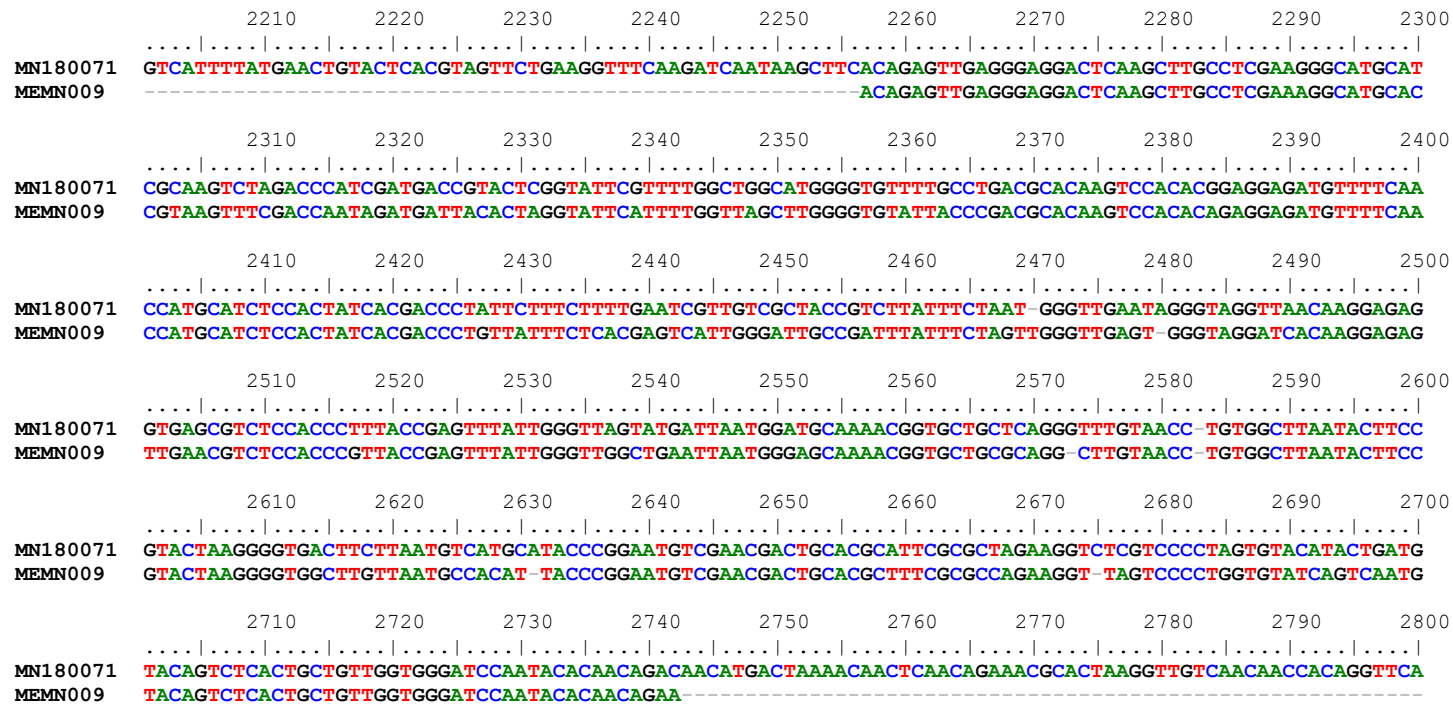
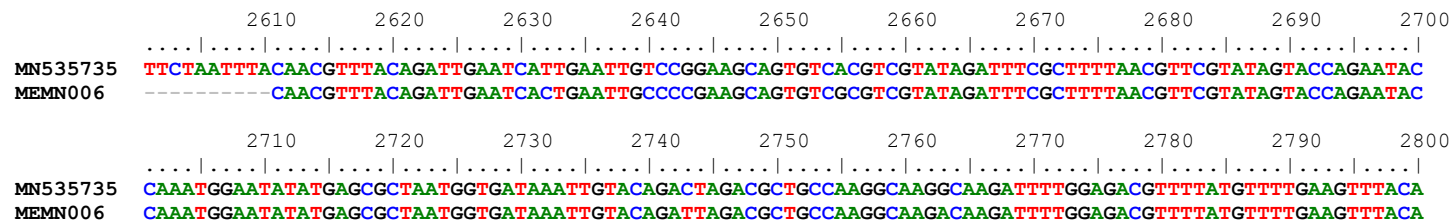


