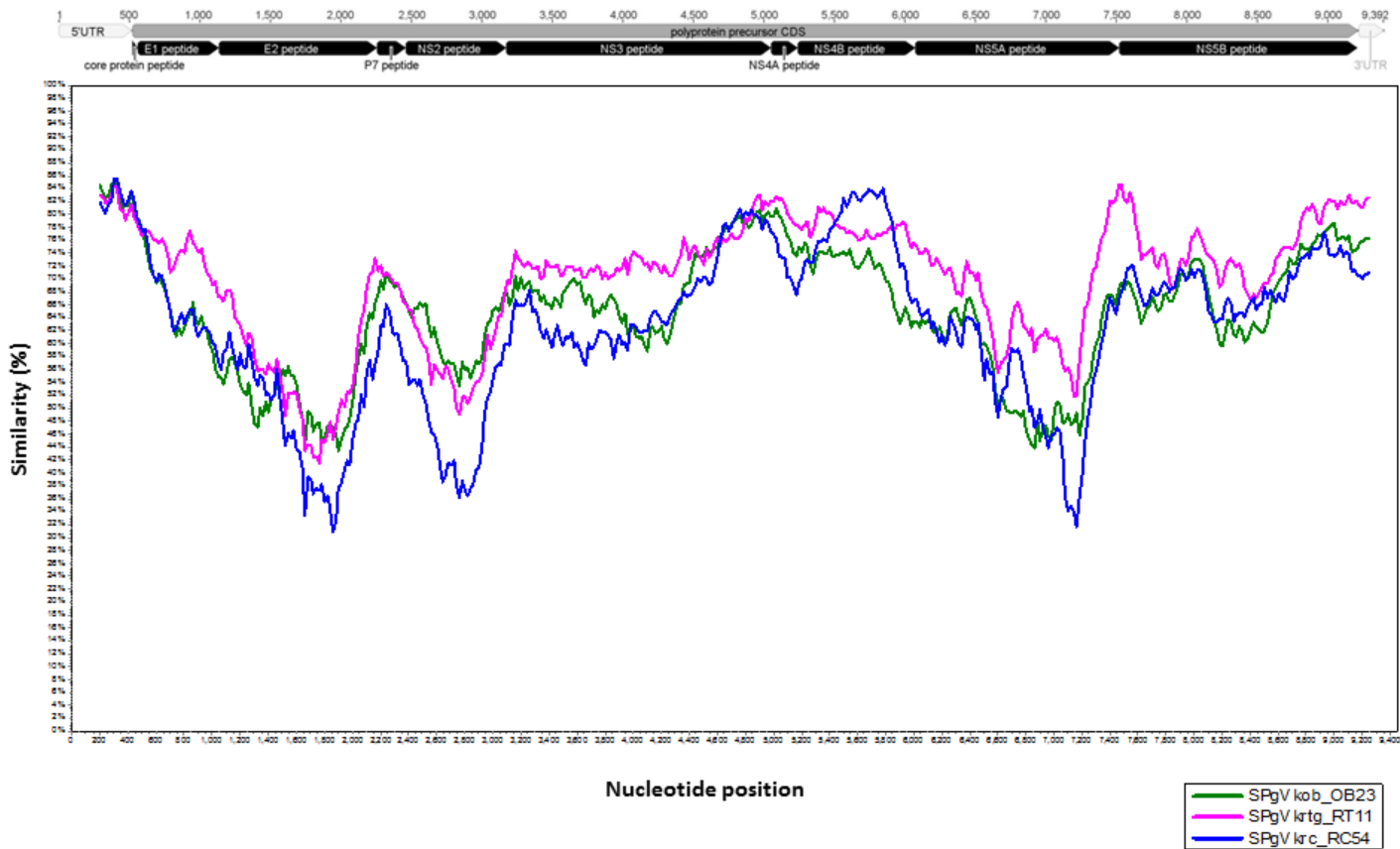
