

SGVB_genome 1 10 20 30 40 50 60
KM229842.1 TAATATTACGGCGTGGCCACCTTATCGCGAGCCCTTTAGGGCGAGCGGTTTAGATTGAT
.....

SGVB_genome 70 80 90 100 110 120
KM229842.1 TTGAAATTTAAAAAGTAAAGTTAGGCGGAAAGTGATTGTGCGATTACACATTTATATAA
.....AT.....GAAAGT.....ATTTGTATCA

SGVB_genome 130 140 150 160 170 180
KM229842.1 AGGGGACATCAGAGTATACCGTATATGGAGCGTCTATTATACCAGGTATTCCTCGTAAAT
...GGTATTT...TCCTCGGATACGA.....TTAT.....T

SGVB_genome 190 200 210 220 230 240
KM229842.1 TATACGCCATCTTACGAGTCTGAGAGTTATCTGCTCCGTGCGCAGGCTTCACGTAAACAAC
CATACG...ATCTCT...CAGTGAG...TGCTGCTCCA...CAGGCTCATCTCAACG

SGVB_genome 250 260 270 280 290 300
KM229842.1 CAGTTGGGAAAGTTGTATCGCTTTGGTTATTTGTTCTGTGCGTGTAGGTTGTCTTAT
GATTTGGTAAAGTTGTATCGCTTTGGTTATTTCTGTGTAGTGTGGTGTGTCTAT

SGVB_genome 310 320 330 340 350 360
KM229842.1 TAGGCTATCTTTATTTTAAAGATTGTATTTGTTATTTAAAGCCAAAGAGCAGAGG
CTGGCTATACCTTCTTTAAAGATTGTATCTCTGTTCAAGGCCAAGAAAGCAGAG

SGVB_genome 370 380 390 400 410
KM229842.1 ACACGACCGAAATAGGGTTTGGAAATACCCCTGCT...AGGCCCG...TTCTCAACCT
ACACATACCGAAATCGGGTTTGGCAACCCCGCTCGAATCAGGATCATCTCAACCT

SGVB_genome 420 430 440 450 460 470
KM229842.1 GCAAAAATGGTGGGACCTTATAAGGTACGTTCTACAAGGAGGAGAGAGGAAGGAACGC
GTA.GGCGGGGTGCATCATGTCGACTGTACGT...GGGAAAGAGAGCGGAAGCGTAGC

SGVB_genome 480 490 500 510 520 530
KM229842.1 TAGGGTTTATGATGCACTGGTGTGTTAACTCCCAAGGGATCTGAGTCAAAGCTCCATCAA
GGAAGGAGATCAAGGGCGAAGAGT.....AGGGATCTGTGTC...CTATGTGCTCA

SGVB_genome 540 550 560 570 580 590
KM229842.1 GGTCTATTTCGAATAGACGTGAATCTTGCAGGTTGCAACGTTCACTTGGACCAAGTTCTG
GGTCCTGTCTTCCAGAGGGAATCTTGCAGGTGCAACCTTTCTCTGGACCAAGTTCTG

SGVB_genome 600 610 620 630 640 650
KM229842.1 GTGCGGGGTGTAAGTTTCTGCTGGTGGGCTGCTTTCTGTGTAAGCAATTTCCACAGG
GTTCGGGTATAAAGTTTCTGCTGGTGGGCTGCTCTACCTGTGAGTAATTTCCACAGG

SGVB_genome 660 670 680 690 700 710
KM229842.1 GTGCCAATGATAACTGCGTCACACCAACAAGACAATCTGTGTACAAAGTTATGTCGAAGA
GTGCCAATGATAACTGCGTCACACCAACAAGACGTCGTATATTAATTATGCTAAGA

SGVB_genome 720 730 740 750 760 770
KM229842.1 ACAGTGTGTATGFGAATGCTCTCACTATCGGAAGGTTTTCGGTGCCCTGTACGTTTT
ATACGTGTGTATTTGGAATCTAGTCACTATTCGAAGGTTTTCAGGTGCCCTTTTACTTTTT

SGVB_genome 780 790 800 810 820 830
KM229842.1 GGTGTGTGTATGACAAATCACTGGGTCTAGTATTTCCTAGTACGGGATATTCTTGAAG
GGCTGTGTGTACGACAAAGCTCCTGGTGTCTATGTTCCAGTACGAGTGACATATTTGAAG

SGVB_genome 840 850 860 870 880 890
KM229842.1 GTCTCTCTGTGTGTTTCCTAATAACCCGAAAGTGTGGTCTAGTTCAGGGCAGCATGTCTATC
GCCATCTCTGTGTTTCCGAACAACTCTTGTGACGTGGATCTGTCTAGGGCTGCATGCTCATC

SGVB_genome 900 910 920 930 940 950
KM229842.1 GCTTTGTGTGTAAAGAAACGTTGGACCGTGATGCTTTGAGTGTAAAGGTGTTGACCAAGC
GTTTTGTGTGTAAAGAAACGTTGGACCGTGATAGTGGAGAGCAATGGGTATTGACCAAGGA

