

1 **First natural crossover recombination of intact ORFs**

2 **between two distinct species of the family**

3 ***Closteroviridae***

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17 Abstract

18 *Lettuce chlorosis virus-SP* (LCV-SP) (family *Closteroviridae*, genus *Crinivirus*), is a
19 new strain of LCV which is able to infect green bean plants and incapable of infecting
20 lettuce crops. In the present study, high throughput and Sanger sequencing of RNA
21 was used to obtain the LCV-SP full-length sequence. The LCV-SP genome comprises
22 8825 nt and 8672 nt equivalent with RNA1 and RNA2 respectively. RNA1 of LCV-SP
23 contains four ORFs, the proteins encoded by the ORF1a and ORF1b are closely related
24 to LCV RNA1 from California (FJ380118) whereas the 3' end encodes proteins which
25 share high amino acid sequence identity with RNA1 of BnYDV (EU191904). The
26 genomic sequence of RNA2 consists of 8 ORFs, instead of 10 ORFs contained in LCV-
27 California isolate. The distribution of vsiRNA (virus-derived small interfering RNA) along
28 the LCV-SP genome suggested the presence of subgenomic RNAs corresponding with
29 HSP70, P6.4 and P60. Results of the analysis using RDP4 and Simplot programs are the
30 proof of the evidence that LCV-SP is the first recombinant of the family *Closteroviridae*
31 by crossover recombination of intact ORFs, being the LCV RNA1 (FJ380118) and BnYDV
32 RNA1 (EU191904) the origin of the new LCV strain. Genetic diversity values of virus
33 isolates in the recombinant region obtained after sampling LCV-SP infected green bean
34 between 2011 and 2017 might suggest that the recombinant virus event occurred in
35 the area before this period. The presence of LCV-SP shows the role of recombination
36 as a driving force of evolution within the genus *Crinivirus*, a globally distributed,
37 emergent genus.

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39 Introduction

40 *Lettuce chlorosis virus* (LCV) belongs to the genus *Crinivirus*, family
41 *Closteroviridae*. Viruses included in this family are the largest among the known plant
42 viruses and present ssRNA, positive-sense genome [1]. Family *Closteroviridae* has been
43 classified in three genera based on vector transmission and phylogenetic relationships:
44 *Closterovirus*, *Ampelovirus*, and *Crinivirus*. Recently, a new genus named *Velarivirus*
45 has been proposed [2]. All members of genus *Crinivirus* include segmented genomes,
46 are whitefly-transmitted and limited to the phloem [3].

47 Many members of genus *Crinivirus* are considered emerging epidemics worldwide [4].
48 LCV was described in the 1990's in California, transmitted by the whitefly *Bemisia*
49 *tabaci* and affecting lettuce and sugar beet crops [5]. The complete sequence and the
50 genomic organization of LCV were described in 2009 by [6] and comprises a bipartite
51 genome formed by RNA1 and RNA2. LCV RNA1 contains the replication module (ORFs
52 1a and 1b), which encodes conserved domains of a papain-like leader proteinase (P-
53 PRo), a methyltransferase (MTR), helicase (HEL) and RNA-dependent RNA polymerase
54 (RdRp), ORF2 encodes a putative 8-kDa protein (P8), and ORF3 encodes a 22.9-kDa
55 protein (P23) recently described as viral suppressor of RNA silencing [7]. LCV RNA2
56 contains the hallmark *Closterovirus* gene array coding for a heat shock protein
57 homolog (Hsp70h, ORF3), a 50-60 kDa protein (ORF5), the major (CP, ORF7) and the
58 minor coat protein (CPm, ORF 8) [1,8]. Furthermore, P5.6, P6, P6.4, P9, P27, and P4.8
59 are encoded by ORF1, ORF2, ORF4, ORF6, ORF9 and ORF10, respectively; the functions
60 of these putative proteins remain unknown [6].

61 LCV share high homology with *Cucurbit chlorotic yellow virus* (CCYV) and with
62 *Bean yellow disorder virus* (BnYDV), [9,6], this last one, was recognized as the first

63 *Crinivirus* that infects Leguminosae family crops [10]. LCV was considered as an
64 endemic infection which had not spread to areas outside Southwestern USA [4]. In
65 2014 however, symptoms similar to BnYDV in green bean crops were attributed to a
66 new strain of LCV, LCV-SP, which was unable to infect lettuce plants and capable of
67 affecting green bean crops [11].

68 Viral RNA-RNA recombination and/or reassortment of genomic segments
69 (pseudo-recombination), between virus strains or virus species, increase the genetic
70 variability and is a powerful tool in virus evolution, responsible for the emergence of
71 new viral strains or species [12]. RNA recombination can also be used to repair viral
72 genomes which will contribute to the fitness of viral populations. The low frequency of
73 its detection is probably the result of selection pressure that removes the majority of
74 recombinants [13]. The first evidence of genetic recombination was described in
75 *Bromo mosaic virus* [14] and it seems to be specially frequent among species belonging
76 to the family *Potyviridae* where crossovers have been described at ORFs and 3'UTR
77 sequences [15-17,13].

78 Within family *Closteroviridae* homologous recombination has been described at
79 CP and P20 in the *Closterovirus* member *Citrus tristeza virus* (CTV) [18,19] and at CP of
80 the *Ampeloviruses* Grapevine leafroll-associated virus 3 (GLRaV-3) and GLRaV-11
81 [19,20]. Although *Closterovirus* members share a core of conserved genes, they
82 present high variability in the set of ORFs located in the 3'end of RNA or in the 3'end of
83 RNA 1 if the genome is bipartite, as is the case of genus *Crinivirus* [1,21]. The presence
84 of mechanisms capable of increasing genetic variability such as genome recombination

85 may have important evolutionary implications because some of these proteins have
86 been characterized as RNA-suppressing proteins (RSS)[22-25,7].

87 In this study we describe a recombinant *Crinivirus*, LCV-SP, originating from a crossover
88 of intact ORFs and analyse a population of isolates collected in the area. Sequencing
89 was achieved by combining primer walking strategy and high-throughput sequencing.
90 The implications in emergence of *Crinivirus* epidemiology are discussed.

91

92 **Material and methods**

93 **Virus isolate**

94

95 Between 2011 and 2017 samples of green bean leaves showing symptoms that
96 could be attributed to LCV-SP (interveinal mottling and yellowing in lower and middle
97 leaves [11]) were collected from different geographical locations from Granada,
98 Almeria and Málaga provinces in Southeastern Spain. The plants were analysed by RT-
99 PCR to ensure the presence of LCV-SP [11] and stored at -80°C for subsequent
100 molecular analysis. One of these isolates collected in 2013 and annotated as "Almeria"
101 was used for complete genome determination.

102 **Whole-genome sequencing of LCV-SP and genome analysis**

103 Total RNA from LCV-SP isolate "Almeria" was extracted with Trizol Reagent
104 (Invitrogen) according to the manufacturer's instructions. Partial length viral sequence
105 of RNA1 and RNA2 of LCV genome was determined by RT-PCR using a primer walking
106 strategy with a set of degenerated primers based on LCV (FJ380118, FJ380119) and
107 BnYDV (NC010560, NC010561) sequences (data not shown). Partial sequences of LCV-

108 SP RNA1 and RNA2 previously described [11] were also used to design specific primers
109 and flank the gaps. The sequences were assembled using the software GENEIOUS (v.
110 7.1.9, Biomatters, New Zealand).

111 **Small RNA purification, dsRNA extraction and deep sequencing**

112 Small RNA purification from the Almeria LCV-SP isolate was obtained using the
113 miRCURY RNA isolation kit (Exiqon, Denmark), according to the manufacturer's
114 instructions. Small RNA library was prepared using the Illumina TruSeq Small RNA Kit
115 (Illumina, San Diego, California, USA). The library was sequenced on the Illumina deep
116 sequencing platform using the services provided by CRG (Barcelona, Spain).
117 Sequencing adapters and reads shorter than 18 nucleotides (nt) were removed using
118 GENEIOUS and reads ranging from 18 to 24 nt were selected. These reads were
119 assembled into contigs larger than 33 nt using the *de novo* assembly function of
120 VELVET v. 1.2.08 implemented in the SCBI Picasso server (<http://www.scbi.uma.es>)
121 with a k-mer = 18. Partial RNA1 and RNA2 LCV-SP sequence obtained for Sanger
122 sequencing was used as a reference for contigs sequences. RNA1 and RNA2 consensus
123 draft sequences obtained were ensured through RT-PCR amplification using specific
124 primer pair based on the assembled genomes (not shown). The 5'/3' Smart™ RACE
125 cDNA Amplification Kit (Clontech, California, USA) was used to complete the 5' and
126 3'ends. PCR fragments were cloned in pGemT vector and at least two cDNA clones
127 were sequenced in both directions. To obtain the profile distribution of LCV-SP virus-
128 derived small interfering RNAs (vsRNAs), the 21 and 22 nt reads of the small RNA
129 library were aligned to the assembled LCV-SP genome using MISIS-2 [26].

