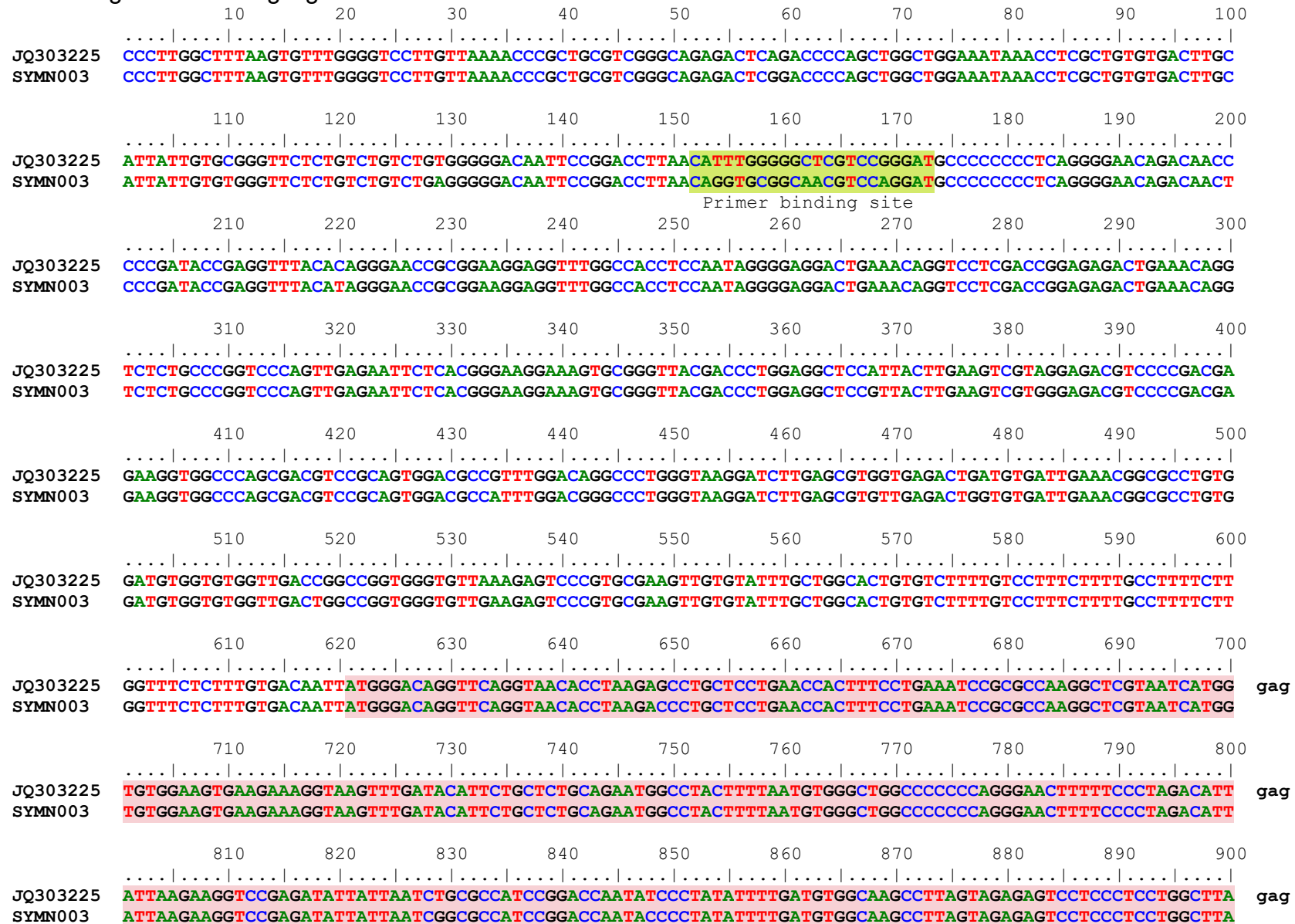


**Supplementary Figure S5:** Alignment of the *Rhinolophus ferrumequinum* retrovirus isolate RFRV (JQ303225) with RFRV-Kenya-SYMN003 (ON893141) characterized in the study. Retroviral gag-pol-env regions and primer binding site on the viral genome are highlighted.