Supplementary Figure S10: Alignment of the Actinidia yellowing virus 2 (A), *Rhopalosiphum padi virus* (B), Bole tick virus 4 (C), Bat herpesvirus (D) and Cyclovirus (E) sequences identified in bat samples. Positions are numbered according to the reference sequence in each alignment

A: MN180071. Actinidia yellowing virus 2 isolate AYV2-Zhouzhi



B: MN535735. Rhopalosiphum padi virus isolate RhPV/OV-157/M.dau/DK/2018



	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900
									
MN535735	GATTTGATTATTTTACGCTTCTAGCCGTCGCAACGTTTTGACTGATTTAACTTACACGGAAGTTGTGAAGTTGTGTCAGGATAAGATGCGCGATCGCGC									
MEMN006	GGTTTGATTATTTGATGCCCTCTAGCCGTCGCAATATTTTACTGATTTAACTTACACGGAAGTTGTGAAGTTGTGTCAG-----									

C: MW561976. Bole tick virus 4 strain Ifin/H.dromedarii/2018

	5010	5020	5030	5040	5050	5060	5070	5080	5090	5100
									
MW561976	CCGCCGCATCGCTATGGCTGGCATCTATGGGGAAGATGAACCTTCAGCCTGGCGGAGATGAAGACACTCTCGCGGTCCGAGGGGCCCTGGCCGCCCTTCACC									
SYMA004	-----CCGCCGAGATGAAGACACTCTCGCGGTCCGAGGGGCCCTGGCCGCCCTTCACC									
	5110	5120	5130	5140	5150	5160	5170	5180	5190	5200
									
MW561976	ACCAGGAAGAGCGCGCCTTACTTTGGGGGCTAGTGTTCGACATCGGATTCCACGCTCCATCGCCGCAAAGATCGGCTTCGACGGTTTCTTTAAGGACGCCG									
SYMA004	ACCAGGAAGAGTGCGCCCTTACTTTGGGGGCTAGTGTTCGACATCGGATTCCACGCTCCATCGCCGCAAAGATCGGCTTCGACGGTTTCTTTAAGGACGCCG									
	5210	5220	5230	5240	5250	5260	5270	5280	5290	5300
									
MW561976	ACATCAACTTTGCGGCCCCAGCTATCTTCCAGATGCAGACCAACACGGGTTGCACGAACACGGGTTTCTGCTTCCAACACCGCGGAGCCGTGTTCAAAA									
SYMA004	ACATCAACTTTGCGGCCCCAGCTATCTTCCAGATGCAGACCAACACGGGTTGCACGAACACGGGTTTCTGCTTCCAACACCGCGGAGCCGTGTTCAAAA									
	5310	5320	5330	5340	5350	5360	5370	5380	5390	5400
									
MW561976	TTACCACGTCACAGAGGGCAGACCCCTCATCCTCCCGACC GTGTTCCAACGAGGGCAAGGTGGATTACTCGCTGATCCGCTGCGTCTTCAAGAATGAGAAA									
SYMA004	TTACCACGTCACAGAGGGCAGACCCCTCATCCTCCCGACC-----									

D: JQ805139. Bat betaherpesvirus B7D8

	10	20	30	40	50	60	70	80	90	100
									
JQ805139	GACACGATAGCGAGTTTATACATCACCGGCGGCGGCGGAACGGTTCATGACGCGTCGGCCGAAACGTGCATCAGAACCGTCCTGGGATGCTATTGGCAGAG									
SYMA008	GACACGATAGCGAATTTTATATAACCGGCGGCGGCGGGAACGCTCACGACGCGTCGGCCGAAACGTGTGTCGGGACCGCTTTCGAGTGTTACTGGCGGAG									
	110	120	130	140	150	160	170	180	190	200
									
JQ805139	GTTGTTCGGGGCGTCTGCGGGAAGCCCTGCGTGTCTCAGTTGGACAGCGGTATGAGCGTGTGCTGGTGTCGGATTGTCGGGTGATCAGTTCGTTTCAGA									
SYMA008	GTTGTTCGGGGGGCTGGACGGAAGCCCGACGTGCTCTCTGCTCGACAGCCACAGGAGCGTGTGCTGGTGTCGGACTGTGCGGACGATCAGCTCGTTCAGA									
	210	220	230	240	250	260	270	280	290	300
									