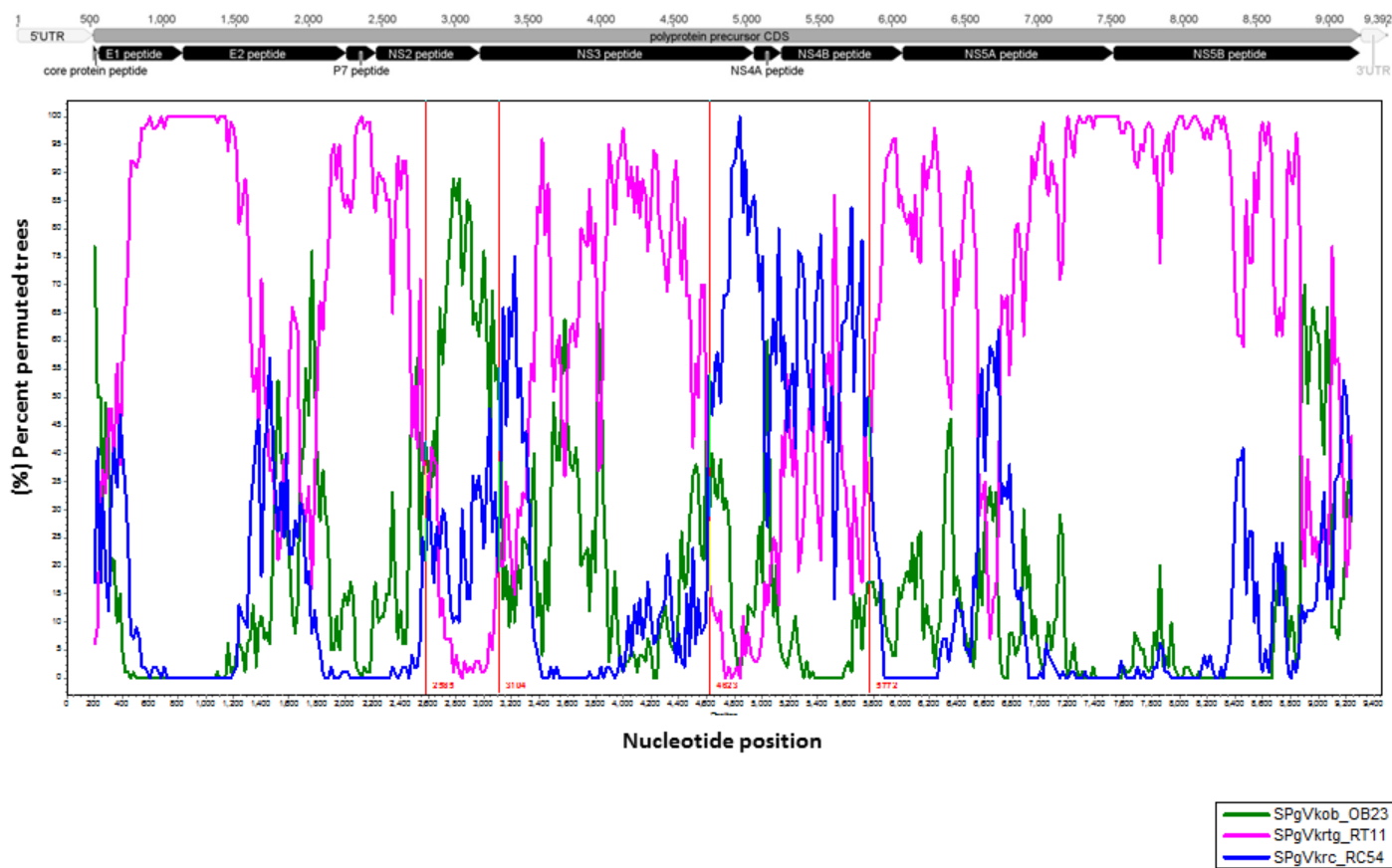


