

**Supplementary Figure S1. Pairwise comparisons of CsRV1 concatenated whole genome based on nucleotide sequences (top) and amino acid sequences (bottom).**

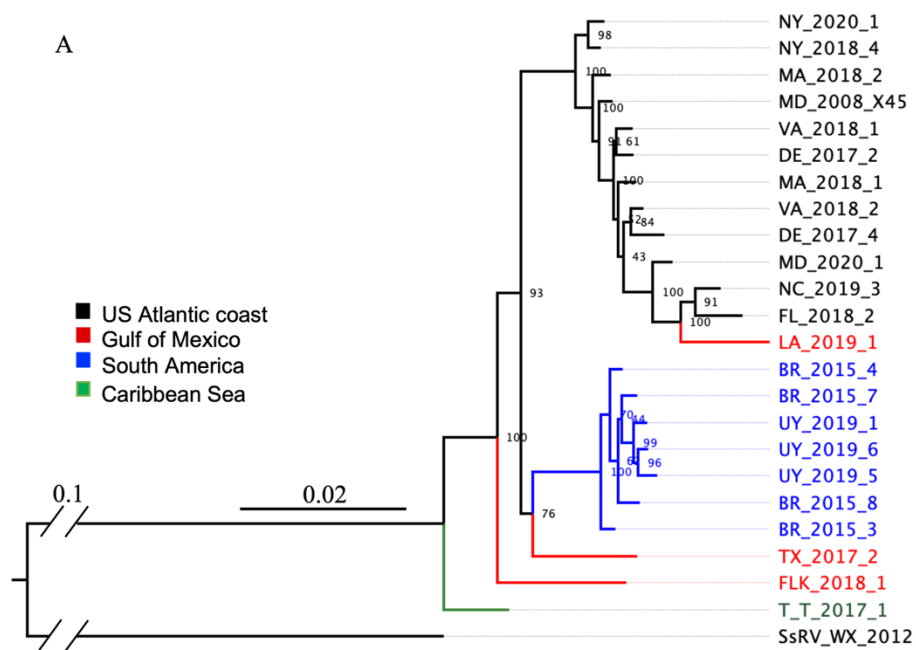
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23
MD_2008_X45	1		99.08	99.32	99.44	99.26	99.26	99.20	99.30	99.11	99.29	98.64	98.53	98.66	98.46	97.77	97.87	98.56	98.50	98.42	98.44	98.44	98.36	98.48
MD_2020_#1	2	182		99.15	98.98	98.89	98.95	99.10	99.21	99.09	99.18	98.84	98.70	98.69	98.22	97.54	97.59	98.28	98.23	98.17	98.18	98.17	98.08	98.21
MA_2018_#1	3	134	169		99.31	99.00	99.24	99.34	99.47	99.32	99.44	98.68	98.51	98.63	98.30	97.69	97.73	98.41	98.38	98.31	98.35	98.36	98.24	98.35
MA_2018_#2	4	110	202	136		99.15	99.29	99.16	99.28	99.10	99.25	98.58	98.50	98.59	98.38	97.72	97.83	98.47	98.41	98.35	98.35	98.36	98.26	98.39
NY_2020_#1	5	146	219	198	168		99.46	98.90	98.95	98.99	99.00	98.60	98.49	98.51	98.41	97.73	97.81	98.52	98.47	98.41	98.40	98.40	98.32	98.45
NY_2018_#4	6	146	208	150	141	107		99.05	99.12	99.14	99.14	98.65	98.56	98.58	98.46	97.79	97.89	98.56	98.51	98.45	98.44	98.45	98.35	98.48
VA_2018_#1	7	159	179	131	167	217	189		99.27	99.21	99.40	98.55	98.37	98.48	98.19	97.53	97.60	98.28	98.23	98.16	98.17	98.17	98.08	98.18
VA_2018_#2	8	139	156	105	143	208	174	144		99.38	99.37	98.73	98.62	98.68	98.29	97.65	97.71	98.40	98.35	98.29	98.30	98.29	98.20	98.31
DE_2017_#4	9	177	180	134	178	201	170	157	123		99.38	98.63	98.51	98.59	98.23	97.63	97.64	98.34	98.29	98.25	98.26	98.24	98.13	98.25
DE_2017_#2	10	140	162	111	148	198	171	119	125	123		98.72	98.50	98.64	98.30	97.65	97.70	98.38	98.33	98.27	98.30	98.28	98.17	98.28
NC_2019_#3	11	269	229	261	281	277	268	287	251	272	254		98.89	98.64	98.05	97.35	97.41	98.08	98.00	97.96	97.96	97.97	97.86	97.96
FL_2018_#2	12	292	258	295	298	300	285	323	274	296	298	219		98.59	97.99	97.34	97.32	97.99	97.94	97.87	97.87	97.77	97.77	97.90
LA_2019_#1	13	265	260	271	279	296	281	302	261	280	269	269	279		98.23	97.52	97.56	98.29	98.23	98.19	98.21	98.17	98.09	98.20
TX_2017_#2	14	305	353	336	321	314	305	358	339	351	337	387	398	350		97.79	97.78	98.52	98.49	98.42	98.44	98.41	98.33	98.45
FLK_2018_#1	15	442	488	458	451	450	438	489	466	470	466	524	527	491	438		97.41	97.76	97.74	97.75	97.70	97.69	97.68	97.77
T&T_2017_#1	16	422	477	450	429	433	418	475	453	467	456	514	530	484	439	514		97.91	97.88	97.87	97.82	97.82	97.76	97.89
BR_2015_#3	17	285	341	314	303	293	286	341	317	328	320	381	399	339	293	443	414		99.67	99.49	99.47	99.36	99.33	99.44
BR_2015_#4	18	297	351	320	315	303	296	350	327	338	330	396	409	350	300	447	419	65		99.59	99.55	99.41	99.40	99.52
BR_2015_#7	19	312	363	334	326	315	307	365	338	347	343	404	422	359	312	445	422	101	82		99.57	99.44	99.43	99.55
BR_2015_#8	20	310	361	327	326	317	309	363	336	345	336	405	421	354	310	456	431	105	90	86		99.37	99.34	99.45
UY_2019_#1	21	309	362	324	325	317	308	362	338	348	340	402	422	363	314	457	432	126	117	111	124		99.57	99.62
UY_2019_#5	22	325	380	348	345	332	326	380	357	370	362	423	442	379	330	460	444	132	119	113	130	86		99.70
UY_2019_#6	23	302	355	327	319	307	301	360	335	346	340	404	416	356	308	442	418	111	96	90	109	76	60	

