

Supplementary Materials

Characterization of a Proposed *Dichorhavirus* Associated with the Citrus Leprosis Disease and Analysis of the Host Response

Figure S1. CiLV-C and HGSV are not present in citrus samples displaying leprosis symptoms. (A) Agarose gel showing no amplified cDNA when total RNA was used as a template sour orange tissue when primers directed against the CP of CiLV-C (**upper panel**) and HGSV (**middle panel**). (**Lower panel**) Amplification of the internal control, COX, from the *Citrus* species. (B) Primers employed in the detection of infected tissue.

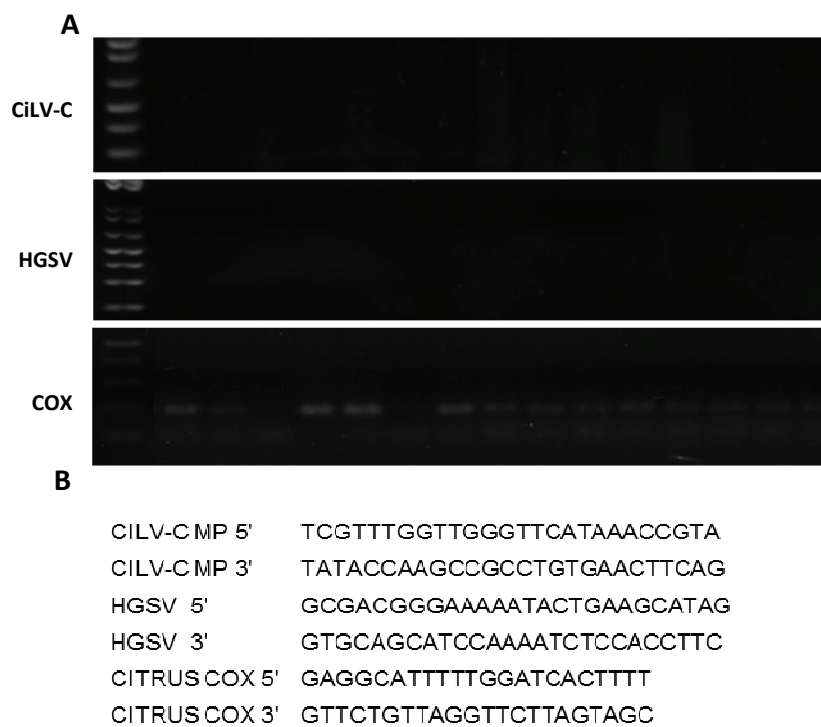
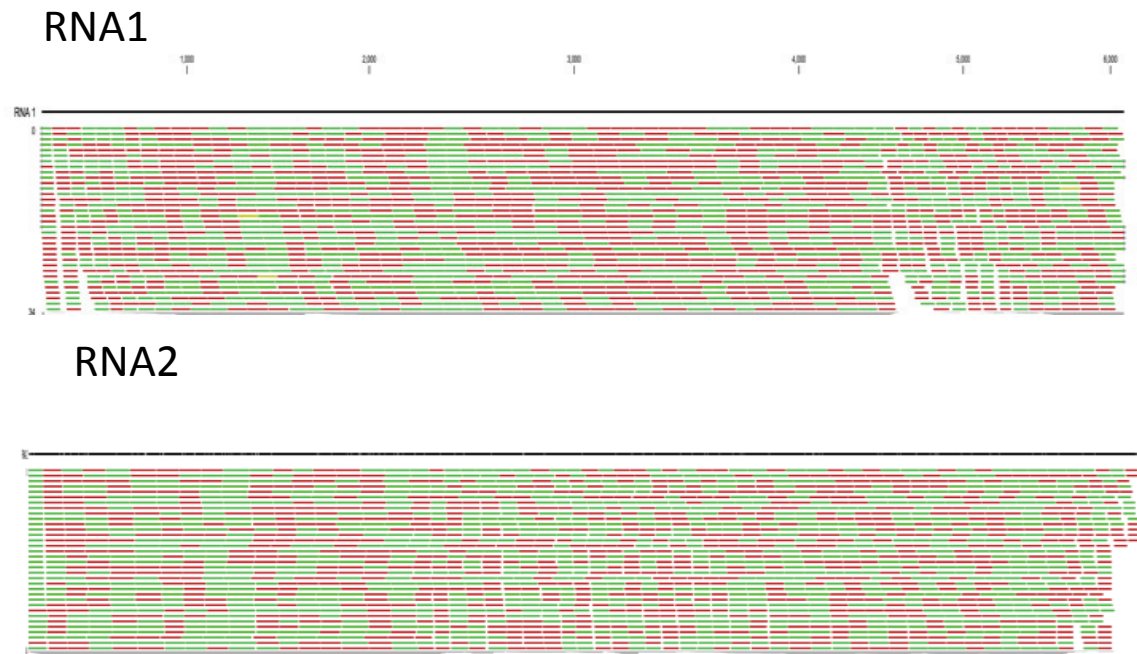


Figure S2. Deep-sequence read coverage of the RNA 1 and RNA2 of the CNSV genome. These are represented as green and red lines under the assembled viral genome. Green lines correspond to sense reads relative to the OFV genome and red lines to antisense reads.



CNSV	CTGTGAAGCCTGCTGAGTCATTCATGAAGGGTGTTCATCAGATTAAACAGGCATATTCAG	840
CILV-N	CTGTGAAGCCTGCTGAGTCATTCATGAAGGGTGTTCATCAGATCAAACAGGCATATTCAG	801
OFV	CTGTGAAGCCGCTGAGTCATTTATGAAGGGTGTTCATCAGATCAAACAGGCATATTCAG	801

CNSV	TCCTGGTGGGAGAGCACTCTGAGTTCCTGTTCAATTATTCATACTCAGAAGGAATGTGCA	900
CILV-N	TCCTGGTGGGAGAGCACTCTGAGTTCCTGTTCAATTATTCATACTCAGAAGGAATGTGCA	861
OFV	TCCTGGTAGGAGAGCATTCTGAAATTCCTGTTCAATTACTCTATTCAGAAGGAATGTGCA	861

CNSV	GAAACATAGCCGACATGTTCAACCAATGCGATGATCTCAAGGCAACTCTTTGTTCATCATT	960
CILV-N	GAAACATAGCCGACATGTTCAACCAATGTGATGATCTCAAGGCAACTCTTTGTTCATCATT	921
OFV	GGAAATATAGCCGACATGTTCAACCAATGTGATGATCTCAAAGCAACTCTTTGCCATCACT	921
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CNSV	GTGCCATAGCAGATGAAACGCACCACCAATAGGAAGAGGCACGGCTTCTCAGATTC	1020
CILV-N	GTGCCATAGCAGATGAAACGCACCACCAATAGGAAGAGGCACGGCTTCTCAGATTC	981
OFV	GCGCCATAGCAGATGAGACGCACCACCAATAGGAAGAGGCACGGACTTCTCAGATTC	981
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CNSV	TGATCCTTCAGCATGTAGATCTCACAGGGATGATCCCATATGGGATGTACATTGACATGA	1080
CILV-N	TGATCCTTCAGCATGTAGATCTCACAGGGATGATCCCATATGGGATGTACATTGACATGC	1041
OFV	TAATCCTTCAACATGTGGATCTTACGGGATGATCCCATATGGAATGTACATTGACATGC	1041
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CNSV	GAAGGCACCTTCACCCCTCTGACACCCGGCCAGTTGCTGACATGGCTCCATGACAACCAGG	1140
CILV-N	GAAGGCACCTTCACCCCTCTTAACACCCGGCCAGTTGCTGACATGGCTCCATGACAACCAGG	1101
OFV	GAAGGTACTTCACCCCTCTTAACACCCGGCCAGTTGCTAACATGGCTTCATGACAACCAGG	1101

CNSV	TATCCAGGCCTCTCAGTGTCAATGCGGACATAAACACCAGGTATGATGTTTCAAACGGAT	1200
CILV-N	TATCCAGGCCTCTCAGTGTCAATGCGGACATCAACACCAGGTATGATGTTTCAAACGGAT	1161
OFV	TATCTAGGCCTCTCAGTGTGATGCGGACATAAACACCAGGTATGATGTTTCTAACGGGT	1161
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CNSV	CAGACCGGTTCTGGAGTACTCAAGGGGCTTGATCCAGGATTCCTTCATAGCATTACAAC	1260
CILV-N	CAGACCGGTTCTGGAGATACTCAAGGGGCTTGATCCAGGATTCCTTCATAGCATTACAAC	1221
OFV	CAGATCGGTTCTGGAGTACTCAAGGGGCTTAGACCAGGATTCCTTATAGCTTACAAC	1221
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CNSV	AATCAAAATGTGTCACCTTGATAGCCAGAATGGCACACATACTGGTGAAGGGAGGAGCCG	1320
CILV-N	AATCAAAATGTGTCACCTGATAGCCAGAATGGCACATATACTGGTGAAGGGAGGAGCCG	1281
OFV	AGTCAAAATGTGTCACCTCTGATAGCCAGGATGGCACATATACTGGTGAAGGGAGGAGCCG	1281
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CNSV	TTGCTGTCAATGAATACTCCGACCCCGAAAGGCAAAGTCACTGGAGAACAAGCCTGGGC	1380
CILV-N	TTGCTGTCAATGATACTCCGACCCCGAAAAGCAAAGTCACTGGAGAACAAGCCTGGGC	1341
OFV	TCGCTGTCAATGAATACTCCGATCCTCGAAAGGCAAAGTCACTGGAGAACAAGCCTGGGC	1341
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CNSV	TGGCAGCGGAGGCTGACAAGTTTGCCACAGAGTTTGTGGAAGCATACAACGGCCTATCAG	1440
CILV-N	TGGCAGCAGAGGCTGACAAGTTTGCCACAGAGTTTGTGGAAGCATACAACGGCCTATCAG	1401
OFV	TGGCAGCGGAGGCAGACAAGTTGCCACTGAGTTCTGTGAGGCATACAACGGCCTATCAG	1401




CNSV	GGTCAAGTGCTAATGCCGGCCCTGTATCCCGTAAACTCTACAACCAAGGCAGAGGTATTC	1500
CILV-N	GGTCAAGTGCTAATGCCGGCCCTGTGTCCCGCAAACCTCTACAACCAAGGCAGAGGTATTC	1461
OFV	GATCAAGTGCAAAAGCCGGCCCTGTGTCCCGCAAACCTCTACAACCAAGGCAGAGGCATCC	1461
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CNSV	CTACCCGCAGAGGCTTATTCACACCTCCCTCCGCCAGACCCGCACCTGTTGTGAATGTGC	1560
CILV-N	CTACCCGCAGAGGCTTATTCACACCTCCCTCCGCCAGACCCGCACCTGTTGTGAATGTGC	1521
OFV	CGACCCGCAGGGGCTTTCACACCCCTCCGCCAGACCTGCGCCCGTTGTGAATGTAC	1521
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CNSV	ATAFCCCAGCCGCTCGTCTCTTTAGCAGGAGCCCTGGATGCTATGAACAGTGAATGAC	1620
CILV-N	ACGTCCCAGCCGCTCGTCTCTTTGGCAGGAGCCCTAGATGCTATGAACAGCGAATGAC	1581
OFV	ACGTCCCTGCCGCTCGTCTCTCTGACAGGGCCCTGGATGCCATGAACAGTGAATGAC	1581






