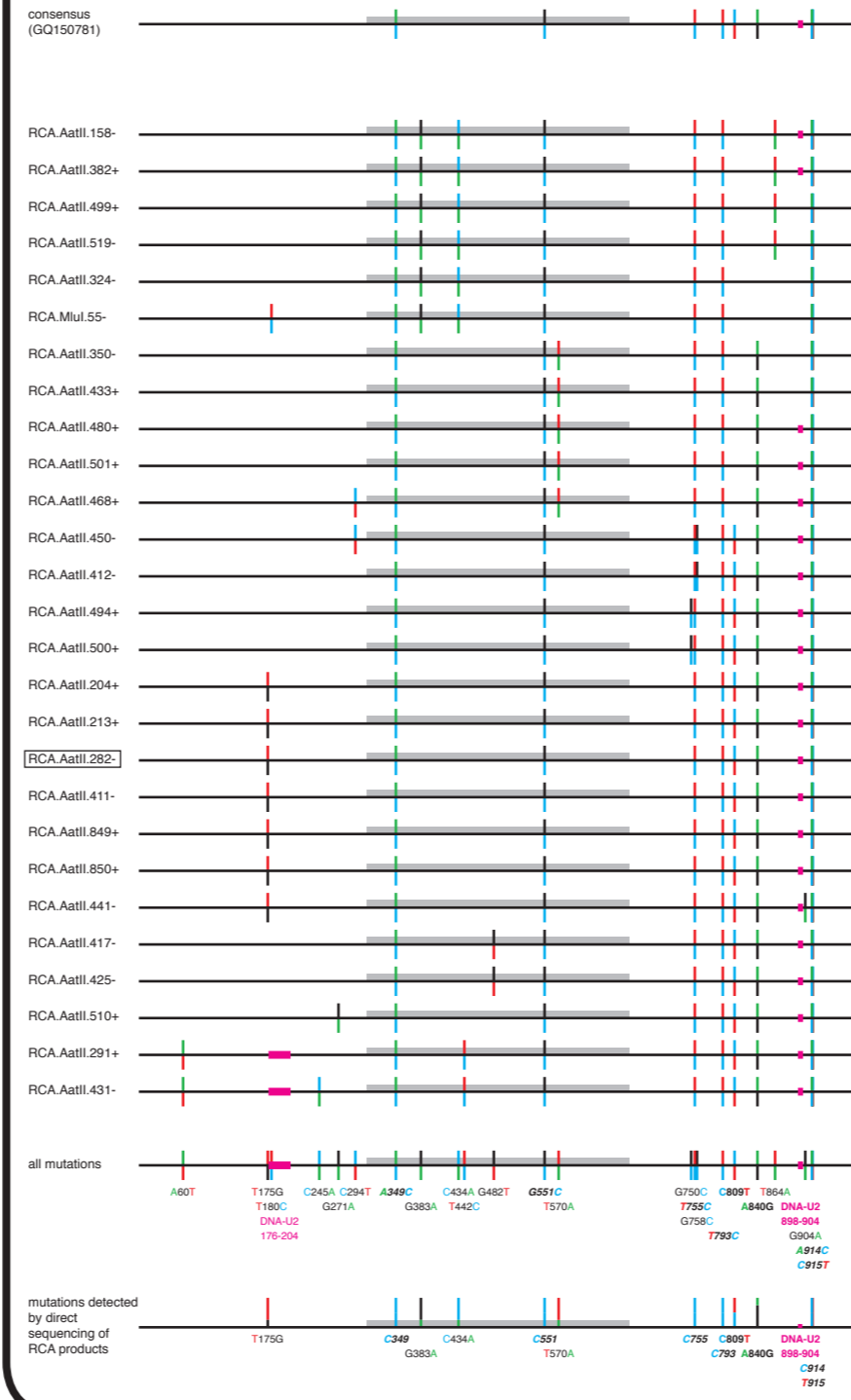
FBNSV-[ET:HoI;JKI-1998/99] DNA-C

AJ749900

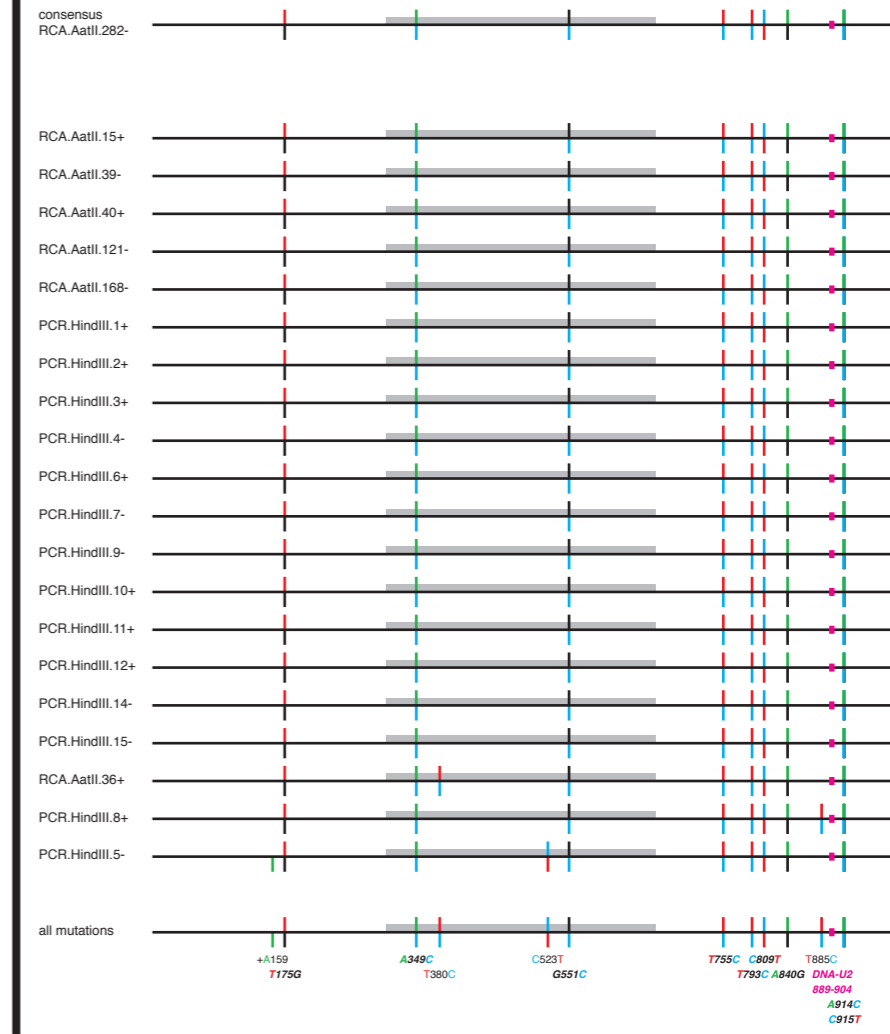
FBNSV-[ET:Hol;1997] DNA-M



FBNSV-[ET:Hol;JKI-2000] DNA-M



FBNSV-[ET:Hol;ISV-T1] DNA-M



FBNSV-[ET:Hol;JKI-1998/99] DNA-M



FBNSV-[ET:Hol;IPO-1998/99] DNA-M



Figure S1 D

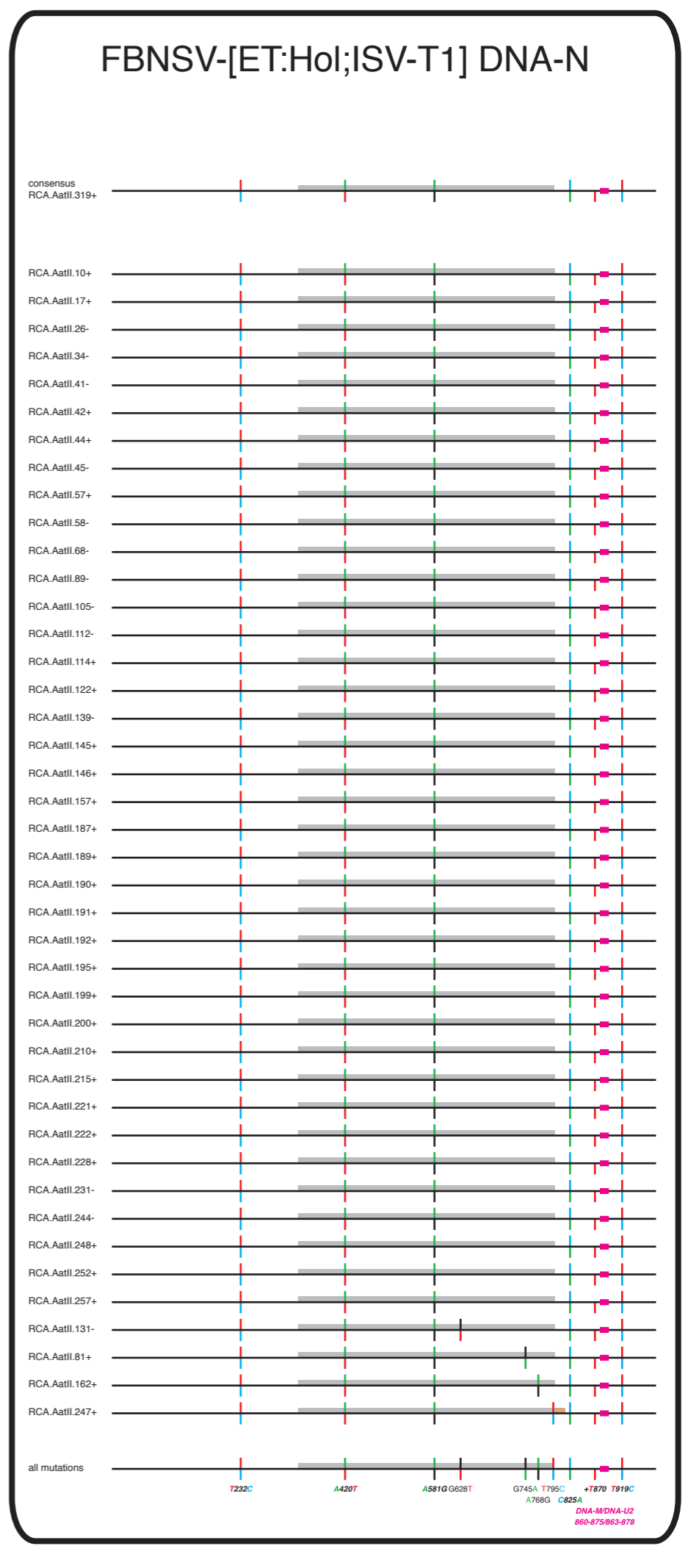
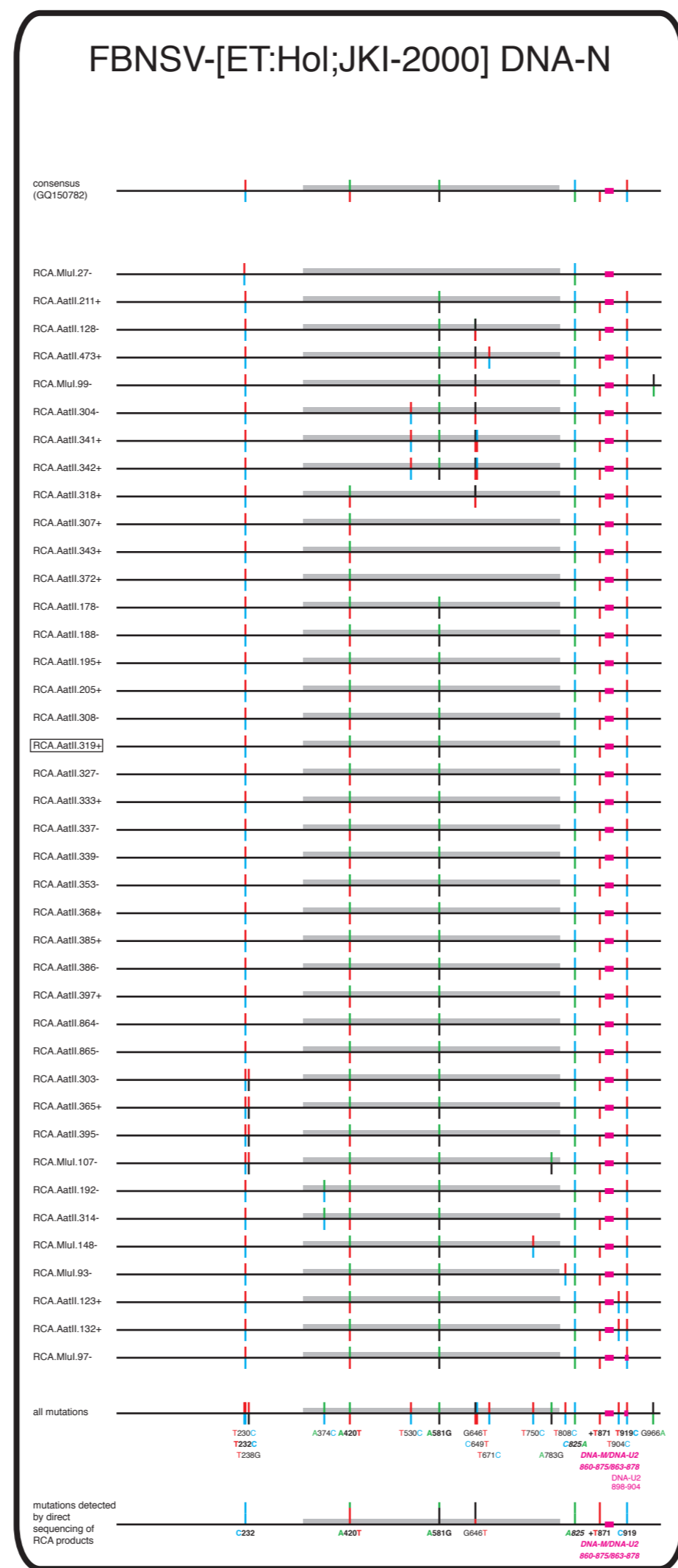
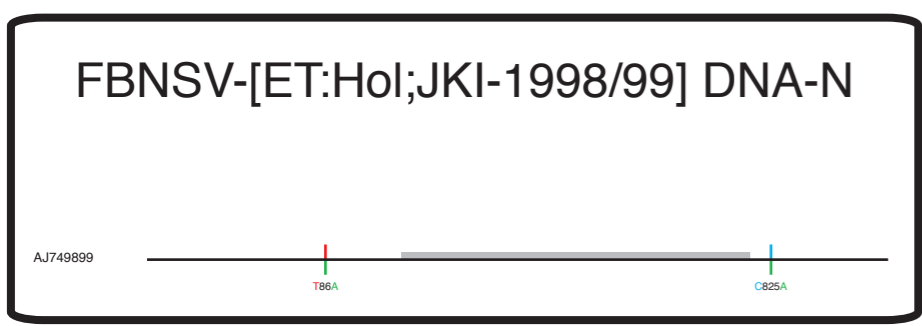