130 **Double stranded RNA purification**

131 Deep sequence from LCV-SP dsRNA was used to confirm the LCV-SP RNA1 and
132 RNA2 genomic sequences. For that, double-stranded RNA was purified from another
133 LCV-SP isolate collected in 2014 [27] followed by S1 nuclease (Promega, Madison,
134 Wisconsin, USA) and DNAase I (Invitrogen, Carlsbad, California, USA) treatments to
135 discard the contamination with genomic DNA and ssRNAs. A library was constructed
136 and sequenced using the Illumina deep sequencing platform with the services provided
137 by CRG (Barcelona, Spain). Contigs were assembled after trimming the low-quality
138 reads by using VELVET (k-mer = 31). Complete sequence of LCV-SP obtained as above is
139 described was used as reference for contigs aligning in GENEIOUS v. 7.1.9.

140 The contigs obtained from both massive deep sequencing were conducted to
141 BLAST analysis against the GenBank database in NCBI (<http://www.ncbi.nlm.nih.gov>)
142 using GENEIOUS. The e-value cut-off was set to 10^{-5} so high confidence matches could
143 be reported. The numbers of reads aligning to LCV or BnYDV genomes were annotated
144 to confirm the presence of sequences belonging to both virus species.

145

146 **Phylogenetic analysis**

147 For phylogenetic analysis, the complete genome sequences from 9 members of
148 genus *Crinivirus*, retrieved from the GenBank database and the complete sequence of
149 LCV-SP were compared. The pairwise percentage of nucleotide sequence identity was
150 performed using the Clustal W algorithm present in MEGA v 7.01 program [28].
151 Appropriate nucleotide substitution models for each genomic region were determined
152 using jModelTest 2.1 [29] and the best model proposed by the Akaike information
153 criterion (AIC) applied in each cases (GTR+I+G for RNA1 and HSP70h; JC for RNA2,
154 GTR+G for CP, CPm and RdRp). Bayesian consensus phylogenetic trees were inferred

155 using Bayesian inference and Markov chain Monte Carlo (MCMC) simulation
156 implemented in MrBayes plugin. MCMC analyses were run with a chain length of 10^7
157 generations, sampling every 1000 trees and with a burn-in of 25% and chain heated to
158 0.2.

159 **Recombination analysis**

160 Recombination Detection Program 4 (RDP4) was used to detect potential
161 recombination events in LCV-SP, likely parental sequences, and localization of
162 recombination breakpoints [30]. The program was executed with default parameter
163 settings which include the RDP, GENECONV, Chimaera, MaxChi, BOOTSCAN, and
164 SISCAN methods. For recombination analysis, sequences of RNA1 and RNA2 of LCV,
165 BnYDV, LCV-SP and CCYV were aligned in MEGA v.7.0.1 software [28] and exported to
166 the RDP4 program for recombination analysis. The program was performed using the
167 default settings and a Bonferroni corrected p -value cut-off ($\alpha=0.05$). Only
168 recombination events detected by four or more methods were considered as
169 significant. The results obtained by RDP were confirmed using a boot scanning method
170 in the SimPlot program v.3.5.1 [31].

171 **Genetic diversity in the recombinant genomic region**

172 The crossover recombination event was confirmed in several isolates by RT-
173 PCR. Eleven isolates obtained in the surveys from 2011 to 2017 were analysed by RT-
174 PCR after RNA extraction using the primers LCVSP-44F
175 5'GCATTCAAGAAATTGTGGGATG 3' (nt 7517-7538) and LCVSP-50R
176 5'ATATTAATGTAATTCTACGGTC 3' (nt 8738-8759) which amplified a region of the LCV-

177 SP genome encompassing 1242 bp corresponding to the entire region of the p26 and
178 p6 proteins. Reverse transcription of the isolates was carried out with a reverse primer
179 using Superscript II (Invitrogen) at 42°C for 60 min. Subsequently, DNA fragments were
180 amplified by PCR with Expand High Fidelity PCR System (Roche, Basel, Switzerland)
181 under the following conditions: 95°C for 3 min, 35 cycles of denaturation for 20s at
182 95°C, annealing for 30s at 55°C and extension for 40s at 72°C followed by one final
183 extension cycle for 5 min at 72°C. PCR products were cloned into pGemT-Easy vector
184 (Promega Corporation, Madison, USA). The clones were bidirectionally sequenced.
185 Nucleotide alignments were performed using Clustal W in MEGA v. 7.01 [28] software
186 with default settings. The aligned sequences were used to calculate the genetic
187 distances for synonymous (dS) and non-synonymous substitution (dNS) as described by
188 [32,33] (PBL method).

189 **Molecular differentiation between yellowing induced by BnYDV** 190 **or LCV recombinant virus (LCV-SP)**

191 In order to determine analytically the presence of the recombinant *Crinivirus*
192 LCV-SP, a RT-PCR-restriction fragment length polymorphism (RFLP) was performed.
193 The set of primers LC-Bn56F 5'GATTTTGGATTTGAAGC 3' and LC-Bn51R
194 5'ACAACAGATCAAAATCCACAATG 3' which amplified fragments of LCV-SP RNA1 and
195 BnYDV RNA1 genome of 739 and 769 bp, corresponding to nucleotides 7190–7928 and
196 7294-8062 respectively were used for a RT-PCR reaction as described above. After
197 that, the PCR products were digested with *KpnI* (Promega) following the
198 manufacturer's instructions. Band patterns were analysed on a 2% agarose gel.

199 Results

200 Genome sequencing of LCV-SP

201 Walking strategy and Sanger sequencing allowed us to obtain 7109 bp and 7821
202 bp corresponding to 80% and 90% of complete genome of RNA1 and RNA2 of LCV-SP.
203 The LCV-SP genome was completed by deep sequencing from small RNAs and RACE
204 strategy. The genome was confirmed through RT-PCR amplification with specific
205 primers (S1 Table) and consisting of 8825 nt and 8672 nt equivalent with RNA1 and
206 RNA2 of GenBank accession numbers MG489894 and MG489895, respectively. Genetic
207 organization of LCV-SP genome is shown in Fig 1. RNA1 of LCV-SP contains four ORFs:
208 ORF1a (nt 73-7561) and ORF1b (nt 6044-7561) contains the replication module and the
209 P-PRO, MTR and RdRp motifs. ORF2 (nt 7637-8338) encodes a predicted protein of 26-
210 kDa (P26) and it is followed by another putative protein of 6-kDa (P6) (ORF3, nt 8339-
211 8512). The proteins encoded by ORF1a and ORF1b share a 93.6 % and 99.6%
212 respectively of amino acid sequence identity with LCV RNA1 from California
213 (FJ380118). Whereas the 5' from LCV-SP RNA1 are closely related to the LCV RNA1
214 genome previously described; the 3' end encodes proteins corresponding to the RNA1
215 of BnYDV (EU191904). The P26 (ORF2) and P6 (ORF3) share a 99.5% and 100% amino
216 acid sequence identity with those present in BnYDV. Both proteins currently have an
217 unknown function; P26 has no homologues in the GenBank database and P6 display
218 only 30% of amino acid sequence identity with a P6a protein of a new unclassified
219 *Crinivirus* named *Tetterwort vein chlorosis virus* (ALE18214). The genomic sequence of
220 RNA2 consists of 8 ORFs, instead of the 10 ORFs contained in LCV-California isolate [6].

221 The genomic sequence comprises the hallmark gene array of the family *Closteroviridae*
222 coding for a HSP70h (ORF5, nt 1817-3483), and three diverged copies of the capsid
223 protein: the ortholog of the coat protein homolog (ORF4, nt 3642–5195), the CP (ORF6,
224 nt 5537–6289) and the CPm (ORF7, nt 6289-7713) which exhibit more than 95% amino
225 acid sequence identity with RNA2 of LCV FJ380119. RNA2 of LCV-SP encodes also three
226 putative small proteins: P5.6 (ORF1, nt 254-421), P6.4 (ORF3, nt 3484-3648) and P9
227 (ORF5, nt 5177-5416), which show 92%, 98% and 96% nucleic acid identity with those
228 in LCV FJ380119. Two putative small proteins in the RNA2 of LCV-Californian isolate
229 (FJ380119), P6 in the 5' end, and P4.8 in the 3' end, which have unknown function are
230 absent in LCV-SP. The last ORF of RNA2 (ORF9) encodes a putative P27, which shows a
231 high amino acid identity (98%) with its counterpart protein in LCV FJ380119.

232 **Fig 1. Diagram of genome organization of LCV-SP genome.** Boxes represent ORFs;
233 putative protein products are also indicated. Solid lines represent the location of
234 contigs assembled from virus-derived small RNAs of LCV-SP.

235 **5' and 3' non coding region**

236 The putative 5'UTR of LCV-SP RNA1 and RNA2 are 72 and 269 nt in length, and
237 share 99% and 96% of nucleotide identity with LCV FJ380118/FJ380119 respectively.
238 The first 5 nucleotides, GAAAT, are identical in both RNAs. This feature has been
239 described in the Californian LCV isolate and in other members of genus *Crinivirus* [6].
240 Table 1 shows the percentage of nucleotide identity among 3'UTR regions
241 corresponding with LCV-SP (RNA1 and 2), BnYDV (RNA1 and 2) and the Californian
242 isolate of LCV (RNA 1 and 2). The 3'UTR of RNAs 1 and 2 are 313 and 256 nt in length

243 respectively and shared high nucleotide sequence similarity (72%). Also, 3'UTR of
 244 RNA1 displays almost identical nucleotide sequence (99%) as its equivalent in BnYDV.
 245 This sequence is next to the putative proteins P26 and P6 corresponding to the 3'end
 246 of RNA1 of BnYDV and LCV-SP. Additionally, 3'UTR of RNA2 of LCV-SP show the highest
 247 homology (89%) with the 3'UTR of RNA1 of the Californian isolate of LCV FJ380118.