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IGR1

CNSV	AACCATCCTCTCATGGCAAACCTCCATCCCTA	CCATGACAATATGCTATATATATATGCG	1680
CILV-N	AACCATCCTCTCATGGCAAACCTCCATCCCTATCG	TGACTACATGCTATATATATGT----	1637
OFV	AGCCACCTCTCATGGAAAGAC-CCCATCTCTATCAT	AACAATATGCTATATATATGCG----	1636
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CNSV	TGCATTTAAATAAAAAAACAACAGGAAACTTATGCT	TTGTTTCATCTCCTCACGCACACAC	1740
CILV-N	TGCATTTAAATAAAAAACAACAGGGAAACTTATGTTG	CTCATCTCCTCACGCACACAC	1697
OFV	TGCATTTAAATAAAAAACAACAGCGAACTTGTGTTG	TATCACTTCAT-----ATAT	1692
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	ORF2: P		
CNSV	ACTAACGGCCTCACATATATTCTCTTTCCA	GGAAAAATGTTCAACCACCAAGGTAAATATGT	1800
CILV-N	ACTAACAGCCTCACATATATTCTCTTTCCA	GGACAATGTTCAACCACCAAGGTAAATATGT	1757
OFV	ATTAAACAGCTTACATATATTTCTCA	TTCCAAGGAAATGTTCAACCACCAAGGTAAATATGT	1752
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CNSV	ACCCAGAGGTCCCAGCTCGTCTCAAGTGTCCGAT	GACATAGACAACGACACACAAGTAG	1860
CILV-N	ACCCAGAGGTCCCAGCTCGTCTCAAGTGTCCGAT	GACATAGACAACGACACACAACATAG	1817
OFV	ACCCAGAGGTCCCAGCTCATCC	CAAGTGTCCGACGACATAGACAACGACACACAGTAG	1812
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CNSV	ACGAGGTCGCAGCATTGTGAGGAAATGGT	CGGCTGCCGGACTATCTCCCCCTGTCACCC	1920
CILV-N	ACGAGGTCGCAGCATTGTGAGGAAATGGT	CGGCTGCCGGACTATCTCCCCCTGTCACCC	1877
OFV	ATGAGGTCGCAGCATTGTGAGGAAATGGT	CAGCTGCCGGACTATCTCCCCCTGTCACCC	1872
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CNSV	TTGCAAAGAACCCTTAGAGCATGGATAGCAAG	CAACACCAACCCAGGGAACCCCTTGGTGC	1980
CILV-N	TTGCAAAGAACCCTTAGAGCATGGATAGCAAG	CAACACCAACCCAGGGAACCCCTTGGTGC	1937
OFV	TTGCAAAGAACCCTCAGAGCATGG	GTAGCGAGCAACACCAACCCAGGGAACCCCTTGGTGC	1932
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CNSV	TGGACGACAGGATGCTAAGTCTCACAACCA	TGATATGGAACACAGCAGCGGAGCATTATA	2040
CILV-N	TGGACGACAGGATGCTAAGTCTCACAACCA	TGATATGGAACACAGCAGCGGAGCATTATA	1997
OFV	TGGACGACAGGATGCTTAGTCTCAG	CACCATGATATGGAACACAGCAGCGGAGCATTATA	1992
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CNSV	CTATGATCGGCAAATCCAGGTCAATCGCAT	GTGCATCACTCATCGACCAGCTGGGGGAGA	2100
CILV-N	CCATGATCGGCAAATCCAGGTCAATCGCAT	GTGCATCACTCATCGACCAGCTGGGGGAGA	2057
OFV	CTATGATCGGTA	AAATCTCAGGTCAATCGTATGTCAAGCCTTATTGACCAGCTGGGGGAGA	2052
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CNSV	TCTCCGGCCGCA	GACCAACAGCAGGGTCCCTCGCTCGATATGCCACCTCCCCCTCCTAAGA	2160
CILV-N	TCTCCGGCCGCAAG	CCACAACAGGGTCCCTCGTTCGATATGCCACCTCCCCCTCCTAAGA	2117
OFV	TCTCCGGCCGAAAACC	GAGCAGGGTCCCTCATTCGACATGCCACCTCCCCCTCCTAAGA	2112
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CNSV	GGAACACCCAGATTCACTAGACACTAACCC	TATCTTAGGCTTAATAGGTCAGGACTGGG	2220
CILV-N	GGAACACCCAGACTCT	CTAGACACTAACCCATTTTAGGCTTAATAGGTCAGGACTGGG	2177
OFV	GGAACACCCG	GATTCACTAGACACTAACCCATCTTAGGCTTAATAGGTCAGGACTGGG	2172
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CNSV	ATGAAAAGAAGGACAAACAGTGGAGG	GAGAAGCCAGCAGACAAGAAACATCTAGTGCTCA	2280
CILV-N	ACGAAAAGAAGGACAAACAGTGGAGG	GAGAAGCCAGCAGACAAGAAACATCTAGTGCTCA	2237
OFV	ACGAAAGAAGGACAAA	CAGTGGAGGAGAAGCCAGCAGATAAGAAACATCTAGTGCTCA	2232
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CNSV	ACTGGGTGTTACACGAGTAC	CTGGGGTTCTAACAAAACCGGTAACAATCAAGTGGATAA	2340
CILV-N	ACTGGGTGTTACACGAGTACT	TGGGAGTCTTAACAAAACCGGTGACAATCAAGTGGATAA	2297
OFV	ACTGGGTGTTACAT	GAAATTTGGGAGTCTTAACAAAACCGGTAACGATCAAGTGGATAA	2292
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CNSV	CAGACAATCCATCGTCCCTGGAGTTGGGAG	CAGTTTCAGCATATGCCCTAAGACATCAGG	2400
CILV-N	CAGACAATCCATCGTCCCTGGAGTTGGGAG	CAGTTTCAGCATATGCCCTAAGACATCAGG	2357
OFV	CAGACAATCCG	TTCGTTCTGGAGTTGGGAGCAGTTTCAGCATATGCCCTGAAACATCAGG	2352
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CNSV	CCAGCTTGTCCGACTG	CGATAAAGAGGCCCTCAGAGCACTCGTGGTCCAGACAGTGAAGA	2460
CILV-N	CCAGCTTGTCCGACTGTGATAAAGAGGCCCT	CAGAGCACTCGTGAATCCAGACAGTGAAGA	2417
OFV	CCAGCTTGTCCGACTGTGAC	AAAGAGGCCCTCAGAGCACTTGTGGTTCAAACAGTGAAGA	2412

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	IGR2	
		
CNSV	ACACCCCCAAGAGGCCATGCCTGGACTAGGTGATATCCTATCAGCCCTATCATATATATG	2520
CILV-N	ACACCCCCAAGAGGCCATGCCTGGACTAGGTGATATCCTATCAGCCCTATCATATATATG	2477
OFV	ACACCCCCAAAAGGCCATGCCTGGACTAGGTGATATCTATCAGCTTATCATATATATG	2472
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CNSV	TTTCTCATGTGTCAGTCATGCATATGATAATAGAGATGCTCAACAGTGACTCACCAGACTC	2580
CILV-N	TTTCTCATGTGTCAGTCATGCATATGATAATAGAGATGCTCAACAGCGACTCACCAGACTC	2537
OFV	TTTCTCATGTGTCGTGCATGCATATGATAATAGAAAATGCTCAATAGTGACTCACCAGACTC	2532
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	ORF3: MP	
CNSV	CATAATATATGTACTAGGCATTTATGCAGTACGTTGTTGTGATACATGCATTTAAATAACA	2640
CILV-N	CATAATATATGTACTAGGCATTTATGCAGTACGTTGTTGTGATAACATGCATTTAAATAAAA	2597
OFV	CATAATATATGTACTAGGCATTTATGCAGTACGTCGTTGTAATTCATGCATTTAAATAAAA	2592
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CNSV	CATCAACTAATGTCAATTGACTGGTATCATATTTGCTATAATTATAATATATATACTTGTG	2700
CILV-N	CATCAACTCATGTCAATTGACTGGTATCATATTTGCTATAATTATAATATATATACTTGTG	2657
OFV	CATCAACTTATGTCAATTAAGTGTATCATATTTCTATAATCATAATATATATACTTGTG	2652
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CNSV	CTTGACTGACCCCTCCTGCAGGATCTAAGATGTCCACATTTGCCAGTGTCCACTCTTCACA	2760
CILV-N	CTTATACTGACCCCTCCTGCAGGATCTAAGATGTCCACATTTGCCAGTGTCCACTCTTCACA	2717
OFV	CTTGTGTCAACCATCCTGCAGGAGCTAAGATGTCCACACTGCCAGTGTCTACTCTTCACA	2712
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CNSV	GGTCCAACGCTAGGGACGAGGTCGAGAGACGGCAGGCCGTAGGATGGCCACGGGTTCG	2820
CILV-N	GGTCCAACGCTAGGGACGAGGTCGAGAGACGGCAGGCCGTAGGATGGCCACGGGTTCG	2777
OFV	GGTCCAACGCTAGGGACGAGGTCAGGAGACGGCAAGTCGTAGGATGGCCACGGGTTCG	2772
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CNSV	ACAGCAATGTGACAGACTTCAACAAGAATCTGCAAAGTCTGAGGCTTGGCAGAAACGTC	2880
CILV-N	ACAGCAATGTGACAGACTTCAACAAGAATCTGCAAAGTCTGAGGCTTGGCAGAAACGTC	2837
OFV	ACAGCAATGTGACGACTTCAACAAGAAATCTGCAAAGTCTGAGGCTTGGCAGAAACGTC	2832
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CNSV	TAATACACAAGACAACCATTAAGGTGACCGGAACAAGAGGTTGAGGGAAGGATCACCATGG	2940
CILV-N	TAATACACAAGACAACCATTAAGGTGACTGGGTCGAGGTTGAGGGAAGGATCACCATGG	2897
OFV	TAATACACAAGAAAGCTCCATCAAGGTGACTGGGTCGGAAGGTGAGGGGAGGATCACCATGG	2892
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CNSV	TGAGGAAGCCCATATTGTTTGACATCATGAACAGCCTGAGCAGCATACTTCCCACATCAA	3000
CILV-N	TGAGGAAGCCCATATTGTTTGACATCATGAACAGCCTGAACAGCATACTTCCCACATCAA	2957
OFV	TGAGAAAGCCCATCTGTTTGACATCATGAACAGTCTAACAGCATACTTCCCACATCGA	2952
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CNSV	CAAAACCTACATGGATCATGGGGATGGCCATTAATGGGTCCCAACATGTGACCTATCCA	3060
CILV-N	CGAAACCTACATGGATCATGGGGATGGCCATTAATGGGTCCCAACATGTGACCTATCCA	3017
OFV	CAAAAGCCAAACATGGATCATGGGGATGGCCATCAAGTGGGTTCGACATGTGACCTGTCCA	3012
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CNSV	CCACAGGGACCATCAAAGTATCGATTGAGAATAAGGCTGTCAATAATCCTGTTCTAAGGG	3120
CILV-N	CCACAGGGACCATCAAAGTGTGATTGAGAATAAGGCTGTCAATAATCCTGTTCTAAGGG	3077
OFV	CAACAGGGACCATCAAAGTATCAATCCAGAATAAGGCTGTCAACAATCCTGTTTAAAGGG	3072
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CNSV	ATCATACTGTCTGCTCCATGACCCAAAGAGCTACAACCCCATTTGAAGTCAATACACAT	3180
CILV-N	ATCATACTGTTGTTCTCCATGACCCAAAGAGTTACAACCCCATTCGAAGTCCAATACACAT	3137
OFV	ATCACTGTTGTTCTCCATGACCCAAAGAGTACAACCCCATTTGAGTCCAATACACAT	3132
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CNSV	CATCCTCCAAGCTCGCCAATAGAACAGGCACAAGGGGGAATCCCTGGATGTATACATACT	3240
CILV-N	CATCCTCCAAGCTCGCCAATAGAACAGGCACAAGGGGGAATCCCTGGATGTATACATACT	3197
OFV	CATCCTCCAAGCTAGCCAAAGGACAGGCACAAGGGGGAATCCCTGGATGTATACATACT	3192
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CNSV	GCATAGAGGGGAATGGATGACGCTCCGATAGACATGGAGGTGGGGGATATTGTTGTTATGC	3300
CILV-N	GCATAGAGGGGAATGAATGACGCTCCGATAGACATGGAGGTGGGGGATATTGTTGTTATGC	3257
OFV	GCATAGAGGGGAATGGATGACGCCCGGATAGACATGGAGGTGGGGGATATTGTTGTTATGC	3252