[illegible]

	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	AAAGCCCCGGCCGTGTTTTTAGAACGCCCTCATGATGCTTATAGACAGTACACCCCGTTGGACCCCTCGCAGAGGAAAACCAAGTCGGCTGTAATTATGTC											gag
JQ303225	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	CTTTATAAACCAAGGCTGCCCGAGATATTAGGAAGAAATTGTACAAACAGGAGGGACTGGGAGAAATGCTATTCTGGGATTTAATGAAAGTAGCGGAGAGA											gag
JQ303225	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	GTCTTCAACACTCGAGAGACTCCCGAAGAAAGGGAGGATAGAAATTAGAAAAGAAAATCAGGAATTACAGGAACGAATCAGGAAGGAAGACAGAGAGCATC											gag
JQ303225	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	AGAGCAGGGAGAACAGGAGGCAGCAGAGGGAGATGGCCAAAGATCTTGTGGCAGGCGTGCAAAGCACAGTCAGGGTGGGACCGAGTCCGGCCGGACCAGC											gag
JQ303225	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	CCGACCGTGGAGACCGCGGCCCCGACTGGATAGGGGACAGTGTGCAAACTGCAAAAGAGTATGGACATTGGAAGAGGGAGTGCCCCAAGCGCCAGGGCCAA											gag
JQ303225	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	ACAGGGCAAGACGCACGGGTCTTGCTGGCGGGGATGGAGAGTGACTAGGGGAGACGGGACTCGGATCCCCTCCCCGAGTCTTGGGTAACTGCGTATGTGG											pol
JQ303225	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	AGGGGAAGCCAGTAGGATTCAATGGTAGACACAGGAGCCCAGTACTCAGTTTTGAATAAGCCTACAGAGCCCTTATCTCAGAAAACCAAGTTTGGTGCAAGG											pol
JQ303225	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	GGCAACTGGGTCCAAGGCTTATCGGTGGACTAGTAGGCGCAAGTGGACTTAGGCCGCCCAAGTGACCCACTCCTTCCAGTTATCCCTGAATGCCCT											pol
JQ303225	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700		
JQ303225	.... .... .... .... .... .... .... .... .... .... ....											
SYM003	GCCCCCTTATTGGGGCGCATCTCCTGACTAAGATCAGGGCTCAGATCCATTTTGAGCCGGATGGCATTAAAGCTATTGGATGGCCAAGGACAGCCCCCTCC											pol

	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	
JQ303225	ACATTTTGAACCTGTCTCTTGTGGATGAACATCGCCTGTTGCGCCCTGCAGGACAAACCCCTACAACCCCTCCCTCTACAGAATGGCCCCGTGATATGGATTAT										
SYM003	ACATTTTGAACCTGTCTCTTGTGGATGAACATCGCCTGTACGCCCTGCAGGACAAACCCCTACAACCCCTCCCTCTACAGAATGGCCCTGTGACATGGATTAT										
	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	
JQ303225	TTGGCTTAAACGTACCCCTCAGGCGTGGGCGGAAATAGCGGGTGTGGGCCGGGCGGCCCGCCGAGCACCAGTAGTGGTGGAACTTAAAGCCTCGGCCAG										pol
SYM003	TTGGCTTAAACGTACCCCTCAGGCGTGGGCGGAAATAGCGGGTGTGGGCCGGGCGGCCCGCAGAGCACCAGTAGTGGTCGAACTTAAAGCCTCGGCCAG										
	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	
JQ303225	CCTATCCGGATCCGCCAGTACCCCATGTCTGCAGAGGCGCGGAAAGGGATCGCCCCGCACATTAACCGTTTACTGGAAGCTGGAATACTGAAACCTTGCC										pol
SYM003	CCTATCCGGGTCCGCCAGTACCCCATGTCTGCAGAAGCGCGGAAAGGGATTGCCCCGCACATTAACCGTTTACTGGAAGCTGGAATACTGAAACCTTGCC										
	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	
JQ303225	ATTCTGCCGTGGAACACCCCACTTCTCCCCGTTAAGAAACCGGGGGGAAAAGATTATAGGCCAGTCCAGGACTTGAGGGAAGTGAATAAGAGGGTTGAAGA										pol
SYM003	ATTCTGCCGTGGAACACCCCACTTCTCCCCGTTAAGAAACCGGGGGGAAAAGATTATAGGCCAGTCCAGGACTTGAGGGAAGTGAATAAGAGGGTTGAAGA										
	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	