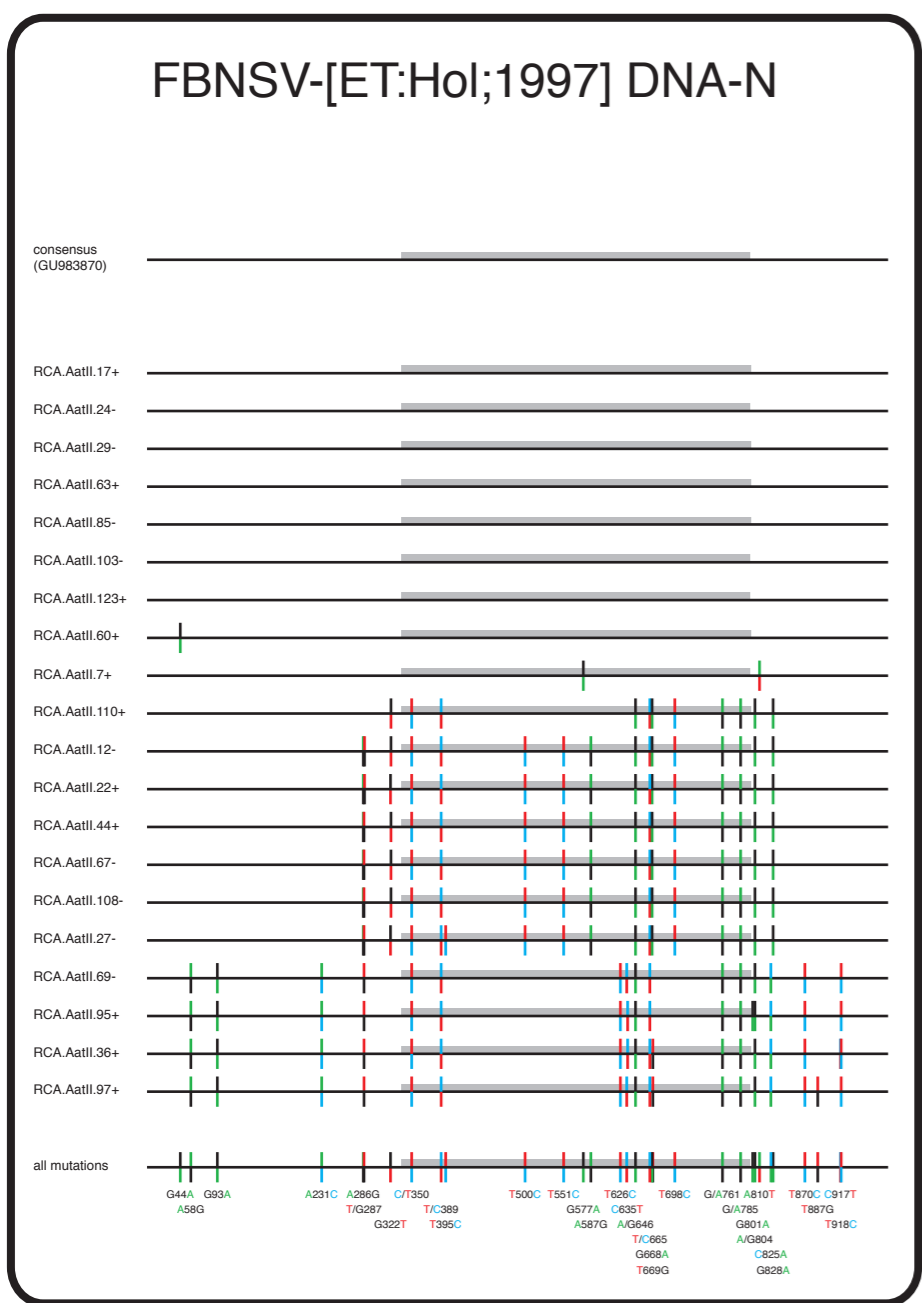
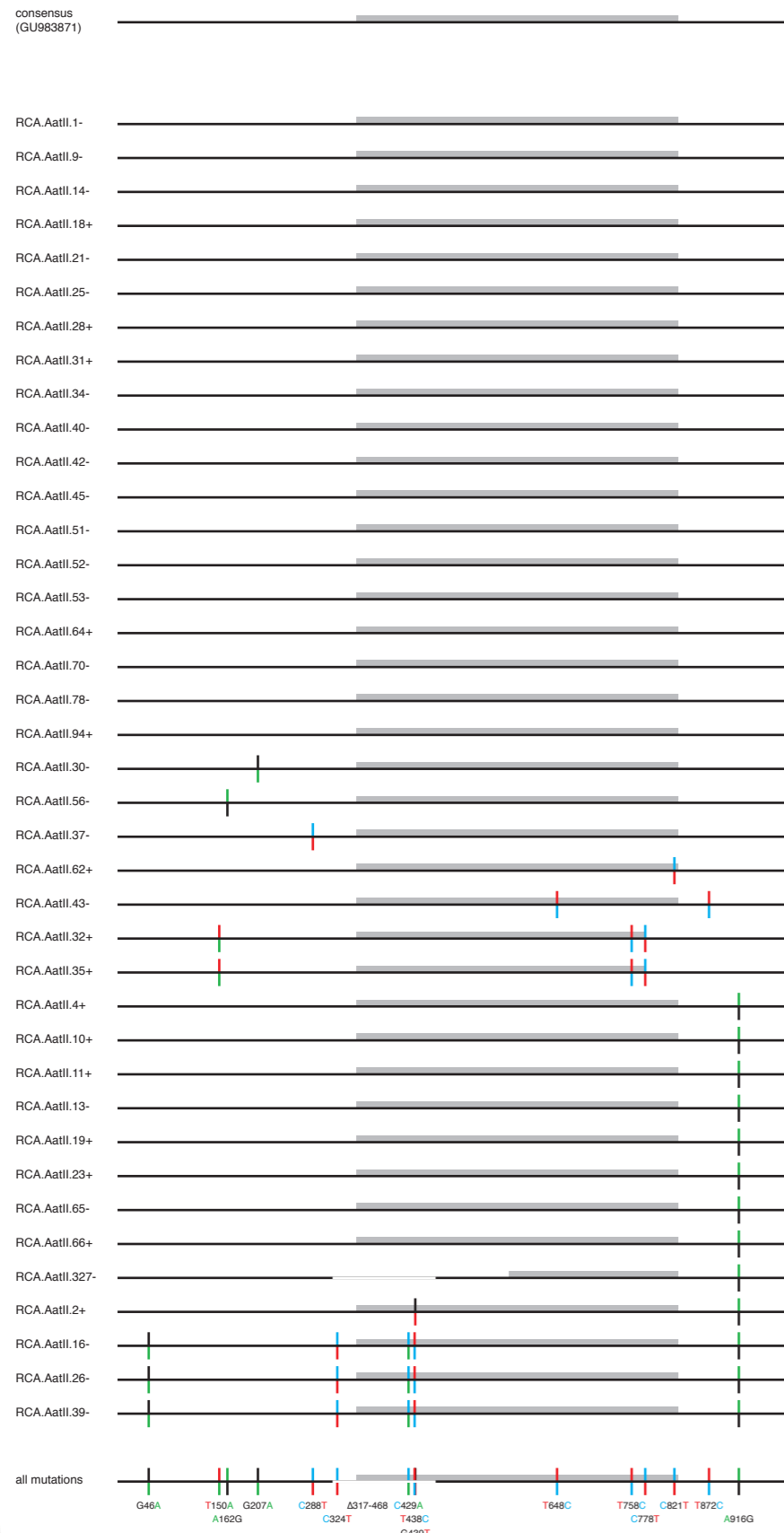
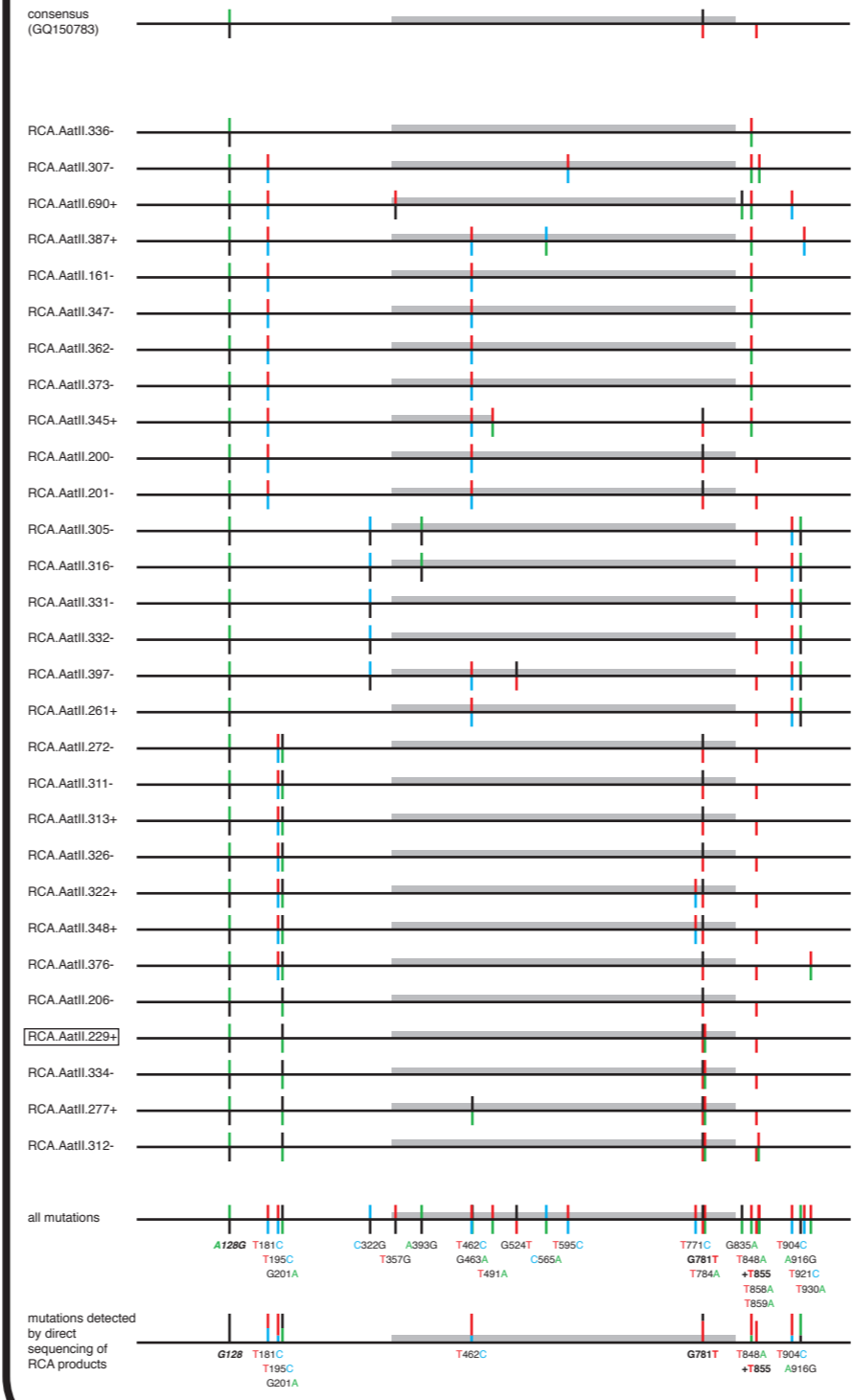


Figure S1 E

FBNSV-[ET:HoI;1997] DNA-U1



FBNSV-[ET:HoI;JKI-2000] DNA-U1



FBNSV-[ET:HoI;JKI-1998/99] DNA-U1



FBNSV-[ET:HoI;ISV-T1] DNA-U1

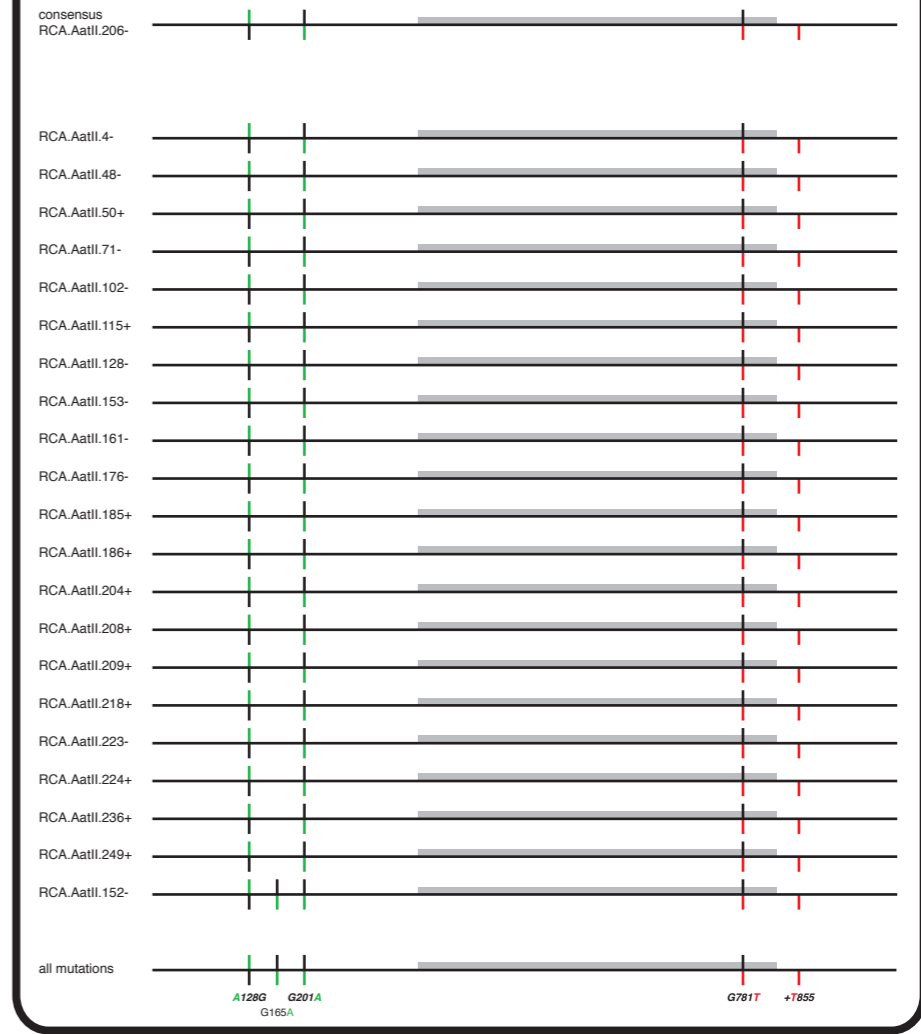
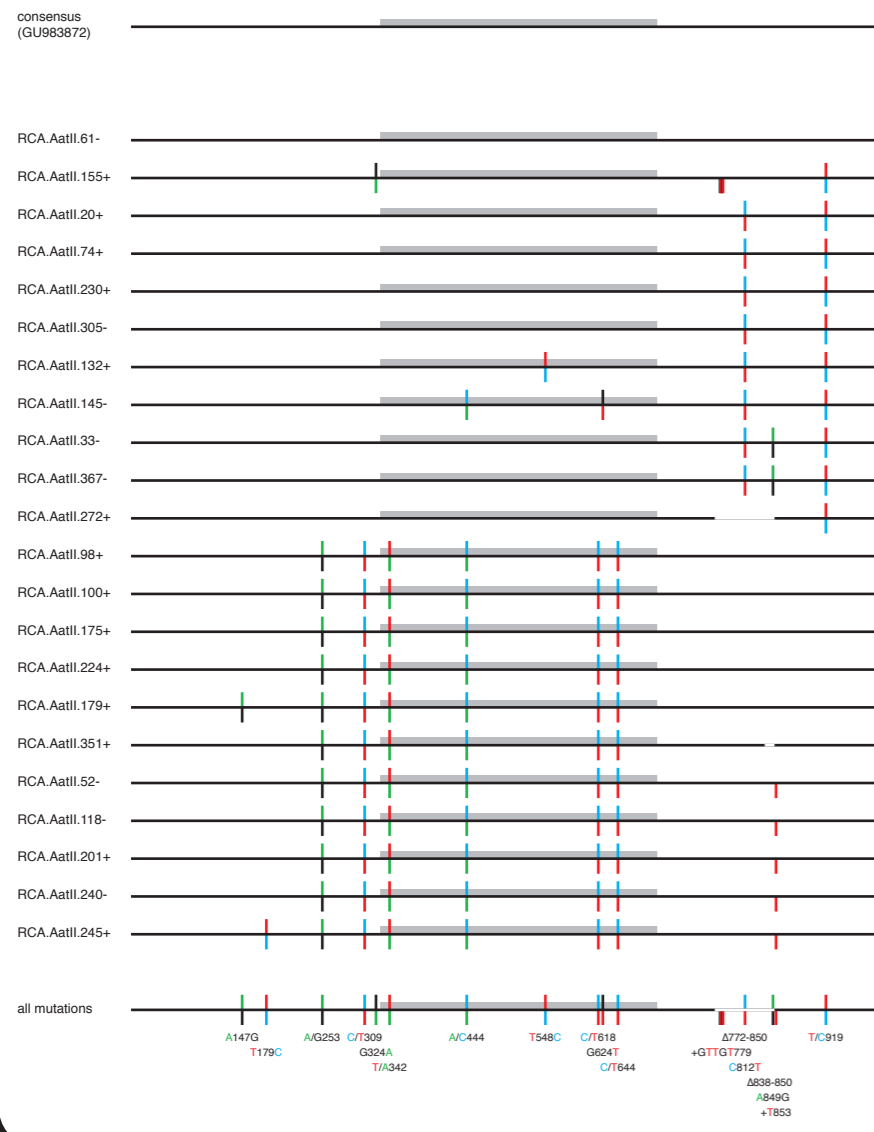
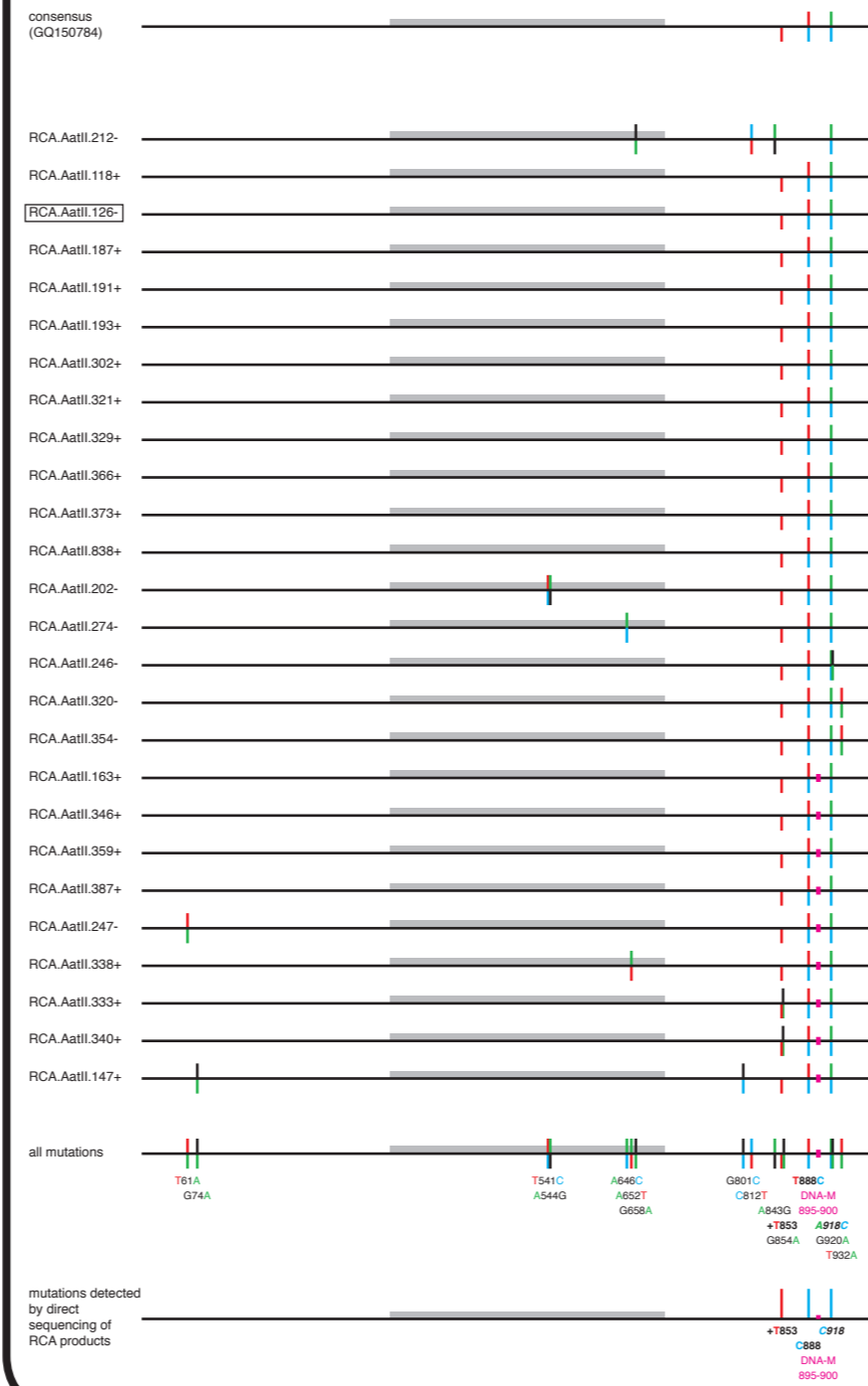