CNSV	CCATGATTAAGTCTGATGAAACTAATACACAGTGGTATGAGGGCGTGAAGTGTAAATGTGT	3360	
CILV-N	CCATGATCAAGTCTGATGACACTAATACACAGTGGTATGAGGGCGTGAAGTGTAAATGTGT	3317	
OFV	CTATGATTAGGTCGGATGACACACACTACACAGTGGTATGAGGGTGTGAAGTGCATATGTGT	3312	
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CNSV	ATGGGGTTATTTCCTCTGAACATACTGTGGTCACCTACTGTGCACCCGGACCTAGGT	3420	
CILV-N	ATGGGGTTATTTCCTCTGAACATACTGTGGTCACCTACTGTGCACCCGGACCTAGGT	3377	
OFV	ATGGAGGTTACTTCCCTCTGAATATACCGTGGTGCACCTACTGTGCACCCGGACCTAGGT	3372	
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CNSV	TCAAGACCAATATGAATGAGATAAGGTCAAACATAGAAATGCTCAGGAGGTATCTCAACG	3480	
CILV-N	TCAAGACCAATATGAATGAGATAAGGTCAAACATAGAGATGCTCAGGAGGTATCTCAACG	3437	
OFV	TCAAGACCAATATGAATGAGATAAAAATCAAACATAGAGATGCTCAGGAGGTATCTCAACG	3432	

CNSV	TCCAGGGTTCACTGATATAGATGAGGATCTGGTCTTCAAATGATACAGTGTGCGACG	3540	
CILV-N	TCCAGGGTTCACTGATGTGGATGAGGATTTGGTCTTCAAATGATACAGTGTGCGACG	3497	
OFV	TCCAGGGATTTACCGATATAGATGAAGATCTGGTCTTCAAATGATACAGTGTGCGACG	3492	
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CNSV	GAGAGCTGCAGGGTCCATAATGAAAGGGATAAGATCCTCCGTGTGGGCCCTTTAGCTA	3600	
CILV-N	GAGAGACTGCAGGGTCCATAATGAAAGGGATAAGATCCTCCGTGTGGGCCCTTTAGCTA	3557	
OFV	GGGAGACTGCAGGATCTATAATGAAGGGGATAAGATCCTCAGTGTGGGCCCTTTGGCCA	3552	
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CNSV	AGACTGACAGGGATTATGTTGTTATTAAGGAGATGCTCCACGACTGTCTGTGGGCAGAA	3660	
CILV-N	AGACTGACAAGGATTATGTTGTCATTAAGGAGATGCTTCATGACTGTCTGTGGGCAGAA	3617	
OFV	AGACTGACAGGGATTATGTTGTAATTAAGGAGATGCTTCATGACTGTCTGGGTAGGCAGAG	3612	
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CNSV	TACTGAGCTACATCACCTCAGCGAGGTGGAGGGTCTTAGCACTATGGGAGGGGATAAAA	3720	
CILV-N	TACTGAGCTACATCACCTCAGCGAGGTGGAGGGTCTTAGCACTATGGGAGGGGACAAAA	3677	
OFV	TACTGAGCTACATCACCTCAGCGAGGTAGAGGGTCTCAGCACCATGGGAGGTGACAAAA	3672	
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CNSV	GCCACAGTTATCGTTAAGTATGACTCAGGCGAAGTACCCTGGAGAAGAATCCCGCCTATC	3780	
CILV-N	GCCACAGTTATCGTTAAGTGTGACTCAGGCGAAGTACCCTGGAGAAGAATCCCGCCTATC	3737	
OFV	GCCACAGCTATCGTTAATTTGTTACTCGGGCTAAGGACCCTGACGGAGAATGCTGCTTCC	3732	
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CNSV	CAATAAACATGTCTACTTACCTACCATAAATTTAAATAAAAATAAATCATCGAATCATTG	3840	
CILV-N	CAATAAACATGTCTACTTACCTACCATAAATTTAAATAAAAACAACAATCATCGAATCATTG	3797	
OFV	CAATAAGCATACTACTTATCTACCCTAATTTAAATAAAAACAACAATCTCGAATCATTG	3792	
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	 ORF4: M		
CNSV	ATTATTATATATCGGATCTAACAATTTGTCTTTTGTGATGCTAAAACAGATTAATATGTG	3900	
CILV-N	ATTATTATATATCAGATCTAACAATTTGTCTTTTGTGATGCTAAAACAGATTAATATGTG	3857	
OFV	ATCATTATATATCAGATCTAACGATTTGTCTTTTATCATGCTAAACAGATCAATATGTG	3852	
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CNSV	CACCGTGTATGTCCTTCAGGTCACTAATCACGTGATAGGACCCAGATCAGTGGATCTTGG	3960	
CILV-N	CACGTGTATGTCCTTCAGGTCCCTAATCACCGTGTATAGGACCCAGATCAGTGGATCTTGG	3917	
OFV	CACGTGTATGTCCTTCAGATCACTCATCACTGTGATAGGACCCAGGTCACTGGATCTTGG	3912	
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CNSV	AGCCGGTTCAAGGAGGCGGTGCTGCGTCTATCACTTCACTCAAGATCAAGGCTAAGGA	4020	
CILV-N	AGCCGGTTCAAGGAGGCGGTGCTGCGTCTATCACTTCACTCAGGATCAAGGCTAAGGA	4077	
OFV	AGCCGGATTCAAGGAGGCGGTGCTGCGAGCAATCACTTCACTCAAGGTCAAGGCTAAGGA	3972	
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CNSV	CCCAAAAGGGACAGAGATTGATGGTCCCTGGCAGGAGCTGTGGTGGAGATTGCCACTAT	4080	
CILV-N	CCCCAAAGGGACAGAGATTGAGGGTCCCTGGCAGGAGCTGTGGTGGAGATTGCCACTAT	4037	
OFV	CCCGAAAGGGCCGAGATAGATGGCCCTGGCAAGAGCTACTGGTGGAGATTGCCACTAT	4032	
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CNSV	GACAAAGTCAGCATTACCCGGCCCTACCATCAAGAAAGACCTGGAGCAGGGGAATGTCTA	4140	
CILV-N	GACAAAGTCAGCATTACCCGGCCCTACCATCAAGAAAGACCTGGAGCAGGGGAATGTCTA	4097	
OFV	GACCAAAATCAGCATTACCCGGCCGACCATCAAGAAAGATCTAGAGCAGGGGAATGTCTA	4092	

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CNSV      CCGTTATGCAATGACAGTTGGCGGCATGTTGAGCACCTCACACAACACAAACGGGAGGCT 4200
CILV-N    TCGTTACGCAATGACAGTTGGCGGCATGTTGAGCACCTCACACAACACAAACGAGAGGCT 4157
OFV       CCGATATGCGATGACAGTTGGCGGCATGTTGAGCACATCACACAATACTAATGGAAGATT 4152
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CNSV      GATGACTGTCGGACTGGACCACTATATGATACTGACCACTACCATGTGTCTGGGGGAGGT 4260
CILV-N    GATGACTGTCAGGACTGGACCACTATATGATACTGACCACTACCATGTGTCTGGGGGAGGT 4217
OFV       GATGACTGTCAGGACTGGACCTCTATATGATACAGACCACTATCATGTGTCTGGGGAGGT 4212
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CNSV      TGATATCGACAAAATGGATGGTTCAAGGCTTCGATAACATTATCTGTGGCCACTGTTAA 4320
CILV-N    TGATATCGACAAAATGGATGGTTCAAGGCTTCGATAACATTATCTGTGGCCACTGTTAA 4277
OFV       TGATATTGATAAAAATGGATGGTTCAAAGCAAAGATAACACTGTCTGTGGCCACTGTCAA 4272
          ***** ** *****
CNSV      GAGAGAACGTCAACAGTGCAGGCGAGGCATCGGGGAATACCATGTTTTGCCGATCAAGGG 4380
CILV-N    GAGAGAACGTCAACAGTGCAGGCGAGGCATCGGGGAATACCATGTTTTGCCGATCAAGGG 4337
OFV       AAGAGAACGTCAACAGTGCAGGCGAGGCATCGGGGAATACCATGTTTTGCCGATCAAGGG 4332
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                                     IGR4
                                     →
CNSV      CAAAAATCCCCACGATCCTCCAGCAACACCGCGGGACCCAGTGGTTAGAGCCATCAACA 4440
CILV-N    CAAAAATCCCCACGATCCTCCAGCAACACCGCGGGACCCAGTGGTTAGAGCCATCAACA 4397
OFV       CAAAAATCCCCACGATCCGCCAGCAACACCGCGGGACCCAGTGGTTAGAGCCATCAACA 4392
          *****
          →
CNSV      GCTCAGGGCCTGCTCTCCCTCCTATCAGACGTGGATAATTACTTACGGAGGAAGAAGTCT 4500
CILV-N    GCTCAGGGCCTGCTCTCCCTCCTATCAGACGTGGATGATTACTTACGGAGGAAGAAGTCT 4457
OFV       GCTCAGGGCCTGCTCTCCCTCCTATCAGCGCTGGATGATTACTTACGGAGGAAGAAGTCT 4452
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CNSV      CGACTGCTCTTATGTTCTGAAGGACCGTGAATGAAACATATAATCATATACATGTCTTAAT 4560
CILV-N    CGACTATCCTATGTTTTGAAGGACCGTGAATGAAACATATAATCATATACATGTCTTAAT 4517
OFV       CGACTATCCTATGTTTTAAAGGACCGTGAATGAAACATATAAACCATATGCATATCTTAAT 4512
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                                     ORF 5: G
                                     →
CNSV      GATATGATCTATATAACCTGATTTAAATAAAACAATAATGATGGCACAGACAAACCAGCC 4620
CILV-N    GATATGATCTATATACCTTATTTAAATAAAACAATAATGATGGCACAGACAAACCAGCC 4577
OFV       GATATGCCCTATATAAATTGATTTAAATAAAACAATAATGATAGTACAACGAAACAGCC 4572
          ***** ** *****
CNSV      CGACACTATGTCAATCTTCCGATCTTCAATCATATTAATGCTTTTCCCTTATCTCAGGGTC 4680
CILV-N    CGACACTATGTCAATCTTCCGCTCTCAATCATATTAATGCTTTTCCCTTATCTCAGGTTT 4637
OFV       CCGCAGCATGTCAAACCTTCTGCTCTTAAACCGTATTAATGTTCTTCTTATCTCAGGTTT 4632
          ** ** * *****
CNSV      TGGAGCACTATCCTTGGTTCCCTAAGACAGTTTGTGAAAAAGAGGTGGGGCTGCATGTGGA 4740
CILV-N    CGGAGCGCTATCCTTGGTTCCCTAAGACAGTTTGTGAGAAAGAGGTGGGGCTGCATGTGGA 4697
OFV       TGAGGCTTTGTCCCTGGTCCCAAGACAGTTTGTGAAAAAGAGGTGGGGCTACATGTGGA 4692
          * ** * *****
CNSV      TGAATGGCTCCAATCATGTTTGGGGGATGCAAGAGCAGCGACAACGATCTAGATATGAC 4800
CILV-N    TGAATGGCTCCAATCATGTTTGGGGGATGCAAGAGCAGCGACAACGATCTAGATCTGAC 4757
OFV       TGAATGGCTCCAATCATGTTTGGGGGCTGCAAGAGCAGCGATAACGACCTTATGATATGAC 4752
          ***** ** *****
CNSV      TCCACACATGTTAATGGAGCCACATTTGGGGTATTTCAAGGCCTTCGGGTATTTTACATA 4860
CILV-N    TCCACACATGTTAATGGAGCCACATTTGGGGTATTTCAAGGCCTTCGGATACTTCATACA 4817
OFV       ACCCACATGTTGATGGAGCCACATTAAGTACTTTAAGGCCTTCGGGTACTTCATACA 4812
          ** *****
CNSV      TGTATCAACCCCTACCAAATCTTCACACACTTCTGTTTCGGCGGGTGTACATCACATC 4920
CILV-N    TGTGTCAACCCCTACCAAATCTTCACACACTTCTGTTTCGGAGGGTGTACATCACATC 4877
OFV       TGTATCAACCCCTACCAAGTCTTCACATACCTTCTTACTCGGTGGGTGTACATCACCTC 4872
          *** *****
CNSV      ACAAGAGACTCCTAGTGATTCTCAGGAGCTTCCCACCAATATGGCCGAGAATATACTGAG 4980
CILV-N    ACAAGAGACTCCTAGTGATTCTCAGGAGCTTCCCACCAATATGGCCGAGAATATACTGAG 4937
OFV       ACAAGGAGACCCCAGCGATTCTAAGAGCTCCCACCAATATGGCTGAGAATATAATTGAG 4932