JQ303225	CATCCACCCCAACGGTCCCCAACCCCTTATACCTTACTAAGTCACCTTGCCCCCTTCACATGTCTGGTATACTACCTTAGACCTAAAGGATGCGTTTTTTAGC										pol
SYM003	CATCCACCCCAACGGTCCCCAACCCCTTATACCTTACTAAGTCACCTTGCCCCCTTCACATGTCTGGTATACTACCTTAGACCTAAAGGATGCTTTTTTTAGC										
	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	
JQ303225	ATAGCCCTGGCACCCAGCAGCCAACACATTTTTCCTTCGAATGGAATAATGGCAATACGGGAACCCCCGGGCAGCTGACCTGGACTAGACTACCGCAAG										pol
SYM003	ATAGCCCTGGCACCCAGCAGCCAACACATATTTGCTTCGAATGGAATGATGGCAATACAGGAACCCCCGGGCAGCTGACCTGGACTAGACTACCGCAAG										
	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	
JQ303225	GCTTCAAAACTCTCCAACCTCTGTTTAAATGAAGCCCTAAATCAGGATTTGGAATCGTTTCGCCAGAGCCATAATTCAGTTACGCTCCTGCAGTACGTAGA										pol
SYM003	GCTTCAAAACTCTCCAACCTCTGTTTAAATGAAGCCCTAAATCAGGATTTGGAATCGTTTCGCCAGAGCCATAATTCAGTTACGCTCCTGCAATACGTAGA										
	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	
JQ303225	TGACTTGCTTCTGGCGGCCCTCCGAAGCAGAATGCCGACAGGCCACTGGAGACCTCCTCCAGGAGCTGGGGCAGTTGGGCTATCGGGCCAGTGCAAG										pol
SYM003	TGACTTGCTTCTGGCGGCCCTCCGAAGCCGAATGCCGACAGGCCACTGGAGACCTCCTCCAGGAGCTGGGGCAGTTGGGCTATCGGGCAAGTGCAAG										
	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	
JQ303225	AAGGCTCAAAATATGCAGGCAAAACAGTCACCTACCTGGGGTATAAACTGAAAGAGGGAACCAAGATGGCTGACAGAGGCCATGAAAGAGACTATTCTTAGAC										pol
SYM003	AAGGCTCAAAATATGCAGGCAAAACATTCACCTACCTGGGGTATAAGCTGAAAGAGGGAACCAAGATGGCTGACTGAGGCCATGAAAGAGACTATTCTTAGAC										

	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	TTCCAGTCCCGACCTCAGCACGAGAGGTC	CGTGAGTTTTTAGGGACGACAGGCTACTG	CCGGCTGTGGATTTTGGGGTATGCTGAAATAGCAAAACCTCT								pol	
	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	GATGAGGCAACCAAGGATAAGGTCCCTTGGGCCTGGGGTCAGACCAACAGAAGGCC	TACGATGA	ACTCAAGGTCGCTCCTAAGAGCCCCGGCTCTG								pol	
	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	GCATTGCCAGACCCCTGAAGCCCTTCACTCTCTTTGTTGATGAGAGGAGGGGAATAGCGAAAGGAGTGCTAATGCAGCGTCTGGGGCCCTGGAACGTC											pol
	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	CGGTTGCCATTTATCCAAGAAGCTAGATCCAGTTGCAGCAGGATGGCCCCGTGCTTAAGGATCATTTGCGGCAGTAGCCCTAATGGTGAAGGATGCTGA											pol
	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	TAAACTCACTTTTGGGCAACATCTGAAGGTAGTGACCCCCCATGCGATCGAGGGGGTCCTGAAATATCCCCCTGGTAGGTGGATGACTAATGCCCGACTA											pol
	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	ACGCATTACCAAGGACTCTTGCTAGATGCACCCCGGATCATCTTCGCTGAACCCACCGCTCTGAATCCAGCCACCTGCTGCCGACCCCGGATCTGAGAG											pol
	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	CTCCCCTGCGATGATTGCCAAGAGATCATGGCAGAAGTCACCCAGGTGCGCCCCGACCTCCAGGACACCGCACTACCCAACAGTGAGTTGGTATGGTACAC											pol
	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	TGATGGAAGCAGCTTCGTTATAGATGGTGTGCGGAGGGCAGGCGCAGCGGTGGTAGACCAAGGGGGAACATCATTTGGAGTGCTTCGCTTTCCCCGGGG											pol
	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500		
JQ303225	.... .... .... .... .... .... .... .... .... .... .... ....											