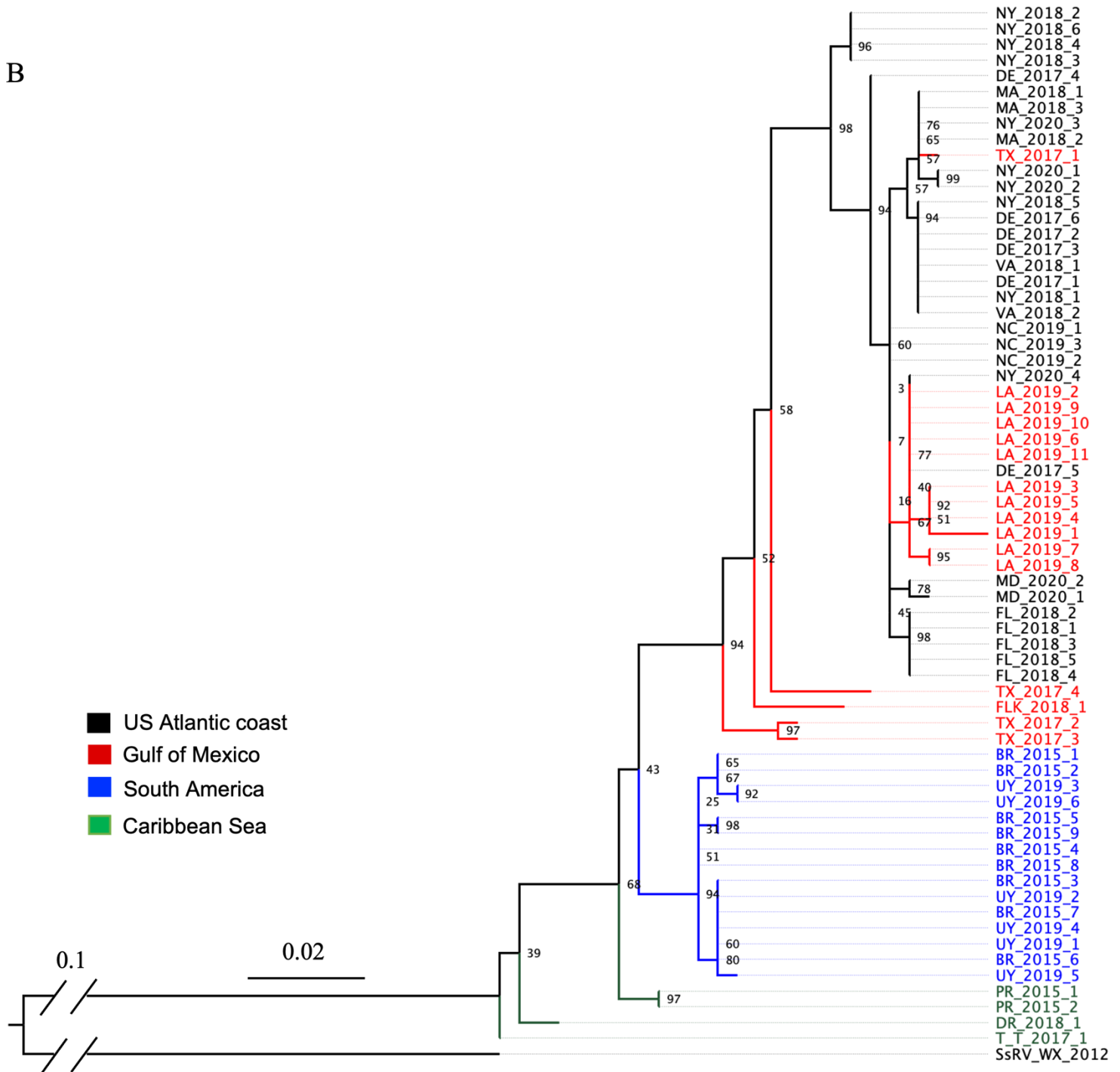
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MD_2008_#X45	1		99.06	99.44	99.56	99.38	99.32	99.43	99.35	99.11	99.41	98.67	98.37	98.26	97.75	97.35	97.57	98.05	97.96	97.87	97.88	98.05	97.90	97.97
MD_2020_#1	2	62		99.15	98.96	98.87	98.87	99.18	99.18	99.02	99.21	99.06	98.75	98.38	97.57	97.07	97.28	97.76	97.67	97.64	97.66	97.76	97.61	97.72
MA_2018_#1	3	37	56		99.38	99.08	99.18	99.53	99.56	99.30	99.55	98.70	98.40	98.23	97.67	97.32	97.44	97.99	97.93	97.84	97.88	97.99	97.84	97.91
MA_2018_#2	4	29	69	41		99.29	99.35	99.38	99.27	99.02	99.40	98.61	98.34	98.14	97.67	97.31	97.54	97.99	97.87	97.81	97.79	97.96	97.81	97.91
NY_2020_#1	5	41	75	61	47		99.65	99.06	98.97	98.88	99.08	98.62	98.37	98.05	97.76	97.38	97.54	98.05	97.96	97.90	97.88	98.02	97.87	97.97
NY_2018_#4	6	45	75	54	43	23		99.08	99.03	98.94	99.08	98.61	98.40	98.08	97.79	97.44	97.61	98.11	98.02	97.96	97.94	98.08	97.93	98.03
VA_2018_#1	7	38	54	31	41	62	61		99.43	99.27	99.59	98.68	98.38	98.17	97.61	97.26	97.40	97.91	97.84	97.75	97.76	97.90	97.75	97.82
VA_2018_#2	8	43	54	29	48	68	64	38		99.47	99.41	98.73	98.52	98.35	97.61	97.26	97.41	97.94	97.85	97.76	97.81	97.91	97.76	97.84
DE_2017_#4	9	59	65	46	65	74	70	48	35		99.38	98.53	98.35	98.16	97.44	97.11	97.22	97.78	97.69	97.63	97.64	97.72	97.57	97.67
DE_2017_#2	10	39	52	30	40	61	61	27	39	41		98.75	98.38	98.29	97.63	97.25	97.41	97.94	97.85	97.76	97.81	97.91	97.76	97.84
NC_2019_#3	11	88	62	86	92	91	92	87	84	97	83		99.12	98.50	97.57	97.04	97.16	97.63	97.52	97.46	97.51	97.67	97.49	97.57
FL_2018_#2	12	108	83	106	110	108	106	107	98	109	107	58		98.37	97.37	96.89	97.01	97.35	97.31	97.16	97.20	97.31	97.19	97.29
LA_2019_#1	13	115	107	117	123	129	127	121	109	122	113	99	108		97.35	96.79	96.87	97.44	97.37	97.34	97.35	97.49	97.32	97.41
TX_2017_#2	14	149	161	154	154	148	146	158	158	169	157	161	174	175		97.13	97.16	97.79	97.72	97.63	97.69	97.78	97.57	97.70
FLK_2018_#1	15	175	194	177	178	173	169	181	181	191	182	196	206	212	190		97.11	97.34	97.23	97.20	97.20	97.37	97.26	97.35
T&T_2017_#1	16	161	180	169	163	163	158	172	171	184	171	188	198	207	188	191		97.51	97.41	97.37	97.37	97.48	97.29	97.43
BR_2015_#3	17	129	148	133	133	129	125	138	136	147	136	157	175	169	146	176	165		99.59	99.36	99.41	99.40	99.24	99.35
BR_2015_#4	18	135	154	137	141	135	131	143	142	153	142	164	178	174	151	183	171	27		99.56	99.49	99.44	99.32	99.43
BR_2015_#7	19	141	156	143	145	139	135	149	148	157	148	168	188	176	157	185	174	42	29		99.53	99.52	99.40	99.50
BR_2015_#8	20	140	155	140	146	140	136	148	145	156	145	165	185	175	153	185	174	39	34	31		99.40	99.27	99.38
UY_2019_#1	21	129	148	133	135	131	127	139	138	151	138	154	178	166	147	174	167	40	37	32	40		99.58	99.65
UY_2019_#5	22	139	158	143	145	141	137	149	148	161	148	166	186	177	161	181	179	50	45	40	48	28		99.65
UY_2019_#6	23	134	151	138	138	134	130	144	143	154	143	161	179	171	152	175	170	43	38	33	41	23	23	