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*** ***** ** ** ***** ***** ***** ***** ***** ***
CNSV      ACATGGCGGTCTCGAGGAGAGGTTTTTATGACGAAAGAGCCCCAATGCAGCCTCTGGAG 5040
CILV-N    ACATGGCGGCCCTGAGGGAGAGGTTATTTATGACAAAAGAGCCCCAATGCAGCCTCTGGAG 4997
OFV       GCATGGCGGCCCTGAGGGAGAGATATTTATGACAAAAGAGCCCCAATGCAGCCTCTGGAG 4992
          ***** ***** * ***** ***** ***** ***** *****
CNSV      TGACAATTATGTGAAAGGCATGCTTGTGAAGTATCACAGGGTGATTTTGACTGTCTCGCA 5100
CILV-N    CGACAATTATGTGAAAGGCATGCTTGTGAAGTATCACAGGGTGATTTTGACTGTCTCGCA 5057
OFV       TGACAATTATGTGAAAGGCATGCTTGTGAAGTATCACAGGGTGATTTTGACTGTCTCACA 5052
          ***** ***** ***** ***** ***** ***** ***** **
CNSV      CACCGAAAGAGGGATAACGGTTCCTTTACGAGCAGGAGGGAGTGA CGGCCATGGCAAGGT 5160
CILV-N    CACCGAAAGAGGGATAACGGTTCCTTTACGAGCAGGAGGGAGTGA TAGGCCA CCGCAAGGT 5117
OFV       CACCAAGAGCGGGATAACGGTTCCTTTACGAGCAGGAGGGAGTGA TAGGCCATGGCAAGGT 5112
          **** * ** ***** ***** ***** ***** ***** *****
CNSV      CGGTAAAACCGTGTATCATCCGGTACTCTCGTGTGGGACATACGGGCACAATACCCAAA 5220
CILV-N    CGGTAAAGCCATGTATCATCCGGTACTCTCGTGTGGGACATACGGGCACAATACCCAAA 5177
OFV       CGGCAAAACCACTTATCATCAGGAACCTTGTGTGGGACGTGAGAGCACAATACCCGAA 5172
          *** ** * ***** ** * ** ***** * * ***** **
CNSV      GTGCAGCTATAGACCTACGGGGTCTTAGCTGTAAACGAGAGGGATCCTACATACGTTG 5280
CILV-N    GTGCAACTATCGACCTACGGGGTCTTAGCTGTAAACGAGAGGGATCCTACATACGTTG 5237
OFV       GTGCAACTATCGCCTACAGGGTCTTAGCTGTAAAGAGAGAATCATACATACGTTG 5232
          ***** ** * ***** ***** ***** ***** * ** *****
CNSV      CAGAGGTATGTCGAGGAGAGAATCTCATCCACCAAGGAGGACTGCGGGGTCA CCGTATT 5340
CILV-N    CAGAGGTATGTCAGAGGAGAGAATCTCATCCACCAAGGAGGACTGCGGGGTCA TATATATT 5297
OFV       CAGAGGTATGTCAGAGGAGAAATTTTCATCCATCACGAGGACTGTGGAGTCATCATATT 5292
          ***** ***** ** ***** ** ***** ** * ** *****
CNSV      AACGACGGACACAAGGAATATATATGGGTACCATAAACATGATGGTGCACTGGCCACCAC 5400
CILV-N    AACGACGGACACAAGGAATATATACGGGTACCATAAACATGATGGTGCACTGGCCACCAC 5357
OFV       AACGACAGACACAAGGAATATATATGGGTACCATAAACATGATGGAGCATTGACTACCAC 5352
          ***** ***** ***** * ** ***** ***** ***** ** * **
CNSV      TCAGACGGATGACAATCAGATAGGCTATGGTGAAGAAGATCATAGAGATAGAGAATCTCAT 5460
CILV-N    TCAGACGGATGACAATCAGATAGGATGGTGAAGAAGATCATAGAGATAGAGAATCTTAT 5417
OFV       TCAGACGGATGACAATCAGATAGGATGGTGAAGAAGATCATCGAGATAGAGAATCTCAT 5412
          ***** ***** ***** ***** ***** ***** ***** **
CNSV      GTGTCATCATCTATGTGAGTCTCATCCGAGGAGGGGGAGTTACACCCATGAATATTT 5520
CILV-N    GTGTCATCATCTATGTGAGTCTCATCTGAGGAGGGGGAGTGACACCCATGAATATTT 5477
OFV       GTGTCATCATCTATGTGAGTCTCATCTGAGGAGGGGGAGTGACACCCATGAATATTT 5472
          ***** ***** ***** ***** ***** ***** ***** *****
CNSV      GGTTCCTCACTCCATAGGACCATGGCTATCCGTATCCACAGAGTCCCATCGCACCATGTT 5580
CILV-N    GGTTCCTCACTCCATAGGACCATGGCTATCTGTATCCACAGAGTCCCATCGCACCATGTT 5537
OFV       GGTTCCTCACACCGATAGGCGCGTGGCTAGCCGTCTCTACGAGTCCCATCGCACCATGTT 5532
          *** ***** ** ***** ** ***** * ** * ** ***** *****
CNSV      CATGTGTACAGATGAAAGCACAGTGTATTGGTGAATTCCTGTGGTACTATGTGGCAATGG 5640
CILV-N    CATGTGTACAGATGAAAGCATAGTGTCACTGGTGGTTCCTGTGGTACTATGTGGCAATGG 5597
OFV       TATGTGTACGGATGAGGTGAGTGTGAGTGTATTGGTGGTTCAGTGGTATTGTGGCAATGG 5592
          ***** ***** * ***** ***** ***** ***** * *****
CNSV      ACCCTTGGTGAAAGTAAGGGTCAATGAGAAGGAACAATGGTGGAAATATCTCCTCTCCGTA 5700
CILV-N    ACCCTTGGTGAAAGTAAGGGTCAATGAGAAGGAACAATGGTGGAAATATCTCCTCTCCGTA 5657
OFV       GCCCTTGGTGAAAGTAAGGGTAAATGAGAGGAGCAATGGTGGAAATATCTCCTCTCCATA 5652
          ***** ***** ***** ** ***** ***** ** ***** **
CNSV      TGTGGCATGGGACTCATTGTGTCCAGGATTGTCTACAGGATTATCTACTGTGATGG 5760
CILV-N    TGTGGCATGGGACTCATTGTGTCCAGGCTGTCTACAGGCTTATCTACTGTGACGG 5717
OFV       TGTGGTATGGGACTCATTGTGTCCAGGCTGTCTACTGGATTATCTACTGTGATGG 5712
          ***** ***** ***** ** ***** ** ***** ** * **
CNSV      TGTGATAAACACATGGTTAGGACAAGTCACCATAGTGAATGGATCCTTCACTTTCAAGCG 5820
CILV-N    TGTGATAAACACATGGTTAGGACAAGTCACCATAGTGAATGGATCCTTCACTTTCAAGCG 5777
OFV       TGTGATAAACACATGGTTGGACAAGTCACCATAGTGAACGGATTTTCACTTTCAAGCG 5772
          ***** ***** ***** ***** ***** ***** ***** *****
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CNSV	TGATTTTATCAATAAGAATTTCCATGGGGCTTTCAGGCCAAGCCAGTTTAGCTGGTCCCA	5880
CILV-N	TGATTTTATCAATAAGAATTTCCACGGGGCTTTCAGGCCAAGCCAGTTTAGCTGGTCCCA	5837
OFV	TGATTTTATCAATAAGAACTTTCACGGGGCTTTCAGGCCAAGCCAGTTTAGCTGGTCTCA	5832

CNSV	CAAAACAGGCAATGATCTTGAACACATCATAGATGCTCTGAATACACAGGAGAAAGTCCT	5940
CILV-N	CAAAACAGGCAATGATCTTGAACACATCATAGATGCTCTGAATACACAGGAGAAAGTCCT	5897
OFV	CAAGACAGGCAATGATCTTGAACACATCATAGATGCTCTTAAACACACAGGAGAAAGTCCT	5892

CNSV	AAGCCACTCTCATGTGATAGAATCACACAGTGTGGGAGCTGGAGAGAACGCGTTGCACTC	6000
CILV-N	AAGCCACTCTCATGTAATAGAATCACACAGTGTGGGAGCCGGAGAGAACGCGTTGCACTC	5957
OFV	AAGCCACTCTCATGTGATAGAATCACACAGTGTGGGGCCCGGGAGAAATGCTGTGCACTC	5952

CNSV	GTTTCATCGGTATGTTCCAGACTGTATTTCGAATGGATACAGAACTTAATCCCAAATGTCAA	6060
CILV-N	GTTTCATGGTATGTTCCAGACTGTATTTCGAATGGATACAGAGCTTAATCCCAAATGTCAA	6017
OFV	GTTTCATCGGTATGTTCCAGACTGTGTTTCGAGTGGATACAAAGCTTGATCCCAAATGTCAA	6012

CNSV	AGGGTGGATCATCAAATCTTCTGTGGGCATTGTTGGCAGCCCTGGCAGTATTGTTACT	6120
CILV-N	AGGGTGGATCATCAAAGTCTTCTGTGGGCATTGTTAGCAGCTCTGGCAGTATTGTTACT	6077
OFV	AGGGTGGATAATCAAGATCTTCTGTGGGCATTGTTGGCAGCCCTGGTAATCCGTTGCT	6072

CNSV	ATGGATATTGTTGGAAGGTATTATGGTTGTTTCATCAAATCTGTGTTTAAAGGCAGTCTAT	6180
CILV-N	ATGGATATTATGGAAGATATTATGGTTGTTTCATCAAATCTGTGTTGTAAGGCGGTCTAT	6137
OFV	CTGGATATTGTTGGAAGGTATTATGGTTGTTTCATCAAATCTGTATTCTTAAGGCGGACCAT	6132

CNSV	TCGGGCAATCCCAACATCGGAAAATTTCAGACACATCACTGAATCGGGCCATCCACAATTG	6240
CILV-N	TCGGGCAATCCCAACATCGGAAAATTTCAGACACATCACTGAATCGGGCCATCCACAATTG	6197
OFV	TCAGGCAGTCCCAACATCGGAGAACTTCAGACACATCGCTGAATCGGGCCATCCACAATTG	6192
	**	
	Trailer	
CNSV	GGCCAAGATGGATTAA CAAGGTCAGTTCGGGGCTCTTCACATATATACATATAGCTAATA	6300
CILV-N	GGCCAAGATGGATTAA CCAGGTCAGTTCGGGGCTCTTCATATATATATATATAGCTAATA	6257
OFV	GGCCAAGATGGATTAA CAAGGTCAGTTAGGGACTTTTATATATATACATATAGCTGATA	6252

CNSV	AATTTAAATAAAACTACCCCTCTAGGGTCTTTGTCTAGTTAGGGATGTAGGGGAAAGGAC	6360
CILV-N	AATTTAAATAAAA-----	6269
OFV	AATTTAAATAAAACTATCTCTGGGGGCCTTTCCTAGTTAGGGATGTAGGGTAAAGGAC	6312

CNSV	CAATAGAGTCGCATAAGAGATCGTAGCGTTCGTCAACATCATCAACGTTGGTCGATGCGG	6420
CILV-N	-----	
OFV	CAATAGAGTCGCATAAGAGATCGTAGCGTTCGTCAACATCATCAACGTTGGTCGATGCGG	6372

CNSV	GATATGTTGACTATTTACAACAGTTACTCATGGCTCTGTGTCCCATGTA CTCTGCTTGA	6480
CILV-N	-----	
OFV	AATATGTTGACTATTTACAACAGTTACTCATGGCTCTGTGT-----	6413

CNSV	TACCACTGCTTAGAT	6495
CILV-N	-----	
OFV	-----	

Comparison of RNA2.