JQ805139	TCCGTGTTTGCACGCGACGGAGACGCTCACTGGACGTGCGTTATGGGCGATGCGATCTCGGACACGCTCTCTAGATGTACGCGCGACCCAGATTGGTTCG									
SYMA008	TCGGCGTTTGCACGCGCACAGGGAACGCACTGGACGTGCGTTCATGGGTGATGCGGATGTGCGGACATCCTTTCTAGATGTACACCGACCCGGAATGGTTCG									
	310	320	330	340	350	360	370	380		
									
JQ805139	GAGCGGAAAAATATAAAAAGCGTGTACGATCGTTGTTTTTTAAGTTTATAAGCATGAGACATAGACCGGAATTTTGGTTGG									
SYMA008	GGTCCGAAAAATATAAAAACGTGTACGATCCCTATTTTTTTAAGTTTATAGCTATGAGACACCGGCGGGAGTTCTGGTTGG									

E: AB937982. Cyclovirus ZM36a, AB937980. Cyclovirus ZM32

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      810      820      830      840      850      860      870      880      890      900
AB937982  ....|....|....|....|....|....|....|....|....|....|....|....|....|
AB937980  CCAGAAATAAAATAAAATGT-----TTCAATTCAAAATGTATTTCTTTATTCAATCTCCTCCTTAAACTACTACAATCATACGCTAAAAATCTATACACCT
SYM011    -----TTTCCTTTATTCAACCTTCTCCTCAAACACTACTACAATCATAGCTAAGAACTCTGTACACTT

      910      920      930      940      950      960      970      980      990     1000
AB937982  CCTCTAGAGGTCTTTCGCTTGTGATCCATATATATTTAGATACGAAGTTTTCATATCCTCCTTTGACAGGGACTCTGTAAGGATATCTGTTCGAGATCTT
AB937980  CCTCTAGAGGTCTTTCGCTTGTGATCCATATATATTTAGATACGAAGTTTTCATATCCTCCTTTGACAGGGACTCGATAAGGATATCTGTTCGAGATCTT
SYM011    CCTCTAGAGGTCTGTTCACTTGTGATCCATATATATTTAGATACGAAGTTTTCATATCCTCCTTTGACAGGGACTCTGTAAGGATATCTGTTCGAGATCTT

      1010     1020     1030     1040     1050     1060     1070     1080     1090     1100
AB937982  GAGAAGCTCGTCGTATTTGATCCATCCGTAGAAGTCATCGATAACAACGCAGGGTTGTCCGGTGTATCCATCCCACCATTTCCCGCGCGGCTTGTAGTAG
AB937980  GAGAAGCTCATCGTATTTAATCCATCCGTAGAAGTCATCGATAACAACGCACGGTTGTCCGGTGTATCCATCCCACCATTTCCCGCGCGGCTTGTAGTAG
SYM011    GAGAAGCTCATCGTACTTGTATCCATCCGTAGAAGTCATCGATAACAACGCAGGGTTGTCCGGTGTATCCATCCCACCATTTCCCGTGGTTTGTAGTAG

      1110     1120     1130     1140     1150     1160     1170     1180     1190     1200
AB937982  GTTTCACCGAGAGCGCGGCTTTCCCTCGCGCGCTTTCACGGGACTTTCCAGTTCAGTTGATCCCCAAAAGTAAAAGACTTCGTTTTAAAGTCTCGTTCTT
AB937980  GTGTCACCAAGAGCGCGGCTTTCTTCGCGCGCTTTCACGGGACTTTCCCTGTTCCAGTCGCTCCCCAAAAGTAAAAGACTTCGTTTTAAAGTCTCGTTCTG
SYM011    GTTTCACCGAGAGCAGGACTTTCTTCGCGCGCTTTCACGGGACTTTCCAGTTCAGTCCGTCCTCCAAAAGTAAAAGACTTCGTTTTAAAGTCTCGTTCTT

      1210     1220     1230     1240     1250     1260     1270     1280     1290     1300
AB937982  GATTTCCATGAGCGACTCTAATGTATTGTTCAATTCTTTGAAATACTTGATGTACGCGACTGGGAACCTGAATGGCCAAAGCTTTAATGTCTCTTCTCC
AB937980  GATTTCCATGAGCGATTCTAATGTATTGTTCAATTCCCTTGAAATACTTGATATACGCTGTGGGAACCTGAAGGGCCAGGTTTTTAATGTCTTCTCTCC
SYM011    GATTTCCATGAGCGATTCTAATGTATTGTTCAATTCTTTGTAATACTTGATATACGCGACTGGGAACCTGAAGGGCCAAAGTTTTAAGGTCTCTCTCTCC