248 **Table 1. Percentage of nucleotide identity between 3'UTRs region of LCV-SP, LCV and**
 249 **BnYDV.**

	LCV-SP RNA1	BnYDV RNA1	LCV RNA1	LCV-SP RNA2	LCV RNA2	BnYDV RNA2
LCV-SP RNA1		99.7	70.1	71.4	72.2	56.2
BnYDV RNA1	99.7		69.8	71.4	71.4	57.0
LCV RNA1	70.1	69.8		89.5	79.8	57.8
LCV-SP RNA2	71.4	71.4	89.5		79.6	61.3
LCV RNA2	72.2	71.4	79.8	79.6		52.8
BnYDV RNA2	56.2	57.0	57.8	61.3	52.8	

250 LCV RNA1: FJ380118; LCV RNA2: FJ380119; BnYDV RNA1: EU191904; BnYDV RNA2: EU191905; LCV-SP-

251 RNA1 : MG489894; LCV-SP RNA2: MG489895

252

253 Libraries of small RNAs and dsRNAs

254 After removal of adapters and reads shorter than 18, deep sequencing from
 255 small RNAs library produced a set of 44,578 million reads, which were subjected to the
 256 novo assembled, generating 19,739 contigs. A total of 113 and 125 sequences of these
 257 contigs assembled with LCV-SP RNA1 and RNA2, respectively. Fig 1 shows the location
 258 of the contigs derived from small RNA reads and assembled to the LCV-SP RNA1 and
 259 RNA2 genome components. The recombinant genome of LCV-SP was confirmed also
 260 by deep sequencing library obtained from dsRNA extracted from a LCV-SP green bean-
 261 infected plant that resulted in 31,353,455 reads. These sequences were assembled

262 resulting in 3642 contigs. These contigs covered 90% of the LCV-SP RNA1 genome and
263 the consensus sequence result was 100% identical. Contigs assembled with LCV-SP
264 RNA2 covered 94% of LCV-SP RNA2 genome with 99.7% coincidence.

265 The result of BLASTN is shown in S2 Table. Only sequences matching the RNA1
266 and RNA2 of different LCV isolates and the 3' end of the RNA1 of BnYDV (EU191904),
267 corresponding to P26 and the 3'UTR, were identified. All the sequences identified in
268 BLASTN as part of the genome of RNA1 of LCV showed high nucleotide identity (more
269 than 80%) with ORFs 1a and 1b. No sequences corresponding to the 3' end of RNA1 of
270 LCV were identified, confirming the presence of the first *Crinivirus* arising by crossover
271 recombination of entire ORFs and discarding the presence of a native LCV in the plants.
272 The profiles of vsRNAs aligned to LCV-SP RNA1 and 2 were analysed. The 21-nt vsRNA
273 class population was most prevalent, followed by the 22-nt (10.1 and 2.6 million
274 respectively.) From this 21-nt population, 58 675 and 80 904 reads matched to LCV-SP
275 RNA1 and 2 genome. In the case of 22-nt class population, 53.932 and 68.146 matched
276 with LCV-SP RNA1 and 2. The analysis of 21 and 22-nt (not shown) vsRNA strand
277 polarity showed similar pictures, 53% of 21 and 22-nt vsRNA class populations aligned
278 to LCV-SP RNA1 were negative, whereas more than 50% of 21-nt and 22-nt vsRNA
279 class populations aligning to LCV-SP RNA2 were positive (53% and 51%, respectively).
280 The profile distribution of both vsRNAs populations aligning to the LCV-SP RNA1 and
281 RNA2 genome components were also very similar. The distribution of 21-nt vsRNAs
282 along LCV-SP RNA1 and 2 genome is shown in the Fig 2. Several vsRNA-generating
283 regions (named as hot spots) were identified in both genomic RNAs of LCV-SP. Hot
284 spots in RNA1 were located between MTR and HEL domains. The distribution of vsRNA

285 hotspots in the RNA2 genome corresponding with ORF 2 (HSP70), 3 (P6.4) and 4 (P60)
286 are correlated with the position of subgenomic RNAs in LCV described by [6]. A hotspot
287 located in the position 1361 of RNA2 does not correspond with any putative coding
288 region.

289 **Fig 2. Profiles distribution of 21-nt vsRNAs along LCV-SP RNA1 (A) and RNA2 (B).**

290 Sense and antisense of 21-nt vsRNAs orientations are above and below the axis
291 respectively. Schema of LCV-SP RNA1 and RNA2, genome is represented as reference.

292 Investigating the 5'- and 3'-terminal nucleotides of the vsRNAs provides insight
293 into the specific silencing machinery active in the plant. In S1 Fig we represent the
294 percentages of nucleotides at each terminal position for the 21 to 24-nt vsRNA
295 populations matching LCV-SP RNA1 and RNA2. For both RNAs, there is a bias towards
296 A/U in the 5' and 3' nucleotide positions in the 21 to 24-nt classes of vsRNAs.

297 **Phylogenetic analysis**

298 The phylogenetic trees generated with the complete sequence of RNA1 and
299 RNA2 of LCV-SP and other members of genus *Crinivirus* show two well differentiated
300 lineages; one comprising LCV-SP, LCV, CCYV, BnYDV and CYSDV and the other is formed
301 by BPYV, ToCV, PVYV and LIYV (Fig 3) Then, two clades were generated where the
302 divergence is clear.

303 **Fig 3. Bayesian phylogenetic trees of RNA1 and RNA2 full-length of selected viruses**

304 **from the genus *Crinivirus*.** *Citrus tristeza virus* (CTV, NC001661), was used as an
305 outgroup. *Lettuce chlorosis virus* (LCV, FJ380118, FJ380119), *Lettuce chlorosis virus-SP*
306 (LCV-SP, MG489894, MG489895), *Lettuce infectious yellows virus* (LIYV, NC003617,
307 NC003618), *Cucurbit yellow disorder virus* (CYSDV, NC004809, NC004810), *Cucurbit*

308 *chlorotic yellow virus* (CCYV, JQ904628, JQ904629), *Bean yellow disorder virus* (BnYDV),
309 *Beet pseudo yellows virus* (BPYV, AY330918, AY330919), *Tomato chlorosis virus* (ToCV,
310 KP137100, KP137101), *Potato yellow vein virus* (PYVV, NC006062). PYVV genome is
311 tripartite and only its RNA1 has been considered in this analysis. Posterior probability
312 is indicated.

313 Identical typology is observed when the Bayesian analysis is done for the RdRp
314 region (Fig 4). When the analysis is done for other genomic relevant regions for
315 *Crinivirus* species demarcation as CP and CPm, two clades are also generated where
316 LCV-SP group with LCV, CCYV, BnYDV and CYSDV. Although in the same genetic clade,
317 CYSDV is particularly distant from LCV-SP, LCV, CCYV and BnYDV. The topology
318 generated in the phylogenetical analysis carried out for the HSP70 region was slightly
319 different from the CP gene tree because LCV-SP was located nearer BnYDV than CCYV
320 (Fig 4). This may indicate distinct recombination events in the *Crinivirus* genus. All the
321 phylogenetic trees presented in this work show that, independently of the gene
322 analysed, BnYDV and CCYV are closely related to LCV-SP and LCV although LCV, LCV-SP
323 and CCYV, have different host ranges and also have not been described in the same
324 geographic area.

325 **Fig 4. Bayesian phylogenetic trees for genomic relevant regions for *Crinivirus* genus**
326 **demarcation as HSP70, RdRp, CP and CPm.** Accession numbers and virus acronyms are
327 as in Fig 3. NC006063 and NC006061 corresponding with RNA2 and RNA3 of PYVV
328 were added for HSP70, CP and CPm analysis.

329

330 **Recombination analysis and variability in the recombinant** 331 **genomic region**

332 RDP4 package program was used to further confirm the putative existence of
333 first recombinant *Crinivirus* detected by Sanger and deep sequencing. Genomic
334 sequence of RNA1 and RNA 2 belonging to LCV, BnYDV, CCYV and LCV-SP aligned were
335 scanned in RDP4 using multiple methods. The full recombination scan of both RNA
336 genomes (1 and 2) of LCV, BnYDV, CCYV and LCV-SP resulted in four recombination
337 events detected (Figure 5, Table 2). The analysis detected LCV RNA1 and BnYDV RNA1
338 as possible major and minor parental sequences for LCV-SP RNA1 (event 1) with a 99%
339 level of confidence (Table 2, event 1). This event was identified by all seven methods
340 implemented in this package and, all of them show higher p value than any other
341 algorithm executed in the rest of the events detected. BnYDV RNA1 was also suggested
342 as a major parental sequence for CCYV RNA1 using five algorithms and with unknown
343 minor parental (Table 2, event 2). Event 3 was detected by seven algorithms and
344 signaled to LCV RNA2 as minor parental and CCYV-RNA2 as a possible recombinant.
345 Although this event was suggested for seven methods as event number 1 was, the
346 highest p -value ($7,181 \times 10^{-9}$, RDP) is much lower than in event 1 ($5,710 \times 10^{-103}$, RDP).
347 LCV RNA2 was identified for six methods as a putative recombinant in event 4 with
348 LCV-SP RNA2 and CCYV RNA2 as major and minor possible parental respectively (Table
349 2, event 4).