**Supplementary Figure S2. Maximum Likelihood phylogenetic tree based on amino acid sequences of the concatenated genomes(A) and segment 9 (B) of CsRV1 isolates from different geographic locations. Bootstrap > 50% was shown on the tree. SsRV WX\_2012 was used as the outgroup.**

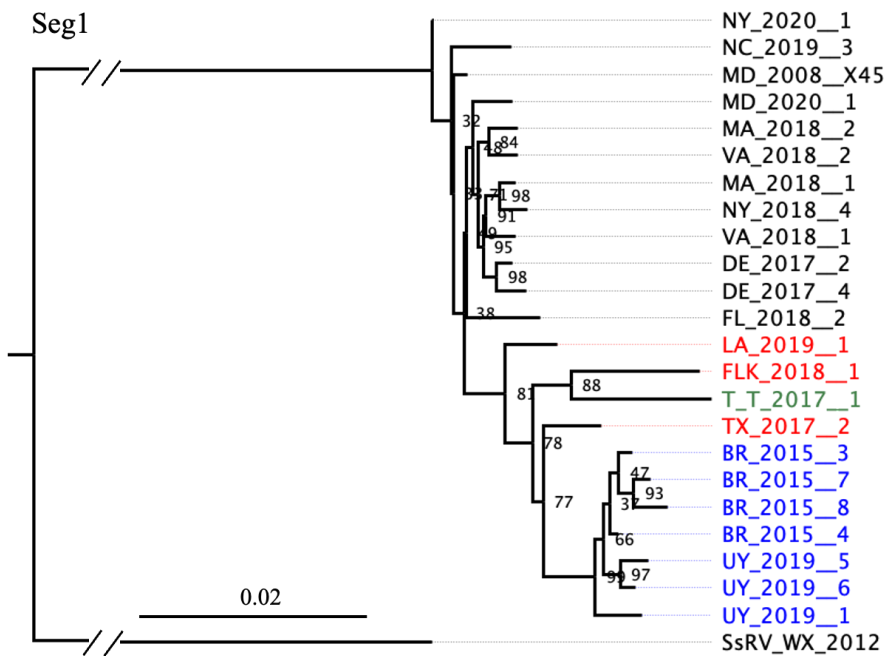
A

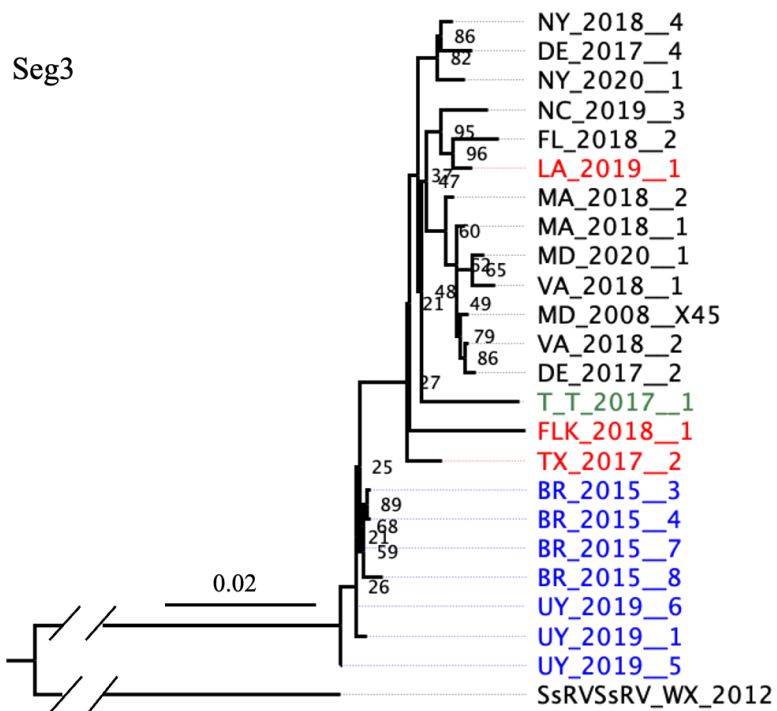