	Leader	
CNSV	GAGGAGTCATGGGGACACAGGACAACCAACTGTCTCATTGCGAAGTCAAATCCGTGATG	60
CILV-N	-----ACACAGGACAACCAACTGTCTCATTGCGAAGTCAAATCCGTGATG	46
OFVRNA2	-----ACACAGGACAACCAACTGTCTCATTGCGAAGTCAAATCCGTGATG	46

CNSV	GGTCCGTCTTTCCTAGAATAAGGGAAGGATACTATAGGATTGATCCTAGTTCTTCTCTAC	120
CILV-N	GGTCCGTCTTTCCTAGAATAAGGGAAGGATACTATAGGATTGATCCTAGTTCTTCTCTAC	106
OFVRNA2	GGTCCGTCTTTCCTAGAATAAGGGAAGGATACTATAGGATTGATCCTAGTTCTTCTCTAC	106

CNSV	GCTGGGTGCTACCGGATCATGCAAAAACAACCAATATCATATATTATTGCACATACACT	180
CILV-N	GCTGGGTGCTACCGGATCATGCAAAAACAACCAATATCATATATTATTGGCGCATACT	166
OFVRNA2	GCTGGGTGCTTACCGGATCATAAAAACAACCAATCATATATTATTACGCATACACT	166

	ORF 6: L	
CNSV	TTTGAACCTAATCAGATATGAATTCACCTATTTAAGCAGTGGTATCAACCGCAGAGTACT-AA	239
CILV-N	TTTGAACCTAATCAGATATGAATTCACCTTTTCAGGAATGTTA---CACAGAGTCCCTTAA	222
OFVRNA2	TTTGAACCTAATCAGATATGAATTCACCTATTTCAGGAATGTTA---CACCGAGTCCCTGA	222

CNSV	TGGCGGATAACACGGACACCGTTCATCACCGGTAAGGGGAGATCCGCCATAACGAGGGAG	299
CILV-N	TGGACGATAACACGGACACCATCATCACCGGTAAGGGGAGATCTGCCATAATGAGGGAG	282
OFVRNA2	TGGACGATAATACGGACACCATCATCACCGGTAAGGGGAGTCTGCCCAATGAGGGAG	282
	*** *****	
CNSV	AATACCATCTAAAGTCTGCCTTGAGAAGCCACAGTGATTATGTGAAGAACAAGCATCAAG	359
CILV-N	AATACCATCTAAAGTCTGCCCTGAGGAGCCACAGTGATTATGTGAAGAACAAGCATCAAG	342
OFVRNA2	AATACCACCTAAAGTCTGCCCTGAGAAGCCACAGTGATTATGTGAAAAACAAGCATCAAG	342

CNSV	CCAAGGATCTGCTGAAGCTCAGTGAGCATAACATCCGTATATGCATCAAGAATCCATGCA	419
CILV-N	CCAAGGATCTGCTAAAGCTCAGTGAGCATAACATCCGTATATGCATCGAAGAATCCATGCA	402
OFVRNA2	CCAAGGATCTGCTAAAGCTCAGTGAAACATACATCTGTATATGCAACGAAAAACCATGCA	402

CNSV	AATGCTACCCACTCTATGGAAGGGAGTGATCGAGGGGAGGAGTGGTGAAGATGAGG	479
CILV-N	AATGCTACCCACTCTATGGAAGGGAGTGGTCGAAGGGGAGGAGTGGTTCGAGGATGAGG	462
OFVRNA2	AGTTACTGCCACTCTATGGAAGGGGTGATTGAAGGGGAGGAGTGGTGAAGATGAGG	462
	* * * * *	
CNSV	TTGTAATATATCTAAAAGAGCTCTATCATGATGACGAGACTGATGATTGTGCTCTTGAGC	539
CILV-N	TTGCAATATATCTAAAAGAGCTCTATCATGATGACGAGACTGATGATTGTGCTCTTGAGC	522
OFVRNA2	TTATAATATACTTGAGAGAGCTCTATCATGACGACGAAACAGACGACTGTGCTCTTGAGC	522
	** ***** * *	
CNSV	TCCTCGATGCAGAGCTGGAGCATGTGTGCCCGATGATGACAAAACAGGGATAATGCAGG	599
CILV-N	TCCTCGATGCAGAGCTGGAGCATGTGTGCCCGATGATGACAAAACAGGGATAATGCAGG	582
OFVRNA2	TCCTTGATGCAGAGCTGGAAACATGTGTTCATGACGATGACAAAACAGGGATAATGCAGG	582
	*** *****	
CNSV	GGTTCGTACAGTGTGAGGAGGATGCATGGAACAAACACACCATCTACGGTAGAGCTAATA	659
CILV-N	GGTTCGTACAGTGTGAGGAGGATGCATGGAACAAACACACCATCTACGGTAGAGCTAATA	642
OFVRNA2	GAGTCGTACAGTGTGAGGAGGATGCATGGAACAAACATACCATCTACGGTAGGGCCAATA	642
	* *****	
CNSV	TCCTCCGGTGGGCCCTGACAAGGATAGTGATAGATCATAATAAAGCAGTGGTATCAACGC	719
CILV-N	TCCTTCGGTGGGCCCTGACAAGGATAGTGATAGATCATAATAAAGAGGACCAACAGAGC	702
OFVRNA2	TCCTTCGATGGGCCCTTGACAAGGATAGTGATCGATCAATAAAGAGGAGCCTACAGAAC	702

CNSV	AGAGTACCATGGGGAGAAAGTTGGATGATAAGGTGTTGCTTATTCATTGAGCAGCTCAT	779
CILV-N	TTAGTCCCATGGGGAGGAAGTTGGATGCGGGGTGTTGCTTATTCATTGAGCAGCTCAT	762
OFVRNA2	TCAGCCCATGGGGAGGAAATTGGCCGATAAGGTGTTGCTTATTCATTGAGCAGCTCAT	762
	* * ***** * *****	

CNSV	TATCTATGATGATAAGCAGAAGTTGGTGTCTCTGATGATCAATGACAGCCCCGGAACCA	839
CILV-N	TATCTATGATGATAAGCAGAAGTTGGTGTCTCTGATGATCAATGACAGCCCCGGAACCA	822
OFVRNA2	TATCTATGATGATAAGCAGAAGTTGGTGTCTCTGATGATTAATGACAGCCCAGGCACCA	822

CNSV	TCAACATTCAGCACCTGATCAACACCCTGGATAAACTGACAGAACGAGTGAACATAATGA	899
CILV-N	TCAACATTCAGCATCTGATCAACACCCTGGATAAACTGACAGAACGAGTGAACATAATGA	882
OFVRNA2	TCAACATTCAGCACCTGATCAACACCCTGGATAAACTGACGGAACGAGTGAACATAATGA	882

CNSV	CTTATCTAACCCCTCTGCAACAAGACTGGGCTCTCAAGCATTTATCCGTCAAGTTGACATCA	959
CILV-N	CTTATCTAACCCCTCTGCAACAAGACTGGGCTCTCAAGCATTTATCCGTCAAGTTGACATCA	942
OFVRNA2	CCTAACCCTAAGACTGGACTTTCAAGCATTTATCCATCAGTAGACATCA	942
	* * * * *	
CNSV	CTCTGAGAATCATTCAGCTAGGTGACCAATTGATACTGAATGAGGGCAATAATGCCTTTC	1019
CILV-N	CTCTGAGAATCATTCAGCTAGGTGACCAATTGATACTGAATGAGGGCAATAATGCCTTTC	1002
OFVRNA2	CTTTGAAATAATTGAGTGGTGCATTTAATAATAAATGAAGGCAATGATGCTTTC	1002
	** * * * *	
CNSV	GCGGGCTGGCCAGTTATGAAGCTATCTGTGTCGGTGAGATAATCAATAGGGGGGACTCAT	1079
CILV-N	GCGGGCTGGCCAGTTATGAAGCTATCTGTGTAAGTGAGATAATCAACAGGGGGGACTCAT	1062
OFVRNA2	GCGGGTTGGCCAGTTACGAAGCATCTGTGTCGGTGCATAATCAACAGGGGCGATTTCGT	1062

CNSV	CAGTGTGGGATGTCGGGAGATTTCTCAACACCATGTACAGGAGTTGGTGCATGTTGGGAG	1139
CILV-N	CAGTGTGGGATGTCGGGAGATTTCTCAACACCATGTACAGGAGTTGGTGCATGTTGGGAG	1122
OFVRNA2	CTGTGTGGGATGTTGGTAGATTCTCAACACTATGTTACAGAGTTGGATCATGTTGGGAG	1122
	* * * * *	
CNSV	AGAAGTACAAGACATGGTTCATCAGATGTTCTGGTAATACTTCAAGGCTAAGGATACAAC	1199
CILV-N	AGAAGTACAAGACATGGTTCATCAGATGTTCTAGTAATACTTCAAGGCTAAGGATACAAC	1182
OFVRNA2	AGAAGTACAAGACATGGTTCATGATGTCCTGGTGATACTGCAAGTTCGAAGATCCAGC	1182

CNSV	AAGTGTGATGCCTGCATGGCATAATATCGCATCTGGGGACACCCGGTGTGTGATCTTGAGA	1259
CILV-N	AAGTGTGATGCCTGCATGGCATAATATCGCATCTGGGGACATCCGGTGTGTGATCTTGAGA	1242
OFVRNA2	AAGTGTGATGCCTGCATGGCATAATATCGTATCTGGGGACATCCAGTGTGTGATCTTGAGA	1242

CNSV	AAGGCCTCATGAAGCTCCGCTCGGTGGCTTTGATGGAGAAAGAGATTCGGCCTGAATGTG	1319
CILV-N	AAGGCCTCATGAAGCTCCGCTCGGTGGCTCTGATGGAGAAAGAGATTCGGCCTGAATGTG	1302
OFVRNA2	AGGCCTCATGAAGCTTCGTTCAAGTACTAATGGAGAAAGAGATCCCAACGAATGTG	1302
	* * * * *	
CNSV	CCAGAAATACCTCCAATATGTTCAAGGAGATATTCTTCCACACAGTATTTAGGGCGCCACA	1379
CILV-N	CCAGAAATACCTCCAATATGTTCAAGGAGATATTCTTCCACACAGTATTTAGGGCGCCACA	1362
OFVRNA2	CCAGAAATACCTCCAATATGTTCAAGGAGATATTCTTCCAGCAATACTTCAGACGCCACA	1362

CNSV	AGTTTACCCTCCACATACCTGGACCGGTCTGAAGGAGGCAATTACATCAAGCAGGTCC	1439
CILV-N	AGTTTACCCTCCACATACCTGGACTGGTCTGAAGGAAGCAATTACATCAAGCAGGTCC	1422
OFVRNA2	AGTTTACCCTCCACACACCTGGACCGGTCCGGAAGGAAGCAATTACATCAAGCAGGTCC	1422

CNSV	TATCACTTGAGAAAGAGTTGGATATACACAACATAAGATATCACTTGAGGACTGGGGGA	1499
CILV-N	TATCACTTGAGAAAGAGTTAGATATACACAACATAAGATATCACTTGAGGACTGGGGGA	1482
OFVRNA2	TATCACTTGAGAAAGAGTTGGATATACACAACATAAGATATCACTTGAGGACTGGGGGA	1482

CNSV	ATATCAGATGTGAGAAGACATTCGAGATCCCGGCCACATACAGCCTTGCATCATGTATCA	1559
CILV-N	ATATCAGATGTGAGAAGACATTCGAGATCCCGGCCACATACAGCCTTGCATCATGTATCA	1542
OFVRNA2	ACATCAGATGTGAGAAGACTTCGAGATTCGGGCCACATACAGTCTTGCATCATGTATCA	1542
	* * * * *	
CNSV	AAGACAGAGCAATATCCCCAAAACGATCAGAGTTGGTATCCATGATCATCAGAGGAGGAT	1619
CILV-N	AAGATAGAGCAATATCCCCAAAACGATCAGAGTTGGTATCCATGATCATCAGAGGAGGAT	1602
OFVRNA2	AAGACAGAGCTATATCCCCGAAACGTCAGAGTTGGTATCCATGATCATCAGAGGGGAT	1602