350 **Fig 5. Recombination analysis of RNA1 and RNA2 of LCV, BnYDV, LCV-SP and CCYV**
351 **using the recombination detection program (RDP-4).**

352

353 **Table 2. Unique recombination events identified by Recombination Detection Program v 4.80 (RDP4).**

354

Event	Recombinant	Major parent	Minor parent	RDP	Geneconv	Bootscan	Maxchi	Chimaera	Siscan	3Seq	Begin	End
1	LCV-SP RNA1	LCV RNA1	BnYDV RNA1	$5,710 \times 10^{-103}$	$6,418 \times 10^{-63}$	$2,665 \times 10^{-107}$	$5,521 \times 10^{-29}$	$4,462 \times 10^{-28}$	$2,232 \times 10^{-36}$	$1,332 \times 10^{-15}$	7580	8815
2	CCYV RNA1	BnYDV RNA1	Unknown	$2,182 \times 10^{-4}$			$1,403 \times 10^{-2}$	$6,949 \times 10^{-4}$	$3,625 \times 10^{-5}$	$2,131 \times 10^{-2}$	7044	8225
3	CCYV RNA2	Unknown	LCV RNA2	$1,498 \times 10^{-9}$	$1,498 \times 10^{-4}$	$3,316 \times 10^{-9}$	$2,801 \times 10^{-2}$	$4,708 \times 10^{-4}$	$6,834 \times 10^{-6}$	$7,181 \times 10^{-9}$	7858	75
4	LCV RNA2	LCV-SP RNA2	CCYV RNA2	$6,581 \times 10^{-6}$	$2,614 \times 10^{-2}$	$6,247 \times 10^{-3}$	$5,859 \times 10^{-9}$	$5,244 \times 10^{-6}$		$1,109 \times 10^{-4}$	585	1046

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360 To confirm the result obtained from RDP4, BootScan analysis using each
361 putative recombinant as query sequence were executed with the Simplot package.
362 When the analysis was performed for LCV-SP RNA1, a point of recombination was
363 detected in the same genomic area described by RDP4 (Fig 6). This result supports the
364 evidence that LCV RNA1 (FJ380118) and BnYDV RNA1 (EU191904) are the origin of the
365 LCV-SP RNA1 genome. The recombination events 2 and 4 however, were not
366 recognized by the Simplot package. Bootscan analysis using CCYV RNA2 as query (Fig 7)
367 suggested a recombination point at 3'UTR as is described in RDP4 (Fig 5) but not in the
368 5'UTR region (Fig 6).

369 **Fig 6. Bootscan analysis with Simplot program using LCV-SP RNA1 as the query**
370 **sequence.** CCYV, LCV, and BnYDV RNA1 were compared. Analysis was carried out with
371 a sliding window of 200 bp and a step size of 20 bp.

372 **Fig 7. Bootscan analysis with Simplot program using CCYV RNA2 as the query**
373 **sequence.** CCYV, LCV, and BnYDV RNA2 were compared. Analysis was carried out with
374 a sliding window of 200 bp and a step size of 20 bp.

375 Eleven DNA fragments corresponding with the entire P26 and P6 sequence of
376 the RNA1 of LCV-SP were submitted to the GenBank database with the accession
377 numbers assigned (MH170031-MH170041). These sequences confirmed the presence
378 of the recombinant LCV-SP in the south of Spain since at least 2011. Values of genetic
379 distance sequences at non-synonymous positions for both ORFs were of the same
380 magnitude (Table 3). The ratio between nucleotide diversity values in non-synonymous
381 and synonymous positions (dNS/dS ratio) indicates the amount of variation in the

382 nucleic acid which results in variation in the encoded protein [34-36]. For P26, genetic
383 distance at synonymous positions was null, and consequently, it was not possible to
384 calculate the dNS/dS ratio. In the case of P6, The dNS/dS ratio was below unity, which
385 could indicate a negative selection against protein change. However, the value of the
386 standard error is too high to consider the data conclusively.

387 **Table 3. Nucleotide diversity for the 3' end LCVSP genome**

Sequence	dNS	SE	dS	SE	D	SE
p26	0.00126	0.00087	0	0	0.0009	0.00072
p6	0.00167	0.00166	0.00305	0.00321	0.00212	0.00153

388 Nucleotide diversities computed for nonsynonymous (dNS) and synonymous (dS) positions using the
389 PBL method (see Methods). Standard errors (SE) were calculated by bootstrap method with 500
390 replicates.

391 **Molecular differentiation between yellowing induced by BnYDV** 392 **or LCV-SP**

393 Restriction analysis with *KpnI* after RT-PCR with the primers LC-BnF/LC-BnL ,
394 which amplified partial sequence of RdRp and P26 in both viruses, yielded two
395 fragments of 582 y 157 bp when the virus was LCV-SP and a single band of 769 bp
396 when the virus present was BnYDV. This RFLP test is then capable of distinguishing
397 yellowing disease originating from recombinant or non-recombinant virus isolates (Fig
398 8).

399 **Fig 8. RFLP analysis with *KpnI* after RT-PCR with by primers LC-BnF/LC-BnL.** Lanes 1, 3:
400 cut amplification products of LCV-SP isolates obtained in 2013 and 2017 respectively.
401 Lanes 2 and 4: same amplification products uncut. Lane 5 and 7: cut amplification

402 product of BnYDV isolates obtained in 2005 and 2009. Lanes 6 and 8: same
403 amplification products uncut.

404 Discussion

405 Members of genus *Crinivirus* represent a worldwide emerging disease as
406 evidence of the increasing number of new species identified during the past 20 years
407 [37-39, 9, 4]. Or, as in another example, a species already described increases its host
408 range [40]. New LCV isolates have been recently described affecting ornamental
409 plants, tobacco and tomato crops [41-43]; but there is no information about the
410 capability of these LCV isolates to infect lettuce crops. Primer walking method and
411 deep sequencing of vsRNA allowed the elucidation of the sequence and genome
412 organization of the first recombinant closterovirus resulting after crossover
413 recombination of intact ORFs. The 5' from LCV-SP RNA1 includes the replication
414 module (ORF 1a and 1b), which share high homology (more than 90%) with the LCV
415 type isolate (FJ380118); however, the 3' end, which encompass P26 and P6, shares high
416 amino acid identity with the 3' end of BnYDV RNA1 (99 and 100%, respectively). These
417 ORFs, are described to be expressed in LCV from 3' coterminal subgenomic RNAs
418 (sgRNAs), a typical strategy among closteroviruses [8,6,44] that increases the
419 probability of recombination events [45].

420 The genomic sequence of LCV-SP RNA2 share 8 ORFs with the Californian
421 isolate of LCV (FJ380119); P6, and P4.8, located in the 5' and 3' end of the Californian
422 isolate, respectively, and with unknown function, are absent in LCV-SP. Both putative

423 proteins are also absent in the LCV Chinese isolates recently reported [41,42], which
424 could indicate that these genes are not essential in the biology of LCV.

425 3'UTRs sequences in both genomic RNAs are highly conserved, sharing 72% of
426 nucleotide sequence identity. This feature is common among criniviruses [46] and it
427 agrees with the notion that sequence identity is essential to generate structures that
428 facilitate the synthesis of the negative sense RNA during replication [47,48,44].

429 The accumulation of vsiRNAs observed in different genome regions probably
430 involve gene expression strategies common within closteroviruses as translational
431 frameshift and the production of 3'coterminial sgRNAs [8]. The lower presence of
432 vsiRNAs along ORF 1b, compared with ORF 1a, suggest that this ORF is presumably
433 expressed by translation via a +1 ribosomal frameshift rather than by sgRNA
434 production as it was proposed before for LCV and other closteroviruses [49-51,6]. The
435 presence of vsiRNAs hot spots along ORF 2, 3 and 4 of LCV-SP RNA2, could correspond
436 with the production of sgRNAs, as was described in LCV [6].

437 Higher number of 21-nt class vsiRNAs populations with respect to 22-nt support
438 the prevalence of a Dicer like protein 4 (DCL4) in the production of vsiRNAs in beans, as
439 has been suggested in others plants [52,53]. 21- and 22-nt vsiRNAs populations,
440 showed the same preference for sense or antisense polarity in RNA1 and RNA2,
441 indicating that the mechanisms responsible for strand polarity are not dependent on
442 the preference of DCL enzymes but on other factors specific to this virus species. The
443 nucleotides present at the 5' and 3' terminal positions were investigated and resulted
444 in an overall preference for A/U nucleotides. This prevalence is widespread among
445 plant virus-pathosystems [54] and indicates the involvement of similar AGO complexes

446 in the silencing of LCV-SP by green beans. Although the function of P26 and P6 in LCV-
447 SP RNA1 (and hence BnYDV-RNA1) is unknown, the reduction of vsiRNA populations in
448 this region could suggest that P26 or P6 interfered with the accumulation of vsiRNA.
449 Recently, P23 of LCV, the closest homologous protein of P26, and also located at the
450 3' end of RNA1, has been described as a viral suppressor of RNA silencing (VSRs) and
451 whose suppressor activity produces a reduction of siRNA [7]. To elucidate this
452 hypothesis additional experiments are required.