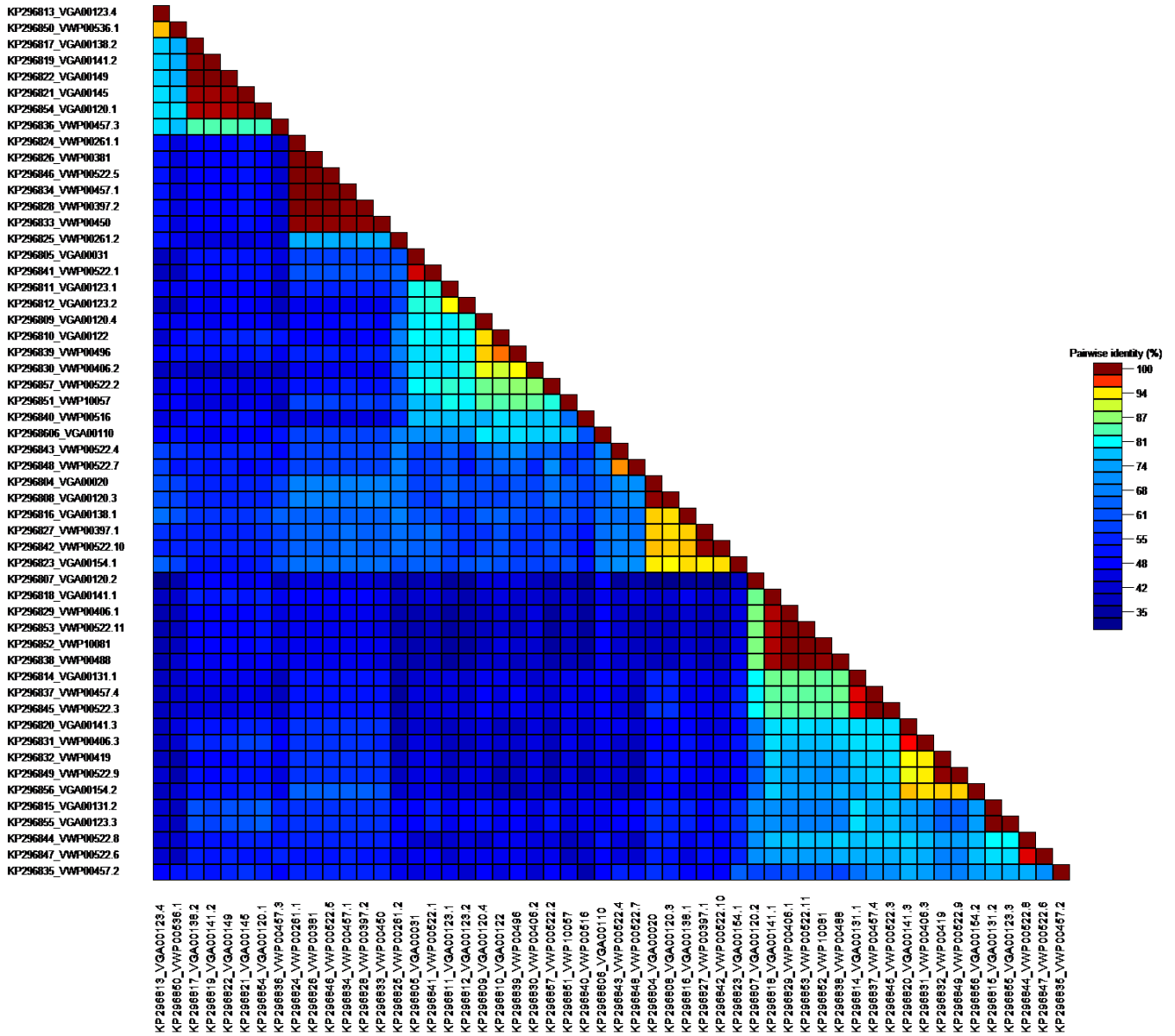
**Figure S1.** Satellite map of Gambia and the Caribbean (St. Kitts, Nevis) depicting the collection sites for samples used in this study.