      1310     1320     1330     1340     1350     1360     1370     1380     1390     1400
AB937982  TCCTTCAATGACAGATACAACCTTTTGGAGGTCTGTTTCGAGTTCCTTGAGTACTGGGTGATCCGCATTGCCAGACATCGCCACTCTTAGAGCAATATTCC
AB937980  TCCTTCAATGACAGAAACAACCTTTTGGAGGTCTGTTCTAGTTCCTTGAGTACTGGGTGATCCACATTGCCATACATCGCCACCTTTAGAGCAGTATTCC
SYM011    TCCTTCAATGACAGAAACAACCTTTTGGAGGTCTGTTCTAGTTCCTTGAGCACTGGGCTCTCCGCATTCCCAGACATCGCCACTCTTAGAGCAATATTCC

      1410     1420     1430     1440     1450     1460     1470     1480     1490     1500
AB937982  TGATTTTCAATATCACTCCCTTTAGCTCGCTCAATGTGCGCACGGCCTCCAAATATTTGCCGTATGCTGTTGAATCGTTTGGGTTCGCTGCAGATTGCTGA
AB937980  TGATTTTCGAGATCACTTCCCTTTAGCTCTTTCAATGTGCGCTCGTCCGCCAAATATTTGCGTATGCTGTTAAATCTTTTGGGTTCGCTGCAAAATGCTGT
SYM011    TTATTTTCGAGATCAGTTCCTTTAGCTCTTTCAATGTGCGCTCTACCTCCAAATATTTTCCGAATGCTGTTGAATCGTTTGGGTTCGCTGCAGATTGCTGT

      1510     1520     1530     1540     1550     1560     1570     1580     1590     1600
AB937982  AAATAAAATCAATAAGTCGT-ACACTATGCACGGAGCCCCGCCGCGAGAGGGGTGGACGGGGCCCCGGCGGGCGTAGCCGCGCCAGGGGGTGGTCCACC
AB937980  AATAGAACAACCATATGTTACGACACTATGTCGGAGCCCCGCCGCGAGAGAGGGGGGGGGGGCCCCCGCGCGCCGAGGCGCGCGTAGGGGTGCCCC-CC
SYM011    AATACAACACGATAAATTAATATCTAATTCTCGGAGCCCCGCCGCGAGAGAGGGGGGGGGGGCCCCCGCGGGCGTAGCCGCGCGTAGGGGTGCCCC-CC
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      1610      1620      1630      1640      1650      1660      1670      1680      1690      1700
AB937982  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AB937980  CCGGAGCGGGATCGGGCGGCTCTATCCAACGTGACTTTCCACTTGCA-CTAGGAGGTTATATAAAAAA--ATTACCAAAATCCCTGGAGATGTTTGT
SYMN011   TCGGCGCGGGATCGGGCGGTTCTATCCAACGTGAGACTATCCAACTGAAACAAGGAGGTTATATT-----TACCAAAATCCCTGGAGATGTTTGT

      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
AB937982  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AB937980  TCCAGTTGTAGGACAAATCTCTCGACCAAAATATAGCAAAATTACATAGCTCAGCGAGGTCCTTCTGAAGCACATCGACATCGTCCCTCCGTATAATTATTC
SYMN011   TCCAGTACTAGGACATGTCTCTCGACCAAAATATAGCAAAATTACAAAGCTCAGCGAGGTCCTTCTGAAGCACATCGACATCCTCGTCGGTATAGTTATTC

      1810      1820      1830      1840      1850      1860      1870      1880      1890
AB937982  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
AB937980  AGCGTCCAGCAGAAATCTACGCACGTGCTGTGTGTTAGCCATAATGATGAGACCGAGCGTTACAGCGCCT-ATATATAACAACGAAGTGGCGGTA
SYMN011   AGCGTCCAGCAGAAATCTTCGAGCGTGTGTTTTTAGCCATAATGGTGAGACCGAGCGTTACAACGTTGCTTATAAACTCCCAGAGTGGCGGTA
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