453 Phylogenetic analysis grouped LCV-SP closely in the same lineage as LCV, CCYV and
454 BnYDV as was already reported [9,6]. Recombination analysis completed with RDP4
455 and Simplot programs, demonstrates the existence of natural crossover recombination
456 of intact ORFs between LCV-RNA1 and BnYDV-RNA1 (event 1). The recombinant virus,
457 LCV-SP, shifted its host range by affecting green bean crops and not lettuce, its original
458 host [11,5]. No other evident recombination events were detected in our analyses.
459 Events 2, 3 and 4 have been discarded as possible recombinants although, alternatively
460 they could be indicative of the close genetic relationship between LCV, LCV-SP, BnYDV
461 and CCYV, as has been observed in the phylogenetic analysis. Plant virus with
462 segmented genomes seem to frequently accumulate recombinants [45,55]. Within
463 genus *Crinivirus*, which shows the lowest variability within the family *Closteroviridae*
464 [19], only *Sweet potato chlorotic stunt virus* (SPCV) and *Beet pseudo yellows virus*
465 (BPYV) have been reported as examples of recombination-mediated gene gain [39,21].
466 The existence of LCV-SP changes the perspectives of the possible epidemiological
467 scenarios within the genus *Crinivirus*, an emergent genus and, as we have
468 demonstrated, with more recombination possibilities than previously shown.

469

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473 **Author Contributions**

474 Conceived and designed the experiments: LR, DJ. Performed the experiments: LR, AS,
475 CG, LV Analyzed the data: LR, LV, DJ. Wrote the paper: LR, DJ.

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640

641 **Supporting information**

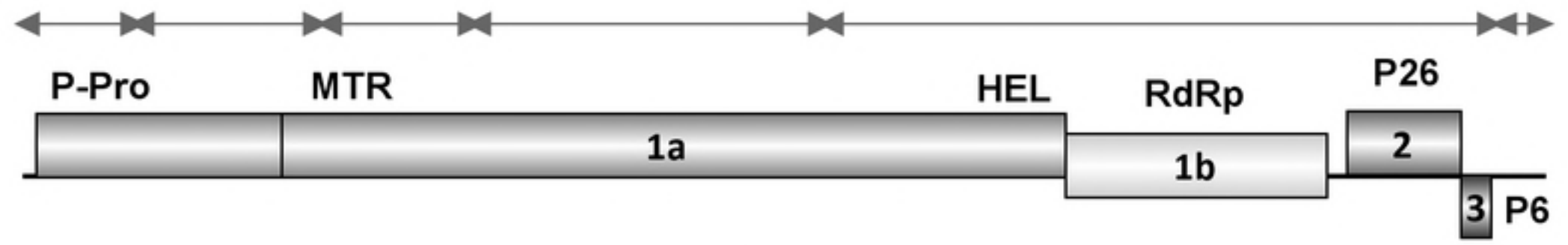
642 **S1 Table. Primers list used to confirm the LCV-SP genome by RT-PCR.**

643 **S2 Table. Numbers of reads homologies identified by BLASTN from contigs obtained**
644 **from small RNAs and dsRNAs libraries.**

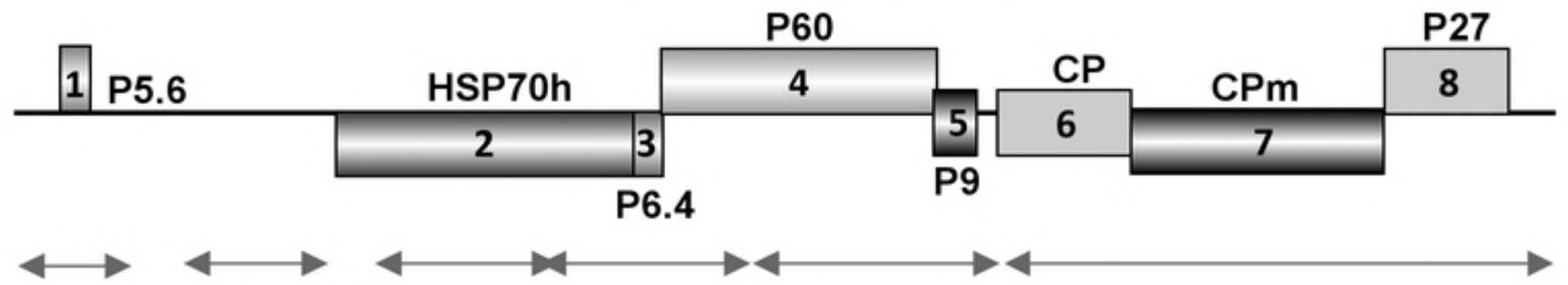
645 **S1 Fig. Percentages of nucleotide species at the 5' and 3' ends of redundant vsiRNAs**
646 **derived from LCV-SP RNA1 (A) and RNA2 (B) according to the size of the reads.**