SYMN003	ACATCAGCACAGAAGGCCGAAC	TGATCGCGCTGGCGGAGGCGCTGGAACGGGCCGAAGGGAGACGAGTGACTGTCTACACCGATAGCCGCTACGCCTTTG								pol		

	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	GCACTGTCCATGTGCATGGCGCCATCTACCGGGAAAGAGGCTTTGTTACAGCGGAAGGAAAGGCTCTGCGCAATCTTCCTGAGGTACGAAGACTACTGAT										pol
	GCACTGTCCATGTGCATGGCGCTATCTACCGGGAAAGAGTCTTTGTTACAGCGGAAGGAAAGACTCTGCGCAATCTTCCTGAGGTACGAAGACTGCTAAT										
	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	GGCCGTGCAAAATGCCCGGGCAGTCGCAGTTGTCCACATCCCTGGGCACCAGTCTGCCAGACCCCGGAAGCTGAAGGAAACCGGCAGCGGATGAAGCC										pol
	GGCTGTGCAAAATGCCCGGGCGGTTCGCAGTTGTCCACATCCCTGGGCACCAGTCTGCACAGAGCCCAAGCTGAAGGAAACCGGCAGCGGATGAAGCC										
	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	GCCAAGACAGCGGCAGTAGCTTCATCAGCTTTAGCACTCACCCCTGCCACACCCGAGCTCCCTCGCCTGCCCGCGACCTGACTACACTCCGAAGACC										pol
	GCCAAGGCAGTGGCAGTAGCTTCATCAGCTTTAGCACTCACCCCTGCCACACCCGAGCTCCCTCGCCTGCCCGCGACCTGACTACACTCCGGAAGACC										
	4810	4820	4830	4840	4850	4860	4870	4880	4890	4900	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	TGCGATGGATCCAGAACCACCACTGCCCGGAATCTGATCAGCAGGGGTGGCATCGGGATACAGAAGGAAGATTGATACGCGGGCACAGCTAGACTGTTT										pol
	TGCGATGGATCCAGAACCACCACTGCCCGGAATCTGATCAGCAGGGGTGGCGTCGGGATACAGAAGGAAGATTGATACGCGGGCACAGCTAGACTGTTT										
	4910	4920	4930	4940	4950	4960	4970	4980	4990	5000	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	CTTCTCTCCAACCTGCATCAAGCCACCCACTTAGGAAAAAAGAAGTTGCTGACAATTCTCGAGTCCGCCCGCCTCCGGTTTCCCCGACAAGCGGCTCAGA										
	CTTCTCTCCAACCTGCATCAAGCCACCCACTTAGGAAAAAAGAAGTTGCTGACAATTCTCGAGTCCGCCCGCCTCCGGTTTCCCCGACAAGCAGCTCAGA										
	5010	5020	5030	5040	5050	5060	5070	5080	5090	5100	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	TTCAAGAGATTGTAGATCAGTGCATTGGGTGCCAGGCTATGAGACCCAGTAGGAAAGGACCCCAACATACAGGTACGAGGGTACGGGGAAGAGCGCCGGG										
	TTCAAGAGATTGTAGATCAGTGCATTGGGTGCCAGGCTATGAGACCCAGTAGGAAAGGACCCCAACATACAGGTACGAGGGTACGGGGAAGAGCGCCGGG										
	5110	5120	5130	5140	5150	5160	5170	5180	5190	5200	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	ACGGAATTGGGAAGTGGATTTTACTGAGGTAAAGCCTGGGAGGTATGGGTATAAGTACTTGCTAGTAATGGTTGACACATTTTCGGGCTGGGTGGAAGCC										
	ACGGAGTTGGGAAGTGGATTTTACGGAGGTAAAGCCTGGGAGGTATGGGTGTAAGTACTTGCTAGTAATGGTTGACACATTTTCTGGCTGGGTGGAAGCC										
	5210	5220	5230	5240	5250	5260	5270	5280	5290	5300	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	TTCCCCACGAAACGGGAGACTGCCCAAGTGGTTGCTAAGGCATTACTAGAAGAAATTAATCCAGATATGGGGTTCTGAGGTTTTAGGCTCCGATAACG										