**Figure S2.** Sequence similarity plots based on entire genome of Gambian SPgVgm\_VGA00020 genome against 3 related genomes from Old World Monkeys in Uganda: isolate SPgVkob\_OB23 from olive baboon (*Papio anubis*), GenBank Accession No. KF234530; SPgVkrtg\_RT11 from red tailed guenon (*Cercopithecus ascanius*), GenBank Accession No. KF234529; SPgVkrc\_RC54 from red colobus monkey (*Piliocolobus tephrosceles*) GenBank Accession No. KF234520.



**Figure S3.** Bootscan analysis with SPgVagm\_VGA00020 as a query sequence. The analysis was done with a sliding window of 400 nt and a step size of 20 nt. The y-axis shows the percentage of the permuted tree in which the selected SPgV strains cluster with the query sequence. Recombination breakpoints were detected around genome positions 2585 and 3104. The potential recombination partner is SpgVkob\_OB23 isolate (olive baboon). The second breakpoint was detected around positions 4623 and 5772, with SPgVkrc\_RC54 (red colobus monkey) as recombination partner. All nucleotide positions are relative to SPgVkrc\_RC54 reference genome (GenBank Accession No. KF234520).



**Figure S4.** Color coded pairwise identity matrix generated from the partial ORF1 (positions 410-657aa, relative to GenBank reference: AB017610). Each colored cell represents a percentage identity score between two sequences.

	KP296841_V...	KP296842_V...	KP296843_V...	KP296844_V...	KP296845_V...	KP296846_V...	KP296847_V...	KP296848_V...	KP296849_V...	KP296853_V...	KP296857_V...
KP296841_VWP00522.1		44%	43%	37%	37%	44%	37%	42%	38%	34%	58%
KP296842_VWP00522.10	44%		47%	39%	37%	46%	39%	47%	38%	34%	43%
KP296843_VWP00522.4	43%	47%		37%	37%	44%	36%	82%	37%	36%	45%
KP296844_VWP00522.8	37%	39%	37%		54%	41%	94%	35%	50%	53%	35%
KP296845_VWP00522.3	37%	37%	37%	54%		41%	52%	35%	54%	63%	36%
KP296846_VWP00522.5	44%	46%	44%	41%	41%		41%	44%	43%	38%	40%
KP296847_VWP00522.6	37%	39%	36%	94%	52%	41%		36%	48%	51%	36%
KP296848_VWP00522.7	42%	47%	82%	35%	35%	44%	36%		34%	35%	47%
KP296849_VWP00522.9	38%	38%	37%	50%	54%	43%	48%	34%		50%	34%
KP296853_VWP00522.11	34%	34%	36%	53%	63%	38%	51%	35%	50%		33%
KP296857_VWP00522.2	58%	43%	45%	35%	36%	40%	36%	47%	34%	33%	

**Figure S5.** Identity plot generated from multiple alignment of partial ORF1 sequence (247 aa). The 11 anellovirus sequences used , were derived from a single plasma sample (VWP00522).

	KP296857_V...	KP296856_V...	KP296855_V...	KP296853_V...	KP296854_V...
KP296857_VWP00522.2		45%	42%	45%	40%
KP296856_VGA00120.1	45%		46%	48%	44%
KP296855_VWP00522.11	42%	46%		58%	53%
KP296853_VGA00123.3	45%	48%	58%		52%
KP296854_VGA00154.2	40%	44%	53%	52%	

**Figure S6.** Nucleotide identity plot of five full genome anelloviruses sequenced from African green monkeys. VGA is the code for Gambian samples; VWP is for Caribbean samples.