Figure S1 F

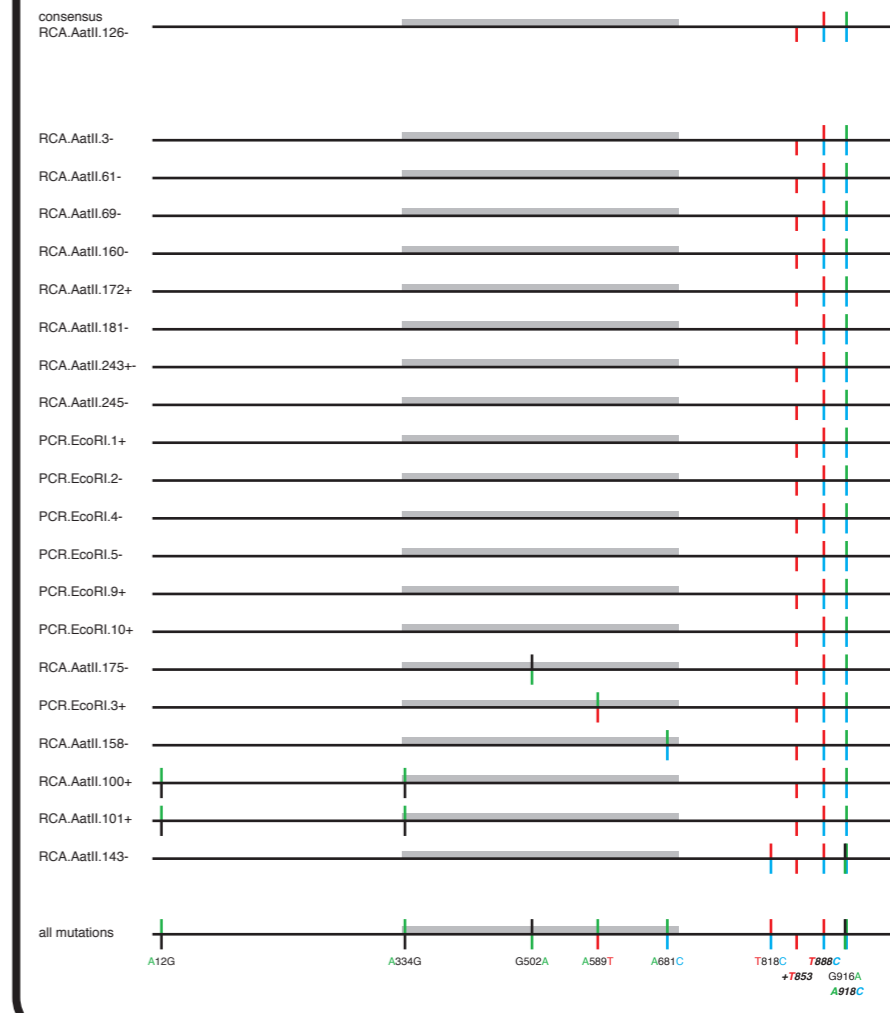
FBNSV-[ET:Hol;1997] DNA-U2



FBNSV-[ET:Hol;JKI-2000] DNA-U2



FBNSV-[ET:Hol;ISV-T1] DNA-U2



FBNSV-[ET:Hol;JKI-1998/99] DNA-U2



Figure S1 G

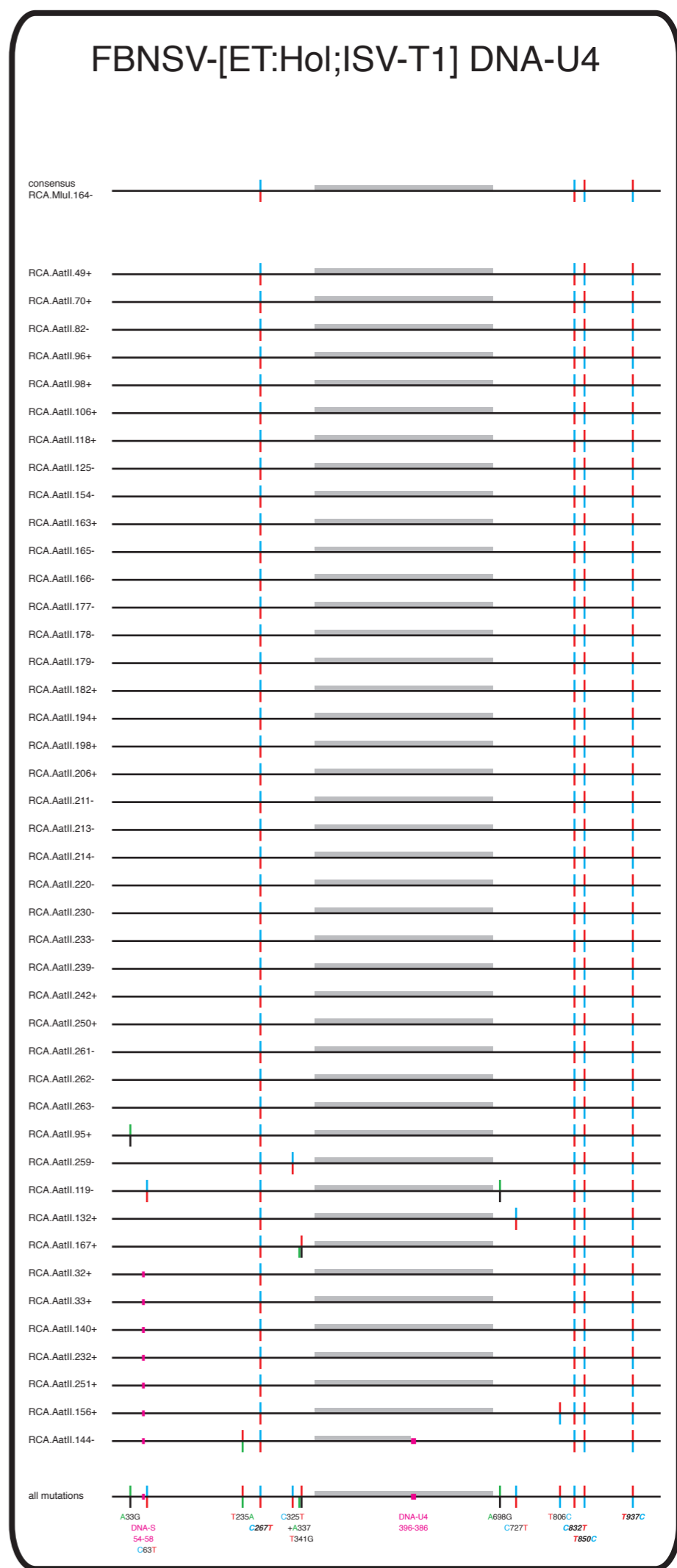
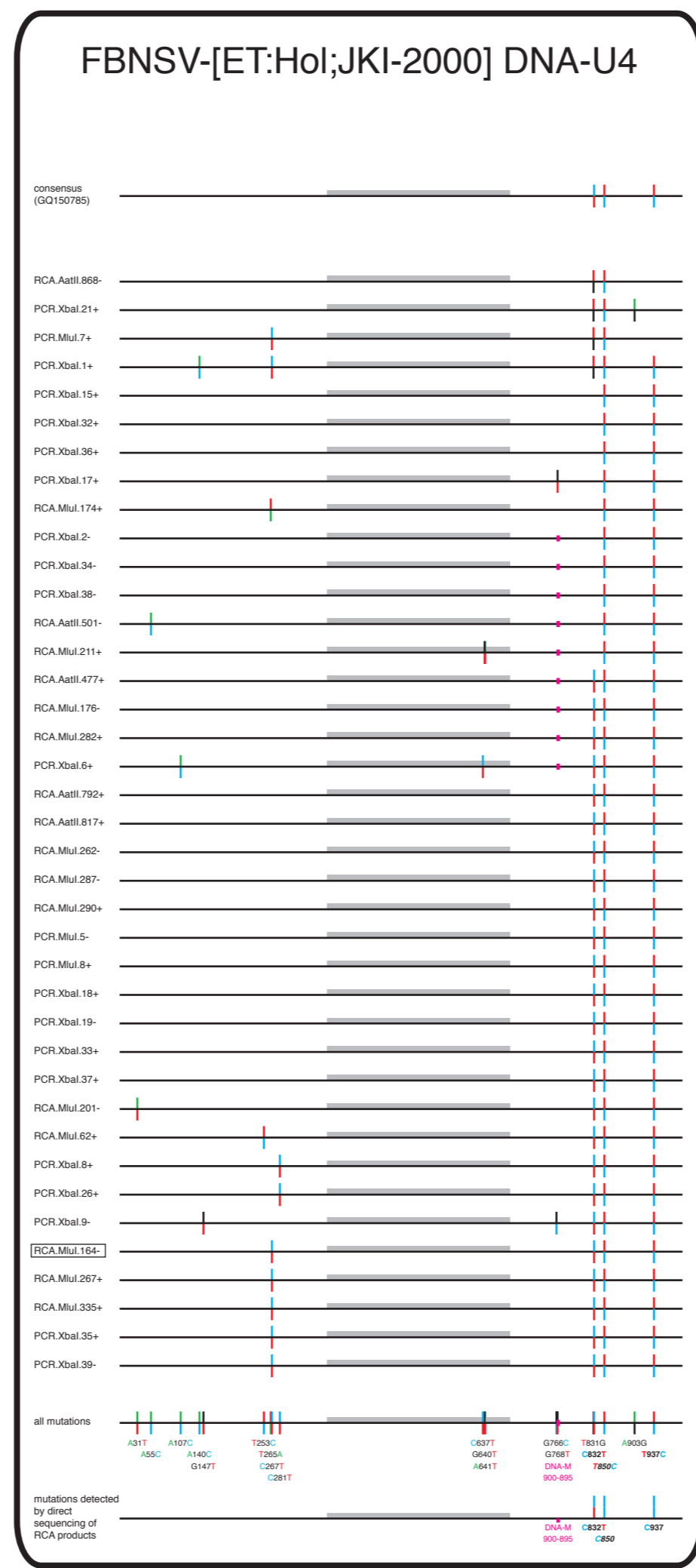
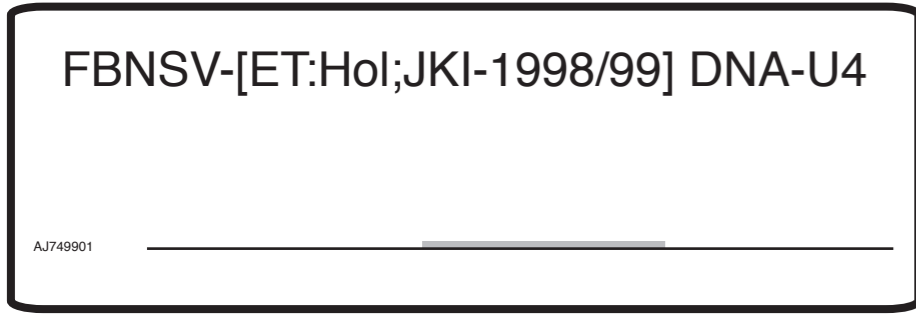
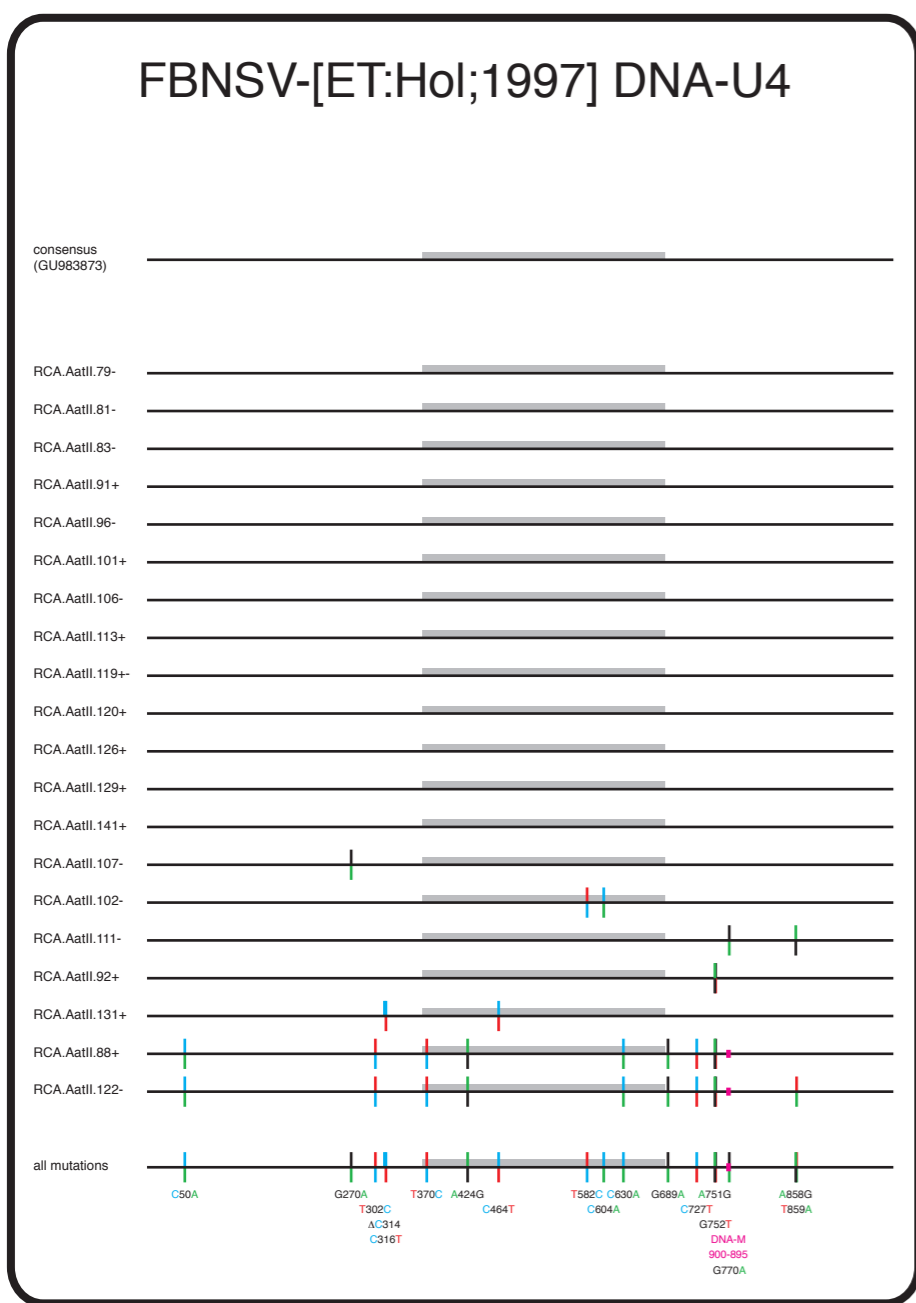