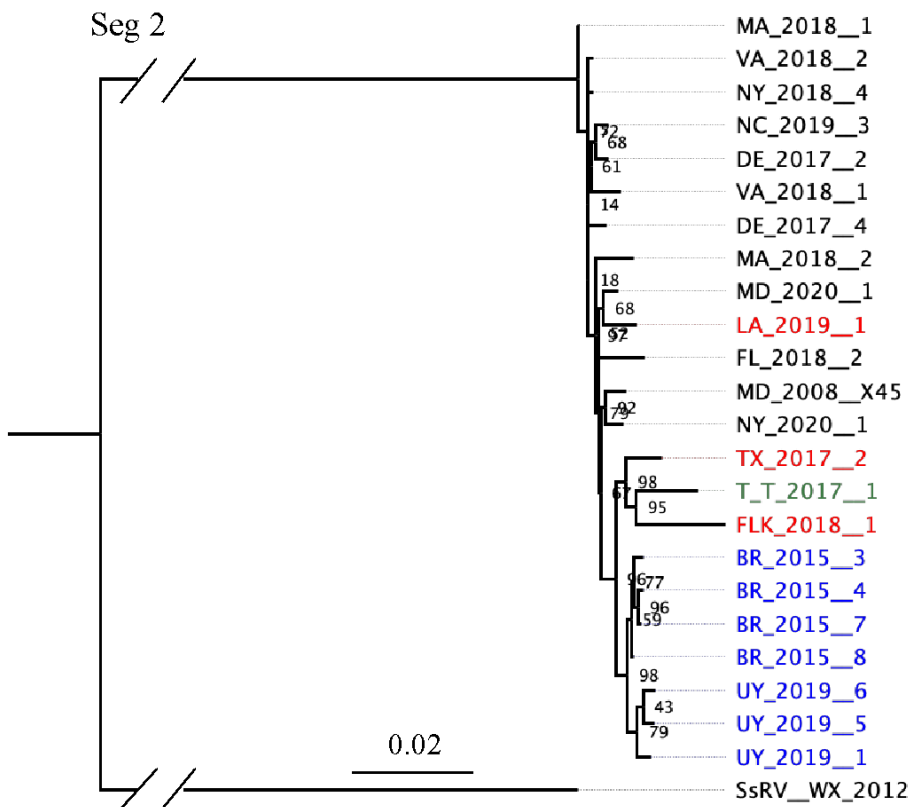


B

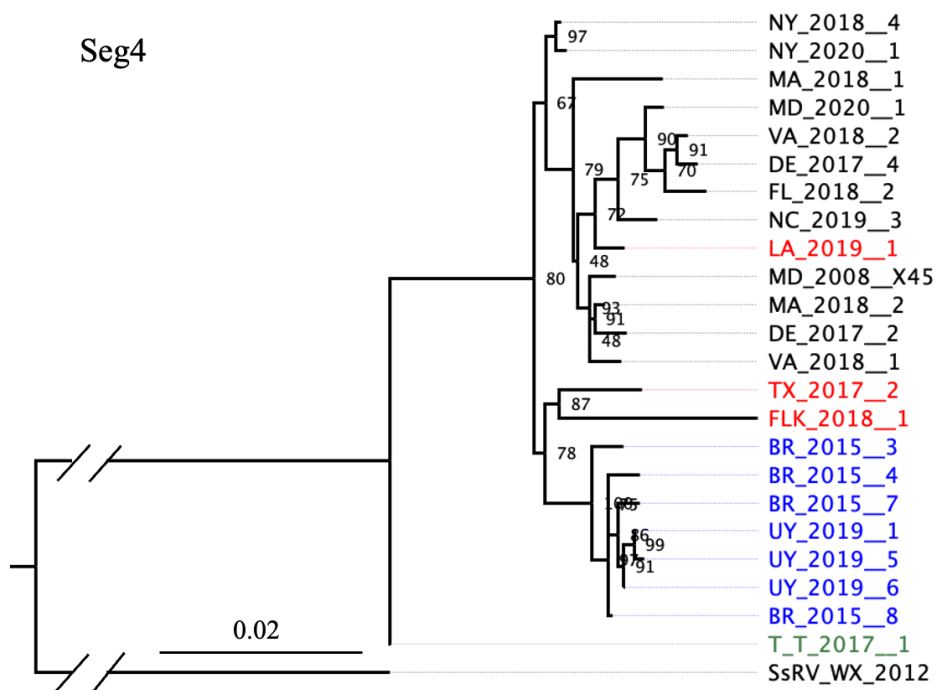


**Supplementary Figure S3. Maximum likelihood phylogenetic tree based on the nucleotide sequences of each segment of 23 strains of CsRV1 collected from different geographic locations.** Best Models based on BIC for each tree were shown in Supplementary Table 3.