	TTCCCCACGAAACGGGAGACTGCCCAAGTGGTTGCTAAGGCATTACTAGAAGAAATTAATCCAGATATGGGGTTCTGAGGTTTTAGGTTCCGATAACG										
	5310	5320	5330	5340	5350	5360	5370	5380	5390	5400	
JQ303225	..... ..... ..... ..... ..... ..... ..... ..... ..... ..... .....										
SYM003	GCCCAGCTTTTCATCAGTAACGTCTCTACAGGGACTAGCCCCGGCGATAGGGATCAATTGGAAGTTACATTGTGAATATAATCCCCAGAGCTCAGGGCAGGT										
	GCCCAGCTTTTCATCAGTAACGTCTCTACAGGGACTAGCCCCGAGCGATAGGGATCAATTGGAAGTTACATTGTGAATATAATCCCCAGAGCTCAGGGCAGGT										

	5410	5420	5430	5440	5450	5460	5470	5480	5490	5500	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	AGAGAGAATGAATCGGACTCTAAGAGGAGACCTTTGTCCAAACTAGCCATCGAGACTGGCGGGGACTGGGTGACCCCTTTACCCATGCCATCTTCCGGG										
	5510	5520	5530	5540	5550	5560	5570	5580	5590	5600	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TCCGGAATCACCATATGTACATGGTTTGACACCTTCGAAATTCTGTATGGGGCACCACCCCCATTATTGTTCTACTCTACCAGATCATGACCCCAA										
	5610	5620	5630	5640	5650	5660	5670	5680	5690	5700	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TGTGGCCCCAAGTTATCTGGCCAGTTTAAAGGCCCTACAGGGGTCCAAACATGAGATATGGCCCCCTAGTGAGTTCCCTGTATGAAATTAAGGACGCCCCG										
	5710	5720	5730	5740	5750	5760	5770	5780	5790	5800	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	AACCCGGAACATGGCATCGTTCCAGGGGATTGGGTATGGGTAAGGAGACACAGGTCCCGGACACTGGAGGAAAGATGGAAAGGTCCTTATGTGGTTATTCT										
	5810	5820	5830	5840	5850	5860	5870	5880	5890	5900	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TGGTTACCCCCACTGCCTTAAAGGTTGACGGCATTGGGCCCTTGGGTCCATCACTCTCACGTGCGCCGAGCCAGCCAGCTGGAGAAGACGCAAGCTAAGGA										
	5910	5920	5930	5940	5950	5960	5970	5980	5990	6000	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GTGGATCGTACGGCGACACCCCTGATAACCCCTCTGAAGCTGCAGCTCTCCCACCTCGGGGAAGCGTCAAGCCCCCTGCCTCAGCTAACGATGGAATGGTT										
	6010	6020	6030	6040	6050	6060	6070	6080	6090	6100	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GCTAGCCCTAACTCTGCTCAACATCTGGGAGAAGAGCCACGCGGGGATCAACCCACACCAACCCCATAGCTAACATGGACCCCTAACAGATGGACAGACC										
	6110	6120	6130	6140	6150	6160	6170	6180	6190	6200	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CAAAACAACCCCTTAATAGCACCAACATACATGCCCCCATCAATACGTGGTGGCCAGATTTGTTTTTCGACCTGCGTGACATTTTCGGCACATAAAGCTGGAC										
	6210	6220	6230	6240	6250	6260	6270	6280	6290	6300	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GGCAGTATGACTACTCAGTCAGGTCCAAGCGGGCTGTAAATTGACACCTCTCAAGGACATAGTGCACAAGGGTTTTGGGCCCTGCCAGGGAACCTAAGAAA										