Figure S1 H

Supplementary Figure S2. Sequences between CR-II and CR-I and their transpositional inversion in DNA-U4.

A. Multialignment of sequences between CR-II, highlighted in blue, and the 5' part of CR-I, highlighted in green, that are mutated, probably due to sequence conversion. Arrows mark iteron-like sequences (a) and their inversions (a') in the CR-I. The 5' stem- and the loop sequence are marked. A vertical arrow indicates position zero. Genome component names and virus isolates are shown at the left, along with the proportion of the respective DNAs among the sequenced molecules. The >16 nt sequences in CR-II of DNA-N from the FBNSV-[ET:Hol;1997] population that had disappeared in the FBNSV-[ET:Hol;JKI-2000] population due to sequence conversion by recombination are highlighted in dark blue. The two versions of the three informative nucleotide changes are highlighted in yellow (AG-TCTT) or magenta (TGCTCTC), respectively. The 60/61-nt sequences of DNA-M and DNA-U2 that occur inverted and transposed in DNA-U4 are highlighted in purple.

B. Line drawing illustrating the position in DNA-U4 of the 60/61-nt sequences similar to, or derived from, sequences between CR-II and CR-I of DNA-M or DNA-U2 as transposed inversion (purple arrows). Grey bars represent coding sequences.

C. Multialignment of individual DNA-U4 sequences defining the common region M-U2-U4, shown as reverse complement and highlighted in purple. The two versions of the three informative nucleotide changes are highlighted in yellow (AG-TCTT) or magenta (TGCTCTC), respectively.

Table S1. Oligonucleotides used in this study.

Specific for:	Name	Sequence 5'-3'	FBNSV-[ET:Hol] isolate:			
			1997	JKI-1998/99	JKI-2000	ISV-T1
DNA-R	Hol-R-EcoRI-dir	TAGAGAATTCAGAGGAGAACTGAAGAAGAA	x			x
	Hol-R-EcoRI-rev	CTCTGAATTCTCTAAGCGTACTTGCAGACT	x			x
	P3	ATATGCTGGTGCTTTACA		x		
	P20	AATTACAATCCTATCCTCACT		x		
	P45	AACTCTCCATACTCCCA(A/T)GGACCTTCAA		x		
	P47	TATGGCCCACAAGGTGGAGAAGGG		x		
DNA-S	Hol-S-PstI-dir	TGGTCTGCAGCTTTCACAGCACCTGCTCTA				x
	Hol-S-PstI-rev	AAAGCTGCAGACCAATTAACAATAGGTGAA				x
	P67	CTCCATCTCAGCCGTTTCATTG		x		
	P68	ACAGCCTTAACAGCTTCACTGG		x		
DNA-C	Hol-C-HindIII-dir	TAAAAAAGCTTCGTCTTCTTCGTTGTTTCAT				x
	Hol-C-HindIII-rev	GACGAAGCTTTTTTATAGAAGAGAGAGAAA				x
	P69	AGGTCTTCAGTTGATGGGT		x		
	P70	TGGCATGTAGAGAGTTGCTG		x		
DNA-M	Hol-M-HindIII-dir	TATGAAGCTTGTTATGTTGTATATTTCATGT				x
	Hol-M-HindIII-rev	TAACAAGCTTCATATTTTCTTGAACACTTA				x
	P51	ACGAAGCAAAGCATATATTTCAGTGC		x		
	P53	TGGAAGCGTGGTTGAATTCTTCATC		x		
DNA-N	P65	GCTCACACTGCAACTAACAAG		x		
	P66	ACAGGAACGTTCTGGTCA		x		
DNA-U1	P71	TATAACATAATCTGAACTTC		x		
	P72	TTAACGCTTCTTGGCTGTCG		x		
DNA-U2	Hol-U2-EcoRI-dir	TGGTGAATTCTGCAGACTCCATGGAAGAAG				x
	Hol-U2-EcoRI-rev	TGCAGAATTCACCAAGAACATCTTTCGTGGG				x
	P50	TTAAGTTAATAAATGACATCTATC		x		
	P55	GCTGATACTATCCTTCCATG		x		
DNA-U4	Hol-U4-XbaI-dir	TTATTCTAGATTAAGAAGTTACTGTCCAGG			x	
	Hol-U4-XbaI-rev	TTAATCTAGAATAATTACTTCTGAATAAAG			x	
	Hol-U4-MluI-dir	CTTCACGCGTTTTGAAGCTACTGTGATTA			x	
	Hol-U4-MluI-rev	CAAAACGCGTGAAGAGATAAAGTGTACAAT			x	
	P58	GGTTGAAGGCGATGATCTTG		x		
	P59	GTTTCCAGACCCAGAGTCTTTAG		x		
DNA-S,-C,-N, -U1,-U4	P23	CACGAATCACAGATCCTGAT		x		
	P44	AAGCGAA(A/T/C)CTGACGGAAGA		x		
DNA-S,-C,-U1	P22	ATGGTTCTCTCTCTATAAAAGCT		x		
	P23	CACGAATCACAGATCCTGAT		x		
DNA-M,-U2	P60	GATGGTCCCCTCCGCACTA		x		
	P61	AATAGCATGTGCGTCTCACGTG		x		

Table S2. Variability of field isolated and laboratory propagated FBNSV.

A: FBNSV-[ET:Hol;1997]									
Genome component	Length (nt)	Number sequenced clones	Number different clone types	Variable sites		Mutation frequency ($\times 10^{-4}$)	Shannon entropy	Genetic Distance ($\times 10^{-3}$) (Tamura-Nei method)	
				Total	Maximum per clone			Distance	Std.Err.
DNA-R	1003	20	5	8	5	3.99	0.37	2.28	0.86
DNA-S	992	26	10	12	2	4.65	0.46	1.01	0.29
DNA-C	994	20	10	20	10	10.06	0.62	5.57	1.47
DNA-M	979	20	11	18	10	9.41	0.70	1.54	0.41
DNA-N	980	20	10	32	10	16.33	0.64	11.85	2.35
DNA-U1	985	39	11	16	5	4.18	0.46	1.46	0.61
DNA-U2	983	22	12	18	9	8.35	0.73	4.59	1.58
DNA-U4	987	20	8	19	10	9.63	0.44	3.01	0.74
Entire genome	7903	187	77	143	61	7.77			

B: FBNSV-[ET:Hol;JKI-2000]									
Genome component	Length (nt)	Number sequenced clones	Number different clone types	Variable sites		Mutation frequency ($\times 10^{-4}$)	Shannon entropy	Genetic Distance ($\times 10^{-3}$) (Tamura-Nei method)	
				Total	Maximum per clone			Distance	Std.Err.
DNA-R	1003	22	8	8	3	3.63	0.52	1.20	0.44
DNA-S	992	29	10	13	6	4.52	0.56	3.32	0.98
DNA-C	994	20	6	5	1	2.52	0.36	0.59	0.25
DNA-M	980	27	14	19	8	7.18	0.72	6.62	1.26
DNA-N	981	40	17	18	6	4.59	0.60	1.96	0.61
DNA-U1	986	29	18	24	7	8.40	0.82	5.17	1.29
DNA-U2	984	26	11	16	5	6.26	0.59	2.21	0.78
DNA-U4	987	39	18	19	6	4.94	0.68	2.64	0.80
Entire genome	7907	232	102	122	42	5.33			

C: FBNSV-[ET:Hol;ISV-T1]									
Genome component	Length (nt)	Number sequenced clones	Number different clone types	Variable sites		Mutation frequency ($\times 10^{-4}$)	Shannon entropy	Genetic Distance ($\times 10^{-3}$) (Tamura-Nei method)	
				Total	Maximum per clone			Distance	Std.Err.
DNA-R	1003	20	3	4	3	2.00	0.13	0.31	0.17
DNA-S	992	20	5	5	2	2.52	0.30	0.67	0.32
DNA-C	994	20	4	3	1	1.51	0.20	0.30	0.17
DNA-M	980	20	4	4	2	2.04	0.20	0.31	0.18
DNA-N	981	42	5	4	1	0.97	0.12	0.19	0.10
DNA-U1	986	21	2	1	1	0.48	0.06	0.10	0.09
DNA-U2	984	20	6	7	2	3.56	0.36	0.90	0.36
DNA-U4	987	43	9	11	3	2.59	0.29	1.23	0.43
Entire genome	7907	206	38	39	15	1.92			

Table S3. Substitution rate from the field isolated to laboratory propagated FBNSV.

Genome component	A: entire genome			B: coding region			C: non coding region		
	Length (nt)	Mutations fixed as consensus	Substitution rate ($\times 10^{-3}$)	Length (nt)	Mutations fixed as consensus	Substitution rate ($\times 10^{-3}$)	Length (nt)	Mutations fixed as consensus	Substitution rate ($\times 10^{-3}$)
DNA-R	1003	2	0.83	861	2	0.96	142	0	0.00
DNA-S	992	5	2.09	519	5	3.99	473	0	0.00
DNA-C	994	2	0.83	510	0	0.00	484	2	1.71
DNA-M	979	9	3.80	357	2	2.32	622	7	4.66
DNA-N	980	7	2.96	462	2	1.79	518	5	3.99
DNA-U1	985	3	1.26	474	1	0.87	511	2	1.62
DNA-U2	983	3	1.26	366	0	0.00	617	3	2.01
DNA-U4	987	3	1.26	312	0	0.00	675	3	1.84
Entire genome	7903	34	1.78	3861	12	1.29	4042	22	2.25

Table S4. Mutant spectra of field isolated and laboratory propagated FBNSV

Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	38	22.33	16.4851	4.90E-05	28	15.67	14.5638	0.0001	8	5.33	2	0.1573
A → G	2 (+3)*	6.93	3.9167 to 0.6020	0.0478 to 0.4378	5	4.86	0.0048	0.9446	2	1.65	0.0813	0.7755
G → A	5 (+3)	5.24	0.0117 to 1.5811	0.9140 to 0.2086	5	3.67	0.5265	0.4681	2	1.25	0.4915	0.4833
C → T	9 (+6)	3.24	10.7564 to 44.8417	0.0010 to 2.14E-11	3	2.30	0.2230	0.6368	1	0.78	0.0629	0.8019
T → C	13 (+6)	6.92	5.9543 to 23.5089	0.0147 to 1.24E-06	15	4.84	23.7387	1.10E-06	3	1.65	1.2339	0.2667
Transversions (Tv)	29	44.67	16.4851	4.90E-05	19	31.33	14.5638	0.0001	8	10.67	2	0.1573
A → C	2 (+2)	6.93	3.9167 to 1.3852	0.0478 to 0.2392	4	4.86	0.1680	0.6819	2	1.65	0.0813	0.7755
C → A	6 (+2)	3.24	2.4692 to 7.3455	0.1161 to 0.0067	2	2.30	0.0415	0.8386	0	0.78	0.8238	0.3641
A → T	2 (+1)	6.93	3.9167 to 2.4901	0.0478 to 0.1146	4	4.86	0.1680	0.6819	2	1.65	0.0813	0.7755
T → A	3 (+1)	6.92	2.4774 to 1.3749	0.1155 to 0.2410	3	4.84	0.7827	0.3763	0	1.65	1.8386	0.1751
C → G	2	3.24	0.4991	0.4799	0	2.30	2.4199	0.1198	0	0.78	0.8238	0.3641
G → C	1	5.24	3.7188	0.0538	0	3.67	3.9761	0.0461	0	1.25	1.3536	0.2447
G → T	5 (+2)	5.24	0.0117 to 0.6437	0.9140 to 0.4224	5	3.67	0.5265	0.4681	4	1.25	6.5819	0.0103
T → G	3 (+2)	6.92	2.4774 to 0.5947	0.1155 to 0.4406	1	4.84	3.4011	0.0652	0	1.65	1.8386	0.1751
Ts/Tv	1.3	0.5			1.5	0.5			1	0.5		
Deletions	2				0				0			
Insertions	0				0				0			
Recombination events	0				0				1			

Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	48	21.33	50	1.54E-12	34	22	9.8172	0.0017	13	6	12.25	0.0005
A → G	9 (+4)	5.83	1.9022 to 9.7180	0.1678 to 0.0018	5	5.97	0.1733	0.6772	3	1.63	1.2671	0.2603
G → A	11 (+4)	4.38	10.7657 to 27.6917	0.0010 to 1.42E-07	9	4.53	4.7238	0.0297	2	1.24	0.5060	0.4769
C → T	13 (+2)	4.05	21.1235 to 31.6178	4.31E-06 to 1.88E-08	6	4.22	0.8077	0.3688	3	1.15	3.1925	0.0740
T → C	9 (+2)	7.08	0.5836 to 2.4362	0.4449 to 0.1186	14	7.28	6.9677	0.0083	5	1.99	5.1414	0.0234
Transversions (Tv)	16	42.67	50	1.54E-12	32	44	9.8172	0.0017	5	12	12.25	0.0005
A → C	2	5.83	2.7643	0.0964	3	5.97	1.6245	0.2025	1	1.63	0.2675	0.6050
C → A	3	4.05	0.2902	0.5901	1	4.22	2.6190	0.1056	0	1.15	1.2260	0.2682
A → T	2	5.83	2.7643	0.0964	4	5.97	0.7148	0.3979	0	1.63	1.7918	0.1807
T → A	3	7.08	2.6462	0.1038	9	7.28	0.4560	0.4995	2	1.99	0.0001	0.9916
C → G	1	4.05	2.4511	0.1174	2	4.22	1.2431	0.2649	0	1.15	1.2260	0.2682
G → C	1	4.38	2.7951	0.0946	4	4.53	0.0675	0.7951	0	1.24	1.3278	0.2492
G → T	2 (+1)	4.38	1.3843 to 0.4641	0.2394 to 0.4957	4	4.53	0.0675	0.7951	0	1.24	1.3278	0.2492
T → G	1 (+1)	7.08	5.8739 to 4.1013	0.0154 to 0.0429	5	7.28	0.8033	0.3701	2	1.99	0.0001	0.9916
Ts/Tv	3	0.5			1.1	0.5			2.6	0.5		
Deletions	4				0				1			
Insertions	3				3				2			
Recombination events	3				6				1			

* Numbers in brackets refer to potential additional mutations resulting from 50±10% ambiguities of the consensus (reference) base and the respective change. Note that these numbers have to be identical for reciprocal changes, e.g. A→G and G→A, etc. and they are counted only once for the total number of transitions or transversions.