CNSV	CTGTGATGAGTCAAAGCTCCAGAAGGGGGGTGTTAAAATGGCTAGACAGCACCATGATCC	1679
CILV-N	CTGTAAATGAGTCAAGCTCCAGAAGGGGGGTGTTAAAATGGCTGGACAGTACCATGATCC	1662
OFVRNA2	CTGTGATGAGTCAAAGCTCAAGAGGGGGGTTCGAAATGGCTGGAATAGTACCATGATTC	1662
	*** **	
CNSV	CTGTGAGAGAATTCCTGGATGGTATAAATGAGTCGGGTAATGTCAAAGGCAACTCAATTA	1739
CILV-N	CCGTGAGAGAATTCCTGGATGGTATAAATGAGTCGGGATTGTCAAAGGCAACTCAATTA	1722
OFVRNA2	CTGTGAGAGAATTCCTGGATGGCATAAGATAAATCAGGATTGTCAAAGGCAACTCAATTA	1722
	* **	
CNSV	TTGGCCTATATCCCAAAGAACGAGAGTTGAAGATGGAGGCCAGGTTCCTTTGCTCTGATGT	1799
CILV-N	TTGGCCTATATCCCAAAGAACGAGAGTTGAAGATGGAGGCCAGGTTCCTTTGCTCTGATGT	1782
OFVRNA2	TTCGGCCTATATCCCAAAGGAAAGAGAGTTGAAGATGGAGGCCAGGTTCCTTTGCTCTAATGT	1782
	* **	
CNSV	CTTTCCAAATGAGGTTACTTTCACAACGACAGAGTACATGGCGAATGACAACCTCCTGG	1859
CILV-N	CCTTTCAAATGAGGTTACTTTCACAATTAACAGAGCATATGGCGAATGACAACCTCCTGG	1842
OFVRNA2	CCTTTCAAATGAGGTTACTTTACAATCACAGAGCATATGGCAATGACAACCTCTTGG	1842
	* **	
CNSV	ACTACTTTCCCATGGTCACAATGTCCGACAGCATGTGGAGCTGAACAAAAGCTGGACA	1919
CILV-N	ACTACTTTCCCATGGTCACAATGTCCGACAGCATGTGGAGCTGAACAAAAGCTGGACA	1902
OFVRNA2	ACTACTTTCCCATGGTCACAATGTCTGACAGCATGTGGAGCTAAACAAGAAGCTGGACA	1902

CNSV	CTCTAAGTAGAAAGCAGGTCAACAAGAAGGAGGGTGTGGTACATTATGTGGTCAATATAG	1979
CILV-N	CTCTAAGTAGAAAGCAAAATCAACAAGAAGGAGGGTGTGGTACATTATGTGGTCAATATAG	1962
OFVRNA2	CTCTGAGCCGAAAGCAGGTACAAAAGAGGAGGGTGTGGTGCATTATGTGGTCAACATCG	1962
	*** **	
CNSV	ATTTTCAGAAAATGGAACCAACAGATGAGGGAAGAGATGACTGTCCCTATGTTTCTTGATG	2039
CILV-N	ATTTTCAGAAAATGGAACCAACAGATGAGGGAAGAGATGACTGTCCCTATGTTTCTTGATG	2022
OFVRNA2	ATTTTCAGAAAATGGAACCAACAGATGAGAGAGGAGATGACTGTCCCTATGTTTCTTGATG	2022

CNSV	CTGACAGACTGTTTCGGTTACACCAATCTGGTGGGGCGGACGCATGAGATCTTCAAGTCCT	2099
CILV-N	CTGATAGACTGTTTCGGTTACACCAATCTGGTGGGGCGGACGCATGAGATCTTCAAGTCCT	2082
OFVRNA2	CTGATAGACTGTTTGGCTACACCAATCTGGTGGGGAGGACACATGAGATTTTCAAGTCCT	2082
	*** **	
CNSV	CATATATATATCTATCCCTCAGGGGAATACGTACCGCAAGTCTCACTCAGAGGAAGGTTGG	2159
CILV-N	CATATATATACTTATCCCTCAGGGGAATACGTACCACAAGTCTCACTCAGAGGAAGGTTGG	2142
OFVRNA2	CATATATATACTTATCCCTCAGGGGAATAATGTACCACAAGTCTCACTCAGAGGAAGGTTGG	2142

CNSV	TGCATGAGGAGCCCTACAGTTGGACCAACGACCCCTCGGGAAAGAAGGTCTGAGGCAAA	2219
CILV-N	TGCATGAGGAGCCCTACAGTTGGACCAATGACCCCTCTGGGAAAGAAGGTCTGAGGCAAA	2202
OFVRNA2	TGCAGAGGAGCCCTACAGTTGGACCAATGACCCCTCTGGGAAAGAAGGTCTGAGGCAAA	2202
	*** **	
CNSV	AATATCTGGACCATCATGACTGCATGTGATCTGATGTATGTAGCCAGACAACACCGAATGA	2279
CILV-N	AATATCTGGACCATCATGACTGCATGTGATTTGATGTATGTGGCTAGACAACATGGGCTGA	2262
OFVRNA2	AATATCTGGACCATCATGACTGCTGTGACTTAATGTATGTAGCTAGACAACATGGGTTGA	2262
	*** **	
CNSV	AGATTGATCTGGTAGGCGGGGGTGACAATCAGGTCCTGATTGTGGAAAGTGACCACAGACA	2339
CILV-N	AGATTGATCTGGTAGGCGGGGGTGACAATCAGGTCCTGATTGTGGAAAGTGACCACAGACA	2322
OFVRNA2	AGATTGATCTGGTAGGCGGGGGGACAATCAGGTCCTGATTGTGGAAAGTGACCACAGACA	2322

CNSV	AAGTCGGGGATGGAGGTGAATTGACCACGGAAAGGGAAGTCTGAGTGCAAATTCAGATGG	2399
CILV-N	AAGTCGGGGATGGAGGTGAATTGACCACGGAGGGGAAGTCTGAGTGCAAATTCAGATGG	2382
OFVRNA2	AGGTTGGAGATGGAGGTGAATTAAACCGGAGGGGAATCCGAGTGCAAATTCAGATGG	2382
	* **	
CNSV	GGACATTCATGAGCCATCTGTCCAATTACATGGAGAAGAAAGGCCTGCCGTTAAAAACAG	2459
CILV-N	GGACATTCATGAGCCATCTGTCCAATTACATGGAGAAGAAAGGCCTGCCGTTAAAAACAG	2442
OFVRNA2	AAACATTCATGCGCCATCTGTCCAATTACATGGAGAAGAAAGGCCTGCCGCTAAAGACAG	2442

CNSV	AGGAAACCTGGATTTCAACCAACCTACTCATGTTCTTCAAGATGATGTATTATGATCATA	2519
CILV-N	AGGAGACCTGGATTTCAACCAACCTACTCATGTTCTTCAAGATGATGTATTATGATCATA	2502
OFVRNA2	AGGAAACCTGGATCTCCCCAACCTGCTCATGTTCTTCAAGATGATGTATTATGACATA	2502
	***** **	
CNSV	CTACTCTGGTGTACCTCTCAAGCAAGCCTCGAGAGTGTTCGCTGTCAAATGATCAAG	2579
CILV-N	CTACTCTGGTGTACCTCTCAAGCAAGCCTCGAGAGTGTTCGCTGTCAAATGATCAAG	2562
OFVRNA2	CCACTCTGGTGTACCTCTCAAACAGGCCTCGAGGCTGTTCGCTTATCTAATGATCAAG	2562
	* *****	
CNSV	TCATGACTATTGGCAACATGGCAGCCACTGTCCTTCAGGGGTTACAGTACTATCCTCCA	2639
CILV-N	TCATGACTATTGGCAACATGGCAGCCACTGTAATCTTCGGGGTTACAGTACTATCCTCCA	2622
OFVRNA2	TCATGACTATTGGCAACATGGCAGCCACTGTCTCCAGGAGTCAAGTACTATCCTCCA	2622
	***** **	
CNSV	AGGACATGCAGATTGGCCAGCAGCCGATTCGGAAGACTCATATGTGCTGATTTAGCAT	2699
CILV-N	AAGACATGCAGATTGGCCAGCAGCTGCTTTTGGAAGACTCATATGTGCTGATTTAGCAT	2682
OFVRNA2	AGGACATGCAGATTGGCCAGCAGCTGCATTGGAAGCTAATATGTGCTGACTTAGCAT	2682
	* *****	
CNSV	CGTTGGTCAACAAGGATCATCCCTTGCTGTGATGGAGGAGAGATGGGTGAGACAGCATAA	2759
CILV-N	CGCTGGTCAACAAGGATCATCCCTTGCTGTGATGGAGGAGAGATGGGTGAGACAGCATAA	2742
OFVRNA2	CATTGGTCAACAAGGATCATCCCTGCTGTGATGGAGGAGAGATGGGTGGACAGCATAA	2742
	* *****	
CNSV	ATATTTGCAGAGGTGGCTCTAGGAGGAAGGTCAACGTTAGGCCGACCTCAAACTCCGA	2819
CILV-N	ATATTTGCAGAGGTGGCTCTAGGAGGAAGGTCAACGTTAGGCCGACCTCAAACTCCGA	2802
OFVRNA2	GCATTTGCAGGGGAGGCTCAAGGAGGAAGGTCAACGTTAAGCCGACCTCAAAACCCAA	2802
	***** **	
CNSV	TGAGAATTTTCTGTCAATTAACACTCCTGCACAAGGTCATGGGAGGCCAGCCATAGTCT	2879
CILV-N	TGAGGATTTTCTGTCAATTAACACTCCTGCACAAGGTCATGGGAGGCCAGCCATAGTAT	2862
OFVRNA2	TGAGAATCTTCTGTCAATTAACACTCCTACACAAAGTCATGGGAGGCCAGCCATAGTAT	2862
	**** * * *****	
CNSV	CACCCCTGGGTATGATGATGAGGGGATTTCTGTATCCGCTTTGTGAACACTTGACTTGG	2939
CILV-N	CACCCCTGGGTATGATGATGAGGGGATTTCTGTATCCGCTTTGTGAACACTTGACTTGG	2922
OFVRNA2	CACCCCTGGGTATGATGATGAGGGGATTTCTGTATCCACTCTGTGAGCATTTGACTGGG	2922
	***** **	
CNSV	TCAGTATGATAAAGACAAAATTTCTCACCAAGCCACTAACTTTGCTTGATGTCCATCAATA	2999
CILV-N	TCAGTATGATAAAGACAAAATTTCCCACCAAGCCACTAACTTTGCTTGATGTCCATCAACA	2982
OFVRNA2	TCAGTATGATTAACTCAAAAATTTCTCACAGCCGCTAACTTCTGCTTGATGTCTATCAACA	2982
	***** **	
CNSV	CCAAGGTCCTTTGGGCTCACCTACTAGAAGACCCGCTCAGTGTCACCAATGATGCTCCCA	3059
CILV-N	CCAAGGTCCTTTGGGCTCACCTACTTGAAGACCCGCTCAGTGTCACCAATGATGCTCCCA	3042
OFVRNA2	CCAAGGTCCTTTGGGCTCATCTGCTTGAAGACCCGCTCAGTGTCACCAATGATGCTCCCA	3042
	***** *****	
CNSV	TGCATGGGCTGGCTGTGCTTAGAAGAGAGGAGAGCAAGCCCTTGTAAAGCCCTCTGGTT	3119
CILV-N	TGCATGGGCTGGCTGTGCTTAGAAGAGAGGAGAGCAAGCCCTCGCTAAAGCCCTCTGGTT	3102
OFVRNA2	TGCATGGATGGCTGTAATTAGAAGAGAGGAGAGCAAGCTCTCGCTAAAGCCCTCTGGCT	3102
	***** *****	
CNSV	ATAAGAATCGAGACTTTATGGATCTGGCCCGCTGTTGTAACAAGAGTCAAGTGGAGGGAC	3179
CILV-N	ATAAGAATCGAGACTTTATGGATCTGGCCCGCTGTTGTAACAAGAGTCAAGTGGAGGGAC	3162
OFVRNA2	ATAAGAATCGAGATTTTATGGACCTGGCTCGCTGTTGTAACAAGAGTCAATGGAGGGAT	3162
	***** *****	
CNSV	TGGCTGAGGCACTATGCTCTGGCAAGAATGTGGATATAAGGGTGTGTCATGATGTCATGG	3239
CILV-N	TGGCTGAGGCACTATGCTCTGGCAAGAATGTGGATATAAGGGTGTGTCATGATGTCATGG	3222
OFVRNA2	TGGCTGAGGCACTATGCTCCGGCAAGAATGTAAGATATAAGGGTGTACATGATGTTATGG	3222
	***** *****	
CNSV	GGCAAGCTTAGGAGGATATTTCAACTCCATAGCCCTCAAGGTTAAACAAGACTGCCACTG	3299
CILV-N	GTGCAAGCTTAGGAGGATATTTCAACTCCATAGCCCTCAAGGTTAAACAAGACTGCCACTG	3282
OFVRNA2	GTGCAAGCTTAGGAGGATATTTCAACTCCATAGCCCTAAGGTTAAACAAGACTGCCACTG	3282
	* *****	