SGVB_genome 960 970 980 990 1000 1010
KM229842.1 AAGGCCCAGAGTGCAGAGTTATTATGGGCCTGGTCCGTGTAAACAGGTGAAGTTGTCTCC
AAGGCCCAGAGTGTCTACATATTATGGGCCTGGTCCGTGTAAACAGATTAACTCTGTAAT

SGVB_genome 1020 1030 1040 1050 1060 1070
KM229842.1 AAGTTCTTCAAGAGATTGGGTGTAGCACTGAGTGGAAAGATAGTTCTACGGGTGATGTA
AAGTTCTTTAAGAGATTGGGTGTGTCAACGGAGTGGAAAGATAGTTCTACGGGTGATGTT

SGVB_genome 1080 1090 1100 1110 1120 1130
KM229842.1 GGTGATATAAAAGAAAGGCGCAATGTACATTGTTGTTCCTCTCCAGAAAGTCTGATGTG
GGTGATATAAAAGAAAGGAGCCCTTTACATTGTTGTTCCTCTCCAGAAAGTCTGATGTAT

SGVB_genome 1140 1150 1160 1170 1180 1190
KM229842.1 TATGTAAATGGTTATTTCCGAGTGTACTTCAAGTCCGTTGGTAATCAATAAAATAAGTTT
TATGTAAATGGTTATTTCCGAGTGTACTTCAAGTCCGTTGGTAATCAATAAAATAATTTT

SGVB_genome 1200 1210 1220 1230 1240
KM229842.1 TATTATGTTTATTAATATATGCTTCAAGTATGAGAGAAAATTACAAAGTACAA
TATTATGAAATATGTAATATGCTTCAAGTATGAGAGAAAATTACAAATACAAATACACACG

SGVB_genome 1250 1260 1270 1280 1290 1300
KM229842.1 ACATAAACACACAAAAACACACAAAAAAAGAGAAACAAATCACACCCCAACATATTAC
AAATAAACATAAAAAACACACCTAAAAAAGAGCAAAACACACCCATAACATATAC

SGVB_genome 1310 1320 1330 1340 1350 1360
KM229842.1 AGTATAGTGAACCTCTAGTTAGAGAGAGGCACGTTTAGTGACTCGACGCAACCTGAGCA
ACTAGAATACCTCTGCTTGGAGAGAGGCACGTTTCTGACTCGACGATTCTCGAGCA

SGVB_genome 1370 1380 1390 1400 1410 1420
KM229842.1 AAAAAATGTTCTTCGATCAACATGTATGGATTACACAATTAGCTTCAAAGTATCTTTC
AAAAAAGTCTCCGTCATACATGTATGGGTGAGACAATTATCTTCAAAGTATCTCTTC

1430 1440 1450 1460 1470 1480
SGVB_genome TGTGAGATGTCATATTATGCATCCAGTCTTCGTCTCATTGCAAAATGATTATGAAGGG
KM229842.1 TGTGAGCTGACATTGAGAGCATCCAGTCTTCGTCTGGATTACAAAGATTATGAAGGG

1490 1500 1510 1520 1530 1540
SGVB_genome ATCCACCTTTTATTTCTTCTTTTTCATATTTAGGGTTGACAGTGTAGTCACTGG
KM229842.1 ATCCACCTTTTATTTCTTCTTTTTCATATTTAGGGTTGACAGTAAATCACTGG

1550 1560 1570 1580 1590 1600
SGVB_genome CAACCTATTAATTGCTTCCAAGTGGGACGAAATTGAAGGGGATGTCGTCAATGACGTTG
KM229842.1 CAACCTATTAATTGCTTCCAAGTGGGACGAACTGAAGGGGATGTCGTCAATGACGTTG

1610 1620 1630 1640 1650 1660
SGVB_genome TAGGTGCGATGTCGTCGTAGTGTGTAGTCGATGGTCCGTTCCAGTAAATTGTGTCTGT
KM229842.1 TAGGTGCGATGTCGTCGTAGTGTGTGTAGTCGATGGTCCGTTCCAGTAAATTGTGTCTGT

1670 1680 1690 1700 1710 1720
SGVB_genome CCGAGGCTTCTTGCCCATGTGTCTCTTGCCGGTCTGTGTTGGTCCGCAGATGTAGAGGGA
KM229842.1 CCGAGGCTTCTTGCCCATGTGTCTCTTGCCGGTCTGTGTTGGTCCGCAGATGTAGAGGCTG

1730 1740 1750 1760 1770 1780
SGVB_genome GGGTCTCTGGTTCAGTCCCTCTCGTCTGGTTAAATCGCCATCCATTCAAGGTCAG
KM229842.1 GGGTCTCTGGTTCAGTCCCTCTCGTCTGGTTAAATCGCCATCCATTCAAGGTCAG

1790 1800 1810 1820 1830 1840
SGVB_genome CTTGGGCTTCACTATATGGGACTGGATGTTATATGTGTAGCGTCAATACCTTACATGAT
KM229842.1 CTTGGGCTTCACTATATGAACTGGATGTTATATGTGTAGCGTCAATACCTTACATGAT