Sample ID	Total number of reads	Number of contigs or reads to blast virus RefSeq	Number of sequences hit virus	Number of virus hits passed NVNR filter
VGA00001	160518	51412	304	72
VGA00010	213054	60641	358	184
VGA00100	221970	53145	431	422
VGA00101	213118	63925	370	50
VGA00102	17354	9241	78	6
VGA00107	192466	63382	341	43
VGA00108	511296	35208	2891	1860
VGA00109	859244	49514	1168	636
VGA00110	1039024	59740	2299	1242
VGA00119	53480	5210	35	14
VGA00012	258532	72419	350	137
VGA00120	935148	87529	4045	2255
VGA00122	1064696	74594	1286	488
VGA00123	1361876	115018	4064	2392
VGA00128	392916	13563	9	4
VGA00129	751976	53464	768	233
VGA00130	1349668	103912	1165	114
VGA00132	1320880	106599	1117	152
VGA00135	531828	42758	561	206
VGA00138	920732	70820	2354	1357
VGA00141	881500	91721	4351	2230
VGA00145	335232	40372	817	415
VGA00147	522772	50516	573	250
VGA00149	456520	41939	1665	1000
VGA00154	274080	20941	829	473
VGA00155	305796	25868	454	149
VGA00017	197740	67714	338	108
VGA00019	277456	73949	897	806
VGA00002	189318	55071	290	62
VGA00020	147794	48029	1223	1455
VGA00131	1149460	82315	2411	1227
VGA00025	126898	36842	264	239
VGA00026	130662	47564	295	46
VGA00028	18782	5855	22	2
VGA00003	113350	37125	435	323
VGA00031	139180	41885	667	609
VGA00004	181900	47607	251	165
VGA00040	184502	48692	246	37
VGA00041	93958	23910	213	202
VGA00042	29796	10069	47	6
VGA00096	268732	137047	510	57
VGA00098	205152	55738	549	457
VGA00099	93458	26214	167	149
VWP10010	185208	51692	237	27
VWP10019	136202	36376	106	17
VWP00204	215886	63680	388	134
VWP00224	157218	37481	79	23
VWP00232	190960	52823	272	75
VWP10025	154234	39029	139	37
VWP00261	291958	66714	228	87
VWP00305	248362	72313	303	76
VWP10031	128742	26169	2	1
VWP00328	184852	45759	180	55
VWP00334	118146	32939	150	39
VWP00359	184162	46874	177	31
VWP10036	274372	84662	456	156
VWP00374	245290	69267	264	85
VWP00376	334976	82340	260	67
VWP00381	259268	71698	728	574
VWP00384	999800	58034	521	158
VWP00386	1141116	119960	3144	295
VWP00397	1222748	81797	2570	940
VWP00405	809876	46688	399	124
VWP00406	1768100	109277	3742	1999
VWP00407	1156044	86266	1774	781
VWP00419	1542292	105784	1310	294
VWP00431	1341232	46552	126	64
VWP00437	1412964	86749	581	26
VWP00449	1170640	85371	545	32
VWP10045	156932	49130	271	135
VWP00450	1081232	73402	889	339
VWP00457	1098988	66912	3169	1970
VWP00465	704740	54962	569	61
VWP00466	382952	31203	431	139
VWP00474	1082608	85863	1402	511
VWP10048	353810	72923	83	18
VWP00488	1037500	88049	1578	570
VWP00496	537732	46403	1364	710
VWP10050	290360	73405	213	86
VWP00516	292808	23684	1420	894
VWP00518	1232040	41038	136	73
VWP00522	1389000	120456	5285	3134
VWP00536	914084	127160	4625	1825
VWP10057	290814	71736	912	734
VWP10064	93212	32861	231	59
VWP10081	188600	51552	534	454
VWP10009	273534	71416	256	92
<b>Total</b>	<b>45969408</b>	<b>5197526</b>	<b>83557</b>	<b>40335</b>

**Table S2.** Number of sequencing reads and virus specific sequences and hits generated during deep sequencing on MiSeq Illumina platform.



	All other Alpha	Infants, Japan/China	Japanese macaques	Gambia												Caribbean													
				VGA00110	VGA00120.1	VGA00120.2	VGA00120.3	VGA00123.3	VGA00123.4	VGA00138.2	VGA00141.1	VGA00141.2	VGA00145	VGA00149	VGA00154.2	VWP00406.1	VWP00457.2	VWP00457.4	VWP00496	VWP00516	VWP00522.10	VWP00522.11	VWP00522.2	VWP00522.3	VWP00522.4	VWP00522.7	VWP00522.9	VWP00536.1	
All other Alpha																													
Infants, Japan/China	30%	51%																											
Japanese macaques	26%	33%	33%																										
Gambia																													
Caribbean																													

**Table S3.** Percentage amino acid identity plotted across the alignments of complete ORF1 sequences (64-697 aa, relative to TTV1, isolate TA278) from Gambia (n=12) and the Caribbean (n=13) including other members of Alphatorquevirus genus. Different groups are represented by multiple species derived from the GenBank: All other Alpha (BAA25131 Torque teno virus 1, isolate TA278), Chinese and Japanese infants (YP\_003587845 Torque teno virus 27, BAA93583 Torque teno virus 29), and Japanese macaques (YP003587873 Torque teno virus 25, YP003587859 Torque teno virus 26).