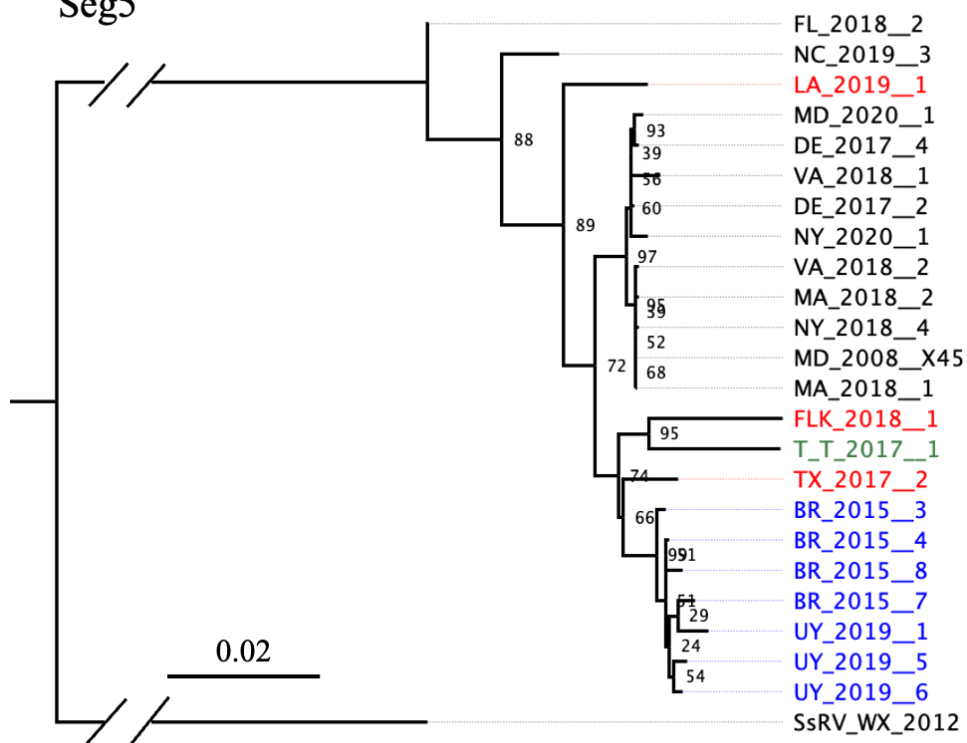




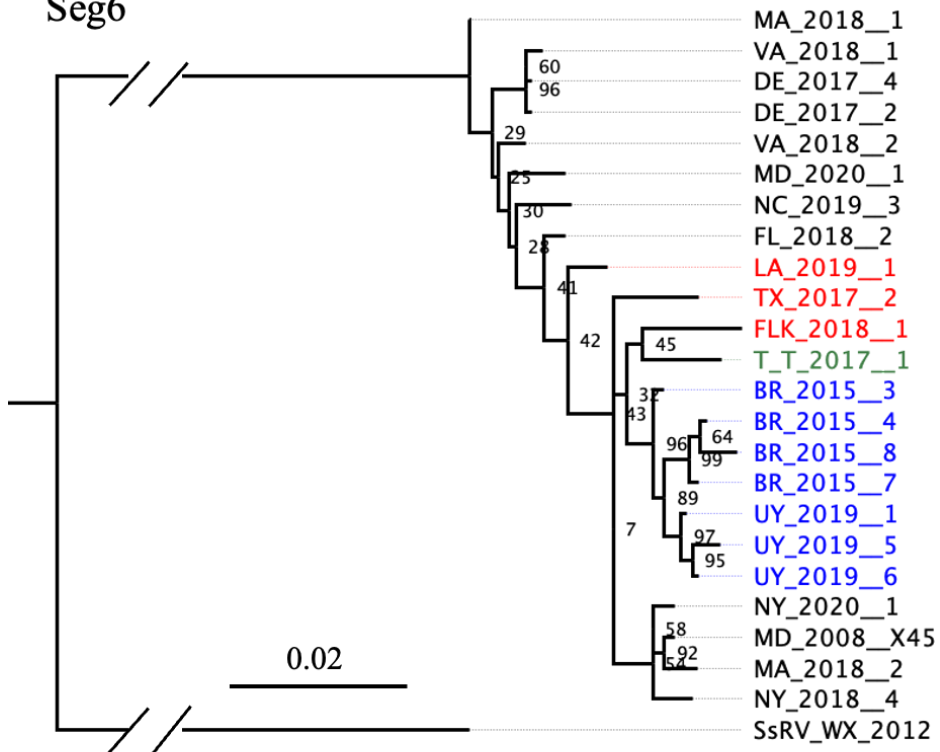
Seg4



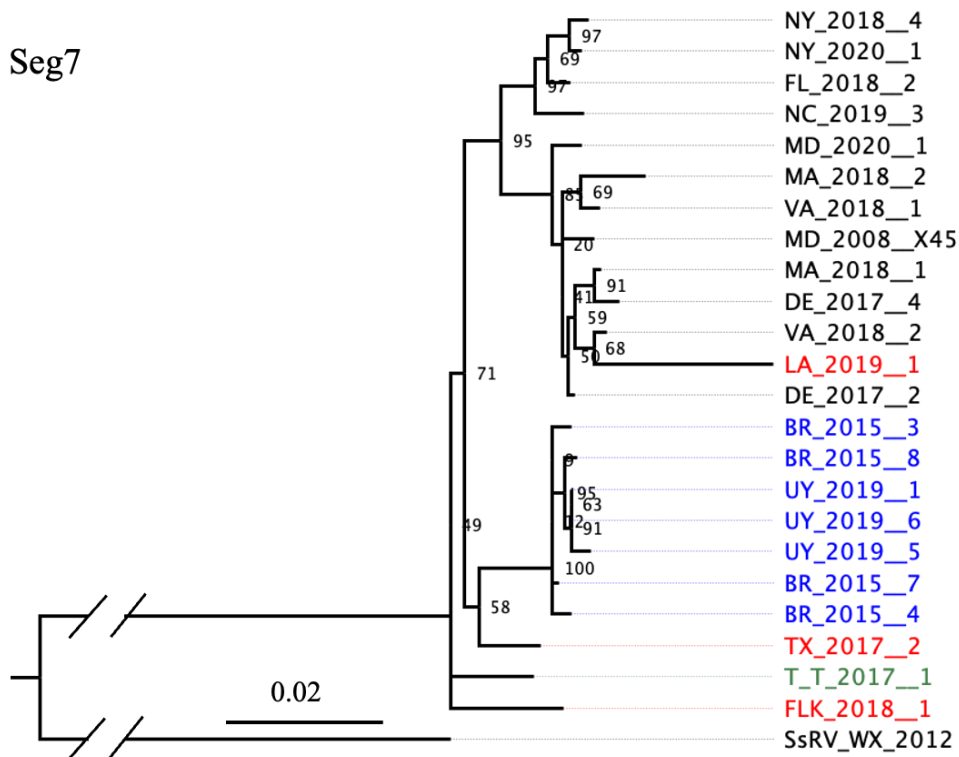
Seg5



Seg6

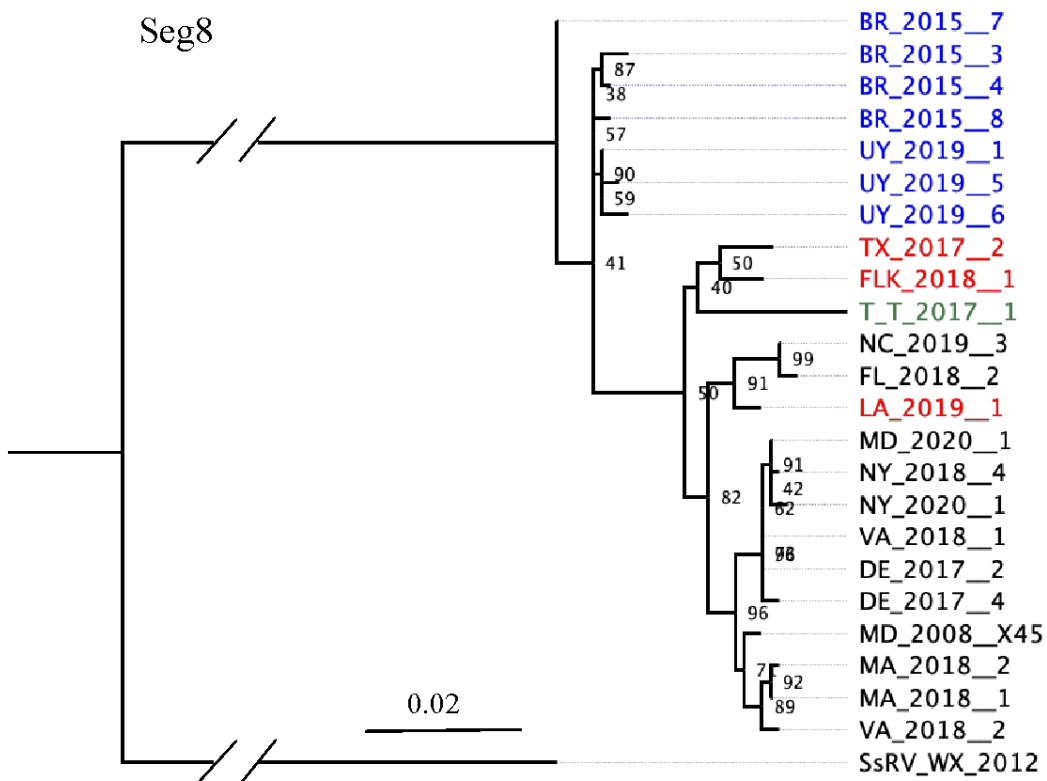


Seg7

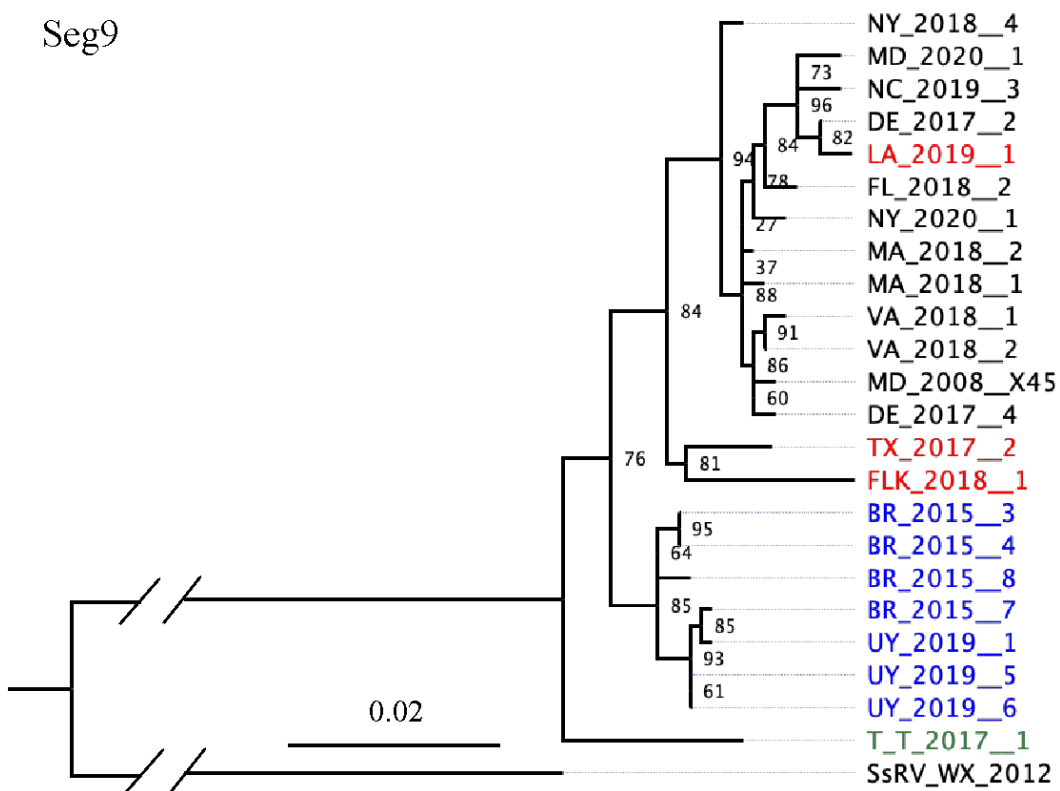




Seg8

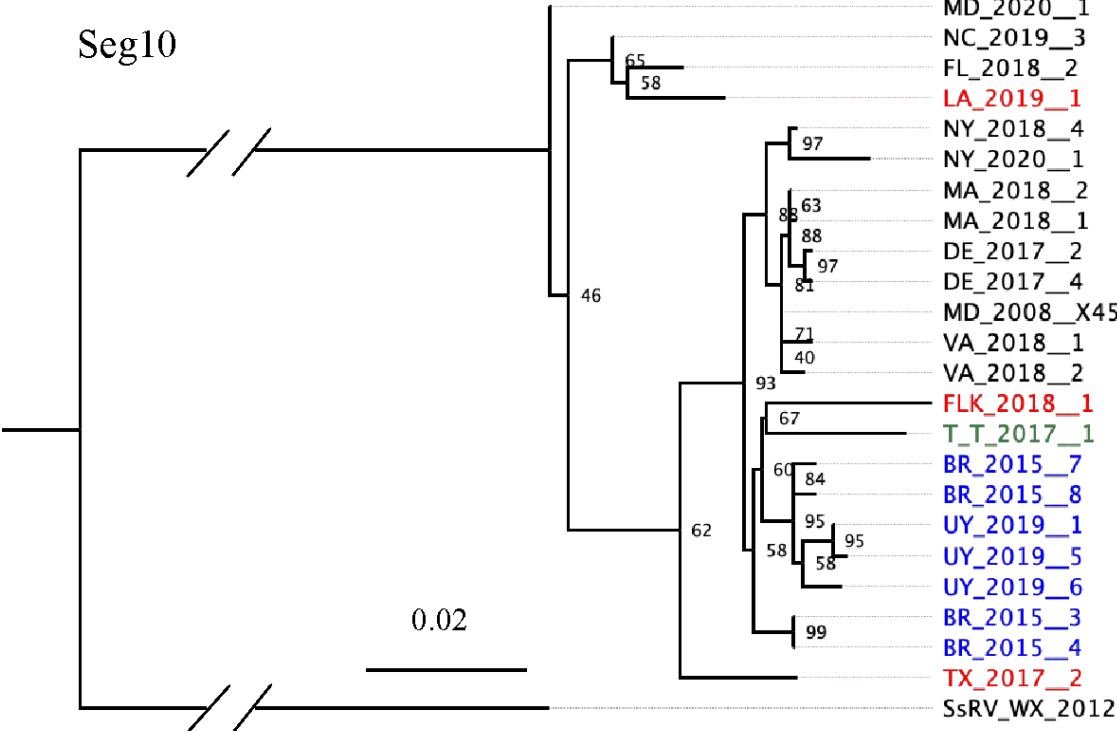


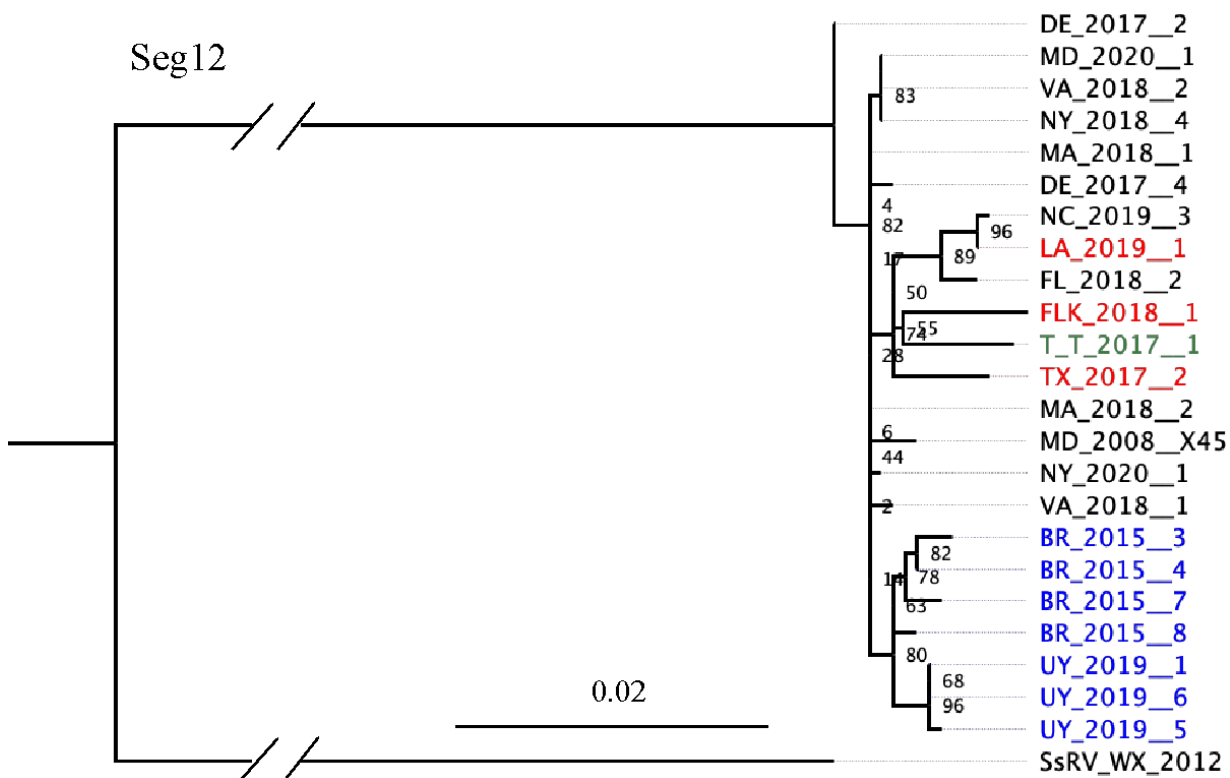
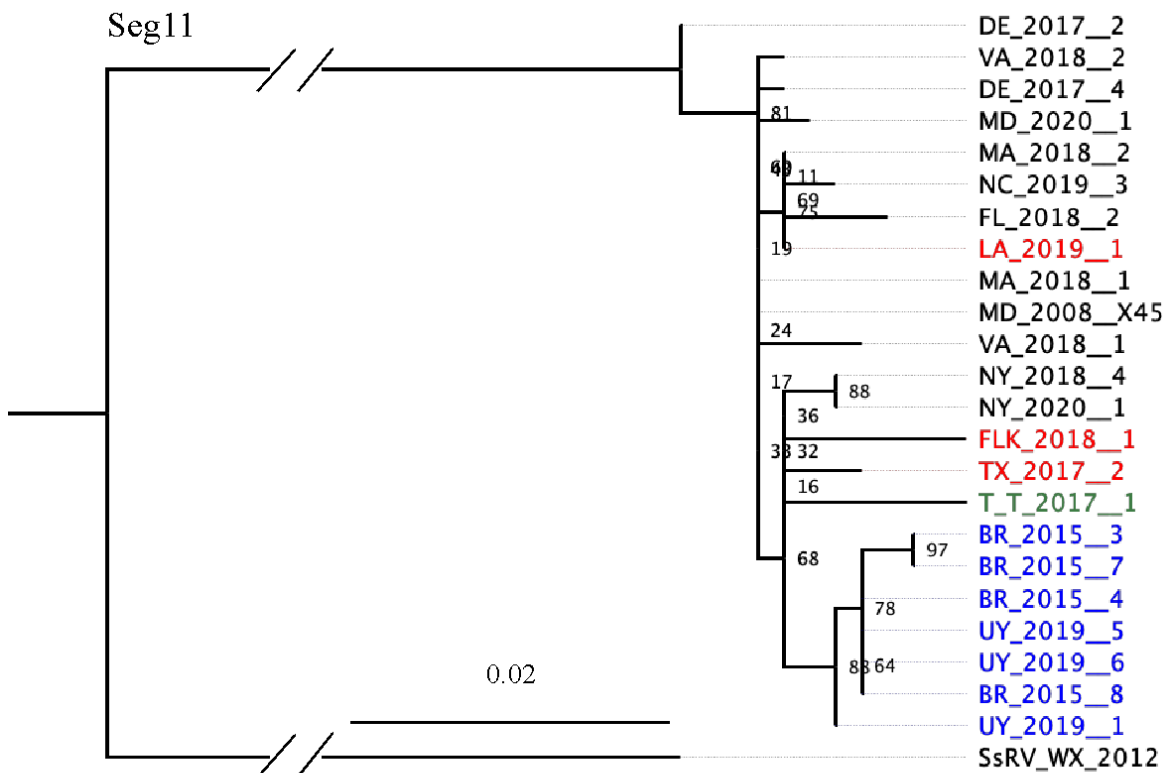
Seg9





Seg10





**Supplementary Table S1. Primers used in this study.**  
(See attached excel)