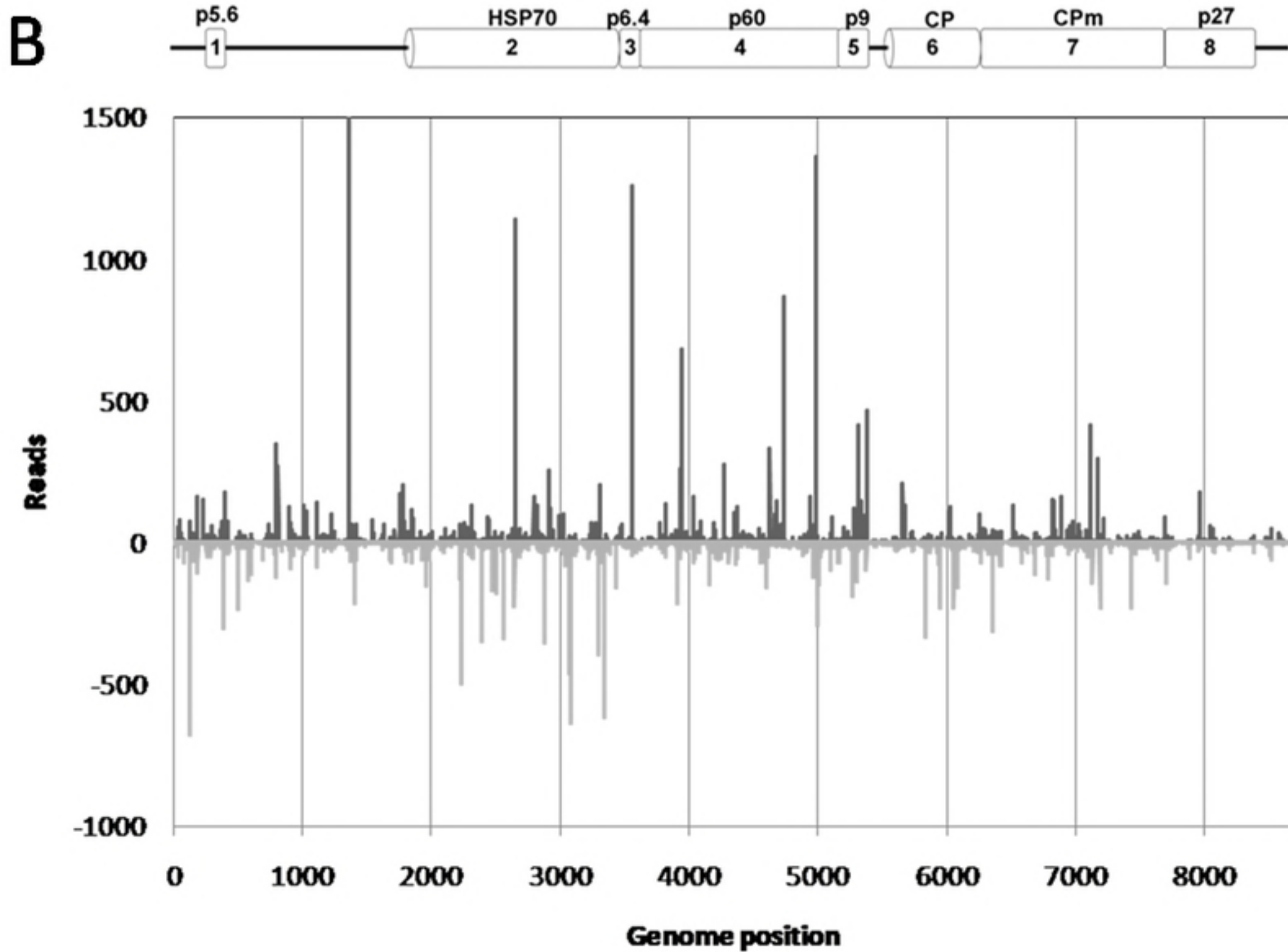
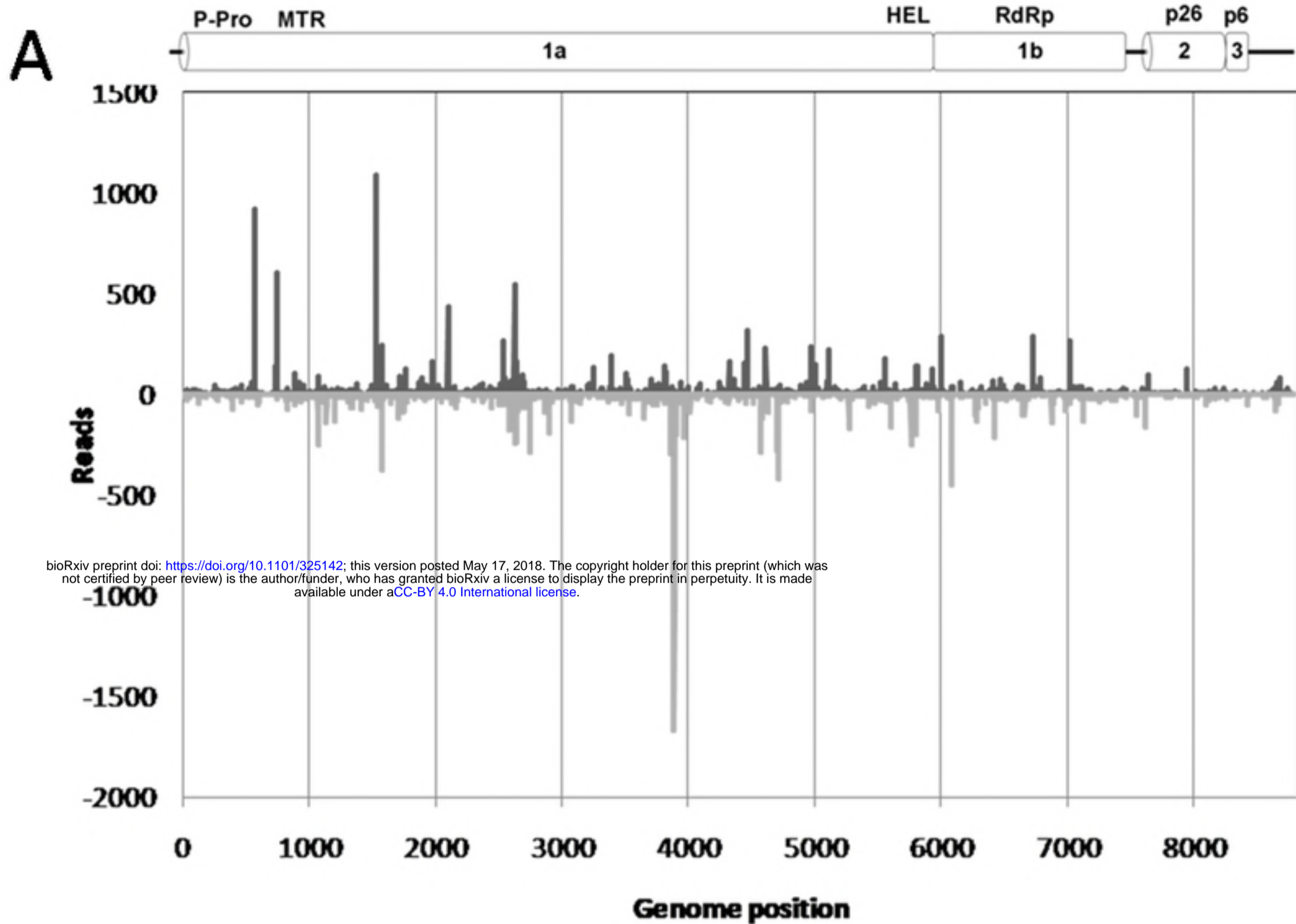
647

RNA 1 (8.85 kb)

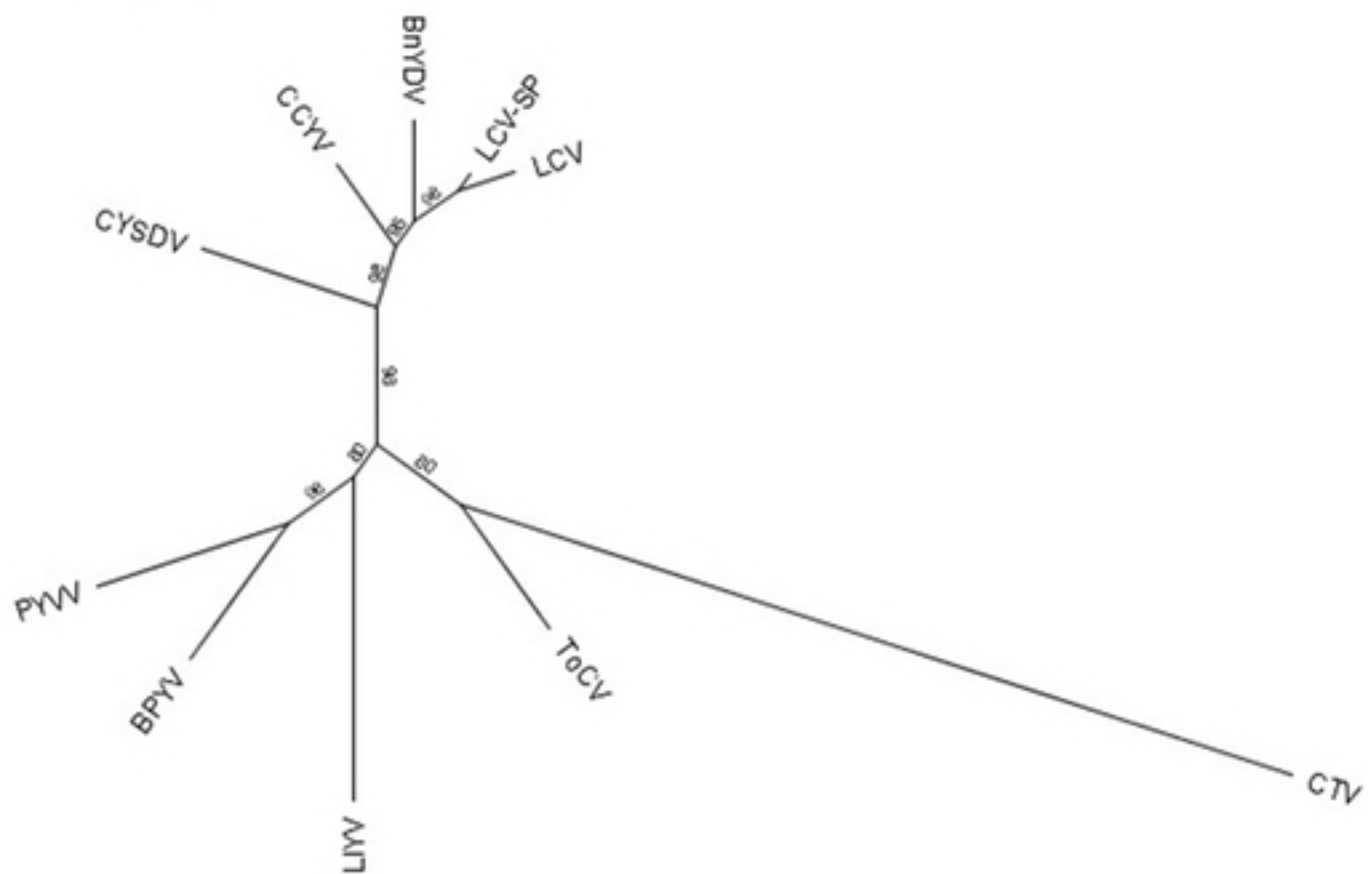


RNA 2 (8.67 kb)