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	6310	6320	6330	6340	6350	6360	6370	6380	6390	6400	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CAATTGGAAAACTGTGGCGGCCAGACCGCTACTATTGTGGTAGTTGGAGTTGTGTCACCTCCAATGACGGGCCCGACAGTGGGACGTTGGGAACAGG										
	6410	6420	6430	6440	6450	6460	6470	6480	6490	6500	env
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GATCTAGTCAAATTCTCCTTAGGGACCCCCCTCAACCAGGTACCCCAGGTACGTGTCCAAATTAACCAAGACGCGGCACGAAAAGAGCGTGGTTGGTTAT										
	6510	6520	6530	6540	6550	6560	6570	6580	6590	6600	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CAGGATTAACTTGGGGGTTCCAATTAGATATAGGCCGTTGGGCATGGATAGGCCCCCCACCCCCGGCGGTCTCCTAACTATTCGACTATCGGTTCGAAACGAT										
	6610	6620	6630	6640	6650	6660	6670	6680	6690	6700	env
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CAGCACTCAGGTGGGTCCAAATAAGGTACTGGCTCCTCTCGTCCCTACCAAGAACCAGGTATATCAAGGGATAAGGACACCACAGGAAGGATCGCGGGA										
	6710	6720	6730	6740	6750	6760	6770	6780	6790	6800	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	ACCCAGCCAAAGACCTCTGTAACTCCTTCGACACCTGTACGCAGACAACCGAAGACTCATTTGCGGAACTGGTGCGCACTGTATACGAGACCCCTTAATG										
	6810	6820	6830	6840	6850	6860	6870	6880	6890	6900	env
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CCACCAGTCCCTCACCTCACACCTCCTGTTGGCTGTGCTATGATGTAAAGCCCCCGTTCTATGAGGCAATAGGACTTAATGCCACTTACAACGCCTCTAA										
	6910	6920	6930	6940	6950	6960	6970	6980	6990	7000	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CGGTAAAGAACCCCTTCTCAGTGTTCATGGGGGATCGTAAAAATTGGCTTAACCCCTGCAACTAGTGAGCGGCAATGGGACCTGTCTAGGGAAGGTGCCCCAG										
	7010	7020	7030	7040	7050	7060	7070	7080	7090	7100	env
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GCTAAACAAAGTTTATGTGCCTCCATAGACAGCTCCCCTAGTTGGAAAAAGTGACACTAAGTGGTTAATCCCCAGAAGTGTATGGATGGTGGATATGTTCAA										
	7110	7120	7130	7140	7150	7160	7170	7180	7190	7200	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	AGACTGGCCTCACCCCGTGCCTATCTACCTCGGTCTTTAATGCCGCCAATGAATTCTGTGTCCTAGTAACTGTGCTGCCCGCATCCTCTATCACCCCTGA										



	7210	7220	7230	7240	7250	7260	7270	7280	7290	7300	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GGAGAGTATGTATTTCGCATTGGGATAGTGACACAAGTACGAGAAGTAAAGAGAGCCCATCACCGCCTAACCATTTGCCACCTGTTTCAGTTTGAGAATA										
	7310	7320	7330	7340	7350	7360	7370	7380	7390	7400	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GCCGGAGCTGGGACCCGGCATAGCGTCCCTGGCTACTCAACAATCAGGCATAACCTCCCTAAGGGCGGCCATAGATGAGGACATAGAAAGTTGGAACCT										
	7410	7420	7430	7440	7450	7460	7470	7480	7490	7500	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	CGATTAGTCATTTAGAGAAGTCGCTCACCTCTCTATCCGAGGTAGTACTCCAGAATAGAAGAGGACTTGATTTGTTGTTCTCCAACAAGGGGGACTGTG										