Ts/Tv, Transition Transversion ratio

ND, not determined

DNA-R Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	3	2.67	0.0625	0.8026	8	3	16	6.33E-05	1	1	0	1
A → G	0	0.83	0.9256	0.3360	2	1	1.8422	0.1747	0	0.31	0.3471	0.5558
G → A	1	0.67	0.1776	0.6735	3	1	8.8461	0.0029	0	0.25	0.2742	0.6006
C → T	1	0.43	0.7955	0.3725	1	0	0.7716	0.3797	0	0.16	0.1729	0.6775
T → C	1	0.74	0.1038	0.7473	2	1	2.4231	0.1196	1	0.27	2.1144	0.1459
Transversions (Tv)	5	5.33	0.0625	0.8026	0	5	16	6.33E-05	2	2	0	1
A → C	1	0.83	0.0390	0.8434	0	1	0.9256	0.3360	1	0.31	1.7020	0.1920
C → A	0	0.43	0.4552	0.4999	0	0	0.4611	0.4971	0	0.16	0.1729	0.6775
A → T	1	0.83	0.0390	0.8434	0	1	0.9256	0.3360	0	0.31	0.3471	0.5558
T → A	0	0.74	0.8112	0.3678	0	1	0.8048	0.3697	0	0.27	0.3018	0.5828
C → G	0	0.43	0.4552	0.4999	0	0	0.4611	0.4971	0	0.16	0.1729	0.6775
G → C	1	0.67	0.1776	0.6735	0	1	0.7311	0.3925	0	0.25	0.2742	0.6006
G → T	1	0.67	0.1776	0.6735	0	1	0.7311	0.3925	1	0.25	2.4361	0.1186
T → G	1	0.74	0.1038	0.7473	0	1	0.8048	0.3697	0	0.27	0.3018	0.5828
Ts/Tv	0.6	0.5			ND	0.5			0.5	0.5		
Deletions	0				0				1			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-R Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	2	2	0	1	6	2	12	0.0005	1	1	0	1
A → G	0	0.64	0.7207	0.3959	1	0.64	0.2214	0.6380	0	0.32	0.3603	0.5483
G → A	1	0.51	0.5133	0.4737	2	0.51	4.7516	0.0293	0	0.26	0.2789	0.5974
C → T	0	0.31	0.3218	0.5705	1	0.31	1.6195	0.2032	0	0.16	0.1634	0.6860
T → C	1	0.54	0.4285	0.5127	2	0.54	4.3883	0.0362	1	0.27	2.1941	0.1385
Transversions (Tv)	4	4	0	1	0	4	12	0.0005	2	2	0	1
A → C	1	0.64	0.2214	0.6380	0	0.64	0.7207	0.3959	1	0.32	1.6020	0.2056
C → A	0	0.31	0.3218	0.5705	0	0.31	0.3269	0.5675	0	0.16	0.1634	0.6860
A → T	1	0.64	0.2214	0.6380	0	0.64	0.7207	0.3959	0	0.32	0.3603	0.5483
T → A	0	0.54	0.5944	0.4407	0	0.54	0.5888	0.4429	0	0.27	0.2944	0.5874
C → G	0	0.31	0.3218	0.5705	0	0.31	0.3269	0.5675	0	0.16	0.1634	0.6860
G → C	0	0.51	0.5579	0.4551	0	0.51	0.5579	0.4551	0	0.26	0.2789	0.5974
G → T	1	0.51	0.5133	0.4737	0	0.51	0.5579	0.4551	1	0.26	2.3758	0.1232
T → G	1	0.54	0.4285	0.5127	0	0.54	0.5888	0.4429	0	0.27	0.2944	0.5874
Ts/Tv	0.5	0.5			ND	0.5			0.5	0.5		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-R Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	1	0.67	0.25	0.6171	2	0.67	4	0.0455	0	0	ND	ND
A → G	0	0.17	0.1805	0.6710	1	0.17	4.5862	0.0322	0	0	ND	ND
G → A	0	0.15	0.1642	0.6853	1	0.15	5.1316	0.0235	0	0	ND	ND
C → T	1	0.14	5.5543	0.0184	0	0.14	0.1535	0.6952	0	0	ND	ND
T → C	0	0.21	0.2307	0.6310	0	0.21	0.2307	0.6310	0	0	ND	ND
Transversions (Tv)	1	1.33	0.25	0.6171	0	1.33	4	0.0455	0	0	ND	ND
A → C	0	0.17	0.1805	0.6710	0	0.17	0.1805	0.6710	0	0	ND	ND
C → A	0	0.14	0.1535	0.6952	0	0.14	0.1535	0.6952	0	0	ND	ND
A → T	0	0.17	0.1805	0.6710	0	0.17	0.1805	0.6710	0	0	ND	ND
T → A	0	0.21	0.2307	0.6310	0	0.21	0.2307	0.6310	0	0	ND	ND
C → G	0	0.14	0.1535	0.6952	0	0.14	0.1535	0.6952	0	0	ND	ND
G → C	1	0.15	5.1316	0.0235	0	0.15	0.1642	0.6853	0	0	ND	ND
G → T	0	0.15	0.1642	0.6853	0	0.15	0.1642	0.6853	0	0	ND	ND
T → G	0	0.21	0.2307	0.6310	0	0.21	0.2307	0.6310	0	0	ND	ND
Ts/Tv	1	0.5			ND	0.5			ND	ND		
Deletions	0				0				1			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-S Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	6	3.33	3.2	0.0736	6	4	1.5	0.2207	0	2	2.5	0.1138
A → G	0	0.95	1.0469	0.3062	0	1.14	1.2611	0.2614	0	0	0.5255	0.4685
G → A	2	0.75	2.2779	0.1312	0	0.89	0.9627	0.3265	0	0	0.4011	0.5265
C → T	3	0.55	11.5197	0.0007	0	0.67	0.7132	0.3984	0	0	0.2972	0.5857
T → C	1	1.09	0.0081	0.9283	6	1.29	19.1748	1.19E-05	0	1	0.6045	0.4368
Transversions (Tv)	4	6.67	3.2	0.0736	6	8	1.5	0.2207	5	3	2.5	0.1138
A → C	0	0.95	1.0469	0.3062	0	1.14	1.2611	0.2614	0	0	0.5255	0.4685
C → A	0	0.55	0.5831	0.4451	0	0.67	0.7132	0.3984	0	0	0.2972	0.5857
A → T	0	0.95	1.0469	0.3062	2	1.14	0.7142	0.3981	1	0	0.6394	0.4239
T → A	2	1.09	0.8561	0.3548	0	1.29	1.4509	0.2284	1	1	0.4410	0.5066
C → G	1	0.55	0.3872	0.5338	1	0.67	0.1681	0.6818	0	0	0.2972	0.5857
G → C	0	0.75	0.8061	0.3693	0	0.89	0.9627	0.3265	0	0	0.4011	0.5265
G → T	1	0.75	0.0935	0.7598	3	0.89	5.3903	0.0202	2	0	7.7164	0.0055
T → G	0	1.09	1.2217	0.2690	0	1.29	1.4509	0.2284	1	1	0.4410	0.5066
Ts/Tv	1.5	0.5			1	0.5			0	0.5		
Deletions	0				0				0			
Insertions	1				0				0			
Recombination events	1				1				0			

DNA-S Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	4	2.67	1	0.3173	5	2	6.75	0.0094	0	1	1.5	0.2207
A → G	0	0.79	0.8711	0.3506	0	0.59	0.6580	0.4173	0	0.30	0.3290	0.5662
G → A	2	0.68	2.7834	0.0952	0	0.51	0.5548	0.4564	0	0.25	0.2774	0.5984
C → T	2	0.40	6.7891	0.0092	0	0.31	0.3269	0.5675	0	0.16	0.1634	0.6860
T → C	0	0.80	0.8902	0.3454	5	0.59	36.6152	1.44E-09	0	0.29	0.3267	0.5676
Transversions (Tv)	4	5.33	1	0.3173	1	4	6.75	0.0094	3	2	1.5	0.2207
A → C	0	0.79	0.8711	0.3506	0	0.59	0.6580	0.4173	0	0.30	0.3290	0.5662
C → A	0	0.40	0.4187	0.5176	0	0.31	0.3269	0.5675	0	0.16	0.1634	0.6860
A → T	0	0.79	0.8711	0.3506	1	0.59	0.3100	0.5777	1	0.30	1.8522	0.1735
T → A	2	0.80	1.9941	0.1579	0	0.59	0.6534	0.4189	0	0.29	0.3267	0.5676
C → G	1	0.40	0.9590	0.3274	0	0.31	0.3269	0.5675	0	0.16	0.1634	0.6860
G → C	0	0.68	0.7457	0.3878	0	0.51	0.5548	0.4564	0	0.25	0.2774	0.5984
G → T	1	0.68	0.1619	0.6874	0	0.51	0.5548	0.4564	2	0.25	13.1184	0.0003
T → G	0	0.80	0.8902	0.3454	0	0.59	0.6534	0.4189	0	0.29	0.3267	0.5676
Ts/Tv	1	0.5			5	0.5			0	0.5		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-S Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	2	0.67	4	0.0455	1	2	0.75	0.3865	0	0.67	1	0.3173
A → G	0	0.18	0.2003	0.6545	0	0.55	0.6009	0.4382	0	0.18	0.2003	0.6545
G → A	0	0.13	0.1345	0.7138	0	0.38	0.4036	0.5252	0	0.13	0.1345	0.7138
C → T	1	0.12	6.7381	0.0094	0	0.37	0.3893	0.5327	0	0.12	0.1298	0.7187
T → C	1	0.24	2.7925	0.0947	1	0.71	0.1343	0.7140	0	0.24	0.2684	0.6044
Transversions (Tv)	0	1.33	4	0.0455	5	4	0.75	0.3865	2	1.33	1	0.3173
A → C	0	0.18	0.2003	0.6545	0	0.55	0.6009	0.4382	0	0.18	0.2003	0.6545
C → A	0	0.12	0.1298	0.7187	0	0.37	0.3893	0.5327	0	0.12	0.1298	0.7187
A → T	0	0.18	0.2003	0.6545	1	0.55	0.4148	0.5195	0	0.18	0.2003	0.6545
T → A	0	0.24	0.2684	0.6044	0	0.71	0.8053	0.3695	1	0.24	2.7925	0.0947
C → G	0	0.12	0.1298	0.7187	1	0.37	1.1723	0.2789	0	0.12	0.1298	0.7187
G → C	0	0.13	0.1345	0.7138	0	0.38	0.4036	0.5252	0	0.13	0.1345	0.7138
G → T	0	0.13	0.1345	0.7138	3	0.38	19.3978	1.06E-05	0	0.13	0.1345	0.7138
T → G	0	0.24	0.2684	0.6044	0	0.71	0.8053	0.3695	1	0.24	2.7925	0.0947
Ts/Tv	ND	0.5			0.2	0.5			0	0.5		
Deletions	0				0				0			
Insertions	1				0				0			
Recombination events	1				1				0			

DNA-C Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	8	6.33	0.7	0.4173	0	1.67	2.5	0.1138	2	1	1.5	0.2207
A → G	(+1)	1.92	2.1409 to 0.4938	0.1434 to 0.4822	0	0.51	0.5654	0.4521	0	0.30	0.3393	0.5603
G → A	(+1)	1.35	1.4543 to 0.0981	0.2278 to 0.7541	0	0.36	0.3827	0.5362	0	0.21	0.2296	0.6318
C → T	4 (+1)	1.02	9.2051 to 16.4186	0.0024 to 5.08E-05	0	0.27	0.2836	0.5944	0	0.16	0.1701	0.6800
T → C	2 (+1)	2.04	0.0008 to 0.5078	0.9771 to 0.4761	0	0.53	0.5989	0.4390	2	0.32	9.8382	0.0017
Transversions (Tv)	11	12.67	0.7	0.4173	5	3.33	2.5	0.1138	1	2	1.5	0.2207
A → C	1 (+1)	1.92	0.4938 to 0.0033	0.4822 to 0.9540	2	0.51	4.8776	0.0272	1	0.30	1.7650	0.1840
C → A	4 (+1)	1.02	9.2051 to 16.4186	0.0024 to 5.08E-05	0	0.27	0.2836	0.5944	0	0.16	0.1701	0.6800
A → T	1	1.92	0.4938	0.4822	1	0.51	0.5304	0.4664	0	0.30	0.3393	0.5603
T → A	1	2.04	0.5928	0.4413	1	0.53	0.4530	0.5009	0	0.32	0.3593	0.5489
C → G	0	1.02	1.0775	0.2993	0	0.27	0.2836	0.5944	0	0.16	0.1701	0.6800
G → C	1	1.35	0.0981	0.7541	0	0.36	0.3827	0.5362	0	0.21	0.2296	0.6318
G → T	(+2)	1.35	1.4543 to 0.3358	0.2278 to 0.5623	0	0.36	0.3827	0.5362	0	0.21	0.2296	0.6318
T → G	(+2)	2.04	2.2837 to 0.0008	0.1307 to 0.9771	1	0.53	0.4530	0.5009	0	0.32	0.3593	0.5489
Ts/Tv	0.7	0.5			0	0.5			2	0.5		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	1				0				0			