		All other Alpha	Infants, Japan/China	Japanese macaques	Gambia										Caribbean																	
					VGA00110	VGA00120.1	VGA00120.2	VGA00120.3	VGA00123.3	VGA00123.4	VGA00138.2	VGA00141.1	VGA00141.2	VGA00145	VGA00149	VGA00154.2	VWP00406.1	VWP00457.2	VWP00457.4	VWP00496	VWP00516	VWP00522.10	VWP00522.11	VWP00522.2	VWP00522.3	VWP00522.4	VWP00522.7	VWP00522.9	VWP00536.1			
All other Alpha		55%																														
Infants, Japan/China		56%	43%																													
Japanese macaques		60%	55%	56%																												
	VGA00110	61%	55%	55%	56%																											
	VGA00120.1	62%	56%	56%	59%	56%																										
	VGA00120.2	59%	56%	53%	48%	55%	55%																									
	VGA00120.3	61%	58%	57%	59%	57%	48%	55%																								
	VGA00123.3	62%	54%	56%	57%	51%	45%	53%	48%																							
	VGA00123.4	61%	58%	56%	57%	58%	57%	54%	49%	55%																						
	VGA00138.2	61%	55%	55%	49%	55%	45%	49%	48%	43%	57%																					
	VGA00141.1	60%	55%	55%	52%	54%	46%	25%	46%	43%	55%	38%																				
	VGA00141.2	62%	60%	58%	62%	59%	49%	56%	29%	48%	50%	48%	46%																			
	VGA00145	60%	55%	55%	52%	55%	46%	25%	46%	43%	55%	38%	1%	47%																		
	VGA00149	60%	56%	55%	52%	55%	46%	25%	46%	43%	54%	38%	3%	46%	4%																	
	VGA00154.2	60%	56%	55%	52%	55%	46%	25%	46%	43%	54%	38%	2%	46%	2%																	
Gambia	VGA00154.2	60%	56%	58%	58%	59%	58%	57%	49%	57%	51%	57%	57%	49%	57%	57%																
	VWP00406.1	61%	60%	59%	62%	60%	48%	57%	29%	48%	50%	49%	47%	6%	47%	47%	47%	47%	49%													
	VWP00457.2	61%	57%	58%	60%	59%	49%	55%	40%	47%	50%	47%	45%	41%	45%	44%	44%	52%	40%													
	VWP00457.4	59%	57%	56%	61%	57%	48%	56%	34%	45%	50%	47%	47%	33%	46%	46%	47%	48%	32%	37%												
	VWP00496	62%	56%	56%	59%	57%	39%	55%	48%	44%	57%	46%	46%	48%	46%	46%	46%	57%	49%	47%	46%											
	VWP00516	61%	57%	56%	59%	57%	41%	54%	50%	45%	57%	45%	45%	49%	45%	46%	46%	58%	49%	50%	47%	39%										
	VWP00522.10	61%	54%	55%	56%	52%	44%	54%	47%	24%	55%	42%	43%	47%	44%	43%	44%	56%	48%	47%	46%	46%	45%									
	VWP00522.11	61%	58%	60%	60%	59%	55%	55%	40%	55%	50%	55%	54%	24%	54%	55%	54%	49%	23%	49%	44%	55%	55%	56%								
	VWP00522.2	59%	54%	56%	57%	57%	52%	55%	60%	56%	57%	56%	56%	59%	56%	56%	58%	60%	60%	59%	58%	46%	51%	55%	58%							
	VWP00522.3	59%	57%	56%	60%	57%	48%	56%	34%	45%	49%	47%	47%	33%	46%	46%	47%	48%	32%	37%	1%	46%	46%	46%	43%	58%						
	VWP00522.4	61%	56%	56%	57%	55%	39%	55%	47%	41%	56%	43%	44%	49%	45%	45%	45%	58%	48%	47%	46%	38%	40%	43%	56%	53%	46%					
	VWP00522.7	62%	56%	55%	57%	55%	37%	54%	47%	43%	56%	44%	44%	49%	44%	45%	45%	58%	48%	48%	46%	39%	41%	44%	55%	53%	46%	16%				
	VWP00522.9	61%	58%	59%	61%	58%	49%	58%	41%	47%	51%	49%	49%	38%	49%	49%	49%	40%	38%	41%	38%	47%	48%	46%	48%	60%	38%	48%	49%			
Caribbean	VWP00536.1	62%	56%	55%	50%	55%	45%	49%	48%	44%	57%	19%	37%	47%	37%	37%	37%	57%	48%	46%	47%	46%	45%	42%	54%	57%	47%	45%	43%	49%		

**Table S4.** Color coded nucleotide distance matrix generated from complete ORF1 (positions 713-2775 nt), relative to GenBank reference: AB017610 (TTV1, isolate TA278). Divergence of >56% defines new genera, >35% is a demarcation for a new species.