**Supplementary Table S2.  $F_{ST}$  estimates of CsRV1 between collection years based on seg9.** Bold values indicate significance ( $P < 0.05$ ).

	NY11-13	NY18-21	MD06-09	MD10-12	MD18-20
NY11-13	-				
NY18-21	<b>0.75</b>	-			
MD06-09	<b>0.31</b>	<b>0.51</b>	-		
MD10-12	<b>0.47</b>	<b>0.59</b>	0.03	-	
MD18-20	<b>0.40</b>	<b>0.54</b>	-0.08	0.17	-

**Supplementary Table S3.  $F_{ST}$  estimates of CsRV1 between locations.** Bold values indicate significance ( $P < 0.05$ ).

	MA	NY	VA	DE	MD	NC	LA	FL	TX	CAR	BR	UY
MA	-											
NY	0.06	-										
VA	0.48	0.21	-									
DE	0.15	0.12	0.12	-								
MD	<b>0.32</b>	<b>0.31</b>	<b>0.35</b>	0.17	-							
NC	0.76	<b>0.47</b>	0.86	0.31	0.23	-						
LA	<b>0.67</b>	<b>0.52</b>	<b>0.73</b>	<b>0.43</b>	<b>0.34</b>	0.45	-					
FL	0.88	<b>0.57</b>	<b>0.95</b>	<b>0.62</b>	<b>0.53</b>	<b>0.96</b>	<b>0.79</b>	-				
TX	0.24	<b>0.42</b>	0.19	<b>0.32</b>	<b>0.5</b>	<b>0.39</b>	<b>0.59</b>	0.52	-			
CAR	0.55	<b>0.68</b>	0.52	<b>0.59</b>	<b>0.7</b>	<b>0.65</b>	<b>0.77</b>	<b>0.74</b>	<b>0.3</b>	-		
BR	<b>0.77</b>	<b>0.72</b>	<b>0.78</b>	<b>0.73</b>	<b>0.74</b>	<b>0.83</b>	<b>0.84</b>	<b>0.87</b>	<b>0.46</b>	<b>0.53</b>	-	
UY	<b>0.91</b>	<b>0.76</b>	<b>0.93</b>	<b>0.8</b>	<b>0.78</b>	<b>0.95</b>	<b>0.9</b>	<b>0.97</b>	<b>0.5</b>	<b>0.6</b>	0.17	-