DNA-C Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	3	4	0.3750	0.5403	0	0.67	1	0.3173	0	0	ND	ND
A → G	0	1.38	1.5603	0.2116	0	0.23	0.2601	0.6101	0	0	ND	ND
G → A	0	0.88	0.9445	0.3311	0	0.15	0.1574	0.6915	0	0	ND	ND
C → T	2 (+1)	0.50	4.6232 to 12.8753	0.0315 to 0.0003	0	0.08	0.0878	0.7670	0	0	ND	ND
T → C	(+1)	1.24	1.3814 to 0.0513	0.2399 to 0.8208	0	0.21	0.2302	0.6313	0	0	ND	ND
Transversions (Tv)	9	8	0.3750	0.5403	2	1.33	1	0.3173	0	0	ND	ND
A → C	1 (+1)	1.38	0.1187 to 0.3138	0.7305 to 0.5754	2	0.23	15.3812	8.79E-05	0	0	ND	ND
C → A	3 (+1)	0.50	12.8753 to 25.2633	0.0003 to 5.00E-07	0	0.08	0.0878	0.7670	0	0	ND	ND
A → T	1	1.38	0.1187	0.7305	0	0.23	0.2601	0.6101	0	0	ND	ND
T → A	0	1.24	1.3814	0.2399	0	0.21	0.2302	0.6313	0	0	ND	ND
C → G	0	0.50	0.5270	0.4679	0	0.08	0.0878	0.7670	0	0	ND	ND
G → C	1	0.88	0.0191	0.8902	0	0.15	0.1574	0.6915	0	0	ND	ND
G → T	(+2)	0.88	0.9445 to 1.5575	0.3311 to 0.2120	0	0.15	0.1574	0.6915	0	0	ND	ND
T → G	(+2)	1.24	1.3814 to 0.5216	0.2399 to 0.4702	0	0.21	0.2302	0.6313	0	0	ND	ND
Ts/Tv	0.3	0.5			0	0.5			ND	ND		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-C Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	5	2.33	4.5714	0.0325	0	0.9999	1.5002	0.2206	2	1	1.5002	0.2206
A → G	(+1)	0.61	0.6665 to 0.2758	0.4143 to 0.5995	0	0.26	0.2881	0.5914	0	0.26	0.2881	0.5914
G → A	(+1)	0.48	0.5199 to 0.5912	0.4709 to 0.4420	0	0.21	0.2228	0.6369	0	0.21	0.2228	0.6369
C → T	2	0.46	5.5201	0.0188	0	0.20	0.2110	0.6460	0	0.20	0.2110	0.6460
T → C	2	0.78	2.1418	0.1433	0	0.33	0.3742	0.5407	2	0.33	9.4011	0.0022
Transversions (Tv)	2	4.67	4.5714	0.0325	3	1.9998	1.5002	0.2206	1	2	1.5002	0.2206
A → C	0	0.61	0.6665	0.4143	0	0.26	0.2881	0.5914	1	0.26	2.2664	0.1322
C → A	1	0.46	0.6789	0.4100	0	0.20	0.2110	0.6460	0	0.20	0.2110	0.6460
A → T	0	0.61	0.6665	0.4143	1	0.26	2.2664	0.1322	0	0.26	0.2881	0.5914
T → A	1	0.78	0.0691	0.7926	1	0.33	1.5061	0.2197	0	0.33	0.3742	0.5407
C → G	0	0.46	0.4922	0.4829	0	0.20	0.2110	0.6460	0	0.20	0.2110	0.6460
G → C	0	0.48	0.5199	0.4709	0	0.21	0.2228	0.6369	0	0.21	0.2228	0.6369
G → T	0	0.48	0.5199	0.4709	0	0.21	0.2228	0.6369	0	0.21	0.2228	0.6369
T → G	0	0.78	0.8790	0.3485	1	0.33	1.5061	0.2197	0	0.33	0.3742	0.5407
Ts/Tv	2.5	0.5			0	0.5			2	0.5		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	1				0				0			

DNA-N Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	25	10.67	28.8906	7.66E-08	12	5.33	12.5	0.0004	3	1.33	3.1250	0.0771
A → G	3 (+4)	2.94	0.0014 to 6.1805	0.9701 to 0.0129	2	1.45	0.2277	0.6332	1	0.36	1.2298	0.2674
G → A	6 (+4)	2.34	6.1747 to 27.0486	0.0130 to 1.98E-07	1	1.19	0.0312	0.8598	1	0.30	1.8053	0.1791
C → T	2 (+3)	1.85	0.0128 to 5.6883	0.9100 to 0.0171	1	0.93	0.0048	0.9447	0	0.23	0.2482	0.6183
T → C	7 (+3)	3.54	3.8117 to 13.2766	0.0509 to 0.0003	8	1.76	24.8255	6.28E-07	1	0.44	0.7990	0.3714
Transversions (Tv)	7	21.33	28.8906	7.66E-08	4	10.67	12.5	0.0004	1	2.67	3.1250	0.0771
A → C	1	2.94	1.4083	0.2353	1	1.45	0.1546	0.6942	0	0.36	0.3991	0.5275
C → A	1	1.85	0.4150	0.5194	0	0.93	0.9930	0.3190	0	0.23	0.2482	0.6183
A → T	1	2.94	1.4083	0.2353	1	1.45	0.1546	0.6942	0	0.36	0.3991	0.5275
T → A	0	3.54	3.9766	0.0461	0	1.76	1.9795	0.1594	0	0.44	0.4949	0.4818
C → G	0	1.85	1.9643	0.1611	0	0.93	0.9930	0.3190	0	0.23	0.2482	0.6183
G → C	0	2.34	2.5249	0.1121	0	1.19	1.2799	0.2579	0	0.30	0.3200	0.5716
G → T	1 (+1)	2.34	0.8281 to 0.0534	0.3628 to 0.8173	1	1.19	0.0312	0.8598	1	0.30	1.8053	0.1791
T → G	2 (+1)	3.54	0.7510 to 0.0917	0.3862 to 0.7620	1	1.76	0.3700	0.5430	0	0.44	0.4949	0.4818
Ts/Tv	3.6	0.5			3	0.5			3	0.5		
Deletions	0				0				0			
Insertions	0				1				0			
Recombination events	0				1				0			

DNA-N Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	15	5.33	26.2813	2.95E-07	6	3	4.5	0.0339	3	1.33	3.1250	0.0771
A → G	1 (+3)	1.58	0.2364 to 4.1112	2.95E-07 to 0.0426	2	0.88	1.5991	0.2060	1	0.39	1.0619	0.3028
G → A	2 (+3)	1.27	0.4611 to 11.9495	0.6268 to 0.0005	0	0.72	0.7815	0.3767	1	0.32	1.5743	0.2096
C → T	1 (+3)	0.79	0.0588 to 13.7240	0.4971 to 0.0002	1	0.44	0.7311	0.3925	0	0.20	0.2077	0.6486
T → C	5 (+3)	1.70	7.1954 to 26.1984	0.8084 to 3.08E-07	3	0.96	4.8443	0.0277	1	0.43	0.8605	0.3536
Transversions (Tv)	1	10.67	26.2813	2.95E-07	3	6	4.5	0.0339	1	2.67	3.1250	0.0771
A → C	0	1.58	1.7534	0.1854	1	0.88	0.0195	0.8888	0	0.39	0.4312	0.5114
C → A	0	0.79	0.8309	0.3620	0	0.44	0.4674	0.4942	0	0.20	0.2077	0.6486
A → T	0	1.58	1.7534	0.1854	1	0.88	0.0195	0.8888	0	0.39	0.4312	0.5114
T → A	0	1.70	1.8978	0.1683	0	0.96	1.0758	0.2996	0	0.43	0.4781	0.4893
C → G	0	0.79	0.8309	0.3620	0	0.44	0.4674	0.4942	0	0.20	0.2077	0.6486
G → C	0	1.27	1.3756	0.2409	0	0.72	0.7815	0.3767	0	0.32	0.3474	0.5556
G → T	0	1.27	1.3756	0.2409	1	0.72	0.1193	0.7298	1	0.32	1.5743	0.2096
T → G	1	1.70	0.3199	0.5717	0	0.96	1.0758	0.2996	0	0.43	0.4781	0.4893
Ts/Tv	15	0.5			2	0.5			3	0.5		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-N Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	10	5.33	6.1244	0.0133	6	2.33	8.6429	0.0033	0	0	ND	ND
A → G	2 (+1)	1.37	0.3149 to 2.1144	0.5747 to 0.1459	0	0.59	0.6497	0.4202	0	0	ND	ND
G → A	4 (+1)	1.09	8.3975 to 15.1479	0.0038 to 9.94E-05	1	0.48	0.5952	0.4404	0	0	ND	ND
C → T	1	1.04	0.0020	0.9643	0	0.46	0.4979	0.4804	0	0	ND	ND
T → C	2	1.83	0.0173	0.8953	5	0.79	25.2405	5.06E-07	0	0	ND	ND
Transversions (Tv)	6	10.67	6.1244	0.0133	1	4.67	8.6429	0.0033	0	0	ND	ND
A → C	1	1.37	0.1101	0.7400	0	0.59	0.6497	0.4202	0	0	ND	ND
C → A	1	1.04	0.0020	0.9643	0	0.46	0.4979	0.4804	0	0	ND	ND
A → T	1	1.37	0.1101	0.7400	0	0.59	0.6497	0.4202	0	0	ND	ND
T → A	0	1.83	2.0691	0.1503	0	0.79	0.8921	0.3449	0	0	ND	ND
C → G	0	1.04	1.1170	0.2906	0	0.46	0.4979	0.4804	0	0	ND	ND
G → C	0	1.09	1.1641	0.2806	0	0.48	0.5185	0.4715	0	0	ND	ND
G → T	1 (+1)	1.09	0.0072 to 0.8271	0.9325 to 0.3631	0	0.48	0.5185	0.4715	0	0	ND	ND
T → G	1 (+1)	1.83	0.4270 to 0.0173	0.5135 to 0.8953	1	0.79	0.0621	0.8032	0	0	ND	ND
Ts/Tv	1.7	0.5			6	0.5			ND	ND		
Deletions	0				0				0			
Insertions	0				1				0			
Recombination events	0				1				0			

DNA-U1 Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	12	5	14.7	0.0001	12	7.67	3.6739	0.0553	1	0.33	2	0.1573
A → G	2	1.43	0.2496	0.6174	2	2.19	0.0173	0.8953	0	0.10	0.1054	0.7455
G → A	2	1.01	1.0558	0.3042	3	1.54	1.4850	0.2230	1	0.07	14.0150	0.0002
C → T	4	0.80	13.4725	0.0002	0	1.23	1.2975	0.2547	0	0.05	0.0564	0.8123
T → C	4	1.76	3.2232	0.0726	7	2.71	7.6741	0.0056	0	0.12	0.1338	0.7145
Transversions (Tv)	3	10	14.7	0.0001	11	15.33	3.6739	0.0553	0	0.67	2	0.1573
A → C	0	1.43	1.5825	0.2084	0	2.19	2.4144	0.1202	0	0.10	0.1054	0.7455
C → A	1	0.80	0.0516	0.8202	1	1.23	0.0448	0.8324	0	0.05	0.0564	0.8123
A → T	0	1.43	1.5825	0.2084	0	2.19	2.4144	0.1202	0	0.10	0.1054	0.7455
T → A	1	1.76	0.3730	0.5414	6	2.71	4.5108	0.0337	0	0.12	0.1338	0.7145
C → G	0	0.80	0.8473	0.3573	1	1.23	0.0448	0.8324	0	0.05	0.0564	0.8123
G → C	0	1.01	1.0772	0.2993	0	1.54	1.6499	0.1990	0	0.07	0.0714	0.7894
G → T	1	1.01	2.67E-05	0.9959	2	1.54	0.1477	0.7008	0	0.07	0.0714	0.7894
T → G	0	1.76	1.9959	0.1577	1	2.71	1.2273	0.2679	0	0.12	0.1338	0.7145
Ts/Tv	4	0.5			1.1	0.5			ND	0.5		
Deletions	1				0				0			
Insertions	0				1				0			
Recombination events	0				0				0			

DNA-U1 Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	5	2.33	4.5719	0.0325	5	3.67	0.7273	0.3937	0	0	ND	ND
A → G	0	0.74	0.8252	0.3637	1	1.16	0.0246	0.8753	0	0	ND	ND
G → A	0	0.48	0.5103	0.4750	1	0.74	0.0983	0.7539	0	0	ND	ND
C → T	2	0.26	11.9484	0.0005	0	0.41	0.4287	0.5126	0	0	ND	ND
T → C	3	0.86	6.1055	0.0135	3	1.35	2.2795	0.1311	0	0	ND	ND
Transversions (Tv)	2	4.67	4.5719	0.0325	6	7.33	0.7273	0.3937	0	0	ND	ND
A → C	0	0.74	0.8252	0.3637	0	1.16	1.2967	0.2548	0	0	ND	ND
C → A	1	0.26	2.1526	0.1423	1	0.41	0.8692	0.3512	0	0	ND	ND
A → T	0	0.74	0.8252	0.3637	0	1.16	1.2967	0.2548	0	0	ND	ND
T → A	0	0.86	0.9768	0.3230	2	1.35	0.3507	0.5537	0	0	ND	ND
C → G	0	0.26	0.2728	0.6015	0	0.41	0.4287	0.5126	0	0	ND	ND
G → C	0	0.48	0.5103	0.4750	0	0.74	0.7930	0.3732	0	0	ND	ND
G → T	1	0.48	0.6205	0.4309	2	0.74	2.3027	0.1291	0	0	ND	ND
T → G	0	0.86	0.9768	0.3230	1	1.35	0.1059	0.7449	0	0	ND	ND
Ts/Tv	2.5	0.5			0.8	0.5			ND	ND		
Deletions	1				0				0			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-U1 Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	7	2.67	10.5625	0.0012	7	4	3.3750	0.0662	1	0.33	1.9998	0.1573
A → G	2	0.69	2.7208	0.0990	1	1.03	0.0007	0.9792	0	0.09	0.0942	0.7589
G → A	2	0.53	4.3792	0.0364	2	0.80	1.9286	0.1649	1	0.07	14.1440	0.0002
C → T	2	0.54	4.1710	0.0411	0	0.82	0.8751	0.3496	0	0.07	0.0729	0.7871
T → C	1	0.90	0.0118	0.9134	4	1.36	5.7862	0.0162	0	0.11	0.1277	0.7208
Transversions (Tv)	1	5.33	10.5625	0.0012	5	8	3.3750	0.0662	0	0.67	1.9998	0.1573
A → C	0	0.69	0.7553	0.3848	0	1.03	1.1210	0.2897	0	0.09	0.0942	0.7589
C → A	0	0.54	0.5846	0.4445	0	0.82	0.8751	0.3496	0	0.07	0.0729	0.7871
A → T	0	0.69	0.7553	0.3848	0	1.03	1.1210	0.2897	0	0.09	0.0942	0.7589
T → A	1	0.90	0.0118	0.9134	4	1.36	5.7862	0.0162	0	0.11	0.1277	0.7208
C → G	0	0.54	0.5846	0.4445	1	0.82	0.0447	0.8325	0	0.07	0.0729	0.7871
G → C	0	0.53	0.5665	0.4516	0	0.80	0.8571	0.3545	0	0.07	0.0707	0.7903
G → T	0	0.53	0.5665	0.4516	0	0.80	0.8571	0.3545	0	0.07	0.0707	0.7903
T → G	0	0.90	1.0175	0.3131	0	1.36	1.5328	0.2157	0	0.11	0.1277	0.7208
Ts/Tv	7	0.5			1.4	0.5			ND	0.5		
Deletions	0				0				0			
Insertions	0				1				0			
Recombination events	0				0				0			