1850 1860 1870 1880 1890 1900
SGVB_genome ATAGATGTGTGTCCTCCAAGTGGCTAGCTCTTCGTGGCAGCGAAGATCTTGTGCTGCT
KM229842.1 ATAGATGTGTGTCCTCCAAGTGGCTAGCTCTTCGTGGCAGCGAAGATCTTGTGCTGCT

1910 1920 1930 1940 1950 1960
SGVB_genome GATGGAAAGGTACATATGTTTGGTTGTGGTGGAAAGAGCCGTGTTGCTGAGTATTCATG
KM229842.1 GATGGAAAGGTACATATGTTTGGTTGTGGTGGAAAGAAATTGTTGCTGAGTATTCATG

1970 1980 1990 2000 2010 2020
SGVB_genome CCACTGTATATTAGTGCCCATTCATGAGGAAATTGTTCTTTGATCATCTCGAGATATTC
KM229842.1 CCACTGTATATTAGTGCCCATTCATGAGGAAATTGTTCTTTGATCATCTCGAGATATTC

2030 2040 2050 2060 2070 2080
SGVB_genome CTCCTTAGATGTTGCAGTCTGGATAAATAGTTCTCCATCGTGCATCAGATTTTGAAGGAGA
KM229842.1 CTCCTTAGACGTTGCAGTCTGGATAAATAGTTCTCCATCGTGCATCAGATTTGCGAGGAGA

2090 2100 2110 2120 2130 2140
SGVB_genome GACTCGATGATCTTTGAAGTCTCCTCTGGTTTGAACATCTCCGTCCTTAGAATGTGATTC
KM229842.1 GACTCTATGATCTCTGAAATCTCCTCTGGTTTGAATATCTCCGTCCTTAGAATGTGATTC

2150 2160 2170 2180 2190 2200

SGVB_genome AAGGACTTGTGTTAGAGTTTCTAGCTGGT TGGATATTAGGGTGATTTCCCTTCAAATCGAA
 KM229842.1 AAGGACTTGTGTTAGAGTTTCTAGCTGGC TGGATATTAGGGTGATTTCCCTTCAAATCGAA

2210 2220 2230 2240 2250 2260

SGVB_genome AAAAGAAGATCCCTAATCAAGGTTTTTTATCAAGTTGATAAAGAGCGTGTA TGGGT
 KM229842.1 AAAAGAAGATCCCTAATCAAGGTTTTTTATCAAGTTGATAAAGAGCA TGA TAG TGGGT

2270 2280 2290 2300 2310 2320

SGVB_genome AGTGCCATCTTGATGAAATTCAGTAGCAATAGCAAGGTAAATAAATAAAGGTGTAG
 KM229842.1 AGTGCCATCTTGATGAAATTCAGTAGCAATAGCAAGGTAAATAAATAAAGGTGTAG

2330 2340 2350 2360 2370 2380

SGVB_genome CTTTCCCAGAGAACTCGAAGAGTTCATCTCTCTGSGAAGAACATTTGGGATGTGAG
 KM229842.1 TTTCCCAGAGAACTCGAAGAGTTCATCTCTCTGSGAAGAACATTTGGGATGTGAG

2390 2400 2410 2420 2430 2440

SGVB_genome GAAAACATATTTTATTGAGTCTGAAATGAGCGTTGGGTCTTCGAGGCATTTGAAGTA
 KM229842.1 GAAAACATATTTTATTGAGTCTGAAATGAGCGTTGGGTCTTCGAGGCATTTGAAGTA

2450 2460 2470 2480 2490

SGVB_genome A GTTGTGACTCCATACAGTGATCCCAAACCTCTATTTATAACAGGCGTGGAGGCATGG
 KM229842.1 GTTGTGACTCCGAGGGGTG.CCAAAACCTCTATCTATAACAGGCGTGGAGGCATGG

2500 2510 2520 2530 2540 2550

SGVB_genome AGGCAAGGGCATTCTGTGTAATTGGAAGATAGTGGAAATTGACGTGGCATTACTTTAGA
 KM229842.1 AGGCAAGGGCATTCTGTGTAATTGGAATATAGTGGAAATGACGTGGCATTACTTTAG

2560 2570 2580

SGVB_genome AA TTAAG.....TT.....TTAAAT.....CTTTCGC.A
 KM229842.1 CG TTAAGGGGGAAATCCACGCCGAAATTAATATTACCGCGTGGTCCCCCTTTCGC.A

2590 2600 2610

SGVB_genome GAA....AGTGC.....CGGCGAT...AAGGTGGG....TCACGCCCATTT.....
 KM229842.1 GCACTTTAGTGCAGCGGTCCAGATTTAAAGTGGTAAATTTCCCGGCCCATAGGGTTTGT

SGVB_genome
 KM229842.1 CTTGCTTTTGCTTTATAAAAGGCGCACTAATGTATAGACCGTAGA

Figure S1. Pairwise sequence alignment of full-length SGVB and CpCDV isolate CpCDV_H_SD_SD180_2013.