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CNSV          TACTGAGAATGAACAAGAGCTCCTCAGTCATCGCGACCATTGCGGGGCAGGAACGACACT 3359
CILV-N        TCCTGAGAATGAACAAAAGCTCCTCAGTCATCGCGACCATTGCGGGGACAGGAACGACACT 3342
OFVRNA2      TCCTAAGGATGAACAAGAGCTCCTCCTCATTTGCCACCATTGCAGGACAGGAAAGACATTT 3342
* * * * *
CNSV          GCATGAGTTATTTTGCCGCATCATCATCAGTGCCTCATGACCTTACTCCCTGAAATGTC 3419
CILV-N        GCATGAGTTATTTTGCCGCATCATCATCAGTGCCTCACGACCTTACTCCCTGAAATGTC 3402
OFVRNA2      GCATGAGTTATTTTGCTGCCATCATCATCAGTGCCTCACGATCTCACTCCCTGAGATGTC 3402
* * * * *
CNSV          CTACAGCCACAGCTAGGAGGTACAGAAGATTGAGCTGGGGCAAGGAAATCCTGTCCATAA 3479
CILV-N        CGACAGCCACAGCTAGGAGGTACAGAAGATTGAGCTGGGGCAAGGAAATCCTGTCCATAA 3462
OFVRNA2      CAACAGCCACAGCTAGACGATACAGAAGACTGAGCTGGGGCAAGGAAATCCTGTCCATCA 3462
* * * * *
CNSV          CTACCCCGCACCTGCAGCCTTCTGAAACCAGTGATTGGAGACCATCAATGTGACCACA 3539
CILV-N        CTACCCCGCATCCTGCAGCCTTCTGACACCGGTGATTGGAGACCATCAATGTGACCACA 3522
OFVRNA2      CCAACCCGCATCCTGCAGCCTTCTTGAACCAGTGATAGGAGACCATCAATGTGACCACA 3522
* * * * *
CNSV          ACTATGTGCAGACCAAGACATCAGGAGGGAACCTGATCAACCCACACTCTAGAGGACCAT 3599
CILV-N        ACTATGTGCAGACCAAAACATCGGGAGGGAACCTGATCAACCCACACTCTAGAGGCCAT 3582
OFVRNA2      ACTATGTGCAGACCAAGACATCAGGAGGGAACCTGATCAATCCCACACTCTAGAGGGCCGT 3582
* * * * *
CNSV          ACCCGGTTTATATGGGCTCATATACCAAGGAGAAGTTCAAGCCACTGAGATGGCAGCGG 3659
CILV-N        ACCCGGTTTACATGGGCTCGTATACCAAGGAGAAGTTCAAGCCACTGAGATGGCGGCGG 3642
OFVRNA2      ATCCGGTTTATATGGGCTCATACACAGGGAGAAGTTCAAGCCTACTGAGATGGCGGCGG 3642
* * * * *
CNSV          CTTACGGAGAGGAGGACCTGCTGTCCAGACCATCCACCTGATGAAGCTGATCAATTGGA 3719
CILV-N        CTTACGGAGAGGAGGACCTACTGTCCAGACCATCCACCTGATGAAGCTGATCAATTGGA 3702
OFVRNA2      CTTACGGAGAAGAGGACCTACTGTCCAGACCATTCATCTGATGAAGCTAATCAATTGGA 3702
* * * * *
CNSV          GATATTCATCATCATCCAACATGGCCAGGATCCTCAAATGCCTGTTGAGCTCCCTGACTG 3779
CILV-N        GATATTCATCATCATCCAACATGGCCCGTACTCCCTCAAATGCCTGTTGAGCTCTCTGACTG 3762
OFVRNA2      GATATTCATCATCATCCAACATGGCCAGGATCCTGAAATGCCTGCTGAGCTCTCTTACTG 3762
* * * * *
CNSV          ATGCTGATGCTACACTTTTCTATGGGATGATGGAGTGGATTGCAGGGGATGCAGAGCATC 3839
CILV-N        ATGCTGATGCTACACTTTTCTATGGGATGATGGAGTGGATTGCAGGAGACGCAGAGCATA 3822
OFVRNA2      ATGCTGATGCCACTCTTTTCTACCGAATGATGGAGTGGATTGCAGGAGATGCAGAGCATA 3822
* * * * *
CNSV          GGTACCAGGATATGGCTACCAAACACGGGGGGTCCCAATGTTGCCACTCTATACTGT 3899
CILV-N        GGTACCAGGACATGGCTACCAAACACGGGGGGTCCCAATGTCGCCACTCTATACTGT 3882
OFVRNA2      GATATCAAGACATGGCGACCAAACATGGGGGAGTTCCCAATGTCGCTCACTCCATACTGT 3882
* * * * *
CNSV          CTTATGTCCGAGCTCACACCACCACATTCAGGAAGCATTCCCGAGGAGGGAAGAATGAGA 3959
CILV-N        CTTATGTCCGAGCTCACACCACCACATTCAGGAAGCATTTCGAGGAGGGAAGAATGAGA 3942
OFVRNA2      CTTATGTCCGAGCTCACACCACCACATTTAGGAAACACTCCCGCGGAGGGAAGAATGAGA 3942
* * * * *
CNSV          CACTTCACTTCCAGGCTGTGATGATATACATCAATGATAGCCCTGTTCAAGAAATACG 4019
CILV-N        CACTTCACTTCCAGGCCTGTCATGATATACATCAATGATAGCCCTGTTCAAGAAATACG 4002
OFVRNA2      CTCTCCACTTCCAGGCTGTGATGATATACATCAATGATAGCCCTGTTCAAGAAATATG 4002
* * * * *
CNSV          GGGGAATCATCCATTGGCATGAGAGCTGTGGAGAGTGCATCCAACAGACTGCTGGCAATG 4079
CILV-N        GGGGAATTCATCCATTGGCATGAGAGCTGTGGAGAGTGCATCCAACAGACTGTCGGCAATG 4062
OFVRNA2      GGGGAATCATCCATTGGCATGAGAGCTGTGGCAGATGCATCCAACAGACTGCTGGCAATG 4062
* * * * *
CNSV          TGGATGTGGTCTGACAAAGAGGGTGGAAATCCCAATATTGAAAGGAAATCTCTTTGCAT 4139
CILV-N        TGGATGTGGTCTGACGAAGAGGGTGGAAATCCCAATATTGAAAGGAAATCTCTTTGCAT 4122
OFVRNA2      TTGATGTGGTACTGACAAAGAGGGTGGAGTTCCCGATCCGTAAGGAAATCTCTTTGCAT 4122
* * * * *
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Trailer

		
CNSV	AAATATCGGGAATAAGTATTTCTGTTTAAATTATATTCATTTAAGGAAAACCGGGTATC	5874
CILV-N	AAATATCGGGAATAAGTAATTTGTTTAAATTATATTCATTTAAGGAAAAA-----	5852
OFVRNA2	AAATATCGGGAATAAGTAATTTGTTTAAATTATATACATTTAAAGAAAACCGGGTATC	5860
	***** ** ***** ***** *****	
		
CNSV	TCGGGTCCTCCC-ACAATCCTCCATCTCTGTTCACTGCGTTAAGAAGGACTAGGAC	5933
CILV-N	-----AAAAAAAA-----	5860
OFVRNA2	TCGGGCTCCCCC CACTATCGTATATTTTGTTCACAACTGCGTTAAGAAGGACTAGGAC	5920
	** * *	
		
CNSV	TAGGTCCCGAAGGTGCAACTGGGTCACACCGGAGTCGCAAGGAGATTTTCATCAATCCATG	5993
CILV-N	-----	
OFVRNA2	TAGGTCCCGGAGGTGCAACTGGGTCACACCGGAGTCGCAAGGAGATTTTCATCAATCCATG	5980
		
CNSV	TACTGTTGATCTGTCCTCTGCTTCC	6018
CILV-N	-----	
OFVRNA2	TACTGTTGATCTGTCCTGTG-----	6001

Figure S4. Gene Ontology terms of upregulated and downregulated genes in CNSV-infected plants, according to RNA expression analyses. A graphic demonstration of genes with altered expression, classified in cell function, metabolism, secondary metabolites and biotic stress. Red, downregulated genes; blue, upregulated genes.

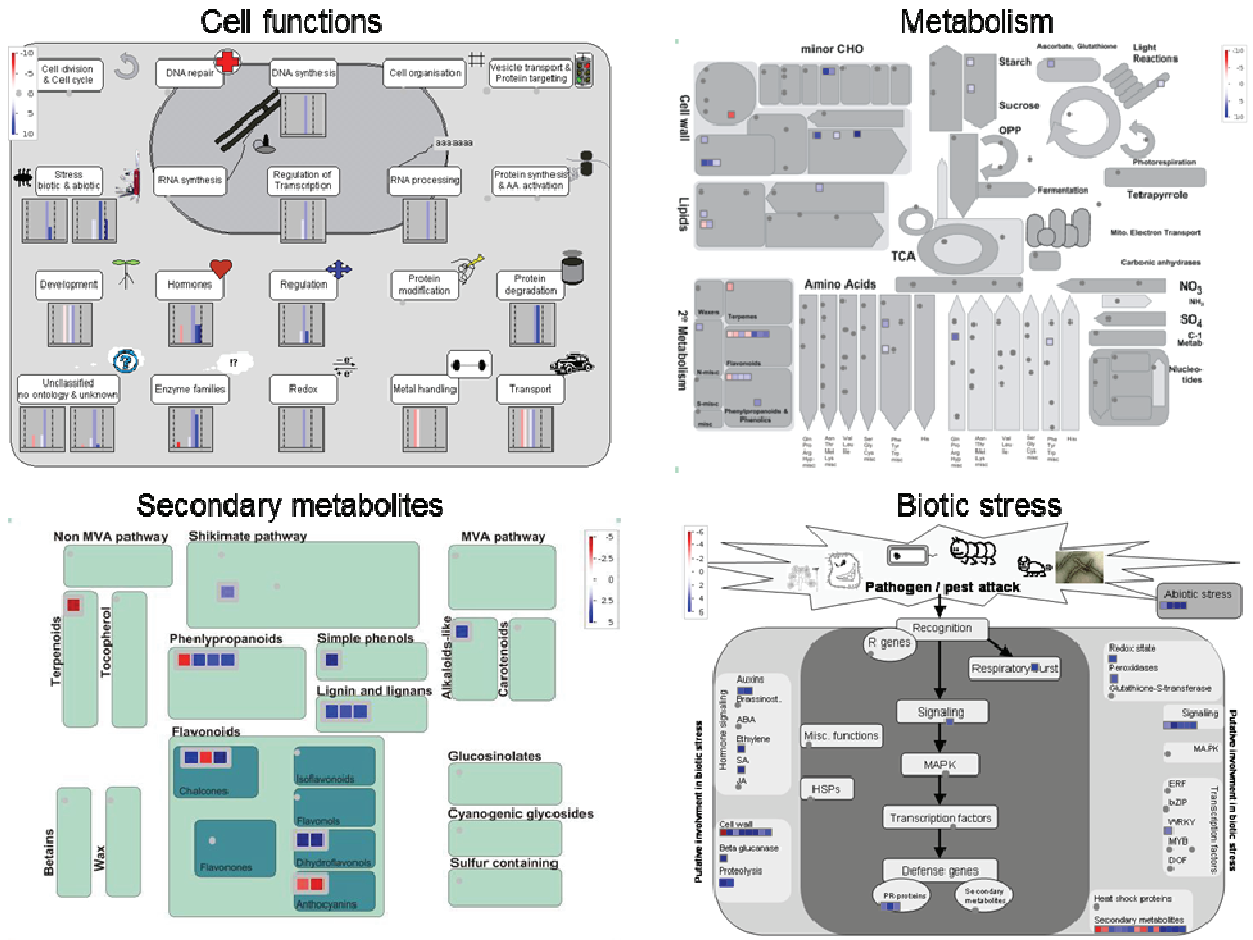


Table S1. Viral Operational Taxonomic Units (OTUs) used for phylogenetic reconstruction.