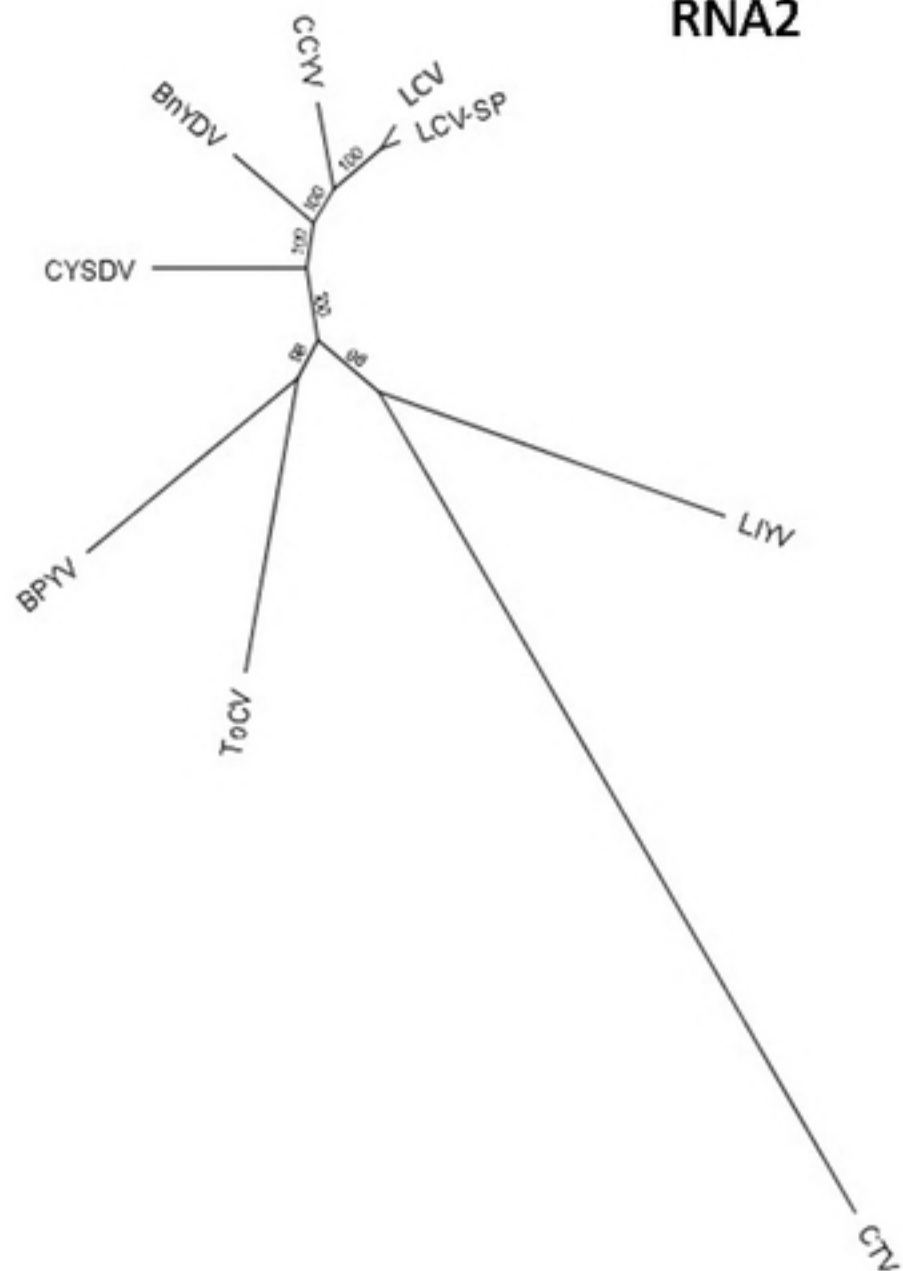


RNA1



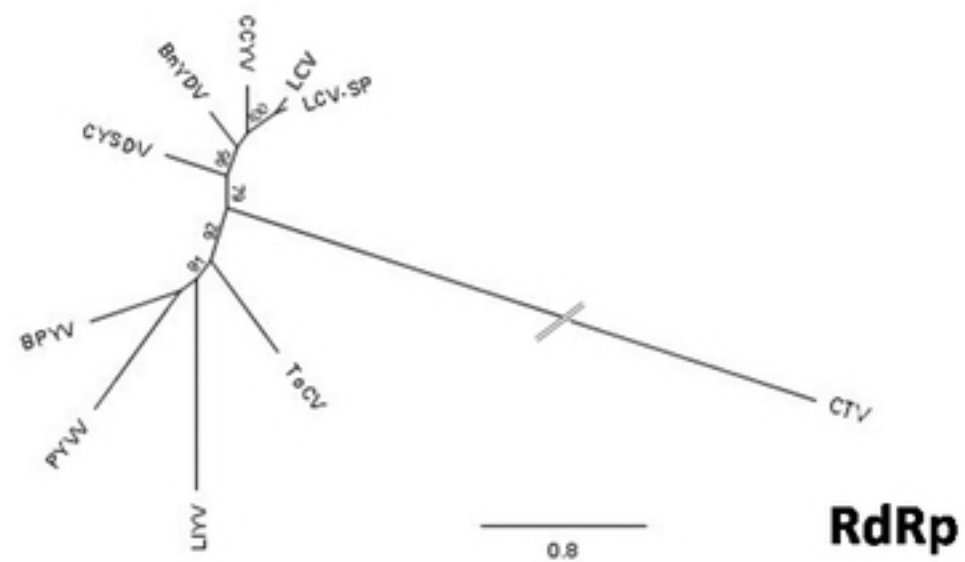
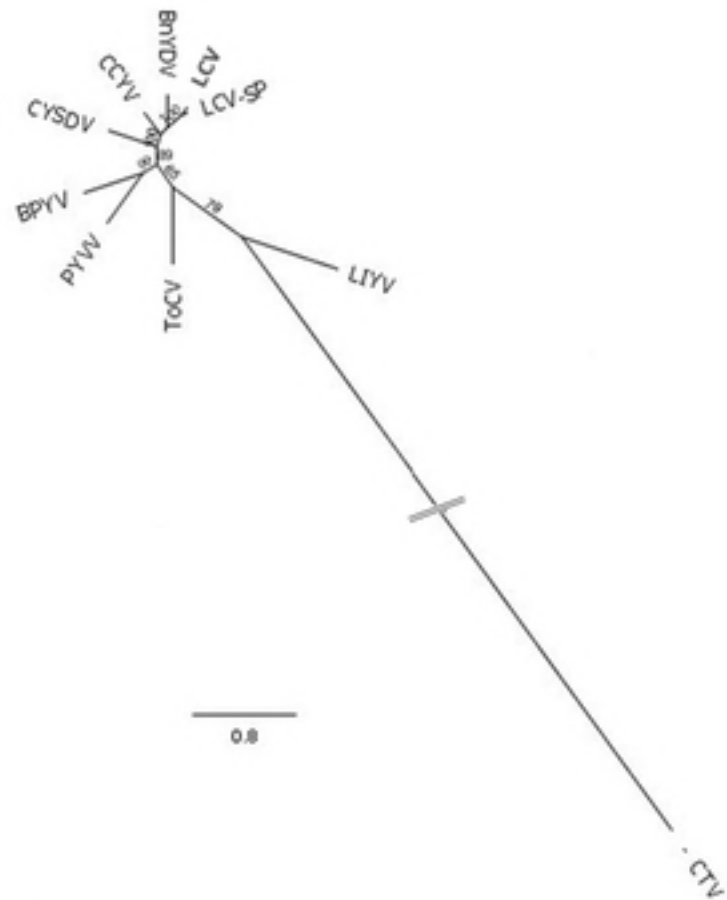
0.8

RNA2

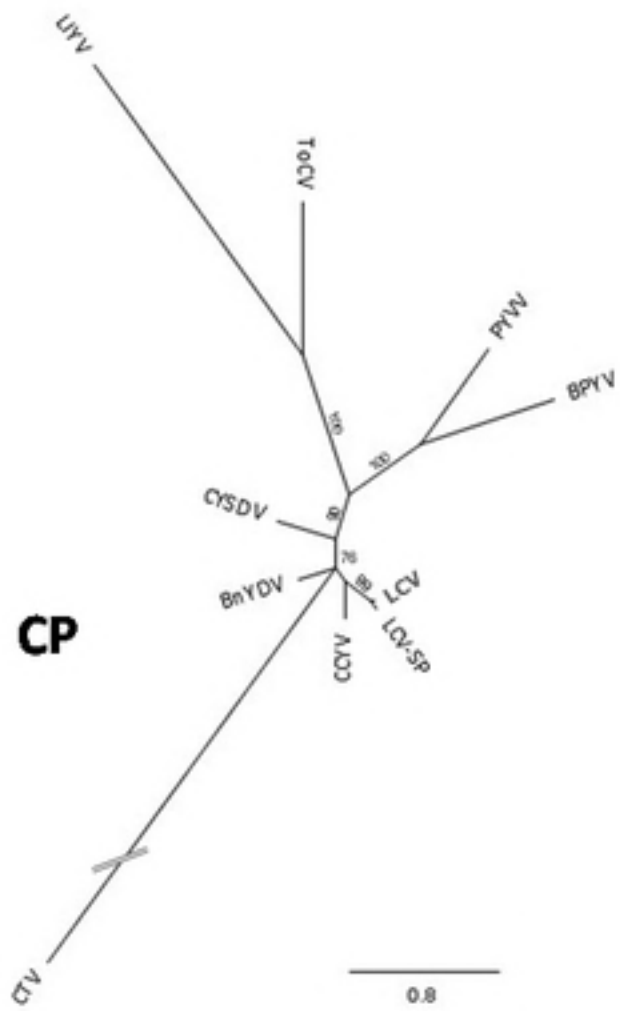


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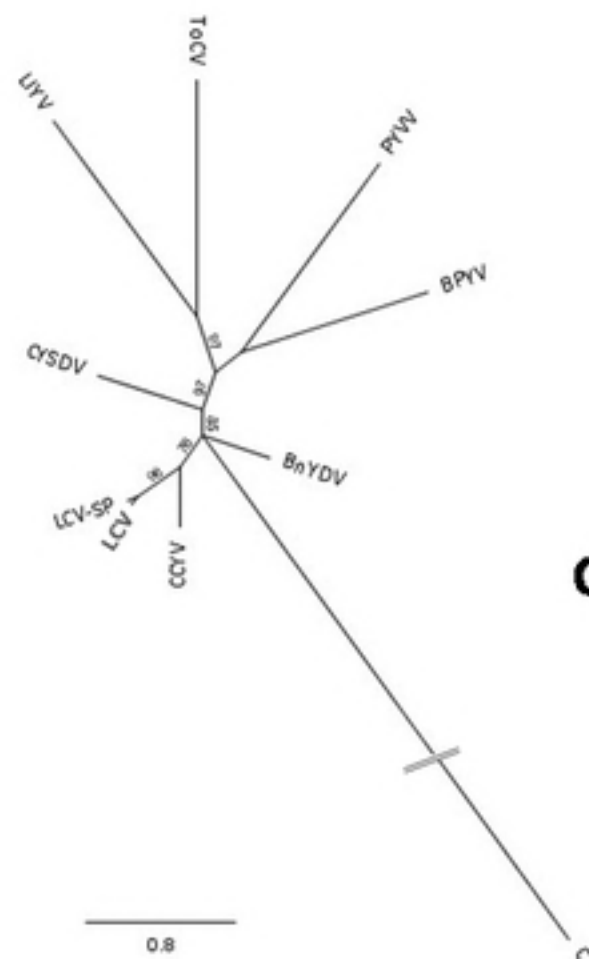
HSP70