	7510	7520	7530	7540	7550	7560	7570	7580	7590	7600	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TGTCGCGCTAGGGGAGGAATGTTGTTTTTATGCTGACCATACTGGTGTAGTAAAAGAAATCCATGGCAAAGGTGAGAGAAGGGTTAGCTAAGAGAAAACGG										
	7610	7620	7630	7640	7650	7660	7670	7680	7690	7700	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	GAAAGGGAAGCTCAGGAGAACTGGTTTGAGGCTTGGTTTAAATAGATCCCCCTGGCTCACCACCTTAGTATCTACCTTAGTGGGCCCGGTTATCTTGCTGG										
	7710	7720	7730	7740	7750	7760	7770	7780	7790	7800	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TGCTTATTTTAACTTTGGCCCTTGCAATTTGAACAAGCTTATTAATTTTGTGAAAGATCGTGTTAATACTGTCCAGCTCATGGTCCTAAGACAACAGTA										
	7810	7820	7830	7840	7850	7860	7870	7880	7890	7900	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TGAGACAGTGCCCACCCGCGAGGACCTCTACGGCTGGCCCGTACATGAGCAAGATTCCCTCATTATGAACAACAACCGCGGGGAAATGTAAGAGACCTTT										
	7910	7920	7930	7940	7950	7960	7970	7980	7990	8000	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	AGCATGAGAACTGCTATCTTAAGGTGAGGCTTAACAGCCCCTAGCCTGAAACAACCTAATTGTAAATTGTAAGAGACCTTAGCATGAGAACTGCTATCT										
	8010	8020	8030	8040	8050	8060	8070	8080	8090	8100	
JQ303225	.... .... .... .... .... .... .... .... .... .... ....										
SYMN003	TAAAGTCAGGGTTAAACAGCCCCTAGCCTGAAACAACCTAATTGTAAATTCAGGATGTGGGCAGTTGCAGCACGGAGACCGAGAAGTCCTGTAGCTTATC										

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	8110	8120	8130	8140	8150	8160	8170	8180	8190	8200	
	.... .... .... .... .... .... .... .... .... .... .... .... .... .... ....										
JQ303225	TTATA	-----	CTCCTTGT	CCTGTAGT	TAAATCTT	TACTCTTT	GAACTATG	TAAGTCCT	GTAGTTTAT	CTTATACT	CCTTGAAGCTATGTAAGTCCT
SYMN003	TTATACTCCT	GGTCTCCT	TGTCTGTAGT	TAAATCTT	TACTCTTT	GAACTATG	CAAGTCCT	GTAGTTTAT	CTTATACT	CTTTGAAGCTATGCAAGTCCT	

	8210	8220	8230	8240	8250	8260	8270	8280	8290	8300
	.... .... .... .... .... .... .... .... .... .... ....									
JQ303225	GTAGTTTATC	TTGTACTCT	CTGAAGCTAT	GGAAAATTACT	GAGTGCCTT	GAAAATGCTAT	ATAAACCCTT	GGCTTTAAGT	TTTGGGGT	CCTTGTTAAAA
SYMN003	GTAGTTTATC	TAGTACTCT	CTGAAGCTAT	GGAAAATTACT	GAGTGCCTT	GAAAATGCTAT	ATAAACCCTT	GGCTTTAAGT	TTTGGGGT	CCTTGTTAAAA

	8310	8320	8330	8340	8350	8360	8370	8380	8390
	.... .... .... .... .... .... .... .... .... .... ....								
JQ303225	CCCGCTGCGT	CGGGCAGAGACT	CGGACCCCAGCT	GGCTGGAAATAAACCT	CGTTGTGTGACT	TGCAAAAAATA	AAAAAAAAAAAAAAAAAAAAAAAAAAAA		
SYMN003	CCCGCTGCGT	CGGGCAGAGACT	CGGACCCCAGCT	GGCTGGAAATAAACCT	CGTTGTGTGACT	TGCA-----			