Abbreviation	Name	Description	Accession No.
LNYV	Lettuce Necrotic Yellow Virus	Cytorhabdovirus	Q86134.1 (N) Q4W382.1 (L)
LYMV	Lettuce Yellow Mottle Virus	Cytorhabdovirus	NC_011532.1
NCMV	Northern Cereal Mosaic Virus	Cytorhabdovirus	NC_002251.1
CNSV	Citrus Necrotic Spot Virus	Dichorhavirus <i>*This work</i>	KF198064.2 (N) KF198065.1 (L)
CiLV-N	Citrus Leprosis Virus Nuclear Type	Dichorhavirus	KF209275.2 (N) KF209276.1 (L)
OFV	Orchid Fleck Virus	Dichorhavirus	NC_009608.1 (N) AB244418.1 (L)
EMDV	Eggplant Mottled Dwarf Virus	Nucleorhabdovirus	KJ082087.1
MFSV	Maize Fine Streak Virus	Nucleorhabdovirus	NC_005974.1
MIMV	Maize Iranian Mosaic Virus	Nucleorhabdovirus	DQ186554.1
MMV	Maize Mosaic Virus	Nucleorhabdovirus	AY618418.1
PYDV	Potato Yellow Dwarf Virus	Nucleorhabdovirus	NC_016136.1
RYSV	Rice Yellow Stunt Virus	Nucleorhabdovirus	NC_003746.1
SYNV	Sonchus Yellow Net Virus	Nucleorhabdovirus	NC_001615.2
TVCV	Taro Vein Chlorosis Virus	Nucleorhabdovirus	NC_006942.1
CRV	Coffee Ringspot Virus	<i>Unclassified</i> Rhabdovirus	KF812525.1 (N) KF812526.1 (L)
LBVAV	Lettuce Big Vein Associated Virus	Varicosavirus (External Group)	Q91QN9.1 (N) Q8B0U2.1 (L)

Table S2. Oligonucleotides used for validation through qPCR of up- and down-regulated Citrus genes.

Oligonucleotide name	Sequence
Germin-like protein 5'	ATGGGAAGTTCTGCAAGGACCCCAAGCT
Germin-like protein 3'	CAACAGGATTTCACTGGCACGGGGTGAAT
Thaumatococcus-like protein 5'	ATGAGGGAAGAGTACGCAAACTGGACAA
Thaumatococcus-like protein 3'	ACAACAGCCCATTGAGGAAGCCCTCCAAT
PR-3 class IV chitinase 5'	AGCCGAGCCAGGCACAACACTAGAGCCCGCAT
PR-3 class IV chitinase 3'	ATCCGTCAATGTTGGACATGTCAATGAAAT
Proline-rich protein 4-like 5'	AGCAGATGCAGCACTTGATCCATCAGGGCT
Proline-rich protein 4-like 3'	TCCAGTGACAACCTTTGAGGAGGAAGCTGGC
Aquaporin tip-2 like 5'	ATGGTTAGCCATGATTCCAGATTCGGAGCA
Aquaporin tip-2 like 3'	TGTATTTGATGAGGGTTTCCAGAATTCCAG
Cytochrome c oxidase 5'	GAGGCATTTTTGGATCACTTTT
Cytochrome c oxidase 3'	GTTCTGTTAGGTTCTTAGTAGC

Table S3. Upregulated genes in CNSV-infected Citrus.

	Length (bp)	Log2 fold-change
Stress response and defense		
Germin-like protein subfamily 1 member 14	898	11.3
1-aminocyclopropane-1-carboxylate synthase	1,534	9.8
Thaumatin-like protein	681	7.7
Blight-associated protein p12	483	7.2
PR-3 class IV chitinase	864	6.9
Stress-induced protein	213	6.9
Chalcone synthase	1,462	6.7
Beta- glucanase	1,190	7.2
Wound-induced protein win1	716	6.1
Cysteine-rich receptor-like protein kinase	1,869	6.0
Proline dehydrogenase mitochondrial-like	1,812	5.9
Blight-associated protein p12 precursor	632	5.8
Anthocyanidin 3-o-glucosyltransferase 5-like	1,434	5.8
Beta-glucosidase 41-like	1,894	5.8
Xylosyltransferase 1-like	1,293	5.8
Non-specific lipid-transfer protein at2g13820-like	958	5.7
Reticuline oxidase-like	1,617	5.6
Pathogenesis-related protein 1	480	5.5
Bifunctional nuclease I	941	5.5
Flavanone 3-beta-hydroxylase	1,403	5.4
GH3 family protein	2,138	5.4
Respiratory burst oxidase homolog protein b-like	2,855	5.3
Ribonuclease 3-like	925	5.3
Stress-response protein	694	5.3
Laccase 110	1,999	5.2
Methyl esterase	870	5.1
Auxin-induced protein	524	4.9
Serine protease inhibitor	285	4.8
2-oxoglutarate-dependent dioxygenase	1452	4.6
Beta –glucanase	1,404	4.5

Wound-induced protein WIN2	761	4.2
Quinone reductase family protein	853	4.2
Proteinase inhibitor	674	4.2

	Length (bp)	Log2 fold-change
Stress response and defense (<i>continued</i>)		
Phenylalanine ammonia-lyase	2,559	4.1
Stress-induced nucleic acid binding protein	696	4.1
Peroxidase 55-like	1,126	4.0
MLO-like protein 12	1,665	4.0
Monogalactosyldiacylglycerol synthase chloroplastic-like	1,890	3.9
Cinnamoyl- reductase	1,344	3.8
Zinc finger protein zat1 1-like	834	3.8
Protein TIFY 5a-like	882	3.8
Proline-rich protein	702	3.8
Thaumatococcus-like protein	928	3.8
Stress-induced homologue At5g58960	2,040	3.8
Cysteine proteinase	1,452	3.7
15-hydroxyprostaglandin dehydrogenase	857	3.7
Probable ribose-5-phosphate isomerase-like	2,316	3.7
Avr9 cf-9 rapidly elicited protein	1,646	3.6
TMV resistance protein n-like	3,014	3.5
Miraculin-like protein 2	1,099	3.5
Pathogenesis-related protein 4	771	3.5
Probable WRKY transcription factor 28-like	1,472	3.4
Protein TIFY 10 ^a	1,081	3.4
Spx domain-containing protein 3-like	1,179	3.3
Cytochrome P450	1,493	3.2
Protein plant cadmium resistance 2-like	802	3.2
Primary metabolism		
Probable rhamnolacturonate lyase b-like	2,303	10.5
Inositol oxygenase	1,246	8.8
Nucleotide binding protein	2,173	6.9

	Length (bp)	Log2 fold-change
Udp-glycosyltransferase 74f2-like	1,401	6.5
Protein LURP-one-related 6-like	814	6.0
BAHD acyltransferase at5g47980-like	1,623	5.3
Inositol oxygenase 1	1,291	5.2
Sarcoplasmic reticulum His-rich calcium-binding	1,027	5.2
Polygalacturonase qrt3-like	1,545	5.0
	Length (bp)	Log2 fold-change
Primary metabolism (continued)		
Cysteine proteinase	1,326	4.9
Protein Ciclev10006313m	7,51	5.6
UDP-glycosyltransferase 74f2-like	1,401	4.7
Aminotransferase ALD1-like	1,386	4.7
NADPH-dependent codeinone reductase 2	1,307	4.6
Nucleotide-diphospho-sugar transferase family	1,080	4.6
Indole-3-acetic acid-amido synthetase	2,304	4.4
Tryptophan decarboxylase	1,592	4.3
Pectinesterase 2-like	1,722	4.3
Probable acyl-activating enzyme peroxisomal-like	1,689	4.2
Type I inositol- -trisphosphate 5-phosphatase 11	966	4.2
Bahd acyltransferase At5g47980-like	1,314	4.1
Potassium transporter 5-like	2,521	4.0
Alpha beta-hydrolases superfamily	1,628	3.6
Plant cell wall protein 88	681	3.6
4-coumarate: ligase	1,922	3.6
Xyloglucan endotransglucosylase hydrolase	762	3.5
Purple acid phosphatase 3 isoform 1	1,586	3.5
Beta- soluble isoenzyme i-like	2,310	3.4
Aminotransferase family protein	1,816	3.4
Kiwellin	753	3.3
Probable beta-d-xylosidase 2-like	2,604	3.3
Cdp-diacylglycerol--glycerol-3-phosphate 3-	573	3.3
Sulfate transporter -like	2,435	3.0

Cruz-Jaramillo *et al.*, 2014.

Alpha-amylase	1,481	3.0
Arogenate dehydratase prephenate dehydratase	1,756	2.9
Chlorophyll a/b binding protein	1,037	2.9
Hypothetical protein	764	2.8
PRUPE_ppa013271mg		

Plant development

Zinc finger protein constans-like 16-like	1,976	3.2
Homeodomain-like superfamily isoform 1	2,662	2.8

Signal transduction

Wall-associated receptor kinase-like protein	1,845	4.2
Probable LRR receptor-like protein kinase	2,351	4.2
Alpha beta-hydrolases superfamily protein	2,030	3.9
Probable LRR receptor-like Ser-Thr-protein kinase	3,195	3.2
Receptor like protein 1	2,210	4.5

Proteins of unknown function

Uncharacterized protein TCM_007254	605	5.4
Hypothetical 21 kDa protein	1,377	4.0
Ciclev10022285m		
Uncharacterized protein LOC100782360 precursor	810	3.3
Uncharacterized protein TCM_034658	844	3.3

Table S4. Downregulated genes in CNSV infected Citrus.

	Length (bp)	Log₂ Fold Change
Stress response and defense		
Heavy metal transport detox. superfamily protein	1,136	-3.4
Protein aluminum sensitive 3-like	1,208	-3.0
Anthocyanin 5-aromatic	1,638	-4.2
Gibberellin 2-oxidase	1,253	-4.4
S-linalool synthase	2,763	-4.6
Aquaporin TIP2-1-like	1,117	-5.1
Proline-rich protein 4-like	1,384	-6.6
Primary metabolism		
BADH acyltransferase dcr-like	1,810	-3.8
NADH-dependent 6-deoxychalcone synthase-like	1,842	-3.3
Non-functional NADPH-dependent codeinone reduct.	922	-3.6
Respiratory burst oxidase homolog protein b-like	2,855	-3.7
Alpha beta fold family protein	1,119	-3.7
Plant-specific domain tigr01589 family protein	1,530	-5.4
Proteins of unknown function		
21 kDa protein Ciclev10005968m	1,105	-6.4

Table S5. Quantitative RT-PCR of five genes in virus-infected Citrus.

Gene ID	Mass	Mass Fraction	Fold Change	Standard Deviation	<i>p</i> -value	Statistical Significance	
	Fraction	Asymptomatic					
Upregulated*	Germin-like protein	17.0810	3.9332	4.34	0.3113	0.0112	yes
	Thaumatococcus-like protein	0.5848	0.3143	1.86	0.2071	0.0260	yes
	PR-3 class IV chitinase	7.7401	2.6710	2.90	0.1853	0.0441	yes
Downregulated*	Proline-rich protein 4-like	0.1783	0.2848	0.63	0.0384	0.0078	yes
	Aquaporin tip-2 like	0.0335	0.0700	0.48	0.0131	0.0011	yes