DNA-U2 Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	11	4.67	12.8929	3.30E-04	9	4.67	6.0357	0.0140	5	2.33	4.5714	0.0325
A → G	2 (+1)	1.38	0.3130 to 2.1230	0.5758 to 0.1451	2	1.37	0.3262	0.5679	2	0.68	2.8144	0.0934
G → A	1 (+1)	0.98	0.0005 to 1.1477	0.9817 to 0.2840	4	0.98	9.9771	0.0016	2	0.49	4.9885	0.0255
C → T	1 (+4)	0.82	0.0437 to 22.7564	0.8344 to 1.84E-06	1	0.83	0.0394	0.8426	0	0.41	0.4384	0.5079
T → C	2 (+4)	1.50	0.1908 to 15.1951	0.6622 to 9.70E-05	2	1.49	0.1920	0.6612	1	0.75	0.0960	0.7567
Transversions (Tv)	3	9.33	12.8929	3.30E-04	5	9.33	6.0357	0.0140	2	4.67	4.5714	0.0325
A → C	(+1)	1.38	1.5268 to 0.1143	0.2166 to 0.7353	1	1.37	0.1086	0.7417	1	0.68	0.1631	0.6863
C → A	(+1)	0.82	0.8673 to 0.0437	0.3517 to 0.8344	0	0.83	0.8767	0.3491	0	0.41	0.4384	0.5079
A → T	(+1)	1.38	1.5268 to 0.1143	0.2166 to 0.7353	1	1.37	0.1086	0.7417	1	0.68	0.1631	0.6863
T → A	(+1)	1.50	1.6740 to 0.1836	0.1957 to 0.6683	2	1.49	0.1920	0.6612	0	0.75	0.8361	0.3605
C → G	0	0.82	0.8673	0.3517	0	0.83	0.8767	0.3491	0	0.41	0.4384	0.5079
G → C	0	0.98	1.0516	0.3051	1	0.98	0.0004	0.9849	0	0.49	0.5280	0.4675
G → T	1	0.98	0.0005	0.9817	0	0.98	1.0559	0.3041	0	0.49	0.5280	0.4675
T → G	0	1.50	1.6740	0.1957	0	1.49	1.6722	0.1960	0	0.75	0.8361	0.3605
Ts/Tv	3.7	0.5			1.8	0.5			2.5	0.5		
Deletions	2				0				0			
Insertions	2				1				0			
Recombination events	0				1				0			

DNA-U2 Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	3	2	0.7501	0.3865	3	1.67	1.6002	0.2059	2	1.33	0.5001	0.4795
A → G	0	0.61	0.6742	0.4116	1	0.51	0.5396	0.4626	1	0.40	0.9779	0.3227
G → A	0	0.41	0.4439	0.5053	1	0.34	1.3407	0.2469	1	0.28	2.0465	0.1526
C → T	(+2)	0.31	0.3314 to 9.5525	0.5648 to 0.0020	0	0.26	0.2762	0.5992	0	0.21	0.2209	0.6383
T → C	1 (+2)	0.67	0.1875 to 9.1884	0.6650 to 0.0024	1	0.56	0.4000	0.5271	0	0.44	0.5001	0.4795
Transversions (Tv)	3	4	0.7501	0.3865	2	3.33	1.6002	0.2059	2	2.67	0.5001	0.4795
A → C	(+1)	0.61	0.6742 to 0.2849	0.4116 to 0.5935	1	0.51	0.5396	0.4626	1	0.40	0.9779	0.3227
C → A	(+1)	0.31	0.3314 to 1.5813	0.5648 to 0.2086	0	0.26	0.2762	0.5992	0	0.21	0.2209	0.6383
A → T	(+1)	0.61	0.6742 to 0.2849	0.4116 to 0.5935	1	0.51	0.5396	0.4626	1	0.40	0.9779	0.3227
T → A	(+1)	0.67	0.7501 to 0.1875	0.3865 to 0.6650	0	0.56	0.6251	0.4292	0	0.44	0.5001	0.4795
C → G	0	0.31	0.3314	0.5648	0	0.26	0.2762	0.5992	0	0.21	0.2209	0.6383
G → C	0	0.41	0.4439	0.5053	0	0.34	0.3699	0.5431	0	0.28	0.2959	0.5865
G → T	1	0.41	0.8948	0.3442	0	0.34	0.3699	0.5431	0	0.28	0.2959	0.5865
T → G	0	0.67	0.7501	0.3865	0	0.56	0.6251	0.4292	0	0.44	0.5001	0.4795
Ts/Tv	1	0.5			1.5	0.5			1	0.5		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	0				0				0			

DNA-U2 Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	8	2.67	16	6.33E-05	6	3	4.5	0.0339	3	1	6	0.0143
A → G	2 (+1)	0.77	2.1492 to 7.0857	0.1426 to 0.0078	1	0.86	0.0253	0.8737	1	0.29	1.9633	0.1612
G → A	1 (+1)	0.56	0.3638 to 3.9399	0.5464 to 0.0472	3	0.64	9.4161	0.0022	1	0.21	3.1387	0.0765
C → T	1 (+2)	0.49	0.5503 to 13.5250	0.4582 to 0.0002	1	0.57	0.3569	0.5502	0	0.19	0.2010	0.6539
T → C	1 (+2)	0.83	0.0367 to 6.2751	0.8481 to 0.0122	1	0.94	0.0047	0.9454	1	0.31	1.6893	0.1937
Transversions (Tv)	0	5.33	16	6.33E-05	3	6	4.5	0.0339	0	2	6	0.0143
A → C	0	0.77	0.8571	0.3546	0	0.86	0.9506	0.3296	0	0.29	0.3169	0.5735
C → A	0	0.49	0.5273	0.4678	0	0.57	0.6031	0.4374	0	0.19	0.2010	0.6539
A → T	0	0.77	0.8571	0.3546	0	0.86	0.9506	0.3296	0	0.29	0.3169	0.5735
T → A	0	0.83	0.9316	0.3345	2	0.94	1.3453	0.2461	0	0.31	0.3487	0.5548
C → G	0	0.49	0.5273	0.4678	0	0.57	0.6031	0.4374	0	0.19	0.2010	0.6539
G → C	0	0.56	0.6062	0.4362	1	0.64	0.2214	0.6380	0	0.21	0.2288	0.6324
G → T	0	0.56	0.6062	0.4362	0	0.64	0.6864	0.4074	0	0.21	0.2288	0.6324
T → G	0	0.83	0.9316	0.3345	0	0.94	1.0461	0.3064	0	0.31	0.3487	0.5548
Ts/Tv	ND	0.5			2	0.5			ND	0.5		
Deletions	2				0				0			
Insertions	2				1				0			
Recombination events	0				1				0			

DNA-U4 Genome	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	12	5.67	10.6176	0.0011	7	6	0.25	0.6171	6	2.67	6.25	0.0124
A → G	3	1.62	1.3021	0.2538	1	1.71	0.3289	0.5663	2	0.76	2.2239	0.1359
G → A	3	1.17	3.0993	0.0783	0	1.23	1.3251	0.2497	0	0.55	0.5889	0.4428
C → T	3	0.99	4.3050	0.0380	4	1.06	8.6945	0.0032	3	0.47	14.5716	0.0001
T → C	3	1.89	0.7356	0.3911	2	1.99	0.0000	0.9963	1	0.89	0.0157	0.9004
Transversions (Tv)	5	11.33	10.6176	0.0011	11	12	0.25	0.6171	2	5.33	6.25	0.0124
A → C	0	1.62	1.7894	0.1810	3	1.71	1.0660	0.3019	0	0.76	0.8421	0.3588
C → A	3	0.99	4.3050	0.0380	0	1.06	1.1238	0.2891	0	0.47	0.4965	0.4811
A → T	0	1.62	1.7894	0.1810	2	1.71	0.0527	0.8185	0	0.76	0.8421	0.3588
T → A	1	1.89	0.4704	0.4928	1	1.99	0.5571	0.4554	1	0.89	0.0157	0.9004
C → G	0	0.99	1.0550	0.3044	0	1.06	1.1238	0.2891	0	0.47	0.4965	0.4811
G → C	0	1.17	1.2514	0.2633	1	1.23	0.0477	0.8271	0	0.55	0.5889	0.4428
G → T	1	1.17	0.0253	0.8737	2	1.23	0.5101	0.4751	0	0.55	0.5889	0.4428
T → G	0	1.89	2.1248	0.1449	2	1.99	0.0000	0.9963	1	0.89	0.0157	0.9004
Ts/Tv	2.4	0.5			0.6	0.5			3	0.5		
Deletions	1				0				0			
Insertions	0				0				1			
Recombination events	1				1				2			

DNA-U4 Coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	4	2	3	0.0833	1	1	0	1	0	0	ND	ND
A → G	1	0.63	0.2445	0.6210	0	0.31	0.3513	0.5534	0	0	ND	ND
G → A	0	0.45	0.4898	0.4840	0	0.23	0.2449	0.6207	0	0	ND	ND
C → T	1	0.30	1.7008	0.1922	1	0.15	5.0309	0.0249	0	0	ND	ND
T → C	2	0.62	3.4613	0.0628	0	0.31	0.3435	0.5578	0	0	ND	ND
Transversions (Tv)	2	4	3	0.0833	2	2	0	1	0	0	ND	ND
A → C	0	0.63	0.7027	0.4019	0	0.31	0.3513	0.5534	0	0	ND	ND
C → A	2	0.30	10.0617	0.0015	0	0.15	0.1589	0.6902	0	0	ND	ND
A → T	0	0.63	0.7027	0.4019	1	0.31	1.6691	0.1964	0	0	ND	ND
T → A	0	0.62	0.6870	0.4072	0	0.31	0.3435	0.5578	0	0	ND	ND
C → G	0	0.30	0.3178	0.5729	0	0.15	0.1589	0.6902	0	0	ND	ND
G → C	0	0.45	0.4898	0.4840	0	0.23	0.2449	0.6207	0	0	ND	ND
G → T	0	0.45	0.4898	0.4840	1	0.23	2.8591	0.0909	0	0	ND	ND
T → G	0	0.62	0.6870	0.4072	0	0.31	0.3435	0.5578	0	0	ND	ND
Ts/Tv	2	0.5			0.5	0.5			ND	ND		
Deletions	0				0				0			
Insertions	0				0				0			
Recombination events	0				0				1			

DNA-U4 Non coding region	A: FBNSV-[ET:Hol;1997]				B: FBNSV-[ET:Hol;JKI-2000]				C: FBNSV-[ET:Hol;ISV-T1]			
	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value	Obs.	Exp.	χ^2	<i>p</i> -value
Transitions (Ts)	8	3.67	7.6826	0.0056	6	5	0.3	0.5839	6	2.67	6.2506	0.0124
A → G	2	1.00	1.1083	0.2924	1	1.36	0.1049	0.7461	2	0.73	2.4631	0.1165
G → A	3	0.72	7.7600	0.0053	0	0.98	1.0476	0.3061	0	0.52	0.5587	0.4548
C → T	2	0.68	2.6923	0.1008	3	0.94	4.8017	0.0284	3	0.50	13.3995	0.0003
T → C	1	1.27	0.0633	0.8014	2	1.72	0.0518	0.8199	1	0.92	0.0077	0.9302
Transversions (Tv)	3	7.33	7.6826	0.0056	9	10	0.3	0.5839	2	5.33	6.2506	0.0124
A → C	0	1.00	1.0970	0.2949	3	1.36	2.1745	0.1403	0	0.73	0.7978	0.3717
C → A	1	0.68	0.1545	0.6943	0	0.94	1.0048	0.3162	0	0.50	0.5313	0.4661
A → T	0	1.00	1.0970	0.2949	1	1.36	0.1049	0.7461	0	0.73	0.7978	0.3717
T → A	1	1.27	0.0633	0.8014	1	1.72	0.3398	0.5599	1	0.92	0.0077	0.9302
C → G	0	0.68	0.7306	0.3927	0	0.94	1.0048	0.3162	0	0.50	0.5313	0.4661
G → C	0	0.72	0.7682	0.3808	1	0.98	0.0005	0.9826	0	0.52	0.5587	0.4548
G → T	1	0.72	0.1185	0.7307	1	0.98	0.0005	0.9826	0	0.52	0.5587	0.4548
T → G	0	1.27	1.4311	0.2316	2	1.72	0.0518	0.8199	1	0.92	0.0077	0.9302
Ts/Tv	11	0.5			0.7	0.5			3	0.5		
Deletions	1				0				0			
Insertions	0				0				1			
Recombination events	1				1				1			

809	Ts	C: 60.0%		C: 40.7% T: 59.3%	T: 100%	→ in CR-M-U2: same mutation was detected in the Holetta-1997 isolate DNA-U2 at equivalent position (C812: 59.1%, T812: 36.4%) → in CR-M-U2: same mutation was detected in the JKI-2000 isolate DNA-U2 at equivalent position (C812: 96.2%, T812: 3.8%) → T809 fixed as consensus in JKI-2000 isolate → detected as variable site by direct sequencing of the JKI-2000 RCA product
840	Ts	A: 60.0%		A: 22.2% G: 77.8%	G: 100%	→ in CR-M-U2: same mutation was detected in the Holetta-1997 isolate DNA-U2 at equivalent position (G849: 81.8%, A846: 9.1%) → G840 fixed as consensus in JKI-2000 isolate → detected as variable site by direct sequencing of the JKI-2000 RCA product
846	Ts	G: 30.0% A: 30.0%		G: 100%	G: 100%	→ in CR-M-U2: same mutation was detected in the Holetta-1997 isolate DNA-U2 at equivalent position (G846: 30.0%, A846: 30.0%)
861	Ts	G: 95.0% A: 5.0%	G: 100%	G: 100%	G: 100%	→ in CR-II: alters the DNA-R/S/M/N/U2/U4 type of CR-II sequence
864	Tv	T: 100%	T: 100%	T: 85.2% A: 14.8%	T: 100%	→ in CR-II: makes the sequence similar to that of DNA-C and DNA-U1 at equivalent positions (A895 on DNA-C and A878 on DNA-U1)
885	Ts	T: 100%	T: 100%	T: 100%	T: 95.0% C: 5.0%	→ in CR-M-U2: same mutation was detected in the JKI-2000 isolate DNA-U2 at equivalent position (T888: 3.8%, C888: 96.2%)
895-900	Rec	AGTCTT: 100%	AGTCTT: 100%	AGTCTT: 22.2% TGCTCTC: 77.8%	TGCTCTC: 100%	→ in CR-M-U2: recombination event with Holetta-1997 isolate DNA-U2 898-904 (TGCTCTC: 100%) → TGCTCTC fixed as consensus in JKI-2000 isolate → in CR-M-U2: same mutations were detected in the JKI-2000 isolate DNA-U2 at equivalent position (898-904: AGTCTT: 34.6%, TGCTCTC: 65.4%) → → in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2. Same mutations were detected in the Holetta-1997 isolate DNA-U4 at equivalent positions (766-772: GAGAGCA: 85.0%, AAGACT: 10.0%) and in the JKI-2000 isolate DNA-U4 at equivalent positions (766-772: GAGAGCA: 71.8%, AAGACT: 23.1%) → in CR-C-M-N-U1-U2: same mutations were detected in the Holetta-1997 isolate DNA-C at equivalent position (908-913: AGTCTC: 65.0%, AGTCTT: 30.0%, TGCTCTC: 5.0%) → in CR-C-M-N-U1-U2: same mutations were detected in the JKI-2000 isolate DNA-N at equivalent position (914-918: AGTCTC: 97.5%, AGTCTT: 2.5%, TGCTCTC: 2.5%) → detected as variable site by direct sequencing of the JKI-2000 RCA product
904	Ts	G: 100%	G: 100%	G: 96.3% A: 3.7%	G: 100%	
914	Tv	A: 95.0% C: 5.0%	A: 100%	C: 100%	C: 100%	→ in CR-M-U2: same mutations were detected in DNA-U2 at equivalent position (A918: 100% in the Holetta-1997 and C918: 100% the JKI-2000 isolate) → in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2 → in CR-M-U2-U4: same mutations were detected in the Holetta-1997 isolate DNA-U4 at equivalent position (G752:85.0%, T752: 15.0%)
915	Ts	C: 95.0% T: 5.0%	A: 100%	T: 100%	T: 100%	→ in CR-M-U2: same mutations were detected in DNA-U2 at equivalent position (C919: 54.5%, T919: 45.5% in the Holetta-1997 and T919:100% the JKI-2000 isolate) → in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2 → in CR-M-U2-U4: same mutations were detected in the Holetta-1997 isolate DNA-U4 at equivalent position (A751:85.0%, G751: 15.0%)