CP



CPm



CCYV RNA1



LCV-SP RNA1

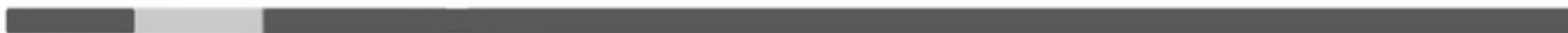


CCYV RNA2



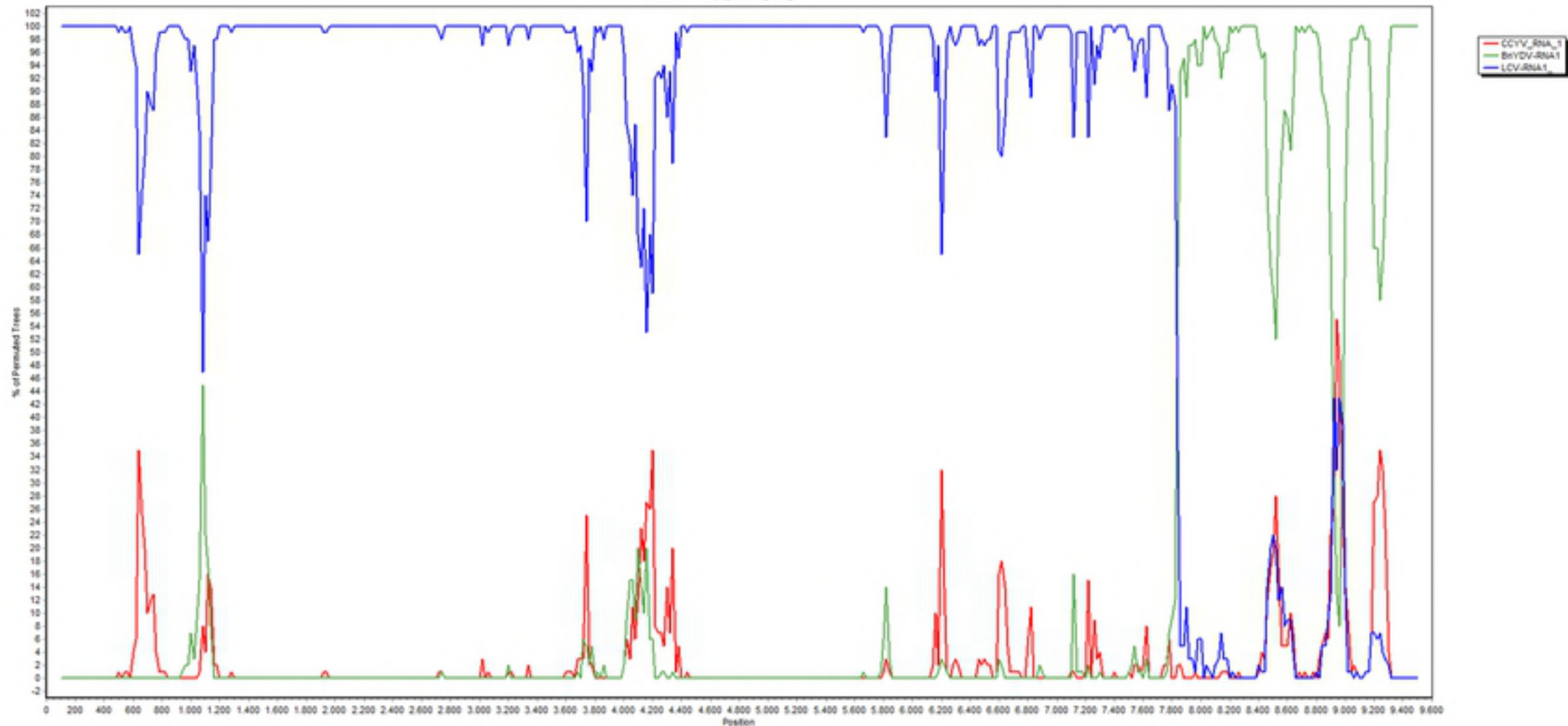
LCV RNA2

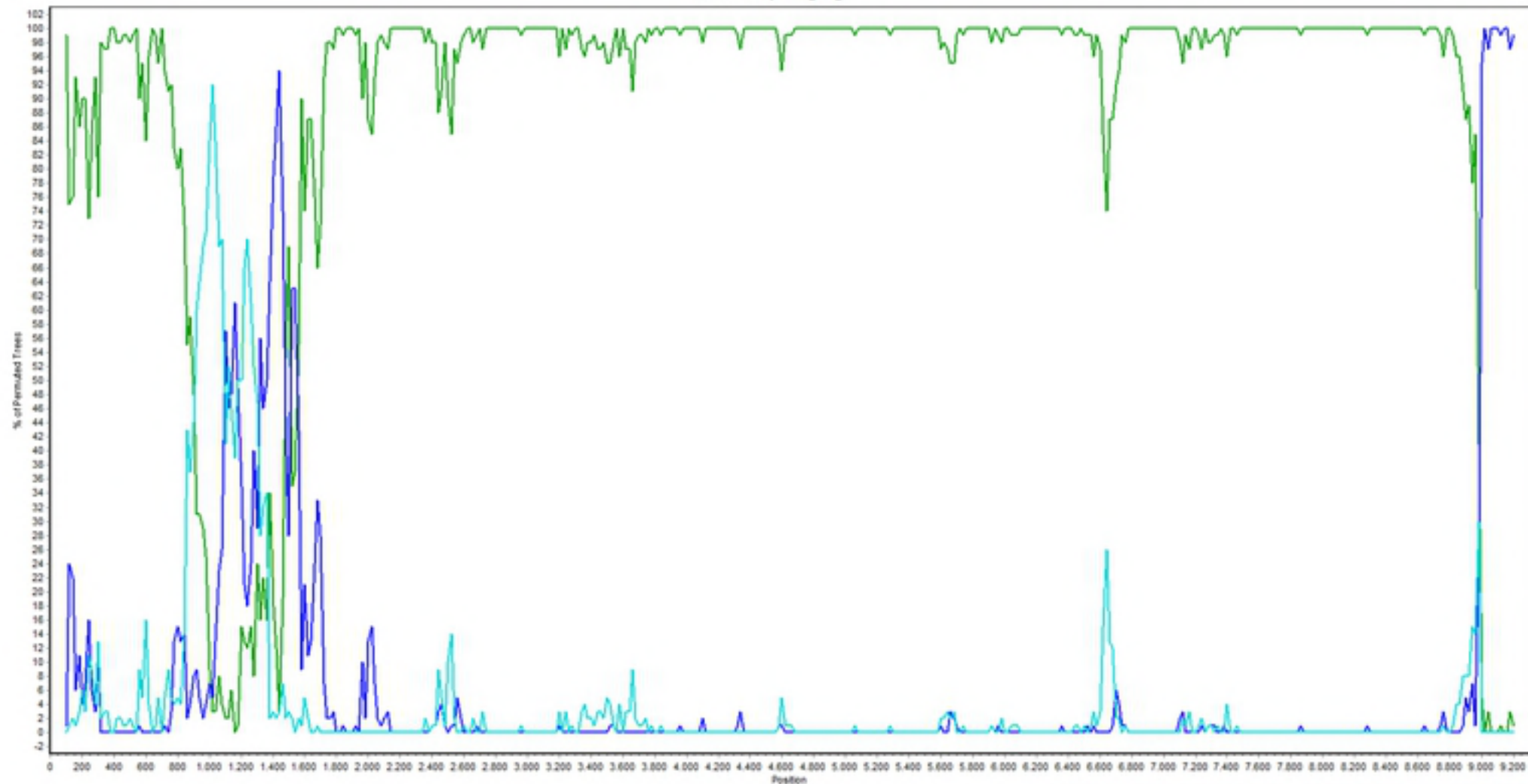
LCV RNA2



4

CCYV RNA2





— BNYDV_RNA_2
— LCV-RNA2
— LCV.SP_RNA_2

1000

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