DNA-N

Sequence changes						Codon changes					Protein changes					
position	type	Holetta-1997	JKI-1998/99	JKI-2000	ISV-T1	Comments	position	Holetta-1997	JKI-1998/99	JKI-2000	ISV-T1	Holetta-1997	JKI-1998/99	JKI-2000	ISV-T1	
44	Ts	G: 95.0% A: 5.0%	G: 100%	G: 100%	G: 100%											
58	Ts	A: 80.0% G: 20.0%	A: 100%	A: 100%	A: 100%	→ in CR-S-N-U4: A58 make the sequence similar to that of DNA-U4 at equivalent position (A58) and G58 make the sequence similar to that of DNA-U4 at equivalent position (G58)										
86	Tv	T: 100%	A: 100%	T: 100%	T: 100%											
93	Ts	G: 80.0% A: 20.0%	G: 100%	G: 100%	G: 100%											
230	Ts	T: 100%	T: 100%	T: 97.5% C: 2.5%	T: 100%											
231	Tv	A: 80.0% C: 20.0%	A: 100%	A: 100%	A: 100%											
232	Ts	T: 100%	T: 100%	T: 2.5% C: 97.5%	C: 100%	→ C232 fixed as consensus in JKI-2000 isolate										
238	Tv	T: 100%	T: 100%	T: 90.0% G: 10.0%	T: 100%											
286	Ts	A: 70.0% G: 30.0%	A: 100%	A: 100%	A: 100%											
287	Tv	T: 50.0% G: 50.0%	T: 100%	T: 100%	T: 100%											
322	Tv	G: 65.0% T: 35.0%	G: 100%	G: 100%	G: 100%											
350	Ts	C: 55.0% T: 45.0%	T: 100%	T: 100%	T: 100%	→ synonymous	5	TTC: 55.0% TTT: 45.0%	TTT: 100%	TTT: 100%	TTT: 100%	Phe: 100%	Phe: 100%	Phe: 100%	Phe: 100%	
374	Tv	A: 100%	A: 100%	A: 95.0% C: 5.0%	A: 100%	→ synonymous	13	ACA: 100%	ACA: 100%	ACA: 95.0% ACC: 5.0%	ACA: 100%	Thr: 100%	Thr: 100%	Thr: 100%	Thr: 100%	
389	Ts	T: 55.0% C: 45.0%	C: 100%	C: 100%	C: 100%	→ synonymous	18	TTT: 55.0% TTC: 45.0%	TTC: 100%	TTC: 100%	TTC: 100%	Phe: 100%	Phe: 100%	Phe: 100%	Phe: 100%	
395	Ts	T: 95.0% C: 5.0%	T: 100%	T: 100%	T: 100%	→ synonymous	20	TCT: 95.0% TCC: 5.0%	TCT: 100%	TCT: 100%	TCT: 100%	Ser: 100%	Ser: 100%	Ser: 100%	Ser: 100%	
420	Tv	A: 100%	A: 100%	A: 20.0% T: 80.0%	T: 100%	→ non synonymous → T420 fixed as consensus in JKI-2000 isolate → detected as variable site by direct sequencing of the JKI-2000 RCA product	29	ATT: 100%	ATT: 100%	ATT: 20.0% TTT: 80.0%	TTT: 100%	Ile: 100%	Ile: 100%	Ile: 20.0% Phe: 80.0%	Phe: 100%	
500	Ts	T: 70.0% C: 30.0%	T: 100%	T: 100%	T: 100%	→ synonymous	55	AAT: 70.0% AAC: 30.0%	AAT: 100%	AAT: 100%	AAT: 100%	Asn: 100%	Asn: 100%	Asn: 100%	Asn: 100%	
530	Ts	T: 100%	T: 100%	T: 92.5% C: 7.5%	T: 100%	→ synonymous	65	GTT: 100%	GTT: 100%	GTT: 92.5% GTC: 7.5%	GTT: 100%	Val: 100%	Val: 100%	Val: 100%	Val: 100%	
551	Ts	T: 70.0% C: 30.0%	T: 100%	T: 100%	T: 100%	→ synonymous	72	TCT: 70.0% TCC: 30.0%	TCT: 100%	TCT: 100%	TCT: 100%	Ser: 100%	Ser: 100%	Ser: 100%	Ser: 100%	
577	Ts	G: 95.0% A: 5.0%	G: 100%	G: 100%	G: 100%	→ non synonymous	81	CGA: 95.0% CAA: 5.0%	CGA: 100%	CGA: 100%	CGA: 100%	Arg 95.0% Gln: 5.0%	Arg: 100%	Arg: 100%	Arg: 100%	Arg: 100%
581	Ts	A: 100%	A: 100%	A: 12.5% G: 87.5%	G: 100%	→ synonymous → G581 fixed as consensus in JKI-2000 isolate → detected as variable site by direct sequencing of the JKI-2000 RCA product	82	CCA: 100%	CCA: 100%	CCA: 12.5% CCG: 87.5%	CCG: 100%	Pro: 100%	Pro: 100%	Pro: 100%	Pro: 100%	
587	Ts	A: 70.0% G: 30.0%	A: 100%	A: 100%	A: 100%	→ synonymous	84	GGA: 70.0% GGG: 30.0%	GGA: 100%	GGA: 100%	GGA: 100%	Gly: 100%	Gly: 100%	Gly: 100%	Gly: 100%	
626	Ts	T: 80.0% C: 20.0%	T: 100%	T: 100%	T: 100%	→ synonymous	97	TAT: 80.0% TAC: 20.0%	TAT: 100%	T: 100%	TAT: 100%	Tyr: 100%	Tyr: 100%	Tyr: 100%	Tyr: 100%	
628	Tv	G: 100%	G: 100%	G: 100%	G: 97.6% T: 2.4%	→ non synonymous	98	GGC: 100%	GGC: 100%	GGC: 100%	GGC: 97.6% GTC: 2.4%	Gly: 100%	Gly: 100%	Gly: 100%	Gly: 97.6% Val: 2.4%	
635	Ts	C: 80.0% T: 20.0%	C: 100%	C: 100%	C: 100%	→ synonymous	100	TAC: 80.0% TAT: 20.0%	TAC: 100%	TAC: 100%	TAC: 100%	Tyr: 100%	Tyr: 100%	Tyr: 100%	Tyr: 100%	
646	Ts Tv	A: 55.0% G: 45.0%	G: 100%	G: 82.5% T: 17.5%	G: 100%	→ non synonymous → detected as variable site by direct sequencing of the JKI-2000 RCA product	104	AAG: 55.0% AGG: 45.0%	AGG: 100%	AGG: 82.5% ATG: 17.5%	AGG: 100%	Lys: 55.0% Arg: 45.0%	Arg: 100%	Arg: 82.5% Met: 17.5%	Arg: 100%	
649	Ts	C: 100%	C: 100%	C: 95.0% T: 5.0%	C: 100%	→ non synonymous	105	ACG: 100%	ACG: 100%	ACG: 95.0% ATG: 5.0%	ACG: 100%	Thr: 100%	Thr: 100%	Thr: 95.0% Met: 5.0%	Thr: 100%	
665	Ts	T: 55.0% C: 45.0%	C: 100%	C: 100%	C: 100%	→ synonymous	110	ATT: 55.0% ATC: 45.0%	ATC: 100%	ATC: 100%	ATC: 100%	Ile: 100%	Ile: 100%	Ile: 100%	Ile: 100%	
668	Ts	G: 65.0% A: 35.0%	G: 100%	G: 100%	G: 100%	→ synonymous	111	GAG: 65.0% GAA: 35.0%	GAG: 100%	GAG: 100%	GAG: 100%	Glu: 100%	Glu: 100%	Glu: 100%	Glu: 100%	
669	Tv	T: 90.0% G: 10.0%	T: 100%	T: 100%	T: 100%	→ non synonymous	112	TCT: 90.0% GCT: 10.0%	TCT: 100%	TCT: 97.5% TCC: 2.5%	TCT: 100%	Ser: 90.0% Ala: 10.0%	Ser: 100%	Ser: 100%	Ser: 100%	
671	Ts	T: 100%	T: 100%	T: 97.5% C: 2.5%	T: 100%	→ synonymous										
698	Tv	T: 65.0% C: 35.0%	T: 100%	T: 100%	T: 100%	→ synonymous	121	TAT: 65.0% TAC: 35.0%	TAT: 100%	TAT: 100%	TAT: 100%	Tyr: 100%	Tyr: 100%	Tyr: 100%	Tyr: 100%	
745	Ts	G: 100%	G: 100%	G: 100%	G: 97.6% A: 2.4%	→ non synonymous	137	AGT: 100%	AGT: 100%	AGT: 100%	AGT: 97.6% AAT: 2.4%	Ser: 100%	Ser: 100%	Ser: 100%	Ser: 97.6% Asn: 2.4%	
750	Ts	T: 100%	T: 100%	T: 97.5% C: 2.5%	T: 100%	→ non synonymous	139	TGT: 100%	TGT: 100%	TGT: 97.5% CGT: 2.5%	TGT: 100%	Cys: 100%	Cys: 100%	Cys: 97.5% Arg: 2.5%	Cys: 100%	
761	Ts	G: 55.0% A: 45.0%	A: 100%	A: 100%	A: 100%	→ synonymous	142	AAG: 55.0% AAA: 45.0%	AAA: 100%	AAA: 100%	AAA: 100%	Lys: 100%	Lys: 100%	Lys: 100%	Lys: 100%	
768	Ts	A: 100%	A: 100%	A: 100%	A: 97.6% G: 2.4%	→ non synonymous	145	ATT: 100%	ATT: 100%	ATT: 100%	ATT: 97.6% GTT: 2.4%	Ile: 100%	Ile: 100%	Ile: 100%	Ile: 97.6% Val: 2.4%	

904	Ts	T: 100%	T: 100%	T: 75.9% C: 24.1%	T: 100%	→ in CR-C-U1: same mutation was detected in Holetta-1997 isolate DNA-C at equivalent position (T913: 70.0% and C913: 30.0%) → detected as variable site by direct sequencing of the JKI-2000 RCA product
916	Ts	A: 68.4% G: 31.6%	A: 100%	A: 79.3% G: 20.7%	A: 100%	→ in CR-C-U1: the sequence with G is similar to that of DNA-C at equivalent position (G925) → detected as variable site by direct sequencing of the JKI-2000 RCA product
921	Ts	T: 100%	T: 100%	T: 96.6% C: 3.4%	T: 100%	
930	Tv	T: 100%	T: 100%	T: 96.6% A: 3.4%	T: 100%	

898-904	Rec	TGCTCTC: 100%	TGCTCTC: 100%	TGCTCTC: 65.4% AGTCTT: 34.6%	TGCTCTC: 100%	<ul style="list-style-type: none"> → in CR-M-U2: recombination event with Holetta-1997 isolate DNA-M 895-900 (AGTCTT: 100%) → in CR-M-U2: same mutations were detected in the JKI-2000 isolate DNA-M at equivalent position (895-900: AGTCTT: 22.2%, TGCTCTC: 77.8%) → in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2. Same mutations were detected in the Holetta-1997 isolate DNA-U4 at equivalent positions (766-772: GAGAGCA: 85.0%, AAGACT: 10.0%) and in the JKI-2000 isolate DNA-U4 at equivalent positions (766-772: GAGAGCA: 71.8%, AAGACT: 23.1%) → in CR-C-M-N-U1-U2: same mutations were detected in the Holetta-1997 isolate DNA-C at equivalent position (908-913: AGTCTC: 65.0%, AGTCTT: 30.0%, TGCTCTC: 5.0%) → in CR-C-M-N-U1-U2: same mutations were detected in the JKI-2000 isolate DNA-N at equivalent position (914-918: AGTCTC: 97.5%, AGTCTT: 2.5%, TGCTCTC: 2.5%) → detected as variable site by direct sequencing of the JKI-2000 RCA product
916	Ts	G: 100%	G: 100%	G: 100%	G: 95.0% A: 5.0%	
918	Tv	A: 100%	A: 100%	C: 100%	C: 100%	<ul style="list-style-type: none"> → in CR-M-U2: same mutations were detected in DNA-M at equivalent position (A914: 95.0%, C914: 5.0% in the Holetta-1997 and C914:100% the JKI-2000 isolate) → in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2 → in CR-M-U2-U4: same mutations were detected in the Holetta-1997 isolate DNA-U4 at equivalent position (G752:85.0%, T752: 15.0%)
919	Ts	T: 54.5% C: 45.5%	T: 100%	T: 100%	T: 100%	<ul style="list-style-type: none"> → in CR-M-U2: same mutations were detected in DNA-M at equivalent position (C915: 95.0%, T915: 5.0% in the Holetta-1997 and T915:100% the JKI-2000 isolate) → in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2 → in CR-M-U2-U4: same mutations were detected in the Holetta-1997 isolate DNA-U4 at equivalent position (A751:85.0%, G751: 15.0%)
920	Ts	G: 100%	G: 100%	G: 96.2% A: 3.8%	G: 100%	
932	Tv	T: 100%	T: 100%	T: 92.3% A: 7.7%	T: 100%	

752	Tv	G: 85.0% T: 15.0%	G: 100%	G: 100%	G: 100%	→ in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2 → in CR-M-U2-U4: same mutations were detected in DNA-M at equivalent position (A914: 95.0%, C914: 5.0% in the Holetta-1997 and C914:100% the JKI-2000 isolate) → in CR-M-U2: same mutations were detected in DNA-U2 at equivalent position (A918: 100% in the Holetta-1997 and C918: 100% the JKI-2000 isolate)
766-772	Rec	GAGAGCA: 85.0% AAGACT: 10.0%	GAGAGCA: 100%	GAGAGCA: 71.8% AAGACT: 23.1%	GAGAGCA: 100%	→ in CR-M-U2-U4: on DNA-U4 this region is inverted when compared to DNA-M and DNA-U2 → in CR-M-U2-U4: recombination event with DNA-M 895-900 → in CR-M-U2-U4: same polymorphisms were detected in the JKI-2000 isolate DNA-M at equivalent position (895-900: AGTCTT: 22.2%, TGCTCTC: 77.8%) → in CR-M-U2-U4: same mutations were detected in the JKI-2000 isolate DNA-U2 at equivalent position (898-904: AGTCTT: 34.6%, TGCTCTC: 65.4%) → in CR-C-M-N-U1-U2: same mutations were detected in the Holetta-1997 isolate DNA-C at equivalent position (908-913: AGTCTC: 65.0%, AGTCTT: 30.0%, TGCTCTC: 5.0%) → in CR-C-M-N-U1-U2: same mutations were detected in the JKI-2000 isolate DNA-N at equivalent position (914-918: AGTCTC: 97.5%, AGTCTT: 2.5%, TGCTCTC: 2.5%) → detected as variable site by direct sequencing of the JKI-2000 RCA product
766	Tv	G: 85.5%	G: 100%	G: 71.8% C: 2.6%	G: 100%	
768	Tv	G: 100%	G: 100%	G: 97.4% T: 2.6%	G: 100%	
770	Ts	G: 85.5% A: 5.0%	G: 100%	G: 71.8%	G: 100%	
806	Ts	T: 100%	T: 100%	T: 100%	T: 97.7% C: 2.3%	
831	Tv	T: 100%	T: 100%	T: 89.7% G: 10.3%	T: 100%	
832	Ts	C: 100%	C: 100%	C: 35.9% T: 64.1	T: 100%	→ T832 fixed as consensus in JKI-2000 isolate → detected as variable site by direct sequencing of the JKI-2000 RCA product
850	Ts	T: 100%	T: 50.0% C: 50.0%	C: 100%	C: 100%	→ C850 completely fixed as consensus in JKI-2000 isolate
858	Ts	A: 95.0% G: 5.0%	A: 100%	A: 100%	A: 100%	
859	Tv	T: 95.0% A: 5.0%	T: 100%	T: 100%	T: 100%	
903	Ts	A: 100%	A: 100%	A: 97.4% G: 2.6%	A: 100%	
937	Ts	T: 100%	T: 100%	T: 7.7% C: 92.3%	C: 100%	→ in CR-S-U4: C937 make the sequence similar to that of DNA-S at equivalent position (C940) → C937 fixed as consensus in JKI-2000 isolate